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Genomic Perturbations Reveal Distinct Regulatory Networks in Intrahepatic Cholangiocarcinoma

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Abstract

Intrahepatic cholangiocarcinoma (iCCA) remains a highly heterogeneous malignancy that has eluded effective patient stratification to date. The extent to which such heterogeneity can be influenced by individual driver mutations remains to be evaluated. Here, we analyzed genomic (whole-exome sequencing, targeted exome sequencing) and epigenomic data from 496 patients, and used the three most recurrently mutated genes to stratify patients (*IDH*, *KRAS*, *TP53*, 'undetermined'). Using this molecular dissection approach, each subgroup was determined to possess unique mutational signature preferences, co-mutation profiles and enriched pathways. High-throughput drug repositioning in seven patient-matched cell lines, chosen to reflect the genetic alterations specific for each patient group, confirmed *in silico* predictions of subgroup-specific vulnerabilities linked to enriched pathways. Intriguingly, patients lacking all 3 mutations ('undetermined') harbored the most extensive structural alterations while IDH mutant tumors displayed the most extensive DNA methylome dysregulation, consistent with previous findings. ***Conclusion***: Stratification of iCCA patients based on occurrence of mutations in three classifier genes (*IDH*, *KRAS*, *TP53*) revealed unique oncogenic programs (mutational, structural, epi-mutational) that influence pharmacologic response in drug repositioning protocols. This genome dissection approach highlights the potential of individual mutations to induce extensive molecular heterogeneity and could facilitate advancement of therapeutic response in this dismal disease.

INTRODUCTION

Intrahepatic cholangiocarcinoma (iCCA) incidence and mortality rates have increased globally over the last three decades, highlighting a growing clinical problem from what was once considered a rare orphan disease (1, 2). The majority of iCCAs are sclerosing adenocarcinomas arising from cholangiocytes lining intra-lobular biliary ductules, as well as peribiliary glands of large intrahepatic bile ducts (1, 3). While the causal biology of this cancer is largely unclear, known risk factors include chronic hepatitis B or C viral infection with cirrhosis (4); chronic liver conditions, such as cholestasis, primary sclerosing cholangitis (5) or liver fluke infestation (6); metabolic disorders, such as diabetes mellitus (DM); and lifestyle or environmental factors, including alcohol consumption and smoking (7). Liver resection remains the only curative treatment, a surgical procedure frequently precluded by early invasion of surrounding tissues. Even among 10-30% patients eligible for resection, 50% recur within the first 12 months. Standard chemotherapy regimens (gemcitabine alongside platin-based compounds) for non-resectable and recurrent iCCA patients are purely palliative, achieving only a limited improvement in survival (8). As most iCCAs are locally advanced or metastatic at presentation, patients have a dismal prognosis with a 5-year survival rate that has persisted below 10% since the 1980s (9). While no targeted therapy has been approved to date, *FGFR2* inhibitors (e.g. BGJ398) may be the first to transform iCCA clinical management, displaying prospective efficacy (though of variable duration) in fusion-positive patients (10). Similarly, future therapeutic advances will likely stem from further molecular stratification of iCCA patients, exposing oncogenic networks against which therapeutics may be strategized.

Recently, several cross-platform integrative analyses have identified broad cholangiocarcinoma subgroups associated with specific clinical and molecular features (11-13). However, inter-study comparison of these subgroups remains difficult given they are enriched by complex molecular characteristics identified in heterogeneous patient cohorts. Identification of single or few genomic alterations which influence downstream oncogenic networks could facilitate refinement of these previously established subgroups, as well as

enhance prediction of therapeutic response to pharmacologic intervention against specific molecular backgrounds. As such, mutations in *IDH1* and *IDH2* have already been associated with unique genomic features (DNA hypermethylation, altered chromatin remodeler expression, increased copy number and expression of mitochondrial genes), as well as sensitivity to dasatinib (14) and PARP inhibitors (15). The potential for individual driver mutations to influence diverse tumor networks is intriguing and remains to be evaluated for other recurrently mutated genes in iCCA, such as *KRAS*, *TP53* and chromatin remodeling enzymes (e.g., *ARID1A* and *BAP1*).

Accordingly, we aimed to deconstruct the molecular programs of iCCA tumors associated with specific individual mutations. To this end, we grouped 496 patients into four subgroups where three were classified based on the most recurrent somatic mutations (*IDH*, *KRAS* and *TP53*) and the remaining based on wild-type status for these genes (referred to as 'undetermined group'). This stratification approach unveiled distinct mutational signatures and co-mutations, pathway-enrichment and pharmacologic response profiles between subgroups, as well as suggesting an enhanced role of structural and epigenomic alterations in undetermined group tumors. These findings uncover the potential of individual mutations to induce substantial downstream molecular heterogeneity which could facilitate prediction of therapeutic sensitivities for iCCA patients using standard targeted genotyping.

MATERIALS AND METHODS

Patients and samples

Data sets from a series of 496 iCCA patients were obtained for analysis (Supporting Fig S1A). Totally, 165 fresh-frozen iCCAs were collected from surgically resected patients. All samples were immediately frozen in liquid nitrogen and stored at -80°C pending genomic DNA isolation. The Danish Regional Ethics Committee and local authorities at contributing institutions approved the study. Written informed patient consent was obtained in accordance to regional regulation. All patient demographic and clinico-pathological data were anonymized and are summarized in Supporting Tables S1-S2. 150 of these tumors were subjected to targeted exome sequencing (TES) (Table S1), performed using the 48-gene TruSeq Amplicon Cancer Panel (TSACP, Illumina). The remaining 15 cases underwent whole-exome sequencing (WES) (Table S2) and were analyzed alongside 262 publically available WES iCCA samples (Table S3).

SNV calling and analysis

FASTQ files were filtered, subjected to quality control and mapped to the human genome assembly (hg19) using BWA. SNVs and short indels were called using a combination of Varscan (v2.3), somaticSnipper (v1.0.4) and Shimmer. Annovar was used to classify SNVs as synonymous or non-synonymous. Potential impacts of amino acid alterations on protein structure and function were assessed by PolyPhen-2. Motif enrichment analysis was performed by HOMER. Inference of mutational signatures was carried out with SomaticSignatures tool. Pathway enrichment of significantly mutated genes encoding SNVs and indels were assessed using genome MuSiC. Further information regarding bioinformatics analysis can be found as Supporting Information.

FGFR2 fusion detection

Totally, 122 of 150 tumors subjected to TES were assessed for known *FGFR2* fusions. RNA isolation was performed and subjected to reverse transcription with SuperScript VILO cDNA Synthesis kit (ThermoFisher Scientific). Fusion

products in *FGFR2* were targeted with primer pairs flanking breakpoints of *FGFR2* and previously reported donor genes. Commercially synthesized DNA with *FGFR2* and all known fusion partner sequence fragments (Integrated DNA Technologies) were cloned into plasmid scaffolds and used as positive controls. Fusions were confirmed by Sanger sequencing. Further information regarding fusion detection can be found as Supporting Information.

Cell culture

Cholangiocarcinoma cell lines were purchased from KCLB (SNU-478, SNU-1079, SNU-1196), DSMZ (EGI-1), RIKEN (HuCCT-1, RBE), and obtained from Mayo Clinic (WITT, KMCH). Cells were cultured in RPMI-1640 or DMEM-F12 (ThermoFisher Scientific), all supplemented with 10% heat-inactivated FBS (GE Healthcare), 1% penicillin-streptomycin and 1% L-glutamine (ThermoFisher Scientific). Cells were maintained at 37°C and 5% CO_2.

High-throughput drug repositioning

Drug screening was carried out using a drug library of 525 compounds (FDA-approved or in late stage clinical trials). Cells were seeded into 384-well plates and treated for 72 hours over 5-fold dilution series. Anti-proliferative cellular effects were measured with CellTiter-Glo Luminescent Cell Viability assay (Promega), as per manufacturers' instructions, and quantified using Drug Sensitivity Score (DSS) metric (16). Further information regarding drug screening can be found as Supporting Information.

CNA calling and analysis

Copy Number Alterations (CNAs) were analyzed using VarScan2, DNAcopy and GISTIC2 packages. *FGFR2* fusions were predicted using BreakDancer. Further information regarding CNA analysis can be found as Supporting Information.

Genome-wide DNA methylation profiling

In house and publically available Infinium Human Methylation 450k BeadChip (Illumina) data were used to identify an independent patient cohort (n=69) to

investigate effects of classifier genes on DNA methylation profiles. Data were processed and analyzed using RnBeads (v1.2.1). Further information regarding methylomics can be found as Supporting Information.

RESULTS

Rational identification of classifier mutations for iCCA patient stratification

To investigate mutational diversity in iCCA, we analyzed 427 patients by targeted exome sequencing ('TES-cohort'; n=150 patients) and whole-exome sequencing ('WES-cohort'; n=277 patients; incorporating 142 tumor/normal matched pairs and 135 tumors) (17-21)) (Supporting Fig. S1A-B). Analysis of TES-cohort of 48 cancer-related genes (Table S1) revealed *IDH1* (n=21/150; 14%), *TP53* (n=19/150; 13%) and *KRAS* (n=18/150; 12%) as the most recurrent mutations (Fig. 1A; Supporting Fig. S2A). Subsequent analysis of WES-cohort (Table S2-3) corroborated our TES-cohort findings where *TP53* (n=57/277; 20%), *KRAS* (n=44/277; 16%) and *IDH1/IDH2* (n=31/277; 11%) were most prevalent (Fig. 1B; Supporting Fig. S2B). Mutations in *IDH1* (R132C/G/L) and *KRAS* (G12A/C/D) were recurrent hotspots, while *TP53* mutations were distributed throughout its entire gene body (Fig. 1C) with prevalent R249S (n=10/45; 22.2%) mutations. Importantly, co-occurrence of *IDH1/KRAS* mutations (TES-cohort: n=1/150; 0.7%; WES-cohort: n=1/277; 0.4%) and *IDH1*/*TP53* (TES-cohort: n=3/150, 2%; WES-cohort: n=1/277, 0.4%) was rare, suggesting mutual exclusivity (Fig. 1A-B). In comparison, dual mutations in *KRAS* and *TP53* are detected in a subset of patients (TES-cohort: n=4/150; 2.7%; WES-cohort: n=14/277; 5.1%) but are not mutually inclusive (*P*=0.07, Fisher's exact test). Accordingly, we selected to stratify iCCA patients into four groups based on mutational status of these genes, referring to them as IDH-gr (including *IDH1* and *IDH2* mutations), KRAS-gr, TP53-gr and Udt-gr ('undetermined', wild type for all 3 driver genes).

FGFR2 fusion events have been identified in between 5.5% (21) to 28% (10) of patients, implicating this event as one of the most recurrent genomic alterations in iCCA. We next analyzed the prevalence of fusions in the TES-cohort by performing targeted analysis against known fusion partners,

followed by confirmation with Sanger sequencing. We observed that 14.8% (n=18/122) of tumors were *FGFR2-BICC1* fusion positive, where 83.3% (n=15/18) cases fused with *BICC1* in exon 3 and the remaining 16.7% (n=3/18) fused in exon 5 (Supporting Fig. S2A; Supporting Fig. S2C). Clinically, *FGFR2* fusion-positive status was associated with shorter overall survival (P<0.0001; Supporting Fig. S2D). The majority of fusion events (n=12/18; 66.7%) fell within Udt-gr. Similarly, in previously reported *FGFR2* fusions from RNAseq data (n=117/277; 42.2%; Japanese patients), *FGFR2* fusions are predominant in Udt-gr (n=3/4; 75%) (Supporting Fig. S2B).

Focusing on tumor/normal matched cases (n=142/277; 51.3%), we annotated 7,921 nonsynonymous SNVs in 5,457 genes (Table S4) and 2,581 synonymous SNVs in 2,229 genes (Table S5) with an average of 2.3 mutations/Mb (Fig. 1D). Apart from the prevalent mutant classifiers (*IDH, KRAS* and *TP53,)* other significantly mutated genes include chromatin modifiers (*ARID1A, BAP1, KDM6B, SETD2*) and genes newly associated with iCCA (Fig. 1E). We next analyzed known clinical risk factors associated with mutational subgroups and observed hepatitis B virus (HBV) infection was significantly associated with TP53-gr (n=26/45; 58%; P = 1.612x10^{-5}, Fisher's exact test) (Fig. 1E). Interestingly, HBV was also associated with a large number of Udt-gr tumors (n=21/63; 33%) but did not reach significance when compared to the entire cohort (Fig. 1E). However, no significant association was determined between mutational subgroups and diabetes mellitus (DM), smoking or alcohol consumption.

Mutation-centric tumor stratification identifies diverse oncogenic processes

The mutational signatures defined by immediate 5'- and 3'- sequences flanking SNVs may reflect specific underlying mutagenic processes (22); thus, we investigated mutagenic signatures associated with the four subgroups. Though C>T transitions and C>A transversions are prevalent overall in iCCA (Supporting Fig. S3A), as previously described (20, 21), mutational signatures are unique between subgroups (Fig. 2A). IDH-gr displayed a specific enrichment of C>A transversions (67%, P=7.01x10^{-132}) (signature 18, 28) (Fig.

2A-B). As such, C>A transversions have been associated with oxidative stress (23), complementing previous studies characterizing the physiological role of wild type *IDH1* in protecting hepatocytes from oxidative stress (24). KRAS-gr was characterized by predominant C>T transitions (Fig. 2A) (55%, P=3.40x10^{-87}, Fisher's exact test), displaying a preference for purine (G or C) upstream of transitions (Fig. 2B), and suggesting a role for APOBEC (signature 2 and 13) (22). Also, promoters of genes mutated in KRAS-gr were enriched for *FOSL2* motif binding sites (Supporting Fig. S4), in agreement with transcriptional signature derived from *KRAS*-driven tumors (25). TP53-gr displayed preferential unique T>A transversions (26%, P = 2.29x10^{-125}) with NpT>ApG associated with aristolochic acid (signature 22). Although, a significant enrichment of R249S mutations were detected in TP53-gr (Fig. 1C), aflatoxin signature was not enriched as in hepatocellular carcinoma (HCC). Also, R249S did not display a significant relationship with HBV status (P=0.48, Fisher's exact test) or overall survival (P=0.917) when comparing with patients manifesting other *TP53*-specific mutations.

Akin to IDH-gr, Udt-gr displayed a preference for C>A transversions (42%, P=4.69x10^{-10}). In fact, non-matrix factorization (NMF) clustering of signature contributions across mutation subgroups in patients and CCA cell lines (n=16) implicated a close association between IDH-gr and Udt-gr (Supporting Fig. S3B-C). Such similarity was also observed at the transcriptome level in our previously published cohort (26) through hierarchical clustering of significant differentially expressed genes (F-test P<0.001; Supporting Fig. S3D). Taken together, these findings suggest that without patient stratification, Udt-gr would have masked the unique genetic patterns elicited by IDH-gr, KRAS-gr and TP53-gr. Furthermore, these data indicate that diversity of oncogenic programs (unique and shared between subgroups) may arise early in tumorigenesis from their initial genetic mutational signatures and possibly transcend different genomic readouts in their consequences.

Inter-group mutational analysis uncovers unique co-mutational profiles

Next, we analyzed the extent of exclusivity of mutated genes among subgroups and observed that the majority of genes encoding nonsynonymous

SNVs were unique (Fig. 3A) and co-occurred (≥2 tumors) within their individual subgroups (Fig. 3B-C; Table S6A-D). Genes encoding somatic synonymous SNVs were also unique to each subgroup (Supporting Fig. S5A; Table S6E), but show minimal overlap (2-4%) (Supporting Fig. S5B) with nonsynonymous SNV genes, suggesting these mutational processes are dissimilar. Furthermore, somatic synonymous SNVs have low recurrence rate and lack significantly mutated genes with iCCA subgroups (Supporting Fig. S5C), which is markedly different from nonsynonymous mutated genes (Fig. 3C).

As expected, *IDH1*, *KRAS* and *TP53* were the most significantly altered genes in their respective groups along with specific enrichment of *BCLAF1* (*P*=0.007) in IDH-gr; *SMAD4* (*P*=0.03) in KRAS-gr; *PTEN* (*P*=9.36x10^{-7}), RB1 (*P*=0.002) and *LATS2* (*P*=0.02) in the TP53-gr; and *KDM6B* in the Udt-gr (*P*=0.08) (Fig. 3C; Table S7). Among the previously reported chromatin modifier genes, *ARID1A* mutations were present in IDH-gr, KRAS-gr and Udt-gr but only significantly enriched with Udt-gr tumors (*P*=8.86x10^{-8}), while *BAP1* was preferentially associated with IDH-gr (*P*=2.57x10^{-8}). Notably, no chromatin modifiers were associated with TP53-gr. Association of significantly mutated genes along with the three classifier genes are represented in Fig. 3D.

We next evaluated any prognostic significance across four mutational subgroups. In the WES-cohort of 142 tumor/normal patient samples, KRAS-gr and TP53-gr were significantly associated with poor overall survival (*P*=0.003; Fig. 3E) and faster time to recurrence (*P*=0.018; Fig. 3F). These findings were confirmed in two independent cohorts whereby KRAS-gr was associated with worse overall survival in TES-cohort (N=150) (*P*=0.0004; Fig. 3G) and both KRAS-gr and TP53-gr were correlated with worse overall survival (*P*=0.0001; Fig. 3H) in Nakamura et al. cohort (N=135) (21). Thus, we conclude that these four mutational subgroups have a distinct association of co-mutated genes and different overall survival.

Intrahepatic CCA subgroups harbor unique dysregulated pathways that are reflected in their drug-response profiles

To understand whether genes associated with each subgroup could contribute to different oncogenic programs through tailored pathway dysregulation, we analyzed perturbed pathways associated with each group (Fig. 4A-B; Table S8). IDH-gr was enriched for metabolic pathways, including glutathione metabolism (P=6.33x10^{-21}) and citrate cycle (P=2.37x10^{-14}), which is consistent with known involvement of *IDH1* in metabolic processes in CCA (27). KRAS-gr was highly enriched for various immune-related pathways, including ErbB (P=4.39x10^{-17}), VEGF (P=2.49x10^{-16}) and actin cytoskeleton rearrangement (P=4.7x10^{-10}). In contrast, MAPK (P=1.44x10^{-33}), WNT (P=2.19x10^{-26}) and p53 signaling (P=3.44x10^{-32}) were enriched in TP53-gr. Since mutations in *KRAS* and *TP53* occur in a small subset of patients, pathway enrichment in dual mutants was independently assessed. Notably, significantly enriched pathways were all present in either KRAS-gr or TP53-gr (Table S8), supporting our previous inclusion of these patients in both KRAS-gr and TP53-gr analyses. Finally, in spite of being the largest group, Udt-gr was exclusively enriched for mTOR signaling (P=4.76x10^{-3}), suggesting that Udt-gr is highly heterogeneous with regards to SNVs. To indirectly test the validity of our classifier genes, we selected the next three most recurrent mutated genes as alternative classifiers: ARID1A-gr (n=14; 9.9%), CDC27-gr (n=12; 8.5%), BAP1-gr (n=9; 6.3%), and Remaining-gr (n=110; 77.5%; analogous to Udt-gr) (Supporting Fig. 6). No pathways were uniquely enriched among these surrogate groups, with significant biological processes emerging only in the 'remaining' tumors, thus justifying our patient classification.

Next, we sought to determine whether mutational subgroups displayed differential sensitivity to diverse classes of compounds *in vitro* and whether these drug responses reflected *in silico* predictions of enhanced pathway dysregulation. To determine the `best fit´ cell models, mimicking the patient groups, we earlier performed NMF clustering of the mutational signatures (genetic substitution patterns) in patients and a panel of 16 CCA cell lines (Supporting Fig. S3B-C). This confirmed genetic signatures under our mutational classifiers were comparable between cell lines and patients.

Accordingly, we selected 7 cell lines with matched mutational profiles representative of each of the patient subgroups, as well as one mixed mutant cell line (RBE; *KRAS*^{G12V} and *IDH1*^{R132S}) not observed in patients (Table S9). Each cell line was subjected to high-throughput screening (HTS) using a drug library of 525 late-stage trial/FDA-approved compounds at clinically-achievable tissue concentrations (Fig. 4C). We classified compounds as biologically-active (Drug Sensitivity Score (DSS) > 10) or -inactive (DSS < 10) (16, 28) and then linked them to the mutational subgroup in which maximal therapeutic effect was observed (Fig. 4D; Table S9). RNA synthesis inhibitors (P=0.029, Fisher's exact test), microtubule-targeting drugs (P=2.93x10^{-4}), topoisomerase inhibitors (P=1.1x10^{-3}) and PLK1 inhibitors (P=0.018), and mTOR pathway modulators (P=7x10^{-6}) displayed maximal efficacy in IDH-gr, KRAS-gr, TP53-gr and Udt-gr, respectively. These modalities largely support earlier observed subgroup-enriched pathway dysregulation (Table S8) as therapeutic vulnerabilities in iCCA. The top 21 most effective drugs with specific mutational subgroup-enrichment are depicted in Fig. 4E. Notably, presence of dual mutations appears to abrogate such observed sensitivities in the RBE cell line (mixed). Taken together, these experimental findings support the concept of preferential pathway deregulation, governed by our mutational sub-classification, which may have important implications for exploitation of pharmacological vulnerabilities.

Structural and epigenomic burden vary across iCCA patient subgroups

In SNVs, Udt-gr tumors showed limited enrichment of specific pathways. This suggests either substantial molecular heterogeneity within Udt-gr or that the causality is related to other genome features (gene fusion, recurrent somatic copy number alteration (SCNA) or epigenetics). We analyzed enriched SCNA segments (total counts) and observed IDH-gr has the lowest, followed by KRAS-gr, Udt-gr and TP53-gr (Fig. 5A; Table S10). Frequencies of SNV and SCNA segments exhibit an inverse trend (Fig. 5B), similar to observations in other cancers (29) with enrichment of DNA repair mismatch genes in cases with high mutational burden. As such, KRAS- and IDH-grs have few recurrent focal SCNAs, while TP53- and Udt-gr tumors have comparably higher

frequency of recurrent structural variants (and encoded genes) (Supporting Fig. S7A; Table S10). Recurrent deletions were significant across all four groups, while recurrent amplifications were only significant in TP53- and Udt-gr (Fig. 5C). The majority of recurrent SCNA segments were unique to each group (Supporting Fig. S7B; Table S11). The only common cytoband 9p21.3 enriched across all groups was the focal segment that encodes the key tumor suppressor gene, *CDKN2B* (q-value reported by GISTIC2: 0.05 (IDH-gr), 0.08 (KRAS-gr), 4.85×10^{-5} (TP53-gr) 1.52×10^{-7} (Udt-gr)). We then examined whether recurrent SCNA segments were correlated with transposons, microsatellite instability (MSI) or HBV integrations but found no significant correlation (Supporting Fig. S7C-G).

Genes within focal SCNA peaks were highly recurrent (70-90% of patients) in their respective subgroups (Fig. 5D; Table S11), suggesting potential causal roles in their pathogenesis. We performed pathway analysis across each subgroup and identified IDH- and TP53-grs as largely silent (Fig. 5E; Table S12), suggesting a diminished contribution of structural variants to their pathogenesis. In contrast, KRAS-gr showed enrichment of multiple immune-related processes (NK cytotoxicity, JAK/STAT and cytokine signaling), complementing our findings from SNVs of widespread immune pathway subversion in these patients (Fig. 4A). Similar enrichment of structural alterations in immune pathway genes (related to viral and/or bacterial infection) was also found in Udt-gr, a patient subgroup with a heterogeneous low SNV burden but high SCNA frequency.

To investigate epigenomic contributions to cholangiocarcinogenesis, we classified an independent iCCA patient cohort (n=69; Table S13) (11, 30) into our four mutational subgroups and compared differential DNA methylation profiles relative to surrounding normal tissues. Consistent with our earlier cohorts (Fig. 3E-H), KRAS-gr was again associated with decreased overall survival within 12 months following surgery (Fig. 6A). While all subgroups displayed predominant hypermethylation over hypomethylation across promoters and gene bodies, the total burden of differentially methylated regions (DMRs) varied between subgroups (Fig. 6B; Table S13).

Unsurprisingly, given its role in DNA demethylation, IDH-gr displayed the greatest number of differentially methylated regions (DMRs) (n=2499/2646; 94.4% hypermethylation). Notably, Udt-gr harbored the next most extensive DNA methylome alterations. Such findings were also emphasized in pathway enrichment, where KRAS-gr and TP53-gr were largely silent, and Udt-gr was particularly enriched in neuronal-related signaling (Fig. 6C; Table S14). Given the fact that the copy number status has been reported to have little effect on DNA methylation alterations (31, 32), here we demonstrate an additional independent molecular patho-mechanism that may positively affect iCCA subtypes and influence tumor behavior as well as therapeutic response.

The most recurrent focal SCNA segment in Udt-gr includes the gene methyltransferase-like 13 (*METTL13*), which is amplified in 70% of patients (Fig. 5D). Comparison of its structural alteration across 36 tumor types (TCGA) revealed it to be most frequently amplified in CCA (Supporting Fig. S8A), correlating with elevated gene expression and DNA methylation (Supporting Fig. S8B-D). Given METTL13s expected role as a SAM methyltransferase, we tested whether this patient subgroup (*METTL13* amp) was readily distinguishable at the epigenetic level, and established a DNA methylation signature that efficiently distinguishes it from surrounding normal tissues and its parent Udt-gr (Fig. 6D). Patients harboring *METTL13* amplification display greater overall survival (*P*=0.00033; Fig. 6E). KEGG pathway analysis of *METTL13* amplification-unique DMRs revealed enrichment of transcriptional control and kinase signaling pathways (Fig 6F). As such, *METTL13* amplification could potentially contribute to the elusive pathogenicity of Udt-gr tumors (Supporting Fig. S8).

DISCUSSION

Arguably the greatest obstacle in the development of therapeutic strategies for cholangiocarcinoma is its extensive molecular heterogeneity, further confounded by mixed patient cohorts of varied clinical and pathological features. Previous efforts have identified individual genomic events responsible for specific therapeutic sensitivities (e.g., *IDH* mutations (14, 15) and *FGFR2* fusions (10)) and broad clusters of patients with diverse

characteristic pathobiological properties (11-13). What remains unclear are the broader network implications of such individual events and the molecular origins of these clusters. Here, we highlight the potential of the three most recurrent SNVs (*IDH*, *KRAS*, *TP53*) to direct unique oncogenic programs in intrahepatic cholangiocarcinoma and, in turn, expose a subset of their network-based vulnerabilities (Fig. 7). Furthermore, we uncover enhanced roles of structural and epigenomic perturbation mechanisms in patients lacking mutations in these three classifier genes, reinforcing the need for integrative approaches to comprehensively stratify patients.

In both TES- (n=150) and WES-cohorts (n=277), the top three recurrently mutated genes were found to be *TP53*, *KRAS* and *IDH1*, as anticipated (17, 20, 21). Intriguingly, these 3 classifier genes are highly distinct with regards to their role in oncogenesis and, as highlighted in this study, in cholangiocarcinogenesis. Hotspot mutations in *KRAS* (G12A/C/D) play a significant role in iCCA initiation in mouse models (33) and are associated with a proliferation subgroup of patients with poor prognosis (26, 34). Mutational inactivation of tumor suppressor *TP53* contributes to this tumor formation *in vivo* (33) and was previously correlated with hypermutated patient tumors (21). Unlike *KRAS*, no mutational hotspot exists in *TP53* and different mutations in this gene have been shown to generate diverse neomorphic mutants with varied cellular effects (reviewed in (35)), indicating the potential for additional network heterogeneity within this subgroup. Functionally nonsynonymous hotspot mutations in *IDH1* (R132) and *IDH2* (R172) promote cholangiocarcinogenesis through repression of hepatocyte differentiation (36). However, mutation of these metabolic enzymes has broad cellular implications as aberrant downstream metabolites impair function of approximately 20 enzymatic families (only one of which are involved in DNA methylation regulation).

Given the diverse nature of these 3 mutational events, we anticipate diverse network consequences downstream. Prediction of sufficiency of 3 mutations to induce invasive carcinoma (37), however, reinforces the missing molecular pathogenicity garnered through use of single-gene dissection of tumors. Here,

we have highlighted the unique co-mutational spectra associated with each of the classifier genes. Interestingly, while *KRAS* and *IDH* mutations are mutually exclusive, *KRAS* and *TP53* mutations coexist in a small subset of patients. Such mutations may be complimentary in a minority of patients given their opposing nature as oncogenes and tumor suppressors, or potentially if they arise at different times during cellular transformation. Indeed, KRAS- and TP53-gr tumors share the greatest similarity in altered pathways. Nonetheless, these findings remain unaltered if *KRAS*/*TP53* dual mutants are excluded, suggesting such pathway similarity arises from a common underlying biology (such as cell cycle regulation) rather than inclusion of co-mutants. Additionally, our patient stratification does not take into account, though may subtly reflect, the heterogeneous cellular origins of iCCA. For example, given recent reports of *IDH* mutant (11) and 'IDH-like' (38) HCC subgroups, this may indicate a putative common origin, further reasoning the continuous spectrum of liver tumors (39). Conversely, *KRAS* mutations are highly recurrent in pancreatic cancer (40) and perihilar CCA (pCCA), potentially suggesting a more likely origin from peribiliary glands.

Initially, a limitation of our genomic stratification appeared to be the relatively large proportion of patients included in Udt-gr (63% TES-cohort, 44% WES-cohort). However, follow-up enquiry of non-mutational mechanisms successfully clarified these cryptogenic tumors. Fusion events involving *FGFR2* are predominant in Udt-gr, identifying a specific fusion-based patient group among these tumors (Fig. 1A-B). More generally, we observed SCNA to inversely correlate with SNV and, therefore, potentially compensate for the lack of SNV-associated genetic and pathway defects in these tumors. This agrees with pan-cancer studies that have identified trade-offs between mutational ('M-class') and structural/copy number ('C-class') (29), as well as large-scale pan-cancer pharmacogenomics studies that identify different contributions from diverse 'cancer functional events' (including mutation, structural alteration and DNA methylation) (41). Specifically, *METTL13* amplification was detected in more than 70% of the Udt-gr tumors with pan-cancer analysis revealing it to be most recurrent in cholangiocarcinoma. Previous studies have reported *METTL13* amplification in HCV-associated

hepatocellular carcinoma (42), conflicting with its downregulation in bladder cancer (43). Furthermore, its family member (*METTL3*) was recently uncovered to exert neoplastic properties in acute myeloid leukemia, in part through its role in RNA methylation (44), indicating METTL13 merits further investigation in iCCA.

To date, clinical trials in cholangiocarcinoma have suffered from both anatomical and molecular heterogeneity reflected in the limited translational and clinical progress made in the past 40 years (45, 46). Here, *in silico* analysis of significantly enriched pathways was successful in identifying broad signaling networks that, through patient stratification, could be exploited to induce enhanced growth arrest *in vitro*. This is further supported by convergent pathway-targeting by different mechanisms (e.g. metabolic subversion by SNV and DNA methylation in IDH-gr, immune insult by SNV and CNA in KRAS-gr). Importantly, lack of specific mutations did not dictate a complete absence of therapeutic response and similarly, co-mutations appeared to be capable of influencing therapeutic benefit (as evident in the dual *KRAS* and *IDH1* mutant RBE cell line). Nonetheless, our stratification successfully identified pathways most responsive to broad classes of repositioned drugs. In conclusion, this study demonstrates the pharmacogenomic potential of mutation- and pathway-driven genetic dissection of tumors. This highlights the potential for driver-gene guided oncogenic network characterization to enable efficient stratification and therapy optimization for intrahepatic cholangiocarcinoma patients, as well as other cancers.

DATA AVAILABILITY

Data is accessible at the European Nucleotide Archive with accession number PRJEB14974.

AUTHOR CONTRIBUTIONS

JBA, CN, CJO, DVO, AT conceived the idea, designed and implemented the study; CN, CJO, DVO, SS, AT, JBA, performed experiments and data

analyses; CN, CJO, DVO, JBA, interpreted omics data; JC, AB, CR, XWW, AL, LRR, JBA patient recruitment, clinical data collection and pathological assessment; CJO, DVO, AT, PG, KW, drug testing, assay development and performance; JBA, CJO, CN, wrote the manuscript; all authors read, edited and approved the manuscript.

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FIGURE LEGENDS

Fig. 1. Genomic alteration landscape of iCCA patients. (**A**) Distribution of the three most prevalently mutated genes, alongside *FGFR2* fusion events, in targeted sequencing (TS)- cohort (n=150). (**B**) Distribution of the three most prevalently mutated genes and *FGFR2* fusion events in whole exome sequencing (WES)-cohort (n=277). **C**) Lollipop plot of mutations reveal mutational hotspots in *IDH1* (R132C/G/L) and *KRAS* (G12A/C/D), while mutations in *TP53* are spread across multiple positions. (**D**) Total number of somatic nonsynonymous (SNVs and short indels) and synonymous mutations in WES-cohort (n=142, paired tumor/normal). (**E**) Mutational catalogue of 45 genes along with their significance score (reported by MuSiC), mutation frequency and select risk factors in WES-cohort (n=142, paired tumor/normal). The genes are sorted based on significance score.

Fig. 2. Mutational spectra in iCCA across four groups. (**A**) Distribution of the 96 substitution patterns, defined by the adjacent 5'- and 3'- sequence of the mutated nucleotide, reveal distinct mutational signatures are preferred across

groups. (**B**) Heatmap represents the frequency of 96 substitution patterns for each patient across four mutational subgroups. The numbers of mutations are scaled to 100 and color represents the percentage.

Fig. 3. Comparison of genes encoding nonsynonymous mutations across four groups. (**A**) A large fraction of genes mutated across four subgroups are unique to each subgroup. (**B**) Distribution of recurrently mutated genes that are unique to each group. (**C**) Significantly mutated genes reported by genome MuSiC. Each bubble represents a gene. The size of each bubble is proportional to the gene's mutational frequency. Genes are sorted alphabetically along x-axis and y-axis indicates $-\log_2(P\text{-value})$. (**D**) Circos plot representing the interaction between three classifier genes and other significant genes (representing potential co-driver and passenger genes). The width of the ribbon represents the interaction count, where the smallest width represents a single interaction. (**E-H**) Kaplan-Meier analysis reveals differences in recurrence rates and overall survival between mutational subgroups across 3 different patient cohorts.

Fig. 4. Enrichment of distinct signaling pathways and pharmacogenomic consequences across four mutational subgroups. (**A**) KEGG analysis indicates preferential association of distinct pathways with mutational subgroups. Z-score are computed from MuSiC *P*-values of the pathways by using scale function across groups in R, followed by hierarchical clustering. (**B**) Connectivity of mutated genes across eight pathways. The numbers in boxes represent the percentage of patients in specific mutational subgroups. Different colors represent the four groups. (**C**) Schematic of high-throughput drug repositioning experiments. (**D**) Differential sensitivity of mutational subgroups to diverse compounds. Heatmaps represent mean Drug Sensitivity Scores (DSS) per mutational subgroup, as quantified by viability effects of biologically active compounds (DSS > 10) across 7 CCA cell lines. (**E**) 21 drugs targeting specific pathways and processes established as enriched in specific mutational subgroups.

Fig. 5. Contribution of somatic copy number alterations (SCNAs) across four

mutational subgroups. (**A**) TP53-gr and Udt-gr have higher amplification and deletion frequencies compared to IDH-gr and KRAS-gr. (**B**) Frequencies of SNV and SCNA are inversely correlated. (**C**) Significant recurrent amplifications (red) and deletions (blue) reported by GISTIC2. X-axis on the bottom represents q-values of false discovery rate (FDR) and x-axis on top defines G-score (represents amplitude of aberration and frequency of occurrences across samples). Black horizontal line indicates FDR of 0.1. Y-axis represents the chromosomes. (**D**) The frequency of copy number gain and loss of genes across four subgroups. Each bubble represents a gene and the size of bubble indicates the total frequency of gain and loss. (**E**) Inter-group pathway-association of genes encoded in recurrent SCNA segments.

Fig. 6. Genome-wide DNA methylation analysis of mutational subgroups. (**A**) Kaplan-Meier analysis of DNA methylation cohort. (**B**) Hierarchical clustering of top 1% most variable probes. Each mutational subgroup is represented by geometric mean of probe methylation within that group. Number of DMRs are scaled against most epigenetically dysregulated group. (**C**) KEGG pathway analysis of total DMRs by patient subgroup. Significance was set at Q-value < 0.05. (**D**) *METTL13* amplification DNA methylation signature compared to Udt-gr and surrounding normal tissue. Probes are unique to amplification positive patients compared to surrounding normal with minimum methylation difference of 0.2 to Udt-gr. (**E**) Kaplan-Meier analysis of *METTL13* amplification positive and negative patients in TCGA cohort. (**F**) KEGG pathway analysis of *METTL13* amplification positive DMRs. Black bars indicate Q-value, grey bars indicate P-value. DMR: Differentially Methylated Regions.

Fig. 7. Mutation-centric diversity of cholangiocarcinogenesis. Incidence of SNV, recurrent SCNA and differentially methylated regions across groups are shown as a relative ratio (scaled to 1). Integrating 'omic' and pathway analysis, confirmed by *in vitro* drug testing, suggests enhanced activity of specific compounds in specific mutational subgroups.

SUPPORTING FIGURE LEGENDS

Supporting Fig. S1. Schematic representation of patient cohorts and experimental pipeline used to analyze data. (**A**) Workflow depicting the sequential flow of different patient cohorts and different data types (from various sources) analyzed in the study. (**B**) Raw sequence reads were mapped to the human genome (hg19) using BWA and were further processed to contain only high quality mapped reads. Multiple tools were used for variant (SNV and indels) calling and somatic copy number alterations (SCNA). Variants were further filtered to remove germline and low confidence variants, thus resulting high confidence SNV and SCNA.

Supporting Fig. S2. Mutational landscape and *FGFR2* fusion status of targeted sequencing (TES-) and whole exome sequencing (WES)-cohorts. (**A**) Mutational catalogue of 48 genes in TES-cohort (n=150) alongside qPCR- and sequencing-based assessment of known *FGFR2* fusions. (**B**) Mutational catalog of *TP53*, *KRAS* and *IDH1* with incidence of *FGFR2* fusion events across WES-cohort (n=277) along with additional information regarding HBV infection, ethnicity and availability of matched normal for tumor samples. WES samples with only tumor samples have higher predicted SNVs compared to matched tumor/normal samples. (**C**) Representative sequencing results spanning fusion points from *FGFR2* exon 19 to *BICC1* exon 3 (n=15) and to *BICC1* exon 5 (n=3). Alternative splicing is possible within the same patient sample. (**D**) Kaplan-Meier overall survival analysis of *FGFR2* fusion events with respect to Udt-gr in iCCA patients.

Supporting Fig. S3. Mutational and transcriptomic spectra of iCCA across four groups. (**A**) The frequencies of mutational spectra are represented as heatmaps, where each row represents a patient. (**B** and **C**) Non-matrix factorization (NMF) and hierarchical clustering of genetic substitution patterns in patients (**B**) and CCA cell lines (**C**), respectively. (**D**) Hierarchical clustering of significantly deregulated genes (F-test, nominal $P<0.001$) in an independent cohort of 135 patients.

Supporting Fig. S4. Heatmap of motifs enrichment among SNVs across

mutational subgroups. Scale bar represents motif enrichment above background, as computed with HOMER.

Supporting Fig. S5. Genes encoding somatic synonymous mutations, list of significantly mutated genes and comparison with nonsynonymous mutation. (**A**) Majority of genes encoding synonymous mutations are largely unique across each group. (**B**) Genes encoding synonymous mutations have minimum overlap with genes encoding nonsynonymous mutations. (**C**) Genes encoding synonymous mutations did not reveal significantly mutated genes within the group, which is different compared to nonsynonymous mutations in each group. Each bubble represents a gene and bubble size represents count. X-axes are sorted alphabetically based upon gene name and y-axis indicates $-\log_2$(*P*-value).

Supporting Fig. S6. KEGG pathway analysis using alternative classifier genes and resulting subgroups. The successive three most recurrently mutated genes (*CDC27*, *ARID1A* and *BAP1*) were used to group patients instead of *IDH1*, *KRAS* and *TP53*, with those wild type (i.e. no nonsynonymous mutations in *CDC27*, *ARID1A* and *BAP1*) classified as "remaining". Three control groups showed no specific enrichment, as all terms are enriched in "remaining" group.

Supporting Fig. S7. Recurrent somatic copy number alterations (SCNA) among groups. (**A**) *TP53*- and Udt-gr have more recurrent SCNA segments (and underlying genes) compared to *IDH1* and *KRAS* groups. No significant difference in length of SCNA segments exists between groups. (**B**) Mutational subgroups have few recurrently altered cytobands (reported by GISTIC2) in common. The cytoband 9p21.3 that encodes *CDKN2B* and *CDKN2B-AS1* genes is significantly recurrent in all groups. Cancer-related genes listed in COSMIC database are shown for each group. (**C**) Distribution of transposons around recurrent SCNA segments. (**D**) Incidences of recurrent somatic microsatellite instability (MSI) revealed no differences among subgroups. (**E**) SCNA burden displayed no differences among TP53- and Udt-gr patients when stratified by HBV status. (**F-G**) No common recurrent SCNA were

shared by HBV positive patients across TP53- and Udt-gr. X-axis on the bottom represents Q-values of false discovery rate (FDR) and x-axis on top defines G-score (represents amplitude of aberration and frequency of occurrences across samples). Black horizontal line indicates FDR of 0.1. Y-axis represents the chromosomes.

Supporting Fig. S8. Incidence and implications of *METTL13* alterations. (**A**) Comparison of *METLL13* alterations across 51 different cancers reveal it to be most frequently altered in intrahepatic cholangiocarcinoma. **(B**) *METTL13* amplification status is positively correlated with its expression. (**C**) *METTL13* methylation is inversely correlated with its amplified status. (**D**) *METTL13* expression is inversely correlated with its methylation status.

SUPPORTING TABLES

Table S1: Clinicopathologic features of patients in TES cohort (n=150)

Table S2: Clinicopathologic features and WES mapping statistics of 15 novel iCCA patients

Table S3: WES libraries used in the study (n=277)

Table S4: Predicted nonsynonymous SNVs and indels

Table S5: Predicted synonymous SNVs

Table S6A-E: List of mutated genes, unique genes and recurrent genes in each group

Table S7: Significantly mutated genes across four groups

Table S8: Enriched KEGG pathways among SNV-affected genes

Table S9: Drug repositioning

Table S10: Recurrent CNA cytobands across each group

Table S11: Genes that are significantly amplified or deleted within recurrent CNA

Table S12: Enriched KEGG pathways among CNA-affected genes

Table S13: Genome-wide DNA methylation analysis

Table S14: Enriched KEGG pathways among differentially methylated regions

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Genomic Perturbations Reveal Distinct Regulatory Networks in Intrahepatic Cholangiocarcinoma

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Abstract

Intrahepatic cholangiocarcinoma (iCCA) remains a highly heterogeneous malignancy that has eluded effective patient stratification to date. The extent to which such heterogeneity can be influenced by individual driver mutations remains to be evaluated. Here, we analyzed genomic (whole-exome sequencing, targeted exome sequencing) and epigenomic data from 496 patients, and used the three most recurrently mutated genes to stratify patients (*IDH*, *KRAS*, *TP53*, 'undetermined'). Using this molecular dissection approach, each subgroup was determined to possess unique mutational signature preferences, co-mutation profiles and enriched pathways. High-throughput drug repositioning in seven patient-matched cell lines, chosen to reflect the genetic alterations specific for each patient group, confirmed *in silico* predictions of subgroup-specific vulnerabilities linked to enriched pathways. Intriguingly, patients lacking all 3 mutations ('undetermined') harbored the most extensive structural alterations while IDH mutant tumors displayed the most extensive DNA methylome dysregulation, consistent with previous findings. ***Conclusion***: Stratification of iCCA patients based on occurrence of mutations in three classifier genes (*IDH*, *KRAS*, *TP53*) revealed unique oncogenic programs (mutational, structural, epi-mutational) that influence pharmacologic response in drug repositioning protocols. This genome dissection approach highlights the potential of individual mutations to induce extensive molecular heterogeneity and could facilitate advancement of therapeutic response in this dismal disease.

INTRODUCTION

Intrahepatic cholangiocarcinoma (iCCA) incidence and mortality rates have increased globally over the last three decades, highlighting a growing clinical problem from what was once considered a rare orphan disease (1, 2). The majority of iCCAs are sclerosing adenocarcinomas arising from cholangiocytes lining intra-lobular biliary ductules, as well as peribiliary glands of large intrahepatic bile ducts (1, 3). While the causal biology of this cancer is largely unclear, known risk factors include chronic hepatitis B or C viral infection with cirrhosis (4); chronic liver conditions, such as cholestasis, primary sclerosing cholangitis (5) or liver fluke infestation (6); metabolic disorders, such as diabetes mellitus (DM); and lifestyle or environmental factors, including alcohol consumption and smoking (7). Liver resection remains the only curative treatment, a surgical procedure frequently precluded by early invasion of surrounding tissues. Even among 10-30% patients eligible for resection, 50% recur within the first 12 months. Standard chemotherapy regimens (gemcitabine alongside platin-based compounds) for non-resectable and recurrent iCCA patients are purely palliative, achieving only a limited improvement in survival (8). As most iCCAs are locally advanced or metastatic at presentation, patients have a dismal prognosis with a 5-year survival rate that has persisted below 10% since the 1980s (9). While no targeted therapy has been approved to date, *FGFR2* inhibitors (e.g. BGJ398) may be the first to transform iCCA clinical management, displaying prospective efficacy (though of variable duration) in fusion-positive patients (10). Similarly, future therapeutic advances will likely stem from further molecular stratification of iCCA patients, exposing oncogenic networks against which therapeutics may be strategized.

Recently, several cross-platform integrative analyses have identified broad cholangiocarcinoma subgroups associated with specific clinical and molecular features (11-13). However, inter-study comparison of these subgroups remains difficult given they are enriched by complex molecular characteristics identified in heterogeneous patient cohorts. Identification of single or few genomic alterations which influence downstream oncogenic networks could facilitate refinement of these previously established subgroups, as well as

enhance prediction of therapeutic response to pharmacologic intervention against specific molecular backgrounds. As such, mutations in *IDH1* and *IDH2* have already been associated with unique genomic features (DNA hypermethylation, altered chromatin remodeler expression, increased copy number and expression of mitochondrial genes), as well as sensitivity to dasatinib (14) and PARP inhibitors (15). The potential for individual driver mutations to influence diverse tumor networks is intriguing and remains to be evaluated for other recurrently mutated genes in iCCA, such as *KRAS*, *TP53* and chromatin remodeling enzymes (e.g., *ARID1A* and *BAP1*).

Accordingly, we aimed to deconstruct the molecular programs of iCCA tumors associated with specific individual mutations. To this end, we grouped 496 patients into four subgroups where three were classified based on the most recurrent somatic mutations (*IDH*, *KRAS* and *TP53*) and the remaining based on wild-type status for these genes (referred to as 'undetermined group'). This stratification approach unveiled distinct mutational signatures and co-mutations, pathway-enrichment and pharmacologic response profiles between subgroups, as well as suggesting an enhanced role of structural and epigenomic alterations in undetermined group tumors. These findings uncover the potential of individual mutations to induce substantial downstream molecular heterogeneity which could facilitate prediction of therapeutic sensitivities for iCCA patients using standard targeted genotyping.

MATERIALS AND METHODS

Patients and samples

Data sets from a series of 496 iCCA patients were obtained for analysis (Supporting Fig S1A). Totally, 165 fresh-frozen iCCAs were collected from surgically resected patients. All samples were immediately frozen in liquid nitrogen and stored at -80°C pending genomic DNA isolation. The Danish Regional Ethics Committee and local authorities at contributing institutions approved the study. Written informed patient consent was obtained in accordance to regional regulation. All patient demographic and clinico-pathological data were anonymized and are summarized in Supporting Tables S1-S2. 150 of these tumors were subjected to targeted exome sequencing (TES) (Table S1), performed using the 48-gene TruSeq Amplicon Cancer Panel (TSACP, Illumina). The remaining 15 cases underwent whole-exome sequencing (WES) (Table S2) and were analyzed alongside 262 publically available WES iCCA samples (Table S3).

SNV calling and analysis

FASTQ files were filtered, subjected to quality control and mapped to the human genome assembly (hg19) using BWA. SNVs and short indels were called using a combination of Varscan (v2.3), somaticSnipper (v1.0.4) and Shimmer. Annovar was used to classify SNVs as synonymous or non-synonymous. Potential impacts of amino acid alterations on protein structure and function were assessed by PolyPhen-2. Motif enrichment analysis was performed by HOMER. Inference of mutational signatures was carried out with SomaticSignatures tool. Pathway enrichment of significantly mutated genes encoding SNVs and indels were assessed using genome MuSiC. Further information regarding bioinformatics analysis can be found as Supporting Information.

FGFR2 fusion detection

Totally, 122 of 150 tumors subjected to TES were assessed for known *FGFR2* fusions. RNA isolation was performed and subjected to reverse transcription with SuperScript VILO cDNA Synthesis kit (ThermoFisher Scientific). Fusion

products in *FGFR2* were targeted with primer pairs flanking breakpoints of *FGFR2* and previously reported donor genes. Commercially synthesized DNA with *FGFR2* and all known fusion partner sequence fragments (Integrated DNA Technologies) were cloned into plasmid scaffolds and used as positive controls. Fusions were confirmed by Sanger sequencing. Further information regarding fusion detection can be found as Supporting Information.

Cell culture

Cholangiocarcinoma cell lines were purchased from KCLB (SNU-478, SNU-1079, SNU-1196), DSMZ (EGI-1), RIKEN (HuCCT-1, RBE), and obtained from Mayo Clinic (WITT, KMCH). Cells were cultured in RPMI-1640 or DMEM-F12 (ThermoFisher Scientific), all supplemented with 10% heat-inactivated FBS (GE Healthcare), 1% penicillin-streptomycin and 1% L-glutamine (ThermoFisher Scientific). Cells were maintained at 37°C and 5% CO_2.

High-throughput drug repositioning

Drug screening was carried out using a drug library of 525 compounds (FDA-approved or in late stage clinical trials). Cells were seeded into 384-well plates and treated for 72 hours over 5-fold dilution series. Anti-proliferative cellular effects were measured with CellTiter-Glo Luminescent Cell Viability assay (Promega), as per manufacturers' instructions, and quantified using Drug Sensitivity Score (DSS) metric (16). Further information regarding drug screening can be found as Supporting Information.

CNA calling and analysis

Copy Number Alterations (CNAs) were analyzed using VarScan2, DNAcopy and GISTIC2 packages. *FGFR2* fusions were predicted using BreakDancer. Further information regarding CNA analysis can be found as Supporting Information.

Genome-wide DNA methylation profiling

In house and publically available Infinium Human Methylation 450k BeadChip (Illumina) data were used to identify an independent patient cohort (n=69) to

investigate effects of classifier genes on DNA methylation profiles. Data were processed and analyzed using RnBeads (v1.2.1). Further information regarding methylomics can be found as Supporting Information.

RESULTS

Rational identification of classifier mutations for iCCA patient stratification

To investigate mutational diversity in iCCA, we analyzed 427 patients by targeted exome sequencing ('TES-cohort'; n=150 patients) and whole-exome sequencing ('WES-cohort'; n=277 patients; incorporating 142 tumor/normal matched pairs and 135 tumors) (17-21)) (Supporting Fig. S1A-B). Analysis of TES-cohort of 48 cancer-related genes (Table S1) revealed *IDH1* (n=21/150; 14%), *TP53* (n=19/150; 13%) and *KRAS* (n=18/150; 12%) as the most recurrent mutations (Fig. 1A; Supporting Fig. S2A). Subsequent analysis of WES-cohort (Table S2-3) corroborated our TES-cohort findings where *TP53* (n=57/277; 20%), *KRAS* (n=44/277; 16%) and *IDH1/IDH2* (n=31/277; 11%) were most prevalent (Fig. 1B; Supporting Fig. S2B). Mutations in *IDH1* (R132C/G/L) and *KRAS* (G12A/C/D) were recurrent hotspots, while *TP53* mutations were distributed throughout its entire gene body (Fig. 1C) with prevalent R249S (n=10/45; 22.2%) mutations. Importantly, co-occurrence of *IDH1/KRAS* mutations (TES-cohort: n=1/150; 0.7%; WES-cohort: n=1/277; 0.4%) and *IDH1*/*TP53* (TES-cohort: n=3/150, 2%; WES-cohort: n=1/277, 0.4%) was rare, suggesting mutual exclusivity (Fig. 1A-B). In comparison, dual mutations in *KRAS* and *TP53* are detected in a subset of patients (TES-cohort: n=4/150; 2.7%; WES-cohort: n=14/277; 5.1%) but are not mutually inclusive (*P*=0.07, Fisher's exact test). Accordingly, we selected to stratify iCCA patients into four groups based on mutational status of these genes, referring to them as IDH-gr (including *IDH1* and *IDH2* mutations), KRAS-gr, TP53-gr and Udt-gr ('undetermined', wild type for all 3 driver genes).

FGFR2 fusion events have been identified in between 5.5% (21) to 28% (10) of patients, implicating this event as one of the most recurrent genomic alterations in iCCA. We next analyzed the prevalence of fusions in the TES-cohort by performing targeted analysis against known fusion partners,

followed by confirmation with Sanger sequencing. We observed that 14.8% (n=18/122) of tumors were *FGFR2-BICC1* fusion positive, where 83.3% (n=15/18) cases fused with *BICC1* in exon 3 and the remaining 16.7% (n=3/18) fused in exon 5 (Supporting Fig. S2A; Supporting Fig. S2C). Clinically, *FGFR2* fusion-positive status was associated with shorter overall survival (P<0.0001; Supporting Fig. S2D). The majority of fusion events (n=12/18; 66.7%) fell within Udt-gr. Similarly, in previously reported *FGFR2* fusions from RNAseq data (n=117/277; 42.2%; Japanese patients), *FGFR2* fusions are predominant in Udt-gr (n=3/4; 75%) (Supporting Fig. S2B).

Focusing on tumor/normal matched cases (n=142/277; 51.3%), we annotated 7,921 nonsynonymous SNVs in 5,457 genes (Table S4) and 2,581 synonymous SNVs in 2,229 genes (Table S5) with an average of 2.3 mutations/Mb (Fig. 1D). Apart from the prevalent mutant classifiers (*IDH, KRAS* and *TP53,)* other significantly mutated genes include chromatin modifiers (*ARID1A, BAP1, KDM6B, SETD2*) and genes newly associated with iCCA (Fig. 1E). We next analyzed known clinical risk factors associated with mutational subgroups and observed hepatitis B virus (HBV) infection was significantly associated with TP53-gr (n=26/45; 58%; P = 1.612x10^{-5}, Fisher's exact test) (Fig. 1E). Interestingly, HBV was also associated with a large number of Udt-gr tumors (n=21/63; 33%) but did not reach significance when compared to the entire cohort (Fig. 1E). However, no significant association was determined between mutational subgroups and diabetes mellitus (DM), smoking or alcohol consumption.

Mutation-centric tumor stratification identifies diverse oncogenic processes

The mutational signatures defined by immediate 5'- and 3'- sequences flanking SNVs may reflect specific underlying mutagenic processes (22); thus, we investigated mutagenic signatures associated with the four subgroups. Though C>T transitions and C>A transversions are prevalent overall in iCCA (Supporting Fig. S3A), as previously described (20, 21), mutational signatures are unique between subgroups (Fig. 2A). IDH-gr displayed a specific enrichment of C>A transversions (67%, P=7.01x10^{-132}) (signature 18, 28) (Fig.

2A-B). As such, C>A transversions have been associated with oxidative stress (23), complementing previous studies characterizing the physiological role of wild type *IDH1* in protecting hepatocytes from oxidative stress (24). KRAS-gr was characterized by predominant C>T transitions (Fig. 2A) (55%, P=3.40x10^{-87}, Fisher's exact test), displaying a preference for purine (G or C) upstream of transitions (Fig. 2B), and suggesting a role for APOBEC (signature 2 and 13) (22). Also, promoters of genes mutated in KRAS-gr were enriched for *FOSL2* motif binding sites (Supporting Fig. S4), in agreement with transcriptional signature derived from *KRAS*-driven tumors (25). TP53-gr displayed preferential unique T>A transversions (26%, P = 2.29x10^{-125}) with NpT>ApG associated with aristolochic acid (signature 22). Although, a significant enrichment of R249S mutations were detected in TP53-gr (Fig. 1C), aflatoxin signature was not enriched as in hepatocellular carcinoma (HCC). Also, R249S did not display a significant relationship with HBV status (P=0.48, Fisher's exact test) or overall survival (P=0.917) when comparing with patients manifesting other *TP53*-specific mutations.

Akin to IDH-gr, Udt-gr displayed a preference for C>A transversions (42%, P=4.69x10^{-10}). In fact, non-matrix factorization (NMF) clustering of signature contributions across mutation subgroups in patients and CCA cell lines (n=16) implicated a close association between IDH-gr and Udt-gr (Supporting Fig. S3B-C). Such similarity was also observed at the transcriptome level in our previously published cohort (26) through hierarchical clustering of significant differentially expressed genes (F-test P<0.001; Supporting Fig. S3D). Taken together, these findings suggest that without patient stratification, Udt-gr would have masked the unique genetic patterns elicited by IDH-gr, KRAS-gr and TP53-gr. Furthermore, these data indicate that diversity of oncogenic programs (unique and shared between subgroups) may arise early in tumorigenesis from their initial genetic mutational signatures and possibly transcend different genomic readouts in their consequences.

Inter-group mutational analysis uncovers unique co-mutational profiles

Next, we analyzed the extent of exclusivity of mutated genes among subgroups and observed that the majority of genes encoding nonsynonymous

SNVs were unique (Fig. 3A) and co-occurred (≥2 tumors) within their individual subgroups (Fig. 3B-C; Table S6A-D). Genes encoding somatic synonymous SNVs were also unique to each subgroup (Supporting Fig. S5A; Table S6E), but show minimal overlap (2-4%) (Supporting Fig. S5B) with nonsynonymous SNV genes, suggesting these mutational processes are dissimilar. Furthermore, somatic synonymous SNVs have low recurrence rate and lack significantly mutated genes with iCCA subgroups (Supporting Fig. S5C), which is markedly different from nonsynonymous mutated genes (Fig. 3C).

As expected, *IDH1*, *KRAS* and *TP53* were the most significantly altered genes in their respective groups along with specific enrichment of *BCLAF1* (P=0.007) in IDH-gr; *SMAD4* (P=0.03) in KRAS-gr; *PTEN* (P=9.36x10^{-7}), RB1 (P=0.002) and *LATS2* (P=0.02) in the TP53-gr; and *KDM6B* in the Udt-gr (P=0.08) (Fig. 3C; Table S7). Among the previously reported chromatin modifier genes, *ARID1A* mutations were present in IDH-gr, KRAS-gr and Udt-gr but only significantly enriched with Udt-gr tumors (P=8.86x10^{-8}), while *BAP1* was preferentially associated with IDH-gr (P=2.57x10^{-8}). Notably, no chromatin modifiers were associated with TP53-gr. Association of significantly mutated genes along with the three classifier genes are represented in Fig. 3D.

We next evaluated any prognostic significance across four mutational subgroups. In the WES-cohort of 142 tumor/normal patient samples, KRAS-gr and TP53-gr were significantly associated with poor overall survival (P=0.003; Fig. 3E) and faster time to recurrence (P=0.018; Fig. 3F). These findings were confirmed in two independent cohorts whereby KRAS-gr was associated with worse overall survival in TES-cohort (N=150) (P=0.0004; Fig. 3G) and both KRAS-gr and TP53-gr were correlated with worse overall survival (P=0.0001; Fig. 3H) in Nakamura et al. cohort (N=135) (21). Thus, we conclude that these four mutational subgroups have a distinct association of co-mutated genes and different overall survival.

Intrahepatic CCA subgroups harbor unique dysregulated pathways that are reflected in their drug-response profiles

To understand whether genes associated with each subgroup could contribute to different oncogenic programs through tailored pathway dysregulation, we analyzed perturbed pathways associated with each group (Fig. 4A-B; Table S8). IDH-gr was enriched for metabolic pathways, including glutathione metabolism (P=6.33x10^{-21}) and citrate cycle (P=2.37x10^{-14}), which is consistent with known involvement of *IDH1* in metabolic processes in CCA (27). KRAS-gr was highly enriched for various immune-related pathways, including ErbB (P=4.39x10^{-17}), VEGF (P=2.49x10^{-16}) and actin cytoskeleton rearrangement (P=4.7x10^{-10}). In contrast, MAPK (P=1.44x10^{-33}), WNT (P=2.19x10^{-26}) and p53 signaling (P=3.44x10^{-32}) were enriched in TP53-gr. Since mutations in *KRAS* and *TP53* occur in a small subset of patients, pathway enrichment in dual mutants was independently assessed. Notably, significantly enriched pathways were all present in either KRAS-gr or TP53-gr (Table S8), supporting our previous inclusion of these patients in both KRAS-gr and TP53-gr analyses. Finally, in spite of being the largest group, Udt-gr was exclusively enriched for mTOR signaling (P=4.76x10^{-3}), suggesting that Udt-gr is highly heterogeneous with regards to SNVs. To indirectly test the validity of our classifier genes, we selected the next three most recurrent mutated genes as alternative classifiers: ARID1A-gr (n=14; 9.9%), CDC27-gr (n=12; 8.5%), BAP1-gr (n=9; 6.3%), and Remaining-gr (n=110; 77.5%; analogous to Udt-gr) (Supporting Fig. 6). No pathways were uniquely enriched among these surrogate groups, with significant biological processes emerging only in the 'remaining' tumors, thus justifying our patient classification.

Next, we sought to determine whether mutational subgroups displayed differential sensitivity to diverse classes of compounds *in vitro* and whether these drug responses reflected *in silico* predictions of enhanced pathway dysregulation. To determine the `best fit´ cell models, mimicking the patient groups, we earlier performed NMF clustering of the mutational signatures (genetic substitution patterns) in patients and a panel of 16 CCA cell lines (Supporting Fig. S3B-C). This confirmed genetic signatures under our mutational classifiers were comparable between cell lines and patients.

Accordingly, we selected 7 cell lines with matched mutational profiles representative of each of the patient subgroups, as well as one mixed mutant cell line (RBE; *KRAS*^{G12V} and *IDH1*^{R132S}) not observed in patients (Table S9). Each cell line was subjected to high-throughput screening (HTS) using a drug library of 525 late-stage trial/FDA-approved compounds at clinically-achievable tissue concentrations (Fig. 4C). We classified compounds as biologically-active (Drug Sensitivity Score (DSS) > 10) or -inactive (DSS < 10) (16, 28) and then linked them to the mutational subgroup in which maximal therapeutic effect was observed (Fig. 4D; Table S9). RNA synthesis inhibitors (P=0.029, Fisher's exact test), microtubule-targeting drugs (P=2.93x10^{-4}), topoisomerase inhibitors (P=1.1x10^{-3}) and PLK1 inhibitors (P=0.018), and mTOR pathway modulators (P=7x10^{-6}) displayed maximal efficacy in IDH-gr, KRAS-gr, TP53-gr and Udt-gr, respectively. These modalities largely support earlier observed subgroup-enriched pathway dysregulation (Table S8) as therapeutic vulnerabilities in iCCA. The top 21 most effective drugs with specific mutational subgroup-enrichment are depicted in Fig. 4E. Notably, presence of dual mutations appears to abrogate such observed sensitivities in the RBE cell line (mixed). Taken together, these experimental findings support the concept of preferential pathway deregulation, governed by our mutational sub-classification, which may have important implications for exploitation of pharmacological vulnerabilities.

Structural and epigenomic burden vary across iCCA patient subgroups

In SNVs, Udt-gr tumors showed limited enrichment of specific pathways. This suggests either substantial molecular heterogeneity within Udt-gr or that the causality is related to other genome features (gene fusion, recurrent somatic copy number alteration (SCNA) or epigenetics). We analyzed enriched SCNA segments (total counts) and observed IDH-gr has the lowest, followed by KRAS-gr, Udt-gr and TP53-gr (Fig. 5A; Table S10). Frequencies of SNV and SCNA segments exhibit an inverse trend (Fig. 5B), similar to observations in other cancers (29) with enrichment of DNA repair mismatch genes in cases with high mutational burden. As such, KRAS- and IDH-grs have few recurrent focal SCNAs, while TP53- and Udt-gr tumors have comparably higher

frequency of recurrent structural variants (and encoded genes) (Supporting Fig. S7A; Table S10). Recurrent deletions were significant across all four groups, while recurrent amplifications were only significant in TP53- and Udt-gr (Fig. 5C). The majority of recurrent SCNA segments were unique to each group (Supporting Fig. S7B; Table S11). The only common cytoband 9p21.3 enriched across all groups was the focal segment that encodes the key tumor suppressor gene, *CDKN2B* (q-value reported by GISTIC2: 0.05 (IDH-gr), 0.08 (KRAS-gr), 4.85×10^{-5} (TP53-gr) 1.52×10^{-7} (Udt-gr)). We then examined whether recurrent SCNA segments were correlated with transposons, microsatellite instability (MSI) or HBV integrations but found no significant correlation (Supporting Fig. S7C-G).

Genes within focal SCNA peaks were highly recurrent (70-90% of patients) in their respective subgroups (Fig. 5D; Table S11), suggesting potential causal roles in their pathogenesis. We performed pathway analysis across each subgroup and identified IDH- and TP53-grs as largely silent (Fig. 5E; Table S12), suggesting a diminished contribution of structural variants to their pathogenesis. In contrast, KRAS-gr showed enrichment of multiple immune-related processes (NK cytotoxicity, JAK/STAT and cytokine signaling), complementing our findings from SNVs of widespread immune pathway subversion in these patients (Fig. 4A). Similar enrichment of structural alterations in immune pathway genes (related to viral and/or bacterial infection) was also found in Udt-gr, a patient subgroup with a heterogeneous low SNV burden but high SCNA frequency.

To investigate epigenomic contributions to cholangiocarcinogenesis, we classified an independent iCCA patient cohort (n=69; Table S13) (11, 30) into our four mutational subgroups and compared differential DNA methylation profiles relative to surrounding normal tissues. Consistent with our earlier cohorts (Fig. 3E-H), KRAS-gr was again associated with decreased overall survival within 12 months following surgery (Fig. 6A). While all subgroups displayed predominant hypermethylation over hypomethylation across promoters and gene bodies, the total burden of differentially methylated regions (DMRs) varied between subgroups (Fig. 6B; Table S13).

Unsurprisingly, given its role in DNA demethylation, IDH-gr displayed the greatest number of differentially methylated regions (DMRs) (n=2499/2646; 94.4% hypermethylation). Notably, Udt-gr harbored the next most extensive DNA methylome alterations. Such findings were also emphasized in pathway enrichment, where KRAS-gr and TP53-gr were largely silent, and Udt-gr was particularly enriched in neuronal-related signaling (Fig. 6C; Table S14). Given the fact that the copy number status has been reported to have little effect on DNA methylation alterations (31, 32), here we demonstrate an additional independent molecular patho-mechanism that may positively affect iCCA subtypes and influence tumor behavior as well as therapeutic response.

The most recurrent focal SCNA segment in Udt-gr includes the gene methyltransferase-like 13 (*METTL13*), which is amplified in 70% of patients (Fig. 5D). Comparison of its structural alteration across 36 tumor types (TCGA) revealed it to be most frequently amplified in CCA (Supporting Fig. S8A), correlating with elevated gene expression and DNA methylation (Supporting Fig. S8B-D). Given METTL13s expected role as a SAM methyltransferase, we tested whether this patient subgroup (*METTL13* amp) was readily distinguishable at the epigenetic level, and established a DNA methylation signature that efficiently distinguishes it from surrounding normal tissues and its parent Udt-gr (Fig. 6D). Patients harboring *METTL13* amplification display greater overall survival (*P*=0.00033; Fig. 6E). KEGG pathway analysis of *METTL13* amplification-unique DMRs revealed enrichment of transcriptional control and kinase signaling pathways (Fig 6F). As such, *METTL13* amplification could potentially contribute to the elusive pathogenicity of Udt-gr tumors (Supporting Fig. S8).

DISCUSSION

Arguably the greatest obstacle in the development of therapeutic strategies for cholangiocarcinoma is its extensive molecular heterogeneity, further confounded by mixed patient cohorts of varied clinical and pathological features. Previous efforts have identified individual genomic events responsible for specific therapeutic sensitivities (e.g., *IDH* mutations (14, 15) and *FGFR2* fusions (10)) and broad clusters of patients with diverse

characteristic pathobiological properties (11-13). What remains unclear are the broader network implications of such individual events and the molecular origins of these clusters. Here, we highlight the potential of the three most recurrent SNVs (*IDH*, *KRAS*, *TP53*) to direct unique oncogenic programs in intrahepatic cholangiocarcinoma and, in turn, expose a subset of their network-based vulnerabilities (Fig. 7). Furthermore, we uncover enhanced roles of structural and epigenomic perturbation mechanisms in patients lacking mutations in these three classifier genes, reinforcing the need for integrative approaches to comprehensively stratify patients.

In both TES- (n=150) and WES-cohorts (n=277), the top three recurrently mutated genes were found to be *TP53*, *KRAS* and *IDH1*, as anticipated (17, 20, 21). Intriguingly, these 3 classifier genes are highly distinct with regards to their role in oncogenesis and, as highlighted in this study, in cholangiocarcinogenesis. Hotspot mutations in *KRAS* (G12A/C/D) play a significant role in iCCA initiation in mouse models (33) and are associated with a proliferation subgroup of patients with poor prognosis (26, 34). Mutational inactivation of tumor suppressor *TP53* contributes to this tumor formation *in vivo* (33) and was previously correlated with hypermutated patient tumors (21). Unlike *KRAS*, no mutational hotspot exists in *TP53* and different mutations in this gene have been shown to generate diverse neomorphic mutants with varied cellular effects (reviewed in (35)), indicating the potential for additional network heterogeneity within this subgroup. Functionally nonsynonymous hotspot mutations in *IDH1* (R132) and *IDH2* (R172) promote cholangiocarcinogenesis through repression of hepatocyte differentiation (36). However, mutation of these metabolic enzymes has broad cellular implications as aberrant downstream metabolites impair function of approximately 20 enzymatic families (only one of which are involved in DNA methylation regulation).

Given the diverse nature of these 3 mutational events, we anticipate diverse network consequences downstream. Prediction of sufficiency of 3 mutations to induce invasive carcinoma (37), however, reinforces the missing molecular pathogenicity garnered through use of single-gene dissection of tumors. Here,

we have highlighted the unique co-mutational spectra associated with each of the classifier genes. Interestingly, while *KRAS* and *IDH* mutations are mutually exclusive, *KRAS* and *TP53* mutations coexist in a small subset of patients. Such mutations may be complimentary in a minority of patients given their opposing nature as oncogenes and tumor suppressors, or potentially if they arise at different times during cellular transformation. Indeed, KRAS- and TP53-gr tumors share the greatest similarity in altered pathways. Nonetheless, these findings remain unaltered if *KRAS*/*TP53* dual mutants are excluded, suggesting such pathway similarity arises from a common underlying biology (such as cell cycle regulation) rather than inclusion of co-mutants. Additionally, our patient stratification does not take into account, though may subtly reflect, the heterogeneous cellular origins of iCCA. For example, given recent reports of *IDH* mutant (11) and 'IDH-like' (38) HCC subgroups, this may indicate a putative common origin, further reasoning the continuous spectrum of liver tumors (39). Conversely, *KRAS* mutations are highly recurrent in pancreatic cancer (40) and perihilar CCA (pCCA), potentially suggesting a more likely origin from peribiliary glands.

Initially, a limitation of our genomic stratification appeared to be the relatively large proportion of patients included in Udt-gr (63% TES-cohort, 44% WES-cohort). However, follow-up enquiry of non-mutational mechanisms successfully clarified these cryptogenic tumors. Fusion events involving *FGFR2* are predominant in Udt-gr, identifying a specific fusion-based patient group among these tumors (Fig. 1A-B). More generally, we observed SCNA to inversely correlate with SNV and, therefore, potentially compensate for the lack of SNV-associated genetic and pathway defects in these tumors. This agrees with pan-cancer studies that have identified trade-offs between mutational ('M-class') and structural/copy number ('C-class') (29), as well as large-scale pan-cancer pharmacogenomics studies that identify different contributions from diverse 'cancer functional events' (including mutation, structural alteration and DNA methylation) (41). Specifically, *METTL13* amplification was detected in more than 70% of the Udt-gr tumors with pan-cancer analysis revealing it to be most recurrent in cholangiocarcinoma. Previous studies have reported *METTL13* amplification in HCV-associated

hepatocellular carcinoma (42), conflicting with its downregulation in bladder cancer (43). Furthermore, its family member (*METTL3*) was recently uncovered to exert neoplastic properties in acute myeloid leukemia, in part through its role in RNA methylation (44), indicating METTL13 merits further investigation in iCCA.

To date, clinical trials in cholangiocarcinoma have suffered from both anatomical and molecular heterogeneity reflected in the limited translational and clinical progress made in the past 40 years (45, 46). Here, *in silico* analysis of significantly enriched pathways was successful in identifying broad signaling networks that, through patient stratification, could be exploited to induce enhanced growth arrest *in vitro*. This is further supported by convergent pathway-targeting by different mechanisms (e.g. metabolic subversion by SNV and DNA methylation in IDH-gr, immune insult by SNV and CNA in KRAS-gr). Importantly, lack of specific mutations did not dictate a complete absence of therapeutic response and similarly, co-mutations appeared to be capable of influencing therapeutic benefit (as evident in the dual *KRAS* and *IDH1* mutant RBE cell line). Nonetheless, our stratification successfully identified pathways most responsive to broad classes of repositioned drugs. In conclusion, this study demonstrates the pharmacogenomic potential of mutation- and pathway-driven genetic dissection of tumors. This highlights the potential for driver-gene guided oncogenic network characterization to enable efficient stratification and therapy optimization for intrahepatic cholangiocarcinoma patients, as well as other cancers.

DATA AVAILABILITY

Data is accessible at the European Nucleotide Archive with accession number PRJEB14974.

AUTHOR CONTRIBUTIONS

JBA, CN, CJO, DVO, AT conceived the idea, designed and implemented the study; CN, CJO, DVO, SS, AT, JBA, performed experiments and data

analyses; CN, CJO, DVO, JBA, interpreted omics data; JC, AB, CR, XWW, AL, LRR, JBA patient recruitment, clinical data collection and pathological assessment; CJO, DVO, AT, PG, KW, drug testing, assay development and performance; JBA, CJO, CN, wrote the manuscript; all authors read, edited and approved the manuscript.

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FIGURE LEGENDS

Fig. 1. Genomic alteration landscape of iCCA patients. (**A**) Distribution of the three most prevalently mutated genes, alongside *FGFR2* fusion events, in targeted sequencing (TS)- cohort (n=150). (**B**) Distribution of the three most prevalently mutated genes and *FGFR2* fusion events in whole exome sequencing (WES)-cohort (n=277). **C**) Lollipop plot of mutations reveal mutational hotspots in *IDH1* (R132C/G/L) and *KRAS* (G12A/C/D), while mutations in *TP53* are spread across multiple positions. (**D**) Total number of somatic nonsynonymous (SNVs and short indels) and synonymous mutations in WES-cohort (n=142, paired tumor/normal). (**E**) Mutational catalogue of 45 genes along with their significance score (reported by MuSiC), mutation frequency and select risk factors in WES-cohort (n=142, paired tumor/normal). The genes are sorted based on significance score.

Fig. 2. Mutational spectra in iCCA across four groups. (**A**) Distribution of the 96 substitution patterns, defined by the adjacent 5'- and 3'- sequence of the mutated nucleotide, reveal distinct mutational signatures are preferred across

groups. (**B**) Heatmap represents the frequency of 96 substitution patterns for each patient across four mutational subgroups. The numbers of mutations are scaled to 100 and color represents the percentage.

Fig. 3. Comparison of genes encoding nonsynonymous mutations across four groups. (**A**) A large fraction of genes mutated across four subgroups are unique to each subgroup. (**B**) Distribution of recurrently mutated genes that are unique to each group. (**C**) Significantly mutated genes reported by genome MuSiC. Each bubble represents a gene. The size of each bubble is proportional to the gene's mutational frequency. Genes are sorted alphabetically along x-axis and y-axis indicates $-\log_2(P\text{-value})$. (**D**) Circos plot representing the interaction between three classifier genes and other significant genes (representing potential co-driver and passenger genes). The width of the ribbon represents the interaction count, where the smallest width represents a single interaction. (**E-H**) Kaplan-Meier analysis reveals differences in recurrence rates and overall survival between mutational subgroups across 3 different patient cohorts.

Fig. 4. Enrichment of distinct signaling pathways and pharmacogenomic consequences across four mutational subgroups. (**A**) KEGG analysis indicates preferential association of distinct pathways with mutational subgroups. Z-score are computed from MuSiC *P*-values of the pathways by using scale function across groups in R, followed by hierarchical clustering. (**B**) Connectivity of mutated genes across eight pathways. The numbers in boxes represent the percentage of patients in specific mutational subgroups. Different colors represent the four groups. (**C**) Schematic of high-throughput drug repositioning experiments. (**D**) Differential sensitivity of mutational subgroups to diverse compounds. Heatmaps represent mean Drug Sensitivity Scores (DSS) per mutational subgroup, as quantified by viability effects of biologically active compounds (DSS > 10) across 7 CCA cell lines. (**E**) 21 drugs targeting specific pathways and processes established as enriched in specific mutational subgroups.

Fig. 5. Contribution of somatic copy number alterations (SCNAs) across four

mutational subgroups. (**A**) TP53-gr and Udt-gr have higher amplification and deletion frequencies compared to IDH-gr and KRAS-gr. (**B**) Frequencies of SNV and SCNA are inversely correlated. (**C**) Significant recurrent amplifications (red) and deletions (blue) reported by GISTIC2. X-axis on the bottom represents q-values of false discovery rate (FDR) and x-axis on top defines G-score (represents amplitude of aberration and frequency of occurrences across samples). Black horizontal line indicates FDR of 0.1. Y-axis represents the chromosomes. (**D**) The frequency of copy number gain and loss of genes across four subgroups. Each bubble represents a gene and the size of bubble indicates the total frequency of gain and loss. (**E**) Inter-group pathway-association of genes encoded in recurrent SCNA segments.

Fig. 6. Genome-wide DNA methylation analysis of mutational subgroups. (**A**) Kaplan-Meier analysis of DNA methylation cohort. (**B**) Hierarchical clustering of top 1% most variable probes. Each mutational subgroup is represented by geometric mean of probe methylation within that group. Number of DMRs are scaled against most epigenetically dysregulated group. (**C**) KEGG pathway analysis of total DMRs by patient subgroup. Significance was set at Q-value < 0.05. (**D**) *METTL13* amplification DNA methylation signature compared to Udt-gr and surrounding normal tissue. Probes are unique to amplification positive patients compared to surrounding normal with minimum methylation difference of 0.2 to Udt-gr. (**E**) Kaplan-Meier analysis of *METTL13* amplification positive and negative patients in TCGA cohort. (**F**) KEGG pathway analysis of *METTL13* amplification positive DMRs. Black bars indicate Q-value, grey bars indicate P-value. DMR: Differentially Methylated Regions.

Fig. 7. Mutation-centric diversity of cholangiocarcinogenesis. Incidence of SNV, recurrent SCNA and differentially methylated regions across groups are shown as a relative ratio (scaled to 1). Integrating 'omic' and pathway analysis, confirmed by *in vitro* drug testing, suggests enhanced activity of specific compounds in specific mutational subgroups.

SUPPORTING FIGURE LEGENDS

Supporting Fig. S1. Schematic representation of patient cohorts and experimental pipeline used to analyze data. (**A**) Workflow depicting the sequential flow of different patient cohorts and different data types (from various sources) analyzed in the study. (**B**) Raw sequence reads were mapped to the human genome (hg19) using BWA and were further processed to contain only high quality mapped reads. Multiple tools were used for variant (SNV and indels) calling and somatic copy number alterations (SCNA). Variants were further filtered to remove germline and low confidence variants, thus resulting high confidence SNV and SCNA.

Supporting Fig. S2. Mutational landscape and *FGFR2* fusion status of targeted sequencing (TES-) and whole exome sequencing (WES)-cohorts. (**A**) Mutational catalogue of 48 genes in TES-cohort (n=150) alongside qPCR- and sequencing-based assessment of known *FGFR2* fusions. (**B**) Mutational catalog of *TP53*, *KRAS* and *IDH1* with incidence of *FGFR2* fusion events across WES-cohort (n=277) along with additional information regarding HBV infection, ethnicity and availability of matched normal for tumor samples. WES samples with only tumor samples have higher predicted SNVs compared to matched tumor/normal samples. (**C**) Representative sequencing results spanning fusion points from *FGFR2* exon 19 to *BICC1* exon 3 (n=15) and to *BICC1* exon 5 (n=3). Alternative splicing is possible within the same patient sample. (**D**) Kaplan-Meier overall survival analysis of *FGFR2* fusion events with respect to Udt-gr in iCCA patients.

Supporting Fig. S3. Mutational and transcriptomic spectra of iCCA across four groups. (**A**) The frequencies of mutational spectra are represented as heatmaps, where each row represents a patient. (**B** and **C**) Non-matrix factorization (NMF) and hierarchical clustering of genetic substitution patterns in patients (**B**) and CCA cell lines (**C**), respectively. (**D**) Hierarchical clustering of significantly deregulated genes (F-test, nominal $P<0.001$) in an independent cohort of 135 patients.

Supporting Fig. S4. Heatmap of motifs enrichment among SNVs across

mutational subgroups. Scale bar represents motif enrichment above background, as computed with HOMER.

Supporting Fig. S5. Genes encoding somatic synonymous mutations, list of significantly mutated genes and comparison with nonsynonymous mutation. (**A**) Majority of genes encoding synonymous mutations are largely unique across each group. (**B**) Genes encoding synonymous mutations have minimum overlap with genes encoding nonsynonymous mutations. (**C**) Genes encoding synonymous mutations did not reveal significantly mutated genes within the group, which is different compared to nonsynonymous mutations in each group. Each bubble represents a gene and bubble size represents count. X-axes are sorted alphabetically based upon gene name and y-axis indicates $-\log_2$(*P*-value).

Supporting Fig. S6. KEGG pathway analysis using alternative classifier genes and resulting subgroups. The successive three most recurrently mutated genes (*CDC27*, *ARID1A* and *BAP1*) were used to group patients instead of *IDH1*, *KRAS* and *TP53*, with those wild type (i.e. no nonsynonymous mutations in *CDC27*, *ARID1A* and *BAP1*) classified as "remaining". Three control groups showed no specific enrichment, as all terms are enriched in "remaining" group.

Supporting Fig. S7. Recurrent somatic copy number alterations (SCNA) among groups. (**A**) *TP53*- and Udt-gr have more recurrent SCNA segments (and underlying genes) compared to *IDH1* and *KRAS* groups. No significant difference in length of SCNA segments exists between groups. (**B**) Mutational subgroups have few recurrently altered cytobands (reported by GISTIC2) in common. The cytoband 9p21.3 that encodes *CDKN2B* and *CDKN2B-AS1* genes is significantly recurrent in all groups. Cancer-related genes listed in COSMIC database are shown for each group. (**C**) Distribution of transposons around recurrent SCNA segments. (**D**) Incidences of recurrent somatic microsatellite instability (MSI) revealed no differences among subgroups. (**E**) SCNA burden displayed no differences among TP53- and Udt-gr patients when stratified by HBV status. (**F-G**) No common recurrent SCNA were

shared by HBV positive patients across TP53- and Udt-gr. X-axis on the bottom represents Q-values of false discovery rate (FDR) and x-axis on top defines G-score (represents amplitude of aberration and frequency of occurrences across samples). Black horizontal line indicates FDR of 0.1. Y-axis represents the chromosomes.

Supporting Fig. S8. Incidence and implications of *METTL13* alterations. (**A**) Comparison of *METLL13* alterations across 51 different cancers reveal it to be most frequently altered in intrahepatic cholangiocarcinoma. **(B**) *METTL13* amplification status is positively correlated with its expression. (**C**) *METTL13* methylation is inversely correlated with its amplified status. (**D**) *METTL13* expression is inversely correlated with its methylation status.

SUPPORTING TABLES

Table S1: Clinicopathologic features of patients in TES cohort (n=150)

Table S2: Clinicopathologic features and WES mapping statistics of 15 novel iCCA patients

Table S3: WES libraries used in the study (n=277)

Table S4: Predicted nonsynonymous SNVs and indels

Table S5: Predicted synonymous SNVs

Table S6A-E: List of mutated genes, unique genes and recurrent genes in each group

Table S7: Significantly mutated genes across four groups

Table S8: Enriched KEGG pathways among SNV-affected genes

Table S9: Drug repositioning

Table S10: Recurrent CNA cytobands across each group

Table S11: Genes that are significantly amplified or deleted within recurrent CNA

Table S12: Enriched KEGG pathways among CNA-affected genes

Table S13: Genome-wide DNA methylation analysis

Table S14: Enriched KEGG pathways among differentially methylated regions

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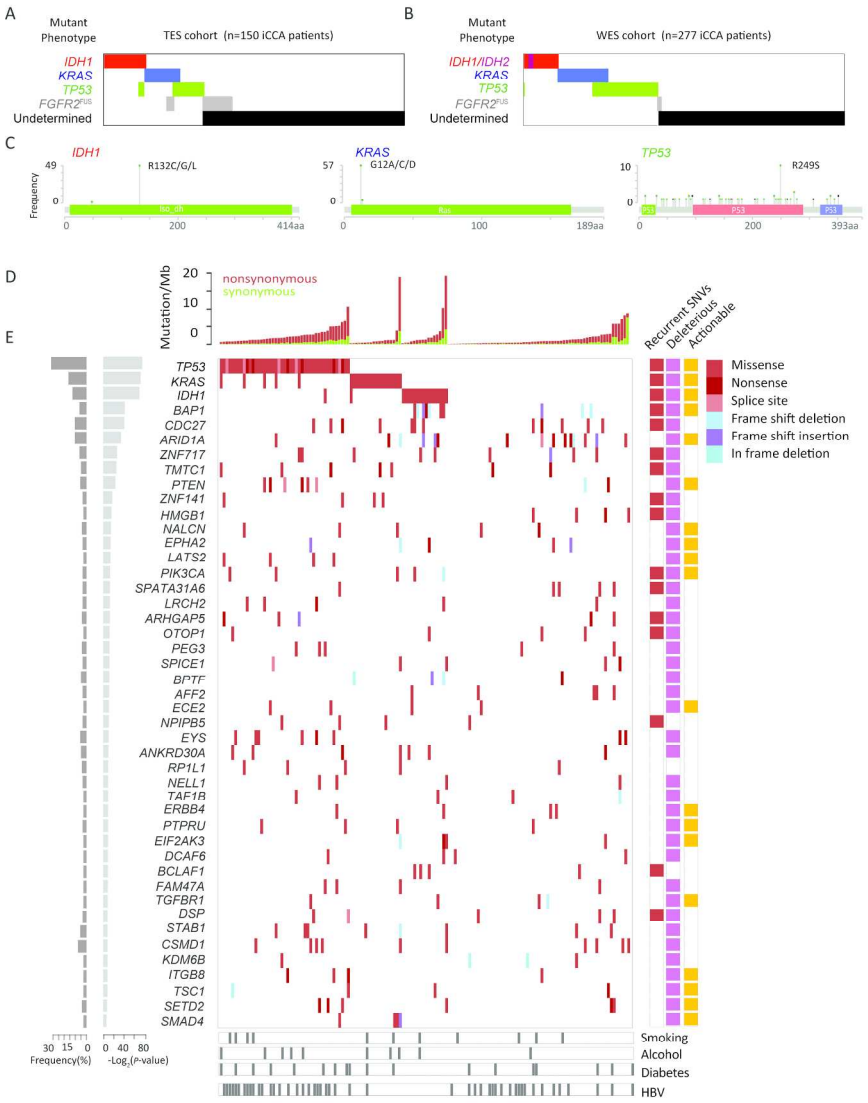

Figure 1

Figure 1

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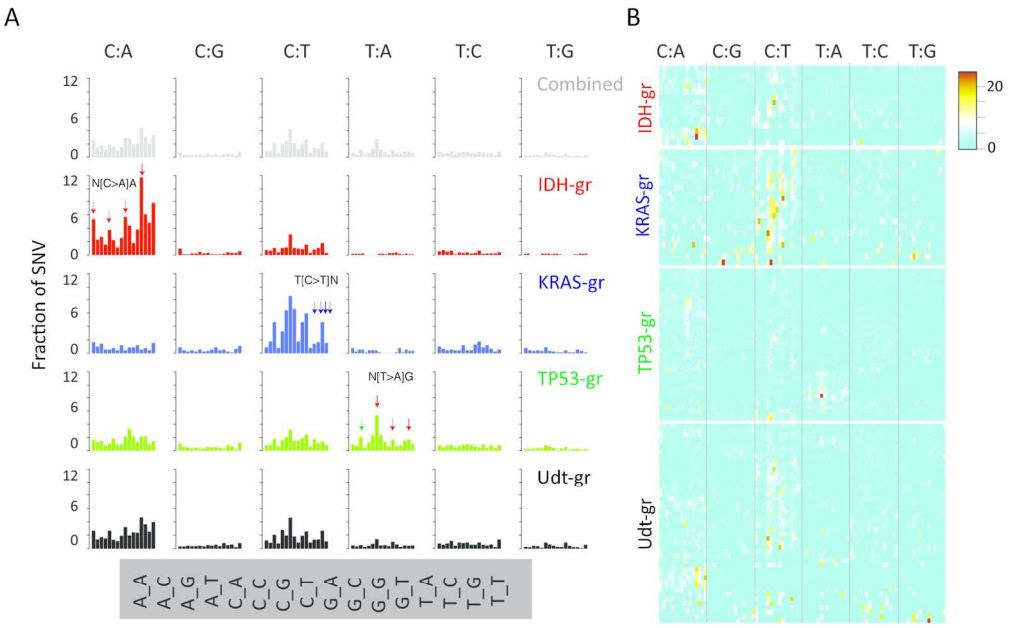

Figure 2

Figure 2

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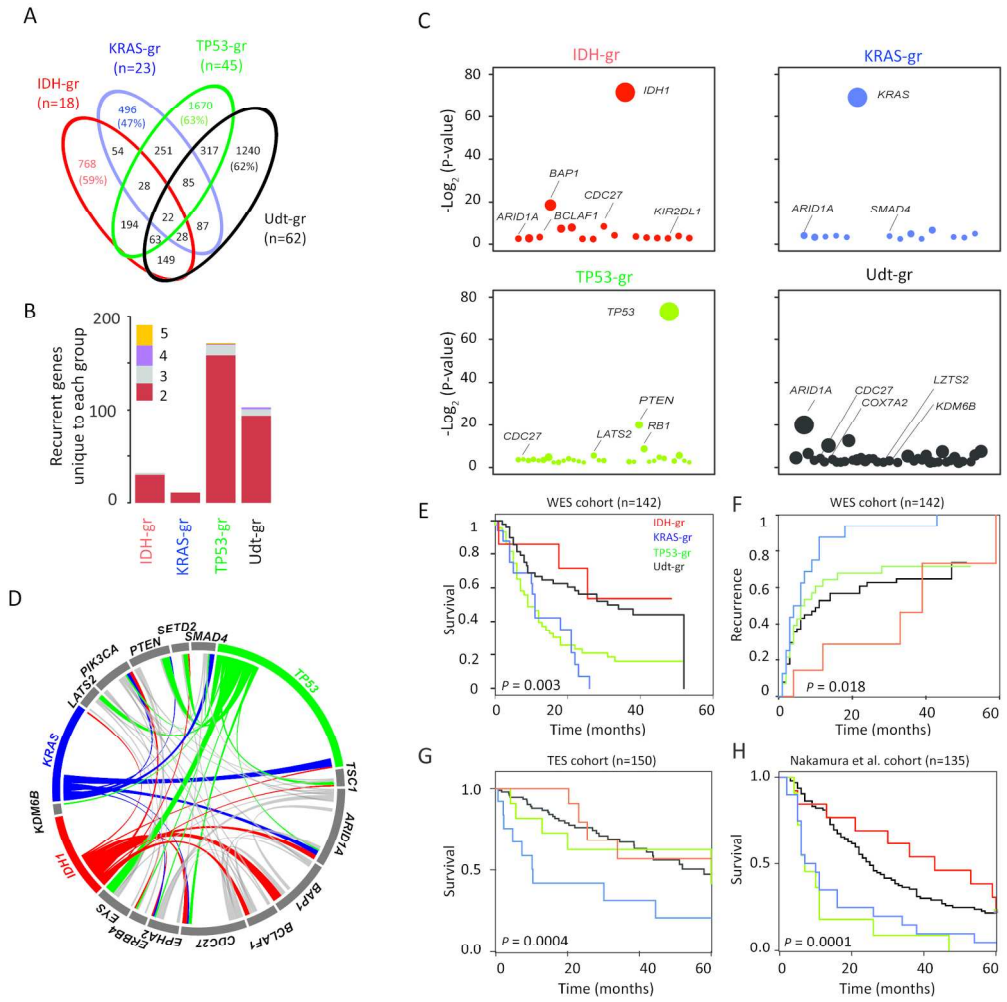

Figure 3

Figure 3

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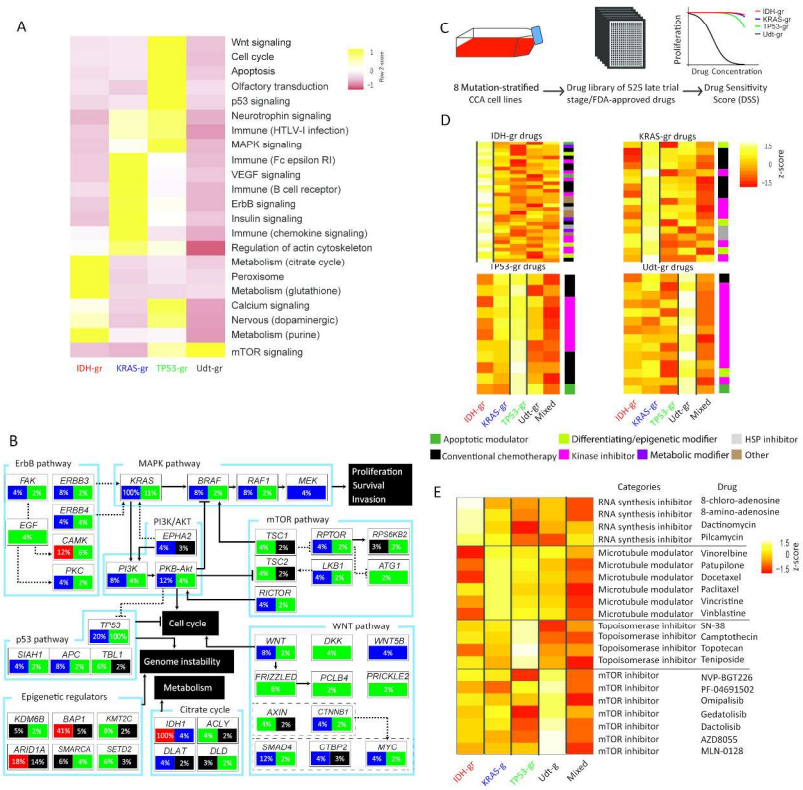

Figure 4

Figure 4

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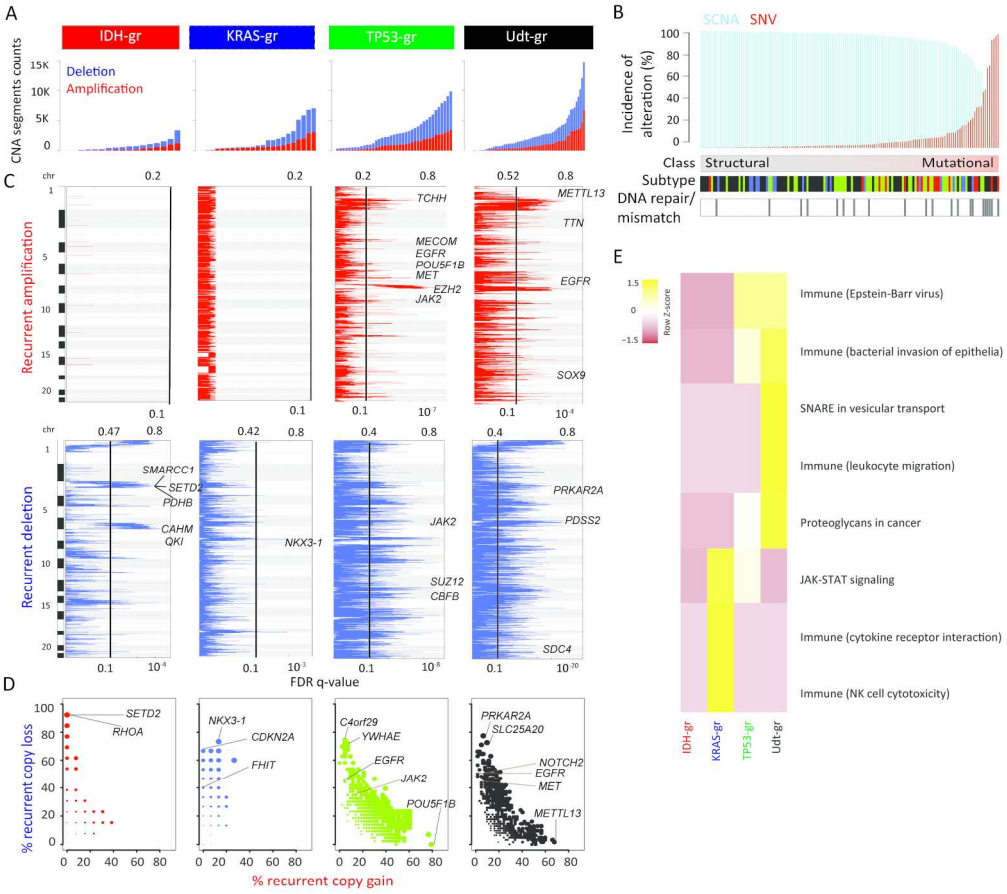

Figure 5

Figure 5

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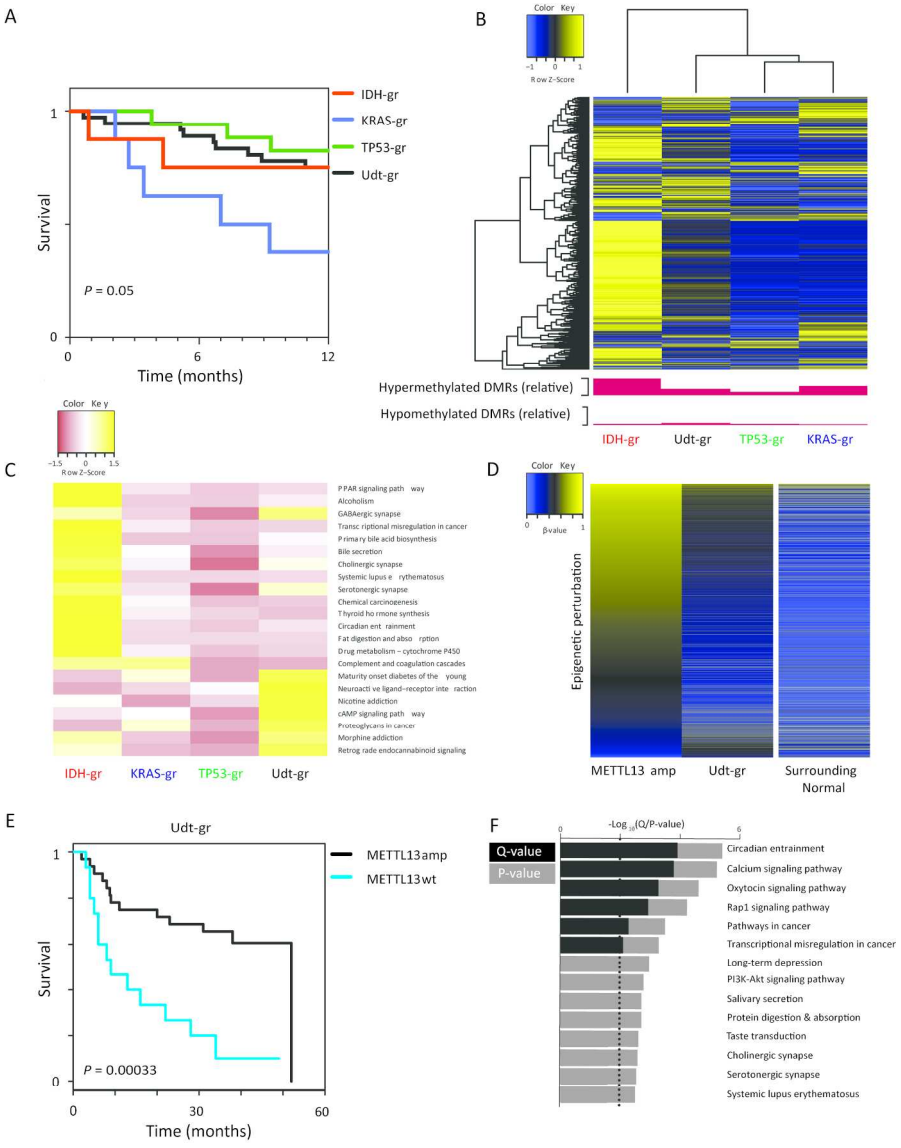

Figure 6

Figure 6

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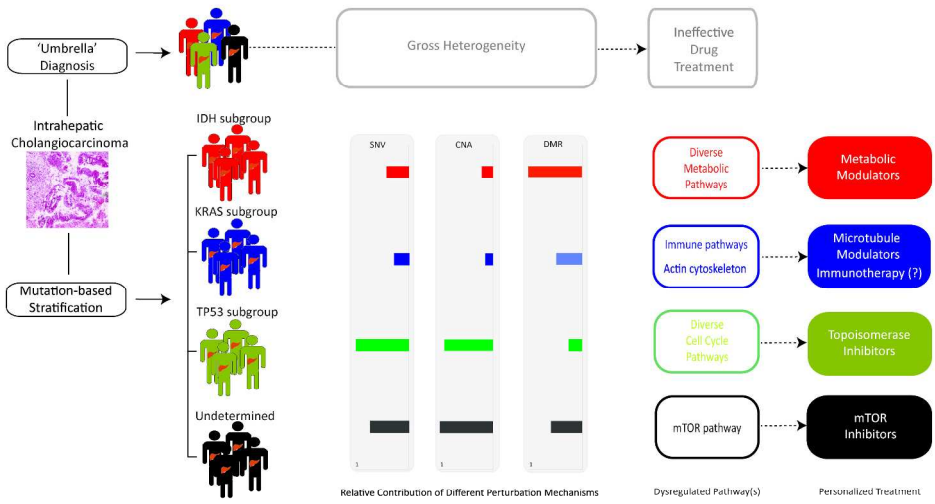

Figure 7

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SUPPORTING INFORMATION

Genomic DNA extraction, exome capture, library construction and sequencing

Genomic DNA was isolated following manufacturer's protocol (AllPrep Universal kit, Qiagen). Quality control and quantification were performed using Qubit fluorescent dsDNA HS assay (ThermoFisher) and loaded on a 0.8% agarose gel. Exome capture, library construction and sequencing were performed at the ATC facility at NIH, USA. Agilent in-solution enrichment was used with biotinylated oligonucleotide probe library (SureSelect Human All-Exon kit v4-70Mb, Agilent Technologies) according to manufacturer's recommendations, and sequenced on an Illumina HiSeq 2000 sequencer as 101bp paired-end reads. Base calling and pre-analysis were performed using RTA v1.12 and CASAVA v1.8.2 pipelines (Illumina). Each sample was sequenced to an average coverage of 220x (ranging from 115x to 303x) with >90% of the targeted regions covered (Table S2).

Targeted exome sequencing was performed using the 48-gene TruSeq Amplicon Cancer Panel (TSACP, Illumina). Genomic DNA was extracted as described above. Library construction and sequencing were performed according to manufacturer's instruction, and sequenced on an Illumina MiSeq as 2x150bp reads to an average depth of >1000X. A total of 23 samples (and PhiX sequencing control) were loaded on each flow cell. Data were analyzed real time using the somatic variant caller (SVC). Called variants were further filtered based on i) coverage (minimum 1000 reads), ii) overlapping germline mutations and iii) dbSNP142.

Dataset analyses

All bioinformatics analyses were done using Perl, bash and R scripts including multiple tools and software described below. We performed high coverage WES on genomic DNA isolated from tumor and adjacent normal liver tissues from 15 iCCA patients. An additional 127 tumors and matched normal samples from previous studies (accession ID: PRJEB4445; SRP025150; GSE63420; SRP045202) (1-4) and 135 tumors were downloaded from EGA (Table S3). We processed raw sequences (FASTQ files) to filter low quality reads and trimmed adapter sequences (if present). Resulting sequences were mapped to the human genome assembly (hg19) using BWA (5). Mapped BAM files were filtered to remove PCR duplicates and excluded multi-mapping reads using samtools (6).

Only unique mapping reads were used for downstream analysis. The purity of the samples were computed using BubbleTree (7) with an average purity of the samples at 0.85 (ranged from 0.42-1). Average as well as range of purity across the four subgroups are similar.

Transposons elements were downloaded from UCSC genome browser (8) and focused only on SINE, LINE and LTR elements. We compared the distribution of transposons around 200 KB of gene transcription start sites (TSS). As some genes are in close proximity, we clustered the genes within 50 KB. The TSS of the clustered regions was expanded by 200 KB on both sides and the number of transposons in each expanded region was counted. Microsatellite instability detection was performed using MSIsensor with default parameters (9).

Annotation and prioritization of SNVs and short indels

We used a combination of Varscan2 (v2.3; (–mpileup 1) (10)), somaticSnipper (v.1.0.4; -q 1 –Q 15) (11) and shimmer (12) to make initial somatic SNV calls. To select high confidence somatic SNVs, we first used filtering scripts provided by each tool. Varscan2 predictions were filtered by *processSomatic* (--max-normal-freq 0.075 –min-tumor-freq 0.15) and *somaticFilter* (–indel-file –min-coverage 8 –min-reads 3 –min-var-freq 0.15). SomaticSnipper predictions were filtered by *snpfilter.pl* (default parameters) and *highconfidence.pl* (–Q 25). Secondly, we excluded SNVs overlapping with common SNPs from dbSNP142 (13). We also compiled high confidence germline mutations from 142 iCCA samples and thus excluded them from predicted somatic SNVs. Thirdly, we ensured predicted SNVs had a minimum coverage of 8 (tumor) and 6 (normal) reads and a minimum 3 reads in a variant allele. In addition, the variant allele should be ≤7.5% of total reads in normal, while the variant allele in tumor must be ≥15% of total reads. Fourthly, SNVs proximal (within 10 bases) to indels and SNVs in clusters (two or more SNVs within 10 bases) were excluded. Short indels were predicted using varscan2 and filtered using the same criteria as mentioned above for SNVs. In cases of patients with dual mutations in either *KRAS, IDH1, IDH2* or *TP53*, these cases are included for analysis in both subgroups. As a control, co-mutated samples were also excluded but this did not result in any different outcome across the analyses.

High confidence SNVs and indels were annotated as synonymous and nonsynonymous using Annovar (14) and focused only on exonic variants. The potential impact of an amino acid substitution on structure and function of human protein was analyzed by PolyPhen-2 (15). To identify enriched motifs, we selected promoter regions (500 nucleotides up- and downstream of transcription start sites) for each gene across four groups and employed HOMER tool to identify motifs enriched in the region compared to background (16). For the inference of mutational signatures by non-matrix factorization and the hierarchical clustering prediction, the patient data were analyzed by SomaticSignatures (17).

Identification of significantly mutated genes and enriched pathways

The significantly mutated genes encoding SNVs and indels were estimated using genome MuSiC (18) by using --merge-concurrent-muts. VCF annotations are converted to MAF annotations by using vcf2Maf script and used as input to genome MuSiC. From the list of significant mutated genes reported, we used *P*-value cut-off ($P < 0.05$) and a minimum of 2 counts in each group. The significantly altered pathways were identified using genome MuSiC and incorporated KEGG pathway database (19). For the enrichment of pathways based on recurrent CNAs, we used ConsensusPathDB (20) and KEGG pathway database.

Annotation of Somatic Copy Number Alterations

Raw copy number for each tumor/normal sample was predicted using VarScan2 (*copynumber*). Raw copy number calls were analyzed using Circular binary segmentation (CBS) from DNAcopy (21). On average, VarScan2 reported 171,400 raw copy number regions per exome and CBS analysis yielded 1,357 segments. The resulting segments were merged using MergeSegments algorithm (mergeSegments.pl) and classified as amplification (log ratio > 0.25), deletion (log ratio < -0.25), or neutral (between -0.25 and 0.25). Amplifications and deletions were categorized as large-scale if they encompassed at least 25% of the chromosome arm or, otherwise, focal. For recurrent CNAs, raw copy number calls from VarScan2 were directly fed to GISTIC2 (22). GISTIC2 outputs significantly amplified and deleted arms and the enriched peak within the arms. The coordinates of the peaks were intersected with gene coordinates and identified amplified

or deleted genes within the arms. *FGFR2* fusion events were investigated using BreakDancer (23).

Gene sets excluded

Meta-analysis of mutational heterogeneity across multiple cancers have shown that some members of certain gene families, such as, *MUCIN*, *NEUROBLASTOMA BREAKPOINT FAMILY* and *TTN* are significantly mutated across multiple cancers (24). Similarly, we observed *TTN*, *MUCIN* (*MUC4, MUC16, MUC17, MUC14*) and *NEUROBLASTOMA BREAKPOINT FAMILY* (*NBPF20, NBPF18, NBPF12, NBPF14*) are enriched in all groups. These genes are unlikely to have association in the context of iCCA pathogenesis and thus excluded from downstream analysis.

Transcriptome analysis

Two gene expression datasets (25, 26) were analyzed to assess the degree of transcriptional (dis)similarity of mutational subgroups. Significantly informative transcripts were identified by F-test ($P < 0.001$).

Detection of *FGFR2* fusion events

In the TES cohort, 122/150 tumors and matched normal tissues were analyzed for *FGFR2* fusions. RNA was isolated from fresh frozen tumor tissues using AllPrep Universal kit (Qiagen) and 1µg subjected to reverse transcription with SuperScript VILO cDNA Synthesis kit (Thermo Fisher Scientific). Fusion products in *FGFR2* were targeted with primer pairs flanking breakpoints of *FGFR2* and previously reported donor genes. Quantitative PCR reactions were run in duplicates with Maxima SYBR Green/ROX qPCR Master Mix 2X (Thermo Fisher Scientific) on CFX Connect ThermoCycler (BioRad) with 40 cycles of 95°C for 30 secs, primer-dependent annealing temperature for 30 secs and 68°C for 1 min. Commercially synthesized DNA with *FGFR2* and all known fusion partner sequence fragments (Integrated DNA Technologies) were cloned into plasmid scaffolds and used as positive controls. Samples showing positive signal in qPCR were re-amplified with Platinum Taq DNA Polymerase High Fidelity and cloned into TOPO TA Cloning vector (Thermo Fisher Scientific) with fusion status subsequently confirmed by Sanger sequencing following bacterial expansion.

Cell culture and mutational subgrouping

Cholangiocarcinoma cell lines were purchased from KCLB (SNU-478, SNU-1079, SNU-1196), DSMZ (EGI-1), RIKEN (HuCCT-1, RBE), and obtained from Mayo Clinic (WITT, KMCH). All cell line identities were verified by STR analysis at time of purchase and routinely mycoplasma tested. Cells were cultured in RPMI-1640 or DMEM-F12 (ThermoFisher Scientific), all supplemented with 10% heat-inactivated FBS (GE Healthcare), 1% penicillin-streptomycin and 1% L-glutamine (ThermoFisher Scientific). Cells were maintained at 37°C and 5% CO_2. A panel of 16 CCA cell lines was analyzed by targeted sequencing TruSeq Amplicon Cancer Panel (TSACP, Illumina) and a subset (n=7) by whole-exome sequencing. The mutational profiles were clustered using NMF from SomaticSignatures (17).

High-throughput drug repositioning and quantification of drug sensitivity

CCA cell lines for drug treatment were selected based on their mutational classification, identical to patient subgrouping. Drug screening was carried out using a drug library of 525 compounds (FDA-approved or in late stage clinical trials) across 8 CCA cell lines treated for 72 hours over 5-fold dilution series. Anti-proliferative cellular effects were measured with CellTiter-Glo Luminescent Cell Viability assay (Promega), as per manufacturers' instructions, and quantified using Drug Sensitivity Score (DSS) metric (27). Compounds with DSS > 10 were deemed to be significantly biologically active.

Genome-wide DNA methylation profiling

DNA was subjected to bisulfite modification using EZ DNA Methylation-Gold kit (Zymo Research). Genome-wide methylation profiling experiments were carried out using Infinium HumanMethylation450 BeadChips (Illumina), as per manufacturer's instructions. Bead chips were scanned using iScan system (Illumina) and resulting IDAT files analyzed using RnBeads (version 1.2.1) (28). Briefly, SNP-enriched probes (>2 SNPs in 50 base pair probe sequence), X chromosome probes and poor quality probes (as determined by Greedycut algorithm) were excluded. Data were normalized using Beta Mixture Interquartile (BMIQ) normalization (29) and processed methylation values exported as β-values. Differentially methylated probes (DMPs) and differentially methylated regions (DMRs) were computed using the RnBeads-integrated limma method (hierarchical linear

model) followed by model fitting using an empirical Bayes approach. Pathway enrichment analysis was carried out via KEGG database (19).

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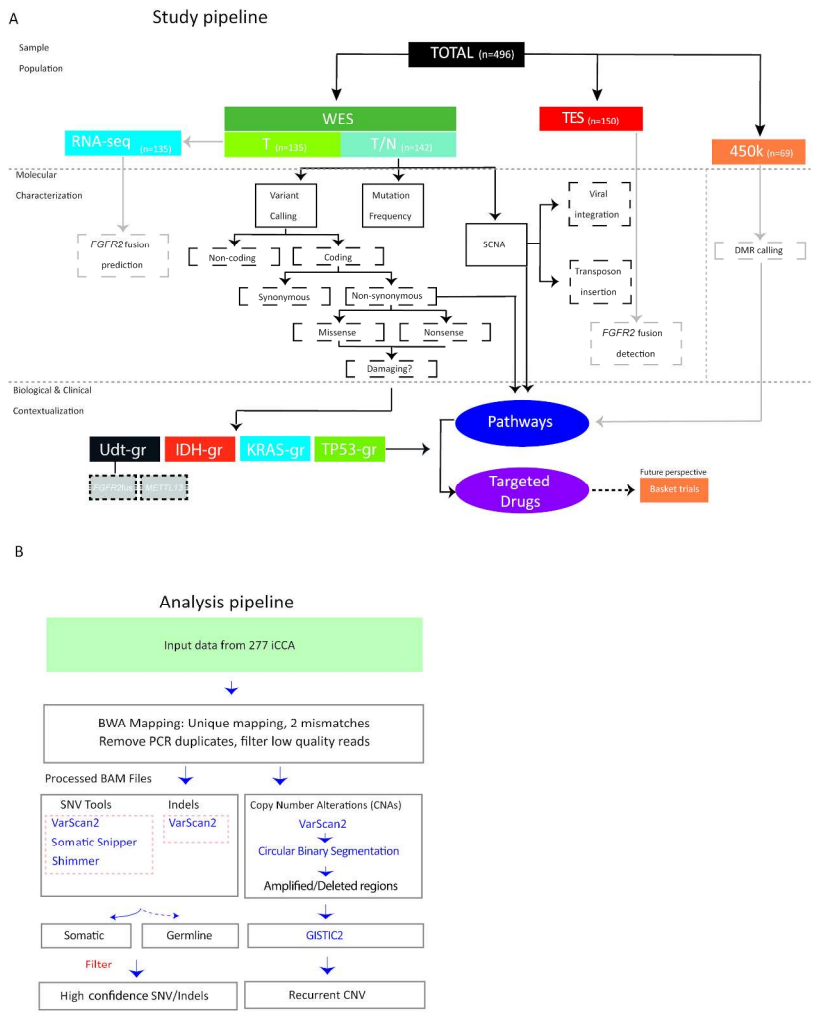

Supporting Figure S1

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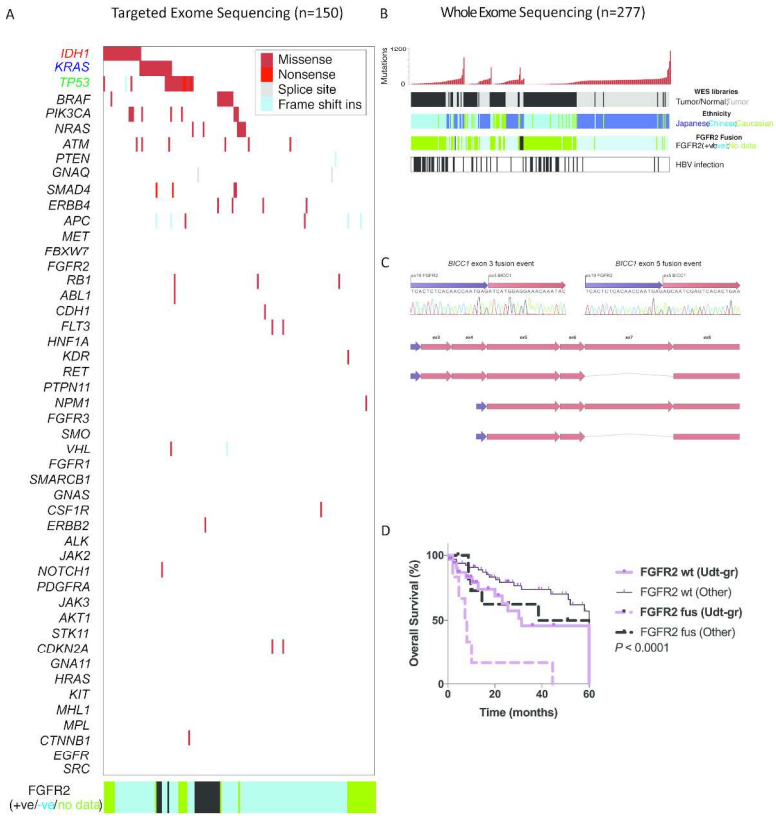
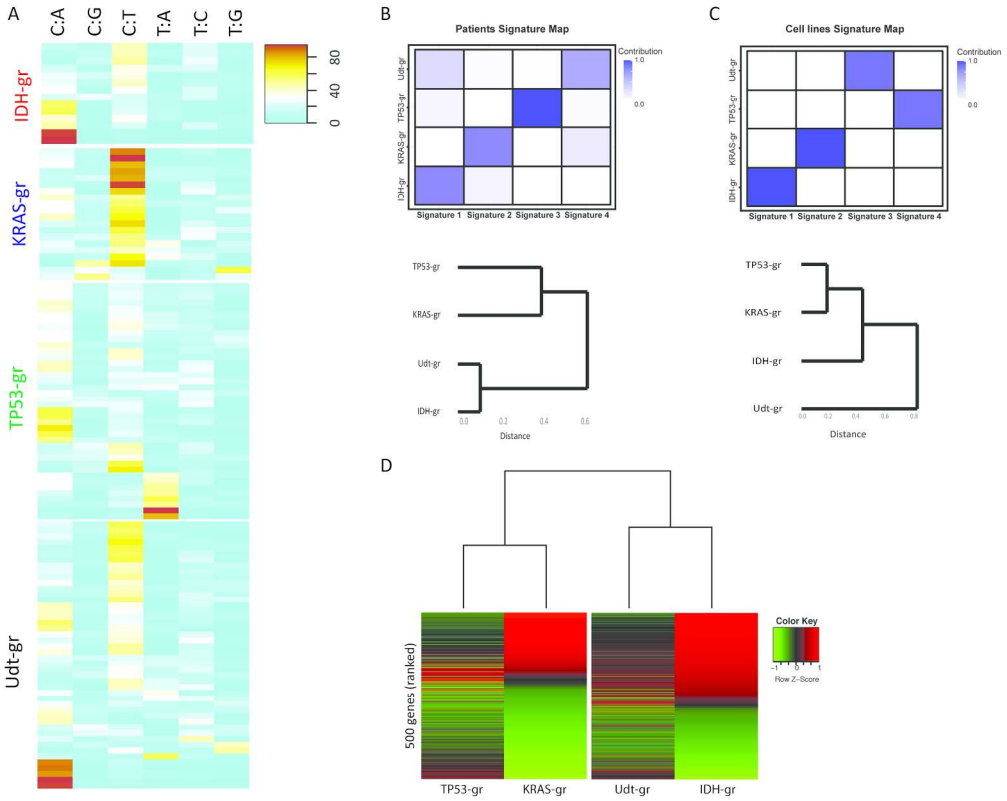


Supporting Figure S2

270x297mm (300 x 300 DPI)



Supporting Figure S3

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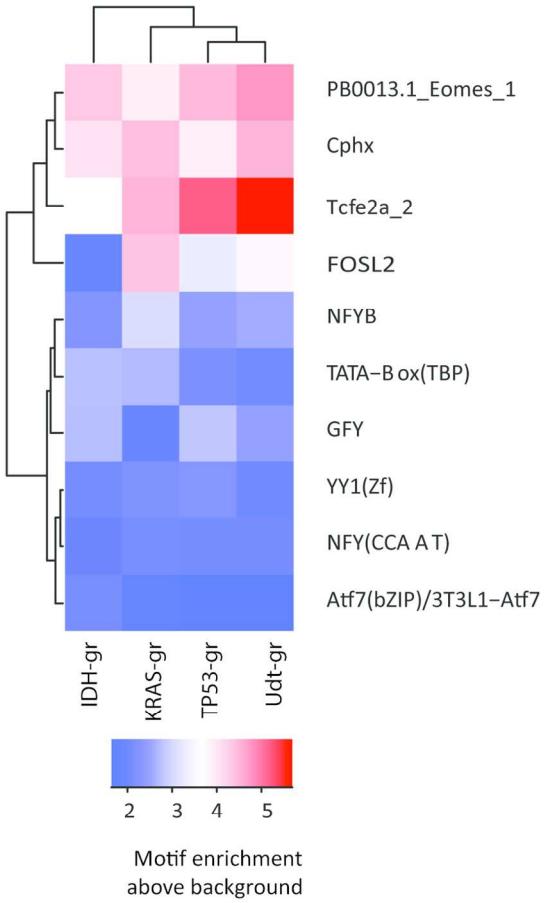
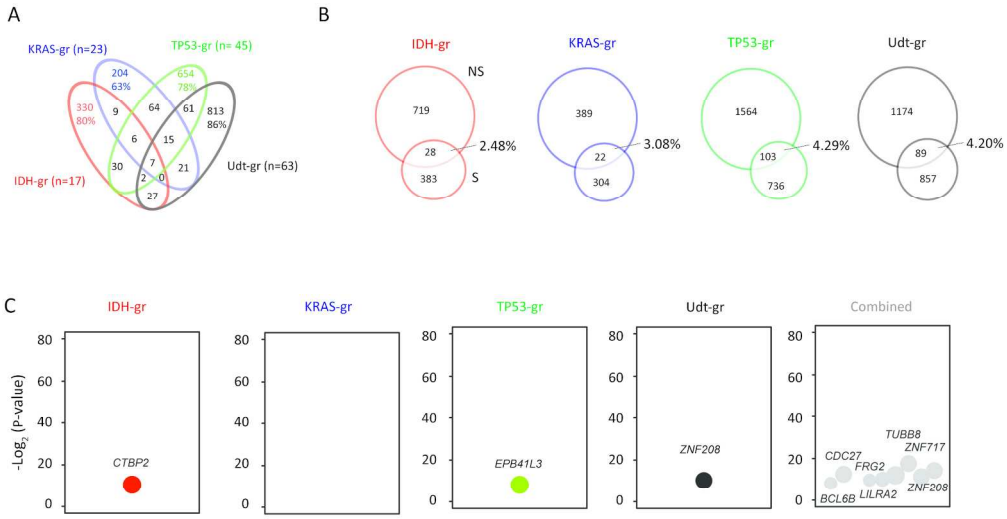


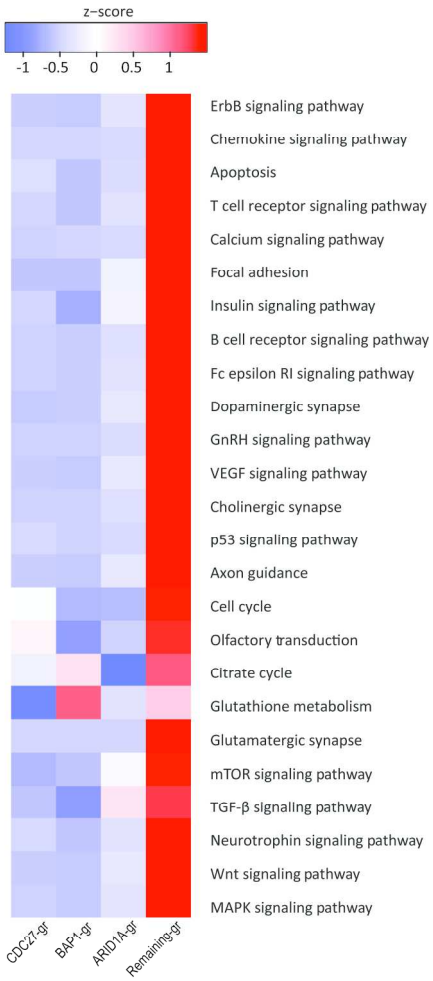
Supporting Figure S4

134x135mm (300 x 300 DPI)



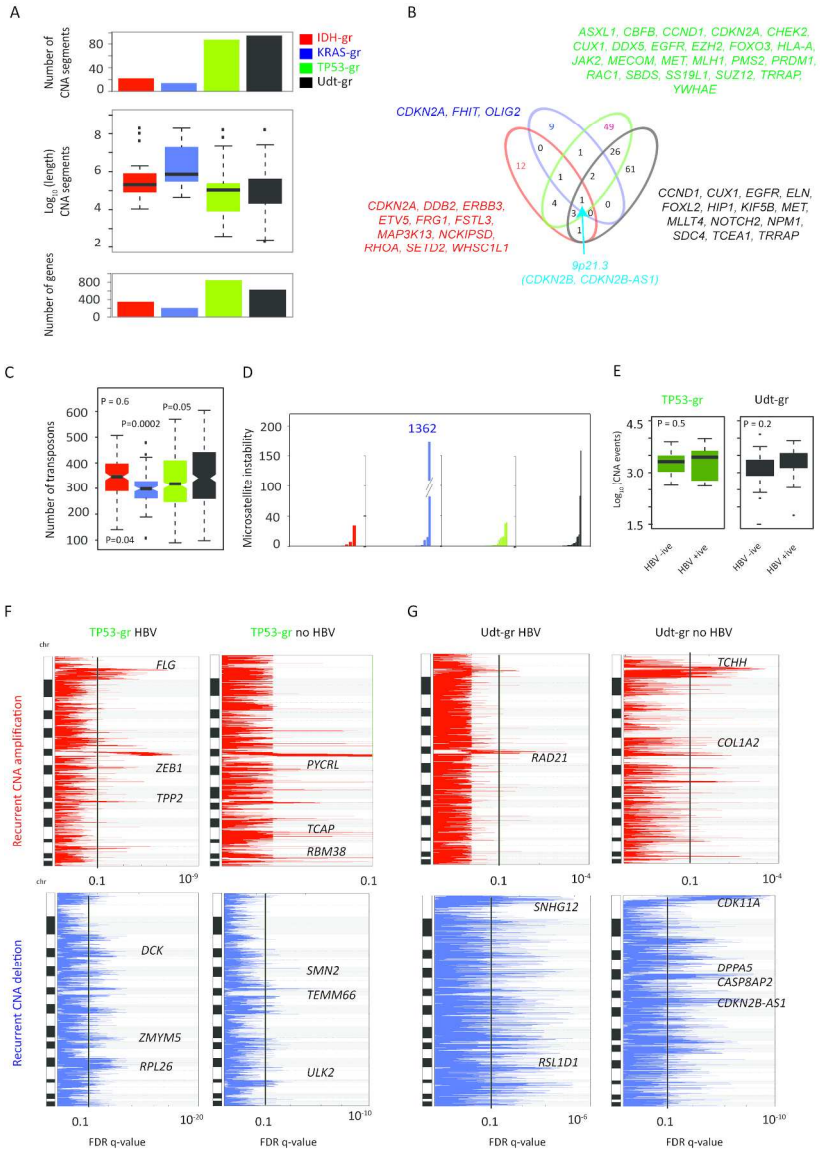
Supporting Figure S5

190x147mm (300 x 300 DPI)



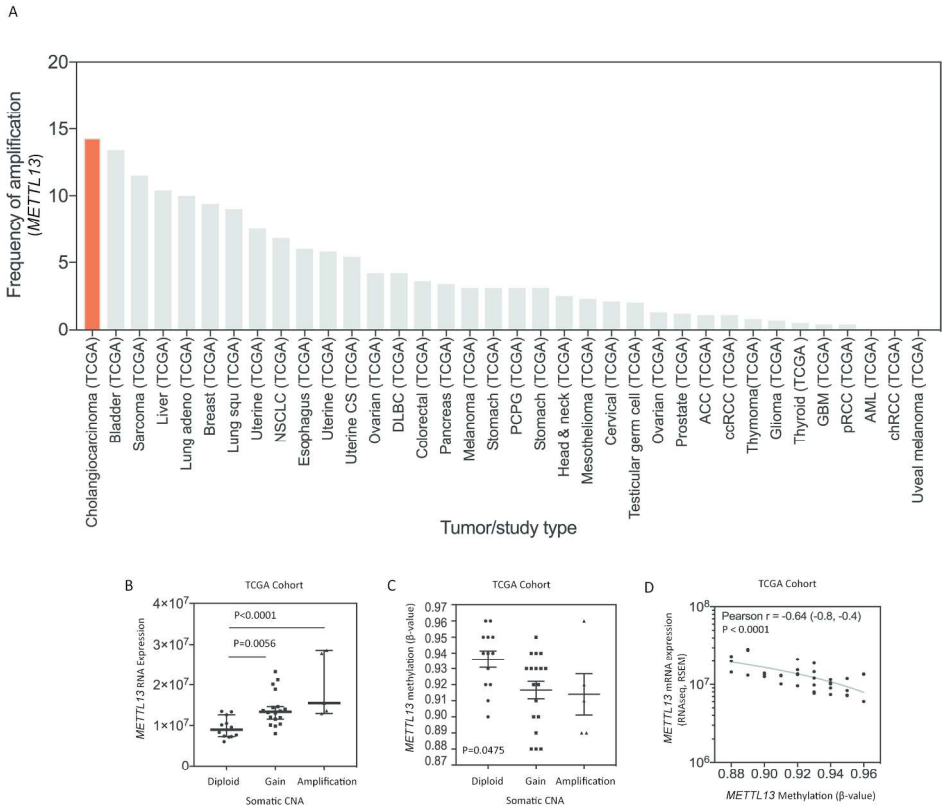
Supporting Figure S6

141x232mm (300 x 300 DPI)



Supporting Figure S7

196x286mm (300 x 300 DPI)



Supporting Figure S8

180x228mm (300 x 300 DPI)

Table S1: Clinicopathologic features of patients in targeted sequencing cohort (n=150)

Characteristics	Number
Total number of patients (Tumor versus Normal)	150
Tumor location (intrahepatic)	150
Age at diagnosis (years, median)	64 (range: 32-85)
Tumor size (mm, median)	60 (range: 5-200)
Gender *	
Female	67 (44.7%)
Male	79 (52.7%)
Stage grouping	
Stage 0	0 (0%)
Stage I	15 (10%)
Stage II	29 (19.3%)
Stage III	27 (18%)
Stage IVa	31 (20.7%)
Stage IVb	27 (18%)
ND	21 (14%)
Etiology	
Cholecystitis	9 (6%)
Steatosis	5 (3.3%)
PBC/PSC	2 (1.3%)
HCV	8 (5.3%)
HBV	5 (3.3%)
Alcohol	3 (2%)
Hemochromatosis	3 (2%)
Cryptogenic	114 (76%)
Resection Status (R0/R1/R2/ND)	
R0	114 (76%)
R1	12 (8%)
R2	2 (1.3%)
ND	22 (14.7%)
Lymph Node Status (N0/N1/Nx)	
N0	81 (54%)
N1	45 (30%)
Nx	24 (16%)
Metastatic Disease (M0/M1/Mx)	
M0	110 (73.3%)
M1	27 (18%)
Mx	13 (8.7%)
Recurrence status	
Yes	65 (43.3%)

No	79 (52.7%)
ND	6 (4%)
Lymphovascular Invasion (Yes/No/ND)	
Yes	90 (60%)
No	44 (29.3%)
ND	16 (10.7%)
Perineural Invasion (Yes/No/ND)	
Yes	100 (66.7%)
No	32 (21.3%)
ND	18 (12%)
Necrosis (Yes/No/ND)	
Yes	32 (21.3%)
No	16 (10.7%)
ND	102 (68%)

ND: Not determined or unknown status

* Gender was not recordered in 4 out of 150 cases

** Cryptogenic: no discernable disease-associated etiology

Table S2: Clinicopathologic features and WES mapping statistics of 15 novel iCCA patients

Characteristics	Number of patients
Total number of patients (Tumor versus Normal)	15
Tumor location (intrahepatic)	15
Age at diagnosis (years, median)	64 (range 45-80)
Tumor size (mm, median)	36 (range 20-125)
Gender	
Female	9 (60%)
Male	6 (40%)
Stage grouping	
Stage 0	0 (0%)
Stage I	0 (0%)
Stage II	3 (20%)
Stage III	4 (27%)
Stage IVa	6 (40%)
Stage Ivb	2 (13%)
Mutational status #	
IDH1 (R132G)	5 (33%)
KRAS (G12D)	5 (33%)
IDH2 (R172S)	1 (6.6%)
EGFR (28 sites)	0 (0%)
BRAF (V600E)	0 (0%)
FGFR2 fusions	0 (0%)
Etiology	
HBV (Yes/No)	0/15 (0%/100%)
HCV (Yes/No)	0/15 (0%/100%)
Alcohol (Yes/No)	0/15 (0%/100%)
Resection Status (R0)	15 (100%)
Lymph Node Status (N0/N1/Nx)	4/7/4 (26.7%/46.7%/26.7%)
Metastatic Disease (M0/M1/Mx)	12/3/0 (80%/20%/0%)
Lymphovascular Invasion (Yes/No/ND)	4/7/4 (26.7%/46.7%/26.7%)
Perineural Invasion (Yes/No/ND)	4/7/4 (33.3%/46.7%/20%)
Portal tract (Yes/No/ND)	2/10/3 (13.3%/66.7%/20%)
Necrosis (Yes/No)	0/15 (0%/100%)
Treatment (naive/palliative chemo/radiation)	12/3/1 (80%/20%/6.7%)

ND: Not determined or unknown status
Genomic DNA isolated from tumor and surrounding noncancerous liver tissue was analyzed for mutations of KRAS, BRAF, and EGFR by quantitative polymerase chain reaction–based assays approved for in vitro diagnostics (CE-IVD). The mutation test kits, which use allele-specific probes to identify the presence of 11 mutations in KRAS codons 12, 13, and 61, one mutation in BRAF (V600E) (EntroGen Inc, Torzana, CA), and 28 mutations in EGFR (Qiagen, Valencia, CA), are designed to detect a low percentage of mutant DNA in a background of wild-type genomic DNA.

WES mapping statistics of 15 iCCA patients					
Patient-ID	**Tissue**	**Mapped reads**	**Coverage**	**% Coverage of targeted region**	**% Coverage of targeted region with >30X coverage**
Patient_ST1_CC008T	Tumor	103425888	161X	95.30	79.55
Patient_ST2_CC008N	Normal	94256664	146X	95.04	77.03
Patient_ST3_CC010T	Tumor	106977362	166X	94.70	73.76
Patient_ST4_CC010N	Normal	74401192	115X	94.34	76.11
Patient_ST5_CC011T	Tumor	117136364	182X	94.68	73.13
Patient_ST6_CC011N	Normal	101140328	157X	94.42	75.61
Patient_ST7_CC021T	Tumor	169775164	264X	94.63	76.40
Patient_ST8_CC021N	Normal	91151812	142X	94.33	75.51
Patient_ST9_CC035T_2	Tumor	142786976	222X	94.36	75.28
Patient_ST10_CC035N	Normal	99918490	155X	92.35	69.62
Patient_ST11	Tumor	192018644	299X	95.30	79.55
Patient_ST12	Normal	155966384	242X	95.04	77.03
Patient_ST13	Tumor	131491382	204X	94.70	73.76
Patient_ST14	Normal	145540306	226X	94.34	76.11
Patient_ST15	Tumor	125381786	195X	94.68	73.13
Patient_ST16	Normal	146177716	227X	94.42	75.61
Patient_ST17	Tumor	149189538	232X	94.63	76.40
Patient_ST18	Normal	143253156	223X	94.33	75.51
Patient_ST19	Tumor	137074370	213X	94.36	75.28
Patient_ST20	Normal	121192120	188X	94.06	72.29
Patient_ST21	Tumor	153780820	239X	94.63	76.53
Patient_ST22	Normal	170753926	266X	94.34	78.10
Patient_ST23	Tumor	150740628	234X	94.31	75.95
Patient_ST24	Normal	141119182	219X	94.18	75.32
Patient_ST25	Tumor	187929354	292X	95.40	78.87
Patient_ST26	Normal	173796182	270X	95.00	78.24
Patient_ST27	Tumor	192117450	299X	95.31	79.39
Patient_ST28	Normal	194790630	303X	95.34	79.65
Patient_ST29	Tumor	188424760	293X	95.43	79.00
Patient_ST30	Normal	156615274	243X	94.31	76.93

Table S3: WES libraries used in the study					
	WES (matched tumor/normal)		Targeted sequencing		Accession ID
Datasets	Patients	Type	Patients count	Genes	
Data generated for this study	15	iCCA	150	48	PRJEB14974
Chan-On et a.l (PMID: 24185513)	10	iCCA	-	-	PRJEB4445
Gao et al. (PMID: 24503127)	8	iCCA	-	-	SRP025150
Sia et al. (PMID: 25608663)	7	iCCA	-	-	GSE63420
Zou et al. (PMID: 25526346)	102	iCCA	-	-	SRP045202
Total	142				
	WES (only tumor)				
Nakamura et al (PMID: 26258846)	135	iCCA			EGA00001000950

Table S4: Predicted nonsynonymous SNVs and indels

Chr	Start	End	Gene	MutationType	NA	SNVType	Ref	Tumor_ref	Tumor_variant	DNSNP142	LibraryName	Annotation	EnsemblGeneID	EnsemblTranscriptID	Transcript	Mutation Description	Description
chr1	152285080	152285080	*FLG*	Nonsense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P10	p.S761*	ENSG00000143631	ENST00000368799	Transcript	stop_gained	NA
chr1	156954142	156954142	*ARHGEF11*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.S71Y	ENSG00000132694	ENST00000368194	Transcript	missense_variant	probably_damaging(0.987)
chr1	173265778	173265778	*ATP13A2*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.E323*	ENSG00000159363	ENST00000326735	Transcript	stop_gained	NA
chr1	208207871	208207871	*PLXNA2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.A1611S	ENSG00000076356	ENST00000367033	Transcript	missense_variant	probably_damaging(0.989)
chr1	225267167	225267167	*DNAH14*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.D895Y	ENSG00000185842	ENST00000430092	Transcript	missense_variant	possibly_damaging(0.814)
chr1	270927070	270927070	*ARID1A*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.G931*	ENSG00000117713	ENST00000324856	Transcript	stop_gained	NA
chr1	372717747	372717747	*GRIK3*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P10	p.G758S	ENSG00000163873	ENST00000373091	Transcript	missense_variant	probably_damaging(1)
chr1	46159087	46159087	*TMEM69*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.S85N	ENSG00000159596	ENST00000372025	Transcript	missense_variant	benign(0.005)
chr1	53980305	53980305	*GLIS1*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.R451W	ENSG00000174332	ENST00000312233	Transcript	missense_variant	probably_damaging(0.976)
chr1	6679876	6679876	*PHF13*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.R52M	ENSG00000116273	ENST00000377648	Transcript	missense_variant	probably_damaging(0.942)
chr10	105752404	105752404	*SLK*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.E122*	ENSG00000065613	ENST00000369755	Transcript	stop_gained	NA
chr10	11908641	11908641	*PROSER2*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.G84R	ENSG00000148426	ENST00000277570	Transcript	missense_variant	probably_damaging(0.918)
chr10	27326243	27326243	*ANKRD26*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.E857*	ENSG00000107890	ENST00000376087	Transcript	stop_gained	NA
chr10	96076322	96076322	*PLCE1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.D2051Y	ENSG00000138193	ENST00000371380	Transcript	missense_variant	benign(0.385)
chr11	130131419	130131420	*ZBTB44*	Frame_Shift_Ins	.	INS	-	-	C	novel	chan_et_al_P10	p.A117Gfs*22	ENSG00000196323	ENST00000525842	Transcript	frameshift_variant	NA
chr11	18339377	18339377	*HPS5*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.S10Y	ENSG00000110756	ENST00000349215	Transcript	missense_variant	possibly_damaging(0.837)
chr11	59623344	59623344	*TCN1*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.S312*	ENSG00000134827	ENST00000257264	Transcript	stop_gained	NA
chr12	123060103	123060103	*KNTC1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P10	p.A799V	ENSG00000184445	ENST00000333479	Transcript	missense_variant	probably_damaging(0.978)
chr12	55356855	55356855	*TESPA1*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.P276L	ENSG00000135426	ENST00000449076	Transcript	missense_variant	probably_damaging(0.977)
chr13	31850845	31850845	*B3GALTL*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.P263T	ENSG00000187676	ENST00000343307	Transcript	missense_variant	probably_damaging(0.93)
chr13	46425653	46425653	*SIAH3*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.V38F	ENSG00000215475	ENST00000400405	Transcript	missense_variant	possibly_damaging(0.809)
chr14	25443939	25443939	*STXBP6*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.T29K	ENSG00000168952	ENST00000323944	Transcript	missense_variant	benign(0.36)
chr14	64568744	64568744	*SYNE2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.S4159Y	ENSG00000054654	ENST00000358025	Transcript	missense_variant	probably_damaging(0.999)
chr14	80164092	80164092	*NRXN3*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P10	p.M873L	ENSG00000021645	ENST00000554719	Transcript	missense_variant	benign(0)
chr14	95236216	95236216	*GSC*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P10	p.A46G	ENSG00000133937	ENST00000238558	Transcript	missense_variant	benign(0)
chr15	41272638	41272638	*INO80*	Missense_Mutation	.	SNP	C	C	A	rs538601631	chan_et_al_P10	p.G1485V	ENSG00000128908	ENST00000361937	Transcript	missense_variant	probably_damaging(0.998)
chr15	42115192	42115192	*MAPKBP1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.P1130T	ENSG00000137802	ENST00000456763	Transcript	missense_variant	benign(0.028)
chr15	65112178	65112178	*PIF1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.D401Y	ENSG00000140451	ENST00000268043	Transcript	missense_variant	possibly_damaging(0.882)
chr15	85147356	85147356	*ZSCAN2*	Missense_Mutation	.	SNP	G	G	T	rs201278787	chan_et_al_P10	p.Q66H	ENSG00000176371	ENST00000448803	Transcript	missense_variant	benign(0.002)
chr16	20029005	20029005	*RPL3L*	Missense_Mutation	.	SNP	T	T	A	rs535291876	chan_et_al_P10	p.D112V	ENSG00000140986	ENST00000268661	Transcript	missense_variant	benign(0.153)
chr16	50655590	50655590	*NKD1*	Missense_Mutation	.	SNP	C	C	A	rs186587113	chan_et_al_P10	p.P113T	ENSG00000140807	ENST00000268459	Transcript	missense_variant	benign(0.024)
chr16	67189526	67189526	*TRADD*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.M61I	ENSG00000102871	ENST00000345057	Transcript	missense_variant	benign(0.003)
chr17	14139240	14139241	*CDRT15*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	chan_et_al_P10	p.W167Yfs*14	ENSG00000223510	ENST00000420162	Transcript	frameshift_variant	NA
chr17	46937752	46937752	*CALCOCO2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.T386N	ENSG00000136436	ENST00000448105	Transcript	missense_variant	benign(0.174)

chr17	4793910	4793910	*MINK1*	Missense_Mutation	.	SNP	g	g	T	novel	chan_et_al_P10	p.Q482H	ENSG00000141503	ENST00000355280	Transcript	missense_variant	benign(0.216)
chr17	59481859	59481859	*TBX2*	Splice_Site	.	SNP	G	G	A	novel	chan_et_al_P10	p.X296_splice	ENSG00000121068	ENST00000240328	Transcript	splice_donor_variant	NA
chr17	73570320	73570320	*LLGL2*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P10	p.R978C	ENSG00000073350	ENST00000395550	Transcript	missense_variant	possibly_damaging(0.453)
chr17	80207315	80207315	*CSNK1D*	Nonsense_Mutation	.	SNP	G	G	T	rs78642182	chan_et_al_P10	p.S350*	ENSG00000141551	ENST00000314028	Transcript	stop_gained	NA
chr18	69999947	69999947	*LAMA1*	Missense_Mutation	.	SNP	C	C	T	rs372497706	chan_et_al_P10	p.A1478T	ENSG00000101680	ENST00000389658	Transcript	missense_variant	probably_damaging(0.993)
chr19	22498210	22498210	*ZNF729*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.A664D	ENSG00000196350	ENST00000601693	Transcript	missense_variant	possibly_damaging(0.81)
chr19	44891043	44891043	*ZNF285*	Missense_Mutation	.	SNP	G	G	T	rs77661661	chan_et_al_P10	p.P455Q	ENSG00000267508	ENST00000330997	Transcript	missense_variant	benign(0.323)
chr19	6458235	6458235	*SLC25A23*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P10	p.F86Y	ENSG00000125648	ENST00000301454	Transcript	missense_variant	probably_damaging(0.999)
chr2	10008447	10008447	*TAF1B*	Missense_Mutation	.	SNP	C	C	A	rs368173816	chan_et_al_P10	p.P148T	ENSG00000115750	ENST00000263663	Transcript	missense_variant	benign(0.021)
chr2	170048520	170048520	*LRP2*	Missense_Mutation	.	SNP	C	C	T	rs138894447	chan_et_al_P10	p.E2952K	ENSG00000081479	ENST00000263816	Transcript	missense_variant	benign(0.362)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	chan_et_al_P10	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	27423868	27423868	*SLC5A6*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.Q588K	ENSG00000138074	ENST00000310574	Transcript	missense_variant	benign(0.007)
chr2	97595052	97595052	*FAM178B*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.D362Y	ENSG00000168754	ENST00000490605	Transcript	missense_variant	probably_damaging(0.967)
chr20	29857441	29857441	*PTPRA*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.A260T	ENSG00000132670	ENST00000380393	Transcript	missense_variant	probably_damaging(0.999)
chr22	17072690	17072690	*CCT8L2*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P10	p.A251T	ENSG00000198445	ENST00000359963	Transcript	missense_variant	benign(0.076)
chr3	124536551	124536551	*ITGB5*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P10	p.T349S	ENSG00000082781	ENST00000296181	Transcript	missense_variant	benign(0.126)
chr3	173322838	173322838	*NLGN1*	Missense_Mutation	.	SNP	C	C	G	rs140286287	chan_et_al_P10	p.S150R	ENSG00000169760	ENST00000457714	Transcript	missense_variant	benign(0.115)
chr3	37114356	37114356	*LRRFIP2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.Q463H	ENSG00000093167	ENST00000421307	Transcript	missense_variant	probably_damaging(0.981)
chr3	46751098	46751098	*TMIE*	Missense_Mutation	.	SNP	a	a	G	rs201683042	chan_et_al_P10	p.K131E	ENSG00000181585	ENST00000326431	Transcript	missense_variant	possibly_damaging(0.801)
chr3	4725409	4725409	*ITPR1*	Nonsense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.W1127*	ENSG00000150995	ENST00000302640	Transcript	stop_gained	NA
chr3	52513816	52513816	*NISCH*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.V452L	ENSG00000010322	ENST00000345716	Transcript	missense_variant	probably_damaging(0.965)
chr3	78734925	78734925	*ROBO1*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P10	p.I438N	ENSG00000169855	ENST00000464233	Transcript	missense_variant	benign(0.371)
chr4	26426337	26426337	*RBPJ*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.S253*	ENSG00000168214	ENST00000342295	Transcript	stop_gained	NA
chr4	4239589	4239589	*TMEM128*	Missense_Mutation	.	SNP	C	C	T	rs202215273	chan_et_al_P10	p.V134I	ENSG00000132406	ENST00000254742	Transcript	missense_variant	benign(0.025)
chr4	89421083	89421083	*HERC5*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.L817F	ENSG00000138646	ENST00000264350	Transcript	missense_variant	possibly_damaging(0.452)
chr5	10649972	10649972	*ANKRD33B*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.R411L	ENSG00000164236	ENST00000296657	Transcript	missense_variant	benign(0.001)
chr5	111602019	111602019	*EPB41L4A*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P10	p.F115S	ENSG00000129595	ENST00000261486	Transcript	missense_variant	probably_damaging(0.999)
chr5	133686064	133686064	*CDKL3*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P10	p.T139S	ENSG00000006837	ENST00000265334	Transcript	missense_variant	possibly_damaging(0.734)
chr5	146889091	146889091	*DPYSL3*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.R111W	ENSG00000113657	ENST00000343218	Transcript	missense_variant	benign(0.183)
chr5	41201668	41201668	*C6*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.E98*	ENSG00000039537	ENST00000263413	Transcript	stop_gained	NA
chr5	93800633	93800633	*KIAA0825*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P10	p.S668R	ENSG00000185261	ENST00000513200	Transcript	missense_variant	benign(0.054)
chr6	116905934	116905934	*RWDD1*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P10	p.D62H	ENSG00000111832	ENST00000466444	Transcript	missense_variant	possibly_damaging(0.537)
chr6	151671982	151671982	*AKAP12*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.P819Q	ENSG00000131016	ENST00000402676	Transcript	missense_variant	possibly_damaging(0.756)
chr6	43222387	43222387	*TTBK1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.P192T	ENSG00000146216	ENST00000259750	Transcript	missense_variant	probably_damaging(0.994)
chr7	122759289	122759289	*SLC13A1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.G453V	ENSG00000081800	ENST00000194130	Transcript	missense_variant	probably_damaging(0.99)
chr8	20771211	20771211	*MYOM2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.S1234Y	ENSG00000036448	ENST00000262113	Transcript	missense_variant	possibly_damaging(0.817)

chr8	41583359	41583359	*ANK1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.H211N	ENSG00000029534	ENST00000265709	Transcript	missense_variant	probably_damaging(0.998)
chr8	95704999	95704999	*ESRP1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.G639C	ENSG00000104413	ENST00000433389	Transcript	missense_variant	probably_damaging(0.95)
chr9	101891233	101891233	*TGFBR1*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P10	p.V65G	ENSG00000106799	ENST00000374994	Transcript	missense_variant	benign(0.038)
chr9	114305170	114305170	*ZNF483*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P10	p.R652H	ENSG00000173258	ENST00000309235	Transcript	missense_variant	possibly_damaging(0.694)
chr9	72933430	72933430	*SMC5*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P10	p.V603L	ENSG00000198887	ENST00000361138	Transcript	missense_variant	probably_damaging(0.941)
chrX	134948056	134948056	*CT45A5*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.S90I	ENSG00000242284	ENST00000463085	Transcript	missense_variant	possibly_damaging(0.461)
chrX	153994632	153994632	*DKC1*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P10	p.C135*	ENSG00000130826	ENST00000369550	Transcript	stop_gained	NA
chr1	185276150	185276150	*IVNS1ABP*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P4	p.E218A	ENSG00000116679	ENST00000367498	Transcript	missense_variant	benign(0.052)
chr1	91406354	91406354	*ZNF644*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P4	p.N186S	ENSG00000122482	ENST00000370440	Transcript	missense_variant	benign(0.023)
chr14	77493471	77493471	*IRF2BPL*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P4	p.A222G	ENSG00000119669	ENST00000238647	Transcript	missense_variant	possibly_damaging(0.515)
chr17	41143106	41143106	*RUNDC1*	Frame_Shift_Del	.	DEL	C	C	-	novel	chan_et_al_P4	p.I406Sfs*17	ENSG00000198863	ENST00000361677	Transcript	frameshift_variant	NA
chr19	36631944	36631944	*CAPNS1*	Missense_Mutation	.	SNP	g	g	A	novel	chan_et_al_P4	p.G11S	ENSG00000126247	ENST00000246533	Transcript	missense_variant	possibly_damaging(0.862)
chr2	209113112	209113112	*IDH1*	Missense_Mutation	.	SNP	C	C	A	rs121913500	chan_et_al_P4	p.R132L	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.833)
chr2	97910937	97910937	*ANKRD36*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P4	p.R1538L	ENSG00000135976	ENST00000420699	Transcript	missense_variant	benign(0.063)
chr6	17826082	17826082	*KIF13A*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P4	p.A568V	ENSG00000137177	ENST00000259711	Transcript	missense_variant	benign(0.007)
chrX	30873412	30873412	*TAB3*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P4	p.P124T	ENSG00000157625	ENST00000378933	Transcript	missense_variant	probably_damaging(0.997)
chr1	10720257	10720257	*CASZ1*	Missense_Mutation	.	SNP	C	C	A	rs564195343	chan_et_al_P5	p.S281I	ENSG00000130940	ENST00000377022	Transcript	missense_variant	benign(0.008)
chr1	11576218	11576218	*PTCHD2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.Q583H	ENSG00000204624	ENST00000294484	Transcript	missense_variant	probably_damaging(0.999)
chr1	11766730	11766730	*DRAXIN*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P5	p.H139Y	ENSG00000162490	ENST00000294485	Transcript	missense_variant	possibly_damaging(0.597)
chr1	12233777	12233777	*SCNN1D*	Missense_Mutation	.	SNP	T	T	A	rs574988244	chan_et_al_P5	p.V541E	ENSG00000162572	ENST00000379116	Transcript	missense_variant	possibly_damaging(0.858)
chr1	13424022	13424022	*PRAMEF9*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P5	p.T7I	ENSG00000204501	ENST00000376152	Transcript	missense_variant	benign(0.02)
chr1	15832562	15832562	*CD1E*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.P211T	ENSG00000158488	ENST00000368167	Transcript	missense_variant	probably_damaging(0.996)
chr1	19820171	19820171	*NEK7*	Translation_Start_Site	.	SNP	G	G	A	novel	chan_et_al_P5	p.M1?	ENSG00000151414	ENST00000367385	Transcript	initiator_codon_variant	benign(0.001)
chr1	22157534	22157534	*HSPG2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.C3871F	ENSG00000142798	ENST00000374695	Transcript	missense_variant	possibly_damaging(0.673)
chr1	27097622	27097622	*ARID1A*	Frame_Shift_Ins	.	INS	-	-	A	novel	chan_et_al_P5	p.W1073Mfs*32	ENSG00000117713	ENST00000324856	Transcript	frameshift_variant	NA
chr1	40228240	40228240	*PPIE*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P5	p.D297H	ENSG00000084072	ENST00000372830	Transcript	missense_variant	benign(0.052)
chr1	79403660	79403660	*ELTD1*	Missense_Mutation	.	SNP	C	C	T	rs201448012	chan_et_al_P5	p.V198M	ENSG00000162618	ENST00000370742	Transcript	missense_variant	benign(0.316)
chr10	51585100	51585100	*NCOA4*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P5	p.V416G	ENSG00000138293	ENST00000452682	Transcript	missense_variant	possibly_damaging(0.548)
chr11	113268064	113268064	*ANKK1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.E319D	ENSG00000170209	ENST00000303941	Transcript	missense_variant	benign(0.007)
chr11	43428700	43428700	*TTC17*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.R592S	ENSG00000052841	ENST00000399989	Transcript	missense_variant	probably_damaging(0.977)
chr11	65350434	65350434	*EHBP1L1*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P5	p.I764R	ENSG00000173442	ENST00000309295	Transcript	missense_variant	benign(0.14)
chr12	11174515	11174515	*TAS2R19*	Missense_Mutation	.	SNP	G	G	A	rs201112051	chan_et_al_P5	p.P219L	ENSG00000212124	ENST00000390673	Transcript	missense_variant	benign(0.007)
chr12	122242756	122242756	*SETD1B*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.P38Q	ENSG00000139718	ENST00000267197	Transcript	missense_variant	probably_damaging(1)
chr12	132547068	132547068	*EP400*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P5	p.R2719K	ENSG00000183495	ENST00000389561	Transcript	missense_variant	benign(0.14)
chr12	48375180	48375180	*COL2A1*	Splice_Site	.	SNP	C	C	A	novel	chan_et_al_P5	p.X804_splice	ENSG00000139219	ENST00000380518	Transcript	splice_acceptor_variant	NA
chr12	49689977	49689977	*PRPH*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.R188S	ENSG00000135406	ENST00000257860	Transcript	missense_variant	benign(0.013)

chr12	58006727	58006727	*ARHGEF25*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.A77S	ENSG00000240771	ENST00000333972	Transcript	missense_variant	benign(0.183)
chr13	26343365	26343365	*ATP8A2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.Q856K	ENSG00000132932	ENST00000381655	Transcript	missense_variant	probably_damaging(0.998)
chr13	76414548	76414548	*LMO7*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.A934S	ENSG00000136153	ENST00000465261	Transcript	missense_variant	benign(0.056)
chr14	104643925	104643925	*KIF26A*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.E1600D	ENSG00000066735	ENST00000423312	Transcript	missense_variant	probably_damaging(0.97)
chr14	45587268	45587268	*FKBP3*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.E195*	ENSG00000100442	ENST00000216330	Transcript	stop_gained	NA
chr14	59992064	59992064	*CCDC175*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P5	p.N644T	ENSG00000151838	ENST00000537690	Transcript	missense_variant	possibly_damaging(0.824)
chr14	68251097	68251097	*ZFYVE26*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.Q1194K	ENSG00000072121	ENST00000347230	Transcript	missense_variant	probably_damaging(0.979)
chr14	73743858	73743858	*NUMB*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.P462T	ENSG00000133961	ENST00000355058	Transcript	missense_variant	benign(0.009)
chr15	30384258	30384258	*GOLGA8J*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P5	p.E430D	ENSG00000179938	ENST00000567927	Transcript	missense_variant	benign(0.088)
chr15	75980959	75980959	*CSPG4*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P5	p.P816L	ENSG00000173546	ENST00000308508	Transcript	missense_variant	benign(0.007)
chr16	71571439	71571439	*CHST4*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P5	p.T287S	ENSG00000140835	ENST00000338482	Transcript	missense_variant	probably_damaging(0.999)
chr16	87453433	87453433	*ZCCHC14*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.R197M	ENSG00000140948	ENST00000268616	Transcript	missense_variant	possibly_damaging(0.525)
chr17	26948185	26948185	*KIAA0100*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.W1688L	ENSG00000007202	ENST00000528896	Transcript	missense_variant	possibly_damaging(0.731)
chr19	20229366	20229366	*ZNF90*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.H335N	ENSG00000213988	ENST00000418063	Transcript	missense_variant	probably_damaging(0.996)
chr19	36120126	36120126	*RBM42*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.G24V	ENSG00000126254	ENST00000262633	Transcript	missense_variant	unknown(0)
chr19	45818739	45818741	*CKM*	In_Frame_Del	.	DEL	CTC	CTC	-	novel	chan_et_al_P5	p.E156del	ENSG00000104879	ENST00000221476	Transcript	inframe_deletion	NA
chr19	58370298	58370298	*ZNF587*	Missense_Mutation	.	SNP	G	G	A	rs144186084	chan_et_al_P5	p.R173H	ENSG00000198466	ENST00000339656	Transcript	missense_variant	benign(0)
chr2	172398182	172398182	*CYBRD1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.A94D	ENSG00000071967	ENST00000321348	Transcript	missense_variant	possibly_damaging(0.821)
chr2	189854821	189854821	*COL3A1*	Splice_Site	.	SNP	G	G	T	novel	chan_et_al_P5	p.X231_splice	ENSG00000168542	ENST00000304636	Transcript	splice_acceptor_variant	NA
chr2	203378549	203378549	*BMPR2*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P5	p.T176A	ENSG00000204217	ENST00000374580	Transcript	missense_variant	benign(0)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	chan_et_al_P5	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	225661703	225661703	*DOCK10*	Nonsense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P5	p.S1602*	ENSG00000135905	ENST00000258390	Transcript	stop_gained	NA
chr2	37284560	37284560	*HEATR5B*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P5	p.N708I	ENSG00000008869	ENST00000233099	Transcript	missense_variant	benign(0.29)
chr2	46707884	46707884	*TMEM247*	Missense_Mutation	.	SNP	A	A	G	rs201742486	chan_et_al_P5	p.Q153R	ENSG00000187600	ENST00000434431	Transcript	missense_variant	benign(0.008)
chr20	43142589	43142589	*SERINC3*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.F44L	ENSG00000132824	ENST00000342374	Transcript	missense_variant	benign(0.02)
chr20	45004417	45004417	*ELMO2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.G274W	ENSG00000062598	ENST00000290246	Transcript	missense_variant	possibly_damaging(0.874)
chr22	19459208	19459208	*UFD1L*	Splice_Site	.	SNP	A	A	T	novel	chan_et_al_P5	p.X97_splice	ENSG00000070010	ENST00000263202	Transcript	splice_donor_variant	NA
chr22	40745936	40745936	*ADSL*	Missense_Mutation	.	SNP	G	G	T	rs540648461	chan_et_al_P5	p.R85L	ENSG00000239900	ENST00000216194	Transcript	missense_variant	probably_damaging(0.933)
chr3	14177320	14177320	*TMEM43*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.A265D	ENSG00000170876	ENST00000306077	Transcript	missense_variant	probably_damaging(0.995)
chr3	29248669	29248669	*CNTN4*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.F231L	ENSG00000144619	ENST00000397461	Transcript	missense_variant	benign(0.044)
chr3	57323102	57323102	*ASB14*	Nonsense_Mutation	.	SNP	C	C	A	rs567329875	chan_et_al_P5	p.E58*	ENSG00000239388	ENST00000487349	Transcript	stop_gained	NA
chr3	75788394	75788394	*ZNF717*	Missense_Mutation	.	SNP	C	C	G	rs201974353	chan_et_al_P5	p.R127T	ENSG00000227124	ENST00000422325	Transcript	missense_variant	possibly_damaging(0.587)
chr5	147469180	147469180	*SPINK5*	Missense_Mutation	.	SNP	C	C	A	rs114784178	chan_et_al_P5	p.L200M	ENSG00000133710	ENST00000359874	Transcript	missense_variant	probably_damaging(0.988)
chr5	159626119	159626119	*FABP6*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.K2N	ENSG00000170231	ENST00000398680	Transcript	missense_variant	unknown(0)
chr6	26157009	26157009	*HIST1H1E*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.P131T	ENSG00000168298	ENST00000304218	Transcript	missense_variant	unknown(0)
chr6	43170522	43170522	*CUL9*	Missense_Mutation	.	SNP	G	G	T	rs200509434	chan_et_al_P5	p.G1239V	ENSG00000112659	ENST00000252050	Transcript	missense_variant	probably_damaging(1)

chr7	141921283	141921283	*RP11-1220K2.2*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P5	p.F2324L	ENSG00000257743	ENST00000477922	Transcript	missense_variant	benign(0.016)
chr7	44268438	44268439	*CAMK2B*	Frame_Shift_Ins	.	INS	-	-	G	novel	chan_et_al_P5	p.P476Afs*20	ENSG00000058404	ENST00000395749	Transcript	frameshift_variant	NA
chr7	48467469	48467469	*ABCA13*	Splice_Site	.	SNP	G	G	T	novel	chan_et_al_P5	p.X4189_splice	ENSG00000179869	ENST00000435803	Transcript	splice_donor_variant	NA
chr8	20003368	20003368	*SLC18A1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P5	p.C495Y	ENSG00000036565	ENST00000440926	Transcript	missense_variant	probably_damaging(0.928)
chr8	37690557	37690557	*GPR124*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.A376D	ENSG00000020181	ENST00000412232	Transcript	missense_variant	probably_damaging(0.949)
chr8	42231664	42231664	*DKK4*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P5	p.R210Q	ENSG00000104371	ENST00000220812	Transcript	missense_variant	benign(0.027)
chr8	72246390	72246390	*EYA1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.S48R	ENSG00000104313	ENST00000340726	Transcript	missense_variant	possibly_damaging(0.53)
chr9	100326320	100326320	*TMOD1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P5	p.S163I	ENSG00000136842	ENST00000259365	Transcript	missense_variant	possibly_damaging(0.732)
chr9	135802593	135802593	*TSC1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P5	p.D69N	ENSG00000165699	ENST00000298552	Transcript	missense_variant	possibly_damaging(0.876)
chr9	137716453	137716453	*COL5A1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P5	p.P1569L	ENSG00000130635	ENST00000371817	Transcript	missense_variant	unknown(0)
chrX	135432584	135432584	*GPR112*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P5	p.K2240R	ENSG00000156920	ENST00000394143	Transcript	missense_variant	benign(0.053)
chrX	30236993	30236993	*MAGEB2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P5	p.A99D	ENSG00000099399	ENST00000378988	Transcript	missense_variant	benign(0.11)
chr1	43215980	43215980	*LEPRE1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P9	p.Q533K	ENSG00000117385	ENST00000236040	Transcript	missense_variant	benign(0.018)
chr1	65088400	65088400	*ESPN*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P9	p.P535L	ENSG00000187017	ENST00000377828	Transcript	missense_variant	possibly_damaging(0.813)
chr12	114395857	114395857	*RBM19*	Splice_Site	.	SNP	T	T	A	rs368981792	chan_et_al_P9	p.X191_splice	ENSG00000122965	ENST00000545145	Transcript	splice_acceptor_variant	NA
chr12	123351949	123351949	*VPS37B*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P9	p.Y191S	ENSG00000139722	ENST00000267202	Transcript	missense_variant	benign(0.041)
chr12	45803172	45803172	*ANO6*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P9	p.R659K	ENSG00000177119	ENST00000423947	Transcript	missense_variant	benign(0.065)
chr14	64568690	64568690	*SYNE2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.S4141Y	ENSG00000054654	ENST00000358025	Transcript	missense_variant	possibly_damaging(0.617)
chr15	52433408	52433408	*GNB5*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P9	p.A186T	ENSG00000069966	ENST00000261837	Transcript	missense_variant	benign(0.017)
chr16	47007443	47007443	*DNAJA2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.G14V	ENSG00000069345	ENST00000317089	Transcript	missense_variant	probably_damaging(0.992)
chr16	55513446	55513446	*MMP2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.L19I	ENSG00000087245	ENST00000219070	Transcript	missense_variant	benign(0)
chr16	72821644	72821644	*ZFHX3*	Missense_Mutation	.	SNP	c	c	T	novel	chan_et_al_P9	p.G3511S	ENSG00000140836	ENST00000268489	Transcript	missense_variant	unknown(0)
chr17	18071025	18071025	*MYO15A*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P9	p.Y3357S	ENSG00000091536	ENST00000205890	Transcript	missense_variant	unknown(0)
chr17	42636651	42636651	*FZD2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P9	p.G532V	ENSG00000180340	ENST00000315323	Transcript	missense_variant	probably_damaging(0.999)
chr19	10657515	10657515	*ATG4D*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P9	p.D165V	ENSG00000130734	ENST00000309469	Transcript	missense_variant	probably_damaging(0.947)
chr19	21991504	21991504	*ZNF43*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P9	p.N445K	ENSG00000198521	ENST00000359599	Transcript	missense_variant	benign(0.002)
chr19	3959203	3959203	*DAPK3*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P9	p.E421K	ENSG00000167657	ENST00000545797	Transcript	missense_variant	benign(0.251)
chr2	100916262	100916262	*LONRF2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P9	p.P395H	ENSG00000170500	ENST00000393437	Transcript	missense_variant	possibly_damaging(0.819)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	chan_et_al_P9	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	85570849	85570849	*RETSAT*	Missense_Mutation	.	SNP	C	C	T	rs4832168	chan_et_al_P9	p.G536R	ENSG00000042445	ENST00000295802	Transcript	missense_variant	probably_damaging(0.998)
chr20	62311244	62311244	*RTEL1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P9	p.Q384H	ENSG00000258366	ENST00000508582	Transcript	missense_variant	benign(0.029)
chr22	18644597	18644597	*USP18*	Missense_Mutation	.	SNP	G	G	A	rs143481018	chan_et_al_P9	p.V99I	ENSG00000184979	ENST00000215794	Transcript	missense_variant	possibly_damaging(0.595)
chr22	25280055	25280055	*SGSM1*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P9	p.T566A	ENSG00000167037	ENST00000400359	Transcript	missense_variant	possibly_damaging(0.777)
chr3	108818291	108818291	*MORC1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.D113Y	ENSG00000114487	ENST00000232603	Transcript	missense_variant	probably_damaging(0.999)
chr3	42240727	42240727	*TRAK1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P9	p.A391V	ENSG00000182606	ENST00000327628	Transcript	missense_variant	benign(0.027)
chr3	52236607	52236607	*ALAS1*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P9	p.H95P	ENSG00000023330	ENST00000394965	Transcript	missense_variant	benign(0.021)

chr3	52437163	52437163	*BAP1*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P9	p.Y627*	ENSG00000163930	ENST00000460680	Transcript	stop_gained	NA
chr4	137769 8	137769 8	*UVSSA*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P9	p.R669H	ENSG00000163945	ENST00000389851	Transcript	missense_variant	probably_damaging(0.999)
chr4	166231812	166231812	*KLHL2*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P9	p.V387I	ENSG00000109466	ENST00000514860	Transcript	missense_variant	benign(0.008)
chr5	141049295	141049295	*ARAP3*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.W778L	ENSG00000120318	ENST00000239440	Transcript	missense_variant	probably_damaging(0.999)
chr5	72798817	72798817	*BTF3*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.T131N	ENSG00000145741	ENST00000380591	Transcript	missense_variant	probably_damaging(0.965)
chr5	90136481	90136481	*GPR98*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P9	p.L5566F	ENSG00000164199	ENST00000405460	Transcript	missense_variant	possibly_damaging(0.86)
chr7	139762431	139762431	*PARP12*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P9	p.R73C	ENSG00000059378	ENST00000263549	Transcript	missense_variant	probably_damaging(0.999)
chr7	150746361	150746361	*ASIC3*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P9	p.G130D	ENSG00000213199	ENST00000297512	Transcript	missense_variant	probably_damaging(0.981)
chr9	130578264	130578264	*ENG*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.A604S	ENSG00000106991	ENST00000373203	Transcript	missense_variant	probably_damaging(0.96)
chr9	134165792	134165792	*PPAPDC3*	Missense_Mutation	.	SNP	C	C	A	rs367916447	chan_et_al_P9	p.S136R	ENSG00000160539	ENST00000372264	Transcript	missense_variant	probably_damaging(0.997)
chr9	140707873	140707873	*EHMT1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P9	p.P1024H	ENSG00000181090	ENST00000460843	Transcript	missense_variant	probably_damaging(0.994)
chr9	36191242	36191242	*CLTA*	Missense_Mutation	.	SNP	g	g	T	rs529517129	chan_et_al_P9	p.Q63H	ENSG00000122705	ENST00000242285	Transcript	missense_variant	benign(0.389)
chrX	102612920	102612920	*WBP5*	Nonsense_Mutation	.	SNP	t	t	A	novel	chan_et_al_P9	p.L103*	ENSG00000185222	ENST00000372661	Transcript	stop_gained	NA
chr1	151341496	151341496	*SELENBP1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.A115D	ENSG00000143416	ENST00000368868	Transcript	missense_variant	possibly_damaging(0.783)
chr1	152883290	152883290	*IVL*	Missense_Mutation	.	SNP	g	g	T	novel	chan_et_al_P1	p.Q339H	ENSG00000163207	ENST00000368764	Transcript	missense_variant	probably_damaging(0.999)
chr1	154947234	154947234	*CKS1B*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.Q5K	ENSG00000173207	ENST00000308987	Transcript	missense_variant	benign(0.05)
chr1	159904604	159904604	*IGSF9*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.V228I	ENSG00000085552	ENST00000368094	Transcript	missense_variant	benign(0.026)
chr1	159907478	159907478	*IGSF9*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P1	p.N133S	ENSG00000085552	ENST00000368094	Transcript	missense_variant	benign(0.041)
chr1	185933003	185933003	*HMCN1*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P1	p.Q692E	ENSG00000143341	ENST00000271588	Transcript	missense_variant	probably_damaging(0.926)
chr1	21051102	21051102	*SH2D5*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.C139*	ENSG00000189410	ENST00000444387	Transcript	stop_gained	NA
chr1	240977000	240977000	*RGS7*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.E292*	ENSG00000182901	ENST00000366565	Transcript	stop_gained	NA
chr1	33631155	33631155	*TRIM62*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.D141N	ENSG00000116525	ENST00000291416	Transcript	missense_variant	benign(0.001)
chr1	36204969	36204969	*CLSPN*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P1	p.H1102R	ENSG00000092853	ENST00000318121	Transcript	missense_variant	possibly_damaging(0.529)
chr1	43888843	43888843	*SZT2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.P704H	ENSG00000198198	ENST00000562955	Transcript	missense_variant	probably_damaging(0.997)
chr1	45469241	45469241	*HECTD3*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.V837I	ENSG00000126107	ENST00000372172	Transcript	missense_variant	benign(0.158)
chr1	46106054	46106054	*GPBP1L1*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P1	p.Q191R	ENSG00000159592	ENST00000355105	Transcript	missense_variant	benign(0.225)
chr1	91981358	91981358	*CDC7*	Nonsense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.Q369*	ENSG00000097046	ENST00000428239	Transcript	stop_gained	NA
chr10	127462903	127462903	*MMP21*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P1	p.V65G	ENSG00000154485	ENST00000368808	Transcript	missense_variant	benign(0.002)
chr10	134218621	134218621	*PWWP2B*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.S206N	ENSG00000171813	ENST00000305233	Transcript	missense_variant	probably_damaging(0.986)
chr10	28824497	28824497	*WAC*	Nonsense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P1	p.K29*	ENSG00000095787	ENST00000354911	Transcript	stop_gained	NA
chr10	71211361	71211361	*TSPAN15*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.G4V	ENSG00000099282	ENST00000373290	Transcript	missense_variant	possibly_damaging(0.835)
chr10	73585614	73585614	*PSAP*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.I253F	ENSG00000197746	ENST00000394936	Transcript	missense_variant	benign(0.279)
chr10	98129930	98129930	*TLL2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.F935L	ENSG00000095587	ENST00000357947	Transcript	missense_variant	possibly_damaging(0.604)
chr11	10580752	10580752	*LYVE1*	Frame_Shift_Ins	.	INS	-	-	T	novel	chan_et_al_P1	p.N294*	ENSG00000133800	ENST00000256178	Transcript	frameshift_variant	NA
chr11	124561655	124561655	*SPA17*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.E97*	ENSG00000064199	ENST00000532692	Transcript	stop_gained	NA
chr11	125267906	125267906	*PKNOX2*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P1	p.D179G	ENSG00000165495	ENST00000298282	Transcript	missense_variant	possibly_damaging(0.78)

chr11	20982041	20982041	*NELL1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.T412K	ENSG00000165973	ENST00000357134	Transcript	missense_variant	possibly_damaging(0.461)
chr11	46812097	46812097	*CKAP5*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.P563T	ENSG00000175216	ENST00000529230	Transcript	missense_variant	benign(0.011)
chr11	64525923	64525923	*PYGM*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P1	p.L137Q	ENSG00000068976	ENST00000164139	Transcript	missense_variant	probably_damaging(0.957)
chr11	64575073	64575073	*MEN1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.P250H	ENSG00000133895	ENST00000337652	Transcript	missense_variant	probably_damaging(0.995)
chr11	66610482	66610482	*C11orf80*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.R637L	ENSG00000173715	ENST00000360962	Transcript	missense_variant	benign(0.003)
chr11	66999141	66999141	*KDM2A*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.A397T	ENSG00000173120	ENST00000529006	Transcript	missense_variant	benign(0.023)
chr11	67260453	67260453	*PITPNM1*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P1	p.Q1141H	ENSG00000110697	ENST00000356404	Transcript	missense_variant	benign(0.03)
chr11	82644474	82644474	*C11orf82*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.Q698H	ENSG00000165490	ENST00000535365	Transcript	missense_variant	possibly_damaging(0.838)
chr11	92531452	92531452	*FAT3*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P1	p.Q1758L	ENSG00000165323	ENST00000298047	Transcript	missense_variant	possibly_damaging(0.877)
chr12	11174542	11174542	*TAS2R19*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.R210Q	ENSG00000212124	ENST00000390673	Transcript	missense_variant	benign(0.003)
chr12	1702503	1702503	*FBXL14*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.A244S	ENSG00000171823	ENST00000339235	Transcript	missense_variant	benign(0.005)
chr12	32895654	32895654	*DNM1L*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.R709H	ENSG00000087470	ENST00000549701	Transcript	missense_variant	probably_damaging(0.983)
chr12	85449324	85449324	*LRRIQ1*	Splice_Site	.	SNP	G	G	T	novel	chan_et_al_P1	p.X252_splice	ENSG00000133640	ENST00000393217	Transcript	splice_acceptor_variant	NA
chr12	93564666	93564666	*PZP*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.E55D	ENSG00000126838	ENST00000261336	Transcript	missense_variant	possibly_damaging(0.755)
chr13	103296946	103296946	*TPP2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.A739S	ENSG00000134900	ENST00000376065	Transcript	missense_variant	benign(0.119)
chr13	103386147	103386147	*CCDC168*	Missense_Mutation	.	SNP	C	C	T	rs187250826	chan_et_al_P1	p.V1005I	ENSG00000175820	ENST00000322527	Transcript	missense_variant	benign(0.208)
chr13	22246322	22246322	*FGF9*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P1	p.R91G	ENSG00000102678	ENST00000382353	Transcript	missense_variant	benign(0.108)
chr13	48955538	48955538	*RB1*	Nonsense_Mutation	.	SNP	C	C	T	rs121913303	chan_et_al_P1	p.R552*	ENSG00000139687	ENST00000267163	Transcript	stop_gained	NA
chr14	20345235	20345235	*OR4K2*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P1	p.I270S	ENSG00000165762	ENST00000298642	Transcript	missense_variant	benign(0.297)
chr14	75416199	75416199	*PGF*	Missense_Mutation	.	SNP	A	A	C	rs200471804	chan_et_al_P1	p.V59G	ENSG00000119630	ENST00000555567	Transcript	missense_variant	probably_damaging(0.998)
chr14	99976643	99976643	*CCNK*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.P423S	ENSG00000090061	ENST00000389879	Transcript	missense_variant	unknown(0)
chr15	25947103	25947103	*ATP10A*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P1	p.D907G	ENSG00000206190	ENST00000356865	Transcript	missense_variant	benign(0.022)
chr15	89861809	89861809	*POLG*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.A1149T	ENSG00000140521	ENST00000268124	Transcript	missense_variant	probably_damaging(1)
chr16	24993848	24993848	*CCNF*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P1	p.T442P	ENSG00000162063	ENST00000397066	Transcript	missense_variant	benign(0.049)
chr16	46956249	46956249	*GPT2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.P378Q	ENSG00000166123	ENST00000340124	Transcript	missense_variant	probably_damaging(0.972)
chr16	75670358	75670358	*KARS*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P1	p.N187S	ENSG00000065427	ENST00000319410	Transcript	missense_variant	benign(0.047)
chr16	88789685	88789685	*PIEZO1*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.Q1463E	ENSG00000103335	ENST00000301015	Transcript	missense_variant	benign(0.011)
chr16	88964527	88964527	*CBFA2T3*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.G113D	ENSG00000129993	ENST00000268679	Transcript	missense_variant	possibly_damaging(0.575)
chr16	89006622	89006622	*RP11-830F9.6*	Missense_Mutation	.	SNP	C	C	A	rs564878768	chan_et_al_P1	p.P7Q	ENSG00000205018	ENST00000378347	Transcript	missense_variant	possibly_damaging(0.908)
chr16	92127274	92127274	*LMF1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.C322Y	ENSG00000103227	ENST00000262301	Transcript	missense_variant	possibly_damaging(0.737)
chr16	98582556	98582556	*GRIN2A*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.P1049T	ENSG00000183454	ENST00000396573	Transcript	missense_variant	benign(0.428)
chr17	15809331	15809331	*PRPF8*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.L638I	ENSG00000174231	ENST00000572621	Transcript	missense_variant	benign(0.032)
chr17	36997536	36997536	*C17orf98*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P1	p.L36P	ENSG00000214556	ENST00000398575	Transcript	missense_variant	probably_damaging(0.921)
chr17	37761958	37761958	*NEUROD2*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.L299F	ENSG00000171532	ENST00000302584	Transcript	missense_variant	possibly_damaging(0.69)
chr17	40695585	40695585	*NAGLU*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.P521S	ENSG00000108784	ENST00000225927	Transcript	missense_variant	probably_damaging(1)
chr17	74064622	74064622	*POLR2A*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.E927Q	ENSG00000181222	ENST00000322644	Transcript	missense_variant	possibly_damaging(0.516)

chr17	7578457	7578457	*TP53*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.R158H	ENSG00000141510	ENST00000269305	Transcript	missense_variant	benign(0.438)
chr17	76046039	76046039	*TNRC6C*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P1	p.D299V	ENSG00000078687	ENST00000335749	Transcript	missense_variant	possibly_damaging(0.743)
chr18	44775400	44775400	*SKOR2*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P1	p.V52G	ENSG00000215474	ENST00000425639	Transcript	missense_variant	probably_damaging(0.977)
chr18	67806882	67806882	*RTTN*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.R914L	ENSG00000176225	ENST00000255674	Transcript	missense_variant	probably_damaging(1)
chr19	1231136	1231137	*C19orf26*	Frame_Shift_Ins	.	INS	-	-	G	novel	chan_et_al_P1	p.R373Pfs*22	ENSG00000099625	ENST00000590083	Transcript	frameshift_variant	NA
chr19	13002330	13002330	*GCDH*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.A41P	ENSG00000105607	ENST00000222214	Transcript	missense_variant	benign(0.001)
chr19	14703147	14703147	*CLEC17A*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P1	p.Y85C	ENSG00000187912	ENST00000417570	Transcript	missense_variant	probably_damaging(0.999)
chr19	21205686	21205686	*ZNF430*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P1	p.K32T	ENSG00000118620	ENST00000261560	Transcript	missense_variant	benign(0.05)
chr19	35551565	35551565	*HPN*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.A219S	ENSG00000105707	ENST00000262626	Transcript	missense_variant	benign(0.055)
chr19	37413686	37413686	*ZNF568*	Missense_Mutation	.	SNP	C	C	A	rs573204075	chan_et_al_P1	p.S5Y	ENSG00000198453	ENST00000333987	Transcript	missense_variant	benign(0)
chr19	45494151	45494151	*CLPTM1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.S456Y	ENSG00000104853	ENST00000337392	Transcript	missense_variant	possibly_damaging(0.56)
chr19	47774903	47774903	*CCDC9*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.P522T	ENSG00000105321	ENST00000222192	Transcript	missense_variant	unknown(0)
chr19	55870813	55870813	*FAM71E2*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P1	p.I475V	ENSG00000180043	ENST00000424985	Transcript	missense_variant	benign(0)
chr19	57672127	57672128	*DUXA*	Frame_Shift_Ins	.	INS	-	-	T	novel	chan_et_al_P1	p.F22Ifs*48	ENSG00000258873	ENST00000554048	Transcript	frameshift_variant	NA
chr19	8203371	8203371	*FBN3*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.R315W	ENSG00000142449	ENST00000600128	Transcript	missense_variant	possibly_damaging(0.897)
chr19	8495749	8495749	*Mar/02*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.L194M	ENSG00000099785	ENST00000602117	Transcript	missense_variant	probably_damaging(0.909)
chr19	984516	984516	*WDR18*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.A55S	ENSG00000065268	ENST00000251289	Transcript	missense_variant	possibly_damaging(0.556)
chr2	108868821	108868821	*SULT1C3*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.G58A	ENSG00000196228	ENST00000329106	Transcript	missense_variant	probably_damaging(0.987)
chr2	113764298	113764298	*IL36A*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.P83H	ENSG00000136694	ENST00000259211	Transcript	missense_variant	probably_damaging(0.982)
chr2	1460055	1460055	*TPO*	Splice_Site	.	SNP	G	G	C	novel	chan_et_al_P1	p.X273_splice	ENSG00000115705	ENST00000345913	Transcript	splice_donor_variant	NA
chr2	148683685	148683686	*ACVR2A*	Frame_Shift_Ins	.	INS	-	-	A	novel	chan_et_al_P1	p.R438Efs*19	ENSG00000121989	ENST00000241416	Transcript	frameshift_variant	NA
chr2	168107563	168107563	*XIRP2*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P1	p.L3221V	ENSG00000163092	ENST00000409195	Transcript	missense_variant	probably_damaging(0.999)
chr2	190541733	190541733	*ANKAR*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.E173*	ENSG00000151687	ENST00000520309	Transcript	stop_gained	NA
chr2	21229859	21229859	*APOB*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.S3294*	ENSG00000084674	ENST00000232432	Transcript	stop_gained	NA
chr2	212522491	212522491	*ERBB4*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.P645R	ENSG00000178568	ENST00000342788	Transcript	missense_variant	benign(0.01)
chr2	233271767	233271767	*ALPPL2*	Missense_Mutation	.	SNP	T	T	C	rs372446876	chan_et_al_P1	p.V23A	ENSG00000163286	ENST00000295453	Transcript	missense_variant	benign(0.002)
chr2	234732209	234732209	*MROH2A*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P1	p.M1338V	ENSG00000185038	ENST00000389758	Transcript	missense_variant	benign(0.002)
chr2	55181282	55181282	*EML6*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.R1492Q	ENSG00000214595	ENST00000356458	Transcript	missense_variant	benign(0.185)
chr2	74733866	74733866	*PCGF1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.L115F	ENSG00000115289	ENST00000233630	Transcript	missense_variant	probably_damaging(0.976)
chr2	75347789	75347789	*TACR1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.Q165H	ENSG00000115353	ENST00000305249	Transcript	missense_variant	probably_damaging(0.99)
chr20	36742529	36742529	*SIGLEC1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.A1115T	ENSG00000088827	ENST00000344754	Transcript	missense_variant	benign(0.113)
chr21	42749862	42749862	*MX2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.S132R	ENSG00000183486	ENST00000330714	Transcript	missense_variant	probably_damaging(1)
chr22	19338924	19338924	*HIRA*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.P965L	ENSG00000100084	ENST00000263208	Transcript	missense_variant	possibly_damaging(0.676)
chr22	35804399	35804399	*MCM5*	Splice_Site	.	SNP	A	A	G	novel	chan_et_al_P1	p.X199_splice	ENSG00000100297	ENST00000216122	Transcript	splice_acceptor_variant	NA
chr22	40708595	40708595	*TNRC6B*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.G1508S	ENSG00000100354	ENST00000454349	Transcript	missense_variant	possibly_damaging(0.507)
chr3	122419629	122419629	*PARP14*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P1	p.V743G	ENSG00000173193	ENST00000474629	Transcript	missense_variant	possibly_damaging(0.467)

chr3	128889359	128889359	*CNBP*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.N159K	ENSG00000169714	ENST00000441626	Transcript	missense_variant	benign(0.044)
chr3	129249760	129249760	*RHO*	Missense_Mutation	.	SNP	C	C	T	rs104893775	chan_et_al_P1	p.R135W	ENSG00000163914	ENST00000296271	Transcript	missense_variant	probably_damaging(1)
chr3	133486887	133486887	*TF*	Nonsense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.E501*	ENSG00000091513	ENST00000402696	Transcript	stop_gained	NA
chr3	151163859	151163859	*IGSF10*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P1	p.K1304E	ENSG00000152580	ENST00000282466	Transcript	missense_variant	benign(0.211)
chr3	160951196	160951196	*NMD3*	Missense_Mutation	.	SNP	G	G	T	rs200743323	chan_et_al_P1	p.V96L	ENSG00000169251	ENST00000460469	Transcript	missense_variant	benign(0.04)
chr3	183580583	183580583	*PARL*	Nonsense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.K157*	ENSG00000175193	ENST00000317096	Transcript	stop_gained	NA
chr3	197249589	197249589	*BDH1*	Nonsense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.Q111*	ENSG00000161267	ENST00000392379	Transcript	stop_gained	NA
chr3	50683572	50683572	*MAPKAPK3*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.L236I	ENSG00000114738	ENST00000446044	Transcript	missense_variant	possibly_damaging(0.839)
chr3	64527600	64527600	*ADAMTS9*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.C1704F	ENSG00000163638	ENST00000498707	Transcript	missense_variant	probably_damaging(1)
chr4	146651094	146651094	*C4orf51*	Nonsense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.R160*	ENSG00000237136	ENST00000438731	Transcript	stop_gained	NA
chr4	79421007	79421007	*FRAS1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.T3083M	ENSG00000138759	ENST00000264895	Transcript	missense_variant	probably_damaging(1)
chr5	10411578	10411578	*Mar/06*	Missense_Mutation	.	SNP	C	C	A	rs200779854	chan_et_al_P1	p.Q609K	ENSG00000145495	ENST00000274140	Transcript	missense_variant	possibly_damaging(0.49)
chr5	134113281	134113281	*DDX46*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.A211S	ENSG00000145833	ENST00000354283	Transcript	missense_variant	benign(0.054)
chr5	150663759	150663759	*SLC36A3*	Nonsense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.K315*	ENSG00000186334	ENST00000377713	Transcript	stop_gained	NA
chr5	169310247	169310247	*FAM196B*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.S219Y	ENSG00000204767	ENST00000377365	Transcript	missense_variant	possibly_damaging(0.568)
chr5	43653312	43653312	*NNT*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P1	p.I686V	ENSG00000112992	ENST00000266463	Transcript	missense_variant	benign(0.054)
chr5	74651190	74651190	*HMGCR*	Frame_Shift_Del	.	DEL	C	C	-	novel	chan_et_al_P1	p.G576Vfs*13	ENSG00000113161	ENST00000287936	Transcript	frameshift_variant	NA
chr5	95067704	95067704	*RHOBTB3*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.S48R	ENSG00000164292	ENST00000379982	Transcript	missense_variant	benign(0.376)
chr6	160453730	160453730	*IGF2R*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.L344I	ENSG00000197081	ENST00000356956	Transcript	missense_variant	probably_damaging(1)
chr6	27424685	27424685	*ZNF184*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.K73I	ENSG00000096654	ENST00000211936	Transcript	missense_variant	benign(0.386)
chr6	38851651	38851651	*DNAH8*	Splice_Site	.	SNP	G	G	T	novel	chan_et_al_P1	p.X2496_splice	ENSG00000124721	ENST00000359357	Transcript	splice_acceptor_variant	NA
chr6	43223505	43223505	*TTBK1*	Missense_Mutation	.	SNP	C	C	T	rs373096251	chan_et_al_P1	p.R258W	ENSG00000146216	ENST00000259750	Transcript	missense_variant	probably_damaging(0.995)
chr6	90455020	90455020	*MDN1*	Nonsense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.E1384*	ENSG00000112159	ENST00000369393	Transcript	stop_gained	NA
chr7	100454745	100454745	*SLC12A9*	Missense_Mutation	.	SNP	G	G	A	rs375275857	chan_et_al_P1	p.R235Q	ENSG00000146828	ENST00000354161	Transcript	missense_variant	benign(0.006)
chr7	104702721	104702721	*KMT2E*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P1	p.Y61C	ENSG00000005483	ENST00000311117	Transcript	missense_variant	possibly_damaging(0.759)
chr7	141795494	141795494	*MGAM*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.V1634L	ENSG00000257335	ENST00000549489	Transcript	missense_variant	benign(0.384)
chr7	150935685	150935685	*CHPF2*	Missense_Mutation	.	SNP	G	G	T	rs138308089	chan_et_al_P1	p.R746L	ENSG00000033100	ENST00000035307	Transcript	missense_variant	benign(0.007)
chr7	18067213	18067213	*PRPS1L1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.D65N	ENSG00000229937	ENST00000506618	Transcript	missense_variant	possibly_damaging(0.49)
chr7	25191228	25191228	*C7orf31*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.G224D	ENSG00000153790	ENST00000409280	Transcript	missense_variant	benign(0.009)
chr7	42005062	42005062	*GLI3*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.N1203K	ENSG00000106571	ENST00000395925	Transcript	missense_variant	benign(0.075)
chr7	82595367	82595367	*PCLO*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.K1246I	ENSG00000186472	ENST00000333891	Transcript	missense_variant	unknown(0)
chr7	94750074	94750074	*PPP1R9A*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.A527P	ENSG00000158528	ENST00000433360	Transcript	missense_variant	probably_damaging(0.979)
chr8	133153487	133153487	*KCNQ3*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.A452S	ENSG00000184156	ENST00000388996	Transcript	missense_variant	benign(0.101)
chr8	15519792	15519792	*TUSC3*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.A232V	ENSG00000104723	ENST00000503731	Transcript	missense_variant	possibly_damaging(0.862)
chr8	41467320	41467320	*AGPAT6*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.D128N	ENSG00000158669	ENST00000396987	Transcript	missense_variant	benign(0.143)
chr9	140772670	140772670	*CACNA1B*	Splice_Site	.	SNP	A	A	T	rs200491212	chan_et_al_P1	p.X95_splice	ENSG00000148408	ENST00000371372	Transcript	splice_donor_variant	NA

chr9	73233860	73233860	*TRPM3*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.A749T	ENSG00000083067	ENST00000377110	Transcript	missense_variant	possibly_damaging(0.662)
chr9	74313020	74313020	*TMEM2*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P1	p.S1160T	ENSG00000135048	ENST00000377043	Transcript	missense_variant	possibly_damaging(0.576)
chr9	88207597	88207597	*AGTPBP1*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P1	p.V776L	ENSG00000135049	ENST00000376083	Transcript	missense_variant	benign(0.001)
chr9	98775024	98775024	*ERCC6L2*	Missense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P1	p.N379Y	ENSG00000182150	ENST00000407474	Transcript	missense_variant	benign(0.025)
chrX	104463911	104463911	*TEX13A*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.A322E	ENSG00000133149	ENST00000413579	Transcript	missense_variant	benign(0.074)
chrX	123871003	123871003	*TENM1*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P1	p.P194A	ENSG00000009694	ENST00000422452	Transcript	missense_variant	possibly_damaging(0.542)
chrX	130678903	130678903	*OR13H1*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P1	p.P286T	ENSG00000171054	ENST00000338616	Transcript	missense_variant	probably_damaging(1)
chrX	135431185	135431185	*GPR112*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.F1774I	ENSG00000156920	ENST00000394143	Transcript	missense_variant	benign(0.049)
chrX	135431214	135431214	*GPR112*	Missense_Mutation	.	SNP	T	T	A	novel	chan_et_al_P1	p.N1783K	ENSG00000156920	ENST00000394143	Transcript	missense_variant	benign(0.004)
chrX	153595114	153595114	*FLNA*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P1	p.G325R	ENSG00000196924	ENST00000369850	Transcript	missense_variant	probably_damaging(0.998)
chrX	153667414	153667414	*GDI1*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.E106K	ENSG00000203879	ENST00000447750	Transcript	missense_variant	possibly_damaging(0.604)
chrX	154033642	154033642	*MPP1*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P1	p.L3F	ENSG00000130830	ENST00000369534	Transcript	missense_variant	possibly_damaging(0.894)
chrX	154157131	154157131	*F8*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P1	p.W1645S	ENSG00000185010	ENST00000360256	Transcript	missense_variant	benign(0.157)
chrX	34149642	34149642	*FAM47A*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P1	p.P252T	ENSG00000185448	ENST00000346193	Transcript	missense_variant	probably_damaging(0.991)
chr1	116380892	116380892	*NHLH2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P2	p.S34R	ENSG00000177551	ENST00000369506	Transcript	missense_variant	benign(0.062)
chr1	155629490	155629490	*YY1AP1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P2	p.M875I	ENSG00000163374	ENST00000368339	Transcript	missense_variant	benign(0.006)
chr1	155629714	155629714	*YY1AP1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P2	p.E801K	ENSG00000163374	ENST00000368339	Transcript	missense_variant	probably_damaging(0.959)
chr1	247921543	247921543	*OR1C1*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P2	p.H56Y	ENSG00000221888	ENST00000408896	Transcript	missense_variant	benign(0.245)
chr1	46212076	46212076	*IPP*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P2	p.N3S	ENSG00000197429	ENST00000396478	Transcript	missense_variant	benign(0)
chr1	54678210	54678210	*MRPL37*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P2	p.T290N	ENSG00000116221	ENST00000360840	Transcript	missense_variant	probably_damaging(1)
chr10	70673036	70673036	*DDX50*	Splice_Site	.	SNP	G	G	A	novel	chan_et_al_P2	p.X253_splice	ENSG00000107625	ENST00000373585	Transcript	splice_donor_variant	NA
chr11	117079626	117079626	*PCSK7*	Missense_Mutation	.	SNP	G	G	C	rs202038275	chan_et_al_P2	p.R560G	ENSG00000160613	ENST00000320934	Transcript	missense_variant	probably_damaging(0.999)
chr11	94353238	94353238	*PIWIL4*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P2	p.D790E	ENSG00000134627	ENST00000299001	Transcript	missense_variant	probably_damaging(0.99)
chr12	112892433	112892433	*PTPN11*	Nonsense_Mutation	.	SNP	T	T	G	rs76982592	chan_et_al_P2	p.Y197*	ENSG00000179295	ENST00000351677	Transcript	stop_gained	NA
chr12	51550156	51550156	*KCNA5*	Missense_Mutation	.	SNP	G	G	A	rs71581017	chan_et_al_P2	p.G568E	ENSG00000130037	ENST00000252321	Transcript	missense_variant	benign(0.311)
chr12	83081402	83081402	*TMTC2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P2	p.A13S	ENSG00000179104	ENST00000321196	Transcript	missense_variant	benign(0.005)
chr13	53216985	53216985	*HNRNPA1L2*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P2	p.H120Y	ENSG00000139675	ENST00000342657	Transcript	missense_variant	benign(0.046)
chr15	51741321	51741321	*DMXL2*	Nonsense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P2	p.R2992*	ENSG00000104093	ENST00000543779	Transcript	stop_gained	NA
chr15	52356196	52356196	*MAPK6*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P2	p.T389A	ENSG00000069956	ENST00000261845	Transcript	missense_variant	benign(0.081)
chr17	60601655	60601655	*TLK2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P2	p.R109L	ENSG00000146872	ENST00000346027	Transcript	missense_variant	benign(0.054)
chr19	1010836	1010836	*TMEM259*	Missense_Mutation	.	SNP	C	C	T	rs202006160	chan_et_al_P2	p.R459H	ENSG00000182087	ENST00000356663	Transcript	missense_variant	benign(0.071)
chr19	46351159	46351159	*SYMPK*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P2	p.N176S	ENSG00000125755	ENST00000245934	Transcript	missense_variant	benign(0.436)
chr19	54783903	54783903	*LILRB2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P2	p.A33D	ENSG00000131042	ENST00000391749	Transcript	missense_variant	probably_damaging(0.99)
chr2	232029971	232029971	*PSMD1*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P2	p.E847K	ENSG00000173692	ENST00000308696	Transcript	missense_variant	benign(0)
chr2	242814938	242814938	*CXXC11*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P2	p.G411C	ENSG00000188011	ENST00000343216	Transcript	missense_variant	possibly_damaging(0.756)
chr20	35400455	35400455	*ATRN*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P2	p.D373A	ENSG00000088812	ENST00000262919	Transcript	missense_variant	possibly_damaging(0.489)

chr4	70360987	70360987	*UGT2B4*	Missense_Mutation	.	SNP	A	A	T	rs188797000	chan_et_al_P2	p.M198K	ENSG00000156096	ENST00000305107	Transcript	missense_variant	benign(0.275)
chr5	140201551	140201551	*PCDHA5*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P2	p.R64Q	ENSG00000204965	ENST00000529859	Transcript	missense_variant	benign(0.248)
chr5	140236750	140236750	*PCDHA10*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P2	p.V373I	ENSG00000250120	ENST00000307360	Transcript	missense_variant	probably_damaging(0.944)
chr5	149755736	149755736	*TCOF1*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P2	p.G662V	ENSG00000070814	ENST00000504761	Transcript	missense_variant	probably_damaging(0.99)
chr5	76028495	76028495	*F2R*	Missense_Mutation	.	SNP	G	G	A	rs560811435	chan_et_al_P2	p.V149M	ENSG00000181104	ENST00000319211	Transcript	missense_variant	probably_damaging(0.948)
chr5	82832995	82832995	*VCAN*	Missense_Mutation	.	SNP	a	a	T	novel	chan_et_al_P2	p.E1391D	ENSG00000038427	ENST00000265077	Transcript	missense_variant	benign(0.012)
chr6	136593183	136593183	*BCLAF1*	Missense_Mutation	.	SNP	G	G	C	rs73555557	chan_et_al_P2	p.H665D	ENSG00000029363	ENST00000531224	Transcript	missense_variant	benign(0.402)
chr6	159044616	159044616	*TMEM181*	Nonsense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P2	p.R448*	ENSG00000146433	ENST00000367090	Transcript	stop_gained	NA
chr7	102045117	102045117	*PRKRIP1*	Missense_Mutation	.	SNP	C	C	A	rs570900028	chan_et_al_P2	p.R127S	ENSG00000128563	ENST00000496391	Transcript	missense_variant	possibly_damaging(0.683)
chr7	127235557	127235557	*FSCN3*	Missense_Mutation	.	SNP	G	G	A	rs199821862	chan_et_al_P2	p.R114H	ENSG00000106328	ENST00000265825	Transcript	missense_variant	benign(0.016)
chr7	128478481	128478481	*FLNC*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P2	p.A403V	ENSG00000128591	ENST00000325888	Transcript	missense_variant	probably_damaging(0.999)
chr8	120101984	120101984	*COLEC10*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P2	p.P72S	ENSG00000184374	ENST00000332843	Transcript	missense_variant	benign(0.018)
chr9	35811508	35811508	*SPAG8*	Missense_Mutation	.	SNP	a	a	G	novel	chan_et_al_P2	p.S179P	ENSG00000137098	ENST00000340291	Transcript	missense_variant	unknown()
chrX	140983193	140983193	*MAGEC3*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P2	p.G350R	ENSG00000165509	ENST00000298296	Transcript	missense_variant	probably_damaging(0.953)
chr1	145562459	145562459	*ANKRD35*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P3	p.R716K	ENSG00000198483	ENST00000355594	Transcript	missense_variant	benign(0.02)
chr1	227842973	227842973	*ZNF678*	Missense_Mutation	.	SNP	G	G	A	rs201014624	chan_et_al_P3	p.R341K	ENSG00000181450	ENST00000343776	Transcript	missense_variant	benign(0.175)
chr13	52439594	52439594	*CCDC70*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P3	p.R27Q	ENSG00000123171	ENST00000242819	Transcript	missense_variant	benign(0.016)
chr15	32688550	32688550	*GOLGA8K*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P3	p.I357L	ENSG00000249931	ENST00000512626	Transcript	missense_variant	benign(0)
chr18	21750417	21750417	*OSBPL1A*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P3	p.S764R	ENSG00000141447	ENST00000319481	Transcript	missense_variant	possibly_damaging(0.566)
chr22	42910199	42910199	*RRP7A*	Missense_Mutation	.	SNP	G	G	A	rs146958654	chan_et_al_P3	p.R224W	ENSG00000189306	ENST00000323013	Transcript	missense_variant	probably_damaging(0.998)
chr7	106508260	106508260	*PIK3CG*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P3	p.A85V	ENSG00000105851	ENST00000359195	Transcript	missense_variant	benign(0.002)
chr1	111932026	111932026	*MTOR*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P6	p.L1759V	ENSG00000198793	ENST00000361445	Transcript	missense_variant	benign(0.171)
chr1	113650265	113650265	*LRIG2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P6	p.L455I	ENSG00000198799	ENST00000361127	Transcript	missense_variant	benign(0.007)
chr1	152187251	152187251	*HRNR*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P6	p.Q2285R	ENSG00000197915	ENST00000368801	Transcript	missense_variant	unknown()
chr1	152280164	152280164	*FLG*	Missense_Mutation	.	SNP	T	T	C	rs200642470	chan_et_al_P6	p.T2400A	ENSG00000143631	ENST00000368799	Transcript	missense_variant	benign(0.023)
chr10	47193377	47193377	*AGAP10*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P6	p.M293V	ENSG00000204172	ENST00000413193	Transcript	missense_variant	unknown()
chr11	10742762	10742762	*ALKBH8*	Missense_Mutation	.	SNP	G	G	T	rs78396710	chan_et_al_P6	p.N79K	ENSG00000137760	ENST00000428149	Transcript	missense_variant	benign(0.261)
chr11	85988997	85988997	*EED*	Frame_Shift_Del	.	DEL	T	T	-	novel	chan_et_al_P6	p.W389Gfs*3	ENSG00000074266	ENST00000263360	Transcript	frameshift_variant	NA
chr12	120152068	120152068	*CIT*	Missense_Mutation	.	SNP	G	G	C	rs200963622	chan_et_al_P6	p.R1414G	ENSG00000122966	ENST00000392521	Transcript	missense_variant	possibly_damaging(0.796)
chr12	122337639	122337639	*PSMD9*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P6	p.E114A	ENSG00000110801	ENST00000541212	Transcript	missense_variant	possibly_damaging(0.824)
chr12	53494946	53494946	*IGFBP6*	Splice_Site	.	SNP	T	T	G	novel	chan_et_al_P6	NA	ENSG00000167779	ENST00000301464	Transcript	splice_donor_variant	NA
chr12	55641827	55641827	*OR6C74*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P6	p.S252R	ENSG00000197706	ENST00000343870	Transcript	missense_variant	probably_damaging(0.999)
chr12	58162799	58162799	*METTL1*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P6	p.T271P	ENSG00000037897	ENST00000324871	Transcript	missense_variant	benign(0)
chr12	6645733	6645733	*GAPDH*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P6	p.D35Y	ENSG00000111640	ENST00000229239	Transcript	missense_variant	probably_damaging(0.989)
chr12	76424952	76424952	*PHLDA1*	Missense_Mutation	.	SNP	c	c	G	rs200070422	chan_et_al_P6	p.Q190H	ENSG00000139289	ENST00000266671	Transcript	missense_variant	benign(0.387)
chr13	80911531	80911531	*SPRY2*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P6	p.R104G	ENSG00000136158	ENST00000377102	Transcript	missense_variant	benign(0.41)

chr14	32561316	32561316	*ARHGAP5*	Nonsense_Mutation	.	SNP	G	G	T	rs200628183	chan_et_al_P6	p.E481*	ENSG00000100852	ENST00000345122	Transcript	stop_gained	NA
chr14	64686090	64686090	*SYNE2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P6	p.D6608Y	ENSG00000054654	ENST00000358025	Transcript	missense_variant	possibly_damaging(0.905)
chr15	90622990	90622990	*ZNF710*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P6	p.D642Y	ENSG00000140548	ENST00000268154	Transcript	missense_variant	benign(0.135)
chr16	30409387	30409387	*ZNF48*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P6	p.D272E	ENSG00000180035	ENST00000320159	Transcript	missense_variant	benign(0.028)
chr16	66919412	66919412	*PDP2*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P6	p.L409V	ENSG00000172840	ENST00000311765	Transcript	missense_variant	possibly_damaging(0.901)
chr17	74004338	74004338	*EVPL*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P6	p.D1650H	ENSG00000167880	ENST00000301607	Transcript	missense_variant	probably_damaging(0.936)
chr18	9122638	9122638	*NDUFV2*	Missense_Mutation	.	SNP	G	G	C	rs148158107	chan_et_al_P6	p.R143P	ENSG00000178127	ENST00000318388	Transcript	missense_variant	probably_damaging(0.964)
chr19	37961264	37961264	*ZNF570*	Missense_Mutation	.	SNP	T	T	G	rs201383469	chan_et_al_P6	p.V3G	ENSG00000171827	ENST00000330173	Transcript	missense_variant	benign(0.249)
chr19	44896564	44896564	*ZNF285*	Missense_Mutation	.	SNP	C	C	A	rs113465092	chan_et_al_P6	p.A28S	ENSG00000267508	ENST00000330997	Transcript	missense_variant	benign(0.207)
chr19	46825086	46825086	*HIF3A*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P6	p.A400T	ENSG00000124440	ENST00000377670	Transcript	missense_variant	benign(0.271)
chr2	130832929	130832929	*POTEF*	Missense_Mutation	.	SNP	C	C	T	rs373944612	chan_et_al_P6	p.A706T	ENSG00000196604	ENST00000357462	Transcript	missense_variant	probably_damaging(0.945)
chr2	3392037	3392037	*TRAPPC12*	Missense_Mutation	.	SNP	G	G	C	rs200331319	chan_et_al_P6	p.A215P	ENSG00000171853	ENST00000324266	Transcript	missense_variant	benign(0.286)
chr2	64085017	64085017	*UGP2*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P6	p.E68K	ENSG00000169764	ENST00000337130	Transcript	missense_variant	benign(0.068)
chr21	34142132	34142134	*PAXBP1*	In_Frame_Del	.	DEL	TGA	TGA	-	novel	chan_et_al_P6	p.S156del	ENSG00000159086	ENST00000331923	Transcript	inframe_deletion	NA
chr3	138186996	138186996	*ESYT3*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P6	p.E423G	ENSG00000158220	ENST00000389567	Transcript	missense_variant	benign(0.039)
chr3	27460082	27460082	*SLC4A7*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P6	p.D509E	ENSG00000033867	ENST00000295736	Transcript	missense_variant	probably_damaging(0.999)
chr3	52437650	52437650	*BAP1*	Frame_Shift_Del	.	DEL	T	T	-	novel	chan_et_al_P6	p.N504Tfs*67	ENSG00000163930	ENST00000460680	Transcript	frameshift_variant	NA
chr4	48994086	48994086	*CWH43*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P6	p.T164A	ENSG00000109182	ENST00000226432	Transcript	missense_variant	benign(0.011)
chr4	90756766	90756766	*SNCA*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P6	p.A18G	ENSG00000145335	ENST00000394986	Transcript	missense_variant	probably_damaging(0.989)
chr4	93426029	93426029	*USP17L5*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P6	p.P494L	ENSG00000227140	ENST00000507227	Transcript	missense_variant	benign(0)
chr5	134678948	134678948	*H2AFY*	Splice_Site	.	SNP	A	A	C	novel	chan_et_al_P6	p.X318_splice	ENSG00000113648	ENST00000511689	Transcript	splice_donor_variant	NA
chr5	137801506	137801506	*EGR1*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P6	p.P19R	ENSG00000120738	ENST00000239938	Transcript	missense_variant	unknown(0)
chr5	147480120	147480120	*SPINK5*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P6	p.T399I	ENSG00000133710	ENST00000359874	Transcript	missense_variant	possibly_damaging(0.848)
chr5	176939587	176939587	*DDX41*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P6	p.V487L	ENSG00000183258	ENST00000507955	Transcript	missense_variant	benign(0.032)
chr5	37169038	37169038	*C5orf42*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P6	p.Y2363S	ENSG00000197603	ENST00000425232	Transcript	missense_variant	benign(0.158)
chr6	118015332	118015332	*NUS1*	Missense_Mutation	.	SNP	C	C	G	rs76776814	chan_et_al_P6	p.A227G	ENSG00000153989	ENST00000368494	Transcript	missense_variant	benign(0)
chr6	31962929	31962929	*C4A*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P6	p.M968V	ENSG00000244731	ENST00000428956	Transcript	missense_variant	benign(0.001)
chr6	31995667	31995667	*C4B*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P6	p.M968V	ENSG00000224389	ENST00000435363	Transcript	missense_variant	benign(0.001)
chr6	43608019	43608019	*MAD2L1BP*	Missense_Mutation	.	SNP	C	C	G	rs201593032	chan_et_al_P6	p.R224G	ENSG00000124688	ENST00000451025	Transcript	missense_variant	probably_damaging(0.994)
chr6	73332249	73332249	*KCNQ5*	Missense_Mutation	.	SNP	T	T	G	rs200862397	chan_et_al_P6	p.V111G	ENSG00000185760	ENST00000342056	Transcript	missense_variant	benign(0.071)
chr7	26295999	26295999	*IQCE*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P6	p.P368L	ENSG00000106012	ENST00000402050	Transcript	missense_variant	benign(0.021)
chr8	101727792	101727792	*PABPC1*	Missense_Mutation	.	SNP	C	C	T	rs201575415	chan_et_al_P6	p.A181T	ENSG00000070756	ENST00000318607	Transcript	missense_variant	benign(0.005)
chr8	65493507	65493507	*BHLHE22*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P6	p.P54S	ENSG00000180828	ENST00000321870	Transcript	missense_variant	benign(0.068)
chr8	73202477	73202477	*SPAG11B*	Missense_Mutation	.	SNP	G	G	A	rs369319310	chan_et_al_P6	p.R66C	ENSG00000164871	ENST00000398462	Transcript	missense_variant	probably_damaging(0.957)
chr9	74817561	74817561	*GDA*	Missense_Mutation	.	SNP	A	A	C	novel	chan_et_al_P6	p.D96A	ENSG00000119125	ENST00000238018	Transcript	missense_variant	possibly_damaging(0.902)
chrX	135957700	135957700	*RBMX*	Missense_Mutation	.	SNP	T	T	C	rs139954333	chan_et_al_P6	p.R196G	ENSG00000147274	ENST00000320676	Transcript	missense_variant	possibly_damaging(0.893)

chrX	21985436	21985436	*SMS*	Splice_Site	.	SNP	T	T	G	novel	chan_et_al_P6	p.X57_splice	ENSG00000102172	ENST00000404933	Transcript	splice_donor_variant	NA
chr1	146756034	146756034	*CHD1L*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P7	p.M572I	ENSG00000131778	ENST00000369258	Transcript	missense_variant	benign(0.03)
chr1	27089777	27089777	*ARID1A*	Splice_Site	.	SNP	G	G	T	novel	chan_et_al_P7	p.X911_splice	ENSG00000117713	ENST00000324856	Transcript	splice_donor_variant	NA
chr11	124294542	124294542	*OR8B4*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P7	p.V76L	ENSG00000198657	ENST00000356130	Transcript	missense_variant	probably_damaging(0.978)
chr11	26719951	26719951	*SLC5A12*	Splice_Site	.	SNP	A	A	G	novel	chan_et_al_P7	p.X317_splice	ENSG00000148942	ENST00000396005	Transcript	splice_donor_variant	NA
chr12	91348068	91348068	*CCER1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P7	p.R151H	ENSG00000197651	ENST00000358859	Transcript	missense_variant	probably_damaging(0.923)
chr17	45247362	45247362	*CDC27*	Nonsense_Mutation	.	SNP	G	G	A	rs73319503	chan_et_al_P7	p.Q100*	ENSG00000004897	ENST00000531206	Transcript	stop_gained	NA
chr19	48244651	48244651	*EHD2*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P7	p.P532S	ENSG00000024422	ENST00000263277	Transcript	missense_variant	probably_damaging(0.999)
chr2	144193228	144193228	*ARHGAP15*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P7	p.L178S	ENSG00000075884	ENST00000295095	Transcript	missense_variant	benign(0.114)
chr2	158971770	158971770	*UPP2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P7	p.S170I	ENSG00000007001	ENST00000605860	Transcript	missense_variant	probably_damaging(0.996)
chr2	63282672	63282672	*OTX1*	Nonsense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P7	p.Q96*	ENSG00000115507	ENST00000282549	Transcript	stop_gained	NA
chr22	43019796	43019796	*CYB5R3*	Missense_Mutation	.	SNP	T	T	G	novel	chan_et_al_P7	p.E277D	ENSG00000100243	ENST00000361740	Transcript	missense_variant	benign(0.006)
chr3	52437801	52437802	*BAP1*	Frame_Shift_Ins	.	INS	-	-	T	novel	chan_et_al_P7	p.E454Rfs*15	ENSG00000163930	ENST00000460680	Transcript	frameshift_variant	NA
chr4	42282423	42282423	*OTOP1*	Missense_Mutation	.	SNP	G	G	T	rs200057225	chan_et_al_P7	p.H117N	ENSG00000163982	ENST00000296358	Transcript	missense_variant	benign(0.009)
chr4	88047344	88047346	*AFF1*	In_Frame_Del	.	DEL	TAA	TAA	-	novel	chan_et_al_P7	p.K890del	ENSG00000172493	ENST00000395146	Transcript	inframe_deletion	NA
chr6	36181711	36181711	*BRPF3*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P7	p.S846F	ENSG00000096070	ENST00000357641	Transcript	missense_variant	possibly_damaging(0.736)
chr7	20444469	20444469	*ITGB8*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P7	p.E636K	ENSG00000105855	ENST00000222573	Transcript	missense_variant	benign(0.005)
chr9	117186796	117186796	*DFNB31*	Missense_Mutation	.	SNP	G	G	T	rs200905454	chan_et_al_P7	p.Q412K	ENSG00000095397	ENST00000362057	Transcript	missense_variant	possibly_damaging(0.776)
chr9	136699461	136699461	*VAV2*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P7	p.P128T	ENSG00000160293	ENST00000371850	Transcript	missense_variant	possibly_damaging(0.706)
chr9	41505511	41505511	*SPATA31A5*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P7	p.T928M	ENSG00000233788	ENST00000377621	Transcript	missense_variant	NA
chrX	54566670	54566670	*GNL3L*	Nonsense_Mutation	.	SNP	A	A	T	novel	chan_et_al_P7	p.K62*	ENSG00000130119	ENST00000336470	Transcript	stop_gained	NA
chrX	69366608	69366608	*IGBP1*	Missense_Mutation	.	SNP	T	T	C	rs61755732	chan_et_al_P7	p.I203T	ENSG00000089289	ENST00000342206	Transcript	missense_variant	benign(0.012)
chr1	185959470	185959470	*HMCN1*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P8	p.V1091A	ENSG00000143341	ENST00000271588	Transcript	missense_variant	benign(0.009)
chr11	17635225	17635225	*OTOG*	Missense_Mutation	.	SNP	A	A	C	rs74727929	chan_et_al_P8	p.T2181P	ENSG00000188162	ENST00000399391	Transcript	missense_variant	possibly_damaging(0.895)
chr11	280422	280422	*NLRP6*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P8	p.D230Y	ENSG00000174885	ENST00000312165	Transcript	missense_variant	probably_damaging(1)
chr12	122261624	122261624	*SETD1B*	Nonsense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P8	p.W1670*	ENSG00000139718	ENST00000267197	Transcript	stop_gained	NA
chr12	130830972	130830972	*PIWIL1*	Missense_Mutation	.	SNP	C	C	G	novel	chan_et_al_P8	p.P125R	ENSG00000125207	ENST00000245255	Transcript	missense_variant	probably_damaging(0.99)
chr12	132210016	132210016	*SFSWAP*	Nonsense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P8	p.Q225*	ENSG00000061936	ENST00000541286	Transcript	stop_gained	NA
chr12	56676244	56676244	*CS*	Missense_Mutation	.	SNP	C	C	T	rs116165297	chan_et_al_P8	p.R183Q	ENSG00000062485	ENST00000351328	Transcript	missense_variant	benign(0.003)
chr17	45219311	45219311	*CDC27*	Missense_Mutation	.	SNP	T	T	C	rs140737545	chan_et_al_P8	p.I493V	ENSG00000004897	ENST00000531206	Transcript	missense_variant	benign(0.006)
chr17	45917737	45917737	*SCRN2*	Missense_Mutation	.	SNP	C	C	A	novel	chan_et_al_P8	p.C59F	ENSG00000141295	ENST00000290216	Transcript	missense_variant	probably_damaging(1)
chr17	65971920	65971920	*BPTF*	Nonsense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P8	p.R2858*	ENSG00000171634	ENST00000306378	Transcript	stop_gained	NA
chr19	11094919	11094919	*SMARCA4*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P8	p.S31N	ENSG00000127616	ENST00000429416	Transcript	missense_variant	unknown(0)
chr19	2039787	2039787	*MKNK2*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P8	p.Q408R	ENSG00000099875	ENST00000250896	Transcript	missense_variant	benign(0.002)
chr19	47673078	47673078	*SAE1*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P8	p.V211M	ENSG00000142230	ENST00000270225	Transcript	missense_variant	benign(0.027)
chr19	58420682	58420682	*ZNF417*	Missense_Mutation	.	SNP	T	T	C	rs202194085	chan_et_al_P8	p.R322G	ENSG00000173480	ENST00000312026	Transcript	missense_variant	benign(0.005)

chr2	131803638	131803638	*ARHGEF4*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P8	p.R650H	ENSG00000136002	ENST00000326016	Transcript	missense_variant	benign(0.06)
chr3	125650525	125650525	*ALG1L*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P8	p.D77E	ENSG00000189366	ENST00000340333	Transcript	missense_variant	possibly_damaging(0.699)
chr3	196812529	196812529	*DLG1*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P8	p.D620G	ENSG00000075711	ENST00000346964	Transcript	missense_variant	probably_damaging(0.959)
chr3	98002446	98002446	*OR5H2*	Missense_Mutation	.	SNP	G	G	A	rs111235306	chan_et_al_P8	p.V239I	ENSG00000197938	ENST00000355273	Transcript	missense_variant	benign(0.001)
chr4	27461512	27461512	*TNIP2*	Missense_Mutation	.	SNP	T	T	C	novel	chan_et_al_P8	p.K330E	ENSG00000168884	ENST00000315423	Transcript	missense_variant	benign(0.002)
chr4	48636349	48636349	*FRYL*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P8	p.Q27K	ENSG00000075539	ENST00000358350	Transcript	missense_variant	benign(0.236)
chr4	83372349	83372349	*ENOPH1*	Nonsense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P8	p.Q114*	ENSG00000145293	ENST00000273920	Transcript	stop_gained	NA
chr5	113972538	113972538	*CTNND2*	Missense_Mutation	.	SNP	G	G	C	novel	chan_et_al_P8	p.H173D	ENSG00000169862	ENST00000304623	Transcript	missense_variant	possibly_damaging(0.811)
chr5	92923763	92923763	*NR2F1*	Missense_Mutation	.	SNP	C	C	T	novel	chan_et_al_P8	p.R202C	ENSG00000175745	ENST00000327111	Transcript	missense_variant	benign(0.117)
chr6	158288619	158288619	*SNX9*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P8	p.N18S	ENSG00000130340	ENST00000392185	Transcript	missense_variant	possibly_damaging(0.524)
chr6	35856637	35856637	*SRPK1*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P8	p.L86S	ENSG00000096063	ENST00000378825	Transcript	missense_variant	probably_damaging(0.999)
chr8	41476454	41476454	*AGPAT6*	Missense_Mutation	.	SNP	A	A	G	novel	chan_et_al_P8	p.K407R	ENSG00000158669	ENST00000396987	Transcript	missense_variant	probably_damaging(0.956)
chr8	63502340	63502340	*NKAIN3*	Missense_Mutation	.	SNP	G	G	T	novel	chan_et_al_P8	p.G87V	ENSG00000185942	ENST00000523211	Transcript	missense_variant	probably_damaging(1)
chr9	131020452	131020452	*GOLGA2*	Missense_Mutation	.	SNP	G	G	A	novel	chan_et_al_P8	p.A745V	ENSG00000167110	ENST00000421699	Transcript	missense_variant	probably_damaging(0.944)
chr1	100614366	100614366	*TRMT13*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.T479K	ENSG00000122435	ENST00000370141	Transcript	missense_variant	benign(0.022)
chr1	102462321	102462321	*OLFM3*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G18*	ENSG00000118733	ENST00000370103	Transcript	stop_gained	NA
chr1	104631 61	104631 61	*PGD*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D100Y	ENSG00000142657	ENST00000270776	Transcript	missense_variant	probably_damaging(1)
chr1	108115978	108115978	*VAV3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S840Y	ENSG00000134215	ENST00000370056	Transcript	missense_variant	probably_damaging(1)
chr1	110256309	110256309	*GSTM5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.R96S	ENSG00000134201	ENST00000256593	Transcript	missense_variant	possibly_damaging(0.863)
chr1	114340346	114340346	*RSBN1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P1	p.H340Tfs*11	ENSG00000081019	ENST00000261441	Transcript	frameshift_variant	NA
chr1	118644392	118644392	*SPAG17*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.G202E	ENSG00000155761	ENST00000336338	Transcript	missense_variant	probably_damaging(1)
chr1	144922205	144922205	*PDE4DIP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S321R	ENSG00000178104	ENST00000369356	Transcript	missense_variant	probably_damaging(0.999)
chr1	145769498	145769498	*GPR89A*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P1	p.X336_splice	ENSG00000117262	ENST00000313835	Transcript	splice_acceptor_variant	NA
chr1	151265395	151265395	*PI4KB*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G807V	ENSG00000143393	ENST00000368875	Transcript	missense_variant	possibly_damaging(0.535)
chr1	151265430	151265430	*PI4KB*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E795D	ENSG00000143393	ENST00000368875	Transcript	missense_variant	possibly_damaging(0.594)
chr1	151783813	151783813	*RORC*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S461R	ENSG00000143365	ENST00000318247	Transcript	missense_variant	benign(0.373)
chr1	152127677	152127677	*RPTN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G633V	ENSG00000215853	ENST00000316073	Transcript	missense_variant	benign(0.408)
chr1	152129243	152129243	*RPTN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.C111F	ENSG00000215853	ENST00000316073	Transcript	missense_variant	benign(0)
chr1	154309959	154309959	*ATP8B2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L358I	ENSG00000143515	ENST00000368489	Transcript	missense_variant	benign(0.26)
chr1	156910163	156910163	*ARHGEF11*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P1	p.E1191Sfs*61	ENSG00000132694	ENST00000368194	Transcript	frameshift_variant	NA
chr1	168034930	168034930	*DCAF6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L848M	ENSG00000143164	ENST00000367840	Transcript	missense_variant	probably_damaging(0.924)
chr1	169519150	169519150	*F5*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.C500*	ENSG00000198734	ENST00000367797	Transcript	stop_gained	NA
chr1	169798495	169798495	*C1orf112*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G407W	ENSG00000000460	ENST00000286031	Transcript	missense_variant	probably_damaging(1)
chr1	176068 52	176068 52	*PADI3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E521D	ENSG00000142619	ENST00000375460	Transcript	missense_variant	benign(0.003)
chr1	179638407	179638407	*TDRD5*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E910*	ENSG00000162782	ENST00000444136	Transcript	stop_gained	NA
chr1	182429173	182429173	*RGSL1*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P1	p.K70Nfs*46	ENSG00000121446	ENST00000294854	Transcript	frameshift_variant	NA

chr1	183933104	183933104	*COLGALT2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.P295T	ENSG00000198756	ENST00000361927	Transcript	missense_variant	possibly_damaging(0.809)
chr1	186388191	186388191	*C1orf27*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.H450N	ENSG00000157181	ENST00000287859	Transcript	missense_variant	probably_damaging(0.915)
chr1	240979706	240979706	*RGS7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G232C	ENSG00000182901	ENST00000366565	Transcript	missense_variant	probably_damaging(0.999)
chr1	247013006	247013006	*AHCTF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S2110Y	ENSG00000153207	ENST00000326225	Transcript	missense_variant	probably_damaging(0.931)
chr1	248224169	248224170	*OR2L3*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P1	p.S63Kfs*7	ENSG00000198128	ENST00000359959	Transcript	frameshift_variant	NA
chr1	248224243	248224243	*OR2L3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G87V	ENSG00000198128	ENST00000359959	Transcript	missense_variant	possibly_damaging(0.703)
chr1	256554564	256554564	*RHD*	3'UTR	.	SNP	C	C	A	novel	sia_et_al_P1	NA	ENSG00000187010	ENST00000328664	Transcript	3_prime_UTR_variant	NA
chr1	362124557	362124557	*CLSPN*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q922K	ENSG00000092853	ENST00000318121	Transcript	missense_variant	possibly_damaging(0.481)
chr1	362125508	362125508	*CLSPN*	Missense_Mutation	.	SNP	C	C	A	rs145905522	sia_et_al_P1	p.D905Y	ENSG00000092853	ENST00000318121	Transcript	missense_variant	probably_damaging(0.999)
chr1	38006266	38006266	*SNIP1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P1	p.R140Gfs*103	ENSG00000163877	ENST00000296215	Transcript	frameshift_variant	NA
chr1	38435350	38435350	*SF3A3*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E355*	ENSG00000183431	ENST00000373019	Transcript	stop_gained	NA
chr1	43131694	43131694	*PPIH*	Frame_Shift_Del	.	DEL	C	C	-	rs142436431	sia_et_al_P1	p.C128Afs*22	ENSG00000171960	ENST00000304979	Transcript	frameshift_variant	NA
chr1	46827472	46827472	*NSUN4*	Missense_Mutation	.	SNP	C	C	A	rs551888089	sia_et_al_P1	p.A370D	ENSG00000117481	ENST00000474844	Transcript	missense_variant	probably_damaging(0.928)
chr1	48771551	48771551	*SPATA6*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P1	NA	ENSG00000132122	ENST00000371847	Transcript	splice_acceptor_variant	NA
chr1	60463285	60463285	*C1orf87*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.N492K	ENSG00000162598	ENST00000371201	Transcript	missense_variant	probably_damaging(0.974)
chr1	60521104	60521104	*C1orf87*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E38D	ENSG00000162598	ENST00000371201	Transcript	missense_variant	benign(0.118)
chr1	67278043	67278043	*DNAJC11*	Frame_Shift_Del	.	DEL	TC	TC	-	rs374290353	sia_et_al_P1	p.E115Gfs*25	ENSG00000007923	ENST00000377577	Transcript	frameshift_variant	NA
chr1	67306307	67306307	*WDR78*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E447*	ENSG00000152763	ENST00000371026	Transcript	stop_gained	NA
chr10	104592963	104592963	*CYP17A1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E252D	ENSG00000148795	ENST00000369887	Transcript	missense_variant	possibly_damaging(0.901)
chr10	113632641	113632641	*CELF2*	Missense_Mutation	.	SNP	C	C	G	novel	sia_et_al_P1	p.L396V	ENSG00000048740	ENST00000450189	Transcript	missense_variant	possibly_damaging(0.754)
chr10	27406575	27406575	*YME1L1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A607E	ENSG00000136758	ENST00000326799	Transcript	missense_variant	probably_damaging(1)
chr10	32311837	32311837	*KIF5B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S618I	ENSG00000170759	ENST00000302418	Transcript	missense_variant	benign(0.125)
chr10	65405033	65405033	*PRKCQ*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E133*	ENSG00000065675	ENST00000263125	Transcript	stop_gained	NA
chr10	75607088	75607088	*CAMK2G*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.W238C	ENSG00000148660	ENST00000322680	Transcript	missense_variant	probably_damaging(0.999)
chr10	90988046	90988046	*LIPA*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P1	p.F113Lfs*48	ENSG00000107798	ENST00000336233	Transcript	frameshift_variant	NA
chr10	94225589	94225589	*IDE*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.V778F	ENSG00000119912	ENST00000265986	Transcript	missense_variant	possibly_damaging(0.865)
chr10	96534948	96534948	*CYP2C19*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.P101Q	ENSG00000165841	ENST00000371321	Transcript	missense_variant	possibly_damaging(0.765)
chr11	10783557	10783557	*CTR9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.P269T	ENSG00000198730	ENST00000361367	Transcript	missense_variant	possibly_damaging(0.589)
chr11	111575716	111575716	*SIK2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L318F	ENSG00000170145	ENST00000304987	Transcript	missense_variant	probably_damaging(0.996)
chr11	113813800	113813800	*HTR3B*	Frame_Shift_Del	.	DEL	C	C	-	rs138362802	sia_et_al_P1	p.N266Tfs*31	ENSG00000149305	ENST00000260191	Transcript	frameshift_variant	NA
chr11	118250351	118250351	*UBE4A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.Q595K	ENSG00000110344	ENST00000437336	Transcript	missense_variant	possibly_damaging(0.798)
chr11	118422974	118422974	*IFT46*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S238Y	ENSG00000118096	ENST00000264020	Transcript	missense_variant	possibly_damaging(0.603)
chr11	125707872	125707872	*PATE4*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P1	p.F57Sfs*28	ENSG00000237353	ENST00000457514	Transcript	frameshift_variant	NA
chr11	126124209	126124209	*FAM118B*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P1	p.W193R	ENSG00000197798	ENST00000533050	Transcript	missense_variant	probably_damaging(1)
chr11	13729601	13729601	*FAR1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.P174T	ENSG00000197601	ENST00000354817	Transcript	missense_variant	benign(0.248)
chr11	18736088	18736088	*IGSF22*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.D539N	ENSG00000179057	ENST00000513874	Transcript	missense_variant	benign(0.006)

chr11	31815084	31815084	*PAX6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G326C	ENSG00000007372	ENST00000419022	Transcript	missense_variant	probably_damaging(0.957)
chr11	32611129	32611129	*EIF3M*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E159*	ENSG00000149100	ENST00000531120	Transcript	stop_gained	NA
chr11	35223257	35223257	*CD44*	Missense_Mutation	.	SNP	G	G	C	novel	sia_et_al_P1	p.W359S	ENSG00000026508	ENST00000428726	Transcript	missense_variant	possibly_damaging(0.558)
chr11	61015900	61015900	*PGA5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.K222N	ENSG00000256713	ENST00000312403	Transcript	missense_variant	benign(0.002)
chr11	65056548	65056548	*POLA2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E387*	ENSG00000014138	ENST00000265465	Transcript	stop_gained	NA
chr11	88300908	88300908	*GRM5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.R648I	ENSG00000168959	ENST00000418177	Transcript	missense_variant	probably_damaging(0.999)
chr11	89603860	89603860	*TRIM64B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L427I	ENSG00000189253	ENST00000329862	Transcript	missense_variant	possibly_damaging(0.802)
chr11	95467866	95467866	*ZNF143*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P1	p.X563_splice	ENSG00000166478	ENST00000396602	Transcript	splice_acceptor_variant	NA
chr11	95712701	95712701	*MAML2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T961K	ENSG00000184384	ENST00000524717	Transcript	missense_variant	unknown(0)
chr11	99836444	99836444	*SBF2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A574S	ENSG00000133812	ENST00000256190	Transcript	missense_variant	probably_damaging(0.989)
chr12	100774620	100774620	*SLC17A8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.M81I	ENSG00000179520	ENST00000323346	Transcript	missense_variant	benign(0.411)
chr12	101491706	101491706	*ANO4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.F628L	ENSG00000151572	ENST00000392979	Transcript	missense_variant	possibly_damaging(0.891)
chr12	109530429	109530429	*ALKBH2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.P55T	ENSG00000189046	ENST00000429722	Transcript	missense_variant	benign(0.075)
chr12	116446753	116446753	*MED13L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H489N	ENSG00000123066	ENST00000281928	Transcript	missense_variant	unknown(0)
chr12	26864139	26864139	*ITPR2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.K306N	ENSG00000123104	ENST00000381340	Transcript	missense_variant	probably_damaging(0.987)
chr12	30485338	30485338	*TULP3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.N419K	ENSG00000078246	ENST00000397132	Transcript	missense_variant	benign(0.073)
chr12	46318669	46318669	*SCAF11*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H1250N	ENSG00000139218	ENST00000369367	Transcript	missense_variant	possibly_damaging(0.864)
chr12	51470271	51470271	*CSRNP2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S25*	ENSG00000110925	ENST00000228515	Transcript	stop_gained	NA
chr12	52188297	52188297	*SCN8A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.W1556L	ENSG00000196876	ENST00000354534	Transcript	missense_variant	benign(0.41)
chr12	53776772	53776772	*SP1*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P1	p.T349Pfs*20	ENSG00000185591	ENST00000327443	Transcript	frameshift_variant	NA
chr12	66320909	66320909	*NCAPD2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.P687H	ENSG00000010292	ENST00000315579	Transcript	missense_variant	possibly_damaging(0.664)
chr12	76844640	76844640	*OSBPL8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H70N	ENSG00000091039	ENST00000261183	Transcript	missense_variant	benign(0.034)
chr12	82824690	82824690	*METTL25*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.W433L	ENSG00000127720	ENST00000248306	Transcript	missense_variant	benign(0.014)
chr12	95603774	95603774	*FGD6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T429K	ENSG00000180263	ENST00000343958	Transcript	missense_variant	benign(0.002)
chr12	97328974	97328974	*NEDD1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S244*	ENSG00000139350	ENST00000557644	Transcript	stop_gained	NA
chr13	107164913	107164913	*EFNB2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L124I	ENSG00000125266	ENST00000245323	Transcript	missense_variant	probably_damaging(0.995)
chr13	25066723	25066723	*PARP4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A297S	ENSG00000102699	ENST00000381989	Transcript	missense_variant	possibly_damaging(0.872)
chr13	25887066	25887066	*NUPL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G111V	ENSG00000139496	ENST00000381736	Transcript	missense_variant	probably_damaging(0.999)
chr13	31326220	31326220	*ALOX5AP*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L68I	ENSG00000132965	ENST00000380490	Transcript	missense_variant	probably_damaging(0.955)
chr13	44462960	44462960	*LACC1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.C325*	ENSG00000179630	ENST00000441843	Transcript	stop_gained	NA
chr13	77655588	77655588	*MYCBP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H3760N	ENSG00000005810	ENST00000544440	Transcript	missense_variant	probably_damaging(0.921)
chr14	104465039	104465039	*TDRD9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S486Y	ENSG00000156414	ENST00000409874	Transcript	missense_variant	probably_damaging(0.999)
chr14	21869106	21869106	*CHD8*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.R1433H	ENSG00000100888	ENST00000399982	Transcript	missense_variant	possibly_damaging(0.813)
chr14	21884021	21884021	*CHD8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D588Y	ENSG00000100888	ENST00000399982	Transcript	missense_variant	probably_damaging(0.996)
chr14	35252422	35252422	*BAZ1A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E672*	ENSG00000198604	ENST00000360310	Transcript	stop_gained	NA
chr14	36192293	36192293	*RALGAPA1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L682I	ENSG00000174373	ENST00000307138	Transcript	missense_variant	probably_damaging(0.995)

chr14	36218005	36218005	*RALGAPA1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.R346I	ENSG00000174373	ENST00000307138	Transcript	missense_variant	possibly_damaging(0.848)
chr14	36783910	36783910	*MBIP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A154D	ENSG00000151332	ENST00000416007	Transcript	missense_variant	probably_damaging(1)
chr14	50122436	50122436	*POLE2*	Nonsense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.W294*	ENSG00000100479	ENST00000216367	Transcript	stop_gained	NA
chr14	92470239	92470239	*TRIP11*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A1361S	ENSG00000100815	ENST00000267622	Transcript	missense_variant	benign(0.281)
chr14	96788576	96788576	*ATG2B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D918Y	ENSG00000066739	ENST00000359933	Transcript	missense_variant	probably_damaging(0.99)
chr15	102194871	102194871	*TARSL2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H775N	ENSG00000185418	ENST00000335968	Transcript	missense_variant	benign(0.152)
chr15	34065789	34065789	*RYR3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G3037V	ENSG00000198838	ENST00000389232	Transcript	missense_variant	probably_damaging(0.999)
chr15	40462302	40462302	*BUB1B*	Missense_Mutation	.	SNP	C	C	A	rs548540749	sia_et_al_P1	p.D73E	ENSG00000156970	ENST00000287598	Transcript	missense_variant	probably_damaging(0.999)
chr15	52258184	52258184	*LEO1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E192D	ENSG00000166477	ENST00000299601	Transcript	missense_variant	benign(0)
chr15	53815477	53815477	*WDR72*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A1064E	ENSG00000166415	ENST00000396328	Transcript	missense_variant	benign(0.1)
chr15	65559052	65559052	*PARP16*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D123Y	ENSG00000138617	ENST00000261888	Transcript	missense_variant	benign(0.426)
chr15	65917995	65917995	*SLC24A1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G526V	ENSG00000074621	ENST00000261892	Transcript	missense_variant	probably_damaging(0.993)
chr15	85366586	85366586	*ALPK3*	Missense_Mutation	.	SNP	C	C	G	novel	sia_et_al_P1	p.P259A	ENSG00000136383	ENST00000258888	Transcript	missense_variant	benign(0.29)
chr15	86064804	86064804	*AKAP13*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.P60H	ENSG00000170776	ENST00000361243	Transcript	missense_variant	probably_damaging(0.999)
chr15	91037999	91038000	*IQGAP1*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P1	p.Y1563Ifs*8	ENSG00000140575	ENST00000268182	Transcript	frameshift_variant	NA
chr16	11374885	11374885	*PRM1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.C40*	ENSG00000175646	ENST00000312511	Transcript	stop_gained	NA
chr16	11846641	11846641	*ZC3H7A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.K870N	ENSG00000122299	ENST00000396516	Transcript	missense_variant	probably_damaging(0.981)
chr16	17353351	17353351	*XYLT1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G136V	ENSG00000103489	ENST00000261381	Transcript	missense_variant	benign(0.068)
chr16	21181872	21181872	*TMEM159*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L71I	ENSG00000011638	ENST00000233047	Transcript	missense_variant	possibly_damaging(0.846)
chr16	3781860	3781860	*CREBBP*	Missense_Mutation	.	SNP	C	C	A	rs375557093	sia_et_al_P1	p.A1603S	ENSG00000005339	ENST00000262367	Transcript	missense_variant	unknown(0)
chr16	66620993	66620993	*CMTM2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L180I	ENSG00000140932	ENST00000268595	Transcript	missense_variant	benign(0.298)
chr16	90037986	90037986	*CENPBD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E115D	ENSG00000177946	ENST00000314994	Transcript	missense_variant	benign(0.009)
chr17	10302896	10302896	*MYH8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L1276I	ENSG00000133020	ENST00000403437	Transcript	missense_variant	benign(0.031)
chr17	18152710	18152710	*FLII*	Missense_Mutation	.	SNP	C	C	T	rs142586846	sia_et_al_P1	p.D597N	ENSG00000177731	ENST00000327031	Transcript	missense_variant	benign(0.002)
chr17	3476959	3476959	*TRPV1*	Missense_Mutation	.	SNP	C	C	T	rs375905892	sia_et_al_P1	p.A691T	ENSG00000196689	ENST00000571088	Transcript	missense_variant	possibly_damaging(0.626)
chr17	35745692	35745692	*C17orf78*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A199D	ENSG00000167230	ENST00000300618	Transcript	missense_variant	possibly_damaging(0.714)
chr17	46863599	46863599	*TTLL6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.R563I	ENSG00000170703	ENST00000393382	Transcript	missense_variant	possibly_damaging(0.845)
chr17	55704655	55704655	*MSI2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.Q240K	ENSG00000153944	ENST00000284073	Transcript	missense_variant	benign(0.017)
chr17	59934560	59934560	*BRIP1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A80S	ENSG00000136492	ENST00000259008	Transcript	missense_variant	benign(0.009)
chr17	62228317	62228317	*TEX2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G1056C	ENSG00000136478	ENST00000258991	Transcript	missense_variant	probably_damaging(0.959)
chr17	62856320	62856320	*LRRC37A3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T1315N	ENSG00000176809	ENST00000584306	Transcript	missense_variant	benign(0.127)
chr17	65899951	65899951	*BPTF*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P1	p.E867Rfs*16	ENSG00000171634	ENST00000306378	Transcript	frameshift_variant	NA
chr17	76803156	76803156	*USP36*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G657V	ENSG00000055483	ENST00000542802	Transcript	missense_variant	possibly_damaging(0.875)
chr17	95862500	95862500	*USP43*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.V406L	ENSG00000154914	ENST00000285199	Transcript	missense_variant	benign(0.006)
chr18	43620014	43620014	*PSTPIP2*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P1	NA	ENSG00000152229	ENST00000409746	Transcript	splice_acceptor_variant	NA
chr18	45423051	45423051	*SMAD2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G26V	ENSG00000175387	ENST00000402690	Transcript	missense_variant	benign(0.069)

chr18	47810849	47810849	*CXXC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D372E	ENSG00000154832	ENST00000412036	Transcript	missense_variant	benign(0.078)
chr18	50961514	50961514	*DCC*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G1055V	ENSG00000187323	ENST00000442544	Transcript	missense_variant	possibly_damaging(0.573)
chr18	52899890	52899890	*TCF4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G602V	ENSG00000196628	ENST00000398339	Transcript	missense_variant	benign(0.119)
chr18	67671458	67671458	*RTTN*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E2204*	ENSG00000176225	ENST00000255674	Transcript	stop_gained	NA
chr18	74536337	74536337	*ZNF236*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E8D	ENSG00000130856	ENST00000253159	Transcript	missense_variant	benign(0)
chr19	12692330	12692330	*ZNF490*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H187N	ENSG00000188033	ENST00000311437	Transcript	missense_variant	benign(0.001)
chr19	15479059	15479059	*AKAP8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.R383S	ENSG00000105127	ENST00000269701	Transcript	missense_variant	possibly_damaging(0.669)
chr19	15852540	15852540	*OR10H3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S113Y	ENSG00000171936	ENST00000305892	Transcript	missense_variant	probably_damaging(0.966)
chr19	16199930	16199930	*TPM4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.K213N	ENSG00000167460	ENST00000538887	Transcript	missense_variant	probably_damaging(0.916)
chr19	17311538	17311538	*MYO9B*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P1	p.I1488Mfs*35	ENSG00000099331	ENST00000595618	Transcript	frameshift_variant	NA
chr19	21212000	21212000	*AP3D1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.C404*	ENSG00000065000	ENST00000355272	Transcript	stop_gained	NA
chr19	41352903	41352903	*CYP2A6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.Q236H	ENSG00000255974	ENST00000301141	Transcript	missense_variant	benign(0.063)
chr19	42821987	42821987	*TMEM145*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E343*	ENSG00000167619	ENST00000301204	Transcript	stop_gained	NA
chr19	49658299	49658299	*HRC*	Missense_Mutation	.	SNP	C	C	A	rs550534373	sia_et_al_P1	p.D66Y	ENSG00000130528	ENST00000252825	Transcript	missense_variant	benign(0.36)
chr19	57290772	57290772	*ZIM2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D239Y	ENSG00000269699	ENST00000391708	Transcript	missense_variant	probably_damaging(0.936)
chr2	130951705	130951705	*TUBA3E*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S237Y	ENSG00000152086	ENST00000312988	Transcript	missense_variant	probably_damaging(1)
chr2	152423882	152423882	*NEB*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E5986*	ENSG00000183091	ENST00000397345	Transcript	stop_gained	NA
chr2	152499801	152499801	*NEB*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D2675Y	ENSG00000183091	ENST00000397345	Transcript	missense_variant	possibly_damaging(0.804)
chr2	160295116	160295116	*BAZ2B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L331I	ENSG00000123636	ENST00000392783	Transcript	missense_variant	benign(0.364)
chr2	163133201	163133201	*IFIH1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T767K	ENSG00000115267	ENST00000263642	Transcript	missense_variant	probably_damaging(1)
chr2	163230069	163230069	*KCNH7*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E1079*	ENSG00000184611	ENST00000332142	Transcript	stop_gained	NA
chr2	166740399	166740399	*TTC21B*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E1197*	ENSG00000123607	ENST00000243344	Transcript	stop_gained	NA
chr2	170597939	170597939	*KLHL23*	Missense_Mutation	.	SNP	G	G	T	rs144118398	sia_et_al_P1	p.V420F	ENSG00000213160	ENST00000392647	Transcript	missense_variant	probably_damaging(1)
chr2	178494197	178494197	*PDE11A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L914M	ENSG00000128655	ENST00000286063	Transcript	missense_variant	possibly_damaging(0.86)
chr2	183707247	183707247	*FRZB*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.R184I	ENSG00000162998	ENST00000295113	Transcript	missense_variant	benign(0.154)
chr2	190584461	190584461	*ANKAR*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E796D	ENSG00000151687	ENST00000520309	Transcript	missense_variant	possibly_damaging(0.622)
chr2	202260057	202260057	*TRAK2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L294I	ENSG00000115993	ENST00000332624	Transcript	missense_variant	probably_damaging(0.999)
chr2	207834090	207834090	*CPO*	Missense_Mutation	.	SNP	A	A	C	novel	sia_et_al_P1	p.D352A	ENSG00000144410	ENST00000272852	Transcript	missense_variant	benign(0.001)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	C	rs121913499	sia_et_al_P1	p.R132G	ENSG00000138413	ENST00000415913	Transcript	missense_variant	probably_damaging(0.998)
chr2	212566860	212566860	*ERBB4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G441C	ENSG00000178568	ENST00000342788	Transcript	missense_variant	possibly_damaging(0.511)
chr2	219617522	219617522	*TTLL4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D1005Y	ENSG00000135912	ENST00000392102	Transcript	missense_variant	benign(0.265)
chr2	242035505	242035505	*MTERFD2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D352Y	ENSG00000122085	ENST00000391980	Transcript	missense_variant	unknown(0)
chr2	27501134	27501134	*DNAJC5G*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.P152S	ENSG00000163793	ENST00000296097	Transcript	missense_variant	probably_damaging(0.941)
chr2	39025448	39025448	*DHX57*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T1385K	ENSG00000163214	ENST00000295373	Transcript	missense_variant	probably_damaging(0.996)
chr2	60773106	60773106	*BCL11A*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.D129N	ENSG00000119866	ENST00000335712	Transcript	missense_variant	benign(0)
chr2	68691455	68691455	*FBXO48*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.W118C	ENSG00000204923	ENST00000377957	Transcript	missense_variant	probably_damaging(0.999)

chr2	71743355	71743355	*DYSF*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E312*	ENSG00000135636	ENST00000410020	Transcript	stop_gained	NA
chr2	72406504	72406504	*EXOC6B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A799D	ENSG00000144036	ENST00000272427	Transcript	missense_variant	benign(0.361)
chr2	86257323	86257323	*POLR1A*	Missense_Mutation	.	SNP	G	G	C	novel	sia_et_al_P1	p.A1592G	ENSG00000068654	ENST00000263857	Transcript	missense_variant	benign(0.019)
chr2	86386784	86386784	*IMMT*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E303*	ENSG00000132305	ENST00000410111	Transcript	stop_gained	NA
chr2	88892869	88892869	*EIF2AK3*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E230*	ENSG00000172071	ENST00000303236	Transcript	stop_gained	NA
chr20	25656432	25656432	*ZNF337*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P1	p.R498Gfs*10	ENSG00000130684	ENST00000376436	Transcript	frameshift_variant	NA
chr20	37524283	37524283	*PPP1R16B*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E133*	ENSG00000101445	ENST00000299824	Transcript	stop_gained	NA
chr20	44669168	44669168	*SLC12A5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L280I	ENSG00000124140	ENST00000454036	Transcript	missense_variant	probably_damaging(1)
chr20	62854679	62854679	*MYT1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.R832I	ENSG00000196132	ENST00000328439	Transcript	missense_variant	probably_damaging(0.934)
chr21	22696784	22696784	*NCAM2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A234D	ENSG00000154654	ENST00000400546	Transcript	missense_variant	probably_damaging(0.934)
chr21	30359199	30359199	*LTN1*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	sia_et_al_P1	p.F81Yfs*9	ENSG00000198862	ENST00000389194	Transcript	frameshift_variant	NA
chr21	35467916	35467916	*SLC5A3*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S140*	ENSG00000272962	ENST00000608209	Transcript	stop_gained	NA
chr22	22065031	22065031	*YPEL1*	Translation_Start_Site	.	SNP	C	C	A	novel	sia_et_al_P1	p.M1?	ENSG00000100027	ENST00000339468	Transcript	initiator_codon_variant	benign(0.184)
chr22	43040481	43040481	*CYB5R3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S12I	ENSG00000100243	ENST00000361740	Transcript	missense_variant	benign(0)
chr3	10128930	10128930	*FANCD2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.Q1150K	ENSG00000144554	ENST00000287647	Transcript	missense_variant	benign(0.02)
chr3	112260731	112260731	*ATG3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D132Y	ENSG00000144848	ENST00000283290	Transcript	missense_variant	benign(0.192)
chr3	113122793	113122793	*WDR52*	Missense_Mutation	.	SNP	C	C	A	rs567449146	sia_et_al_P1	p.R359L	ENSG00000206530	ENST00000393845	Transcript	missense_variant	benign(0.241)
chr3	123066717	123066717	*ADCY5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.V440F	ENSG00000173175	ENST00000462833	Transcript	missense_variant	probably_damaging(0.98)
chr3	132209847	132209848	*DNAJC13*	Targeted_Region	.	INS	-	-	AGA	novel	sia_et_al_P1	p.F1192_L1193insE	ENSG00000138246	ENST00000260818	Transcript	protein_altering_variant	NA
chr3	132209850	132209851	*DNAJC13*	Frame_Shift_Del	.	DEL	TA	TA	-	novel	sia_et_al_P1	p.L1193Rfs*4	ENSG00000138246	ENST00000260818	Transcript	frameshift_variant	NA
chr3	141682726	141682726	*TFDP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T271N	ENSG00000114126	ENST00000489671	Transcript	missense_variant	possibly_damaging(0.88)
chr3	141723782	141723782	*TMEM43*	Frame_Shift_Del	.	DEL	G	G	-	rs138764471	sia_et_al_P1	p.D75Tfs*39	ENSG00000170876	ENST00000306077	Transcript	frameshift_variant	NA
chr3	145199674	145199674	*SLC6A6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G450C	ENSG00000131389	ENST00000454876	Transcript	missense_variant	probably_damaging(1)
chr3	147130434	147130435	*ZIC1*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	sia_et_al_P1	p.T372Afs*71	ENSG00000152977	ENST00000282928	Transcript	frameshift_variant	NA
chr3	155212306	155212306	*PLCH1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G620V	ENSG00000114805	ENST00000340059	Transcript	missense_variant	probably_damaging(1)
chr3	178927979	178927979	*PIK3CA*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P1	p.C420Vfs*8	ENSG00000121879	ENST00000263967	Transcript	frameshift_variant	NA
chr3	179597756	179597756	*PEX5L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q156K	ENSG00000114757	ENST00000467460	Transcript	missense_variant	benign(0.007)
chr3	180337146	180337146	*CCDC39*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E722D	ENSG00000145075	ENST00000442201	Transcript	missense_variant	possibly_damaging(0.615)
chr3	197619519	197619519	*IQCG*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L359I	ENSG00000114473	ENST00000265239	Transcript	missense_variant	possibly_damaging(0.893)
chr3	38442384	38442384	*XYLB*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L481I	ENSG00000093217	ENST00000207870	Transcript	missense_variant	benign(0.031)
chr3	51266977	51266977	*DOCK3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.F618L	ENSG00000088538	ENST00000266037	Transcript	missense_variant	benign(0)
chr3	51350274	51350274	*DOCK3*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P1	p.X1065_splice	ENSG00000088538	ENST00000266037	Transcript	splice_acceptor_variant	NA
chr3	52682399	52682400	*PBRM1*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P1	p.N258Kfs*6	ENSG00000163939	ENST00000394830	Transcript	frameshift_variant	NA
chr3	56763498	56763498	*ARHGEF3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L493I	ENSG00000163947	ENST00000338458	Transcript	missense_variant	possibly_damaging(0.543)
chr3	62355902	62355902	*FEZF2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.N412K	ENSG00000153266	ENST00000283268	Transcript	missense_variant	benign(0.02)
chr3	71090645	71090645	*FOXP1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.V237L	ENSG00000114861	ENST00000491238	Transcript	missense_variant	benign(0.093)

chr4	103987519	103987519	*SLC9B2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.P79H	ENSG00000164038	ENST00000394785	Transcript	missense_variant	benign(0.426)
chr4	110384533	110384533	*SEC24B*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P1	p.G204S	ENSG00000138802	ENST00000265175	Transcript	missense_variant	benign(0.016)
chr4	110685807	110685807	*CFI*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S123*	ENSG00000205403	ENST00000394634	Transcript	stop_gained	NA
chr4	134084204	134084204	*PCDH10*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S957Y	ENSG00000138650	ENST00000264360	Transcript	missense_variant	probably_damaging(0.996)
chr4	143094862	143094862	*INPP4B*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.A428T	ENSG00000109452	ENST00000513000	Transcript	missense_variant	benign(0.233)
chr4	146572267	146572267	*MMAA*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L263I	ENSG00000151611	ENST00000281317	Transcript	missense_variant	possibly_damaging(0.702)
chr4	153332637	153332637	*FBXW7*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E107*	ENSG00000109670	ENST00000281708	Transcript	stop_gained	NA
chr4	153332760	153332760	*FBXW7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.P66T	ENSG00000109670	ENST00000281708	Transcript	missense_variant	unknown(0)
chr4	155533181	155533181	*FGG*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S99*	ENSG00000171557	ENST00000336098	Transcript	stop_gained	NA
chr4	156643209	156643209	*GUCY1A3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S579Y	ENSG00000164116	ENST00000296518	Transcript	missense_variant	probably_damaging(0.975)
chr4	245424496	245424496	*DHX15*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D521Y	ENSG00000109606	ENST00000336812	Transcript	missense_variant	probably_damaging(0.999)
chr4	378415536	378415536	*PGM2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.Q170K	ENSG00000169299	ENST00000381967	Transcript	missense_variant	benign(0.038)
chr4	424031748	424031748	*SHISA3*	Missense_Mutation	.	SNP	C	C	A	rs200511756	sia_et_al_P1	p.P133T	ENSG00000178343	ENST00000319234	Transcript	missense_variant	probably_damaging(0.999)
chr4	490468424	490468424	*CWH43*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D609Y	ENSG00000109182	ENST00000226432	Transcript	missense_variant	possibly_damaging(0.879)
chr4	559487708	559487708	*KDR*	Missense_Mutation	.	SNP	G	G	T	rs142120845	sia_et_al_P1	p.P1253T	ENSG00000128052	ENST00000263923	Transcript	missense_variant	benign(0.003)
chr4	837857736	837857736	*SEC31A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.V405F	ENSG00000138674	ENST00000395310	Transcript	missense_variant	probably_damaging(0.98)
chr4	838675752	838675752	*LIN54*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A343S	ENSG00000189308	ENST00000340417	Transcript	missense_variant	benign(0.323)
chr4	856940738	856940738	*WDFY3*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P1	p.C1600Lfs*5	ENSG00000163625	ENST00000295888	Transcript	frameshift_variant	NA
chr4	876102756	876102756	*PTPN13*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.C153*	ENSG00000163629	ENST00000436978	Transcript	stop_gained	NA
chr5	102888090	102888090	*NUDT12*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.R369I	ENSG00000112874	ENST00000230792	Transcript	missense_variant	probably_damaging(1)
chr5	121901818	121901818	*SLC6A19*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A392S	ENSG00000174358	ENST00000304460	Transcript	missense_variant	benign(0.009)
chr5	131657943	131657943	*SLC22A4*	Missense_Mutation	.	SNP	C	C	A	rs575829481	sia_et_al_P1	p.A240E	ENSG00000197208	ENST00000200652	Transcript	missense_variant	possibly_damaging(0.883)
chr5	136403460	136403460	*SPOCK1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G178V	ENSG00000152377	ENST00000394945	Transcript	missense_variant	probably_damaging(1)
chr5	141248550	141248550	*PCDH1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D163Y	ENSG00000156453	ENST00000287008	Transcript	missense_variant	probably_damaging(1)
chr5	153085445	153085445	*GRIA1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.Y557*	ENSG00000155511	ENST00000518783	Transcript	stop_gained	NA
chr5	153085484	153085484	*GRIA1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.F570L	ENSG00000155511	ENST00000518783	Transcript	missense_variant	probably_damaging(0.997)
chr5	173040135	173040135	*BOD1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q121K	ENSG00000145919	ENST00000311086	Transcript	missense_variant	probably_damaging(0.921)
chr5	176965086	176965086	*FAM193B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.C159F	ENSG00000146067	ENST00000514747	Transcript	missense_variant	probably_damaging(0.995)
chr5	61876823	61876823	*LRRC70*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E520*	ENSG00000186105	ENST00000334994	Transcript	stop_gained	NA
chr5	78693438	78693438	*HOMER1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S236I	ENSG00000152413	ENST00000334082	Transcript	missense_variant	probably_damaging(0.996)
chr5	98115375	98115376	*RGMB*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P1	p.D119*	ENSG00000174136	ENST00000308234	Transcript	frameshift_variant	NA
chr6	123127483	123127483	*SMPDL3A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.P342H	ENSG00000172594	ENST00000368440	Transcript	missense_variant	possibly_damaging(0.687)
chr6	132891518	132891518	*TAAR6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G20W	ENSG00000146383	ENST00000275198	Transcript	missense_variant	probably_damaging(0.991)
chr6	137466796	137466796	*IL22RA2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q253K	ENSG00000164485	ENST00000296980	Transcript	missense_variant	benign(0.216)
chr6	146266647	146266647	*SHPRH*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P1	p.L483*	ENSG00000146414	ENST00000367505	Transcript	frameshift_variant	NA
chr6	152708419	152708419	*SYNE1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.P2759T	ENSG00000131018	ENST00000367255	Transcript	missense_variant	possibly_damaging(0.682)

chr6	159183131	159183131	*SYTL3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.G480C	ENSG00000164674	ENST00000297239	Transcript	missense_variant	benign(0.179)
chr6	160328431	160328431	*MAS1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q148H	ENSG00000130368	ENST00000252660	Transcript	missense_variant	probably_damaging(0.984)
chr6	176378 73	176378 73	*NUP153*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G659W	ENSG00000124789	ENST00000262077	Transcript	missense_variant	possibly_damaging(0.838)
chr6	374208 40	374208 40	*CMTR1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.L209F	ENSG00000137200	ENST00000373451	Transcript	missense_variant	probably_damaging(1)
chr6	516116 40	516116 40	*PKHD1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.D3293N	ENSG00000170927	ENST00000371117	Transcript	missense_variant	possibly_damaging(0.831)
chr6	564626 44	564626 44	*DST*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A1407E	ENSG00000151914	ENST00000244364	Transcript	missense_variant	benign(0.001)
chr6	883876 20	883876 20	*AKIRIN2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G149W	ENSG00000135334	ENST00000257787	Transcript	missense_variant	probably_damaging(0.999)
chr6	898084 63	898084 63	*SRSF12*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G207V	ENSG00000154548	ENST00000452027	Transcript	missense_variant	probably_damaging(0.972)
chr6	898885 63	898885 63	*GABRR1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D456Y	ENSG00000146276	ENST00000454853	Transcript	missense_variant	probably_damaging(1)
chr6	903639 82	903639 82	*MDN1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D5188Y	ENSG00000112159	ENST00000369393	Transcript	missense_variant	unknown(0)
chr7	100205 286	100205 286	*PCOLCE*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.V347F	ENSG00000106333	ENST00000223061	Transcript	missense_variant	possibly_damaging(0.889)
chr7	120990 596	120990 596	*FAM3C*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.K201N	ENSG00000196937	ENST00000359943	Transcript	missense_variant	possibly_damaging(0.664)
chr7	131833 310	131833 310	*PLXNA4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H1586N	ENSG00000221866	ENST00000359827	Transcript	missense_variant	possibly_damaging(0.874)
chr7	140159 725	140159 725	*MKRN1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S109I	ENSG00000133606	ENST00000255977	Transcript	missense_variant	possibly_damaging(0.616)
chr7	233475 38	233475 38	*MALSU1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D163Y	ENSG00000156928	ENST00000466681	Transcript	missense_variant	probably_damaging(0.981)
chr7	238265 39	238265 39	*STK31*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S828*	ENSG00000196335	ENST00000355870	Transcript	stop_gained	NA
chr7	304690 39	304690 39	*NOD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A914S	ENSG00000106100	ENST00000222823	Transcript	missense_variant	benign(0.077)
chr7	702312 46	702312 46	*AUTS2*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.H539Y	ENSG00000158321	ENST00000342771	Transcript	missense_variant	probably_damaging(0.997)
chr7	702312 70	702312 70	*AUTS2*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P1	p.P547S	ENSG00000158321	ENST00000342771	Transcript	missense_variant	probably_damaging(0.999)
chr7	802993 39	802993 39	*CD36*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P1	p.X273_splice	ENSG00000135218	ENST00000435819	Transcript	splice_donor_variant	NA
chr7	877439 12	877439 12	*ADAM22*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D163Y	ENSG00000008277	ENST00000265727	Transcript	missense_variant	probably_damaging(0.967)
chr7	927336 57	927336 57	*SAMD9*	Missense_Mutation	.	SNP	C	C	A	rs528742571	sia_et_al_P1	p.G585V	ENSG00000205413	ENST00000379958	Transcript	missense_variant	benign(0.002)
chr7	935165 74	935165 74	*TFPI2*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P1	p.A211Lfs*2	ENSG00000105825	ENST00000222543	Transcript	frameshift_variant	NA
chr7	979371 20	979371 20	*BAIAP2L1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.F348L	ENSG00000006453	ENST00000005260	Transcript	missense_variant	probably_damaging(0.999)
chr8	103273 457	103273 457	*UBR5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.P2625T	ENSG00000104517	ENST00000520539	Transcript	missense_variant	probably_damaging(0.988)
chr8	119936 793	119936 793	*TNFRSF11B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L342F	ENSG00000164761	ENST00000297350	Transcript	missense_variant	possibly_damaging(0.568)
chr8	125579 314	125579 314	*MTSS1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q242K	ENSG00000170873	ENST00000518547	Transcript	missense_variant	benign(0.382)
chr8	125864 38	125864 38	*LONRF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A661D	ENSG00000154359	ENST00000398246	Transcript	missense_variant	probably_damaging(1)
chr8	126034 182	126034 182	*SQLE*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.H574N	ENSG00000104549	ENST00000265896	Transcript	missense_variant	benign(0.002)
chr8	130854 416	130854 416	*FAM49B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.S316Y	ENSG00000153310	ENST00000519824	Transcript	missense_variant	possibly_damaging(0.841)
chr8	131072 969	131072 969	*ASAP1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E1016D	ENSG00000153317	ENST00000357668	Transcript	missense_variant	benign(0.001)
chr8	220844 38	220844 39	*PHYHIP*	Frame_Shift_Ins	.	INS	-	-	GA	novel	sia_et_al_P1	p.Q89Hfs*2	ENSG00000168490	ENST00000454243	Transcript	frameshift_variant	NA
chr8	273829 59	273829 59	*EPHX2*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P1	p.V380Dfs*22	ENSG00000120915	ENST00000521400	Transcript	frameshift_variant	NA
chr8	421718 45	421718 45	*IKBKB*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S233*	ENSG00000104365	ENST00000520810	Transcript	stop_gained	NA
chr8	742050 16	742050 16	*RPL7*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P1	p.P12Lfs*17	ENSG00000147604	ENST00000352983	Transcript	frameshift_variant	NA
chr8	742096 20	742096 20	*RDH10*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.L161I	ENSG00000121039	ENST00000240285	Transcript	missense_variant	possibly_damaging(0.676)

chr8	90971061	90971061	*NBN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G339V	ENSG00000104320	ENST00000265433	Transcript	missense_variant	possibly_damaging(0.873)
chr9	100449477	100449477	*XPA*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P1	p.C153Vfs*3	ENSG00000136936	ENST00000375128	Transcript	frameshift_variant	NA
chr9	100672732	100672732	*C9orf156*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D192E	ENSG00000136932	ENST00000375119	Transcript	missense_variant	benign(0.004)
chr9	101061560	101061560	*GABBR2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.H830N	ENSG00000136928	ENST00000259455	Transcript	missense_variant	benign(0.432)
chr9	101829237	101829237	*COL15A1*	Missense_Mutation	.	SNP	G	G	T	rs10988694	sia_et_al_P1	p.R1242I	ENSG00000204291	ENST00000375001	Transcript	missense_variant	probably_damaging(0.98)
chr9	115812098	115812098	*ZFP37*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E63*	ENSG00000136866	ENST00000374227	Transcript	stop_gained	NA
chr9	116836336	116836336	*AMBP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T145N	ENSG00000106927	ENST00000265132	Transcript	missense_variant	possibly_damaging(0.872)
chr9	117793925	117793925	*TNC*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A1943S	ENSG00000041982	ENST00000350763	Transcript	missense_variant	benign(0.021)
chr9	128230379	128230379	*MAPKAP1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.G406V	ENSG00000119487	ENST00000265960	Transcript	missense_variant	possibly_damaging(0.549)
chr9	139976498	139976498	*UAP1L1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P1	p.V472Gfs*8	ENSG00000197355	ENST00000409858	Transcript	frameshift_variant	NA
chr9	20789536	20789536	*FOCAD*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P1	p.E462K	ENSG00000188352	ENST00000380249	Transcript	missense_variant	benign(0.03)
chr9	27455373	27455373	*MOB3B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.W59L	ENSG00000120162	ENST00000262244	Transcript	missense_variant	probably_damaging(1)
chr9	33923921	33923921	*UBAP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q890K	ENSG00000137073	ENST00000379238	Transcript	missense_variant	unknown(0)
chr9	34241258	34241258	*UBAP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A143S	ENSG00000165006	ENST00000545103	Transcript	missense_variant	benign(0.221)
chr9	69256863	69256863	*CBWD6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.V90F	ENSG00000204790	ENST00000377457	Transcript	missense_variant	benign(0.333)
chr9	71395595	71395595	*FAM122A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.P172Q	ENSG00000187866	ENST00000394264	Transcript	missense_variant	probably_damaging(0.953)
chr9	90312085	90312085	*DAPK1*	Missense_Mutation	.	SNP	C	C	A	rs376600898	sia_et_al_P1	p.F859L	ENSG00000196730	ENST00000408954	Transcript	missense_variant	benign(0)
chrX	100615106	100615106	*BTK*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.T270N	ENSG00000010671	ENST00000308731	Transcript	missense_variant	possibly_damaging(0.761)
chrX	101096005	101096005	*NXF5*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E155*	ENSG00000126952	ENST00000537026	Transcript	stop_gained	NA
chrX	101395913	101395913	*TCEAL6*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E131*	ENSG00000204071	ENST00000372774	Transcript	stop_gained	NA
chrX	114400410	114400410	*LRCH2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.Q398K	ENSG00000130224	ENST00000317135	Transcript	missense_variant	benign(0.01)
chrX	129263561	129263561	*AIFM1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.A605S	ENSG00000156709	ENST00000287295	Transcript	missense_variant	possibly_damaging(0.752)
chrX	129813654	129813654	*ENOX2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E137*	ENSG00000165675	ENST00000338144	Transcript	stop_gained	NA
chrX	135095579	135095579	*SLC9A6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.Q407K	ENSG00000198689	ENST00000370695	Transcript	missense_variant	benign(0.058)
chrX	13791105	13791105	*GPM6B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.K294N	ENSG00000046653	ENST00000316715	Transcript	missense_variant	probably_damaging(0.934)
chrX	139038738	139038738	*CXorf66*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E135*	ENSG00000203933	ENST00000370540	Transcript	stop_gained	NA
chrX	150912431	150912431	*CNGA2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.D486Y	ENSG00000183862	ENST00000329903	Transcript	missense_variant	probably_damaging(0.981)
chrX	152602140	152602140	*ZNF275*	Translation_Start_Site	.	SNP	G	G	T	novel	sia_et_al_P1	p.M1?	ENSG00000063587	ENST00000370251	Transcript	initiator_codon_variant	benign(0.107)
chrX	153996665	153996665	*DKC1*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P1	p.M243I	ENSG00000130826	ENST00000369550	Transcript	missense_variant	probably_damaging(0.996)
chrX	2945508	2945507	*ARSH*	Frame_Shift_Del	.	DEL	CC	CC	-	novel	sia_et_al_P1	p.Q398Gfs*5	ENSG00000205667	ENST00000381130	Transcript	frameshift_variant	NA
chrX	49029528	49029528	*PLP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.S50Y	ENSG00000102007	ENST00000376327	Transcript	missense_variant	benign(0.16)
chrX	53245073	53245073	*KDM5C*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.K289N	ENSG00000126012	ENST00000375401	Transcript	missense_variant	benign(0.159)
chrX	53430538	53430538	*SMC1A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E794*	ENSG00000072501	ENST00000322213	Transcript	stop_gained	NA
chrX	53627172	53627172	*HUWE1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.E1023D	ENSG00000086758	ENST00000342160	Transcript	missense_variant	benign(0.036)
chrX	54566621	54566621	*GNL3L*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P1	p.F46Lfs*14	ENSG00000130119	ENST00000336470	Transcript	frameshift_variant	NA
chrX	64749139	64749139	*LAS1L*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P1	NA	ENSG00000001497	ENST00000374811	Transcript	splice_acceptor_variant	NA

chrX	70443955	70443955	*GJB1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.W133L	ENSG00000169562	ENST00000374022	Transcript	missense_variant	benign(0.415)
chrX	72804265	72804265	*CHIC1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.E122*	ENSG00000204116	ENST00000373502	Transcript	stop_gained	NA
chrX	83588835	83588835	*HDX*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P1	p.D586Y	ENSG00000165259	ENST00000299797	Transcript	missense_variant	probably_damaging(0.998)
chrX	91873391	91873391	*PCDH11X*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P1	p.A1166S	ENSG00000102290	ENST00000373094	Transcript	missense_variant	benign(0.004)
chr1	145440658	145440658	*TXNIP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P2	p.K286N	ENSG00000117289	ENST00000369317	Transcript	missense_variant	possibly_damaging(0.491)
chr1	169388367	169388367	*CCDC181*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P2	p.E367*	ENSG00000117477	ENST00000545005	Transcript	stop_gained	NA
chr1	182615914	182615914	*RGS8*	Missense_Mutation	.	SNP	T	T	C	novel	sia_et_al_P2	p.M185V	ENSG00000135824	ENST00000258302	Transcript	missense_variant	benign(0.001)
chr10	37451750	37451750	*ANKRD30A*	Missense_Mutation	.	SNP	T	T	G	novel	sia_et_al_P2	p.L603W	ENSG00000148513	ENST00000361713	Transcript	missense_variant	probably_damaging(0.926)
chr10	86177587	86177587	*CCSER2*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P2	p.D559N	ENSG00000107771	ENST00000224756	Transcript	missense_variant	possibly_damaging(0.864)
chr16	20384428	20384428	*PDILT*	Missense_Mutation	.	SNP	C	C	A	rs141043720	sia_et_al_P2	p.R233L	ENSG00000169340	ENST00000302451	Transcript	missense_variant	benign(0.132)
chr17	34192351	34192351	*C17orf66*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P2	p.P63L	ENSG00000172653	ENST00000311880	Transcript	missense_variant	benign(0.032)
chr17	76457702	76457702	*DNAH17*	Missense_Mutation	.	SNP	C	C	T	rs139755402	sia_et_al_P2	p.G3074D	ENSG00000187775	ENST00000389840	Transcript	missense_variant	probably_damaging(0.935)
chr2	197135974	197135974	*HECW2*	Missense_Mutation	.	SNP	T	T	C	novel	sia_et_al_P2	p.N1093S	ENSG00000138411	ENST00000260983	Transcript	missense_variant	possibly_damaging(0.706)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	C	rs121913499	sia_et_al_P2	p.R132G	ENSG00000138413	ENST00000415913	Transcript	missense_variant	probably_damaging(0.998)
chr4	44697652	44697652	*GUF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P2	p.G579V	ENSG00000151806	ENST00000281543	Transcript	missense_variant	probably_damaging(0.976)
chr7	57529545	57529545	*ZNF716*	Missense_Mutation	.	SNP	G	G	C	novel	sia_et_al_P2	p.G460R	ENSG00000182111	ENST00000420713	Transcript	missense_variant	probably_damaging(0.916)
chr7	93108722	93108722	*CALCR*	Missense_Mutation	.	SNP	T	T	C	rs201946167	sia_et_al_P2	p.D68G	ENSG00000004948	ENST00000355958	Transcript	missense_variant	possibly_damaging(0.763)
chr8	17063216	17063216	*ZDHHC2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P2	p.A177S	ENSG00000104219	ENST00000262096	Transcript	missense_variant	probably_damaging(0.947)
chr1	100605973	100605973	*TRMT13*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S135Y	ENSG00000122435	ENST00000370141	Transcript	missense_variant	benign(0.042)
chr1	11155856	11155856	*EXOSC10*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D111Y	ENSG00000171824	ENST00000376936	Transcript	missense_variant	probably_damaging(0.988)
chr1	113121032	113121032	*ST7L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S359R	ENSG00000007341	ENST00000358039	Transcript	missense_variant	probably_damaging(0.999)
chr1	115110867	115110867	*BCAS2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L188M	ENSG00000116752	ENST00000369541	Transcript	missense_variant	probably_damaging(0.999)
chr1	117131636	117131636	*IGSF3*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.T727I	ENSG00000143061	ENST00000369483	Transcript	missense_variant	possibly_damaging(0.877)
chr1	120307064	120307064	*HMGCS2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S97*	ENSG00000134240	ENST00000369406	Transcript	stop_gained	NA
chr1	12854293	12854293	*PRAMEF1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q173K	ENSG00000116721	ENST00000332296	Transcript	missense_variant	possibly_damaging(0.731)
chr1	149943089	149943089	*OTUD7B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G59V	ENSG00000163113	ENST00000369135	Transcript	missense_variant	benign(0.432)
chr1	151070424	151070424	*GABPB2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E190*	ENSG00000143458	ENST00000368918	Transcript	stop_gained	NA
chr1	155747435	155747435	*GON4L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R690I	ENSG00000116580	ENST00000437809	Transcript	missense_variant	probably_damaging(0.988)
chr1	156438663	156438663	*MEF2D*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P386T	ENSG00000116604	ENST00000348159	Transcript	missense_variant	benign(0.048)
chr1	166818361	166818362	*POGK*	Frame_Shift_Ins	.	INS	-	-	G	novel	sia_et_al_P7	p.A183Gfs*2	ENSG00000143157	ENST00000367875	Transcript	frameshift_variant	NA
chr1	169495233	169495233	*F5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.M1874I	ENSG00000198734	ENST00000367797	Transcript	missense_variant	possibly_damaging(0.821)
chr1	178863125	178863125	*RALGPS2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R466I	ENSG00000116191	ENST00000367635	Transcript	missense_variant	probably_damaging(0.996)
chr1	192992976	192992976	*UCHL5*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E244*	ENSG00000116750	ENST00000367455	Transcript	stop_gained	NA
chr1	19487532	19487532	*UBR4*	Missense_Mutation	.	SNP	G	G	A	rs200629314	sia_et_al_P7	p.S1762F	ENSG00000127481	ENST00000375254	Transcript	missense_variant	benign(0.302)
chr1	196759300	196759300	*CFHR3*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.G247S	ENSG00000116785	ENST00000367425	Transcript	missense_variant	probably_damaging(0.996)
chr1	197030166	197030166	*F13B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S164Y	ENSG00000143278	ENST00000367412	Transcript	missense_variant	possibly_damaging(0.904)

chr1	197391043	197391044	*CRB1*	Frame_Shift_Del	.	DEL	GT	GT	-	novel	sia_et_al_P7	p.C696*	ENSG00000134376	ENST00000367400	Transcript	frameshift_variant	NA
chr1	202984164	202984164	*TMEM183A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R172M	ENSG00000163444	ENST00000367242	Transcript	missense_variant	probably_damaging(0.983)
chr1	204403024	204403024	*PIK3C2B*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.G1247Vfs*35	ENSG00000133056	ENST00000367187	Transcript	frameshift_variant	NA
chr1	205308856	205308856	*KLHDC8A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D153Y	ENSG00000162873	ENST00000367156	Transcript	missense_variant	probably_damaging(0.96)
chr1	207753921	207753921	*CR1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q1727K	ENSG00000203710	ENST00000367049	Transcript	missense_variant	possibly_damaging(0.583)
chr1	211093171	211093171	*KCNH1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D425Y	ENSG00000143473	ENST00000271751	Transcript	missense_variant	possibly_damaging(0.68)
chr1	213161882	213161882	*VASH2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D298Y	ENSG00000143494	ENST00000366965	Transcript	missense_variant	possibly_damaging(0.863)
chr1	226420203	226420203	*LIN9*	Nonstop_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.*559Lext*45	ENSG00000183814	ENST00000328205	Transcript	stop_lost	NA
chr1	234088052	234088052	*KDM1A*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.P814Hfs*27	ENSG00000004487	ENST00000400181	Transcript	frameshift_variant	NA
chr1	237060933	237060933	*MTR*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D1263Y	ENSG00000116984	ENST00000366577	Transcript	missense_variant	possibly_damaging(0.819)
chr1	244479480	244479480	*IL22RA1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S347Y	ENSG00000142677	ENST00000270800	Transcript	missense_variant	possibly_damaging(0.789)
chr1	246740437	246740437	*GRHL3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R541S	ENSG00000158055	ENST00000350501	Transcript	missense_variant	probably_damaging(0.997)
chr1	248569976	248569976	*OR2T1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.F227L	ENSG00000175143	ENST00000366474	Transcript	missense_variant	possibly_damaging(0.717)
chr1	28120108	28120108	*STX12*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G85W	ENSG00000117758	ENST00000373943	Transcript	missense_variant	probably_damaging(0.973)
chr1	37400031	37400031	*CEP104*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F820L	ENSG00000116198	ENST00000378230	Transcript	missense_variant	benign(0)
chr1	38338676	38338676	*INPP5B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G705W	ENSG00000204084	ENST00000373024	Transcript	missense_variant	probably_damaging(1)
chr1	38406394	38406394	*INPP5B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R119S	ENSG00000204084	ENST00000373024	Transcript	missense_variant	possibly_damaging(0.665)
chr1	40656481	40656481	*RLF*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E144*	ENSG00000117000	ENST00000372771	Transcript	stop_gained	NA
chr1	43895399	43895399	*SZT2*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.P1341Lfs*20	ENSG00000198198	ENST00000562955	Transcript	frameshift_variant	NA
chr1	43907209	43907209	*SZT2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G2459W	ENSG00000198198	ENST00000562955	Transcript	missense_variant	probably_damaging(0.999)
chr1	47014940	47014940	*KNCN*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P7	p.X51_splice	ENSG00000162456	ENST00000396314	Transcript	splice_acceptor_variant	NA
chr1	52871468	52871468	*PRPF38A*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E83*	ENSG00000134748	ENST00000257181	Transcript	stop_gained	NA
chr1	60462977	60462977	*NPHP4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P18Q	ENSG00000131697	ENST00000378156	Transcript	missense_variant	possibly_damaging(0.8)
chr1	62380306	62380306	*INADL*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q1180H	ENSG00000132849	ENST00000371158	Transcript	missense_variant	benign(0.014)
chr1	68603582	68603582	*WLS*	Frame_Shift_Del	.	DEL	TG	TG	-	novel	sia_et_al_P7	p.T464Sfs*31	ENSG00000116729	ENST00000354777	Transcript	frameshift_variant	NA
chr1	74540384	74540384	*LRRIQ3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G320C	ENSG00000162620	ENST00000354431	Transcript	missense_variant	possibly_damaging(0.533)
chr1	80377147	80377147	*PARK7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P109T	ENSG00000116288	ENST00000493678	Transcript	missense_variant	possibly_damaging(0.602)
chr1	93168996	93168996	*EVI5*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E218*	ENSG00000067208	ENST00000370331	Transcript	stop_gained	NA
chr1	95363335	95363335	*CNN3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R318I	ENSG00000117519	ENST00000370206	Transcript	missense_variant	benign(0.372)
chr10	103845151	103845151	*GTPBP4*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S24*	ENSG00000107937	ENST00000360803	Transcript	stop_gained	NA
chr10	104594687	104594687	*CYP17A1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A174E	ENSG00000148795	ENST00000369887	Transcript	missense_variant	probably_damaging(0.953)
chr10	105761224	105761224	*SLK*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S296Y	ENSG00000065613	ENST00000369755	Transcript	missense_variant	probably_damaging(0.995)
chr10	112650397	112650397	*PDCD4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G320V	ENSG00000150593	ENST00000280154	Transcript	missense_variant	probably_damaging(0.997)
chr10	114186097	114186097	*ACSL5*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E663*	ENSG00000197142	ENST00000356116	Transcript	stop_gained	NA
chr10	120830441	120830441	*EIF3A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R233I	ENSG00000107581	ENST00000369144	Transcript	missense_variant	unknown(0)
chr10	120830469	120830469	*EIF3A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E224*	ENSG00000107581	ENST00000369144	Transcript	stop_gained	NA

chr10	12197813	12197813	*SEC61A2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E167*	ENSG00000065665	ENST00000298428	Transcript	stop_gained	NA
chr10	129906346	129906346	*MKI67*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S1253Y	ENSG00000148773	ENST00000368654	Transcript	missense_variant	probably_damaging(0.997)
chr10	15559202	15559202	*ITGA8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.M1049I	ENSG00000077943	ENST00000378076	Transcript	missense_variant	benign(0.014)
chr10	17107567	17107567	*CUBN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D1027Y	ENSG00000107611	ENST00000377833	Transcript	missense_variant	probably_damaging(0.974)
chr10	32101753	32101754	*ARHGAP12*	Splice_Site	.	DEL	TT	TT	-	novel	sia_et_al_P7	p.X612_splice	ENSG00000165322	ENST00000344936	Transcript	splice_acceptor_variant	NA
chr10	34671716	34671716	*PARD3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P384H	ENSG00000148498	ENST00000374789	Transcript	missense_variant	benign(0.013)
chr10	43869941	43869941	*FXYD4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D21Y	ENSG00000150201	ENST00000476166	Transcript	missense_variant	probably_damaging(0.961)
chr10	43870071	43870071	*FXYD4*	Missense_Mutation	.	SNP	C	C	A	rs140710266	sia_et_al_P7	p.D27E	ENSG00000150201	ENST00000476166	Transcript	missense_variant	unknown(0)
chr10	51890704	51890704	*FAM21A*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.R1252Efs*22	ENSG00000099290	ENST00000282633	Transcript	frameshift_variant	NA
chr10	63810658	63810658	*ARID5B*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.G250Afs*34	ENSG00000150347	ENST00000279873	Transcript	frameshift_variant	NA
chr10	74987902	74987902	*FAM149B1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R328L	ENSG00000138286	ENST00000242505	Transcript	missense_variant	benign(0.341)
chr10	75675140	75675140	*PLAU*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.T369Qfs*20	ENSG00000122861	ENST00000372764	Transcript	frameshift_variant	NA
chr10	88477746	88477746	*LDB3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R573S	ENSG00000122367	ENST00000429277	Transcript	missense_variant	probably_damaging(0.988)
chr10	94834291	94834291	*CYP26A1*	Splice_Site	.	DEL	T	T	-	novel	sia_et_al_P7	p.X138_splice	ENSG00000095596	ENST00000224356	Transcript	splice_donor_variant	NA
chr10	99243899	99243899	*MMS19*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S41Y	ENSG00000155229	ENST00000438925	Transcript	missense_variant	possibly_damaging(0.617)
chr11	107375765	107375765	*ALKBH8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q538H	ENSG00000137760	ENST00000428149	Transcript	missense_variant	benign(0.004)
chr11	107904540	107904540	*CUL5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L13I	ENSG00000166266	ENST00000393094	Transcript	missense_variant	benign(0.001)
chr11	112085495	112085495	*BCO2*	Missense_Mutation	.	SNP	C	C	A	rs150993927	sia_et_al_P7	p.S448Y	ENSG00000197580	ENST00000357685	Transcript	missense_variant	benign(0.219)
chr11	114453403	114453403	*NXPE4*	Missense_Mutation	.	SNP	G	G	T	rs200548586	sia_et_al_P7	p.A146E	ENSG00000137634	ENST00000375478	Transcript	missense_variant	possibly_damaging(0.743)
chr11	117061398	117061398	*SIDT2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.M559I	ENSG00000149577	ENST00000324225	Transcript	missense_variant	possibly_damaging(0.843)
chr11	117352765	117352765	*DSCAML1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.K884N	ENSG00000177103	ENST00000321322	Transcript	missense_variant	possibly_damaging(0.877)
chr11	121036048	121036048	*TECTA*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G1780V	ENSG00000109927	ENST00000392793	Transcript	missense_variant	probably_damaging(0.989)
chr11	124740147	124740148	*ROBO3*	Frame_Shift_Del	.	DEL	CC	CC	-	novel	sia_et_al_P7	p.P286Tfs*18	ENSG00000154134	ENST00000397801	Transcript	frameshift_variant	NA
chr11	125776044	125776044	*DDX25*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.L85Yfs*12	ENSG00000109832	ENST00000263576	Transcript	frameshift_variant	NA
chr11	125792744	125792744	*DDX25*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D474Y	ENSG00000109832	ENST00000263576	Transcript	missense_variant	probably_damaging(0.952)
chr11	132180054	132180054	*NTM*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.K238Rfs*25	ENSG00000182667	ENST00000425719	Transcript	frameshift_variant	NA
chr11	134086969	134086969	*NCAPD3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E81D	ENSG00000151503	ENST00000534548	Transcript	missense_variant	possibly_damaging(0.751)
chr11	144902081	144902081	*COPB1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.M697I	ENSG00000129083	ENST00000249923	Transcript	missense_variant	benign(0)
chr11	148655531	148655531	*PDE3B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G827W	ENSG00000152270	ENST00000282096	Transcript	missense_variant	probably_damaging(1)
chr11	184210787	184210787	*LDHA*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S108Y	ENSG00000134333	ENST00000540430	Transcript	missense_variant	possibly_damaging(0.531)
chr11	187504782	187504782	*PTPN5*	Nonstop_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.*566Lext*93	ENSG00000110786	ENST00000358540	Transcript	stop_lost	NA
chr11	206912994	206912994	*NELL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.V9L	ENSG00000165973	ENST00000357134	Transcript	missense_variant	benign(0)
chr11	32610269	32610269	*EIF3M*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R102I	ENSG00000149100	ENST00000531120	Transcript	missense_variant	benign(0.082)
chr11	32674756	32674756	*CCDC73*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F284L	ENSG00000186714	ENST00000335185	Transcript	missense_variant	benign(0.381)
chr11	33308810	33308810	*HIPK3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D284Y	ENSG00000110422	ENST00000303296	Transcript	missense_variant	probably_damaging(0.999)
chr11	36296209	36296209	*COMMD9*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D190E	ENSG00000110442	ENST00000263401	Transcript	missense_variant	possibly_damaging(0.666)

chr11	3752735	3752735	*NUP98*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P539H	ENSG00000110713	ENST00000324932	Transcript	missense_variant	probably_damaging(0.991)
chr11	4103578	4103578	*STIM1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.A380Lfs*4	ENSG00000167323	ENST00000300737	Transcript	frameshift_variant	NA
chr11	45832355	45832355	*SLC35C1*	Frame_Shift_Del	.	DEL	G	G	-	rs543075977	sia_et_al_P7	p.A190Qfs*41	ENSG00000181830	ENST00000314134	Transcript	frameshift_variant	NA
chr11	47289480	47289480	*NR1H3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.F335L	ENSG00000025434	ENST00000467728	Transcript	missense_variant	possibly_damaging(0.576)
chr11	48511099	48511099	*OR4A47*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.C252*	ENSG00000237388	ENST00000446524	Transcript	frameshift_variant	NA
chr11	55681261	55681264	*OR5W2*	Frame_Shift_Del	.	DEL	ATAG	ATAG	-	novel	sia_et_al_P7	p.Y266Lfs*2	ENSG00000187612	ENST00000345144	Transcript	frameshift_variant	NA
chr11	56020573	56020573	*OR5T3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.H300N	ENSG00000172489	ENST00000303059	Transcript	missense_variant	benign(0.071)
chr11	60183566	60183566	*MS4A14*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.M408I	ENSG00000166928	ENST00000531783	Transcript	missense_variant	benign(0.022)
chr11	61607893	61607893	*FADS2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L136I	ENSG00000134824	ENST00000278840	Transcript	missense_variant	benign(0.002)
chr11	62063889	62063889	*SCGB1D4*	Nonsense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.W82*	ENSG00000197745	ENST00000358585	Transcript	stop_gained	NA
chr11	64361182	64361182	*SLC22A12*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G246V	ENSG00000197891	ENST00000377574	Transcript	missense_variant	benign(0.001)
chr11	65308371	65308372	*LTBP3*	In_Frame_Ins	.	INS	-	-	TGT	novel	sia_et_al_P7	p.I983_V984insN	ENSG00000168056	ENST00000301873	Transcript	inframe_insertion	NA
chr11	67266415	67266416	*PITPNM1*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P7	p.S410Rfs*12	ENSG00000110697	ENST00000356404	Transcript	frameshift_variant	NA
chr11	71196687	71196687	*NADSYN1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D519Y	ENSG00000172890	ENST00000319023	Transcript	missense_variant	probably_damaging(0.988)
chr11	73753241	73753241	*C2CD3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A1840S	ENSG00000168014	ENST00000313663	Transcript	missense_variant	benign(0.037)
chr11	94134094	94134094	*GPR83*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S107I	ENSG00000123901	ENST00000243673	Transcript	missense_variant	probably_damaging(0.99)
chr11	95825433	95825433	*MAML2*	Nonsense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.Q588*	ENSG00000184384	ENST00000524717	Transcript	stop_gained	NA
chr12	10544590	10544590	*ALDH1L2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G499*	ENSG00000136010	ENST00000258494	Transcript	stop_gained	NA
chr12	109017377	109017377	*SELPLG*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P252Q	ENSG00000110876	ENST00000228463	Transcript	missense_variant	probably_damaging(0.972)
chr12	109661706	109661706	*ACACB*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L1293F	ENSG00000076555	ENST00000338432	Transcript	missense_variant	probably_damaging(0.998)
chr12	110641729	110641729	*IFT81*	Nonsense_Mutation	.	SNP	G	G	T	rs549244328	sia_et_al_P7	p.E540*	ENSG00000122970	ENST00000242591	Transcript	stop_gained	NA
chr12	112370416	112370416	*TMEM116*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L261I	ENSG00000198270	ENST00000552374	Transcript	missense_variant	probably_damaging(0.998)
chr12	117383292	117383292	*FBXW8*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E183*	ENSG00000174989	ENST00000309909	Transcript	stop_gained	NA
chr12	120031758	120031758	*TMEM233*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.K35N	ENSG00000224982	ENST00000426426	Transcript	missense_variant	benign(0.049)
chr12	120535172	120535172	*RAB35*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F161L	ENSG00000111737	ENST00000229340	Transcript	missense_variant	probably_damaging(1)
chr12	122995654	122995654	*RSRC2*	Splice_Site	.	SNP	A	A	T	novel	sia_et_al_P7	NA	ENSG00000111011	ENST00000331738	Transcript	splice_donor_variant	NA
chr12	123907694	123907694	*RILPL2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P168T	ENSG00000150977	ENST00000280571	Transcript	missense_variant	benign(0.124)
chr12	124816947	124816947	*NCOR2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E2274D	ENSG00000196498	ENST00000405201	Transcript	missense_variant	probably_damaging(0.999)
chr12	125299546	125299546	*SCARB1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Y133*	ENSG00000073060	ENST00000261693	Transcript	stop_gained	NA
chr12	125397953	125397953	*UBC*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A122D	ENSG00000150991	ENST00000536769	Transcript	missense_variant	possibly_damaging(0.634)
chr12	133331517	133331518	*ANKLE2*	Frame_Shift_Del	.	DEL	TG	TG	-	novel	sia_et_al_P7	p.T128Sfs*14	ENSG00000176915	ENST00000357997	Transcript	frameshift_variant	NA
chr12	23687169	23687169	*SOX5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A759E	ENSG00000134532	ENST00000451604	Transcript	missense_variant	benign(0.215)
chr12	310931	310931	*SLC6A12*	Missense_Mutation	.	SNP	C	C	G	novel	sia_et_al_P7	p.W192S	ENSG00000111181	ENST00000428720	Transcript	missense_variant	benign(0.405)
chr12	49099558	49099558	*CCNT1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R122I	ENSG00000129315	ENST00000261900	Transcript	missense_variant	benign(0.053)
chr12	49992573	49992573	*FAM186B*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E777*	ENSG00000135436	ENST00000257894	Transcript	stop_gained	NA
chr12	52864337	52864337	*KRT6C*	Missense_Mutation	.	SNP	G	G	T	rs144142819	sia_et_al_P7	p.N385K	ENSG00000170465	ENST00000252250	Transcript	missense_variant	probably_damaging(0.992)

chr12	53346594	53346594	*KRT18*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E421*	ENSG00000111057	ENST00000388835	Transcript	stop_gained	NA
chr12	54113525	54113525	*CALCOCO1*	Nonsense_Mutation	.	SNP	C	C	A	rs543529054	sia_et_al_P7	p.E283*	ENSG00000012822	ENST00000550804	Transcript	stop_gained	NA
chr12	54118995	54118995	*CALCOCO1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S11Y	ENSG00000012822	ENST00000550804	Transcript	missense_variant	probably_damaging(0.976)
chr12	54367168	54367168	*HOXC11*	Missense_Mutation	.	SNP	C	C	T	rs17849492	sia_et_al_P7	p.S48F	ENSG00000123388	ENST00000546378	Transcript	missense_variant	probably_damaging(0.989)
chr12	57397738	57397738	*ZBTB39*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L322M	ENSG00000166860	ENST00000300101	Transcript	missense_variant	probably_damaging(0.997)
chr12	62943610	62943610	*MON2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L972F	ENSG00000061987	ENST00000393632	Transcript	missense_variant	probably_damaging(0.937)
chr12	67815577	67815577	*ZNF384*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q351H	ENSG00000126746	ENST00000396801	Transcript	missense_variant	possibly_damaging(0.722)
chr12	68720708	68720708	*MDM1*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.S76L	ENSG00000111554	ENST00000303145	Transcript	missense_variant	possibly_damaging(0.543)
chr12	76453947	76453947	*NAP1L1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A107S	ENSG00000187109	ENST00000261182	Transcript	missense_variant	benign(0.14)
chr12	80648941	80648942	*OTOGL*	Frame_Shift_Del	.	DEL	TT	TT	-	novel	sia_et_al_P7	p.L513Tfs*6	ENSG00000165899	ENST00000458043	Transcript	frameshift_variant	NA
chr12	95502296	95502296	*FGD6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D1059Y	ENSG00000180263	ENST00000343958	Transcript	missense_variant	probably_damaging(0.995)
chr12	96312744	96312744	*CCDC38*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.D17Mfs*34	ENSG00000165972	ENST00000344280	Transcript	frameshift_variant	NA
chr12	96386527	96386528	*HAL*	Frame_Shift_Ins	.	INS	-	-	GA	novel	sia_et_al_P7	p.N216Tfs*4	ENSG00000084110	ENST00000261208	Transcript	frameshift_variant	NA
chr12	99102462	99102462	*APAF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D941Y	ENSG00000120868	ENST00000551964	Transcript	missense_variant	probably_damaging(0.989)
chr13	107822900	107822900	*FAM155A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G441V	ENSG00000204442	ENST00000375915	Transcript	missense_variant	benign(0.079)
chr13	23929438	23929438	*SACS*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S438Y	ENSG00000151835	ENST00000382298	Transcript	missense_variant	benign(0.372)
chr13	25281560	25281560	*ATP12A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G834W	ENSG00000075673	ENST00000218548	Transcript	missense_variant	probably_damaging(1)
chr13	25480191	25480191	*CENPJ*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S662Y	ENSG00000151849	ENST00000381884	Transcript	missense_variant	benign(0.169)
chr13	37401781	37401781	*RFXAP*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S237*	ENSG00000133111	ENST00000255476	Transcript	stop_gained	NA
chr13	42277540	42277540	*VWA8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L1042M	ENSG00000102763	ENST00000379310	Transcript	missense_variant	possibly_damaging(0.78)
chr13	77785428	77785428	*MYCBP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P1059H	ENSG00000005810	ENST00000544440	Transcript	missense_variant	possibly_damaging(0.642)
chr13	93879801	93879801	*GPC6*	Missense_Mutation	.	SNP	G	G	T	rs376392142	sia_et_al_P7	p.G31V	ENSG00000183098	ENST00000377047	Transcript	missense_variant	benign(0.063)
chr13	95839064	95839064	*ABCC4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S479Y	ENSG00000125257	ENST00000376887	Transcript	missense_variant	probably_damaging(0.981)
chr14	10357478	10357478	*EXOC3L4*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.E634Rfs*55	ENSG00000205436	ENST00000380069	Transcript	frameshift_variant	NA
chr14	21897236	21897236	*CHD8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P368T	ENSG00000100888	ENST00000399982	Transcript	missense_variant	benign(0.018)
chr14	23745370	23745370	*HOMEZ*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.R356H	ENSG00000215271	ENST00000357460	Transcript	missense_variant	benign(0.009)
chr14	23944513	23944513	*NGDN*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R93L	ENSG00000129460	ENST00000408901	Transcript	missense_variant	probably_damaging(1)
chr14	24787653	24787653	*ADCY4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R1068L	ENSG00000129467	ENST00000310677	Transcript	missense_variant	probably_damaging(0.997)
chr14	35482586	35482586	*SRP54*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S224Y	ENSG00000100883	ENST00000556994	Transcript	missense_variant	benign(0.145)
chr14	53521165	53521165	*DDHD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D810Y	ENSG00000100523	ENST00000323669	Transcript	missense_variant	probably_damaging(0.961)
chr14	55510035	55510036	*SOCS4*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	sia_et_al_P7	p.Q93Efs*16	ENSG00000180008	ENST00000395472	Transcript	frameshift_variant	NA
chr14	64608106	64608107	*SYNE2*	Frame_Shift_Del	.	DEL	TA	TA	-	novel	sia_et_al_P7	p.I5009Qfs*13	ENSG00000054654	ENST00000358025	Transcript	frameshift_variant	NA
chr14	68191216	68191216	*RDH12*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R32I	ENSG00000139988	ENST00000551171	Transcript	missense_variant	benign(0.11)
chr14	71513823	71513823	*PCNX*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P7	p.X1387_splice	ENSG00000100731	ENST00000304743	Transcript	splice_donor_variant	NA
chr14	75643266	75643266	*TMED10*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.G6Afs*11	ENSG00000170348	ENST00000303575	Transcript	frameshift_variant	NA
chr15	10235877	10235877	*OR4F15*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L130I	ENSG00000182854	ENST00000332238	Transcript	missense_variant	possibly_damaging(0.908)

chr15	21051164	21051164	*POTEB2*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.H432Qfs*26	ENSG00000230031	ENST00000454856	Transcript	frameshift_variant	NA
chr15	22958230	22958230	*CYFIP1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E625*	ENSG00000068793	ENST00000313077	Transcript	stop_gained	NA
chr15	22958262	22958262	*CYFIP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R635S	ENSG00000068793	ENST00000313077	Transcript	missense_variant	possibly_damaging(0.791)
chr15	27114481	27114481	*GABRA5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G29V	ENSG00000186297	ENST00000335625	Transcript	missense_variant	benign(0.006)
chr15	42731268	42731268	*ZNF106*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E1480*	ENSG00000103994	ENST00000263805	Transcript	stop_gained	NA
chr15	43495420	43495420	*EPB42*	Nonsense_Mutation	.	SNP	C	C	A	rs75424023	sia_et_al_P7	p.E588*	ENSG00000166947	ENST00000300215	Transcript	stop_gained	NA
chr15	44106760	44106760	*MFAP1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E186*	ENSG00000140259	ENST00000267812	Transcript	stop_gained	NA
chr15	44862773	44862773	*SPG11*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H2143N	ENSG00000104133	ENST00000261866	Transcript	missense_variant	benign(0.002)
chr15	48784689	48784689	*FBN1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.M941I	ENSG00000166147	ENST00000316623	Transcript	missense_variant	benign(0.211)
chr15	49061271	49061271	*CEP152*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.T597K	ENSG00000103995	ENST00000380950	Transcript	missense_variant	benign(0.015)
chr15	59179642	59179642	*SLTM*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D825Y	ENSG00000137776	ENST00000380516	Transcript	missense_variant	probably_damaging(0.983)
chr15	59497621	59497621	*MYO1E*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E532*	ENSG00000157483	ENST00000288235	Transcript	stop_gained	NA
chr15	64495367	64495367	*CSNK1G1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H341N	ENSG00000169118	ENST00000303052	Transcript	missense_variant	benign(0.004)
chr15	65993514	65993514	*DENND4A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.T859N	ENSG00000174485	ENST00000443035	Transcript	missense_variant	benign(0.146)
chr15	86251305	86251305	*AKAP13*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.K1844N	ENSG00000170776	ENST00000361243	Transcript	missense_variant	probably_damaging(1)
chr16	11967002	11967002	*GSPT1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L630M	ENSG00000103342	ENST00000434724	Transcript	missense_variant	possibly_damaging(0.586)
chr16	12669400	12669400	*CACNA1H*	Missense_Mutation	.	SNP	C	C	A	rs57181695	sia_et_al_P7	p.N1751K	ENSG00000196557	ENST00000348261	Transcript	missense_variant	probably_damaging(0.998)
chr16	15186466	15186466	*RRN3*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S32*	ENSG00000085721	ENST00000198767	Transcript	stop_gained	NA
chr16	19485472	19485472	*TMC5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G655V	ENSG00000103534	ENST00000396229	Transcript	missense_variant	benign(0.218)
chr16	20373783	20373783	*PDILT*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q453H	ENSG00000169340	ENST00000302451	Transcript	missense_variant	benign(0.024)
chr16	20380952	20380952	*PDILT*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F326L	ENSG00000169340	ENST00000302451	Transcript	missense_variant	probably_damaging(0.999)
chr16	28913332	28913332	*ATP2A1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G750V	ENSG00000196296	ENST00000357084	Transcript	missense_variant	probably_damaging(1)
chr16	29828533	29828533	*PAGR1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P162Q	ENSG00000185928	ENST00000320330	Transcript	missense_variant	probably_damaging(1)
chr16	30419389	30419389	*ZNF771*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q5H	ENSG00000179965	ENST00000319296	Transcript	missense_variant	possibly_damaging(0.447)
chr16	30748754	30748754	*SRCAP*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P2465T	ENSG00000080603	ENST00000262518	Transcript	missense_variant	unknown(0)
chr16	31230508	31230508	*TRIM72*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.E162Rfs*51	ENSG00000177238	ENST00000322122	Transcript	frameshift_variant	NA
chr16	49456577	49456577	*PPL*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.Q345Rfs*72	ENSG00000118898	ENST00000345988	Transcript	frameshift_variant	NA
chr16	50102776	50102776	*HEATR3*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E133*	ENSG00000155393	ENST00000299192	Transcript	stop_gained	NA
chr16	53495681	53495681	*RBL2*	Missense_Mutation	.	SNP	A	A	T	rs61747628	sia_et_al_P7	p.I459F	ENSG00000103479	ENST00000262133	Transcript	missense_variant	probably_damaging(0.991)
chr16	53720475	53720475	*RPGRIP1L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q216K	ENSG00000103494	ENST00000379925	Transcript	missense_variant	benign(0.017)
chr16	66885576	66885576	*CA7*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E155*	ENSG00000168748	ENST00000338437	Transcript	stop_gained	NA
chr16	67100690	67100690	*CBFB*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E130*	ENSG00000067955	ENST00000412916	Transcript	stop_gained	NA
chr16	69996935	69996935	*CLEC18A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R423L	ENSG00000157322	ENST00000288040	Transcript	missense_variant	possibly_damaging(0.878)
chr16	70358494	70358494	*DDX19B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q132H	ENSG00000157349	ENST00000288071	Transcript	missense_variant	benign(0.327)
chr16	70389414	70389414	*DDX19A*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E45*	ENSG00000168872	ENST00000302243	Transcript	stop_gained	NA
chr16	775830	775830	*CCDC78*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E77D	ENSG00000162004	ENST00000293889	Transcript	missense_variant	probably_damaging(0.92)

chr16	786362	786362	*NARFL*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.S115Rfs*16	ENSG00000103245	ENST00000251588	Transcript	frameshift_variant	NA
chr16	8728922	8728922	*METTL22*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D181Y	ENSG00000067365	ENST00000381920	Transcript	missense_variant	probably_damaging(1)
chr16	9024150	9024150	*USP7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D62Y	ENSG00000187555	ENST00000344836	Transcript	missense_variant	probably_damaging(0.959)
chr17	10406526	10406526	*MYH1*	Missense_Mutation	.	SNP	G	G	T	rs370123454	sia_et_al_P7	p.Q911K	ENSG00000109061	ENST00000226207	Transcript	missense_variant	benign(0.006)
chr17	1584248	1584248	*PRPF8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L323I	ENSG00000174231	ENST00000572621	Transcript	missense_variant	benign(0.001)
chr17	19708085	19708085	*ULK2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q406K	ENSG00000083290	ENST00000395544	Transcript	missense_variant	probably_damaging(0.983)
chr17	2236895	2236895	*TSR1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G366V	ENSG00000167721	ENST00000301364	Transcript	missense_variant	probably_damaging(0.988)
chr17	26888453	26888454	*PIGS*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P7	p.L221Qfs*7	ENSG00000087111	ENST00000308360	Transcript	frameshift_variant	NA
chr17	26959141	26959141	*KIAA0100*	Missense_Mutation	.	SNP	G	G	T	rs372600965	sia_et_al_P7	p.L1308M	ENSG00000007202	ENST00000528896	Transcript	missense_variant	benign(0.007)
chr17	27086226	27086227	*FAM222B*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	sia_et_al_P7	p.L251Ffs*16	ENSG00000173065	ENST00000341217	Transcript	frameshift_variant	NA
chr17	27401842	27401842	*MYO18A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H2037Q	ENSG00000196535	ENST00000527372	Transcript	missense_variant	benign(0.035)
chr17	27958800	27958800	*SSH2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L1111M	ENSG00000141298	ENST00000269033	Transcript	missense_variant	possibly_damaging(0.498)
chr17	30351796	30351796	*LRRC37B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E582D	ENSG00000185158	ENST00000341671	Transcript	missense_variant	benign(0.006)
chr17	33738720	33738720	*SLFN12*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F458L	ENSG00000172123	ENST00000394562	Transcript	missense_variant	benign(0.034)
chr17	33771677	33771677	*SLFN13*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L341F	ENSG00000154760	ENST00000285013	Transcript	missense_variant	probably_damaging(0.997)
chr17	35914137	35914137	*SYNRG*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S563Y	ENSG00000006114	ENST00000339208	Transcript	missense_variant	probably_damaging(0.998)
chr17	38978213	38978213	*KRT10*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q209K	ENSG00000186395	ENST00000269576	Transcript	missense_variant	benign(0.006)
chr17	39139311	39139311	*KRT40*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D173Y	ENSG00000204889	ENST00000377755	Transcript	missense_variant	probably_damaging(1)
chr17	40717556	40717556	*COASY*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E514D	ENSG00000068120	ENST00000590958	Transcript	missense_variant	probably_damaging(0.933)
chr17	41061371	41061371	*G6PC*	Silent	.	SNP	C	C	A	novel	sia_et_al_P7	p.V166V	ENSG00000131482	ENST00000253801	Transcript	synonymous_variant	NA
chr17	41610084	41610084	*ETV4*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.V257Wfs*2	ENSG00000175832	ENST00000319349	Transcript	frameshift_variant	NA
chr17	42635705	42635705	*FZD2*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	sia_et_al_P7	p.G217Rfs*3	ENSG00000180340	ENST00000315323	Transcript	frameshift_variant	NA
chr17	46690650	46690650	*HOXB8*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E216*	ENSG00000120068	ENST00000239144	Transcript	stop_gained	NA
chr17	49157023	49157023	*SPAG9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D116Y	ENSG00000008294	ENST00000262013	Transcript	missense_variant	probably_damaging(0.972)
chr17	57465728	57465728	*YPEL2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S53*	ENSG00000175155	ENST00000312655	Transcript	stop_gained	NA
chr17	59668540	59668541	*NACA2*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P7	p.M1?	ENSG00000253506	ENST00000521764	Transcript	frameshift_variant	NA
chr17	61907502	61907502	*PSMC5*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E92*	ENSG00000087191	ENST00000310144	Transcript	stop_gained	NA
chr17	62045469	62045469	*SCN4A*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S317*	ENSG00000007314	ENST00000435607	Transcript	stop_gained	NA
chr17	62078474	62078476	*C17orf72*	In_Frame_Del	.	DEL	GAG	GAG	-	rs559317966	sia_et_al_P7	p.E95del	ENSG00000224383	ENST00000425164	Transcript	inframe_deletion	NA
chr17	66992059	66992059	*ABCA9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G1178C	ENSG00000154258	ENST00000340001	Transcript	missense_variant	possibly_damaging(0.549)
chr17	67161811	67161811	*TEKT1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A274D	ENSG00000167858	ENST00000338694	Transcript	missense_variant	probably_damaging(0.988)
chr17	68128288	68128288	*KCNJ16*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Y20*	ENSG00000153822	ENST00000392670	Transcript	stop_gained	NA
chr17	73170911	73170911	*SUMO2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S54*	ENSG00000188612	ENST00000420826	Transcript	stop_gained	NA
chr17	73238534	73238534	*GGA3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.K210N	ENSG00000125447	ENST00000245541	Transcript	missense_variant	probably_damaging(0.996)
chr17	73836612	73836613	*UNC13D*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P7	p.G244Wfs*25	ENSG00000092929	ENST00000207549	Transcript	frameshift_variant	NA
chr17	73854577	73854577	*SLC35G6*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.G52Afs*116	ENSG00000259224	ENST00000412468	Transcript	frameshift_variant	NA

chr17	73929107	73929107	*FBF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q32K	ENSG00000188878	ENST00000319129	Transcript	missense_variant	benign(0.058)
chr17	77922754	77922754	*TBC1D16*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F486L	ENSG00000167291	ENST00000310924	Transcript	missense_variant	benign(0.297)
chr17	80439061	80439061	*NARF*	Frame_Shift_Del	.	DEL	G	G	-	rs375187791	sia_et_al_P7	p.G249Afs*6	ENSG00000141562	ENST00000309794	Transcript	frameshift_variant	NA
chr17	86474648	86474648	*CCDC42*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P40T	ENSG00000161973	ENST00000293845	Transcript	missense_variant	probably_damaging(0.997)
chr18	12479738	12479738	*SPIRE1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R455I	ENSG00000134278	ENST00000409402	Transcript	missense_variant	benign(0.305)
chr18	19147954	19147954	*ESCO1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E544D	ENSG00000141446	ENST00000269214	Transcript	missense_variant	benign(0.02)
chr18	21416973	21416973	*LAMA3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.H1005N	ENSG00000053747	ENST00000313654	Transcript	missense_variant	benign(0.002)
chr18	21913041	21913041	*OSBPL1A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P164T	ENSG00000141447	ENST00000319481	Transcript	missense_variant	benign(0.042)
chr18	22806935	22806935	*ZNF521*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S316Y	ENSG00000198795	ENST00000361524	Transcript	missense_variant	probably_damaging(0.982)
chr18	45423125	45423125	*SMAD2*	Translation_Start_Site	.	SNP	C	C	A	novel	sia_et_al_P7	p.M1?	ENSG00000175387	ENST00000402690	Transcript	initiator_codon_variant	benign(0.018)
chr18	47500720	47500720	*MYO5B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G441V	ENSG00000167306	ENST00000285039	Transcript	missense_variant	probably_damaging(0.992)
chr18	52896182	52896182	*TCF4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G694V	ENSG00000196628	ENST00000398339	Transcript	missense_variant	probably_damaging(1)
chr18	53957000	53957000	*EPB41L3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P994T	ENSG00000082397	ENST00000341928	Transcript	missense_variant	benign(0.003)
chr18	54340222	54340222	*EPB41L3*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S235*	ENSG00000082397	ENST00000341928	Transcript	stop_gained	NA
chr18	56367802	56367802	*MALT1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D210Y	ENSG00000172175	ENST00000348428	Transcript	missense_variant	possibly_damaging(0.833)
chr18	61231230	61231230	*SERPINB12*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.F174L	ENSG00000166634	ENST00000269491	Transcript	missense_variant	possibly_damaging(0.601)
chr18	74627666	74627666	*ZNF236*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.H1041Tfs*6	ENSG00000130856	ENST00000253159	Transcript	frameshift_variant	NA
chr19	10694306	10694306	*AP1M2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Y81*	ENSG00000129354	ENST00000250244	Transcript	stop_gained	NA
chr19	11941165	11941165	*ZNF440*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S24Y	ENSG00000171295	ENST00000304060	Transcript	missense_variant	possibly_damaging(0.597)
chr19	12849415	12849415	*ASNA1*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.Q85Rfs*41	ENSG00000198356	ENST00000591090	Transcript	frameshift_variant	NA
chr19	13184309	13184309	*NFIX*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q232H	ENSG00000008441	ENST00000397661	Transcript	missense_variant	probably_damaging(0.987)
chr19	13221093	13221093	*TRMT1*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.L301Sfs*80	ENSG00000104907	ENST00000592062	Transcript	frameshift_variant	NA
chr19	14161595	14161598	*IL27RA*	Frame_Shift_Del	.	DEL	CCTG	CCTG	-	novel	sia_et_al_P7	p.P478Tfs*11	ENSG00000104998	ENST00000263379	Transcript	frameshift_variant	NA
chr19	14521923	14521923	*DDX39A*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.C164Ffs*23	ENSG00000123136	ENST00000242776	Transcript	frameshift_variant	NA
chr19	15472548	15472548	*AKAP8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P463H	ENSG00000105127	ENST00000269701	Transcript	missense_variant	probably_damaging(1)
chr19	15508349	15508349	*AKAP8L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D463Y	ENSG00000011243	ENST00000397410	Transcript	missense_variant	probably_damaging(0.998)
chr19	17759375	17759375	*UNC13A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A561S	ENSG00000130477	ENST00000519716	Transcript	missense_variant	probably_damaging(0.929)
chr19	17986900	17986900	*SLC5A5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R228L	ENSG00000105641	ENST00000222248	Transcript	missense_variant	possibly_damaging(0.578)
chr19	19675765	19675765	*PBX4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S301I	ENSG00000105717	ENST00000251203	Transcript	missense_variant	possibly_damaging(0.726)
chr19	22846739	22846739	*ZNF492*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E90*	ENSG00000229676	ENST00000456783	Transcript	stop_gained	NA
chr19	34859522	34859522	*GPI*	Missense_Mutation	.	SNP	G	G	T	rs143827313	sia_et_al_P7	p.R145L	ENSG00000105220	ENST00000415930	Transcript	missense_variant	possibly_damaging(0.732)
chr19	36237334	36237334	*PSENEN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L26M	ENSG00000205155	ENST00000587708	Transcript	missense_variant	probably_damaging(1)
chr19	38847447	38847447	*CATSPERG*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E421*	ENSG00000099338	ENST00000409235	Transcript	stop_gained	NA
chr19	40996133	40996133	*SPTBN4*	Nonsense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.W158*	ENSG00000160460	ENST00000352632	Transcript	stop_gained	NA
chr19	42754057	42754057	*ERF*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G99W	ENSG00000105722	ENST00000222329	Transcript	missense_variant	probably_damaging(1)
chr19	43372228	43372228	*PSG1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.A423Efs*2	ENSG00000231924	ENST00000244296	Transcript	frameshift_variant	NA

chr19	47228839	47228839	*STRN4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D446Y	ENSG00000090372	ENST00000391910	Transcript	missense_variant	probably_damaging(0.999)
chr19	52658370	52658370	*ZNF836*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H856N	ENSG00000196267	ENST00000322146	Transcript	missense_variant	probably_damaging(0.96)
chr19	55452952	55452952	*NLRP7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.W43L	ENSG00000167634	ENST00000588756	Transcript	missense_variant	benign(0.017)
chr19	6190632	6190632	*ACSBG2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q655H	ENSG00000130377	ENST00000586696	Transcript	missense_variant	possibly_damaging(0.726)
chr2	107040695	107040695	*RGPD3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.T1243N	ENSG00000153165	ENST00000409886	Transcript	missense_variant	benign(0.258)
chr2	128408920	128408920	*GPR17*	Missense_Mutation	.	SNP	C	C	A	rs375357809	sia_et_al_P7	p.P232Q	ENSG00000144230	ENST00000544369	Transcript	missense_variant	probably_damaging(0.998)
chr2	133543261	133543261	*NCKAP5*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.S375Vfs*31	ENSG00000176771	ENST00000409261	Transcript	frameshift_variant	NA
chr2	145158859	145158859	*ZEB2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q275K	ENSG00000169554	ENST00000558170	Transcript	missense_variant	probably_damaging(0.977)
chr2	167142877	167142877	*SCN9A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A524E	ENSG00000169432	ENST00000409672	Transcript	missense_variant	benign(0.01)
chr2	170034397	170034397	*LRP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D3437Y	ENSG00000081479	ENST00000263816	Transcript	missense_variant	possibly_damaging(0.655)
chr2	172691356	172691356	*SLC25A12*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S211*	ENSG00000115840	ENST00000422440	Transcript	stop_gained	NA
chr2	175742585	175742585	*CHN1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.G178R	ENSG00000128656	ENST00000409900	Transcript	missense_variant	benign(0)
chr2	178415946	178415946	*TTC30B*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E516*	ENSG00000196659	ENST00000408939	Transcript	stop_gained	NA
chr2	191865882	191865882	*STAT1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S127*	ENSG00000115415	ENST00000361099	Transcript	stop_gained	NA
chr2	208434928	208434929	*CREB1*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P7	p.D144Cfs*8	ENSG00000118260	ENST00000432329	Transcript	frameshift_variant	NA
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	C	rs121913499	sia_et_al_P7	p.R132G	ENSG00000138413	ENST00000415913	Transcript	missense_variant	probably_damaging(0.998)
chr2	209198099	209198099	*PIKFYVE*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E1342*	ENSG00000115020	ENST00000264380	Transcript	stop_gained	NA
chr2	216236835	216236835	*FN1*	Missense_Mutation	.	SNP	C	C	A	rs369532159	sia_et_al_P7	p.V2171L	ENSG00000115414	ENST00000354785	Transcript	missense_variant	benign(0.005)
chr2	219540836	219540836	*STK36*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.E174Sfs*22	ENSG00000163482	ENST00000295709	Transcript	frameshift_variant	NA
chr2	219558617	219558617	*STK36*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P7	p.X750_splice	ENSG00000163482	ENST00000295709	Transcript	splice_acceptor_variant	NA
chr2	220101826	220101826	*GLB1L*	Missense_Mutation	.	SNP	C	C	T	rs147840034	sia_et_al_P7	p.A645T	ENSG00000163521	ENST00000295759	Transcript	missense_variant	benign(0)
chr2	220473912	220473912	*STK11IP*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P646T	ENSG00000144589	ENST00000295641	Transcript	missense_variant	benign(0.439)
chr2	225346740	225346740	*CUL3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S633Y	ENSG00000036257	ENST00000264414	Transcript	missense_variant	probably_damaging(0.997)
chr2	231937054	231937054	*PSMD1*	Missense_Mutation	.	SNP	G	G	T	rs140288102	sia_et_al_P7	p.R269L	ENSG00000173692	ENST00000308696	Transcript	missense_variant	benign(0.004)
chr2	231937114	231937114	*PSMD1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G289V	ENSG00000173692	ENST00000308696	Transcript	missense_variant	benign(0.01)
chr2	232100068	232100068	*ARMC9*	Missense_Mutation	.	SNP	C	C	A	rs370477312	sia_et_al_P7	p.L252I	ENSG00000135931	ENST00000349938	Transcript	missense_variant	probably_damaging(0.926)
chr2	232141474	232141474	*ARMC9*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.C487F	ENSG00000135931	ENST00000349938	Transcript	missense_variant	probably_damaging(1)
chr2	238978025	238978026	*SCLY*	Frame_Shift_Del	.	DEL	GT	GT	-	novel	sia_et_al_P7	p.V139Efs*68	ENSG00000132330	ENST00000256633	Transcript	frameshift_variant	NA
chr2	242460475	242460475	*MFSD2B*	Missense_Mutation	.	SNP	G	G	T	rs371551284	sia_et_al_P7	p.G379C	ENSG00000205639	ENST00000406420	Transcript	missense_variant	probably_damaging(0.999)
chr2	249648 17	249648 17	*NCOA1*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.R1158Vfs*33	ENSG00000084676	ENST00000406961	Transcript	frameshift_variant	NA
chr2	29296614	29296614	*C2orf71*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G172C	ENSG00000179270	ENST00000331664	Transcript	missense_variant	benign(0.113)
chr2	37289133	37289133	*HEATR5B*	Frame_Shift_Del	.	DEL	AA	AA	-	novel	sia_et_al_P7	p.L549Sfs*46	ENSG00000008869	ENST00000233099	Transcript	frameshift_variant	NA
chr2	48692642	48692642	*PPP1R21*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R253L	ENSG00000162869	ENST00000294952	Transcript	missense_variant	probably_damaging(0.998)
chr2	55566779	55566779	*CCDC88A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q447K	ENSG00000115355	ENST00000336838	Transcript	missense_variant	benign(0.087)
chr2	61515838	61515838	*USP34*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G1575C	ENSG00000115464	ENST00000398571	Transcript	missense_variant	possibly_damaging(0.887)
chr2	64113646	64113646	*UGP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D349Y	ENSG00000169764	ENST00000337130	Transcript	missense_variant	benign(0.078)

chr2	64331840	64331840	*PELI1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A66S	ENSG00000197329	ENST00000358912	Transcript	missense_variant	benign(0.016)
chr2	74076614	74076614	*STAMBP*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.M290*	ENSG00000124356	ENST00000394070	Transcript	frameshift_variant	NA
chr2	74450071	74450071	*SLC4A5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F1101L	ENSG00000188687	ENST00000377634	Transcript	missense_variant	benign(0.12)
chr2	85276677	85276677	*KCMF1*	Missense_Mutation	.	SNP	A	A	T	novel	sia_et_al_P7	p.T264S	ENSG00000176407	ENST00000409785	Transcript	missense_variant	benign(0.001)
chr2	88857411	88857411	*EIF2AK3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R1065L	ENSG00000172071	ENST00000303236	Transcript	missense_variant	probably_damaging(1)
chr2	99454601	99454601	*KIAA1211L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D74Y	ENSG00000196872	ENST00000397899	Transcript	missense_variant	probably_damaging(0.963)
chr20	20003119	20003119	*NAA20*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E25*	ENSG00000173418	ENST00000334982	Transcript	stop_gained	NA
chr20	20023138	20023138	*CRNKL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A493E	ENSG00000101343	ENST00000377340	Transcript	missense_variant	possibly_damaging(0.536)
chr20	25939006	25939006	*TMC2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L604I	ENSG00000149488	ENST00000358864	Transcript	missense_variant	benign(0.021)
chr20	35422406	35422406	*SOGA1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S1360*	ENSG00000149639	ENST00000237536	Transcript	stop_gained	NA
chr20	37603911	37603911	*SPEF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F47L	ENSG00000101222	ENST00000379756	Transcript	missense_variant	possibly_damaging(0.873)
chr20	47271903	47271903	*PREX1*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.I712Sfs*41	ENSG00000124126	ENST00000371941	Transcript	frameshift_variant	NA
chr20	47741100	47741100	*STAU1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H212N	ENSG00000124214	ENST00000371856	Transcript	missense_variant	probably_damaging(0.998)
chr20	54824471	54824471	*MC3R*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.C191F	ENSG00000124089	ENST00000243911	Transcript	missense_variant	probably_damaging(0.972)
chr20	56083838	56083838	*CTCFL*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H500N	ENSG00000124092	ENST00000423479	Transcript	missense_variant	probably_damaging(0.993)
chr20	57478842	57478842	*GNAS*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P786H	ENSG00000087460	ENST00000371100	Transcript	missense_variant	probably_damaging(0.987)
chr21	30339327	30339327	*LTN1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E542*	ENSG00000198862	ENST00000389194	Transcript	stop_gained	NA
chr21	31964852	31964852	*KRTAP6-3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L23M	ENSG00000212938	ENST00000391624	Transcript	missense_variant	unknown(0)
chr21	31964876	31964876	*KRTAP6-3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G31C	ENSG00000212938	ENST00000391624	Transcript	missense_variant	unknown(0)
chr21	37741375	37741375	*MORC3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G570V	ENSG00000159256	ENST00000400485	Transcript	missense_variant	benign(0.006)
chr21	41416103	41416103	*DSCAM*	Missense_Mutation	.	SNP	T	T	C	novel	sia_et_al_P7	p.H1762R	ENSG00000171587	ENST00000400454	Transcript	missense_variant	benign(0.01)
chr21	47766092	47766092	*PCNT*	Frame_Shift_Del	.	DEL	GT	GT	-	novel	sia_et_al_P7	p.E231Rfs*2	ENSG00000160299	ENST00000359568	Transcript	frameshift_variant	NA
chr22	18018385	18018385	*CECR2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E424*	ENSG00000099954	ENST00000262608	Transcript	stop_gained	NA
chr22	18387582	18387582	*MICAL3*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.C97Vfs*68	ENSG00000243156	ENST00000441493	Transcript	frameshift_variant	NA
chr22	18568008	18568008	*PEX26*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.V267*	ENSG00000215193	ENST00000329627	Transcript	frameshift_variant	NA
chr22	29932646	29932646	*THOC5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S227R	ENSG00000100296	ENST00000490103	Transcript	missense_variant	benign(0.07)
chr22	32112678	32112678	*PRR14L*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.Y383Ifs*21	ENSG00000183530	ENST00000327423	Transcript	frameshift_variant	NA
chr22	40064378	40064378	*CACNA1I*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D1396Y	ENSG00000100346	ENST00000402142	Transcript	missense_variant	probably_damaging(0.961)
chr22	42120069	42120070	*MEI1*	Frame_Shift_Del	.	DEL	CT	CT	-	novel	sia_et_al_P7	p.L286Qfs*7	ENSG00000167077	ENST00000401548	Transcript	frameshift_variant	NA
chr22	44328845	44328845	*PNPLA3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D192Y	ENSG00000100344	ENST00000216180	Transcript	missense_variant	probably_damaging(1)
chr3	100949960	100949960	*IMPG2*	Missense_Mutation	.	SNP	C	C	A	rs531246692	sia_et_al_P7	p.R1088L	ENSG00000081148	ENST00000193391	Transcript	missense_variant	probably_damaging(0.987)
chr3	10346788	10346788	*SEC13*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D213Y	ENSG00000157020	ENST00000350697	Transcript	missense_variant	probably_damaging(0.999)
chr3	109027034	109027034	*DPPA2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R168I	ENSG00000163530	ENST00000478945	Transcript	missense_variant	possibly_damaging(0.5)
chr3	112357778	112357778	*CCDC80*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E325D	ENSG00000091986	ENST00000206423	Transcript	missense_variant	benign(0)
chr3	113225422	113225422	*SPICE1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P11T	ENSG00000163611	ENST00000295872	Transcript	missense_variant	benign(0.082)
chr3	118866405	118866405	*C3orf30*	Frame_Shift_Del	.	DEL	G	G	-	rs199919487	sia_et_al_P7	p.E457Kfs*6	ENSG00000163424	ENST00000295622	Transcript	frameshift_variant	NA

chr3	128996154	128996154	*COPG1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.H838N	ENSG00000181789	ENST00000314797	Transcript	missense_variant	benign(0.056)
chr3	129196910	129196910	*IFT122*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R451L	ENSG00000163913	ENST00000296266	Transcript	missense_variant	probably_damaging(0.99)
chr3	130140004	130140004	*COL6A5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S1653Y	ENSG00000172752	ENST00000265379	Transcript	missense_variant	benign(0)
chr3	132203476	132203476	*DNAJC13*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R1076I	ENSG00000138246	ENST00000260818	Transcript	missense_variant	probably_damaging(0.985)
chr3	133583458	133583458	*RAB6B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F33L	ENSG00000154917	ENST00000285208	Transcript	missense_variant	possibly_damaging(0.556)
chr3	135768188	135768188	*PPP2R3A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.F818L	ENSG00000073711	ENST00000264977	Transcript	missense_variant	probably_damaging(0.991)
chr3	137843270	137843270	*A4GNT*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L287M	ENSG00000118017	ENST00000236709	Transcript	missense_variant	probably_damaging(0.949)
chr3	140401821	140401821	*TRIM42*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E287*	ENSG00000155890	ENST00000286349	Transcript	stop_gained	NA
chr3	141011483	141011483	*ACPL2*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.I295*	ENSG00000155893	ENST00000286353	Transcript	frameshift_variant	NA
chr3	151158166	151158166	*ZFYVE20*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S593*	ENSG00000131381	ENST00000253699	Transcript	stop_gained	NA
chr3	171965417	171965417	*FNDC3B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.T120N	ENSG00000075420	ENST00000336824	Transcript	missense_variant	benign(0.402)
chr3	183397056	183397056	*KLHL24*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E595D	ENSG00000114796	ENST00000454652	Transcript	missense_variant	benign(0)
chr3	184082983	184082983	*POLR2H*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E74*	ENSG00000163882	ENST00000456318	Transcript	stop_gained	NA
chr3	190106230	190106230	*CLDN16*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E108*	ENSG00000113946	ENST00000264734	Transcript	stop_gained	NA
chr3	195256687	195256687	*PPP1R2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.K46N	ENSG00000184203	ENST00000328432	Transcript	missense_variant	probably_damaging(0.97)
chr3	195965585	195965585	*PCYT1A*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.D360Ifs*137	ENSG00000161217	ENST00000292823	Transcript	frameshift_variant	NA
chr3	196528851	196528851	*PAK2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E81*	ENSG00000180370	ENST00000327134	Transcript	stop_gained	NA
chr3	267511 76	267511 76	*LRRC3B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D5Y	ENSG00000179796	ENST00000396641	Transcript	missense_variant	possibly_damaging(0.843)
chr3	274901 62	274901 62	*SLC4A7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G81V	ENSG00000033867	ENST00000295736	Transcript	missense_variant	possibly_damaging(0.881)
chr3	316585 57	316585 57	*STT3B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L371F	ENSG00000163527	ENST00000295770	Transcript	missense_variant	probably_damaging(0.997)
chr3	323989 79	323989 79	*CMTM8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L88I	ENSG00000170293	ENST00000307526	Transcript	missense_variant	possibly_damaging(0.572)
chr3	329951 46	329951 46	*CCR4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L78M	ENSG00000183813	ENST00000330953	Transcript	missense_variant	probably_damaging(1)
chr3	465714 79	465714 79	*LRRC2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P230Q	ENSG00000163827	ENST00000395905	Transcript	missense_variant	probably_damaging(1)
chr3	471656 11	471656 11	*SETD2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P172Q	ENSG00000181555	ENST00000409792	Transcript	missense_variant	benign(0.002)
chr3	485108 05	485108 05	*SHISA5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P200T	ENSG00000164054	ENST00000296444	Transcript	missense_variant	probably_damaging(0.975)
chr3	485387 20	485387 20	*SHISA5*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.G28Vfs*35	ENSG00000164054	ENST00000296444	Transcript	frameshift_variant	NA
chr3	485729 98	485729 98	*PFKFB4*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E312*	ENSG00000114268	ENST00000232375	Transcript	stop_gained	NA
chr3	486654 43	486654 43	*SLC26A6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S610Y	ENSG00000225697	ENST00000395550	Transcript	missense_variant	benign(0.016)
chr3	493977 19	493977 19	*RHOA*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E169*	ENSG00000067560	ENST00000418115	Transcript	stop_gained	NA
chr3	525553 92	525553 92	*STAB1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P1975H	ENSG00000010327	ENST00000321725	Transcript	missense_variant	possibly_damaging(0.566)
chr3	525554 35	525554 35	*STAB1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.M1989I	ENSG00000010327	ENST00000321725	Transcript	missense_variant	benign(0.001)
chr3	531408 44	531408 44	*RFT1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G273C	ENSG00000163933	ENST00000296292	Transcript	missense_variant	probably_damaging(0.992)
chr3	535357 15	535357 15	*CACNA1D*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E151*	ENSG00000157388	ENST00000288139	Transcript	stop_gained	NA
chr3	555135 01	555135 01	*WNT5A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G78*	ENSG00000114251	ENST00000474267	Transcript	stop_gained	NA
chr3	623559 20	623559 20	*FEZF2*	Missense_Mutation	.	SNP	G	G	T	rs530439929	sia_et_al_P7	p.F406L	ENSG00000153266	ENST00000283268	Transcript	missense_variant	benign(0.014)
chr3	691712 44	691712 44	*LMOD3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E98D	ENSG00000163380	ENST00000420581	Transcript	missense_variant	benign(0.403)

chr3	93813928	93813928	*NSUN3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D225Y	ENSG00000178694	ENST00000314622	Transcript	missense_variant	probably_damaging(0.956)
chr4	110865039	110865039	*EGF*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R184I	ENSG00000138798	ENST00000265171	Transcript	missense_variant	probably_damaging(0.996)
chr4	111026759	111026759	*ELOVL6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L39M	ENSG00000170522	ENST00000394607	Transcript	missense_variant	possibly_damaging(0.507)
chr4	122078287	122078287	*TNIP3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q186K	ENSG00000050730	ENST00000509841	Transcript	missense_variant	benign(0.051)
chr4	122756431	122756431	*BBS7*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S460*	ENSG00000138686	ENST00000264499	Transcript	stop_gained	NA
chr4	124323608	124323608	*SPRY1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D288Y	ENSG00000164056	ENST00000394339	Transcript	missense_variant	probably_damaging(1)
chr4	140587187	140587187	*MGST2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S5*	ENSG00000085871	ENST00000265498	Transcript	stop_gained	NA
chr4	146460970	146460970	*SMAD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L139M	ENSG00000170365	ENST00000515385	Transcript	missense_variant	probably_damaging(0.913)
chr4	153692117	153692117	*TIGD4*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.V15*	ENSG00000169989	ENST00000303437	Transcript	frameshift_variant	NA
chr4	175833 82	175833 82	*LAP3*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P7	p.X73_splice	ENSG00000002549	ENST00000226299	Transcript	splice_acceptor_variant	NA
chr4	177829 06	177829 06	*FAM184B*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.N6Tfs*31	ENSG00000047662	ENST00000265018	Transcript	frameshift_variant	NA
chr4	205411 82	205411 82	*SLIT2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D651Y	ENSG00000145147	ENST00000504154	Transcript	missense_variant	probably_damaging(0.979)
chr4	3105610	3105610	*HTT*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.K176N	ENSG00000197386	ENST00000355072	Transcript	missense_variant	possibly_damaging(0.8)
chr4	3209032	3209032	*HTT*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E2034*	ENSG00000197386	ENST00000355072	Transcript	stop_gained	NA
chr4	41016125	41016125	*APBB2*	Nonsense_Mutation	.	SNP	C	C	A	rs571480915	sia_et_al_P7	p.E104*	ENSG00000163697	ENST00000508593	Transcript	stop_gained	NA
chr4	53610712	53610712	*ERVMER34-1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L326I	ENSG00000226887	ENST00000443173	Transcript	missense_variant	possibly_damaging(0.567)
chr4	7006570	7006570	*TBC1D14*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P7	p.X424_splice	ENSG00000132405	ENST00000409757	Transcript	splice_acceptor_variant	NA
chr4	77969625	77969625	*CCNI*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.S294N	ENSG00000118816	ENST00000237654	Transcript	missense_variant	benign(0.287)
chr4	79372943	79372943	*FRAS1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.H2161N	ENSG00000138759	ENST00000264895	Transcript	missense_variant	probably_damaging(0.996)
chr4	87656891	87656891	*PTPN13*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.L767*	ENSG00000163629	ENST00000436978	Transcript	frameshift_variant	NA
chr5	108713980	108713980	*PJA2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G403V	ENSG00000198961	ENST00000361189	Transcript	missense_variant	benign(0.004)
chr5	123985315	123985315	*ZNF608*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.W413L	ENSG00000168916	ENST00000306315	Transcript	missense_variant	probably_damaging(0.92)
chr5	127595187	127595187	*FBN2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G2900V	ENSG00000138829	ENST00000508053	Transcript	missense_variant	benign(0.013)
chr5	134015292	134015292	*SEC24A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q419K	ENSG00000113615	ENST00000398844	Transcript	missense_variant	benign(0.004)
chr5	13700902	13700902	*DNAH5*	Missense_Mutation	.	SNP	C	C	A	rs199916139	sia_et_al_P7	p.D4524Y	ENSG00000039139	ENST00000265104	Transcript	missense_variant	probably_damaging(0.978)
chr5	137500730	137500730	*BRD8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D468E	ENSG00000112983	ENST00000254900	Transcript	missense_variant	benign(0.002)
chr5	13871769	13871769	*DNAH5*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E1168*	ENSG00000039139	ENST00000265104	Transcript	stop_gained	NA
chr5	139889731	139889731	*ANKHD1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.R1357W	ENSG00000131503	ENST00000297183	Transcript	missense_variant	possibly_damaging(0.898)
chr5	147778671	147778671	*FBXO38*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.R80W	ENSG00000145868	ENST00000394370	Transcript	missense_variant	probably_damaging(0.992)
chr5	149772991	149772991	*TCOF1*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.A1221Pfs*5	ENSG00000070814	ENST00000504761	Transcript	frameshift_variant	NA
chr5	157065587	157065587	*SOX30*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.Q511Nfs*22	ENSG00000039600	ENST00000265007	Transcript	frameshift_variant	NA
chr5	16764454	16764454	*MYO10*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E411*	ENSG00000145555	ENST00000513610	Transcript	stop_gained	NA
chr5	178996418	178996418	*RUFY1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D274Y	ENSG00000176783	ENST00000319449	Transcript	missense_variant	probably_damaging(0.999)
chr5	179755315	179755315	*GFPT2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F186L	ENSG00000131459	ENST00000253778	Transcript	missense_variant	benign(0.104)
chr5	32230053	32230053	*MTMR12*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A692D	ENSG00000150712	ENST00000382142	Transcript	missense_variant	benign(0.209)
chr5	32724803	32724803	*NPR3*	Splice_Site	.	SNP	G	G	T	rs377329316	sia_et_al_P7	p.X257_splice	ENSG00000113389	ENST00000265074	Transcript	splice_acceptor_variant	NA

chr5	35026568	35026568	*AGXT2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L273M	ENSG00000113492	ENST00000231420	Transcript	missense_variant	possibly_damaging(0.877)
chr5	35955856	35955856	*UGT3A1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G396*	ENSG00000145626	ENST00000274278	Transcript	stop_gained	NA
chr5	36257122	36257122	*RANBP3L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S300Y	ENSG00000164188	ENST00000502994	Transcript	missense_variant	possibly_damaging(0.474)
chr5	64079727	64079727	*CWC27*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S106Y	ENSG00000153015	ENST00000381070	Transcript	missense_variant	benign(0.199)
chr5	68411762	68411762	*SLC30A5*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E265*	ENSG00000145740	ENST00000396591	Transcript	stop_gained	NA
chr5	75896647	75896647	*IQGAP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A361D	ENSG00000145703	ENST00000274364	Transcript	missense_variant	benign(0.424)
chr5	76707945	76707945	*PDE8B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.H533N	ENSG00000113231	ENST00000264917	Transcript	missense_variant	benign(0.056)
chr5	81572274	81572274	*RPS23*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.K76N	ENSG00000186468	ENST00000296674	Transcript	missense_variant	possibly_damaging(0.657)
chr5	837592	837592	*ZDHHC11*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A263D	ENSG00000188818	ENST00000283441	Transcript	missense_variant	possibly_damaging(0.588)
chr5	96058347	96058347	*CAST*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S72*	ENSG00000153113	ENST00000395812	Transcript	stop_gained	NA
chr5	96119631	96119631	*ERAP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F699L	ENSG00000164307	ENST00000296754	Transcript	missense_variant	benign(0.006)
chr6	107088760	107088760	*QRSL1*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.G83S	ENSG00000130348	ENST00000369046	Transcript	missense_variant	benign(0.163)
chr6	111196367	111196367	*AMD1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R20L	ENSG00000123505	ENST00000368885	Transcript	missense_variant	benign(0.002)
chr6	11213797	11213797	*NEDD9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R59L	ENSG00000111859	ENST00000379446	Transcript	missense_variant	probably_damaging(1)
chr6	116288843	116288843	*FRK*	Missense_Mutation	.	SNP	C	C	A	rs555269385	sia_et_al_P7	p.V224L	ENSG00000111816	ENST00000606080	Transcript	missense_variant	benign(0.256)
chr6	116757900	116757901	*DSE*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P7	p.K758Efs*12	ENSG00000111817	ENST00000331677	Transcript	frameshift_variant	NA
chr6	117240385	117240385	*RFX6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D370Y	ENSG00000185002	ENST00000332958	Transcript	missense_variant	benign(0.396)
chr6	126199427	126199427	*NCOA7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L124I	ENSG00000111912	ENST00000368357	Transcript	missense_variant	possibly_damaging(0.536)
chr6	131917816	131917816	*MED23*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H874N	ENSG00000112282	ENST00000368068	Transcript	missense_variant	possibly_damaging(0.715)
chr6	135768283	135768283	*AHI1*	Missense_Mutation	.	SNP	G	G	T	rs553366477	sia_et_al_P7	p.R548S	ENSG00000135541	ENST00000367800	Transcript	missense_variant	possibly_damaging(0.693)
chr6	136980407	136980407	*MAP3K5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.M492I	ENSG00000197442	ENST00000359015	Transcript	missense_variant	benign(0)
chr6	151413614	151413614	*MTHFD1L*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.M953I	ENSG00000120254	ENST00000367321	Transcript	missense_variant	benign(0.052)
chr6	154105119	154105119	*JARID2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.K82N	ENSG00000008083	ENST00000341776	Transcript	missense_variant	possibly_damaging(0.723)
chr6	157256631	157256631	*ARID1B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S653Y	ENSG00000049618	ENST00000346085	Transcript	missense_variant	possibly_damaging(0.782)
chr6	160494338	160494338	*IGF2R*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G1595V	ENSG00000197081	ENST00000356956	Transcript	missense_variant	probably_damaging(1)
chr6	160551232	160551232	*SLC22A1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A170S	ENSG00000175003	ENST00000366963	Transcript	missense_variant	benign(0.121)
chr6	165809926	165809926	*PDE10A*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S434*	ENSG00000112541	ENST00000539869	Transcript	stop_gained	NA
chr6	25845746	25845746	*SLC17A3*	Splice_Site	.	DEL	T	T	-	novel	sia_et_al_P7	p.X455_splice	ENSG00000124564	ENST00000397060	Transcript	splice_acceptor_variant	NA
chr6	25862508	25862508	*SLC17A3*	Missense_Mutation	.	SNP	C	C	A	rs370851319	sia_et_al_P7	p.D86Y	ENSG00000124564	ENST00000397060	Transcript	missense_variant	benign(0.378)
chr6	26370805	26370805	*BTN3A2*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.K231Rfs*47	ENSG00000186470	ENST00000356386	Transcript	frameshift_variant	NA
chr6	35911843	35911843	*SLC26A8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S916Y	ENSG00000112053	ENST00000490799	Transcript	missense_variant	benign(0)
chr6	35912096	35912096	*SLC26A8*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	NA	ENSG00000112053	ENST00000490799	Transcript	frameshift_variant	NA
chr6	36368248	36368248	*PXT1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H95N	ENSG00000179165	ENST00000454782	Transcript	missense_variant	benign(0.055)
chr6	43023734	43023734	*MRPL2*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.E178Kfs*43	ENSG00000112651	ENST00000388752	Transcript	frameshift_variant	NA
chr6	43038169	43038170	*KLC4*	Frame_Shift_Del	.	DEL	GC	GC	-	novel	sia_et_al_P7	p.R338Gfs*34	ENSG00000137171	ENST00000259708	Transcript	frameshift_variant	NA
chr6	44394236	44394236	*CDC5L*	Frame_Shift_Del	.	DEL	A	A	-	rs138606198	sia_et_al_P7	p.R557Dfs*3	ENSG00000096401	ENST00000371477	Transcript	frameshift_variant	NA

chr6	99374849	99374849	*FBXL4*	Missense_Mutation	.	SNP	G	G	T	rs549380000	sia_et_al_P7	p.P6T	ENSG00000112234	ENST00000369244	Transcript	missense_variant	probably_damaging(0.999)
chr7	104767450	104767450	*SRPK2*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.R605Efs*6	ENSG00000135250	ENST00000393651	Transcript	frameshift_variant	NA
chr7	107013207	107013208	*COG5*	Splice_Site	.	DEL	TT	TT	-	novel	sia_et_al_P7	p.X255_splice	ENSG00000164597	ENST00000297135	Transcript	splice_acceptor_variant	NA
chr7	107834589	107834589	*NRCAM*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E553*	ENSG00000091129	ENST00000379028	Transcript	stop_gained	NA
chr7	124104 92	124104 92	*VWDE*	Splice_Site	.	DEL	T	T	-	novel	sia_et_al_P7	p.X530_splice	ENSG00000146530	ENST00000275358	Transcript	splice_acceptor_variant	NA
chr7	129909513	129909514	*CPA2*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P7	p.W55Lfs*39	ENSG00000158516	ENST00000222481	Transcript	frameshift_variant	NA
chr7	131194279	131194279	*PODXL*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P290T	ENSG00000128567	ENST00000378555	Transcript	missense_variant	possibly_damaging(0.531)
chr7	131815300	131815300	*PLXNA4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G1875W	ENSG00000221866	ENST00000359827	Transcript	missense_variant	possibly_damaging(0.844)
chr7	135282858	135282858	*NUP205*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G726V	ENSG00000155561	ENST00000285968	Transcript	missense_variant	probably_damaging(0.997)
chr7	138603901	138603901	*KIAA1549*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.M157I	ENSG00000122778	ENST00000422774	Transcript	missense_variant	possibly_damaging(0.889)
chr7	139311466	139311466	*HIPK2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F500L	ENSG00000064393	ENST00000406875	Transcript	missense_variant	possibly_damaging(0.866)
chr7	143175118	143175118	*TAS2R41*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.L51F	ENSG00000221855	ENST00000408916	Transcript	missense_variant	probably_damaging(1)
chr7	148489835	148489835	*CUL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.M608I	ENSG00000055130	ENST00000325222	Transcript	missense_variant	possibly_damaging(0.662)
chr7	165022 78	165022 78	*SOSTDC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H172Q	ENSG00000171243	ENST00000307068	Transcript	missense_variant	probably_damaging(0.995)
chr7	271690 11	271690 11	*HOXA4*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P7	p.R266W	ENSG00000197576	ENST00000360046	Transcript	missense_variant	probably_damaging(1)
chr7	306720 03	306720 03	*GARS*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.H682N	ENSG00000106105	ENST00000389266	Transcript	missense_variant	benign(0.039)
chr7	446056 66	446056 66	*DDX56*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q527K	ENSG00000136271	ENST00000258772	Transcript	missense_variant	benign(0.004)
chr7	662178 3	662178 3	*ZDHHC4*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P7	p.C91S	ENSG00000136247	ENST00000396706	Transcript	missense_variant	probably_damaging(0.972)
chr7	666603 13	666603 13	*TYW1*	Missense_Mutation	.	SNP	G	G	T	rs538199546	sia_et_al_P7	p.A656S	ENSG00000198874	ENST00000359626	Transcript	missense_variant	benign(0.367)
chr7	734743 23	734743 23	*ELN*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G508C	ENSG00000049540	ENST00000252034	Transcript	missense_variant	unknown(0)
chr7	756116 29	756116 29	*POR*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.N274Tfs*22	ENSG00000127948	ENST00000461988	Transcript	frameshift_variant	NA
chr7	761266 4	761266 4	*MIOS*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.C187Vfs*22	ENSG00000164654	ENST00000340080	Transcript	frameshift_variant	NA
chr7	815992 43	815992 43	*CACNA2D1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R754S	ENSG00000153956	ENST00000356860	Transcript	missense_variant	probably_damaging(0.999)
chr7	827636 68	827636 69	*PCLO*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P7	p.I1068Rfs*3	ENSG00000186472	ENST00000333891	Transcript	frameshift_variant	NA
chr7	919724 64	919724 64	*ANKIB1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P305Q	ENSG00000001629	ENST00000265742	Transcript	missense_variant	possibly_damaging(0.54)
chr7	920858 16	920858 16	*GATAD1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.W250C	ENSG00000157259	ENST00000287957	Transcript	missense_variant	probably_damaging(0.98)
chr8	100833 531	100833 531	*VPS13B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q3027K	ENSG00000132549	ENST00000358544	Transcript	missense_variant	benign(0.042)
chr8	103298 818	103298 818	*UBR5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S1662Y	ENSG00000104517	ENST00000520539	Transcript	missense_variant	probably_damaging(0.982)
chr8	117861 236	117861 236	*RAD21*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.Q551H	ENSG00000164754	ENST00000297338	Transcript	missense_variant	probably_damaging(0.979)
chr8	120759 082	120759 082	*TAF2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E991*	ENSG00000064313	ENST00000378164	Transcript	stop_gained	NA
chr8	121463 561	121463 561	*MTBP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D142Y	ENSG00000172167	ENST00000305949	Transcript	missense_variant	benign(0.348)
chr8	135649 913	135649 913	*ZFAT*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S80Y	ENSG00000066827	ENST00000377838	Transcript	missense_variant	possibly_damaging(0.556)
chr8	144906 505	144906 505	*PUF60*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G30V	ENSG00000179950	ENST00000526683	Transcript	missense_variant	benign(0.032)
chr8	144941 784	144941 784	*EPPK1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G1880*	ENSG00000227184	ENST00000525985	Transcript	stop_gained	NA
chr8	307211 1	307211 1	*CSMD1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S1592Y	ENSG00000183117	ENST00000537824	Transcript	missense_variant	possibly_damaging(0.578)
chr8	395643 87	395643 87	*ADAM18*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G661W	ENSG00000168619	ENST00000265707	Transcript	missense_variant	probably_damaging(1)

chr8	444580	444580	*TDRP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.F42L	ENSG00000180190	ENST00000523656	Transcript	missense_variant	benign(0.124)
chr8	48874193	48874193	*MCM4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A63D	ENSG00000104738	ENST00000262105	Transcript	missense_variant	benign(0.021)
chr8	61766994	61766994	*CHD7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.T2283N	ENSG00000171316	ENST00000423902	Transcript	missense_variant	possibly_damaging(0.852)
chr8	64203401	64203401	*ANGPT2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G39W	ENSG00000091879	ENST00000325203	Transcript	missense_variant	probably_damaging(1)
chr8	68150998	68150998	*ARFGEF1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G1037V	ENSG00000066777	ENST00000262215	Transcript	missense_variant	probably_damaging(1)
chr8	70514006	70514006	*SULF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D335Y	ENSG00000137573	ENST00000260128	Transcript	missense_variant	probably_damaging(0.979)
chr8	81412496	81412496	*ZBTB10*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.T581Qfs*16	ENSG00000205189	ENST00000430430	Transcript	frameshift_variant	NA
chr9	101065545	101065545	*GABBR2*	Missense_Mutation	.	SNP	C	C	A	rs80137447	sia_et_al_P7	p.R797L	ENSG00000136928	ENST00000259455	Transcript	missense_variant	benign(0.03)
chr9	101216340	101216340	*GABBR2*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.D387Afs*17	ENSG00000136928	ENST00000259455	Transcript	frameshift_variant	NA
chr9	111911947	111911947	*FRRS1L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D149Y	ENSG00000260230	ENST00000561981	Transcript	missense_variant	benign(0.288)
chr9	113445057	113445057	*MUSK*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.W61C	ENSG00000030304	ENST00000374448	Transcript	missense_variant	probably_damaging(0.999)
chr9	115204045	115204045	*HSDL2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S287*	ENSG00000119471	ENST00000398805	Transcript	stop_gained	NA
chr9	118162642	118162642	*Dec/01*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	NA	ENSG00000173077	ENST00000374016	Transcript	frameshift_variant	NA
chr9	125797120	125797120	*GPR21*	Missense_Mutation	.	SNP	A	A	T	novel	sia_et_al_P7	p.H92L	ENSG00000188394	ENST00000373642	Transcript	missense_variant	benign(0.001)
chr9	127651715	127651715	*GOLGA1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R533L	ENSG00000136935	ENST00000373555	Transcript	missense_variant	benign(0.032)
chr9	131743572	131743572	*NUP188*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.F473L	ENSG00000095319	ENST00000372577	Transcript	missense_variant	benign(0.438)
chr9	131893840	131893840	*PPP2R4*	Missense_Mutation	.	SNP	C	C	A	rs371000314	sia_et_al_P7	p.L128M	ENSG00000119383	ENST00000393370	Transcript	missense_variant	benign(0.091)
chr9	132060092	132060092	*MPDZ*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G433C	ENSG00000107186	ENST00000541718	Transcript	missense_variant	possibly_damaging(0.843)
chr9	140866004	140866004	*CACNA1B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.M501I	ENSG00000148408	ENST00000371372	Transcript	missense_variant	benign(0.017)
chr9	140952524	140952524	*CACNA1B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A1377D	ENSG00000148408	ENST00000371372	Transcript	missense_variant	probably_damaging(0.999)
chr9	19573375	19573375	*SLC24A2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H441N	ENSG00000155886	ENST00000341998	Transcript	missense_variant	benign(0.008)
chr9	20907153	20907153	*FOCAD*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	sia_et_al_P7	p.H877Yfs*47	ENSG00000188352	ENST00000380249	Transcript	frameshift_variant	NA
chr9	34648874	34648874	*GALT*	Frame_Shift_Del	.	DEL	C	C	-	rs111033847	sia_et_al_P7	p.P269Lfs*7	ENSG00000213930	ENST00000378842	Transcript	frameshift_variant	NA
chr9	35399273	35399273	*UNC13B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D1315Y	ENSG00000198722	ENST00000378495	Transcript	missense_variant	probably_damaging(1)
chr9	57536437	57536437	*KIAA1432*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P7	NA	ENSG00000107036	ENST00000414202	Transcript	splice_donor_variant	NA
chr9	86414203	86414203	*GKAP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S86Y	ENSG00000165113	ENST00000376371	Transcript	missense_variant	probably_damaging(0.97)
chr9	96324546	96324546	*FAM120A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.R1002M	ENSG00000048828	ENST00000277165	Transcript	missense_variant	possibly_damaging(0.859)
chrX	101912134	101912134	*GPRASP1*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P7	p.Q1098Rfs*52	ENSG00000198932	ENST00000537097	Transcript	frameshift_variant	NA
chrX	106065404	106065404	*TBC1D8B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S186R	ENSG00000133138	ENST00000357242	Transcript	missense_variant	possibly_damaging(0.908)
chrX	114869358	114869358	*PLS3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.A250S	ENSG00000102024	ENST00000426625	Transcript	missense_variant	benign(0.091)
chrX	118724883	118724883	*NKRF*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.E184*	ENSG00000186416	ENST00000542113	Transcript	stop_gained	NA
chrX	119004778	119004778	*RNF113A*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.Q267Rfs*47	ENSG00000125352	ENST00000371442	Transcript	frameshift_variant	NA
chrX	123615612	123615612	*TENM1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A1307S	ENSG00000009694	ENST00000422452	Transcript	missense_variant	probably_damaging(0.957)
chrX	128657257	128657257	*SMARCA1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P31T	ENSG00000102038	ENST00000371122	Transcript	missense_variant	benign(0)
chrX	129804095	129804095	*ENOX2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D209Y	ENSG00000165675	ENST00000338144	Transcript	missense_variant	probably_damaging(0.999)
chrX	130678378	130678378	*OR13H1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.E111*	ENSG00000171054	ENST00000338616	Transcript	stop_gained	NA

chrX	132888148	132888148	*GPC3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.K131N	ENSG00000147257	ENST00000394299	Transcript	missense_variant	benign(0.102)
chrX	134680808	134680808	*DDX26B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G204V	ENSG00000165359	ENST00000370752	Transcript	missense_variant	probably_damaging(0.999)
chrX	135290644	135290644	*FHL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.D178Y	ENSG00000022267	ENST00000394155	Transcript	missense_variant	probably_damaging(0.996)
chrX	135592263	135592263	*HTATSF1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S316Y	ENSG00000102241	ENST00000535601	Transcript	missense_variant	probably_damaging(0.999)
chrX	149945922	149945922	*CD99L2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G177V	ENSG00000102181	ENST00000370377	Transcript	missense_variant	possibly_damaging(0.809)
chrX	153219981	153219981	*HCFC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S1290Y	ENSG00000172534	ENST00000310441	Transcript	missense_variant	probably_damaging(0.982)
chrX	153695580	153695580	*PLXNA3*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.V1071*	ENSG00000130827	ENST00000369682	Transcript	frameshift_variant	NA
chrX	170403 94	170403 94	*REPS2*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P7	p.Q182Hfs*27	ENSG00000169891	ENST00000357277	Transcript	frameshift_variant	NA
chrX	182134 73	182134 73	*BEND2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.G375*	ENSG00000177324	ENST00000380033	Transcript	stop_gained	NA
chrX	200439 96	200439 96	*MAP7D2*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.R361H	ENSG00000184368	ENST00000379643	Transcript	missense_variant	probably_damaging(0.99)
chrX	200815 93	200815 93	*MAP7D2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.R104L	ENSG00000184368	ENST00000379643	Transcript	missense_variant	probably_damaging(0.997)
chrX	216091 43	216091 43	*CNKSR2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P554H	ENSG00000149970	ENST00000379510	Transcript	missense_variant	benign(0.111)
chrX	292817 9	292817 9	*ARSH*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P7	p.I69Sfs*11	ENSG00000205667	ENST00000381130	Transcript	frameshift_variant	NA
chrX	296865 68	296865 68	*IL1RAPL1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P242H	ENSG00000169306	ENST00000378993	Transcript	missense_variant	possibly_damaging(0.781)
chrX	303263 18	303263 18	*NR0B1*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P7	p.N388Tfs*10	ENSG00000169297	ENST00000378970	Transcript	frameshift_variant	NA
chrX	324029 3	324029 3	*MXRA5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.H1145N	ENSG00000101825	ENST00000217939	Transcript	missense_variant	benign(0.115)
chrX	404504 93	404504 93	*ATP6AP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.S59Y	ENSG00000182220	ENST00000378438	Transcript	missense_variant	possibly_damaging(0.845)
chrX	405738 72	405738 72	*MED14*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.A147S	ENSG00000180182	ENST00000324817	Transcript	missense_variant	probably_damaging(0.998)
chrX	483365 47	483365 47	*FTSJ1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.L38I	ENSG00000068438	ENST00000348411	Transcript	missense_variant	benign(0.316)
chrX	487637 39	487637 39	*SLC35A2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.S119Y	ENSG00000102100	ENST00000247138	Transcript	missense_variant	probably_damaging(0.971)
chrX	535631 76	535631 76	*HUWE1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.Q4155K	ENSG00000086758	ENST00000342160	Transcript	missense_variant	unknown()
chrX	540202 61	540202 61	*PHF8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.P503T	ENSG00000172943	ENST00000357988	Transcript	missense_variant	benign(0.026)
chrX	668631 99	668631 99	*AR*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P7	p.G573V	ENSG00000169083	ENST00000374690	Transcript	missense_variant	probably_damaging(0.997)
chrX	703485 35	703485 35	*MED12*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P7	p.R1148C	ENSG00000184634	ENST00000374080	Transcript	missense_variant	benign(0.161)
chrX	729008 12	729008 12	*CHIC1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.P216Q	ENSG00000204116	ENST00000373502	Transcript	missense_variant	probably_damaging(0.999)
chrX	851662 82	851662 82	*CHM*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P7	p.D410Y	ENSG00000188419	ENST00000357749	Transcript	missense_variant	probably_damaging(0.991)
chr1	120436 817	120436 817	*ADAM30*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P3	p.H715Y	ENSG00000134249	ENST00000369400	Transcript	missense_variant	benign(0)
chr1	120548 048	120548 048	*NOTCH2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.H107N	ENSG00000134250	ENST00000256646	Transcript	missense_variant	benign(0.008)
chr1	145698 952	145698 952	*CD160*	Splice_Site	.	SNP	C	C	T	rs185729292	sia_et_al_P3	p.X180_splice	ENSG00000117281	ENST00000235933	Transcript	splice_donor_variant	NA
chr1	155736 469	155736 469	*GON4L*	Missense_Mutation	.	SNP	C	C	A	rs553583157	sia_et_al_P3	p.R932L	ENSG00000116580	ENST00000437809	Transcript	missense_variant	possibly_damaging(0.835)
chr1	197097 738	197097 738	*ASPM*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P3	p.L940F	ENSG00000066279	ENST00000367409	Transcript	missense_variant	probably_damaging(1)
chr1	491937 04	491937 04	*BEND5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.D374Y	ENSG00000162373	ENST00000371833	Transcript	missense_variant	probably_damaging(0.913)
chr1	914051 64	914051 65	*ZNF644*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P3	p.S583Ifs*7	ENSG00000122482	ENST00000370440	Transcript	frameshift_variant	NA
chr1	919771 55	919771 55	*CDC7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.G113W	ENSG00000097046	ENST00000428239	Transcript	missense_variant	probably_damaging(1)
chr10	284205 88	284205 88	*MPP7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.Q116H	ENSG00000150054	ENST00000337532	Transcript	missense_variant	probably_damaging(0.92)
chr10	374228 81	374228 81	*ANKRD30A*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.E163*	ENSG00000148513	ENST00000361713	Transcript	stop_gained	NA

chr10	70951421	70951421	*SUPV3L1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.C251F	ENSG00000156502	ENST00000359655	Transcript	missense_variant	probably_damaging(0.996)
chr10	96112772	96112772	*NOC3L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.D247Y	ENSG00000173145	ENST00000371361	Transcript	missense_variant	probably_damaging(0.999)
chr11	108155164	108155164	*ATM*	Nonsense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P3	p.Y1319*	ENSG00000149311	ENST00000278616	Transcript	stop_gained	NA
chr11	56043536	56043536	*OR5T1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.P141H	ENSG00000181698	ENST00000313033	Transcript	missense_variant	probably_damaging(0.995)
chr11	68029745	68029745	*C11orf24*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.D240Y	ENSG00000171067	ENST00000304271	Transcript	missense_variant	probably_damaging(0.979)
chr12	19626286	19626286	*AEBP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.F328L	ENSG00000139154	ENST00000398864	Transcript	missense_variant	benign(0.085)
chr12	53071971	53071971	*KRT1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E281D	ENSG00000167768	ENST00000252244	Transcript	missense_variant	probably_damaging(0.996)
chr12	59274556	59274556	*LRIG3*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P3	p.D537Tfs*23	ENSG00000139263	ENST00000320743	Transcript	frameshift_variant	NA
chr12	69991001	69991003	*CCT2*	In_Frame_Del	.	DEL	GAG	GAG	-	novel	sia_et_al_P3	p.E351del	ENSG00000166226	ENST00000299300	Transcript	inframe_deletion	NA
chr13	21364707	21364707	*XPO4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.R937I	ENSG00000132953	ENST00000255305	Transcript	missense_variant	benign(0.019)
chr13	31036824	31036824	*HMGB1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E108*	ENSG00000189403	ENST00000405805	Transcript	stop_gained	NA
chr13	38159012	38159012	*POSTN*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.G317*	ENSG00000133110	ENST00000379747	Transcript	stop_gained	NA
chr13	42875245	42875245	*AKAP11*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.A788D	ENSG00000023516	ENST00000253021	Transcript	missense_variant	probably_damaging(0.915)
chr13	50502074	50502074	*SPRYD7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.P124Q	ENSG00000123178	ENST00000361840	Transcript	missense_variant	probably_damaging(0.992)
chr13	70413295	70413295	*KLHL1*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P3	p.X410_splice	ENSG00000150361	ENST00000377844	Transcript	splice_acceptor_variant	NA
chr13	77595967	77595967	*FBXL3*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P3	p.R10H	ENSG00000005812	ENST00000355619	Transcript	missense_variant	benign(0)
chr14	26917206	26917206	*NOVA1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P3	p.E495K	ENSG00000139910	ENST00000539517	Transcript	missense_variant	probably_damaging(0.985)
chr14	35078930	35078930	*SNX6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.D37Y	ENSG00000129515	ENST00000362031	Transcript	missense_variant	probably_damaging(0.92)
chr15	28474897	28474897	*HERC2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.L1636I	ENSG00000128731	ENST00000261609	Transcript	missense_variant	benign(0.026)
chr15	30927798	30927798	*ARHGAP11B*	Missense_Mutation	.	SNP	C	C	A	rs369518739	sia_et_al_P3	p.L257M	ENSG00000187951	ENST00000428041	Transcript	missense_variant	benign(0.438)
chr15	43708614	43708614	*TP53BP1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.G1561V	ENSG00000067369	ENST00000382044	Transcript	missense_variant	probably_damaging(1)
chr16	14973915	14973915	*NOMO1*	Missense_Mutation	.	SNP	G	G	T	rs377717037	sia_et_al_P3	p.R934L	ENSG00000103512	ENST00000287667	Transcript	missense_variant	possibly_damaging(0.582)
chr17	35346657	35346657	*AATF*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P3	p.G421S	ENSG00000108270	ENST00000225402	Transcript	missense_variant	probably_damaging(0.989)
chr17	35376316	35376316	*AATF*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.L471I	ENSG00000108270	ENST00000225402	Transcript	missense_variant	probably_damaging(0.946)
chr17	35913891	35913891	*SYNRG*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.T645K	ENSG00000006114	ENST00000339208	Transcript	missense_variant	benign(0.156)
chr17	41244748	41244748	*BRCA1*	Missense_Mutation	.	SNP	G	G	T	rs80357223	sia_et_al_P3	p.Q934K	ENSG00000012048	ENST00000471181	Transcript	missense_variant	possibly_damaging(0.805)
chr17	42937822	42937822	*EFTUD2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.T566N	ENSG00000108883	ENST00000426333	Transcript	missense_variant	probably_damaging(0.932)
chr17	49302513	49302513	*MBTD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.G4C	ENSG00000011258	ENST00000586178	Transcript	missense_variant	probably_damaging(0.999)
chr18	18586552	18586552	*ROCK1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E549*	ENSG00000067900	ENST00000399799	Transcript	stop_gained	NA
chr18	55336597	55336597	*ATP8B1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.D684Y	ENSG00000081923	ENST00000536015	Transcript	missense_variant	probably_damaging(0.987)
chr2	149447864	149447864	*EPC2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.A79S	ENSG00000135999	ENST00000258484	Transcript	missense_variant	possibly_damaging(0.823)
chr2	163167401	163167401	*IFIH1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E166*	ENSG00000115267	ENST00000263642	Transcript	stop_gained	NA
chr2	170732312	170732312	*UBR3*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P3	p.P233S	ENSG00000144357	ENST00000418381	Transcript	missense_variant	benign(0.001)
chr2	174820914	174820914	*SP3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.W109L	ENSG00000172845	ENST00000310015	Transcript	missense_variant	probably_damaging(0.932)
chr2	202575792	202575792	*ALS2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E1348D	ENSG00000003393	ENST00000264276	Transcript	missense_variant	benign(0.049)
chr2	88887560	88887560	*EIF2AK3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.D457Y	ENSG00000172071	ENST00000303236	Transcript	missense_variant	probably_damaging(0.945)

chr20	20054979	20054979	*C20orf26*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.A110S	ENSG00000089101	ENST00000245957	Transcript	missense_variant	benign(0.377)
chr20	78949978	78949978	*HAO1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E120*	ENSG00000101323	ENST00000378789	Transcript	stop_gained	NA
chr21	18981457	18981457	*BTG3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.K2N	ENSG00000154640	ENST00000339775	Transcript	missense_variant	possibly_damaging(0.879)
chr3	10116341	10116341	*FANCD2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.T948N	ENSG00000144554	ENST00000287647	Transcript	missense_variant	benign(0.162)
chr3	113169289	113169289	*SPICE1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.M739I	ENSG00000163611	ENST00000295872	Transcript	missense_variant	benign(0.005)
chr3	15123877	15123877	*ZFYVE20*	Nonsense_Mutation	.	SNP	G	G	T	rs372130779	sia_et_al_P3	p.Y279*	ENSG00000131381	ENST00000253699	Transcript	stop_gained	NA
chr3	154139145	154139145	*GPR149*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E436*	ENSG00000174948	ENST00000389740	Transcript	stop_gained	NA
chr3	170723261	170723261	*SLC2A2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.S259I	ENSG00000163581	ENST00000314251	Transcript	missense_variant	probably_damaging(0.965)
chr3	32181729	32181729	*GPD1L*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.E126*	ENSG00000152642	ENST00000282541	Transcript	stop_gained	NA
chr3	37388774	37388774	*GOLGA4*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P3	p.G2203D	ENSG00000144674	ENST00000356847	Transcript	missense_variant	probably_damaging(1)
chr4	110749287	110749287	*RRH*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.A35E	ENSG00000180245	ENST00000317735	Transcript	missense_variant	probably_damaging(0.983)
chr4	36286009	36286009	*DTHD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.T103N	ENSG00000197057	ENST00000456874	Transcript	missense_variant	possibly_damaging(0.499)
chr4	66230873	66230872	*EPHA5*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P3	p.L702Ifs*9	ENSG00000145242	ENST00000273854	Transcript	frameshift_variant	NA
chr4	72363394	72363394	*SLC4A4*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P3	p.Y718Ifs*9	ENSG00000080493	ENST00000425175	Transcript	frameshift_variant	NA
chr4	77244476	77244476	*CCDC158*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.D1082Y	ENSG00000163749	ENST00000388914	Transcript	missense_variant	probably_damaging(0.998)
chr5	140553312	140553312	*PCDHB7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.G299V	ENSG00000113212	ENST00000231137	Transcript	missense_variant	probably_damaging(0.943)
chr5	161322713	161322713	*GABRA1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.A300S	ENSG00000022355	ENST00000428797	Transcript	missense_variant	probably_damaging(0.992)
chr5	180582400	180582400	*OR2V2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.G153V	ENSG00000182613	ENST00000328275	Transcript	missense_variant	probably_damaging(1)
chr5	37351327	37351327	*NUP155*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.G230*	ENSG00000113569	ENST00000231498	Transcript	stop_gained	NA
chr6	101099513	101099513	*ASCC3*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E1000*	ENSG00000112249	ENST00000369162	Transcript	stop_gained	NA
chr6	160485914	160485914	*IGF2R*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.L1366M	ENSG00000197081	ENST00000356956	Transcript	missense_variant	benign(0.026)
chr6	26448858	26448858	*BTN3A3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.E310D	ENSG00000111801	ENST00000244519	Transcript	missense_variant	benign(0.002)
chr7	33312624	33312624	*BBS9*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.V235L	ENSG00000122507	ENST00000242067	Transcript	missense_variant	benign(0.137)
chr8	117782465	117782465	*UTP23*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.D75Y	ENSG00000147679	ENST00000309822	Transcript	missense_variant	possibly_damaging(0.516)
chr8	68536479	68536479	*CPA6*	Missense_Mutation	.	SNP	C	C	A	rs372306981	sia_et_al_P3	p.V42L	ENSG00000165078	ENST00000297770	Transcript	missense_variant	benign(0.015)
chr8	77761243	77761243	*ZFHX4*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P3	p.P1175L	ENSG00000091656	ENST00000521891	Transcript	missense_variant	possibly_damaging(0.851)
chr9	19305375	19305375	*DENND4C*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.C446F	ENSG00000137145	ENST00000602925	Transcript	missense_variant	probably_damaging(1)
chrX	12275763 8	12275763 8	*THOC2*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P3	p.G1168D	ENSG00000125676	ENST00000245838	Transcript	missense_variant	possibly_damaging(0.493)
chrX	13548807 6	13548807 6	*GPR112*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.W2960C	ENSG00000156920	ENST00000394143	Transcript	missense_variant	probably_damaging(0.998)
chrX	21579664	21579664	*CNKSR2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.R460I	ENSG00000149970	ENST00000379510	Transcript	missense_variant	possibly_damaging(0.702)
chrX	31697601	31697601	*DMD*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P3	p.A2588D	ENSG00000198947	ENST00000357033	Transcript	missense_variant	possibly_damaging(0.82)
chrX	57934619	57934619	*ZXDA*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P3	p.E746*	ENSG00000198205	ENST00000358697	Transcript	stop_gained	NA
chrX	64517911	64517911	*VCX3A*	Missense_Mutation	.	SNP	C	C	T	rs743939338	sia_et_al_P3	p.V186M	ENSG00000169059	ENST00000381089	Transcript	missense_variant	unknown(0)
chr1	10074040 0	10074040 0	*RTCA*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P4	p.G178D	ENSG00000137996	ENST00000260563	Transcript	missense_variant	probably_damaging(0.909)
chr1	10977362 7	10977362 7	*SARS*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P4	p.R192Q	ENSG00000031698	ENST00000234677	Transcript	missense_variant	probably_damaging(1)
chr1	14558543 5	14558543 5	*PIAS3*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P4	p.S567Ffs*37	ENSG00000131788	ENST00000390305	Transcript	frameshift_variant	NA

chr1	145765435	145765435	GPR89A	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P4	p.X366_splice	ENSG00000117262	ENST00000313835	Transcript	splice_acceptor_variant	NA
chr1	150082610	150082610	VPS45	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P4	p.X498_splice	ENSG00000136631	ENST00000369130	Transcript	splice_acceptor_variant	NA
chr1	158227216	158227216	CD1A	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.H297N	ENSG00000158477	ENST00000289429	Transcript	missense_variant	benign(0.041)
chr1	165621232	165621232	MGST3	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.P70L	ENSG00000143198	ENST00000367889	Transcript	missense_variant	benign(0.004)
chr1	177030299	177030299	ASTN1	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P129Q	ENSG00000152092	ENST00000361833	Transcript	missense_variant	benign(0.007)
chr1	213251152	213251152	RPS6KC1	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.V86L	ENSG00000136643	ENST00000366960	Transcript	missense_variant	benign(0.075)
chr1	223959550	223959550	CAPN2	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.A648D	ENSG00000162909	ENST00000295006	Transcript	missense_variant	probably_damaging(0.999)
chr1	233388512	233388512	PCNXL2	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.K619N	ENSG00000135749	ENST00000258229	Transcript	missense_variant	benign(0.013)
chr1	235323932	235323932	RBM34	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E87*	ENSG00000188739	ENST00000408888	Transcript	stop_gained	NA
chr1	242253184	242253184	PLD5	Missense_Mutation	.	SNP	G	G	T	rs550275311	sia_et_al_P4	p.T528K	ENSG00000180287	ENST00000536534	Transcript	missense_variant	benign(0.004)
chr1	247769560	247769560	OR2G3	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.V225L	ENSG00000177476	ENST00000320002	Transcript	missense_variant	benign(0.167)
chr1	26227999	26227999	STMN1	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E121*	ENSG00000117632	ENST00000426559	Transcript	stop_gained	NA
chr1	26801609	26801609	HMGN2	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.Q81H	ENSG00000198830	ENST00000361427	Transcript	missense_variant	benign(0.228)
chr1	42896512	42896512	ZMYND12	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.M331I	ENSG00000066185	ENST00000372565	Transcript	missense_variant	benign(0.001)
chr1	49201985	49201985	BEND5	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.G345V	ENSG00000162373	ENST00000371833	Transcript	missense_variant	possibly_damaging(0.858)
chr1	52489177	52489178	TXNDC12	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P4	p.V142Dfs*20	ENSG00000117862	ENST00000371626	Transcript	frameshift_variant	NA
chr1	53267603	53267603	ZYG11B	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P4	p.R533K	ENSG00000162378	ENST00000294353	Transcript	missense_variant	benign(0.003)
chr1	87012917	87012917	CLCA4	Missense_Mutation	.	SNP	G	G	T	rs201894845	sia_et_al_P4	p.D39Y	ENSG00000016602	ENST00000370563	Transcript	missense_variant	probably_damaging(0.968)
chr1	94953135	94953135	ABCD3	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.S312*	ENSG00000117528	ENST00000370214	Transcript	stop_gained	NA
chr10	12819289	12819289	C10orf90	In_Frame_Ins	.	INS	-	-	CGA	rs577186477	sia_et_al_P4	p.S291dup	ENSG00000154493	ENST00000284694	Transcript	inframe_insertion	NA
chr10	15098861	15098861	OLAH	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.L68I	ENSG00000152463	ENST00000378217	Transcript	missense_variant	benign(0.047)
chr10	15115200	15115200	OLAH	Missense_Mutation	.	SNP	T	T	A	rs370998370	sia_et_al_P4	p.L310Q	ENSG00000152463	ENST00000378217	Transcript	missense_variant	probably_damaging(0.999)
chr10	26729729	26729729	ZMYND11	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P4	NA	ENSG00000015171	ENST00000397962	Transcript	splice_donor_variant	NA
chr10	33197323	33197323	ITGB1	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.K768N	ENSG00000150093	ENST00000396033	Transcript	missense_variant	probably_damaging(0.996)
chr10	43659372	43659372	CSGALNACT2	Nonsense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.R347*	ENSG00000169826	ENST00000374466	Transcript	stop_gained	NA
chr10	60553264	60553264	BICC1	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.L356F	ENSG00000122870	ENST00000373886	Transcript	missense_variant	probably_damaging(0.998)
chr10	70516053	70516053	CCAR1	Missense_Mutation	.	SNP	A	A	T	novel	sia_et_al_P4	p.Y550F	ENSG00000060339	ENST00000265872	Transcript	missense_variant	probably_damaging(0.973)
chr10	75290071	75290072	USP54	Frame_Shift_Ins	.	INS	-	-	GA	novel	sia_et_al_P4	p.D554Lfs*5	ENSG00000166348	ENST00000339859	Transcript	frameshift_variant	NA
chr11	116798028	116798028	SIK3	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.A117S	ENSG00000160584	ENST00000292055	Transcript	missense_variant	probably_damaging(1)
chr11	128844220	128844220	ARHGAP32	Nonsense_Mutation	.	SNP	C	C	A	rs371103913	sia_et_al_P4	p.E944*	ENSG00000134909	ENST00000310343	Transcript	stop_gained	NA
chr11	14529207	14529207	PSMA1	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.A250S	ENSG00000129084	ENST00000418988	Transcript	missense_variant	benign(0.001)
chr11	28116332	28116332	KIF18A	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.A114D	ENSG00000121621	ENST00000263181	Transcript	missense_variant	probably_damaging(1)
chr11	61570845	61570846	FADS1	Frame_Shift_Ins	.	INS	-	-	C	novel	sia_et_al_P4	p.S414Vfs*17	ENSG00000149485	ENST00000350997	Transcript	frameshift_variant	NA
chr11	76925024	76925024	MYO7A	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P4	NA	ENSG00000137474	ENST00000409709	Transcript	frameshift_variant	NA
chr11	77702344	77702344	INTS4	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P19Q	ENSG00000149262	ENST00000534064	Transcript	missense_variant	benign(0)
chr11	94219226	94219226	MRE11A	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.D60Y	ENSG00000020922	ENST00000323929	Transcript	missense_variant	probably_damaging(1)

chr12	100787200	100787200	*SLC17A8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.S176Y	ENSG00000179520	ENST00000323346	Transcript	missense_variant	probably_damaging(0.954)
chr12	102190483	102190483	*GNPTAB*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.N59Y	ENSG00000111670	ENST00000299314	Transcript	missense_variant	probably_damaging(0.999)
chr12	108008863	108008863	*BTBD11*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.P642Q	ENSG00000151136	ENST00000280758	Transcript	missense_variant	probably_damaging(0.993)
chr12	124094609	124094609	*DDX55*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P4	p.K226Rfs*66	ENSG00000111364	ENST00000238146	Transcript	frameshift_variant	NA
chr12	270242 4	270242 4	*CACNA1C*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.P859Q	ENSG00000151067	ENST00000347598	Transcript	missense_variant	probably_damaging(0.982)
chr12	39155932	39155932	*CPNE8*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.C221Y	ENSG00000139117	ENST00000331366	Transcript	missense_variant	probably_damaging(0.966)
chr12	56566244	56566245	*SMARCC2*	Frame_Shift_Ins	.	INS	-	-	G	novel	sia_et_al_P4	p.W601Lfs*19	ENSG00000139613	ENST00000267064	Transcript	frameshift_variant	NA
chr12	75678776	75678776	*CAPS2*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.E513K	ENSG00000180881	ENST00000409445	Transcript	missense_variant	probably_damaging(0.911)
chr13	52997774	52997774	*VPS36*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E259*	ENSG00000136100	ENST00000378060	Transcript	stop_gained	NA
chr13	73335612	73335612	*DIS3*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.F854Lfs*2	ENSG00000083520	ENST00000377767	Transcript	frameshift_variant	NA
chr13	76412291	76412291	*LMO7*	Missense_Mutation	.	SNP	C	C	A	rs367627741	sia_et_al_P4	p.S904Y	ENSG00000136153	ENST00000465261	Transcript	missense_variant	probably_damaging(0.987)
chr13	78475256	78475256	*EDNRB*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.M386I	ENSG00000136160	ENST00000377211	Transcript	missense_variant	benign(0.041)
chr13	99115962	99115962	*STK24*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.S316R	ENSG00000102572	ENST00000376547	Transcript	missense_variant	possibly_damaging(0.628)
chr13	99115992	99115992	*STK24*	Missense_Mutation	.	SNP	C	C	A	rs575613052	sia_et_al_P4	p.W306C	ENSG00000102572	ENST00000376547	Transcript	missense_variant	probably_damaging(0.988)
chr14	71524264	71524265	*PCNX*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P4	p.H1559Lfs*4	ENSG00000100731	ENST00000304743	Transcript	frameshift_variant	NA
chr14	73673103	73673103	*PSEN1*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.V293E	ENSG00000080815	ENST00000324501	Transcript	missense_variant	possibly_damaging(0.778)
chr15	28493761	28493761	*HERC2*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P4	p.Q1058Nfs*25	ENSG00000128731	ENST00000261609	Transcript	frameshift_variant	NA
chr15	43023438	43023438	*CDAN1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E611*	ENSG00000140326	ENST00000356231	Transcript	stop_gained	NA
chr15	43446958	43446958	*TMEM62*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.P371S	ENSG00000137842	ENST00000260403	Transcript	missense_variant	probably_damaging(0.999)
chr15	50884133	50884133	*TRPM7*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.D1433Efs*9	ENSG00000092439	ENST00000313478	Transcript	frameshift_variant	NA
chr15	50902109	50902109	*TRPM7*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.K777I	ENSG00000092439	ENST00000313478	Transcript	missense_variant	probably_damaging(0.947)
chr15	64716253	64716253	*TRIP4*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P4	p.H463Tfs*7	ENSG00000103671	ENST00000261884	Transcript	frameshift_variant	NA
chr15	68118819	68118820	*SKOR1*	Frame_Shift_Del	.	DEL	CG	CG	-	novel	sia_et_al_P4	p.P405Qfs*34	ENSG00000188779	ENST00000341418	Transcript	frameshift_variant	NA
chr15	77406901	77406902	*PEAK1*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	sia_et_al_P4	p.P1613Rfs*39	ENSG00000173517	ENST00000560626	Transcript	frameshift_variant	NA
chr16	15829289	15829290	*MYH11*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P4	p.E1156Gfs*37	ENSG00000133392	ENST00000396324	Transcript	frameshift_variant	NA
chr16	22268630	22268631	*EEF2K*	Frame_Shift_Del	.	DEL	CC	CC	-	novel	sia_et_al_P4	p.Q276Gfs*8	ENSG00000103319	ENST00000263026	Transcript	frameshift_variant	NA
chr16	46652276	46652277	*SHCBP1*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	sia_et_al_P4	p.F37Lfs*3	ENSG00000171241	ENST00000303383	Transcript	frameshift_variant	NA
chr16	58589696	58589696	*CNOT1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.V866I	ENSG00000125107	ENST00000317147	Transcript	missense_variant	benign(0.016)
chr16	70573105	70573105	*SF3B3*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.N355Tfs*58	ENSG00000189091	ENST00000302516	Transcript	frameshift_variant	NA
chr16	72821931	72821931	*ZFHX3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.A3415D	ENSG00000140836	ENST00000268489	Transcript	missense_variant	unknown(0)
chr17	10356966	10356966	*MYH4*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P4	p.N977Tfs*3	ENSG00000264424	ENST00000255381	Transcript	frameshift_variant	NA
chr17	10395735	10395736	*MYH1*	Frame_Shift_Ins	.	INS	-	-	CT	novel	sia_et_al_P4	NA	ENSG00000109061	ENST00000226207	Transcript	frameshift_variant	NA
chr17	16456157	16456157	*ZNF287*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.F433L	ENSG00000141040	ENST00000395824	Transcript	missense_variant	probably_damaging(0.981)
chr17	27251233	27251233	*PHF12*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.D137Y	ENSG00000109118	ENST00000332830	Transcript	missense_variant	probably_damaging(0.936)
chr17	33690031	33690031	*SLFN11*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P4	p.D266Tfs*5	ENSG00000172716	ENST00000394566	Transcript	frameshift_variant	NA
chr17	35592012	35592012	*ACACA*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P4	p.H1042Y	ENSG00000132142	ENST00000353139	Transcript	missense_variant	probably_damaging(0.993)

chr17	38573006	38573006	*TOP2A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E55*	ENSG00000131747	ENST00000423485	Transcript	stop_gained	NA
chr17	42882317	42882317	*GJC1*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.Y290F	ENSG00000182963	ENST00000426548	Transcript	missense_variant	probably_damaging(0.935)
chr17	46606998	46606998	*HOXB1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P273T	ENSG00000120094	ENST00000239174	Transcript	missense_variant	benign(0.002)
chr17	48626186	48626186	*SPATA20*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P4	p.H127Tfs*5	ENSG00000006282	ENST00000006658	Transcript	frameshift_variant	NA
chr17	48729288	48729288	*CAMTA2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.K1109N	ENSG00000108509	ENST00000414043	Transcript	missense_variant	probably_damaging(0.997)
chr17	61838605	61838605	*CCDC47*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.M218I	ENSG00000108588	ENST00000225726	Transcript	missense_variant	probably_damaging(0.996)
chr17	66347756	66347756	*ARSG*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.M165I	ENSG00000141337	ENST00000448504	Transcript	missense_variant	possibly_damaging(0.893)
chr17	77279799	77279800	*DNAH2*	Frame_Shift_Del	.	DEL	CC	CC	-	novel	sia_et_al_P4	p.H3931Pfs*48	ENSG00000183914	ENST00000572933	Transcript	frameshift_variant	NA
chr18	46645287	46645287	*DYM*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.L525I	ENSG00000141627	ENST00000269445	Transcript	missense_variant	probably_damaging(1)
chr18	61077533	61077533	*VPS4B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.D96Y	ENSG00000119541	ENST00000238497	Transcript	missense_variant	possibly_damaging(0.691)
chr18	69431882	69431882	*LAMA1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P3022T	ENSG00000101680	ENST00000389658	Transcript	missense_variant	possibly_damaging(0.685)
chr19	10610320	10610320	*KEAP1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P4	p.K131Rfs*26	ENSG00000079999	ENST00000171111	Transcript	frameshift_variant	NA
chr19	15640650	15640650	*CYP4F22*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.L119Wfs*18	ENSG00000171954	ENST00000269703	Transcript	frameshift_variant	NA
chr19	37004922	37004922	*ZNF260*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P4	p.Q407Rfs*25	ENSG00000254004	ENST00000523638	Transcript	frameshift_variant	NA
chr19	58758088	58758088	*ZNF544*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.S58T	ENSG00000198131	ENST00000269829	Transcript	missense_variant	benign(0.002)
chr2	113786618	113786618	*IL36B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.F53L	ENSG00000136696	ENST00000259213	Transcript	missense_variant	benign(0.039)
chr2	136374307	136374307	*R3HDM1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.E95*	ENSG00000048991	ENST00000264160	Transcript	stop_gained	NA
chr2	141607853	141607853	*LRP1B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.G1586V	ENSG00000168702	ENST00000389484	Transcript	missense_variant	probably_damaging(0.953)
chr2	163139040	163139040	*IFIH1*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.L381*	ENSG00000115267	ENST00000263642	Transcript	frameshift_variant	NA
chr2	163167296	163167296	*IFIH1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.D201Y	ENSG00000115267	ENST00000263642	Transcript	missense_variant	benign(0.212)
chr2	166786704	166786704	*TTC21B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E355D	ENSG00000123607	ENST00000243344	Transcript	missense_variant	benign(0.021)
chr2	183792941	183792941	*NCKAP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.N1034K	ENSG00000061676	ENST00000360982	Transcript	missense_variant	possibly_damaging(0.883)
chr2	189856225	189856225	*COL3A1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.L289I	ENSG00000168542	ENST00000304636	Transcript	missense_variant	unknown(0)
chr2	189856953	189856953	*COL3A1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.P332Q	ENSG00000168542	ENST00000304636	Transcript	missense_variant	unknown(0)
chr2	207025358	207025358	*EEF1B2*	Missense_Mutation	.	SNP	A	A	G	novel	sia_et_al_P4	p.S43G	ENSG00000114942	ENST00000392222	Transcript	missense_variant	benign(0)
chr2	210837843	210837844	*UNC80*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P4	p.V2747Dfs*42	ENSG00000144406	ENST00000439458	Transcript	frameshift_variant	NA
chr2	228567024	228567024	*SLC19A3*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.Y4Sfs*5	ENSG00000135917	ENST00000258403	Transcript	frameshift_variant	NA
chr2	228767751	228767751	*DAW1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.V192L	ENSG00000123977	ENST00000309931	Transcript	missense_variant	benign(0.019)
chr2	230657744	230657744	*TRIP12*	Frame_Shift_Del	.	DEL	G	G	-	rs372882810	sia_et_al_P4	p.K1288Rfs*16	ENSG00000153827	ENST00000283943	Transcript	frameshift_variant	NA
chr2	233839598	233839598	*NGEF*	Translation_Start_Site	.	SNP	C	C	A	novel	sia_et_al_P4	p.M1?	ENSG00000066248	ENST00000264051	Transcript	initiator_codon_variant	benign(0.023)
chr2	238934020	238934020	*UBE2F*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.P107H	ENSG00000184182	ENST00000272930	Transcript	missense_variant	probably_damaging(1)
chr2	30791035	30791035	*LCLAT1*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.R246Efs*45	ENSG00000172954	ENST00000309052	Transcript	frameshift_variant	NA
chr2	32696188	32696188	*BIRC6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.L2196F	ENSG00000115760	ENST00000421745	Transcript	missense_variant	benign(0.328)
chr2	38216721	38216721	*RMDN2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.G455C	ENSG00000115841	ENST00000234195	Transcript	missense_variant	probably_damaging(0.999)
chr2	55529183	55529183	*CCDC88A*	Missense_Mutation	.	SNP	C	C	G	novel	sia_et_al_P4	p.M1498I	ENSG00000115355	ENST00000336838	Transcript	missense_variant	probably_damaging(0.92)
chr2	61118955	61118955	*REL*	Missense_Mutation	.	SNP	A	A	G	novel	sia_et_al_P4	p.I50V	ENSG00000162924	ENST00000295025	Transcript	missense_variant	benign(0.057)

chr2	68413632	68413632	*PPP3R1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.D145N	ENSG00000221823	ENST00000234310	Transcript	missense_variant	probably_damaging(0.998)
chr2	74596457	74596457	*DCTN1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.K518N	ENSG00000204843	ENST00000361874	Transcript	missense_variant	benign(0.008)
chr2	84937412	84937412	*DNAH6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.A3085E	ENSG00000115423	ENST00000389394	Transcript	missense_variant	probably_damaging(0.986)
chr2	86281294	86281294	*POLR1A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.G726V	ENSG00000068654	ENST00000263857	Transcript	missense_variant	possibly_damaging(0.892)
chr2	86281334	86281334	*POLR1A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.G713W	ENSG00000068654	ENST00000263857	Transcript	missense_variant	probably_damaging(0.994)
chr2	98263590	98263590	*COX5B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.A55E	ENSG00000135940	ENST00000258424	Transcript	missense_variant	benign(0.113)
chr20	15591578	15591578	*SIRPB1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P87T	ENSG00000101307	ENST00000381605	Transcript	missense_variant	possibly_damaging(0.798)
chr20	31041556	31041557	*C20orf112*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	sia_et_al_P4	p.P132Lfs*18	ENSG00000197183	ENST00000359676	Transcript	frameshift_variant	NA
chr20	33530744	33530744	*GSS*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.G114V	ENSG00000100983	ENST00000216951	Transcript	missense_variant	probably_damaging(0.986)
chr20	37169783	37169783	*RALGAPB*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.P888T	ENSG00000170471	ENST00000262879	Transcript	missense_variant	benign(0.135)
chr20	46295103	46295103	*SULF2*	Missense_Mutation	.	SNP	C	C	A	rs201340688	sia_et_al_P4	p.G569V	ENSG00000196562	ENST00000359930	Transcript	missense_variant	benign(0.008)
chr20	47628564	47628565	*ARFGEF2*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P4	p.M1288Ifs*16	ENSG00000124198	ENST00000371917	Transcript	frameshift_variant	NA
chr20	47648627	47648627	*ARFGEF2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.S1702Y	ENSG00000124198	ENST00000371917	Transcript	missense_variant	probably_damaging(0.947)
chr20	49195713	49195713	*PTPN1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.K237N	ENSG00000196396	ENST00000371621	Transcript	missense_variant	benign(0.421)
chr21	35258664	35258665	*ITSN1*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P4	p.N1640Pfs*33	ENSG00000205726	ENST00000381318	Transcript	frameshift_variant	NA
chr22	19175510	19175510	*CLTCL1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E1473*	ENSG00000070371	ENST00000263200	Transcript	stop_gained	NA
chr22	26219587	26219588	*MYO18B*	Frame_Shift_Del	.	DEL	CC	CC	-	novel	sia_et_al_P4	p.Q880Afs*14	ENSG00000133454	ENST00000335473	Transcript	frameshift_variant	NA
chr3	121417341	121417341	*GOLGB1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P4	p.L677Ffs*18	ENSG00000173230	ENST00000393667	Transcript	frameshift_variant	NA
chr3	122598196	122598197	*DIRC2*	Frame_Shift_Del	.	DEL	CT	CT	-	novel	sia_et_al_P4	p.Y471Sfs*2	ENSG00000138463	ENST00000261038	Transcript	frameshift_variant	NA
chr3	133293911	133293911	*CDV3*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.E92Rfs*14	ENSG00000091527	ENST00000264993	Transcript	frameshift_variant	NA
chr3	182681839	182681839	*DCUN1D1*	Splice_Site	.	DEL	T	T	-	novel	sia_et_al_P4	p.X74_splice	ENSG00000043093	ENST00000292782	Transcript	splice_acceptor_variant	NA
chr3	182925462	182925463	*MCF2L2*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	sia_et_al_P4	p.C882*	ENSG00000053524	ENST00000328913	Transcript	frameshift_variant	NA
chr3	183689489	183689490	*ABCC5*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P4	p.L542Afs*13	ENSG00000114770	ENST00000334444	Transcript	frameshift_variant	NA
chr3	196449383	196449383	*PIGX*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.D51Y	ENSG00000163964	ENST00000314118	Transcript	missense_variant	probably_damaging(0.997)
chr3	197640760	197640760	*IQCG*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E294*	ENSG00000114473	ENST00000265239	Transcript	stop_gained	NA
chr3	197707364	197707364	*LMLN*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.N240Tfs*6	ENSG00000185621	ENST00000420910	Transcript	frameshift_variant	NA
chr3	47125112	47125112	*ITPR1*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	sia_et_al_P4	p.D688Qfs*18	ENSG00000150995	ENST00000302640	Transcript	frameshift_variant	NA
chr3	47676764	47676764	*SMARCC1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.K854N	ENSG00000173473	ENST00000254480	Transcript	missense_variant	possibly_damaging(0.474)
chr4	186112232	186112232	*KIAA1430*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P40Q	ENSG00000164323	ENST00000458385	Transcript	missense_variant	benign(0.007)
chr4	58272677	58272677	*CRMP1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.Q641H	ENSG00000072832	ENST00000324989	Transcript	missense_variant	probably_damaging(0.998)
chr4	60866477	60866477	*JAKMIP1*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.I294Lfs*4	ENSG00000152969	ENST00000409021	Transcript	frameshift_variant	NA
chr4	76572256	76572256	*G3BP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.L338F	ENSG00000138757	ENST00000359707	Transcript	missense_variant	probably_damaging(0.999)
chr4	78113715	78113715	*AFAP1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.Q340H	ENSG00000196526	ENST00000420658	Transcript	missense_variant	probably_damaging(0.993)
chr4	79475588	79475588	*ANXA3*	Splice_Site	.	SNP	A	A	T	novel	sia_et_al_P4	NA	ENSG00000138772	ENST00000264908	Transcript	splice_acceptor_variant	NA
chr5	137627784	137627784	*CDC25C*	Missense_Mutation	.	SNP	G	G	A	rs114224600	sia_et_al_P4	p.R213C	ENSG00000158402	ENST00000323760	Transcript	missense_variant	possibly_damaging(0.908)
chr5	37224416	37224416	*C5orf42*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.L840F	ENSG00000197603	ENST00000425232	Transcript	missense_variant	possibly_damaging(0.721)

chr5	52361715	52361715	*ITGA2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.Y617*	ENSG00000164171	ENST00000296585	Transcript	stop_gained	NA
chr5	68413197	68413197	*SLC30A5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.W471C	ENSG00000145740	ENST00000396591	Transcript	missense_variant	probably_damaging(0.998)
chr5	68875653	68875653	*GTF2H2C*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.P240H	ENSG00000183474	ENST00000510979	Transcript	missense_variant	probably_damaging(0.954)
chr5	70948519	70948519	*MCCC2*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.L505*	ENSG00000131844	ENST00000340941	Transcript	frameshift_variant	NA
chr5	73207231	73207231	*ARHGEF28*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.Y1593*	ENSG00000214944	ENST00000543537	Transcript	stop_gained	NA
chr5	74801914	74801914	*COL4A3BP*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.D170Y	ENSG00000113163	ENST00000380494	Transcript	missense_variant	probably_damaging(0.996)
chr5	77784886	77784886	*LHFPL2*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.Y174F	ENSG00000145685	ENST00000380345	Transcript	missense_variant	benign(0.006)
chr5	86672319	86672319	*RASA1*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P4	p.V708Cfs*18	ENSG00000145715	ENST00000274376	Transcript	frameshift_variant	NA
chr5	94826640	94826640	*TTC37*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.L1301F	ENSG00000198677	ENST00000358746	Transcript	missense_variant	benign(0.365)
chr6	10770343	10770343	*MAK*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P4	p.X573_splice	ENSG00000111837	ENST00000313243	Transcript	splice_donor_variant	NA
chr6	10824611 7	10824611 7	*SEC63*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.G82*	ENSG00000025796	ENST00000369002	Transcript	stop_gained	NA
chr6	11169682 6	11169682 6	*REV3L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.G911V	ENSG00000009413	ENST00000358835	Transcript	missense_variant	probably_damaging(0.917)
chr6	13119931 8	13119931 8	*EPB41L2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E657*	ENSG00000079819	ENST00000337057	Transcript	stop_gained	NA
chr6	13668370 2	13668370 2	*MAP7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.A493E	ENSG00000135525	ENST00000454590	Transcript	missense_variant	probably_damaging(1)
chr6	15550057 7	15550057 7	*TIAM2*	Frame_Shift_Del	.	DEL	GT	GT	-	novel	sia_et_al_P4	p.C900*	ENSG00000146426	ENST00000461783	Transcript	frameshift_variant	NA
chr6	16149173 1	16149173 1	*MAP3K4*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.S600*	ENSG00000085511	ENST00000392142	Transcript	stop_gained	NA
chr6	52370491	52370491	*TRAM2*	Frame_Shift_Del	.	DEL	GT	GT	-	novel	sia_et_al_P4	p.T261Pfs*19	ENSG00000065308	ENST00000182527	Transcript	frameshift_variant	NA
chr6	79698057	79698057	*PHIP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.H777N	ENSG00000146247	ENST00000275034	Transcript	missense_variant	benign(0.001)
chr7	10509831 2	10509831 2	*PUS7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.M637I	ENSG00000091127	ENST00000356362	Transcript	missense_variant	probably_damaging(0.968)
chr7	13822353 2	13822353 2	*TRIM24*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.Y377Ifs*5	ENSG00000122779	ENST00000343526	Transcript	frameshift_variant	NA
chr7	14396559 9	14396559 9	*CTAGE8*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E249*	ENSG00000244693	ENST00000487179	Transcript	stop_gained	NA
chr7	15081472 7	15081472 7	*AGAP3*	Missense_Mutation	.	SNP	C	C	A	rs199715909	sia_et_al_P4	p.A190D	ENSG00000133612	ENST00000397238	Transcript	missense_variant	probably_damaging(0.912)
chr7	15169990 3	15169990 3	*GALNTL5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.L255M	ENSG00000106648	ENST00000392800	Transcript	missense_variant	benign(0.138)
chr7	42950229	42950229	*C7orf25*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.V149F	ENSG00000136197	ENST00000431882	Transcript	missense_variant	possibly_damaging(0.804)
chr7	64398088	64398088	*RAC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.V112F	ENSG00000136238	ENST00000356142	Transcript	missense_variant	possibly_damaging(0.783)
chr7	67307229	67307229	*ZNF12*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.S615Y	ENSG00000164631	ENST00000405858	Transcript	missense_variant	probably_damaging(1)
chr7	77569606	77569606	*PHTF2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.R542I	ENSG00000006576	ENST00000416283	Transcript	missense_variant	probably_damaging(1)
chr7	83610737	83610737	*SEMA3A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.D518Y	ENSG00000075213	ENST00000265362	Transcript	missense_variant	possibly_damaging(0.734)
chr8	12058152 9	12058152 9	*ENPP2*	Frame_Shift_Ins	.	INS	-	-	AG	novel	sia_et_al_P4	p.C719Sfs*21	ENSG00000136960	ENST00000259486	Transcript	frameshift_variant	NA
chr8	12423237 0	12423237 0	*C8orf76*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.F372L	ENSG00000189376	ENST00000276704	Transcript	missense_variant	benign(0.006)
chr8	17581240	17581240	*MTUS1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.T797K	ENSG00000129422	ENST00000262102	Transcript	missense_variant	possibly_damaging(0.798)
chr8	30000003	30000003	*CSMD1*	Missense_Mutation	.	SNP	A	A	C	novel	sia_et_al_P4	p.F2075L	ENSG00000183117	ENST00000537824	Transcript	missense_variant	probably_damaging(0.995)
chr8	30034670	30034670	*DCTN6*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.E75*	ENSG00000104671	ENST00000221114	Transcript	stop_gained	NA
chr8	30469953	30469953	*GTF2E2*	Missense_Mutation	.	SNP	C	C	G	novel	sia_et_al_P4	p.A138P	ENSG00000197265	ENST00000355904	Transcript	missense_variant	possibly_damaging(0.722)
chr8	30511109	30511109	*GTF2E2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P3T	ENSG00000197265	ENST00000355904	Transcript	missense_variant	possibly_damaging(0.764)
chr8	38285954	38285954	*FGFR1*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P4	p.X153_splice	ENSG00000077782	ENST00000425967	Transcript	splice_acceptor_variant	NA

chr8	63351446	63351446	*MCPH1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.P656Q	ENSG00000147316	ENST00000344683	Transcript	missense_variant	benign(0.153)
chr8	86385972	86385972	*CA2*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.H96Tfs*48	ENSG00000104267	ENST00000285379	Transcript	frameshift_variant	NA
chr8	96060736	96060736	*NDUFAF6*	Nonsense_Mutation	.	SNP	A	A	T	novel	sia_et_al_P4	p.R256*	ENSG00000156170	ENST00000396124	Transcript	stop_gained	NA
chr9	104319812	104319812	*RNF20*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.Q772H	ENSG00000155827	ENST00000389120	Transcript	missense_variant	probably_damaging(0.981)
chr9	106860785	106860785	*SMC2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.R126I	ENSG00000136824	ENST00000286398	Transcript	missense_variant	probably_damaging(0.921)
chr9	125438365	125438365	*OR1L3*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P4	p.N319Kfs*?	ENSG00000171481	ENST00000304820	Transcript	frameshift_variant	NA
chr9	129928485	129928485	*RALGPS1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.D250Y	ENSG00000136828	ENST00000259351	Transcript	missense_variant	possibly_damaging(0.819)
chr9	213332161	213332161	*KLHL9*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.R533K	ENSG00000198642	ENST00000359039	Transcript	missense_variant	benign(0.165)
chr9	324593971	324593971	*DDX58*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E827*	ENSG00000107201	ENST00000379883	Transcript	stop_gained	NA
chr9	326307474	326307475	*TAF1L*	Nonsense_Mutation	.	DEL	TA	TA	-	novel	sia_et_al_P4	p.Y1601*	ENSG00000122728	ENST00000242310	Transcript	stop_gained	NA
chr9	342631616	342631616	*KIF24*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.Q500K	ENSG00000186638	ENST00000379166	Transcript	missense_variant	possibly_damaging(0.613)
chr9	803363614	803363614	*GNAQ*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E335D	ENSG00000156052	ENST00000286548	Transcript	missense_variant	benign(0.004)
chrX	101660607	101660607	*CLCN4*	Nonsense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P4	p.L154*	ENSG00000073464	ENST00000380833	Transcript	stop_gained	NA
chrX	118716607	118716607	*UBE2A*	Missense_Mutation	.	SNP	T	T	C	novel	sia_et_al_P4	p.Y100H	ENSG00000077721	ENST00000371558	Transcript	missense_variant	probably_damaging(0.995)
chrX	119589352	119589352	*LAMP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P86H	ENSG00000005893	ENST00000434600	Transcript	missense_variant	possibly_damaging(0.873)
chrX	123699374	123699374	*TENM1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.C705F	ENSG00000009694	ENST00000422452	Transcript	missense_variant	probably_damaging(1)
chrX	128652367	128652367	*SMARCA1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.E78*	ENSG00000102038	ENST00000371122	Transcript	stop_gained	NA
chrX	151900538	151900538	*MAGEA12*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.S88I	ENSG00000213401	ENST00000393900	Transcript	missense_variant	possibly_damaging(0.516)
chrX	153208	153208	*ASB11*	Frame_Shift_Ins	.	INS	-	-	C	novel	sia_et_al_P4	p.L78Cfs*5	ENSG00000165192	ENST00000480796	Transcript	frameshift_variant	NA
chrX	18213427	18213427	*BEND2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.T390N	ENSG00000177324	ENST00000380033	Transcript	missense_variant	benign(0.149)
chrX	30738852	30738852	*GK*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P4	p.P445Qfs*2	ENSG00000198814	ENST00000378943	Transcript	frameshift_variant	NA
chrX	40495950	40495950	*CXorf38*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.D212E	ENSG00000185753	ENST00000327877	Transcript	missense_variant	probably_damaging(0.983)
chrX	43552566	43552566	*MAOA*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.G66V	ENSG00000189221	ENST00000338702	Transcript	missense_variant	probably_damaging(1)
chrX	43552656	43552656	*MAOA*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.R96L	ENSG00000189221	ENST00000338702	Transcript	missense_variant	benign(0.051)
chrX	48970564	48970564	*GPKOW*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.D476Y	ENSG00000068394	ENST00000156109	Transcript	missense_variant	probably_damaging(0.974)
chrX	53562447	53562447	*HUWE1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.V4183F	ENSG00000086758	ENST00000342160	Transcript	missense_variant	unknown(0)
chrX	54014287	54014287	*PHF8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.M643I	ENSG00000172943	ENST00000357988	Transcript	missense_variant	benign(0)
chrX	71870291	71870291	*PHKA1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.P425T	ENSG00000067177	ENST00000373542	Transcript	missense_variant	probably_damaging(1)
chrX	76776372	76776372	*ATRX*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P4	p.S2365*	ENSG00000085224	ENST00000373344	Transcript	stop_gained	NA
chrX	78426918	78426918	*GPR174*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.S138R	ENSG00000147138	ENST00000276077	Transcript	missense_variant	possibly_damaging(0.903)
chrX	84537248	84537248	*POF1B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.Q575H	ENSG00000124429	ENST00000262753	Transcript	missense_variant	benign(0.015)
chrY	14889993	14889993	*USP9Y*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P4	p.P894S	ENSG00000114374	ENST00000338981	Transcript	missense_variant	probably_damaging(0.987)
chrY	15447622	15447622	*UTY*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.T789Pfs*27	ENSG00000183878	ENST00000331397	Transcript	frameshift_variant	NA
chrY	22921802	22921802	*RPS4Y2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P4	p.L44M	ENSG00000157828	ENST00000288666	Transcript	missense_variant	probably_damaging(0.918)
chrY	6948808	6948808	*TBL1Y*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P4	p.F332Lfs*50	ENSG00000092377	ENST00000383032	Transcript	frameshift_variant	NA
chr1	153431360	153431360	*S100A7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.L44I	ENSG00000143556	ENST00000368723	Transcript	missense_variant	probably_damaging(0.951)

chr1	160000627	160000627	*PIGM*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.L301F	ENSG00000143315	ENST00000368090	Transcript	missense_variant	probably_damaging(0.998)
chr1	174652675	174652675	*RABGAP1L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.D614Y	ENSG00000152061	ENST00000251507	Transcript	missense_variant	probably_damaging(1)
chr1	201965287	201965287	*RNPEP*	Missense_Mutation	.	SNP	G	G	T	rs199706738	sia_et_al_P5	p.W250C	ENSG00000176393	ENST00000295640	Transcript	missense_variant	probably_damaging(1)
chr1	237796997	237796997	*RYR2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.S2225R	ENSG00000198626	ENST00000366574	Transcript	missense_variant	probably_damaging(0.999)
chr1	31447606	31447606	*PUM1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.W466C	ENSG00000134644	ENST00000426105	Transcript	missense_variant	probably_damaging(0.998)
chr10	129906949	129906949	*MKI67*	Missense_Mutation	.	SNP	G	G	C	rs189041436	sia_et_al_P5	p.T1052R	ENSG00000148773	ENST00000368654	Transcript	missense_variant	probably_damaging(0.994)
chr10	13228179	13228179	*MCM10*	Missense_Mutation	.	SNP	G	G	T	rs138296691	sia_et_al_P5	p.D373Y	ENSG00000065328	ENST00000484800	Transcript	missense_variant	probably_damaging(1)
chr10	27326137	27326137	*ANKRD26*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.A892D	ENSG00000107890	ENST00000376087	Transcript	missense_variant	benign(0.295)
chr10	71913710	71913710	*SAR1A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E122*	ENSG00000079332	ENST00000373242	Transcript	stop_gained	NA
chr10	93719569	93719569	*BTAF1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.E340*	ENSG00000095564	ENST00000265990	Transcript	stop_gained	NA
chr10	94297129	94297129	*IDE*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.H93N	ENSG00000119912	ENST00000265986	Transcript	missense_variant	benign(0.117)
chr10	99221833	99221834	*MMS19*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P5	p.D686Rfs*9	ENSG00000155229	ENST00000438925	Transcript	frameshift_variant	NA
chr11	111572274	111572274	*SIK2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.F234L	ENSG00000170145	ENST00000309987	Transcript	missense_variant	probably_damaging(0.993)
chr11	113853982	113853982	*HTR3A*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P5	p.S178L	ENSG00000166736	ENST00000355556	Transcript	missense_variant	probably_damaging(0.977)
chr11	118242349	118242349	*UBE4A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.L177I	ENSG00000110344	ENST00000431736	Transcript	missense_variant	probably_damaging(1)
chr11	123894501	123894501	*OR10G9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.P261Q	ENSG00000236981	ENST00000375024	Transcript	missense_variant	probably_damaging(0.968)
chr11	33361070	33361070	*HIPK3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.H535N	ENSG00000110422	ENST00000303296	Transcript	missense_variant	benign(0.347)
chr11	60073579	60073579	*MS4A4A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.D185Y	ENSG00000110079	ENST00000337908	Transcript	missense_variant	possibly_damaging(0.793)
chr12	10530835	10530835	*KLRK1*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P5	p.X144_splice	ENSG00000213809	ENST00000240618	Transcript	splice_acceptor_variant	NA
chr12	10601981	10601981	*KLRC1*	Missense_Mutation	.	SNP	T	T	G	novel	sia_et_al_P5	p.H115P	ENSG00000134545	ENST00000544822	Transcript	missense_variant	benign(0.001)
chr12	34179554	34179554	*ALG10*	Missense_Mutation	.	SNP	G	G	C	novel	sia_et_al_P5	p.A376P	ENSG00000139133	ENST00000266483	Transcript	missense_variant	benign(0.002)
chr12	49315958	49315958	*FKBP11*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E139*	ENSG00000134285	ENST00000550765	Transcript	stop_gained	NA
chr12	72038837	72038837	*ZFC3H1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E367*	ENSG00000133858	ENST00000378743	Transcript	stop_gained	NA
chr12	9256842	9256842	*A2M*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.T420N	ENSG00000175899	ENST00000318602	Transcript	missense_variant	benign(0.003)
chr12	93219946	93219946	*EEA1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.A507D	ENSG00000102189	ENST00000322349	Transcript	missense_variant	probably_damaging(0.967)
chr13	74289640	74289640	*KLF12*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E298*	ENSG00000118922	ENST00000377669	Transcript	stop_gained	NA
chr14	31592254	31592254	*HECTD1*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P5	NA	ENSG00000092148	ENST00000399332	Transcript	splice_acceptor_variant	NA
chr14	55650339	55650339	*DLGAP5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.R124I	ENSG00000126787	ENST00000247191	Transcript	missense_variant	possibly_damaging(0.819)
chr14	57700740	57700740	*EXOC5*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P5	p.H227L	ENSG00000070367	ENST00000413566	Transcript	missense_variant	benign(0.004)
chr16	14978328	14978328	*NOMO1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.P1071T	ENSG00000103512	ENST00000287667	Transcript	missense_variant	benign(0.005)
chr16	15704840	15704840	*KIAA0430*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.P1248H	ENSG00000166783	ENST00000396368	Transcript	missense_variant	probably_damaging(0.951)
chr16	56535367	56535367	*BBS2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.G375C	ENSG00000125124	ENST00000245157	Transcript	missense_variant	probably_damaging(0.985)
chr17	10351729	10351729	*MYH4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.S1547Y	ENSG00000264424	ENST00000255381	Transcript	missense_variant	benign(0.347)
chr17	62045400	62045400	*SCN4A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.A340D	ENSG00000007314	ENST00000435607	Transcript	missense_variant	benign(0.092)
chr17	9583585	9583585	*USP43*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.R336L	ENSG00000154914	ENST00000285199	Transcript	missense_variant	probably_damaging(0.987)
chr19	56416411	56416411	*SAFB*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.G104V	ENSG00000160633	ENST00000588852	Transcript	missense_variant	probably_damaging(0.98)

chr2	102440509	102440510	*MAP4K4*	Frame_Shift_Ins	.	INS	-	-	CT	novel	sia_et_al_P5	p.W102Sfs*17	ENSG00000071054	ENST00000347699	Transcript	frameshift_variant	NA
chr2	128526559	128526559	*WDR33*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.R74I	ENSG00000136709	ENST00000322313	Transcript	missense_variant	unknown(0)
chr2	166773791	166773791	*TTC21B*	Missense_Mutation	.	SNP	G	G	T	rs201527373	sia_et_al_P5	p.D625E	ENSG00000123607	ENST00000243344	Transcript	missense_variant	benign(0.002)
chr2	167313400	167313400	*SCN7A*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P5	p.E424K	ENSG00000136546	ENST00000409855	Transcript	missense_variant	benign(0.146)
chr2	206050582	206050582	*PARD3B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.S611R	ENSG00000116117	ENST00000358768	Transcript	missense_variant	benign(0.012)
chr2	45826953	45826953	*SRBD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.D95Y	ENSG00000068784	ENST00000263736	Transcript	missense_variant	possibly_damaging(0.736)
chr2	68368837	68368837	*WDR92*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.T169N	ENSG00000243667	ENST00000295121	Transcript	missense_variant	possibly_damaging(0.733)
chr20	50007968	50007968	*NFATC2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E915*	ENSG00000101096	ENST00000396009	Transcript	stop_gained	NA
chr20	56098241	56098241	*CTCFL*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.D213Y	ENSG00000124092	ENST00000423479	Transcript	missense_variant	benign(0.405)
chr22	26166111	26166111	*MYO18B*	Missense_Mutation	.	SNP	T	T	C	novel	sia_et_al_P5	p.V516A	ENSG00000133454	ENST00000335473	Transcript	missense_variant	probably_damaging(0.999)
chr22	43976534	43976534	*EFCAB6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.G1013V	ENSG00000186976	ENST00000262726	Transcript	missense_variant	probably_damaging(0.963)
chr3	11372813	11372813	*ATG7*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P5	p.X227_splice	ENSG00000197548	ENST00000354449	Transcript	splice_acceptor_variant	NA
chr3	151538202	151538202	*AADAC*	Missense_Mutation	.	SNP	G	G	T	rs142051669	sia_et_al_P5	p.W131C	ENSG00000114771	ENST00000232892	Transcript	missense_variant	possibly_damaging(0.84)
chr3	179131311	179131311	*GNB4*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P5	p.M196I	ENSG00000114450	ENST00000232564	Transcript	missense_variant	benign(0.034)
chr3	196199523	196199523	*RNF168*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E295*	ENSG00000163961	ENST00000318037	Transcript	stop_gained	NA
chr3	47058678	47058678	*SETD2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E2534*	ENSG00000181555	ENST00000409792	Transcript	stop_gained	NA
chr3	52544398	52544398	*STAB1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P5	p.H888Y	ENSG00000010327	ENST00000321725	Transcript	missense_variant	benign(0.105)
chr4	13601797	13601797	*BOD1L1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.A2243S	ENSG00000038219	ENST00000407348	Transcript	missense_variant	benign(0.001)
chr4	141311807	141311807	*CLGN*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.S576*	ENSG00000153132	ENST00000325617	Transcript	stop_gained	NA
chr4	156269057	156269057	*MAP9*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E608*	ENSG00000164114	ENST00000311277	Transcript	stop_gained	NA
chr4	82353515	82353515	*RASGEF1B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.L445F	ENSG00000138670	ENST00000264400	Transcript	missense_variant	benign(0.013)
chr4	95202735	95202735	*SMARCAD1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.S907Y	ENSG00000163104	ENST00000354268	Transcript	missense_variant	benign(0.081)
chr5	114611157	114611157	*CCDC112*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.T225K	ENSG00000164221	ENST00000379611	Transcript	missense_variant	benign(0.089)
chr5	38964909	38964909	*RICTOR*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.P462H	ENSG00000164327	ENST00000357387	Transcript	missense_variant	benign(0.177)
chr5	89990411	89990411	*GPR98*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.T2613K	ENSG00000164199	ENST00000405460	Transcript	missense_variant	probably_damaging(0.987)
chr6	108375696	108375696	*OSTM1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.Q205K	ENSG00000081087	ENST00000193322	Transcript	missense_variant	benign(0.288)
chr6	116910060	116910060	*RWDD1*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P5	p.K110Nfs*2	ENSG00000111832	ENST00000466444	Transcript	frameshift_variant	NA
chr6	132032154	132032154	*CTAGE9*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E2*	ENSG00000236761	ENST00000314099	Transcript	stop_gained	NA
chr6	17675462	17675462	*NUP153*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.P241T	ENSG00000124789	ENST00000262077	Transcript	missense_variant	benign(0.12)
chr6	17856348	17856348	*KIF13A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E76*	ENSG00000137177	ENST00000259711	Transcript	stop_gained	NA
chr6	55381386	55381386	*HMGCLL1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E135*	ENSG00000146151	ENST00000398661	Transcript	stop_gained	NA
chr6	56035894	56035894	*COL21A1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.A225S	ENSG00000124749	ENST00000244728	Transcript	missense_variant	benign(0.102)
chr6	87953223	87953223	*ZNF292*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.E258*	ENSG00000188994	ENST00000369577	Transcript	stop_gained	NA
chr7	107542834	107542834	*DLD*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.S88Y	ENSG00000091140	ENST00000205402	Transcript	missense_variant	probably_damaging(0.998)
chr8	105511712	105511712	*LRP12*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.C103F	ENSG00000147650	ENST00000276654	Transcript	missense_variant	probably_damaging(0.983)
chr8	30889363	30889363	*PURG*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.E312D	ENSG00000172733	ENST00000475541	Transcript	missense_variant	benign(0.064)

chr8	38189073	38189073	*WHSC1L1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.S314I	ENSG00000147548	ENST00000317025	Transcript	missense_variant	probably_damaging(0.981)
chr8	38205413	38205413	*WHSC1L1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.P93T	ENSG00000147548	ENST00000317025	Transcript	missense_variant	probably_damaging(0.999)
chr8	38940167	38940167	*ADAM9*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.R630I	ENSG00000168615	ENST00000487273	Transcript	missense_variant	benign(0.028)
chr8	56698367	56698367	*TGS1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.E86*	ENSG00000137574	ENST00000260129	Transcript	stop_gained	NA
chr9	102722426	102722426	*STX17*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.L191I	ENSG00000136874	ENST00000259400	Transcript	missense_variant	benign(0.003)
chr9	108097959	108097959	*SLC44A1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.Q129K	ENSG00000070214	ENST00000374720	Transcript	missense_variant	benign(0.001)
chr9	128125014	128125014	*GAPVD1*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P5	p.D1485N	ENSG00000165219	ENST00000394105	Transcript	missense_variant	probably_damaging(0.98)
chr9	128432099	128432099	*MAPKAP1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.S116*	ENSG00000119487	ENST00000265960	Transcript	stop_gained	NA
chr9	130435484	130435484	*STXBP1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.E352*	ENSG00000136854	ENST00000373302	Transcript	stop_gained	NA
chr9	167384 83	167384 83	*BNC2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.A2S	ENSG00000173068	ENST00000380672	Transcript	missense_variant	unknown(0)
chr9	728956 87	728956 87	*SMC5*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P5	p.E231*	ENSG00000198887	ENST00000361138	Transcript	stop_gained	NA
chrX	105179167	105179167	*NRK*	Missense_Mutation	.	SNP	G	G	T	rs377439740	sia_et_al_P5	p.A1170S	ENSG00000123572	ENST00000428173	Transcript	missense_variant	benign(0.131)
chrX	118725253	118725253	*NKRF*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P5	p.K60N	ENSG00000186416	ENST00000542113	Transcript	missense_variant	possibly_damaging(0.892)
chrX	153585992	153585992	*FLNA*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P5	NA	ENSG00000196924	ENST00000369850	Transcript	splice_acceptor_variant	NA
chr1	111493989	111493989	*LRIF1*	Missense_Mutation	.	SNP	C	C	G	novel	sia_et_al_P6	p.S506T	ENSG00000121931	ENST00000369763	Transcript	missense_variant	benign(0.016)
chr1	114510399	114510399	*HIPK1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.S798Y	ENSG00000163349	ENST00000369558	Transcript	missense_variant	possibly_damaging(0.805)
chr1	155451175	155451175	*ASH1L*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P6	p.N496Y	ENSG00000116539	ENST00000392403	Transcript	missense_variant	benign(0.421)
chr1	161334937	161334937	*C1orf192*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.H118N	ENSG00000188931	ENST00000367974	Transcript	missense_variant	benign(0.004)
chr1	167935955	167935955	*DCAF6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R83I	ENSG00000143164	ENST00000367840	Transcript	missense_variant	probably_damaging(0.975)
chr1	169525893	169525894	*F5*	Frame_Shift_Ins	.	INS	-	-	T	novel	sia_et_al_P6	p.L316Ifs*10	ENSG00000198734	ENST00000367797	Transcript	frameshift_variant	NA
chr1	180017834	180017834	*CEP350*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E1596*	ENSG00000135837	ENST00000367607	Transcript	stop_gained	NA
chr1	182908680	182908681	*SHCBP1L*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P6	p.D261*	ENSG00000157060	ENST00000367547	Transcript	frameshift_variant	NA
chr1	183835204	183835204	*RGL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R176M	ENSG00000143344	ENST00000304685	Transcript	missense_variant	possibly_damaging(0.866)
chr1	186270741	186270741	*PRG4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.R73S	ENSG00000116690	ENST00000445192	Transcript	missense_variant	probably_damaging(0.999)
chr1	200618315	200618315	*DDX59*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D452Y	ENSG00000118197	ENST00000331314	Transcript	missense_variant	probably_damaging(0.954)
chr1	207934752	207934752	*CD46*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.D212Y	ENSG00000117335	ENST00000322875	Transcript	missense_variant	possibly_damaging(0.762)
chr1	212238268	212238268	*DTL*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P6	p.Y179Lfs*4	ENSG00000143476	ENST00000366991	Transcript	frameshift_variant	NA
chr1	212911859	212911859	*NSL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.T246N	ENSG00000117697	ENST00000366977	Transcript	missense_variant	benign(0.06)
chr1	227203781	227203781	*CDC42BPA*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.M1584I	ENSG00000143776	ENST00000366769	Transcript	missense_variant	benign(0.005)
chr1	227279598	227279598	*CDC42BPA*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E782*	ENSG00000143776	ENST00000366769	Transcript	stop_gained	NA
chr1	270944 01	270944 01	*ARID1A*	Missense_Mutation	.	SNP	G	G	T	rs144496027	sia_et_al_P6	p.G1037C	ENSG00000117713	ENST00000324856	Transcript	missense_variant	unknown(0)
chr1	398938 07	398938 07	*MACF1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.L3489I	ENSG00000127603	ENST00000545844	Transcript	missense_variant	probably_damaging(0.925)
chr1	438975 11	438975 11	*SZT2*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.R1681Pfs*6	ENSG00000198198	ENST00000562955	Transcript	frameshift_variant	NA
chr1	477673 66	477673 66	*STIL*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P107H	ENSG00000123473	ENST00000371877	Transcript	missense_variant	probably_damaging(0.967)
chr1	516134 02	516134 02	*C1orf185*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P6	NA	ENSG00000204006	ENST00000371759	Transcript	frameshift_variant	NA
chr1	640973 70	640973 70	*PGM1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R218I	ENSG00000079739	ENST00000371083	Transcript	missense_variant	possibly_damaging(0.79)

chr1	66081893	66081893	*LEPR*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.W733L	ENSG00000116678	ENST00000349533	Transcript	missense_variant	benign(0.018)
chr1	67889899	67889899	*SERBP1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.A268T	ENSG00000142864	ENST00000370995	Transcript	missense_variant	possibly_damaging(0.842)
chr1	89578211	89578211	*GBP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q436K	ENSG00000162645	ENST00000370466	Transcript	missense_variant	benign(0.015)
chr1	90470597	90470597	*ZNF326*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G33W	ENSG00000162664	ENST00000340281	Transcript	missense_variant	possibly_damaging(0.841)
chr1	93091350	93091350	*EVI5*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P6	NA	ENSG00000067208	ENST00000370331	Transcript	splice_donor_variant	NA
chr1	99156658	99156658	*SNX7*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E131*	ENSG00000162627	ENST00000306121	Transcript	stop_gained	NA
chr10	103285915	103285915	*BTRC*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R234S	ENSG00000166167	ENST00000370187	Transcript	missense_variant	benign(0.023)
chr10	105923890	105923890	*WDR96*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E1070*	ENSG00000197748	ENST00000357060	Transcript	stop_gained	NA
chr10	112055048	112055048	*SMNDC1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D173Y	ENSG00000119953	ENST00000369603	Transcript	missense_variant	possibly_damaging(0.864)
chr10	115904296	115904296	*C10orf118*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.W394L	ENSG00000165813	ENST00000369287	Transcript	missense_variant	probably_damaging(1)
chr10	126097450	126097450	*OAT*	Missense_Mutation	.	SNP	G	G	T	rs11553551	sia_et_al_P6	p.P95H	ENSG00000065154	ENST00000368845	Transcript	missense_variant	probably_damaging(0.987)
chr10	27425302	27425302	*YME1L1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S205Y	ENSG00000136758	ENST00000326799	Transcript	missense_variant	possibly_damaging(0.62)
chr10	51579282	51579282	*NCOA4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E63D	ENSG00000138293	ENST00000452682	Transcript	missense_variant	probably_damaging(0.983)
chr10	58079799	58079799	*GDI2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G443V	ENSG00000057608	ENST00000380191	Transcript	missense_variant	possibly_damaging(0.77)
chr11	110477297	110477297	*ARHGAP20*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.Q318Sfs*3	ENSG00000137727	ENST00000260283	Transcript	frameshift_variant	NA
chr11	120976636	120976636	*TECTA*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.P54Q	ENSG00000109927	ENST00000393793	Transcript	missense_variant	benign(0.114)
chr11	124135322	124135322	*OR8G5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R200S	ENSG00000255298	ENST00000524943	Transcript	missense_variant	probably_damaging(0.94)
chr11	44076804	44076804	*ACCSL*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E368*	ENSG00000205126	ENST00000378832	Transcript	stop_gained	NA
chr11	57578339	57578339	*OR56B1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.S31R	ENSG00000181023	ENST00000317121	Transcript	missense_variant	benign(0.013)
chr11	74079560	74079560	*PGM2L1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R178S	ENSG00000165434	ENST00000298198	Transcript	missense_variant	benign(0.351)
chr11	76727823	76727823	*ACER3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S235I	ENSG00000078124	ENST00000532485	Transcript	missense_variant	possibly_damaging(0.649)
chr11	78437124	78437124	*TENM4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G1184C	ENSG00000149256	ENST00000278550	Transcript	missense_variant	probably_damaging(0.998)
chr12	104031860	104031860	*STAB2*	Missense_Mutation	.	SNP	G	G	T	rs544012754	sia_et_al_P6	p.R259L	ENSG00000136011	ENST00000388887	Transcript	missense_variant	possibly_damaging(0.557)
chr12	109945437	109945437	*UBE3B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G507W	ENSG00000151148	ENST00000342494	Transcript	missense_variant	probably_damaging(0.999)
chr12	116452921	116452921	*MED13L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q390K	ENSG00000123066	ENST00000281928	Transcript	missense_variant	unknown(0)
chr12	25302672	25302672	*CASC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P159T	ENSG00000118307	ENST00000395987	Transcript	missense_variant	possibly_damaging(0.89)
chr12	57496674	57496674	*STAT6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.H415N	ENSG00000166888	ENST00000300134	Transcript	missense_variant	probably_damaging(0.999)
chr12	62931882	62931882	*MON2*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.W710Gfs*5	ENSG00000061987	ENST00000393632	Transcript	frameshift_variant	NA
chr12	66665667	66665667	*NOP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.Q710H	ENSG00000111641	ENST00000382421	Transcript	missense_variant	possibly_damaging(0.553)
chr12	71016250	71016250	*PTPRB*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P210T	ENSG00000127329	ENST00000334414	Transcript	missense_variant	benign(0.156)
chr12	78553056	78553056	*NAV3*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.A1620V	ENSG00000067798	ENST00000536525	Transcript	missense_variant	possibly_damaging(0.475)
chr12	81536955	81536955	*ACSS3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.D284Y	ENSG00000111058	ENST00000548058	Transcript	missense_variant	possibly_damaging(0.511)
chr12	95418936	95418936	*NR2C1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D543Y	ENSG00000120798	ENST00000333003	Transcript	missense_variant	probably_damaging(0.999)
chr13	23777926	23777926	*SGCG*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.W31C	ENSG00000102683	ENST00000218867	Transcript	missense_variant	probably_damaging(1)
chr13	32705814	32705814	*FRY*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.P241H	ENSG00000073910	ENST00000380250	Transcript	missense_variant	benign(0.065)
chr13	36202381	36202381	*NBEA*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R2538M	ENSG00000172915	ENST00000400445	Transcript	missense_variant	probably_damaging(0.995)

chr13	46066332	46066332	*COG3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q378H	ENSG00000136152	ENST00000349995	Transcript	missense_variant	benign(0.345)
chr13	46543576	46543576	*ZC3H13*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P1035T	ENSG00000123200	ENST00000282007	Transcript	missense_variant	unknown()
chr14	100847322	100847322	*WDR25*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E21*	ENSG00000176473	ENST00000335290	Transcript	stop_gained	NA
chr14	50929481	50929481	*MAP4K5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P280T	ENSG00000012983	ENST00000013125	Transcript	missense_variant	benign(0.022)
chr14	51060615	51060616	*ATL1*	Splice_Site	.	DEL	GT	GT	-	novel	sia_et_al_P6	p.X191_splice	ENSG00000198513	ENST00000358385	Transcript	splice_donor_variant	NA
chr14	51226979	51226979	*NIN*	Frame_Shift_Del	.	DEL	T	T	-	rs144622574	sia_et_al_P6	p.E666Kfs*4	ENSG00000100503	ENST00000382041	Transcript	frameshift_variant	NA
chr14	59790930	59790930	*DAAM1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.A287S	ENSG00000100592	ENST00000395125	Transcript	missense_variant	unknown()
chr14	59965530	59965530	*JKAMP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G182W	ENSG00000050130	ENST00000261247	Transcript	missense_variant	probably_damaging(0.965)
chr14	60212781	60212781	*RTN1*	Missense_Mutation	.	SNP	C	C	A	rs147824671	sia_et_al_P6	p.L220F	ENSG00000139970	ENST00000267484	Transcript	missense_variant	benign(0.235)
chr14	67854154	67854154	*PLEK2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.Q318H	ENSG00000100558	ENST00000216446	Transcript	missense_variant	probably_damaging(0.999)
chr14	70634209	70634209	*SLC8A3*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E311*	ENSG00000100678	ENST00000381269	Transcript	stop_gained	NA
chr14	72932485	72932485	*RGS6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R138S	ENSG00000182732	ENST00000355525	Transcript	missense_variant	probably_damaging(1)
chr14	76173987	76173987	*TTLL5*	Frame_Shift_Del	.	DEL	CT	CT	-	novel	sia_et_al_P6	p.Y227Cfs*7	ENSG00000119685	ENST00000298832	Transcript	frameshift_variant	NA
chr14	92102890	92102890	*CATSPERB*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P541T	ENSG00000133962	ENST00000256343	Transcript	missense_variant	possibly_damaging(0.785)
chr14	97321675	97321675	*VRK1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.D231Y	ENSG00000100749	ENST00000216639	Transcript	missense_variant	probably_damaging(1)
chr15	30925697	30925697	*ARHGAP11B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.L69I	ENSG00000187951	ENST00000428041	Transcript	missense_variant	benign(0.168)
chr15	34651389	34651389	*LPCAT4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P505Q	ENSG00000176454	ENST00000314891	Transcript	missense_variant	benign(0.222)
chr15	34651437	34651437	*LPCAT4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P489H	ENSG00000176454	ENST00000314891	Transcript	missense_variant	possibly_damaging(0.855)
chr15	42481320	42481320	*VPS39*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D112Y	ENSG00000166887	ENST00000318006	Transcript	missense_variant	possibly_damaging(0.882)
chr15	48443708	48443708	*MYEF2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G423V	ENSG00000104177	ENST00000324324	Transcript	missense_variant	benign(0.005)
chr15	54008820	54008820	*WDR72*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.R108M	ENSG00000166415	ENST00000396328	Transcript	missense_variant	possibly_damaging(0.823)
chr15	59224593	59224593	*SLTM*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S71*	ENSG00000137776	ENST00000380516	Transcript	stop_gained	NA
chr15	62176466	62176466	*VPS13C*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.S3115Lfs*7	ENSG00000129003	ENST00000261517	Transcript	frameshift_variant	NA
chr16	50250017	50250017	*PAPD5*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E266*	ENSG00000121274	ENST00000436909	Transcript	stop_gained	NA
chr16	66793074	66793075	*CCDC79*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	sia_et_al_P6	p.E634Tfs*8	ENSG00000249961	ENST00000433154	Transcript	frameshift_variant	NA
chr16	81391518	81391518	*GAN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.H319N	ENSG00000261609	ENST00000568107	Transcript	missense_variant	probably_damaging(0.989)
chr17	10432759	10432759	*MYH2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D1053Y	ENSG00000125414	ENST00000245503	Transcript	missense_variant	probably_damaging(0.946)
chr17	15989751	15989751	*NCOR1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.Q1008Sfs*7	ENSG00000141027	ENST00000268712	Transcript	frameshift_variant	NA
chr17	33258000	33258000	*CCT6B*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S473*	ENSG00000132141	ENST00000314144	Transcript	stop_gained	NA
chr17	57049553	57049553	*PPM1E*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.A345S	ENSG00000175175	ENST00000308249	Transcript	missense_variant	probably_damaging(0.929)
chr17	67152058	67152058	*ABCA10*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P1155Q	ENSG00000154263	ENST00000269081	Transcript	missense_variant	possibly_damaging(0.624)
chr17	84119741	84119741	*MYH10*	Missense_Mutation	.	SNP	G	G	T	rs139985087	sia_et_al_P6	p.R1038S	ENSG00000133026	ENST00000360416	Transcript	missense_variant	probably_damaging(0.997)
chr18	10789303	10789303	*PIEZO2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.A648E	ENSG00000154864	ENST00000503781	Transcript	missense_variant	benign(0.001)
chr18	19761537	19761537	*GATA6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G476W	ENSG00000141448	ENST00000269216	Transcript	missense_variant	probably_damaging(1)
chr18	21644115	21644115	*TTC39C*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.P60Q	ENSG00000168234	ENST00000317571	Transcript	missense_variant	probably_damaging(0.997)
chr18	28609480	28609480	*DSC3*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.Q157Nfs*17	ENSG00000134762	ENST00000360428	Transcript	frameshift_variant	NA

chr18	28728515	28728515	*DSC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P240T	ENSG00000134765	ENST00000257198	Transcript	missense_variant	possibly_damaging(0.759)
chr18	43467763	43467763	*EPG5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P1688T	ENSG00000152223	ENST00000282041	Transcript	missense_variant	probably_damaging(0.991)
chr18	56367689	56367689	*MALT1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.T172K	ENSG00000172175	ENST00000348428	Transcript	missense_variant	benign(0.017)
chr19	10270720	10270720	*DNMT1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R355S	ENSG00000130816	ENST00000359526	Transcript	missense_variant	benign(0.015)
chr19	12541995	12541995	*ZNF443*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.H331N	ENSG00000180855	ENST00000301547	Transcript	missense_variant	probably_damaging(0.998)
chr19	44273948	44273948	*KCNN4*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.V285M	ENSG00000104783	ENST00000262888	Transcript	missense_variant	possibly_damaging(0.839)
chr19	44469158	44469158	*ZNF221*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.L47Wfs*12	ENSG00000159905	ENST00000251269	Transcript	frameshift_variant	NA
chr19	55497646	55497646	*NLRP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.V777F	ENSG00000022556	ENST00000543010	Transcript	missense_variant	possibly_damaging(0.504)
chr2	100915760	100915760	*LONRF2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P430Q	ENSG00000170500	ENST00000393437	Transcript	missense_variant	benign(0)
chr2	128870799	128870800	*UGGT1*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P6	p.I223Nfs*11	ENSG00000136731	ENST00000259253	Transcript	frameshift_variant	NA
chr2	135744901	135744902	*MAP3K19*	Frame_Shift_Del	.	DEL	TT	TT	-	novel	sia_et_al_P6	p.N514Qfs*3	ENSG00000176601	ENST00000375845	Transcript	frameshift_variant	NA
chr2	152521325	152521325	*NEB*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P1764H	ENSG00000183091	ENST00000397345	Transcript	missense_variant	possibly_damaging(0.824)
chr2	153591627	153591627	*ARL6IP6*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.P192S	ENSG00000177917	ENST00000326446	Transcript	missense_variant	probably_damaging(0.999)
chr2	160289393	160289393	*BAZ2B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.R592I	ENSG00000123636	ENST00000392783	Transcript	missense_variant	benign(0.308)
chr2	207527902	207527902	*DYTN*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P453Q	ENSG00000232125	ENST00000452335	Transcript	missense_variant	benign(0.079)
chr2	209189688	209189688	*PIKFYVE*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.M795I	ENSG00000115020	ENST00000264380	Transcript	missense_variant	benign(0.326)
chr2	215848384	215848384	*ABCA12*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E1457*	ENSG00000144452	ENST00000272895	Transcript	stop_gained	NA
chr2	225670177	225670177	*DOCK10*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S1295Y	ENSG00000135905	ENST00000258390	Transcript	missense_variant	probably_damaging(0.998)
chr2	227967532	227967532	*COL4A4*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P6	p.G302Vfs*23	ENSG00000081052	ENST00000396625	Transcript	frameshift_variant	NA
chr2	32434569	32434569	*SLC30A6*	Missense_Mutation	.	SNP	C	C	A	rs139073294	sia_et_al_P6	p.T315N	ENSG00000152683	ENST00000379343	Transcript	missense_variant	probably_damaging(0.991)
chr2	37505044	37505044	*PRKD3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G421W	ENSG00000115825	ENST00000379066	Transcript	missense_variant	probably_damaging(1)
chr2	43801867	43801867	*THADA*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.R446Q	ENSG00000115970	ENST00000405006	Transcript	missense_variant	benign(0.002)
chr2	48896939	48896939	*STON1-GTF2A1L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G1057C	ENSG00000068781	ENST00000394754	Transcript	missense_variant	probably_damaging(0.981)
chr2	48898772	48898772	*STON1-GTF2A1L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.P1132T	ENSG00000068781	ENST00000394754	Transcript	missense_variant	benign(0.02)
chr2	49191001	49191001	*FSHR*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S320Y	ENSG00000170820	ENST00000406846	Transcript	missense_variant	benign(0.009)
chr2	54848606	54848606	*SPTBN1*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.S278F	ENSG00000115306	ENST00000356805	Transcript	missense_variant	probably_damaging(0.987)
chr2	55462008	55462008	*RPS27A*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P6	p.K78Rfs*26	ENSG00000143947	ENST00000272317	Transcript	frameshift_variant	NA
chr2	55563821	55563821	*CCDC88A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.R551I	ENSG00000115355	ENST00000336838	Transcript	missense_variant	probably_damaging(0.947)
chr2	55589455	55589455	*CCDC88A*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E206*	ENSG00000115355	ENST00000336838	Transcript	stop_gained	NA
chr2	75933713	75933713	*GCFC2*	Missense_Mutation	.	SNP	C	C	A	rs529991040	sia_et_al_P6	p.K110N	ENSG00000005436	ENST00000321027	Transcript	missense_variant	benign(0.038)
chr2	87085506	87085506	*CD8B*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P6	p.P26L	ENSG00000172116	ENST00000331469	Transcript	missense_variant	possibly_damaging(0.781)
chr20	3546057	3546057	*ATRN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.H617N	ENSG00000088812	ENST00000262919	Transcript	missense_variant	possibly_damaging(0.903)
chr20	58547125	58547125	*CDH26*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G114*	ENSG00000124215	ENST00000348616	Transcript	stop_gained	NA
chr20	61040911	61040911	*GATA5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.A298S	ENSG00000130700	ENST00000252997	Transcript	missense_variant	benign(0.014)
chr21	17163944	17163944	*USP25*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.K172N	ENSG00000155313	ENST00000285679	Transcript	missense_variant	possibly_damaging(0.728)
chr21	34056396	34056396	*SYNJ1*	Missense_Mutation	.	SNP	C	C	G	novel	sia_et_al_P6	p.L423F	ENSG00000159082	ENST00000433931	Transcript	missense_variant	probably_damaging(1)

chr22	21288266	21288266	*CRKL*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G171W	ENSG00000099942	ENST00000354336	Transcript	missense_variant	probably_damaging(0.999)
chr3	100020942	100020942	*TBC1D23*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.S375*	ENSG00000036054	ENST00000394144	Transcript	stop_gained	NA
chr3	111688709	111688711	*PHLDB2*	In_Frame_Del	.	DEL	GTT	GTT	-	novel	sia_et_al_P6	p.W1164del	ENSG00000144824	ENST00000431670	Transcript	inframe_deletion	NA
chr3	122060397	122060397	*CSTA*	Nonsense_Mutation	.	SNP	G	G	T	rs200394711	sia_et_al_P6	p.E94*	ENSG00000121552	ENST00000264474	Transcript	stop_gained	NA
chr3	124017656	124017656	*KALRN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.H328N	ENSG00000160145	ENST00000240874	Transcript	missense_variant	benign(0.312)
chr3	145806491	145806491	*PLOD2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P296Q	ENSG00000152952	ENST00000282903	Transcript	missense_variant	probably_damaging(0.976)
chr3	152590 72	152590 72	*CAPN7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.D118Y	ENSG00000131375	ENST00000253693	Transcript	missense_variant	possibly_damaging(0.905)
chr3	169896635	169896637	*PHC3*	In_Frame_Del	.	DEL	TGG	TGG	-	novel	sia_et_al_P6	p.T35del	ENSG00000173889	ENST00000495893	Transcript	inframe_deletion	NA
chr3	183476655	183476655	*YEATS2*	Missense_Mutation	.	SNP	C	C	A	rs536285810	sia_et_al_P6	p.P520T	ENSG00000163872	ENST00000305135	Transcript	missense_variant	possibly_damaging(0.521)
chr3	184100184	184100184	*CHRD*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G236V	ENSG00000090539	ENST00000204604	Transcript	missense_variant	probably_damaging(1)
chr3	192993040	192993040	*ATP13A5*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G1150*	ENSG00000187527	ENST00000342358	Transcript	stop_gained	NA
chr3	194180518	194180518	*ATP13A3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.Q136H	ENSG00000133657	ENST00000439040	Transcript	missense_variant	benign(0.043)
chr3	195256652	195256652	*PPP1R2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P58Q	ENSG00000184203	ENST00000328432	Transcript	missense_variant	probably_damaging(0.992)
chr3	196281317	196281317	*WDR53*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P281H	ENSG00000185798	ENST00000332629	Transcript	missense_variant	possibly_damaging(0.695)
chr3	375840 05	375840 05	*ITGA9*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G540C	ENSG00000144668	ENST00000264741	Transcript	missense_variant	probably_damaging(0.948)
chr3	457511 39	457511 39	*SACM1L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R161S	ENSG00000211456	ENST00000389061	Transcript	missense_variant	benign(0.364)
chr3	476767 35	476767 35	*SMARCC1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G864V	ENSG00000173473	ENST00000254480	Transcript	missense_variant	possibly_damaging(0.852)
chr3	477874 28	477874 28	*SMARCC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.A124D	ENSG00000173473	ENST00000254480	Transcript	missense_variant	possibly_damaging(0.512)
chr3	573118 29	573118 29	*ASB14*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P6	p.Q518Rfs*11	ENSG00000239388	ENST00000487349	Transcript	frameshift_variant	NA
chr3	942498 7	942498 7	*THUMPD3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G410V	ENSG00000134077	ENST00000345094	Transcript	missense_variant	probably_damaging(0.994)
chr3	995673 33	995673 33	*FILIP1L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.H1063N	ENSG00000168386	ENST00000354552	Transcript	missense_variant	probably_damaging(0.999)
chr4	100130066	100130066	*ADH6*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P6	p.C196Wfs*52	ENSG00000172955	ENST00000394899	Transcript	frameshift_variant	NA
chr4	100827728	100827728	*DNAJB14*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S226R	ENSG00000164031	ENST00000442697	Transcript	missense_variant	possibly_damaging(0.447)
chr4	103571694	103571694	*MANBA*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.Q623H	ENSG00000109323	ENST00000226578	Transcript	missense_variant	probably_damaging(0.999)
chr4	110221759	110221759	*COL25A1*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S116*	ENSG00000188517	ENST00000399132	Transcript	stop_gained	NA
chr4	123176331	123176332	*KIAA1109*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	sia_et_al_P6	p.T2091Kfs*16	ENSG00000138688	ENST00000264501	Transcript	frameshift_variant	NA
chr4	126373716	126373716	*FAT4*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P6	p.K3849Sfs*13	ENSG00000196159	ENST00000394329	Transcript	frameshift_variant	NA
chr4	129120736	129120736	*LARP1B*	Missense_Mutation	.	SNP	C	C	T	rs201885302	sia_et_al_P6	p.R716C	ENSG00000138709	ENST00000326639	Transcript	missense_variant	possibly_damaging(0.893)
chr4	156274148	156274148	*MAP9*	Missense_Mutation	.	SNP	C	C	A	rs111294648	sia_et_al_P6	p.R535I	ENSG00000164114	ENST00000311277	Transcript	missense_variant	possibly_damaging(0.555)
chr4	169279360	169279360	*DDX60L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q1687K	ENSG00000181381	ENST00000260184	Transcript	missense_variant	benign(0.002)
chr4	178243651	178243651	*NEIL3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.L65F	ENSG00000109674	ENST00000264596	Transcript	missense_variant	benign(0.013)
chr4	185553446	185553446	*CASP3*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E95*	ENSG00000164305	ENST00000308394	Transcript	stop_gained	NA
chr4	185650079	185650079	*CENPU*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E69D	ENSG00000151725	ENST00000281453	Transcript	missense_variant	benign(0.384)
chr4	238143 91	238143 91	*PPARGC1A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E666D	ENSG00000109819	ENST00000264867	Transcript	missense_variant	unknown(0)
chr4	420650 14	420650 14	*SLC30A9*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.S303*	ENSG00000014824	ENST00000264451	Transcript	stop_gained	NA
chr4	705047 71	705047 71	*UGT2A2*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P6	p.A197Hfs*17	ENSG00000271271	ENST00000457664	Transcript	frameshift_variant	NA

chr4	72994332	72994332	*NPFFR2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.N110K	ENSG00000056291	ENST00000308744	Transcript	missense_variant	possibly_damaging(0.859)
chr4	74447979	74447979	*RASSF6*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P6	p.S231L	ENSG00000169435	ENST00000342081	Transcript	missense_variant	possibly_damaging(0.904)
chr4	76570692	76570692	*G3BP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.R457S	ENSG00000138757	ENST00000359707	Transcript	missense_variant	probably_damaging(0.972)
chr4	84015914	84015914	*PLAC8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.L92I	ENSG00000145287	ENST00000426923	Transcript	missense_variant	benign(0.012)
chr4	88979149	88979149	*PKD2*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P6	p.R638H	ENSG00000118762	ENST00000237596	Transcript	missense_variant	probably_damaging(0.976)
chr4	89653250	89653250	*FAM13A*	Nonsense_Mutation	.	SNP	C	C	A	rs371018005	sia_et_al_P6	p.E916*	ENSG00000138640	ENST00000264344	Transcript	stop_gained	NA
chr5	134033703	134033703	*SEC24A*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P6	p.R741Q	ENSG00000113615	ENST00000398844	Transcript	missense_variant	probably_damaging(0.941)
chr5	13920687	13920687	*DNAH5*	Missense_Mutation	.	SNP	G	G	T	rs199974463	sia_et_al_P6	p.L234I	ENSG00000039139	ENST00000265104	Transcript	missense_variant	benign(0.364)
chr5	154311066	154311066	*GEMIN5*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G245*	ENSG00000082516	ENST00000285873	Transcript	stop_gained	NA
chr5	156514276	156514276	*HAVCR2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S248*	ENSG00000135077	ENST00000307851	Transcript	stop_gained	NA
chr5	161576128	161576128	*GABRG2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.L353M	ENSG00000113327	ENST00000414552	Transcript	missense_variant	probably_damaging(0.999)
chr5	177163598	177163598	*FAM153A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P139T	ENSG00000170074	ENST00000440605	Transcript	missense_variant	benign(0.192)
chr5	37002852	37002852	*NIPBL*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.M1251I	ENSG00000164190	ENST00000282516	Transcript	missense_variant	possibly_damaging(0.649)
chr5	37443430	37443430	*WDR70*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.M214I	ENSG00000082068	ENST00000265107	Transcript	missense_variant	probably_damaging(0.967)
chr5	43294884	43294884	*HMGCS1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q329K	ENSG00000112972	ENST00000325110	Transcript	missense_variant	benign(0.001)
chr5	52322649	52322649	*ITGA2*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E46*	ENSG00000164171	ENST00000296585	Transcript	stop_gained	NA
chr5	64957977	64957977	*TRAPPC13*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S333I	ENSG00000113597	ENST00000438419	Transcript	missense_variant	benign(0.32)
chr5	72857054	72857054	*ANKRA2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P117T	ENSG00000164331	ENST00000296785	Transcript	missense_variant	probably_damaging(0.996)
chr5	72857099	72857099	*ANKRA2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.H102N	ENSG00000164331	ENST00000296785	Transcript	missense_variant	benign(0.053)
chr5	78350009	78350010	*DMGDH*	Frame_Shift_Del	.	DEL	TA	TA	-	novel	sia_et_al_P6	p.N179Kfs*8	ENSG00000132837	ENST00000255189	Transcript	frameshift_variant	NA
chr5	90281301	90281301	*GPR98*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q6038H	ENSG00000164199	ENST00000404560	Transcript	missense_variant	benign(0.115)
chr6	11698003	11698003	*ZUFSP*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q241K	ENSG00000153975	ENST00000368576	Transcript	missense_variant	benign(0.018)
chr6	13693530	13693530	*MAP3K5*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G759*	ENSG00000197442	ENST00000359015	Transcript	stop_gained	NA
chr6	13701846	13701846	*MAP3K5*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.G289S	ENSG00000197442	ENST00000359015	Transcript	missense_variant	probably_damaging(1)
chr6	14484325	14484325	*UTRN*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.P1893T	ENSG00000152818	ENST00000367545	Transcript	missense_variant	probably_damaging(0.992)
chr6	14624490	14624490	*SHPRH*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P1140H	ENSG00000146414	ENST00000367505	Transcript	missense_variant	probably_damaging(0.959)
chr6	14983335	14983335	*PPIL4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.H390N	ENSG00000131013	ENST00000253329	Transcript	missense_variant	benign(0.011)
chr6	16010915	16010915	*SOD2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G115W	ENSG00000112096	ENST00000538183	Transcript	missense_variant	probably_damaging(0.985)
chr6	17788078	17788078	*KIF13A*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.R1097K	ENSG00000137177	ENST00000259711	Transcript	missense_variant	probably_damaging(0.997)
chr6	20758874	20758874	*CDKAL1*	Frame_Shift_Del	.	DEL	AG	AG	-	novel	sia_et_al_P6	p.G173Sfs*12	ENSG00000145996	ENST00000274695	Transcript	frameshift_variant	NA
chr6	24658955	24658955	*TDP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.L87I	ENSG00000111802	ENST00000378198	Transcript	missense_variant	possibly_damaging(0.567)
chr6	56494202	56494202	*DST*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.H904N	ENSG00000151914	ENST00000244364	Transcript	missense_variant	probably_damaging(0.997)
chr6	66053933	66053933	*EYS*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.E533*	ENSG00000188107	ENST00000503581	Transcript	stop_gained	NA
chr6	83921651	83921651	*ME1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D571Y	ENSG00000065833	ENST00000369705	Transcript	missense_variant	benign(0.143)
chr6	84644421	84644421	*CYB5R4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G308W	ENSG00000065615	ENST00000369681	Transcript	missense_variant	probably_damaging(1)
chr6	90048020	90048020	*UBE2J1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.A111E	ENSG00000198833	ENST00000435041	Transcript	missense_variant	probably_damaging(0.939)

chr7	103002497	103002497	*PSMC2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q128H	ENSG00000161057	ENST00000435765	Transcript	missense_variant	benign(0.001)
chr7	106768685	106768685	*PRKAR2B*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R142I	ENSG00000005249	ENST00000265717	Transcript	missense_variant	probably_damaging(0.909)
chr7	139416662	139416662	*HIPK2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.P58T	ENSG00000064393	ENST00000406875	Transcript	missense_variant	benign(0.033)
chr7	30094390	30094390	*PLEKHA8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.Q288K	ENSG00000106086	ENST00000449726	Transcript	missense_variant	benign(0.003)
chr7	89933318	89933318	*C7orf63*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E696*	ENSG00000105792	ENST00000389297	Transcript	stop_gained	NA
chr8	109252205	109252205	*EIF3E*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.R102M	ENSG00000104408	ENST00000220849	Transcript	missense_variant	benign(0.153)
chr8	126075778	126075778	*KIAA0196*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.R465I	ENSG00000164961	ENST00000318410	Transcript	missense_variant	probably_damaging(1)
chr8	133855115	133855115	*PHF20L1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P6	p.E915Kfs*37	ENSG00000129292	ENST00000395386	Transcript	frameshift_variant	NA
chr8	136554925	136554925	*KHDRBS3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.P79Q	ENSG00000131773	ENST00000355849	Transcript	missense_variant	probably_damaging(0.992)
chr8	42260891	42260891	*VDAC3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.S206Y	ENSG00000078668	ENST00000521158	Transcript	missense_variant	possibly_damaging(0.691)
chr8	48626072	48626072	*SPIDR*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R737L	ENSG00000164808	ENST00000297423	Transcript	missense_variant	probably_damaging(0.991)
chr8	52339270	52339270	*PXDNL*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.G525V	ENSG00000147485	ENST00000356297	Transcript	missense_variant	probably_damaging(0.999)
chr8	62559381	62559381	*ASPH*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D183Y	ENSG00000198363	ENST00000379454	Transcript	missense_variant	benign(0.008)
chr8	67504719	67504719	*MYBL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.L275I	ENSG00000185697	ENST00000522677	Transcript	missense_variant	probably_damaging(0.999)
chr8	68151118	68151118	*ARFGEF1*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P6	p.D997V	ENSG00000066777	ENST00000262215	Transcript	missense_variant	probably_damaging(0.996)
chr8	71619361	71619361	*XKR9*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E156*	ENSG00000221947	ENST00000408926	Transcript	stop_gained	NA
chr9	112542797	112542797	*PALM2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.R10M	ENSG00000243444	ENST00000314527	Transcript	missense_variant	probably_damaging(0.979)
chr9	123789527	123789527	*C5*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.E262K	ENSG00000106804	ENST00000223642	Transcript	missense_variant	benign(0.022)
chr9	127683459	127683459	*GOLGA1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.K264N	ENSG00000136935	ENST00000373555	Transcript	missense_variant	possibly_damaging(0.694)
chr9	131864180	131864180	*CRAT*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P6	p.Y263Tfs*9	ENSG00000095321	ENST00000318080	Transcript	frameshift_variant	NA
chr9	744588	744588	*KANK1*	Missense_Mutation	.	SNP	C	C	T	rs143775530	sia_et_al_P6	p.P1332L	ENSG00000107104	ENST00000382303	Transcript	missense_variant	possibly_damaging(0.701)
chrX	100356279	100356279	*CENPI*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.E74*	ENSG00000102384	ENST00000372927	Transcript	stop_gained	NA
chrX	100531047	100531047	*TAF7L*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Q409K	ENSG00000102387	ENST00000372907	Transcript	missense_variant	benign(0.025)
chrX	107170208	107170208	*MID2*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.P705S	ENSG00000080561	ENST00000262843	Transcript	missense_variant	probably_damaging(0.988)
chrX	123164939	123164939	*STAG2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.L84F	ENSG00000101972	ENST00000218089	Transcript	missense_variant	probably_damaging(0.997)
chrX	129361732	129361732	*ZNF280C*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.S391*	ENSG00000056277	ENST00000370978	Transcript	stop_gained	NA
chrX	135310834	135310834	*MAP7D3*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P6	p.E612K	ENSG00000129680	ENST00000316077	Transcript	missense_variant	probably_damaging(0.979)
chrX	154019338	154019338	*MPP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.L111I	ENSG00000130830	ENST00000369534	Transcript	missense_variant	possibly_damaging(0.85)
chrX	155649082	155649082	*BMX*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.W578L	ENSG00000102010	ENST00000357607	Transcript	missense_variant	probably_damaging(1)
chrX	21990016	21990016	*SMS*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P6	p.F58Lfs*4	ENSG00000102172	ENST00000404933	Transcript	frameshift_variant	NA
chrX	30870948	30870948	*TAB3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P6	p.D553Y	ENSG00000157625	ENST00000378933	Transcript	missense_variant	possibly_damaging(0.723)
chrX	40464955	40464955	*ATP6AP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.G334V	ENSG00000182220	ENST00000378438	Transcript	missense_variant	probably_damaging(0.99)
chrX	57620765	57620765	*ZXDB*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	sia_et_al_P6	p.H762Sfs*2	ENSG00000198455	ENST00000374888	Transcript	frameshift_variant	NA
chrX	84537320	84537320	*POF1B*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.Y551*	ENSG00000124429	ENST00000262753	Transcript	stop_gained	NA
chrX	87643666	87643666	*FAM9A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P6	p.A144D	ENSG00000183304	ENST00000543214	Transcript	missense_variant	probably_damaging(0.958)
chr1	109650588	109650589	*C1orf194*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	sia_et_al_P8	p.T40Nfs*12	ENSG00000179902	ENST00000369949	Transcript	frameshift_variant	NA

chr1	11087400	11087400	*MASP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L535M	ENSG00000009724	ENST00000400897	Transcript	missense_variant	probably_damaging(1)
chr1	11155876	11155876	*EXOSC10*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.T104N	ENSG00000171824	ENST00000376936	Transcript	missense_variant	possibly_damaging(0.775)
chr1	114319963	114319963	*RSBN1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.W510Gfs*20	ENSG00000081019	ENST00000261441	Transcript	frameshift_variant	NA
chr1	120845994	120845994	*FAM72B*	Splice_Site	.	SNP	G	G	T	novel	sia_et_al_P8	p.X77_splice	ENSG00000188610	ENST00000369390	Transcript	splice_acceptor_variant	NA
chr1	124160 81	124160 81	*VPS13D*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.V3269L	ENSG00000048707	ENST00000358136	Transcript	missense_variant	benign(0.014)
chr1	146751845	146751846	*CHD1L*	Frame_Shift_Ins	.	INS	-	-	A	novel	sia_et_al_P8	p.R563Kfs*14	ENSG00000131778	ENST00000369258	Transcript	frameshift_variant	NA
chr1	160000599	160000600	*PIGM*	Nonsense_Mutation	.	DEL	TG	TG	-	novel	sia_et_al_P8	p.Y310*	ENSG00000143315	ENST00000368090	Transcript	stop_gained	NA
chr1	167744 51	167744 51	*NECAP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.R94S	ENSG00000157191	ENST00000443980	Transcript	missense_variant	probably_damaging(0.974)
chr1	169586552	169586553	*SELP*	Frame_Shift_Del	.	DEL	TG	TG	-	novel	sia_et_al_P8	p.D66Lfs*7	ENSG00000174175	ENST00000263686	Transcript	frameshift_variant	NA
chr1	268734 12	268734 13	*RPS6KA1*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P8	p.K65Gfs*2	ENSG00000117676	ENST00000531382	Transcript	frameshift_variant	NA
chr1	29438885	29438886	*EPB41*	Frame_Shift_Del	.	DEL	AA	AA	-	novel	sia_et_al_P8	p.K808Rfs*9	ENSG00000159023	ENST00000343067	Transcript	frameshift_variant	NA
chr1	43055154	43055154	*CCDC30*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.E461D	ENSG00000186409	ENST00000428554	Transcript	missense_variant	probably_damaging(0.988)
chr1	8000052	8000052	*TNFRSF9*	Translation_Start_Site	.	SNP	C	C	T	novel	sia_et_al_P8	p.M1?	ENSG00000049249	ENST00000377507	Transcript	initiator_codon_variant	probably_damaging(0.993)
chr1	92528830	92528830	*EPHX4*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	NA	ENSG00000172031	ENST00000370383	Transcript	frameshift_variant	NA
chr10	16930425	16930425	*CUBN*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.H2966N	ENSG00000107611	ENST00000377833	Transcript	missense_variant	possibly_damaging(0.686)
chr10	25273744	25273744	*ENKUR*	Missense_Mutation	.	SNP	T	T	C	rs33980615	sia_et_al_P8	p.R229G	ENSG00000151023	ENST00000331161	Transcript	missense_variant	benign(0.371)
chr10	32582621	32582621	*EPC1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E120*	ENSG00000120616	ENST00000263062	Transcript	stop_gained	NA
chr10	96495174	96495174	*CYP2C18*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L482F	ENSG00000108242	ENST00000285979	Transcript	missense_variant	benign(0.008)
chr11	102234438	102234438	*BIRC2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.D372Y	ENSG00000110330	ENST00000227758	Transcript	missense_variant	benign(0.181)
chr11	108031762	108031762	*NPAT*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.P1351T	ENSG00000149308	ENST00000278612	Transcript	missense_variant	probably_damaging(1)
chr11	108127067	108127067	*ATM*	Missense_Mutation	.	SNP	G	G	T	rs1137887	sia_et_al_P8	p.K750N	ENSG00000149311	ENST00000278616	Transcript	missense_variant	probably_damaging(0.996)
chr11	108302502	108302502	*C11orf65*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q49K	ENSG00000166323	ENST00000393084	Transcript	missense_variant	benign(0.069)
chr11	111735971	111735971	*ALG9*	5'UTR	.	SNP	G	G	T	novel	sia_et_al_P8	NA	ENSG00000086848	ENST00000531154	Transcript	5_prime_UTR_variant	NA
chr11	115102181	115102181	*CADM1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q152K	ENSG00000182985	ENST00000452722	Transcript	missense_variant	benign(0.049)
chr11	118636047	118636047	*DDX6*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.R174Efs*23	ENSG00000110367	ENST00000264018	Transcript	frameshift_variant	NA
chr11	123755344	123755344	*TMEM225*	Splice_Site	.	SNP	C	C	A	novel	sia_et_al_P8	p.X61_splice	ENSG00000204300	ENST00000375026	Transcript	splice_acceptor_variant	NA
chr11	134055245	134055245	*NCAPD3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.W741L	ENSG00000151503	ENST00000534548	Transcript	missense_variant	possibly_damaging(0.505)
chr11	19253883	19253883	*E2F8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L322M	ENSG00000129173	ENST00000527884	Transcript	missense_variant	probably_damaging(1)
chr11	20948951	20948951	*NELL1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.W286L	ENSG00000165973	ENST00000357134	Transcript	missense_variant	probably_damaging(0.914)
chr11	22747978	22747978	*GAS2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L136F	ENSG00000148935	ENST00000457584	Transcript	missense_variant	probably_damaging(0.999)
chr11	26664848	26664848	*ANO3*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.R799W	ENSG00000134343	ENST00000256737	Transcript	missense_variant	probably_damaging(0.998)
chr11	34673352	34673352	*EHF*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.A204S	ENSG00000135373	ENST00000531794	Transcript	missense_variant	benign(0.003)
chr11	36614454	36614454	*RAG2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.T422N	ENSG00000175097	ENST00000311485	Transcript	missense_variant	benign(0.166)
chr11	46391102	46391102	*DGKZ*	Splice_Site	.	DEL	T	T	-	novel	sia_et_al_P8	p.X355_splice	ENSG00000149091	ENST00000454345	Transcript	splice_donor_variant	NA
chr11	56345021	56345021	*ORSM10*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.M59I	ENSG00000254834	ENST00000526812	Transcript	missense_variant	benign(0.126)
chr11	59282934	59282934	*OR4D9*	Missense_Mutation	.	SNP	G	G	T	rs562656575	sia_et_al_P8	p.Q183H	ENSG00000172742	ENST00000329328	Transcript	missense_variant	benign(0.35)

chr11	59626684	59626684	*TCN1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.G205W	ENSG00000134827	ENST00000257264	Transcript	missense_variant	probably_damaging(0.968)
chr11	68748023	68748024	*MRGPRD*	Frame_Shift_Del	.	DEL	CC	CC	-	novel	sia_et_al_P8	p.W144Cfs*28	ENSG00000172938	ENST00000309106	Transcript	frameshift_variant	NA
chr11	69426022	69426022	*OR2D3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G124W	ENSG00000178358	ENST00000317834	Transcript	missense_variant	probably_damaging(0.999)
chr11	77639396	77639396	*INTS4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.V455L	ENSG00000149262	ENST00000534064	Transcript	missense_variant	benign(0.231)
chr11	78204209	78204209	*NARS2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.T241N	ENSG00000137513	ENST00000281038	Transcript	missense_variant	probably_damaging(0.962)
chr11	89451029	89451029	*TRIM77*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G448*	ENSG00000214414	ENST00000398290	Transcript	stop_gained	NA
chr11	94113759	94113759	*GPR83*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.T277Qfs*18	ENSG00000123901	ENST00000243673	Transcript	frameshift_variant	NA
chr11	95583011	95583011	*MTMR2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.H274N	ENSG00000087053	ENST00000346299	Transcript	missense_variant	possibly_damaging(0.778)
chr11	96117136	96117136	*CCDC82*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.R259I	ENSG00000149231	ENST00000278520	Transcript	missense_variant	possibly_damaging(0.548)
chr12	120172071	120172071	*CIT*	Missense_Mutation	.	SNP	C	C	T	rs368207202	sia_et_al_P8	p.R1083Q	ENSG00000122966	ENST00000392521	Transcript	missense_variant	probably_damaging(0.961)
chr12	121442138	121442138	*C12orf43*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.V203I	ENSG00000157895	ENST00000288757	Transcript	missense_variant	benign(0.003)
chr12	121756312	121756312	*ANAPC5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.M579I	ENSG00000089053	ENST00000261819	Transcript	missense_variant	benign(0.001)
chr12	132416810	132416811	*PUS1*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P8	p.E132Gfs*32	ENSG00000177192	ENST00000376649	Transcript	frameshift_variant	NA
chr12	46591840	46591840	*SLC38A1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.R376Vfs*33	ENSG00000111371	ENST00000398637	Transcript	frameshift_variant	NA
chr12	65564810	65564810	*LEMD3*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P8	p.T479Lfs*8	ENSG00000174106	ENST00000308330	Transcript	frameshift_variant	NA
chr13	73343040	73343040	*DIS3*	Missense_Mutation	.	SNP	G	G	T	rs199919016	sia_et_al_P8	p.T589K	ENSG00000083520	ENST00000377767	Transcript	missense_variant	probably_damaging(0.995)
chr14	53177860	53177860	*PSMC6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L114F	ENSG00000100519	ENST00000445930	Transcript	missense_variant	probably_damaging(0.972)
chr14	57710971	57710971	*EXOC5*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.R126Q	ENSG00000070367	ENST00000413566	Transcript	missense_variant	probably_damaging(0.981)
chr14	69800300	69800300	*GALNT16*	Frame_Shift_Del	.	DEL	G	G	-	rs144140025	sia_et_al_P8	p.G319Efs*83	ENSG00000100626	ENST00000337827	Transcript	frameshift_variant	NA
chr14	75587252	75587252	*NEK9*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.S162*	ENSG00000119638	ENST00000238616	Transcript	stop_gained	NA
chr15	43678490	43678490	*TUBGCP4*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.E326*	ENSG00000137822	ENST00000560479	Transcript	stop_gained	NA
chr15	50926718	50926719	*TRPM7*	Frame_Shift_Del	.	DEL	AT	AT	-	novel	sia_et_al_P8	p.F290*	ENSG00000092439	ENST00000313478	Transcript	frameshift_variant	NA
chr15	88678584	88678584	*NTRK3*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P8	p.E318Sfs*96	ENSG00000140538	ENST00000360948	Transcript	frameshift_variant	NA
chr16	47628125	47628125	*PHKB*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G402*	ENSG00000102893	ENST00000323584	Transcript	stop_gained	NA
chr16	57490451	57490451	*COQ9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.F138L	ENSG00000088682	ENST00000262507	Transcript	missense_variant	possibly_damaging(0.62)
chr16	69074223	69074223	*TANGO6*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.L1003M	ENSG00000103047	ENST00000261778	Transcript	missense_variant	possibly_damaging(0.808)
chr17	10356966	10356966	*MYH4*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E976D	ENSG00000264424	ENST00000255381	Transcript	missense_variant	possibly_damaging(0.614)
chr17	16612746	16612746	*CCDC144A*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.D459Y	ENSG00000170160	ENST00000443444	Transcript	missense_variant	probably_damaging(0.953)
chr17	36485966	36485966	*GPR179*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.S1162R	ENSG00000188888	ENST00000342292	Transcript	missense_variant	probably_damaging(0.999)
chr17	40630549	40630549	*ATP6V0A1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.R199L	ENSG00000033627	ENST00000264649	Transcript	missense_variant	probably_damaging(1)
chr17	56729356	56729357	*TEX14*	Frame_Shift_Del	.	DEL	GA	GA	-	novel	sia_et_al_P8	p.R3Gfs*18	ENSG00000121101	ENST00000240361	Transcript	frameshift_variant	NA
chr17	82733318	82733318	*KRBA2*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.G205R	ENSG00000184619	ENST00000331336	Transcript	missense_variant	possibly_damaging(0.697)
chr18	11824928	11824928	*GNAL*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.D212E	ENSG00000141404	ENST00000334049	Transcript	missense_variant	benign(0.083)
chr18	13885395	13885395	*MC2R*	Missense_Mutation	.	SNP	C	C	A	rs373074499	sia_et_al_P8	p.E41D	ENSG00000185231	ENST00000327606	Transcript	missense_variant	probably_damaging(0.996)
chr18	28712625	28712625	*DSC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.T715N	ENSG00000134765	ENST00000257198	Transcript	missense_variant	probably_damaging(0.921)
chr18	29101206	29101206	*DSG2*	Missense_Mutation	.	SNP	C	C	T	rs375422019	sia_et_al_P8	p.H175Y	ENSG00000046604	ENST00000261590	Transcript	missense_variant	benign(0.011)

chr18	56247745	56247745	*ALPK2*	Nonsense_Mutation	.	SNP	G	G	T	rs199755126	sia_et_al_P8	p.S88*	ENSG00000198796	ENST00000361673	Transcript	stop_gained	NA
chr19	22363627	22363627	*ZNF676*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P8	p.E298Nfs*200	ENSG00000196109	ENST00000397121	Transcript	frameshift_variant	NA
chr19	33333110	33333110	*SLC7A9*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.M396I	ENSG00000021488	ENST00000023064	Transcript	missense_variant	possibly_damaging(0.542)
chr19	36304169	36304169	*PRODH2*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P8	p.V65fs*17	ENSG00000250799	ENST00000301175	Transcript	frameshift_variant	NA
chr19	37643861	37643861	*ZNF585A*	Missense_Mutation	.	SNP	G	G	T	rs267605449	sia_et_al_P8	p.Q259K	ENSG00000196967	ENST00000292841	Transcript	missense_variant	benign(0.063)
chr19	38028142	38028142	*ZNF793*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.A196Lfs*14	ENSG00000188227	ENST00000445217	Transcript	frameshift_variant	NA
chr19	44792016	44792016	*ZNF235*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.F524L	ENSG00000159917	ENST00000291182	Transcript	missense_variant	probably_damaging(1)
chr19	46663693	46663693	*IGFL2*	Missense_Mutation	.	SNP	G	G	T	rs191441091	sia_et_al_P8	p.C25F	ENSG00000204866	ENST00000434646	Transcript	missense_variant	benign(0)
chr19	48386884	48386884	*SULT2A1*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.L100Sfs*17	ENSG00000105398	ENST00000222002	Transcript	frameshift_variant	NA
chr19	52496328	52496328	*ZNF615*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P8	p.I679Lfs*75	ENSG00000197619	ENST00000594083	Transcript	frameshift_variant	NA
chr19	52825878	52825878	*ZNF480*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.E459*	ENSG00000198464	ENST00000595962	Transcript	stop_gained	NA
chr2	109367763	109367763	*RANBP2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.W439C	ENSG00000153201	ENST00000283195	Transcript	missense_variant	benign(0.425)
chr2	120857824	120857825	*EPB41L5*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	sia_et_al_P8	p.H395Qfs*2	ENSG00000115109	ENST00000263713	Transcript	frameshift_variant	NA
chr2	152989751	152989751	*STAM2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.Q302H	ENSG00000115145	ENST00000263904	Transcript	missense_variant	benign(0.008)
chr2	178082483	178082483	*HNRNPA3*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G291C	ENSG00000170144	ENST00000392524	Transcript	missense_variant	unknown(0)
chr2	204591391	204591391	*CD28*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.V30*	ENSG00000178562	ENST00000324106	Transcript	frameshift_variant	NA
chr2	204821424	204821424	*ICOS*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G146V	ENSG00000163600	ENST00000316386	Transcript	missense_variant	probably_damaging(0.96)
chr2	209025630	209025630	*CRYGA*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P8	p.R142Gfs*5	ENSG00000168582	ENST00000304502	Transcript	frameshift_variant	NA
chr2	214215371	214215371	*SPAG16*	Splice_Site	.	DEL	T	T	-	novel	sia_et_al_P8	p.X254_splice	ENSG00000144451	ENST00000331683	Transcript	splice_donor_variant	NA
chr2	227875053	227875053	*COL4A4*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E1500*	ENSG00000081052	ENST00000396625	Transcript	stop_gained	NA
chr2	61761002	61761002	*XPO1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.H11N	ENSG00000082898	ENST00000401558	Transcript	missense_variant	benign(0.007)
chr2	99945336	99945336	*TAF1B*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.G129Efs*7	ENSG00000115750	ENST00000266633	Transcript	frameshift_variant	NA
chr21	27284135	27284136	*APP*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	sia_et_al_P8	p.N610Wfs*17	ENSG00000142192	ENST00000346798	Transcript	frameshift_variant	NA
chr21	33867459	33867459	*EVA1C*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.L253I	ENSG00000166979	ENST00000300255	Transcript	missense_variant	probably_damaging(0.999)
chr3	100992442	100992442	*IMPG2*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E271*	ENSG00000081148	ENST00000193391	Transcript	stop_gained	NA
chr3	113082360	113082360	*WDR52*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.P912Q	ENSG00000206530	ENST00000393845	Transcript	missense_variant	benign(0.066)
chr3	113187693	113187693	*SPICE1*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E269*	ENSG00000163611	ENST00000295872	Transcript	stop_gained	NA
chr3	119222866	119222866	*TIMMDC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G172V	ENSG00000113845	ENST00000494664	Transcript	missense_variant	probably_damaging(0.944)
chr3	121981235	121981237	*CASR*	In_Frame_Del	.	DEL	CAT	CAT	-	novel	sia_et_al_P8	p.I452del	ENSG00000036828	ENST00000498619	Transcript	inframe_deletion	NA
chr3	12610503	12610504	*MKRN2*	Splice_Site	.	DEL	GC	GC	-	novel	sia_et_al_P8	p.X52_splice	ENSG00000075975	ENST00000170447	Transcript	splice_donor_variant	NA
chr3	132358336	132358336	*ACAD11*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E234D	ENSG00000240303	ENST00000264990	Transcript	missense_variant	possibly_damaging(0.824)
chr3	145806491	145806491	*PLOD2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.P296Q	ENSG00000152952	ENST00000282903	Transcript	missense_variant	probably_damaging(0.976)
chr3	151087230	151087230	*MED12L*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.P1151H	ENSG00000144893	ENST00000474524	Transcript	missense_variant	benign(0.166)
chr3	151156359	151156359	*IGSF10*	Missense_Mutation	.	SNP	G	G	T	rs199577194	sia_et_al_P8	p.P1997H	ENSG00000152580	ENST00000282466	Transcript	missense_variant	probably_damaging(0.992)
chr3	164760926	164760926	*SI*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.T642K	ENSG00000090402	ENST00000264382	Transcript	missense_variant	possibly_damaging(0.894)
chr3	16635178	16635178	*DAZL*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.G260V	ENSG00000092345	ENST00000250863	Transcript	missense_variant	possibly_damaging(0.461)

chr3	196083593	196083593	*UBXN7*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.C478F	ENSG00000163960	ENST00000296328	Transcript	missense_variant	benign(0.061)
chr3	32568398	32568398	*DYNC1LI1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q489K	ENSG00000144635	ENST00000273130	Transcript	missense_variant	probably_damaging(0.926)
chr3	33558658	33558658	*CLASP2*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.L1274*	ENSG00000163539	ENST00000468888	Transcript	frameshift_variant	NA
chr3	41957536	41957536	*ULK4*	Frame_Shift_Del	.	DEL	G	G	-	rs375337313	sia_et_al_P8	p.R246Vfs*24	ENSG00000168038	ENST00000301831	Transcript	frameshift_variant	NA
chr3	62556575	62556575	*CADPS*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.W539L	ENSG00000163618	ENST00000383710	Transcript	missense_variant	possibly_damaging(0.533)
chr3	98188505	98188505	*OR5K1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.V29L	ENSG00000232382	ENST00000332650	Transcript	missense_variant	benign(0.003)
chr4	110862299	110862299	*EGF*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.E109*	ENSG00000138798	ENST00000265171	Transcript	stop_gained	NA
chr4	122747134	122747134	*BBS7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L677I	ENSG00000138686	ENST00000264499	Transcript	missense_variant	probably_damaging(0.941)
chr4	47647178	47647178	*CORIN*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.S626Y	ENSG00000145244	ENST00000273857	Transcript	missense_variant	benign(0.211)
chr4	66467971	66467971	*EPHA5*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q100K	ENSG00000145242	ENST00000273854	Transcript	missense_variant	probably_damaging(0.949)
chr4	68497620	68497620	*UBA6*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q717K	ENSG00000033178	ENST00000322244	Transcript	missense_variant	possibly_damaging(0.685)
chr4	68531012	68531012	*UBA6*	Splice_Site	.	DEL	T	T	-	novel	sia_et_al_P8	p.X265_splice	ENSG00000033178	ENST00000322244	Transcript	splice_acceptor_variant	NA
chr4	82377909	82377909	*RASGEF1B*	Frame_Shift_Del	.	DEL	G	G	-	novel	sia_et_al_P8	p.Q112Nfs*19	ENSG00000138670	ENST00000264400	Transcript	frameshift_variant	NA
chr4	89357033	89357033	*HERC6*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.R803W	ENSG00000138642	ENST00000264346	Transcript	missense_variant	possibly_damaging(0.657)
chr5	140725040	140725041	*PCDHGA3*	Frame_Shift_Ins	.	INS	-	-	AGCA	novel	sia_et_al_P8	p.N482Kfs*46	ENSG00000254245	ENST00000253812	Transcript	frameshift_variant	NA
chr5	154251333	154251333	*CNOT8*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.R173S	ENSG00000155508	ENST00000517876	Transcript	missense_variant	benign(0.174)
chr5	43543167	43543167	*PAIP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L225M	ENSG00000172239	ENST00000306846	Transcript	missense_variant	probably_damaging(1)
chr6	109867219	109867219	*AK9*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.L1026I	ENSG00000155085	ENST00000424296	Transcript	missense_variant	probably_damaging(0.996)
chr6	111995704	111995704	*FYN*	Missense_Mutation	.	SNP	G	G	C	novel	sia_et_al_P8	p.P468R	ENSG00000010810	ENST00000354650	Transcript	missense_variant	possibly_damaging(0.879)
chr6	117704668	117704668	*ROS1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q770K	ENSG00000047936	ENST00000368508	Transcript	missense_variant	benign(0.285)
chr6	126319269	126319269	*TRMT11*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.V95L	ENSG00000066651	ENST00000334379	Transcript	missense_variant	benign(0)
chr6	139565799	139565799	*TXLNB*	Frame_Shift_Del	.	DEL	T	T	-	novel	sia_et_al_P8	p.K400Rfs*20	ENSG00000164440	ENST00000358430	Transcript	frameshift_variant	NA
chr6	143784055	143784055	*PEX3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.L70M	ENSG00000034693	ENST00000367591	Transcript	missense_variant	probably_damaging(0.995)
chr6	144750848	144750848	*UTRN*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P8	p.E276K	ENSG00000152818	ENST00000367545	Transcript	missense_variant	probably_damaging(0.995)
chr6	150267543	150267543	*ULBP2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.Q129K	ENSG00000131015	ENST00000367351	Transcript	missense_variant	benign(0.18)
chr6	159677663	159677663	*FNDC1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.R1725M	ENSG00000164694	ENST00000297267	Transcript	missense_variant	probably_damaging(0.995)
chr6	27222775	27222775	*PRSS16*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P8	p.W449Gfs*4	ENSG00000112812	ENST00000230582	Transcript	frameshift_variant	NA
chr6	65300676	65300676	*EYS*	Nonsense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.S1695*	ENSG00000188107	ENST00000505581	Transcript	stop_gained	NA
chr6	80732173	80732173	*TTK*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.R414L	ENSG00000112742	ENST00000369798	Transcript	missense_variant	benign(0.001)
chr6	87968808	87968809	*ZNF292*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	sia_et_al_P8	p.T1821Kfs*3	ENSG00000188994	ENST00000369577	Transcript	frameshift_variant	NA
chr6	90372617	90372617	*MDN1*	Missense_Mutation	.	SNP	T	T	A	novel	sia_et_al_P8	p.E4769V	ENSG00000112159	ENST00000369393	Transcript	missense_variant	benign(0.295)
chr7	105912976	105912976	*NAMPT*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E149D	ENSG00000105835	ENST00000225523	Transcript	missense_variant	possibly_damaging(0.797)
chr7	107557903	107557903	*DLD*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P8	p.E412Rfs*28	ENSG00000091140	ENST00000205402	Transcript	frameshift_variant	NA
chr7	110625082	110625082	*PHF14*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.M431I	ENSG00000106443	ENST00000403050	Transcript	missense_variant	probably_damaging(0.977)
chr7	114644044	114644044	*THSD7A*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.V1088F	ENSG00000005108	ENST00000423059	Transcript	missense_variant	probably_damaging(0.986)
chr7	130001069	130001069	*CPA5*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.S173Y	ENSG00000158525	ENST00000485477	Transcript	missense_variant	probably_damaging(0.954)

chr7	6029588	6029588	*PMS2*	Splice_Site	.	SNP	T	T	A	novel	sia_et_al_P8	p.X330_splice	ENSG00000122512	ENST00000265849	Transcript	splice_acceptor_variant	NA
chr7	87370891	87370891	*RUNDC3B*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.Q226K	ENSG00000105784	ENST00000338056	Transcript	missense_variant	possibly_damaging(0.792)
chr7	94147635	94147635	*CASD1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.K117N	ENSG00000127995	ENST00000297273	Transcript	missense_variant	possibly_damaging(0.751)
chr7	95664973	95664973	*DYNC1I1*	Missense_Mutation	.	SNP	G	G	A	novel	sia_et_al_P8	p.V442I	ENSG00000158560	ENST00000324972	Transcript	missense_variant	probably_damaging(0.989)
chr7	97944900	97944900	*BAIAP2L1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q171K	ENSG00000006453	ENST00000052600	Transcript	missense_variant	probably_damaging(0.999)
chr9	100243164	100243164	*TDRD7*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.D786Y	ENSG00000196116	ENST00000355295	Transcript	missense_variant	probably_damaging(0.998)
chr9	102713487	102713487	*STX17*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.S112Y	ENSG00000136874	ENST00000259400	Transcript	missense_variant	benign(0.218)
chr9	104071556	104071556	*LPPR1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G150V	ENSG00000148123	ENST00000374874	Transcript	missense_variant	probably_damaging(0.987)
chr9	107298075	107298075	*OR13C3*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.L340F	ENSG00000204246	ENST00000374781	Transcript	missense_variant	possibly_damaging(0.721)
chr9	107594912	107594912	*ABCA1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.W484C	ENSG00000165029	ENST00000374736	Transcript	missense_variant	probably_damaging(0.96)
chr9	114152370	114152370	*KIAA0368*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.S1236Y	ENSG00000136813	ENST00000259335	Transcript	missense_variant	probably_damaging(0.978)
chr9	125748689	125748689	*RABGAP1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.G194V	ENSG00000011454	ENST00000374647	Transcript	missense_variant	possibly_damaging(0.874)
chr9	130942699	130942699	*CIZ1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.L262F	ENSG00000148337	ENST00000393608	Transcript	missense_variant	benign(0.298)
chr9	130942726	130942726	*CIZ1*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E253D	ENSG00000148337	ENST00000393608	Transcript	missense_variant	possibly_damaging(0.755)
chr9	132224220	132224220	*MPDZ*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q187K	ENSG00000107186	ENST00000541718	Transcript	missense_variant	probably_damaging(1)
chr9	134314386	134314386	*PRRC2B*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.S136*	ENSG00000130723	ENST00000357304	Transcript	stop_gained	NA
chr9	135163942	135163942	*SETX*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.R2068I	ENSG00000107290	ENST00000224140	Transcript	missense_variant	probably_damaging(0.991)
chr9	140477473	140477473	*ZMYND19*	Nonsense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.E168*	ENSG00000165724	ENST00000298585	Transcript	stop_gained	NA
chr9	19058308	19058308	*HAUS6*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P8	p.R820Dfs*21	ENSG00000147874	ENST00000380502	Transcript	frameshift_variant	NA
chr9	20546007	20546007	*SMARCA2*	Missense_Mutation	.	SNP	C	C	A	novel	sia_et_al_P8	p.R353S	ENSG00000080503	ENST00000382203	Transcript	missense_variant	benign(0.353)
chr9	432306	432306	*DOCK8*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.M1589I	ENSG00000107099	ENST00000453981	Transcript	missense_variant	benign(0.001)
chr9	79842345	79842345	*VPS13A*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.L466F	ENSG00000197969	ENST00000360280	Transcript	missense_variant	probably_damaging(0.999)
chr9	95285103	95285103	*ECM2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.Q16K	ENSG00000106823	ENST00000344604	Transcript	missense_variant	benign(0.223)
chr9	98683560	98683560	*ERCC6L2*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.C432F	ENSG00000182150	ENST00000288985	Transcript	missense_variant	probably_damaging(1)
chrX	100667466	100667467	*HNRNPH2*	Frame_Shift_Del	.	DEL	AT	AT	-	novel	sia_et_al_P8	p.I164Sfs*2	ENSG00000126945	ENST00000316594	Transcript	frameshift_variant	NA
chrX	31792208	31792208	*DMD*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.A2471T	ENSG00000198947	ENST00000357033	Transcript	missense_variant	possibly_damaging(0.682)
chrX	32486810	32486810	*DMD*	Frame_Shift_Del	.	DEL	C	C	-	novel	sia_et_al_P8	p.Q990Kfs*14	ENSG00000198947	ENST00000357033	Transcript	frameshift_variant	NA
chrX	46898447	46898447	*JADE3*	Frame_Shift_Del	.	DEL	A	A	-	novel	sia_et_al_P8	p.K318Rfs*10	ENSG00000102221	ENST00000218343	Transcript	frameshift_variant	NA
chrX	53617983	53617983	*HUWE1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.P1358T	ENSG00000086758	ENST00000342160	Transcript	missense_variant	benign(0.059)
chrX	70145757	70145757	*SLC7A3*	Missense_Mutation	.	SNP	C	C	G	rs149447856	sia_et_al_P8	p.S589T	ENSG00000165349	ENST00000374299	Transcript	missense_variant	possibly_damaging(0.742)
chrX	70607300	70607300	*TAF1*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.D826Y	ENSG00000147133	ENST00000276072	Transcript	missense_variant	probably_damaging(0.973)
chrX	74289126	74289126	*ABCB7*	Missense_Mutation	.	SNP	C	C	T	novel	sia_et_al_P8	p.G511E	ENSG00000131269	ENST00000253577	Transcript	missense_variant	probably_damaging(1)
chrX	78010916	78010916	*LPAR4*	Missense_Mutation	.	SNP	G	G	T	novel	sia_et_al_P8	p.A184S	ENSG00000147145	ENST00000435339	Transcript	missense_variant	benign(0)
chr1	111216332	111216332	*KCNA3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R367H	ENSG00000177272	ENST00000369769	Transcript	missense_variant	probably_damaging(0.999)
chr1	115222310	115222310	*AMPD1*	Missense_Mutation	.	SNP	G	G	A	rs139003085	gao_et_al_P7	p.R296C	ENSG00000116748	ENST00000520113	Transcript	missense_variant	probably_damaging(1)
chr1	12026353	12026353	*PLOD1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A544T	ENSG00000083444	ENST00000196061	Transcript	missense_variant	benign(0.001)

chr1	1372689	1372689	*VWA1*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.M155Cfs*51	ENSG00000179403	ENST00000476993	Transcript	frameshift_variant	NA
chr1	150444667	150444667	*RPRD2*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	NA	ENSG00000163125	ENST00000369068	Transcript	frameshift_variant	NA
chr1	151315621	151315621	*RFX5*	Missense_Mutation	.	SNP	C	C	T	rs146341254	gao_et_al_P7	p.G298S	ENSG00000143390	ENST00000290524	Transcript	missense_variant	benign(0.004)
chr1	152732678	152732678	*KPRP*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.Q207Sfs*4	ENSG00000203786	ENST00000368773	Transcript	frameshift_variant	NA
chr1	154842105	154842106	*KCNN3*	Frame_Shift_Ins	.	INS	-	-	G	novel	gao_et_al_P7	p.S113Ffs*22	ENSG00000143603	ENST00000271915	Transcript	frameshift_variant	NA
chr1	160853242	160853242	*ITLN1*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P7	p.K45Q	ENSG00000179914	ENST00000326245	Transcript	missense_variant	benign(0.159)
chr1	161200655	161200655	*NR1I3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A298T	ENSG00000143257	ENST00000367980	Transcript	missense_variant	probably_damaging(0.995)
chr1	16269156	16269156	*ZBTB17*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.V636M	ENSG00000116809	ENST00000375743	Transcript	missense_variant	probably_damaging(0.987)
chr1	164621999	164621999	*EPHA2*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.P460Rfs*33	ENSG00000142627	ENST00000358432	Transcript	frameshift_variant	NA
chr1	172410938	172410938	*PIGC*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F275Lfs*32	ENSG00000135845	ENST00000367728	Transcript	frameshift_variant	NA
chr1	174189118	174189118	*PADI2*	Missense_Mutation	.	SNP	C	C	T	rs375141021	gao_et_al_P7	p.V214M	ENSG00000117115	ENST00000375486	Transcript	missense_variant	probably_damaging(0.992)
chr1	181497888	181497888	*ACTL8*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.P97Lfs*2	ENSG00000117148	ENST00000375406	Transcript	frameshift_variant	NA
chr1	202862391	202862391	*KLHL12*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R519Q	ENSG00000117153	ENST00000367261	Transcript	missense_variant	benign(0.001)
chr1	203816503	203816504	*ZC3H11A*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.H415Tfs*23	ENSG00000058673	ENST00000545588	Transcript	frameshift_variant	NA
chr1	207679428	207679428	*CR1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R101C	ENSG00000203710	ENST00000367049	Transcript	missense_variant	probably_damaging(0.965)
chr1	208205029	208205029	*PLXNA2*	Frame_Shift_Del	.	DEL	G	G	-	rs186740123	gao_et_al_P7	p.L1711Wfs*10	ENSG00000076356	ENST00000367033	Transcript	frameshift_variant	NA
chr1	226923855	226923855	*ITPKB*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.R436Vfs*53	ENSG00000143772	ENST00000429204	Transcript	frameshift_variant	NA
chr1	243905968	243905968	*MYOM3*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P7	p.G1206R	ENSG00000142661	ENST00000374434	Transcript	missense_variant	benign(0.342)
chr1	244595877	244595877	*ADSS*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.R126Gfs*73	ENSG00000035687	ENST00000366535	Transcript	frameshift_variant	NA
chr1	24687434	24687434	*STPG1*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.G279C	ENSG00000001460	ENST00000374409	Transcript	missense_variant	probably_damaging(1)
chr1	248512910	248512910	*OR14C36*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.I278M	ENSG00000177174	ENST00000317861	Transcript	missense_variant	benign(0.34)
chr1	27097622	27097622	*ARID1A*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.K1072Nfs*21	ENSG00000117713	ENST00000324856	Transcript	frameshift_variant	NA
chr1	27100111	27100111	*ARID1A*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.A1304Pfs*177	ENSG00000117713	ENST00000324856	Transcript	frameshift_variant	NA
chr1	27121637	27121637	*PIGV*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.D371G	ENSG00000060642	ENST00000374145	Transcript	missense_variant	benign(0.005)
chr1	27440668	27440668	*SLC9A1*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.F155Sfs*36	ENSG00000090020	ENST00000263980	Transcript	frameshift_variant	NA
chr1	27621108	27621108	*WDTC1*	Frame_Shift_Del	.	DEL	G	G	-	rs145339479	gao_et_al_P7	p.E290Nfs*8	ENSG00000142784	ENST00000361771	Transcript	frameshift_variant	NA
chr1	28564412	28564414	*ATPIF1*	In_Frame_Del	.	DEL	AAG	AAG	-	novel	gao_et_al_P7	p.K82del	ENSG00000130770	ENST00000335514	Transcript	inframe_deletion	NA
chr1	33245000	33245003	*YARS*	Frame_Shift_Del	.	DEL	CTTT	CTTT	-	novel	gao_et_al_P7	p.K486Sfs*25	ENSG00000134684	ENST00000373477	Transcript	frameshift_variant	NA
chr1	33998700	33998700	*CSMD2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R3374H	ENSG00000121904	ENST00000373381	Transcript	missense_variant	probably_damaging(0.932)
chr1	34083211	34083211	*CSMD2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G1945D	ENSG00000121904	ENST00000373381	Transcript	missense_variant	probably_damaging(0.98)
chr1	40558135	40558135	*PPT1*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.M57Wfs*14	ENSG00000131238	ENST00000433473	Transcript	frameshift_variant	NA
chr1	41303446	41303446	*KCNQ4*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.V619M	ENSG00000117013	ENST00000347132	Transcript	missense_variant	probably_damaging(0.995)
chr1	43002201	43002201	*CCDC30*	Frame_Shift_Del	.	DEL	AG	AG	-	rs372826618	gao_et_al_P7	p.K21Afs*7	ENSG00000186409	ENST00000428554	Transcript	frameshift_variant	NA
chr1	43912033	43912033	*SZT2*	Frame_Shift_Del	.	DEL	CAAA	CAAA	-	novel	gao_et_al_P7	p.K2949Sfs*33	ENSG00000198198	ENST00000562955	Transcript	frameshift_variant	NA
chr1	46083256	46083254	*NASP*	In_Frame_Del	.	DEL	GGA	GGA	-	novel	gao_et_al_P7	p.E762del	ENSG00000132780	ENST00000350030	Transcript	inframe_deletion	NA
chr1	57373746	57373746	*C8A*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G447E	ENSG00000157131	ENST00000361249	Transcript	missense_variant	probably_damaging(1)

chr1	6257785	6257785	*RPL22*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K15Rfs*5	ENSG00000116251	ENST00000234875	Transcript	frameshift_variant	NA
chr1	6688653	6688653	*THAP3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.E57K	ENSG00000041988	ENST00000054650	Transcript	missense_variant	probably_damaging(0.919)
chr1	67147865	67147867	*SGIP1*	In_Frame_Del	.	DEL	AGA	AGA	-	novel	gao_et_al_P7	p.E377del	ENSG00000118473	ENST00000371037	Transcript	inframe_deletion	NA
chr1	78401649	78401649	*NEXN*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.I467*	ENSG00000162614	ENST00000334785	Transcript	frameshift_variant	NA
chr1	86746900	86746900	*RERE*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.P151Qfs*23	ENSG00000142599	ENST00000337907	Transcript	frameshift_variant	NA
chr1	89298838	89298838	*PKN2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R917W	ENSG00000065243	ENST00000370521	Transcript	missense_variant	probably_damaging(0.992)
chr1	94980738	94980739	*ABCD3*	Frame_Shift_Del	.	DEL	TC	TC	-	novel	gao_et_al_P7	p.W630Efs*4	ENSG00000117528	ENST00000370214	Transcript	frameshift_variant	NA
chr10	105178240	105178240	*PDCD11*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P7	p.E652A	ENSG00000148843	ENST00000369797	Transcript	missense_variant	benign(0.184)
chr10	111893350	111893350	*ADD3*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	NA	ENSG00000148700	ENST00000356080	Transcript	frameshift_variant	NA
chr10	115668266	115668266	*NHLRC2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A718T	ENSG00000196865	ENST00000369301	Transcript	missense_variant	benign(0.002)
chr10	118315557	118315557	*PNLIP*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.Y286C	ENSG00000175535	ENST00000369221	Transcript	missense_variant	probably_damaging(0.999)
chr10	123844422	123844422	*TACC2*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P7	p.Q803E	ENSG00000138162	ENST00000369005	Transcript	missense_variant	benign(0.059)
chr10	128193492	128193492	*C10orf90*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G93R	ENSG00000154493	ENST00000284694	Transcript	missense_variant	benign(0.007)
chr10	16919034	16919034	*CUBN*	Missense_Mutation	.	SNP	C	C	T	rs115888073	gao_et_al_P7	p.V2990I	ENSG00000107611	ENST00000377833	Transcript	missense_variant	benign(0.008)
chr10	17156077	17156077	*CUBN*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.V278M	ENSG00000107611	ENST00000377833	Transcript	missense_variant	probably_damaging(0.984)
chr10	21959612	21959612	*MLLT10*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A344T	ENSG00000078403	ENST00000307729	Transcript	missense_variant	benign(0.015)
chr10	23250921	23250921	*ARMC3*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.G216C	ENSG00000165309	ENST00000298032	Transcript	missense_variant	probably_damaging(0.933)
chr10	27702951	27702951	*PTCHD3*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.R77Gfs*43	ENSG00000182077	ENST00000438700	Transcript	frameshift_variant	NA
chr10	37431020	37431020	*ANKRD30A*	Missense_Mutation	.	SNP	G	G	A	rs202201583	gao_et_al_P7	p.A343T	ENSG00000148513	ENST00000361713	Transcript	missense_variant	possibly_damaging(0.821)
chr10	43659474	43659474	*CSGALNACT2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R381W	ENSG00000169826	ENST00000374466	Transcript	missense_variant	probably_damaging(0.939)
chr10	48390151	48390151	*RBP3*	Missense_Mutation	.	SNP	C	C	T	rs149256669	gao_et_al_P7	p.A243T	ENSG00000107618	ENST00000224600	Transcript	missense_variant	probably_damaging(0.992)
chr10	50531273	50531273	*C10orf71*	Missense_Mutation	.	SNP	C	C	T	rs376805154	gao_et_al_P7	p.A228V	ENSG00000177354	ENST00000374144	Transcript	missense_variant	benign(0.133)
chr10	74267933	74267933	*MICU1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F211Sfs*22	ENSG00000107745	ENST00000361114	Transcript	frameshift_variant	NA
chr10	78729786	78729786	*KCNMA1*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K711Sfs*17	ENSG00000156113	ENST00000404857	Transcript	frameshift_variant	NA
chr10	79782037	79782037	*POLR3A*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.I251V	ENSG00000148606	ENST00000372371	Transcript	missense_variant	benign(0.126)
chr10	82369309	82369309	*SH2D4B*	Splice_Site	.	SNP	T	T	C	novel	gao_et_al_P7	p.X329_splice	ENSG00000178217	ENST00000339284	Transcript	splice_donor_variant	NA
chr10	84738806	84738806	*NRG3*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P7	p.I505F	ENSG00000185737	ENST00000372141	Transcript	missense_variant	benign(0.234)
chr10	86273825	86273825	*CCSER2*	3'UTR	.	DEL	C	C	-	novel	gao_et_al_P7	NA	ENSG00000107771	ENST00000224756	Transcript	3_prime_UTR_variant	NA
chr11	106810467	106810467	*GUCY1A2*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.T309A	ENSG00000152402	ENST00000282249	Transcript	missense_variant	benign(0.005)
chr11	107207381	107207381	*CWF19L2*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.L754Wfs*5	ENSG00000152404	ENST00000282251	Transcript	frameshift_variant	NA
chr11	10820934	10820935	*EIF4G2*	Frame_Shift_Ins	.	INS	-	-	G	novel	gao_et_al_P7	p.S788Tfs*3	ENSG00000110321	ENST00000526148	Transcript	frameshift_variant	NA
chr11	111365969	111365969	*BTG4*	Missense_Mutation	.	SNP	C	C	T	rs201313198	gao_et_al_P7	p.R194H	ENSG00000137707	ENST00000356018	Transcript	missense_variant	benign(0.007)
chr11	111941931	111941932	*PIH1D2*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.N126Kfs*12	ENSG00000150773	ENST00000280350	Transcript	frameshift_variant	NA
chr11	113567677	113567677	*TMPRSS5*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G161R	ENSG00000166682	ENST00000299882	Transcript	missense_variant	possibly_damaging(0.714)
chr11	121031033	121031033	*TECTA*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G1627R	ENSG00000109927	ENST00000392793	Transcript	missense_variant	probably_damaging(1)
chr11	124767660	124767660	*ROBO4*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.G11Afs*25	ENSG00000154133	ENST00000306534	Transcript	frameshift_variant	NA

chr11	14825540	14825540	*PDE3B*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.P489L	ENSG00000152270	ENST00000282096	Transcript	missense_variant	benign(0.165)
chr11	22301099	22301099	*ANO5*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.L845*	ENSG00000171714	ENST00000324559	Transcript	frameshift_variant	NA
chr11	22833369	22833369	*GAS2*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.V250A	ENSG00000148935	ENST00000454584	Transcript	missense_variant	probably_damaging(0.984)
chr11	372141	372142	*B4GALNT4*	Frame_Shift_Ins	.	INS	-	-	G	novel	gao_et_al_P7	p.V64Gfs*11	ENSG00000182272	ENST00000329962	Transcript	frameshift_variant	NA
chr11	44286624	44286624	*ALX4*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.G340Afs*11	ENSG00000052850	ENST00000329255	Transcript	frameshift_variant	NA
chr11	46812114	46812114	*CKAP5*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K557Rfs*26	ENSG00000175216	ENST00000529230	Transcript	frameshift_variant	NA
chr11	51412076	51412076	*OR4A5*	Missense_Mutation	.	SNP	C	C	A	rs368103058	gao_et_al_P7	p.G107V	ENSG00000221840	ENST00000319760	Transcript	missense_variant	possibly_damaging(0.555)
chr11	59271134	59271134	*OR4D11*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.L31Yfs*6	ENSG00000176200	ENST00000313253	Transcript	frameshift_variant	NA
chr11	59554609	59554612	*STX3*	Splice_Site	.	DEL	AGTG	AGTG	-	novel	gao_et_al_P7	p.X72_splice	ENSG00000166900	ENST00000337979	Transcript	splice_donor_variant	NA
chr11	62749334	62749334	*SLC22A6*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.A260Pfs*26	ENSG00000197901	ENST00000377871	Transcript	frameshift_variant	NA
chr11	64004663	64004663	*VEGFB*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.K129Rfs*5	ENSG00000173511	ENST00000309422	Transcript	frameshift_variant	NA
chr11	64009978	64009978	*FKBP2*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.D40G	ENSG00000173486	ENST00000394540	Transcript	missense_variant	benign(0.002)
chr11	64108896	64108896	*CCDC88B*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.E151K	ENSG00000168071	ENST00000356786	Transcript	missense_variant	possibly_damaging(0.805)
chr11	64883014	64883014	*TM7SF2*	Missense_Mutation	.	SNP	G	G	A	rs375149084	gao_et_al_P7	p.R347H	ENSG00000149809	ENST00000279263	Transcript	missense_variant	probably_damaging(1)
chr11	64898751	64898751	*SYVN1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A251V	ENSG00000162298	ENST00000377190	Transcript	missense_variant	possibly_damaging(0.829)
chr11	66006688	66006688	*PACS1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R790Q	ENSG00000175115	ENST00000320580	Transcript	missense_variant	possibly_damaging(0.612)
chr11	67196695	67196696	*RPS6KB2*	Frame_Shift_Ins	.	INS	-	-	G	novel	gao_et_al_P7	p.Y78Lfs*42	ENSG00000175634	ENST00000312629	Transcript	frameshift_variant	NA
chr11	67378538	67378538	*NDUFV1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G258E	ENSG00000167792	ENST00000322776	Transcript	missense_variant	probably_damaging(0.931)
chr11	69425588	69425589	*OR2D3*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.Y111Lfs*27	ENSG00000178358	ENST00000317834	Transcript	frameshift_variant	NA
chr11	72006647	72006647	*CLPB*	Missense_Mutation	.	SNP	C	C	T	rs372344202	gao_et_al_P7	p.A489T	ENSG00000162129	ENST00000294053	Transcript	missense_variant	probably_damaging(0.981)
chr11	76940243	76940243	*GDPD4*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A475V	ENSG00000178795	ENST00000315938	Transcript	missense_variant	benign(0.001)
chr11	83177849	83177850	*DLG2*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	gao_et_al_P7	NA	ENSG00000150672	ENST00000376104	Transcript	frameshift_variant	NA
chr11	84744434	84744434	*STK33*	Missense_Mutation	.	SNP	G	G	A	rs375541480	gao_et_al_P7	p.A269V	ENSG00000130413	ENST00000447869	Transcript	missense_variant	probably_damaging(0.991)
chr11	85375242	85375244	*CREBZF*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	gao_et_al_P7	p.K226del	ENSG00000137504	ENST00000527447	Transcript	inframe_deletion	NA
chr11	86410600	86410600	*TRIM66*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P7	p.I1110N	ENSG00000166436	ENST00000402157	Transcript	missense_variant	probably_damaging(1)
chr12	100451840	100451840	*UHRF1BP1L*	Frame_Shift_Del	.	DEL	G	G	-	rs550401137	gao_et_al_P7	p.P1072Qfs*11	ENSG00000111647	ENST00000279907	Transcript	frameshift_variant	NA
chr12	100731192	100731192	*SCYL2*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.K685E	ENSG00000136021	ENST00000360820	Transcript	missense_variant	benign(0.278)
chr12	102547645	102547645	*PARPBP*	Splice_Site	.	SNP	A	A	G	novel	gao_et_al_P7	p.X130_splice	ENSG00000185480	ENST00000358383	Transcript	splice_acceptor_variant	NA
chr12	104107474	104107474	*STAB2*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.K1489E	ENSG00000136011	ENST00000388887	Transcript	missense_variant	possibly_damaging(0.676)
chr12	112513482	112513482	*NAA25*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.N259Tfs*9	ENSG00000111300	ENST00000261745	Transcript	frameshift_variant	NA
chr12	113544980	113544980	*RASAL1*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.L528Cfs*12	ENSG00000111344	ENST00000546530	Transcript	frameshift_variant	NA
chr12	118517256	118517256	*VSIG10*	Frame_Shift_Del	.	DEL	C	C	-	rs145604064	gao_et_al_P7	p.V274Wfs*4	ENSG00000176834	ENST00000359236	Transcript	frameshift_variant	NA
chr12	119617377	119617377	*HSPB8*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.P89Hfs*12	ENSG00000152137	ENST00000281938	Transcript	frameshift_variant	NA
chr12	122242658	122242658	*SETD1B*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.H8Tfs*27	ENSG00000139718	ENST00000267197	Transcript	frameshift_variant	NA
chr12	123307941	123307941	*CCDC62*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.N679Ifs*18	ENSG00000130783	ENST00000253079	Transcript	frameshift_variant	NA
chr12	134599 1	134599 1	*ERC1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.K805Rfs*7	ENSG00000082805	ENST00000397203	Transcript	frameshift_variant	NA

chr12	140190144	140190144	*GRIN2B*	Frame_Shift_Del	.	DEL	G	G	-	rs77738206	gao_et_al_P7	p.S34Afs*38	ENSG00000273079	ENST00000609686	Transcript	frameshift_variant	NA
chr12	149475110	149475110	*WBP11*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R228C	ENSG00000084463	ENST00000261167	Transcript	missense_variant	unknown(0)
chr12	25148925	25148925	*C12orf77*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P7	p.I75L	ENSG00000226397	ENST00000549828	Transcript	missense_variant	benign(0.003)
chr12	25398281	25398281	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G13D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.506)
chr12	27628630	27628630	*SMCO2*	Frame_Shift_Del	.	DEL	A	A	-	rs545209953	gao_et_al_P7	p.I162*	ENSG00000165935	ENST00000416383	Transcript	frameshift_variant	NA
chr12	49443667	49443667	*KMT2D*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.G1236Afs*94	ENSG00000167548	ENST00000301067	Transcript	frameshift_variant	NA
chr12	50029045	50029045	*PRPF40B*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R389W	ENSG00000110844	ENST00000548825	Transcript	missense_variant	probably_damaging(0.988)
chr12	51442183	51442183	*LETMD1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.G15V	ENSG00000050426	ENST00000418425	Transcript	missense_variant	benign(0.013)
chr12	51863525	51863525	*SLC4A8*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.V493I	ENSG00000050438	ENST00000453097	Transcript	missense_variant	probably_damaging(0.996)
chr12	52579224	52579224	*KRT80*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R150W	ENSG00000167767	ENST00000394815	Transcript	missense_variant	probably_damaging(0.976)
chr12	52946483	52946483	*KRT71*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R127C	ENSG00000139648	ENST00000267119	Transcript	missense_variant	benign(0.021)
chr12	53818535	53818535	*AMHR2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.C92F	ENSG00000135409	ENST00000257863	Transcript	missense_variant	possibly_damaging(0.639)
chr12	57883053	57883053	*MARS*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.L71Cfs*33	ENSG00000166986	ENST00000262027	Transcript	frameshift_variant	NA
chr12	58025102	58025103	*B4GALNT1*	Frame_Shift_Ins	.	INS	-	-	C	novel	gao_et_al_P7	p.L89Pfs*13	ENSG00000135454	ENST00000341156	Transcript	frameshift_variant	NA
chr12	63544097	63544097	*AVPR1A*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A174T	ENSG00000166148	ENST00000299178	Transcript	missense_variant	benign(0.144)
chr12	64812755	64812755	*XPOT*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F126Lfs*6	ENSG00000184575	ENST00000332707	Transcript	frameshift_variant	NA
chr12	64944143	64944144	*LTBR*	Frame_Shift_Ins	.	INS	-	-	C	novel	gao_et_al_P7	p.C116Lfs*32	ENSG00000111321	ENST00000228918	Transcript	frameshift_variant	NA
chr12	70933407	70933407	*PTPRB*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.E1926K	ENSG00000127329	ENST00000334414	Transcript	missense_variant	probably_damaging(0.945)
chr12	72008414	72008414	*ZFC3H1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.T1810Mfs*3	ENSG00000133858	ENST00000378743	Transcript	frameshift_variant	NA
chr12	72808586	72808586	*RBP5*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.V78M	ENSG00000139194	ENST00000266560	Transcript	missense_variant	benign(0.141)
chr12	81111125	81111125	*MYF5*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R95C	ENSG00000111049	ENST00000228644	Transcript	missense_variant	probably_damaging(1)
chr12	88512304	88512305	*CEP290*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.I556Nfs*20	ENSG00000198707	ENST00000552810	Transcript	frameshift_variant	NA
chr12	91448367	91448367	*KLRG1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A40T	ENSG00000139187	ENST00000356986	Transcript	missense_variant	benign(0.028)
chr13	114542743	114542745	*GAS6*	In_Frame_Del	.	DEL	AGA	AGA	-	novel	gao_et_al_P7	p.F141del	ENSG00000183087	ENST00000327773	Transcript	inframe_deletion	NA
chr13	23912864	23912864	*SACS*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K1717Nfs*8	ENSG00000151835	ENST00000382298	Transcript	frameshift_variant	NA
chr13	25356067	25356068	*RNF17*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.D202*	ENSG00000132972	ENST00000255324	Transcript	frameshift_variant	NA
chr13	28539102	28539102	*CDX2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R198W	ENSG00000165556	ENST00000381020	Transcript	missense_variant	probably_damaging(0.996)
chr13	31233003	31233003	*USPL1*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P7	p.N930T	ENSG00000132952	ENST00000255304	Transcript	missense_variant	probably_damaging(0.956)
chr13	32868599	32868599	*FRY*	Missense_Mutation	.	SNP	C	C	T	rs558171569	gao_et_al_P7	p.A2892V	ENSG00000073910	ENST00000380250	Transcript	missense_variant	benign(0.018)
chr13	36241630	36241630	*NBEA*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.Y2841H	ENSG00000172915	ENST00000400445	Transcript	missense_variant	possibly_damaging(0.873)
chr13	36385036	36385036	*DCLK1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G542S	ENSG00000133083	ENST00000255448	Transcript	missense_variant	probably_damaging(0.935)
chr13	38145595	38145595	*POSTN*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G697E	ENSG00000133110	ENST00000379747	Transcript	missense_variant	benign(0.002)
chr13	40273702	40273702	*COG6*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.I413Yfs*6	ENSG00000133103	ENST00000455146	Transcript	frameshift_variant	NA
chr13	46541915	46541915	*ZC3H13*	Nonsense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R1349*	ENSG00000123200	ENST00000282007	Transcript	stop_gained	NA
chr13	49705294	49705294	*FNDC3A*	Nonsense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R92*	ENSG00000102531	ENST00000492622	Transcript	stop_gained	NA
chr13	50235209	50235209	*EBPL*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	NA	ENSG00000123179	ENST00000248227	Transcript	frameshift_variant	NA

chr13	52976711	52976712	*THSD1*	Frame_Shift_Del	.	DEL	AA	AA	-	novel	gao_et_al_P7	p.S9Kfs*9	ENSG00000136114	ENST00000258613	Transcript	frameshift_variant	NA
chr13	53420879	53420879	*PCDH8*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R565C	ENSG00000136099	ENST00000377942	Transcript	missense_variant	probably_damaging(0.936)
chr13	79918806	79918807	*RBM26*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.Q701Tfs*23	ENSG00000139746	ENST00000267229	Transcript	frameshift_variant	NA
chr14	21550028	21550028	*ARHGEF40*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R1001W	ENSG00000165801	ENST00000298694	Transcript	missense_variant	benign(0.01)
chr14	21896280	21896280	*CHD8*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R450H	ENSG00000100888	ENST00000399982	Transcript	missense_variant	probably_damaging(0.98)
chr14	23390144	23390144	*PRMT5*	Missense_Mutation	.	SNP	G	G	T	rs565682196	gao_et_al_P7	p.P628H	ENSG00000100462	ENST00000324366	Transcript	missense_variant	probably_damaging(0.993)
chr14	24572751	24572751	*PCK2*	Missense_Mutation	.	SNP	C	C	T	rs199570303	gao_et_al_P7	p.R501W	ENSG00000100889	ENST00000216780	Transcript	missense_variant	probably_damaging(1)
chr14	24619809	24619809	*RNF31*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.D402Mfs*90	ENSG00000092098	ENST00000324103	Transcript	frameshift_variant	NA
chr14	31381333	31381333	*STRN3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R477H	ENSG00000196792	ENST00000357479	Transcript	missense_variant	possibly_damaging(0.836)
chr14	45523648	45523648	*FAM179B*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.I1432M	ENSG00000198718	ENST00000361577	Transcript	missense_variant	benign(0.004)
chr14	47530771	47530771	*MDGA2*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.G105Dfs*22	ENSG00000139915	ENST00000426342	Transcript	frameshift_variant	NA
chr14	50262615	50262615	*NEMF*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A838V	ENSG00000165525	ENST00000298310	Transcript	missense_variant	benign(0)
chr14	64606785	64606785	*SYNE2*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F4992Lfs*13	ENSG00000054654	ENST00000358025	Transcript	frameshift_variant	NA
chr14	65053978	65053980	*PPP1R36*	In_Frame_Del	.	DEL	GAA	GAA	-	novel	gao_et_al_P7	p.E260del	ENSG00000165807	ENST00000298705	Transcript	inframe_deletion	NA
chr14	67940481	67940481	*TMEM229B*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G54S	ENSG00000198133	ENST00000357461	Transcript	missense_variant	possibly_damaging(0.749)
chr15	101605984	101605984	*LRRK1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.S1781I	ENSG00000154237	ENST00000388948	Transcript	missense_variant	possibly_damaging(0.602)
chr15	101775437	101775437	*CHSY1*	Frame_Shift_Del	.	DEL	C	C	-	rs745456602	gao_et_al_P7	p.P223Lfs*3	ENSG00000131873	ENST00000254190	Transcript	frameshift_variant	NA
chr15	102358903	102358903	*OR4F15*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.N172D	ENSG00000182854	ENST00000332238	Transcript	missense_variant	probably_damaging(0.976)
chr15	25924712	25924712	*ATP10A*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	NA	ENSG00000206190	ENST00000356865	Transcript	frameshift_variant	NA
chr15	25959007	25959007	*ATP10A*	Missense_Mutation	.	SNP	C	C	T	rs367580656	gao_et_al_P7	p.D720N	ENSG00000206190	ENST00000356865	Transcript	missense_variant	benign(0.069)
chr15	34163232	34163233	*AVEN*	Splice_Site	.	INS	-	-	TA	novel	gao_et_al_P7	p.X173_splice	ENSG00000169857	ENST00000306730	Transcript	splice_acceptor_variant	NA
chr15	34640686	34640687	*NUTM1*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.W179Lfs*24	ENSG00000184507	ENST00000333756	Transcript	frameshift_variant	NA
chr15	43814251	43814251	*MAP1A*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.G194C	ENSG00000166963	ENST00000300231	Transcript	missense_variant	probably_damaging(1)
chr15	49935635	49935635	*DTWD1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.V259I	ENSG00000104047	ENST00000251250	Transcript	missense_variant	benign(0.304)
chr15	54626040	54626040	*UNC13C*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F1525Lfs*3	ENSG00000137766	ENST00000260323	Transcript	frameshift_variant	NA
chr15	70352890	70352892	*TLE3*	In_Frame_Del	.	DEL	CTC	CTC	-	novel	gao_et_al_P7	p.E231del	ENSG00000140332	ENST00000558939	Transcript	inframe_deletion	NA
chr15	72432352	72432352	*SENP8*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P7	p.K130Q	ENSG00000166192	ENST00000544411	Transcript	missense_variant	benign(0.073)
chr15	83932762	83932762	*BNC1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.H414R	ENSG00000169594	ENST00000345382	Transcript	missense_variant	probably_damaging(0.997)
chr15	89056193	89056193	*DET1*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.C559R	ENSG00000140543	ENST00000564406	Transcript	missense_variant	benign(0.021)
chr15	91136948	91136948	*CRTC3*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.L106Sfs*48	ENSG00000140577	ENST00000268184	Transcript	frameshift_variant	NA
chr15	99023868	99023868	*FAM169B*	Missense_Mutation	.	SNP	G	G	A	rs141122936	gao_et_al_P7	p.R49C	ENSG00000185087	ENST00000558256	Transcript	missense_variant	possibly_damaging(0.646)
chr16	10867203	10867203	*TVP23A*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F140Lfs*7	ENSG00000166676	ENST00000299866	Transcript	frameshift_variant	NA
chr16	15122825	15122825	*PDXDC1*	Splice_Site	.	SNP	T	T	C	novel	gao_et_al_P7	p.X431_splice	ENSG00000179889	ENST00000396410	Transcript	splice_donor_variant	NA
chr16	19498346	19498346	*TMC5*	Splice_Site	.	DEL	GTGA	GTGA	-	novel	gao_et_al_P7	p.X813_splice	ENSG00000103534	ENST00000396229	Transcript	splice_donor_variant	NA
chr16	22111790	22111790	*VWA3A*	Missense_Mutation	.	SNP	G	G	A	rs377575921	gao_et_al_P7	p.R135H	ENSG00000175267	ENST00000389398	Transcript	missense_variant	benign(0.001)
chr16	23205578	23205579	*SCNN1G*	Frame_Shift_Ins	.	INS	-	-	G	novel	gao_et_al_P7	p.S302Qfs*27	ENSG00000166828	ENST00000300061	Transcript	frameshift_variant	NA

chr16	23347889	23347889	*ABCA3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R1232C	ENSG00000167972	ENST00000301732	Transcript	missense_variant	possibly_damaging(0.892)
chr16	25258441	25258441	*ZKSCAN2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R359H	ENSG00000155592	ENST00000328086	Transcript	missense_variant	probably_damaging(0.998)
chr16	30094730	30094730	*PPP4C*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R107C	ENSG00000149923	ENST00000279387	Transcript	missense_variant	probably_damaging(0.975)
chr16	3065456	3065456	*CLDN6*	Frame_Shift_Del	.	DEL	C	C	-	rs536531302	gao_et_al_P7	p.S190Pfs*70	ENSG00000184697	ENST00000396925	Transcript	frameshift_variant	NA
chr16	31733995	31733995	*ZNF720*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.W18R	ENSG00000197302	ENST00000316491	Transcript	missense_variant	probably_damaging(0.998)
chr16	3778104	3778104	*CREBBP*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P7	p.S2315T	ENSG00000005339	ENST00000262367	Transcript	missense_variant	unknown(0)
chr16	48381427	48381427	*LONP2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R650C	ENSG00000102910	ENST00000285737	Transcript	missense_variant	probably_damaging(1)
chr16	53692704	53692704	*RPGRIP1L*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R444C	ENSG00000103494	ENST00000379925	Transcript	missense_variant	benign(0.042)
chr16	56902236	56902236	*SLC12A3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.V153M	ENSG00000070915	ENST00000438926	Transcript	missense_variant	probably_damaging(1)
chr16	57284324	57284324	*ARL2BP*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.H99Y	ENSG00000102931	ENST00000219204	Transcript	missense_variant	possibly_damaging(0.492)
chr16	64981699	64981699	*CDH11*	Missense_Mutation	.	SNP	G	G	A	rs555349824	gao_et_al_P7	p.T733M	ENSG00000140937	ENST00000268603	Transcript	missense_variant	probably_damaging(0.968)
chr16	67685720	67685720	*RLTPR*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.L854M	ENSG00000159753	ENST00000334583	Transcript	missense_variant	benign(0.183)
chr16	68100541	68100541	*DUS2*	Splice_Site	.	SNP	T	T	C	novel	gao_et_al_P7	p.X185_splice	ENSG00000167264	ENST00000565263	Transcript	splice_donor_variant	NA
chr16	68721490	68721490	*CDH3*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.E549G	ENSG00000062038	ENST00000264012	Transcript	missense_variant	possibly_damaging(0.66)
chr16	70818690	70818690	*VAC14*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.R159S	ENSG00000103043	ENST00000261776	Transcript	missense_variant	probably_damaging(0.995)
chr16	71220808	71220808	*HYDIN*	5'UTR	.	DEL	T	T	-	novel	gao_et_al_P7	NA	ENSG00000157423	ENST00000393567	Transcript	5_prime_UTR_variant	NA
chr16	71748506	71748506	*PHLPP2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.V65I	ENSG00000040199	ENST00000568954	Transcript	missense_variant	probably_damaging(0.99)
chr16	75512979	75512979	*CHST6*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.V250I	ENSG00000183196	ENST00000332272	Transcript	missense_variant	possibly_damaging(0.692)
chr16	77356311	77356311	*ADAMTS18*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F695Lfs*7	ENSG00000140873	ENST00000282849	Transcript	frameshift_variant	NA
chr16	78466513	78466513	*WWOX*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.L307P	ENSG00000186153	ENST00000566780	Transcript	missense_variant	probably_damaging(0.996)
chr16	85682289	85682290	*GSE1*	Frame_Shift_Ins	.	INS	-	-	CC	novel	gao_et_al_P7	p.V123Pfs*3	ENSG00000131149	ENST00000253458	Transcript	frameshift_variant	NA
chr16	87363331	87363331	*METTL22*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.D307N	ENSG00000067365	ENST00000381920	Transcript	missense_variant	possibly_damaging(0.665)
chr16	88498493	88498493	*ZNF469*	Missense_Mutation	.	SNP	G	G	A	rs559565235	gao_et_al_P7	p.A1511T	ENSG00000225614	ENST00000437464	Transcript	missense_variant	benign(0.001)
chr17	18996861	18996863	*AC007952.5*	In_Frame_Del	.	DEL	CTT	CTT	-	rs200553822	gao_et_al_P7	p.L67del	ENSG00000228157	ENST00000428928	Transcript	inframe_deletion	NA
chr17	27829700	27829700	*TAOK1*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P7	p.R433G	ENSG00000160551	ENST00000261716	Transcript	missense_variant	possibly_damaging(0.593)
chr17	33362866	33362866	*OR1E2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A284T	ENSG00000127780	ENST00000248384	Transcript	missense_variant	benign(0.12)
chr17	33807083	33807084	*SLFN12L*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.M49Ifs*12	ENSG00000205045	ENST00000260908	Transcript	frameshift_variant	NA
chr17	37650860	37650862	*CDK12*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	gao_et_al_P7	p.L778del	ENSG00000167258	ENST00000447079	Transcript	inframe_deletion	NA
chr17	38508066	38508066	*ATP2A3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R325H	ENSG00000074370	ENST00000359983	Transcript	missense_variant	probably_damaging(0.943)
chr17	38788534	38788537	*SMARCE1*	Frame_Shift_Del	.	DEL	CTCA	CTCA	-	novel	gao_et_al_P7	p.S208Rfs*26	ENSG00000073584	ENST00000348513	Transcript	frameshift_variant	NA
chr17	40711223	40711223	*ANKFY1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R1196W	ENSG00000185722	ENST00000570535	Transcript	missense_variant	probably_damaging(1)
chr17	40939870	40939870	*WNK4*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.V608Cfs*53	ENSG00000126562	ENST00000246914	Transcript	frameshift_variant	NA
chr17	41245587	41245587	*BRCA1*	Frame_Shift_Del	.	DEL	T	T	-	rs80357522	gao_et_al_P7	p.K654Sfs*47	ENSG00000012048	ENST00000471181	Transcript	frameshift_variant	NA
chr17	44953906	44953906	*WNT9B*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G299D	ENSG00000158955	ENST00000290015	Transcript	missense_variant	probably_damaging(1)
chr17	52646889	52646889	*RABEP1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A428T	ENSG00000029725	ENST00000262477	Transcript	missense_variant	probably_damaging(0.943)
chr17	56388330	56388330	*BZRAP1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.P1109H	ENSG00000005379	ENST00000343736	Transcript	missense_variant	possibly_damaging(0.853)

chr17	56569119	56569119	*MTMR4*	Missense_Mutation	.	SNP	C	C	T	rs148218230	gao_et_al_P7	p.V1165I	ENSG00000108389	ENST00000323456	Transcript	missense_variant	probably_damaging(0.999)
chr17	57247171	57247171	*PRR11*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.E23Kfs*9	ENSG00000068489	ENST00000262293	Transcript	frameshift_variant	NA
chr17	58234015	58234017	*CA4*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	gao_et_al_P7	p.F72del	ENSG00000167434	ENST00000300900	Transcript	inframe_deletion	NA
chr17	59841511	59841511	*WSCD1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A58V	ENSG00000179314	ENST00000574946	Transcript	missense_variant	benign(0.231)
chr17	61744387	61744387	*MAP3K3*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.E190Sfs*59	ENSG00000198909	ENST00000361357	Transcript	frameshift_variant	NA
chr17	62121389	62121389	*ERN1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.P965S	ENSG00000178607	ENST00000433197	Transcript	missense_variant	benign(0.002)
chr17	66426137	66426137	*WIPI1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.T322M	ENSG00000070540	ENST00000262139	Transcript	missense_variant	benign(0.406)
chr17	72595422	72595422	*TMEM95*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.T128Pfs*42	ENSG00000182896	ENST00000330767	Transcript	frameshift_variant	NA
chr17	73460600	73460600	*FGF11*	Nonsense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R186*	ENSG00000161958	ENST00000293829	Transcript	stop_gained	NA
chr17	74003204	74003204	*EVPL*	Missense_Mutation	.	SNP	C	C	T	rs201900469	gao_et_al_P7	p.V2028I	ENSG00000167880	ENST00000301607	Transcript	missense_variant	benign(0)
chr17	74961222	74961222	*FXR2*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.P540Qfs*32	ENSG00000129245	ENST00000250113	Transcript	frameshift_variant	NA
chr17	78028623	78028623	*CHD3*	Splice_Site	.	SNP	T	T	C	novel	gao_et_al_P7	NA	ENSG00000170004	ENST00000380358	Transcript	splice_donor_variant	NA
chr17	79263605	79263605	*SLC38A10*	Missense_Mutation	.	SNP	C	C	T	rs569770411	gao_et_al_P7	p.G35S	ENSG00000157637	ENST00000374759	Transcript	missense_variant	probably_damaging(1)
chr17	86616844	86616844	*SPDYE4*	Missense_Mutation	.	SNP	G	G	A	rs346940479	gao_et_al_P7	p.A6V	ENSG00000183318	ENST00000328794	Transcript	missense_variant	possibly_damaging(0.499)
chr18	13068107	13068107	*CEP192*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.W1543C	ENSG00000101639	ENST00000506447	Transcript	missense_variant	probably_damaging(1)
chr18	14851862	14851862	*ANKRD30B*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.D1188Y	ENSG00000180777	ENST00000358984	Transcript	missense_variant	probably_damaging(0.996)
chr18	19762928	19762928	*GATA6*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.T515I	ENSG00000141448	ENST00000269216	Transcript	missense_variant	probably_damaging(0.997)
chr18	24056513	24056513	*KCTD1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R92Q	ENSG00000134504	ENST00000408011	Transcript	missense_variant	probably_damaging(1)
chr18	30913143	30913143	*CCDC178*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.M292Wfs*3	ENSG00000166960	ENST00000383096	Transcript	frameshift_variant	NA
chr18	31325835	31325835	*ASXL3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.T2008I	ENSG00000141431	ENST00000269197	Transcript	missense_variant	benign(0.022)
chr18	31491411	31491411	*MYOM1*	Splice_Site	.	SNP	A	A	G	novel	gao_et_al_P7	p.X634_splice	ENSG00000101605	ENST00000356443	Transcript	splice_donor_variant	NA
chr18	48584732	48584732	*SMAD4*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.S271Kfs*2	ENSG00000141646	ENST00000342988	Transcript	frameshift_variant	NA
chr18	52918968	52918968	*ZBTB14*	In_Frame_Del	.	DEL	TCT	TCT	-	novel	gao_et_al_P7	p.E103del	ENSG00000198081	ENST00000357006	Transcript	inframe_deletion	NA
chr18	56816778	56816778	*SEC11C*	Missense_Mutation	.	SNP	G	G	A	rs375344740	gao_et_al_P7	p.V41M	ENSG00000166562	ENST00000587834	Transcript	missense_variant	possibly_damaging(0.868)
chr18	58039374	58039374	*MC4R*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A70V	ENSG00000166603	ENST00000299766	Transcript	missense_variant	possibly_damaging(0.862)
chr18	63489354	63489354	*CDH7*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.E221D	ENSG00000081138	ENST00000397968	Transcript	missense_variant	probably_damaging(0.961)
chr18	72775783	72775783	*ZNF407*	Missense_Mutation	.	SNP	G	G	A	rs371814141	gao_et_al_P7	p.E2036K	ENSG00000215421	ENST00000299687	Transcript	missense_variant	benign(0.174)
chr18	77895154	77895154	*ADNP2*	Missense_Mutation	.	SNP	G	G	A	rs372050062	gao_et_al_P7	p.V620M	ENSG00000101544	ENST00000262198	Transcript	missense_variant	possibly_damaging(0.704)
chr19	10578271	10578271	*PDE4A*	Frame_Shift_Del	.	DEL	G	G	-	rs200139989	gao_et_al_P7	p.S881Qfs*92	ENSG00000065989	ENST00000352831	Transcript	frameshift_variant	NA
chr19	11436202	11436202	*RAB3D*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R178C	ENSG00000105514	ENST00000222120	Transcript	missense_variant	benign(0.135)
chr19	11461607	11461607	*CCDC159*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R117H	ENSG00000183401	ENST00000588790	Transcript	missense_variant	benign(0.035)
chr19	13414640	13414640	*CACNA1A*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.G682Afs*15	ENSG00000141837	ENST00000360228	Transcript	frameshift_variant	NA
chr19	14685387	14685387	*APC2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G1746D	ENSG00000115266	ENST00000535453	Transcript	missense_variant	benign(0.055)
chr19	14758173	14758173	*EMR3*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.S235Vfs*15	ENSG00000131355	ENST00000253673	Transcript	frameshift_variant	NA
chr19	14910638	14910638	*OR7C1*	Frame_Shift_Del	.	DEL	A	A	-	rs534928853	gao_et_al_P7	p.F104Lfs*12	ENSG00000127530	ENST00000248073	Transcript	frameshift_variant	NA
chr19	15482788	15482788	*AKAP8*	Missense_Mutation	.	SNP	C	C	T	rs560438541	gao_et_al_P7	p.R338H	ENSG00000105127	ENST00000269701	Transcript	missense_variant	probably_damaging(0.948)

chr19	16905358	16905358	*NWD1*	Missense_Mutation	.	SNP	G	G	A	rs191339575	gao_et_al_P7	p.A1100T	ENSG00000188039	ENST00000524140	Transcript	missense_variant	benign(0.394)
chr19	19136394	19136394	*SUGP2*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.I255Yfs*4	ENSG00000064607	ENST00000601879	Transcript	frameshift_variant	NA
chr19	20229801	20229802	*ZNF90*	Frame_Shift_Del	.	DEL	CT	CT	-	novel	gao_et_al_P7	p.Y481Qfs*6	ENSG00000213988	ENST00000418063	Transcript	frameshift_variant	NA
chr19	33108538	33108538	*ANKRD27*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.V670A	ENSG00000105186	ENST00000306065	Transcript	missense_variant	benign(0.418)
chr19	34263031	34263031	*CHST8*	Missense_Mutation	.	SNP	G	G	A	rs558009314	gao_et_al_P7	p.R113H	ENSG00000124302	ENST00000262622	Transcript	missense_variant	probably_damaging(0.912)
chr19	34890232	34890232	*GPI*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.P475S	ENSG00000105220	ENST00000415930	Transcript	missense_variant	probably_damaging(0.989)
chr19	35175412	35175413	*ZNF302*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.S160Vfs*6	ENSG00000089335	ENST00000505242	Transcript	frameshift_variant	NA
chr19	36111212	36111212	*HAUS5*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.P545L	ENSG00000249115	ENST00000203166	Transcript	missense_variant	benign(0.014)
chr19	36124023	36124023	*RBM42*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.L185I	ENSG00000126254	ENST00000262633	Transcript	missense_variant	possibly_damaging(0.791)
chr19	36276205	36276205	*ARHGAP33*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.G614Afs*18	ENSG00000004777	ENST00000314737	Transcript	frameshift_variant	NA
chr19	36278313	36278313	*ARHGAP33*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.S788N	ENSG00000004777	ENST00000314737	Transcript	missense_variant	benign(0.304)
chr19	36322568	36322568	*NPHS1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R1088Q	ENSG00000161270	ENST00000378910	Transcript	missense_variant	benign(0.003)
chr19	37406932	37406932	*TJP3*	Missense_Mutation	.	SNP	C	C	T	rs148288309	gao_et_al_P7	p.R601C	ENSG00000105289	ENST00000589378	Transcript	missense_variant	probably_damaging(1)
chr19	39559563	39559563	*DAPK3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R301C	ENSG00000167657	ENST00000545797	Transcript	missense_variant	possibly_damaging(0.726)
chr19	40354361	40354362	*FCGBP*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	gao_et_al_P7	NA	ENSG00000090920	ENST00000221347	Transcript	frameshift_variant	NA
chr19	45136365	45136365	*PLIN4*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.V99M	ENSG00000167676	ENST00000301286	Transcript	missense_variant	benign(0.094)
chr19	47503744	47503746	*ARHGAP35*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	gao_et_al_P7	p.F1436del	ENSG00000160007	ENST00000404338	Transcript	inframe_deletion	NA
chr19	48198189	48198190	*GLTSCR1*	Frame_Shift_Ins	.	INS	-	-	G	novel	gao_et_al_P7	p.A979Gfs*86	ENSG00000063169	ENST00000396720	Transcript	frameshift_variant	NA
chr19	49131298	49131298	*SPHK2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.T243M	ENSG00000063176	ENST00000245222	Transcript	missense_variant	probably_damaging(0.99)
chr19	50100691	50100691	*PRR12*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.H1035Tfs*188	ENSG00000126464	ENST00000418929	Transcript	frameshift_variant	NA
chr19	51984736	51984736	*CEACAM18*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.T225A	ENSG00000213822	ENST00000451626	Transcript	missense_variant	benign(0.091)
chr19	52869608	52869608	*ZNF610*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.R326M	ENSG00000167554	ENST00000404036	Transcript	missense_variant	benign(0.326)
chr19	53762248	53762248	*VN1R2*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.T207K	ENSG00000196131	ENST00000341702	Transcript	missense_variant	benign(0.003)
chr19	55815036	55815036	*BRSK1*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.R379Gfs*9	ENSG00000160469	ENST00000309383	Transcript	frameshift_variant	NA
chr19	55912912	55912913	*UBE2S*	Frame_Shift_Ins	.	INS	-	-	C	novel	gao_et_al_P7	p.P188Rfs*5	ENSG00000108106	ENST00000264552	Transcript	frameshift_variant	NA
chr19	56319223	56319223	*NLRP11*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P7	p.L667V	ENSG00000179873	ENST00000443188	Transcript	missense_variant	benign(0.113)
chr19	56423853	56423853	*NLRP13*	Missense_Mutation	.	SNP	C	C	T	rs150988752	gao_et_al_P7	p.D444N	ENSG00000173572	ENST00000342929	Transcript	missense_variant	benign(0.024)
chr19	57133272	57133272	*ZNF71*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R206H	ENSG00000197951	ENST00000328070	Transcript	missense_variant	probably_damaging(0.998)
chr19	58437885	58437885	*ZNF418*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R555Q	ENSG00000196724	ENST00000396147	Transcript	missense_variant	benign(0.136)
chr19	7671182	7671182	*CAMSAP3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A143V	ENSG00000076826	ENST00000446248	Transcript	missense_variant	probably_damaging(0.966)
chr19	989838	989838	*WDR18*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.S133I	ENSG00000065268	ENST00000251289	Transcript	missense_variant	probably_damaging(0.94)
chr2	102029458	102029458	*RFX8*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.G213C	ENSG00000196460	ENST00000428343	Transcript	missense_variant	benign(0.053)
chr2	108487495	108487495	*RGPD4*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A1012V	ENSG00000196862	ENST00000408999	Transcript	missense_variant	benign(0.003)
chr2	128471170	128471170	*WDR33*	Missense_Mutation	.	SNP	G	G	A	rs373594035	gao_et_al_P7	p.R1099C	ENSG00000136709	ENST00000322313	Transcript	missense_variant	possibly_damaging(0.876)
chr2	136566433	136566433	*LCT*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G1162R	ENSG00000115850	ENST00000264162	Transcript	missense_variant	probably_damaging(1)
chr2	141079562	141079562	*LRP1B*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.N4204D	ENSG00000168702	ENST00000389484	Transcript	missense_variant	benign(0.292)

chr2	165551295	165551296	*COBLL1*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.Q908Sfs*24	ENSG00000082438	ENST00000342193	Transcript	frameshift_variant	NA
chr2	168106247	168106248	*XIRP2*	Frame_Shift_Ins	.	INS	-	-	AC	novel	gao_et_al_P7	p.Q2783Hfs*46	ENSG00000163092	ENST00000409195	Transcript	frameshift_variant	NA
chr2	182542972	182542972	*NEUROD1*	Frame_Shift_Del	.	DEL	G	G	-	rs201174472	gao_et_al_P7	p.H206Tfs*56	ENSG00000162992	ENST00000295108	Transcript	frameshift_variant	NA
chr2	192012838	192012838	*STAT4*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R31Q	ENSG00000138378	ENST00000392320	Transcript	missense_variant	probably_damaging(0.999)
chr2	200188600	200188600	*SATB2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.E490K	ENSG00000119042	ENST00000417098	Transcript	missense_variant	probably_damaging(0.987)
chr2	202149799	202149799	*CASP8*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F415Lfs*26	ENSG00000064012	ENST00000358485	Transcript	frameshift_variant	NA
chr2	210561667	210561667	*MAP2*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.T1474Qfs*14	ENSG00000078018	ENST00000360351	Transcript	frameshift_variant	NA
chr2	210798649	210798649	*UNC80*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G1967D	ENSG00000144406	ENST00000439458	Transcript	missense_variant	probably_damaging(0.994)
chr2	219127671	219127671	*GPBAR1*	Nonsense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.W75*	ENSG00000179921	ENST00000522678	Transcript	stop_gained	NA
chr2	219508772	219508772	*ZNF142*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R823W	ENSG00000115568	ENST00000411696	Transcript	missense_variant	possibly_damaging(0.689)
chr2	231077625	231077625	*SP110*	Frame_Shift_Ins	.	INS	-	-	G	novel	gao_et_al_P7	p.Q146Sfs*13	ENSG00000135899	ENST00000258381	Transcript	frameshift_variant	NA
chr2	234915574	234915574	*TRPM8*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P7	p.K1070*	ENSG00000144481	ENST00000324695	Transcript	stop_gained	NA
chr2	235950498	235950498	*SH3BP4*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.P362H	ENSG00000130147	ENST00000409212	Transcript	missense_variant	probably_damaging(0.992)
chr2	238688156	238688156	*LRRFIP1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A635V	ENSG00000124831	ENST00000308482	Transcript	missense_variant	benign(0.048)
chr2	239054422	239054422	*KLHL30*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R367C	ENSG00000168427	ENST00000409223	Transcript	missense_variant	probably_damaging(0.995)
chr2	241492420	241492420	*ANKMY1*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.W42R	ENSG00000144504	ENST00000391987	Transcript	missense_variant	probably_damaging(0.999)
chr2	38178783	38178783	*RMDN2*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F144Lfs*13	ENSG00000115841	ENST00000234195	Transcript	frameshift_variant	NA
chr2	48687007	48687007	*PPP1R21*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P7	p.K164*	ENSG00000162869	ENST00000294952	Transcript	stop_gained	NA
chr2	64109723	64109724	*UGP2*	Frame_Shift_Del	.	DEL	AA	AA	-	novel	gao_et_al_P7	p.L129Dfs*6	ENSG00000169764	ENST00000337130	Transcript	frameshift_variant	NA
chr2	67630497	67630497	*ETAA1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.L228S	ENSG00000143971	ENST00000272342	Transcript	missense_variant	benign(0.093)
chr2	74842219	74842219	*M1AP*	Frame_Shift_Del	.	DEL	TG	TG	-	novel	gao_et_al_P7	p.Q100Efs*77	ENSG00000159374	ENST00000290536	Transcript	frameshift_variant	NA
chr2	75425841	75425841	*TACR1*	Missense_Mutation	.	SNP	G	G	T	rs200411690	gao_et_al_P7	p.L74M	ENSG00000115353	ENST00000305249	Transcript	missense_variant	probably_damaging(1)
chr2	88874270	88874270	*EIF2AK3*	Frame_Shift_Del	.	DEL	CT	CT	-	novel	gao_et_al_P7	p.R911Efs*20	ENSG00000172071	ENST00000303236	Transcript	frameshift_variant	NA
chr2	97526594	97526594	*SEMA4C*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.P759Lfs*36	ENSG00000168758	ENST00000305476	Transcript	frameshift_variant	NA
chr2	97911213	97911213	*ANKRD36*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.Y1630C	ENSG00000135976	ENST00000420699	Transcript	missense_variant	benign(0.005)
chr20	18424086	18424086	*DZANK1*	Frame_Shift_Del	.	DEL	G	G	-	rs190534960	gao_et_al_P7	p.P219Hfs*44	ENSG00000089091	ENST00000262547	Transcript	frameshift_variant	NA
chr20	23472525	23472525	*CST8*	Missense_Mutation	.	SNP	C	C	T	rs574083273	gao_et_al_P7	p.A74V	ENSG00000125815	ENST00000246012	Transcript	missense_variant	benign(0.092)
chr20	31671214	31671214	*BPIFB4*	Frame_Shift_Del	.	DEL	C	C	-	rs139974951	gao_et_al_P7	p.P73Qfs*160	ENSG00000186191	ENST00000375483	Transcript	frameshift_variant	NA
chr20	33337356	33337356	*NCOA6*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.T881M	ENSG00000198646	ENST00000374796	Transcript	missense_variant	probably_damaging(0.998)
chr20	39987370	39987370	*LPIN3*	Missense_Mutation	.	SNP	G	G	A	rs371258106	gao_et_al_P7	p.R807Q	ENSG00000132793	ENST00000373257	Transcript	missense_variant	benign(0.372)
chr20	40050266	40050266	*CHD6*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.D1670G	ENSG00000124177	ENST00000373233	Transcript	missense_variant	benign(0)
chr20	48467301	48467301	*SLC9A8*	Frame_Shift_Del	.	DEL	T	T	-	rs564652819	gao_et_al_P7	p.F182Lfs*16	ENSG00000197818	ENST00000417961	Transcript	frameshift_variant	NA
chr20	48505609	48505609	*SLC23A2*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.I412Sfs*4	ENSG00000089057	ENST00000379333	Transcript	frameshift_variant	NA
chr20	54579062	54579062	*CBLN4*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.S56P	ENSG00000054803	ENST00000064571	Transcript	missense_variant	benign(0.239)
chr20	59486299	59486299	*MCM8*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.Q394R	ENSG00000125885	ENST00000378896	Transcript	missense_variant	benign(0.053)
chr20	62199835	62199835	*HELZ2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R536C	ENSG00000130589	ENST00000467148	Transcript	missense_variant	possibly_damaging(0.862)

chr20	62493530	62493530	*ABHD16B*	Missense_Mutation	.	SNP	G	G	A	rs142426403	gao_et_al_P7	p.V213M	ENSG00000183260	ENST00000369916	Transcript	missense_variant	benign(0.384)
chr21	16338330	16338330	*NRIP1*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.E729Rfs*5	ENSG00000180530	ENST00000400202	Transcript	frameshift_variant	NA
chr21	30341860	30341860	*LTN1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F459Lfs*7	ENSG00000198862	ENST00000389194	Transcript	frameshift_variant	NA
chr21	32638591	32638591	*TIAM1*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P7	p.G233A	ENSG00000156299	ENST00000286827	Transcript	missense_variant	benign(0.019)
chr21	34882122	34882122	*GART*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K807Rfs*7	ENSG00000159131	ENST00000381831	Transcript	frameshift_variant	NA
chr21	43413579	43413579	*ZBTB21*	Missense_Mutation	.	SNP	G	G	A	rs148545576	gao_et_al_P7	p.P209L	ENSG00000173276	ENST00000310826	Transcript	missense_variant	benign(0.002)
chr21	43714712	43714712	*ABCG1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.V584I	ENSG00000160179	ENST00000361802	Transcript	missense_variant	possibly_damaging(0.6)
chr21	47974538	47974538	*DIP2A*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.P1069S	ENSG00000160305	ENST00000417564	Transcript	missense_variant	probably_damaging(0.992)
chr22	20100507	20100507	*TRMT2A*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R525W	ENSG00000099899	ENST00000252136	Transcript	missense_variant	probably_damaging(0.999)
chr22	21991341	21991341	*CCDC116*	Missense_Mutation	.	SNP	g	g	T	novel	gao_et_al_P7	p.K608N	ENSG00000161180	ENST00000292779	Transcript	missense_variant	unknown(0)
chr22	31658637	31658637	*LIMK2*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.V219Sfs*40	ENSG00000182541	ENST00000340552	Transcript	frameshift_variant	NA
chr22	41973855	41973855	*PMM1*	Missense_Mutation	.	SNP	T	T	C	rs199731490	gao_et_al_P7	p.D208G	ENSG00000100417	ENST00000216259	Transcript	missense_variant	benign(0.102)
chr22	50277679	50277679	*ZBED4*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F125Lfs*16	ENSG00000100426	ENST00000216268	Transcript	frameshift_variant	NA
chr3	101284698	101284698	*TRMT10C*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R358H	ENSG00000174173	ENST00000309922	Transcript	missense_variant	benign(0.243)
chr3	108682419	108682419	*MORC1*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.I881Kfs*37	ENSG00000114487	ENST00000232603	Transcript	frameshift_variant	NA
chr3	108724131	108724131	*MORC1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.L600Wfs*5	ENSG00000114487	ENST00000232603	Transcript	frameshift_variant	NA
chr3	113187080	113187080	*SPICE1*	Missense_Mutation	.	SNP	C	C	T	rs376071843	gao_et_al_P7	p.R354H	ENSG00000163611	ENST00000295872	Transcript	missense_variant	benign(0.424)
chr3	113789641	113789643	*QTRTD1*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	gao_et_al_P7	p.L181del	ENSG00000151576	ENST00000485050	Transcript	inframe_deletion	NA
chr3	119134317	119134317	*ARHGAP31*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.V1181M	ENSG00000031081	ENST00000264245	Transcript	missense_variant	benign(0.17)
chr3	122288286	122288288	*DTX3L*	In_Frame_Del	.	DEL	AGA	AGA	-	novel	gao_et_al_P7	p.E451del	ENSG00000163840	ENST00000296161	Transcript	inframe_deletion	NA
chr3	124952158	124952158	*ZNF148*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.L471*	ENSG00000163848	ENST00000360647	Transcript	frameshift_variant	NA
chr3	127819446	127819446	*RUVBL1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R249W	ENSG00000175792	ENST00000322623	Transcript	missense_variant	probably_damaging(0.989)
chr3	128810021	128810021	*RAB43*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.L188Cfs*12	ENSG00000172780	ENST00000315150	Transcript	frameshift_variant	NA
chr3	130403135	130403135	*PIK3R4*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R1189H	ENSG00000196455	ENST00000356763	Transcript	missense_variant	probably_damaging(0.977)
chr3	134670615	134670615	*EPHB1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A176T	ENSG00000154928	ENST00000398015	Transcript	missense_variant	probably_damaging(0.983)
chr3	137843592	137843594	*A4GNT*	In_Frame_Del	.	DEL	CTC	CTC	-	novel	gao_et_al_P7	p.E179del	ENSG00000118017	ENST00000236709	Transcript	inframe_deletion	NA
chr3	148545857	148545857	*CPB1*	Missense_Mutation	.	SNP	C	C	T	rs146537927	gao_et_al_P7	p.T47M	ENSG00000153002	ENST00000491148	Transcript	missense_variant	benign(0.355)
chr3	150421516	150421516	*FAM194A*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P7	p.E57V	ENSG00000163645	ENST00000295910	Transcript	missense_variant	benign(0.192)
chr3	151112597	151112598	*MED12L*	In_Frame_Ins	.	INS	-	-	GCA	novel	gao_et_al_P7	p.L1886_Q1887insQ	ENSG00000144893	ENST00000474524	Transcript	inframe_insertion	NA
chr3	154032978	154032978	*DHX36*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F155Lfs*26	ENSG00000174953	ENST00000496811	Transcript	frameshift_variant	NA
chr3	175473050	175473050	*NAALADL2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R678H	ENSG00000177694	ENST00000454872	Transcript	missense_variant	benign(0.004)
chr3	181430716	181430716	*SOX2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G190S	ENSG00000181449	ENST00000325404	Transcript	missense_variant	benign(0.015)
chr3	183855703	183855703	*EIF2B5*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.N177Mfs*4	ENSG00000145191	ENST00000273783	Transcript	frameshift_variant	NA
chr3	186006602	186006602	*DGKG*	Frame_Shift_Del	.	DEL	G	G	-	rs190526753	gao_et_al_P7	p.V148Sfs*14	ENSG00000058866	ENST00000265022	Transcript	frameshift_variant	NA
chr3	186953596	186953596	*MASP1*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.G688Dfs*53	ENSG00000127241	ENST00000296280	Transcript	frameshift_variant	NA
chr3	190967873	190967873	*OSTN*	Missense_Mutation	.	SNP	G	G	A	rs145144111	gao_et_al_P7	p.R122Q	ENSG00000188729	ENST00000339051	Transcript	missense_variant	possibly_damaging(0.68)

chr3	30691872	30691872	*TGFBR2*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.K153Sfs*35	ENSG00000163513	ENST00000359013	Transcript	frameshift_variant	NA
chr3	41277224	41277224	*CTNNB1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R565C	ENSG00000168036	ENST00000349496	Transcript	missense_variant	possibly_damaging(0.887)
chr3	44489683	44489683	*ZNF445*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.F494L	ENSG00000185219	ENST00000425708	Transcript	missense_variant	benign(0.153)
chr3	46902222	46902222	*MYL3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G84D	ENSG00000160808	ENST00000395869	Transcript	missense_variant	probably_damaging(1)
chr3	48895160	48895160	*SLC25A20*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A297T	ENSG00000178537	ENST00000319017	Transcript	missense_variant	benign(0.004)
chr3	49053694	49053694	*DALRD3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R409H	ENSG00000178149	ENST00000341949	Transcript	missense_variant	probably_damaging(1)
chr3	49723112	49723112	*MST1*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.N435Tfs*91	ENSG00000173531	ENST00000449682	Transcript	frameshift_variant	NA
chr3	49736984	49736984	*RNF123*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R283Q	ENSG00000164068	ENST00000327697	Transcript	missense_variant	benign(0.001)
chr3	50379857	50379857	*ZMYND10*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.T282A	ENSG00000004838	ENST00000237749	Transcript	missense_variant	benign(0.41)
chr3	51457794	51457794	*VPRBP*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.P428L	ENSG00000145041	ENST00000335891	Transcript	missense_variant	probably_damaging(0.959)
chr3	52398724	52398724	*DNAH1*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P7	p.N1772T	ENSG00000114841	ENST00000420323	Transcript	missense_variant	benign(0.316)
chr3	52550119	52550119	*STAB1*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.V1339Cfs*252	ENSG00000010327	ENST00000321725	Transcript	frameshift_variant	NA
chr3	53757832	53757832	*CACNA1D*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.L656M	ENSG00000157388	ENST00000288139	Transcript	missense_variant	probably_damaging(0.999)
chr3	67559272	67559272	*SUCLG2*	Missense_Mutation	.	SNP	T	T	C	rs143813883	gao_et_al_P7	p.Q239R	ENSG00000172340	ENST00000493112	Transcript	missense_variant	probably_damaging(0.979)
chr3	71804090	71804090	*GPR27*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.Y300Tfs*21	ENSG00000170837	ENST00000304411	Transcript	frameshift_variant	NA
chr3	77657038	77657038	*ROBO2*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.P1094Qfs*95	ENSG00000185008	ENST00000487694	Transcript	frameshift_variant	NA
chr4	103500100	103500100	*NFKB1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.V212M	ENSG00000109320	ENST00000226574	Transcript	missense_variant	probably_damaging(0.997)
chr4	109767366	109767366	*COL25A1*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.G482C	ENSG00000188517	ENST00000399132	Transcript	missense_variant	probably_damaging(1)
chr4	118005517	118005517	*TRAM1L1*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.R345Efs*14	ENSG00000174599	ENST00000310754	Transcript	frameshift_variant	NA
chr4	119609096	119609096	*METTL14*	Missense_Mutation	.	SNP	G	G	A	rs200462174	gao_et_al_P7	p.D29N	ENSG00000145388	ENST00000388822	Transcript	missense_variant	probably_damaging(0.985)
chr4	123128369	123128369	*KIAA1109*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.A535S	ENSG00000138688	ENST00000264501	Transcript	missense_variant	probably_damaging(0.91)
chr4	129012266	129012266	*LARP1B*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R157W	ENSG00000138709	ENST00000326639	Transcript	missense_variant	benign(0.308)
chr4	143235866	143235866	*INPP4B*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G141E	ENSG00000109452	ENST00000513000	Transcript	missense_variant	benign(0.033)
chr4	158256907	158256907	*GRIA2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A451T	ENSG00000120251	ENST00000296526	Transcript	missense_variant	benign(0.008)
chr4	184587567	184587567	*TRAPPC11*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.V121A	ENSG00000168538	ENST00000334690	Transcript	missense_variant	benign(0.153)
chr4	2939958	2939958	*NOP14*	3'UTR	.	DEL	A	A	-	novel	gao_et_al_P7	NA	ENSG00000087269	ENST00000416614	Transcript	3_prime_UTR_variant	NA
chr4	38774956	38774956	*TLR10*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.A753Hfs*28	ENSG00000174123	ENST00000308973	Transcript	frameshift_variant	NA
chr4	41984182	41984182	*DCAF4L1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R125W	ENSG00000182308	ENST00000333141	Transcript	missense_variant	probably_damaging(0.995)
chr4	435916	435917	*ZNF721*	Frame_Shift_Del	.	DEL	GG	GG	-	novel	gao_et_al_P7	NA	ENSG00000182903	ENST00000511833	Transcript	frameshift_variant	NA
chr4	47589133	47589133	*ATP10D*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.S1284F	ENSG00000145246	ENST00000273859	Transcript	missense_variant	possibly_damaging(0.899)
chr4	74014742	74014742	*ANKRD17*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.L452S	ENSG00000132466	ENST00000358602	Transcript	missense_variant	probably_damaging(0.999)
chr4	80905986	80905986	*ANTXR2*	Frame_Shift_Ins	.	INS	-	-	G	rs312262690	gao_et_al_P7	p.A359Rfs*13	ENSG00000163297	ENST00000307333	Transcript	frameshift_variant	NA
chr4	88996773	88996773	*PKD2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R945H	ENSG00000118762	ENST00000237596	Transcript	missense_variant	possibly_damaging(0.893)
chr4	941630	941630	*TMEM175*	Missense_Mutation	.	SNP	C	C	T	rs542936413	gao_et_al_P7	p.R35C	ENSG00000127419	ENST00000264771	Transcript	missense_variant	probably_damaging(1)
chr5	111506649	111506649	*EPB41L4A*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.H555N	ENSG00000129595	ENST00000261486	Transcript	missense_variant	benign(0.33)
chr5	118483094	118483094	*DMXL1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.S947L	ENSG00000172869	ENST00000311085	Transcript	missense_variant	possibly_damaging(0.715)

chr5	134015305	134015305	*SEC24A*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.V423A	ENSG00000113615	ENST00000398844	Transcript	missense_variant	benign(0.071)
chr5	138163322	138163322	*CTNNA1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R326H	ENSG00000044115	ENST00000302763	Transcript	missense_variant	probably_damaging(0.997)
chr5	140237321	140237321	*PCDHA10*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A563V	ENSG00000250120	ENST00000307360	Transcript	missense_variant	benign(0.005)
chr5	140263777	140263777	*PCDHA13*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A642T	ENSG00000239389	ENST00000289272	Transcript	missense_variant	benign(0.015)
chr5	140532017	140532017	*PCDHB6*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.E727K	ENSG00000113211	ENST00000231136	Transcript	missense_variant	benign(0.064)
chr5	140574360	140574360	*PCDHB10*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.E745D	ENSG00000120324	ENST00000239446	Transcript	missense_variant	benign(0.062)
chr5	140724711	140724711	*PCDHGA3*	Missense_Mutation	.	SNP	G	G	A	rs369622113	gao_et_al_P7	p.V371M	ENSG00000254245	ENST00000253812	Transcript	missense_variant	probably_damaging(0.992)
chr5	140725881	140725881	*PCDHGA3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A761T	ENSG00000254245	ENST00000253812	Transcript	missense_variant	benign(0.053)
chr5	140797741	140797742	*PCDHGB7*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.L106Ffs*19	ENSG00000254122	ENST00000398594	Transcript	frameshift_variant	NA
chr5	140812373	140812373	*PCDHGA12*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P7	p.N683Y	ENSG00000253159	ENST00000252085	Transcript	missense_variant	benign(0.009)
chr5	140870510	140870510	*PCDHGC5*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R568Q	ENSG00000240764	ENST00000252087	Transcript	missense_variant	benign(0.016)
chr5	145477814	145477814	*PLAC8L1*	Missense_Mutation	.	SNP	C	C	T	rs144848795	gao_et_al_P7	p.R54Q	ENSG00000173261	ENST00000311450	Transcript	missense_variant	possibly_damaging(0.567)
chr5	145969652	145969652	*PPP2R2B*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	NA	ENSG00000156475	ENST00000336640	Transcript	frameshift_variant	NA
chr5	146775200	146775200	*DPYSL3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A630T	ENSG00000113657	ENST00000343218	Transcript	missense_variant	benign(0.008)
chr5	149491	149491	*LPCAT1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A133T	ENSG00000153395	ENST00000283415	Transcript	missense_variant	probably_damaging(1)
chr5	150028358	150028358	*SYNPO*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A418V	ENSG00000171992	ENST00000394243	Transcript	missense_variant	benign(0.014)
chr5	150672992	150672992	*SLC36A3*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.E113*	ENSG00000186334	ENST00000377713	Transcript	stop_gained	NA
chr5	154181832	154181832	*LARP1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R584H	ENSG00000155506	ENST00000336314	Transcript	missense_variant	probably_damaging(0.999)
chr5	167855773	167855773	*WWC1*	Nonsense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R661*	ENSG00000113645	ENST00000521089	Transcript	stop_gained	NA
chr5	176940733	176940733	*DDX41*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.D351N	ENSG00000183258	ENST00000507955	Transcript	missense_variant	benign(0.343)
chr5	179260184	179260184	*SQSTM1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A303T	ENSG00000161011	ENST00000389805	Transcript	missense_variant	benign(0)
chr5	179315313	179315313	*TBC1D9B*	Splice_Site	.	SNP	C	C	A	novel	gao_et_al_P7	p.X349_splice	ENSG00000197226	ENST00000356834	Transcript	splice_acceptor_variant	NA
chr5	180687318	180687318	*TRIM52*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.Y166C	ENSG00000183718	ENST00000327767	Transcript	missense_variant	possibly_damaging(0.784)
chr5	244929	244929	*CDH10*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F526Sfs*3	ENSG00000040731	ENST00000264463	Transcript	frameshift_variant	NA
chr5	269061	269061	*CDH9*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.T257M	ENSG00000113100	ENST00000231021	Transcript	missense_variant	probably_damaging(0.925)
chr5	313231	313231	*CDH6*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R702W	ENSG00000113361	ENST00000265071	Transcript	missense_variant	probably_damaging(0.998)
chr5	349339	349339	*DNAJC21*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.N35Ifs*14	ENSG00000168724	ENST00000382021	Transcript	frameshift_variant	NA
chr5	358746	358746	*IL7R*	Frame_Shift_Del	.	DEL	TG	TG	-	novel	gao_et_al_P7	p.L263Mfs*6	ENSG00000168685	ENST00000303115	Transcript	frameshift_variant	NA
chr5	360110	360110	*IRX1*	Frame_Shift_Ins	.	INS	-	-	C	novel	gao_et_al_P7	p.Q467Afs*40	ENSG00000170549	ENST00000302006	Transcript	frameshift_variant	NA
chr5	373074	373074	*NUP155*	In_Frame_Del	.	DEL	TCT	TCT	-	novel	gao_et_al_P7	p.E957del	ENSG00000113569	ENST00000231498	Transcript	inframe_deletion	NA
chr5	433034	433034	*AHRR*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.L384F	ENSG00000063438	ENST00000316418	Transcript	missense_variant	benign(0.098)
chr5	475728	475728	*SLC9A3*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P7	p.I734Sfs*68	ENSG00000066230	ENST00000264938	Transcript	frameshift_variant	NA
chr5	561818	561818	*MAP3K1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G1356D	ENSG00000095015	ENST00000399503	Transcript	missense_variant	probably_damaging(1)
chr5	618766	618766	*LRRC70*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P7	p.E469D	ENSG00000186105	ENST00000334994	Transcript	missense_variant	possibly_damaging(0.875)
chr5	632565	632565	*HTR1A*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.A319Pfs*26	ENSG00000178394	ENST00000323865	Transcript	frameshift_variant	NA
chr5	661111	661111	*NSUN2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.P394H	ENSG00000037474	ENST00000264670	Transcript	missense_variant	probably_damaging(0.992)

chr5	68868366	68868366	*GTF2H2C*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.M153I	ENSG00000183474	ENST00000510979	Transcript	missense_variant	benign(0.006)
chr5	74400949	74400950	*ANKRD31*	Frame_Shift_Ins	.	INS	-	-	T	rs530301594	gao_et_al_P7	p.Q1479Tfs*12	ENSG00000145700	ENST00000506364	Transcript	frameshift_variant	NA
chr5	76129525	76129525	*F2RL1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R365C	ENSG00000164251	ENST00000296677	Transcript	missense_variant	probably_damaging(1)
chr5	76254662	76254662	*CRHBP*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.V214A	ENSG00000145708	ENST00000274368	Transcript	missense_variant	benign(0.006)
chr5	78746859	78746859	*HOMER1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.N83S	ENSG00000152413	ENST00000334082	Transcript	missense_variant	probably_damaging(0.991)
chr5	95743939	95743939	*PCSK1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A395V	ENSG00000175426	ENST00000311106	Transcript	missense_variant	benign(0.336)
chr5	96090374	96090374	*CAST*	In_Frame_Del	.	DEL	AAG	AAG	-	novel	gao_et_al_P7	p.E507del	ENSG00000153113	ENST00000395812	Transcript	inframe_deletion	NA
chr6	108214755	108214755	*SEC63*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K535Nfs*28	ENSG00000025796	ENST00000369002	Transcript	frameshift_variant	NA
chr6	108214774	108214774	*SEC63*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K529Rfs*4	ENSG00000025796	ENST00000369002	Transcript	frameshift_variant	NA
chr6	110943335	110943335	*CDK19*	Nonsense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R356*	ENSG00000155111	ENST00000368911	Transcript	stop_gained	NA
chr6	111587361	111587361	*KIAA1919*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.C202Vfs*4	ENSG00000173214	ENST00000368847	Transcript	frameshift_variant	NA
chr6	115659441	115659441	*TMEM170B*	Frame_Shift_Del	.	DEL	TGTT	TGTT	-	novel	gao_et_al_P7	p.F48Sfs*8	ENSG00000205269	ENST00000379426	Transcript	frameshift_variant	NA
chr6	116756905	116756905	*DSE*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R425H	ENSG00000111817	ENST00000331677	Transcript	missense_variant	probably_damaging(0.917)
chr6	125379193	125379193	*RNF217*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.H116Y	ENSG00000146373	ENST00000359704	Transcript	missense_variant	possibly_damaging(0.908)
chr6	135784283	135784284	*AHI1*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.T304Nfs*6	ENSG00000135541	ENST00000367800	Transcript	frameshift_variant	NA
chr6	143486315	143486315	*AIG1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G132R	ENSG00000146416	ENST00000357847	Transcript	missense_variant	probably_damaging(0.978)
chr6	146275963	146275964	*SHPRH*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.P167Tfs*6	ENSG00000146414	ENST00000367505	Transcript	frameshift_variant	NA
chr6	160496889	160496889	*IGF2R*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R1726Q	ENSG00000197081	ENST00000356956	Transcript	missense_variant	probably_damaging(0.996)
chr6	161501996	161501996	*MAP3K4*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P7	p.E727D	ENSG00000085511	ENST00000392142	Transcript	missense_variant	possibly_damaging(0.685)
chr6	167550589	167550589	*CCR6*	Missense_Mutation	.	SNP	G	G	A	rs545727839	gao_et_al_P7	p.E291K	ENSG00000112486	ENST00000341935	Transcript	missense_variant	benign(0.006)
chr6	167790057	167790057	*TCP10*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R185W	ENSG00000203690	ENST00000397829	Transcript	missense_variant	benign(0.005)
chr6	35050962	35050962	*ANKS1A*	Nonsense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R956*	ENSG00000064999	ENST00000360359	Transcript	stop_gained	NA
chr6	37250063	37250063	*TBC1D22B*	Frame_Shift_Ins	.	INS	-	-	C	novel	gao_et_al_P7	p.M178Nfs*22	ENSG00000065491	ENST00000373491	Transcript	frameshift_variant	NA
chr6	38883056	38883056	*DNAH8*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.I3133Nfs*4	ENSG00000124721	ENST00000359357	Transcript	frameshift_variant	NA
chr6	43166448	43166448	*CUL9*	Missense_Mutation	.	SNP	C	C	T	rs537266929	gao_et_al_P7	p.R969C	ENSG00000112659	ENST00000252050	Transcript	missense_variant	possibly_damaging(0.582)
chr6	43172205	43172205	*CUL9*	Missense_Mutation	.	SNP	C	C	T	rs368858642	gao_et_al_P7	p.R1423C	ENSG00000112659	ENST00000252050	Transcript	missense_variant	probably_damaging(1)
chr6	50791208	50791208	*TFAP2B*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.L57P	ENSG00000008196	ENST00000393655	Transcript	missense_variant	benign(0.03)
chr6	80751897	80751897	*TTK*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	NA	ENSG00000112742	ENST00000369798	Transcript	frameshift_variant	NA
chr6	84870551	84870551	*KIAA1009*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.I921Nfs*9	ENSG00000135315	ENST00000403245	Transcript	frameshift_variant	NA
chr6	84881347	84881347	*KIAA1009*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P7	p.F753V	ENSG00000135315	ENST00000403245	Transcript	missense_variant	benign(0.006)
chr6	84896233	84896233	*KIAA1009*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F406Lfs*8	ENSG00000135315	ENST00000403245	Transcript	frameshift_variant	NA
chr6	97676884	97676884	*MMS22L*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P7	p.Y642F	ENSG00000146263	ENST00000275053	Transcript	missense_variant	benign(0.143)
chr7	100779016	100779016	*SERPINE1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A341T	ENSG00000106366	ENST00000223095	Transcript	missense_variant	benign(0.406)
chr7	102462538	102462538	*FBXL13*	Missense_Mutation	.	SNP	C	C	T	rs77788049	gao_et_al_P7	p.G656D	ENSG00000161040	ENST00000313221	Transcript	missense_variant	probably_damaging(0.992)
chr7	105177156	105177156	*RINT1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.I78T	ENSG00000135249	ENST00000257700	Transcript	missense_variant	possibly_damaging(0.948)
chr7	110763761	110763761	*LRRN3*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.R312Efs*3	ENSG00000173114	ENST00000451085	Transcript	frameshift_variant	NA

chr7	110764578	110764578	*LRRN3*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.N584D	ENSG00000173114	ENST00000451085	Transcript	missense_variant	benign(0.105)
chr7	117432019	117432019	*CTTNBP2*	Nonsense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.Q411*	ENSG00000077063	ENST00000160373	Transcript	stop_gained	NA
chr7	121650722	121650722	*PTPRZ1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.G541D	ENSG00000106278	ENST00000393386	Transcript	missense_variant	benign(0.005)
chr7	139083424	139083425	*C7orf55-LUC7L2*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P7	p.F82Lfs*2	ENSG00000146963	ENST00000354926	Transcript	frameshift_variant	NA
chr7	141424864	141424864	*WEE2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.L420F	ENSG00000214102	ENST00000397541	Transcript	missense_variant	probably_damaging(1)
chr7	148951130	148951130	*ZNF212*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.C371Y	ENSG00000170260	ENST00000335870	Transcript	missense_variant	probably_damaging(1)
chr7	150095013	150095013	*ZNF775*	Missense_Mutation	.	SNP	C	C	T	rs527417474	gao_et_al_P7	p.R482C	ENSG00000196456	ENST00000329630	Transcript	missense_variant	benign(0.005)
chr7	151874148	151874148	*KMT2C*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.E2798Dfs*25	ENSG00000055609	ENST00000262189	Transcript	frameshift_variant	NA
chr7	27224636	27224636	*HOXA11*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.M43T	ENSG00000005073	ENST00000006015	Transcript	missense_variant	benign(0.117)
chr7	45122153	45122153	*NACAD*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.P1209Qfs*295	ENSG00000136274	ENST00000490531	Transcript	frameshift_variant	NA
chr7	49842307	49842307	*VWC2*	Missense_Mutation	.	SNP	G	G	T	rs375100335	gao_et_al_P7	p.V233L	ENSG00000188730	ENST00000340652	Transcript	missense_variant	possibly_damaging(0.873)
chr7	56127999	56127999	*CCT6A*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.N368S	ENSG00000146731	ENST00000275603	Transcript	missense_variant	benign(0.266)
chr7	6205177	6205177	*CYTH3*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.P324H	ENSG00000008256	ENST00000350796	Transcript	missense_variant	possibly_damaging(0.85)
chr7	64152285	64152285	*ZNF107*	5'UTR	.	DEL	A	A	-	rs377379477	gao_et_al_P7	NA	ENSG00000196247	ENST00000395391	Transcript	5_prime_UTR_variant	NA
chr7	64388187	64388188	*ZNF273*	Frame_Shift_Del	.	DEL	AG	AG	-	novel	gao_et_al_P7	p.G162Lfs*2	ENSG00000198039	ENST00000476120	Transcript	frameshift_variant	NA
chr7	65617292	65617294	*CRCP*	In_Frame_Del	.	DEL	AGA	AGA	-	novel	gao_et_al_P7	p.K134del	ENSG00000241258	ENST00000395326	Transcript	inframe_deletion	NA
chr7	70853334	70853334	*WBSCR17*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.T179M	ENSG00000185274	ENST00000333538	Transcript	missense_variant	probably_damaging(0.95)
chr7	810254	810254	*HEATR2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.G644W	ENSG00000164818	ENST00000297440	Transcript	missense_variant	probably_damaging(0.995)
chr7	87280245	87280245	*RUNDC3B*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R77Q	ENSG00000105784	ENST00000338056	Transcript	missense_variant	probably_damaging(0.985)
chr7	87529652	87529652	*DBF4*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.Q266R	ENSG00000006634	ENST00000265728	Transcript	missense_variant	benign(0.097)
chr7	91652135	91652135	*AKAP9*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P7	p.N1320K	ENSG00000127914	ENST00000356239	Transcript	missense_variant	benign(0.009)
chr7	94183880	94183880	*CASD1*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.S707*	ENSG00000127995	ENST00000297273	Transcript	stop_gained	NA
chr7	94185017	94185017	*CASD1*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.C783Vfs*21	ENSG00000127995	ENST00000297273	Transcript	frameshift_variant	NA
chr7	97833302	97833302	*LMTK2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.M1429I	ENSG00000164715	ENST00000297293	Transcript	missense_variant	benign(0.004)
chr8	10465997	10465997	*RP1L1*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.S1871P	ENSG00000183638	ENST00000382483	Transcript	missense_variant	unknown(0)
chr8	11689115	11689115	*FDFT1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.T323I	ENSG00000079459	ENST00000220584	Transcript	missense_variant	benign(0.029)
chr8	139263124	139263124	*FAM135B*	Missense_Mutation	.	SNP	C	C	T	rs184738153	gao_et_al_P7	p.V168I	ENSG00000147724	ENST00000395297	Transcript	missense_variant	benign(0.004)
chr8	139729082	139729082	*COL22A1*	Nonsense_Mutation	.	SNP	G	G	A	rs373752145	gao_et_al_P7	p.R796*	ENSG00000169436	ENST00000303045	Transcript	stop_gained	NA
chr8	142367803	142367803	*GPR20*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A74V	ENSG00000204882	ENST00000377741	Transcript	missense_variant	probably_damaging(1)
chr8	17829972	17829972	*PCM1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R1240H	ENSG00000078674	ENST00000325083	Transcript	missense_variant	benign(0.002)
chr8	22472975	22472975	*CCAR2*	Frame_Shift_Ins	.	INS	-	-	C	novel	gao_et_al_P7	p.R417Pfs*49	ENSG00000158941	ENST00000308511	Transcript	frameshift_variant	NA
chr8	27888776	27888776	*NUGGC*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F6325fs*2	ENSG00000189233	ENST00000413272	Transcript	frameshift_variant	NA
chr8	32247188	32247188	*CSMD1*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.L984S	ENSG00000183117	ENST00000537824	Transcript	missense_variant	probably_damaging(1)
chr8	53025769	53025769	*ST18*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.I1045V	ENSG00000147488	ENST00000276480	Transcript	missense_variant	benign(0.424)
chr8	54975925	54975925	*LYPLA1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.P60S	ENSG00000120992	ENST00000316963	Transcript	missense_variant	possibly_damaging(0.758)
chr8	56863054	56863054	*LYN*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.E110Kfs*15	ENSG00000254087	ENST00000519728	Transcript	frameshift_variant	NA

chr8	68992721	68992721	*PREX2*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.S565Rfs*10	ENSG00000046889	ENST00000288368	Transcript	frameshift_variant	NA
chr8	72234106	72234106	*EYA1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.Y94C	ENSG00000104313	ENST00000340726	Transcript	missense_variant	possibly_damaging(0.756)
chr8	79710316	79710316	*IL7*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P7	p.D46E	ENSG00000104432	ENST00000263851	Transcript	missense_variant	probably_damaging(0.935)
chr8	82572810	82572810	*IMPA1*	Missense_Mutation	.	SNP	T	T	G	rs202127208	gao_et_al_P7	p.D279A	ENSG00000133731	ENST00000449740	Transcript	missense_variant	probably_damaging(0.99)
chr8	82627040	82627040	*ZFAND1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.D120Ifs*26	ENSG00000104231	ENST00000220669	Transcript	frameshift_variant	NA
chr8	86114470	86114471	*E2F5*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.N110Kfs*13	ENSG00000133740	ENST00000416274	Transcript	frameshift_variant	NA
chr9	105767031	105767031	*CYLC2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R79C	ENSG00000155833	ENST00000374798	Transcript	missense_variant	probably_damaging(0.997)
chr9	111903637	111903637	*FRRS1L*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.G283D	ENSG00000260230	ENST00000561981	Transcript	missense_variant	probably_damaging(0.999)
chr9	117930	117930	*FOXD4*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.A64T	ENSG00000170122	ENST00000382500	Transcript	missense_variant	benign(0.036)
chr9	118949988	118949988	*PAPPA*	Missense_Mutation	.	SNP	C	C	A	rs445154	gao_et_al_P7	p.P324H	ENSG00000182752	ENST00000328252	Transcript	missense_variant	probably_damaging(0.977)
chr9	139299142	139299142	*SDCCAG3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R337W	ENSG00000165689	ENST00000357365	Transcript	missense_variant	possibly_damaging(0.705)
chr9	139302341	139302344	*SDCCAG3*	Frame_Shift_Del	.	DEL	CTCT	CTCT	-	novel	gao_et_al_P7	p.R112Sfs*3	ENSG00000165689	ENST00000357365	Transcript	frameshift_variant	NA
chr9	146189 73	146189 73	*ZDHHC21*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P7	p.N263K	ENSG00000175893	ENST00000380916	Transcript	missense_variant	benign(0.081)
chr9	2086947	2086947	*SMARCA2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.T882I	ENSG00000080503	ENST00000382203	Transcript	missense_variant	benign(0.15)
chr9	32632433	32632433	*TAF1L*	Missense_Mutation	.	SNP	G	G	A	rs535964605	gao_et_al_P7	p.R1049C	ENSG00000122728	ENST00000242310	Transcript	missense_variant	probably_damaging(1)
chr9	405015	405015	*DOCK8*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.F1113Lfs*2	ENSG00000107099	ENST00000453981	Transcript	frameshift_variant	NA
chr9	5080636	5080638	*JAK2*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	gao_et_al_P7	p.S797del	ENSG00000096968	ENST00000381652	Transcript	inframe_deletion	NA
chr9	95069255	95069255	*NOL8*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P7	p.K913Rfs*4	ENSG00000198000	ENST00000545558	Transcript	frameshift_variant	NA
chr9	99581245	99581245	*ZNF782*	Missense_Mutation	.	SNP	T	T	C	rs138537807	gao_et_al_P7	p.S354G	ENSG00000196597	ENST00000481138	Transcript	missense_variant	benign(0.001)
chrX	100088273	100088273	*CSTF2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R438C	ENSG00000101811	ENST00000372972	Transcript	missense_variant	probably_damaging(0.982)
chrX	103360001	103360001	*ZCCHC18*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.S400F	ENSG00000166707	ENST00000537356	Transcript	missense_variant	benign(0.031)
chrX	104464304	104464304	*TEX13A*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P7	p.G192*	ENSG00000133149	ENST00000413579	Transcript	stop_gained	NA
chrX	114425871	114425871	*RBMXL3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.R623C	ENSG00000175718	ENST00000424776	Transcript	missense_variant	benign(0.255)
chrX	118724502	118724502	*NKRF*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.V311M	ENSG00000186416	ENST00000542113	Transcript	missense_variant	probably_damaging(0.974)
chrX	118774684	118774684	*Sep/06*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.A253V	ENSG00000125354	ENST00000343984	Transcript	missense_variant	benign(0.026)
chrX	119389024	119389024	*ZBTB33*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R585H	ENSG00000177485	ENST00000326624	Transcript	missense_variant	benign(0.025)
chrX	120009178	120009178	*CT47B1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.P116L	ENSG00000236446	ENST00000371311	Transcript	missense_variant	probably_damaging(0.998)
chrX	128602849	128602849	*SMARCA1*	Nonsense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.Q867*	ENSG00000102038	ENST00000371122	Transcript	stop_gained	NA
chrX	129155009	129155009	*BCORL1*	Frame_Shift_Del	.	DEL	G	G	-	novel	gao_et_al_P7	p.A1166Lfs*56	ENSG00000085185	ENST00000540052	Transcript	frameshift_variant	NA
chrX	135445742	135445742	*GPR112*	Missense_Mutation	.	SNP	A	A	T	rs201153873	gao_et_al_P7	p.T2462S	ENSG00000156920	ENST00000394143	Transcript	missense_variant	possibly_damaging(0.508)
chrX	138644174	138644174	*F9*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P7	p.Y444H	ENSG00000101981	ENST00000218099	Transcript	missense_variant	probably_damaging(1)
chrX	14883151	14883151	*FANCB*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P7	p.V161A	ENSG00000181544	ENST00000398334	Transcript	missense_variant	benign(0.204)
chrX	149639163	149639164	*MAMLD1*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.G416Rfs*25	ENSG00000013619	ENST00000432680	Transcript	frameshift_variant	NA
chrX	152159281	152159281	*PNMA5*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R288C	ENSG00000198883	ENST00000439251	Transcript	missense_variant	probably_damaging(0.999)
chrX	15841214	15841214	*ZRSR2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R433H	ENSG00000169249	ENST00000307771	Transcript	missense_variant	unknown()
chrX	17745878	17745879	*NHS*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P7	p.N1199Kfs*5	ENSG00000188158	ENST00000380060	Transcript	frameshift_variant	NA

chrX	177501 33	177501 33	*NHS*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P7	p.L1481R	ENSG00000188158	ENST00000380060	Transcript	missense_variant	probably_damaging(1)
chrX	189618 91	189618 91	*PHKA2*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.F218Lfs*10	ENSG00000044446	ENST00000379942	Transcript	frameshift_variant	NA
chrX	341494 62	341494 62	*FAM47A*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.H312Y	ENSG00000185448	ENST00000346193	Transcript	missense_variant	benign(0.099)
chrX	373126 10	373126 11	*PRRG1*	Frame_Shift_Ins	.	INS	-	-	C	novel	gao_et_al_P7	p.P135Tfs*3	ENSG00000130962	ENST00000542554	Transcript	frameshift_variant	NA
chrX	506593 30	506593 30	*BMP15*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R301H	ENSG00000130385	ENST00000252677	Transcript	missense_variant	benign(0.031)
chrX	532235 99	532235 99	*KDM5C*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P7	p.R1254C	ENSG00000126012	ENST00000375401	Transcript	missense_variant	probably_damaging(0.998)
chrX	694973 06	694973 06	*ARR3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P7	p.P179L	ENSG00000120500	ENST00000307959	Transcript	missense_variant	benign(0.055)
chrX	695617 71	695617 71	*KIF4A*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P7	p.R419M	ENSG00000090889	ENST00000374403	Transcript	missense_variant	possibly_damaging(0.823)
chrX	845266 21	845266 21	*ZNF711*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P7	p.K693Nfs*3	ENSG00000147180	ENST00000373165	Transcript	frameshift_variant	NA
chr1	107201 16	107201 16	*CASZ1*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.Q328L	ENSG00000130940	ENST00000377022	Transcript	missense_variant	probably_damaging(0.942)
chr1	152082 899	152082 899	*TCHH*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.E932K	ENSG00000159450	ENST00000368804	Transcript	missense_variant	unknown(0)
chr1	161279 695	161279 695	*MPZ*	Translation_Start_Site	.	SNP	T	T	C	novel	gao_et_al_P3	p.M1?	ENSG00000158887	ENST00000533357	Transcript	initiator_codon_variant	unknown(0)
chr1	170695 497	170695 497	*PRRX1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.P185L	ENSG00000116132	ENST00000239461	Transcript	missense_variant	possibly_damaging(0.603)
chr1	171621 325	171621 325	*MYOC*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P3	p.S143R	ENSG00000034971	ENST00000375032	Transcript	missense_variant	benign(0.382)
chr1	177226 407	177226 407	*BRINP2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.S186C	ENSG00000198797	ENST00000361539	Transcript	missense_variant	possibly_damaging(0.819)
chr1	179077 356	179077 356	*ABL2*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P3	p.S1016A	ENSG00000143322	ENST00000502732	Transcript	missense_variant	benign(0)
chr1	182909 616	182909 616	*SHCBP1L*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.E206D	ENSG00000157060	ENST00000367547	Transcript	missense_variant	benign(0.034)
chr1	210412 865	210412 865	*SERTAD4*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.P68L	ENSG00000082497	ENST00000367012	Transcript	missense_variant	probably_damaging(0.997)
chr1	240969 626	240969 626	*RGS7*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.R361S	ENSG00000182901	ENST00000366565	Transcript	missense_variant	probably_damaging(0.998)
chr1	247875 888	247875 888	*OR6F1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.T57N	ENSG00000169214	ENST00000302084	Transcript	missense_variant	possibly_damaging(0.852)
chr1	373255 06	373255 06	*GRIK3*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.S300Y	ENSG00000163873	ENST00000373091	Transcript	missense_variant	benign(0.032)
chr1	630035 84	630035 84	*DOCK7*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.S1119Y	ENSG00000116641	ENST00000340370	Transcript	missense_variant	probably_damaging(0.997)
chr1	780989 04	780989 04	*ZZZ3*	Nonsense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.R46*	ENSG00000036549	ENST00000370801	Transcript	stop_gained	NA
chr1	863134 11	863134 11	*COL24A1*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.R1133S	ENSG00000171502	ENST00000370571	Transcript	missense_variant	benign(0.16)
chr10	115278 44	115278 44	*USP6NL*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P3	p.K261R	ENSG00000148429	ENST00000277575	Transcript	missense_variant	benign(0.202)
chr10	117045 845	117045 845	*ATRNL1*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.S785T	ENSG00000107518	ENST00000355044	Transcript	missense_variant	probably_damaging(0.993)
chr10	121571 432	121571 432	*INPP5F*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.F617L	ENSG00000198825	ENST00000361976	Transcript	missense_variant	probably_damaging(0.976)
chr10	122650 306	122650 306	*WDR11*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.K808*	ENSG00000120008	ENST00000263461	Transcript	stop_gained	NA
chr10	375079 29	375079 29	*ANKRD30A*	Nonsense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.E1041*	ENSG00000148513	ENST00000361713	Transcript	stop_gained	NA
chr10	719693 22	719693 22	*PPA1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P3	p.K211E	ENSG00000180817	ENST00000373232	Transcript	missense_variant	possibly_damaging(0.883)
chr10	987436 30	987436 30	*C10orf12*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P3	p.A828G	ENSG00000155640	ENST00000286067	Transcript	missense_variant	possibly_damaging(0.731)
chr11	111430 896	111430 896	*LAYN*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.D288Y	ENSG00000204381	ENST00000375615	Transcript	missense_variant	possibly_damaging(0.873)
chr11	189559 92	189559 92	*MRGPRX1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P3	p.S114G	ENSG00000170255	ENST00000302797	Transcript	missense_variant	benign(0.33)
chr11	553218 70	553218 70	*OR4C15*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.K30*	ENSG00000181939	ENST00000314644	Transcript	stop_gained	NA
chr11	589192 86	589192 86	*FAM111A*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.P49T	ENSG00000166801	ENST00000528737	Transcript	missense_variant	benign(0.032)
chr11	592455 42	592455 42	*OR4D10*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.L214I	ENSG00000254466	ENST00000530162	Transcript	missense_variant	possibly_damaging(0.651)

chr11	66029370	66029370	*KLC2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Q129L	ENSG00000174996	ENST00000417856	Transcript	missense_variant	possibly_damaging(0.724)
chr11	69628255	69628255	*ZNF215*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P3	p.L142V	ENSG00000149054	ENST00000278319	Transcript	missense_variant	benign(0.013)
chr11	92539564	92539564	*FAT3*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.S3044T	ENSG00000165323	ENST00000298047	Transcript	missense_variant	benign(0.042)
chr12	10467328	10467328	*KLRD1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.G159V	ENSG00000134539	ENST00000336164	Transcript	missense_variant	benign(0.363)
chr12	10568367	10568367	*KLRC3*	Missense_Mutation	.	SNP	C	C	T	rs370768044	gao_et_al_P3	p.R205H	ENSG00000205810	ENST00000381903	Transcript	missense_variant	benign(0.001)
chr12	25261756	25261756	*CASC1*	Missense_Mutation	.	SNP	A	A	C	rs1908947	gao_et_al_P3	p.V632G	ENSG00000118307	ENST00000395987	Transcript	missense_variant	possibly_damaging(0.607)
chr12	53865524	53865524	*PCBP2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.D333N	ENSG00000197111	ENST00000359462	Transcript	missense_variant	benign(0.253)
chr12	55714543	55714543	*OR6C1*	Nonsense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.Q54*	ENSG00000205330	ENST00000379668	Transcript	stop_gained	NA
chr12	57398203	57398203	*ZBTB39*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.G167S	ENSG00000166860	ENST00000300101	Transcript	missense_variant	benign(0.076)
chr12	58009473	58009473	*ARHGEF25*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Y445F	ENSG00000240771	ENST00000339732	Transcript	missense_variant	probably_damaging(0.999)
chr12	75444978	75444978	*KCNC2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.S269R	ENSG00000166006	ENST00000549446	Transcript	missense_variant	benign(0.01)
chr13	100188947	100188947	*TM9SF2*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P3	p.Y183D	ENSG00000125304	ENST00000376387	Transcript	missense_variant	possibly_damaging(0.723)
chr13	35630193	35630193	*NBEA*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.S340N	ENSG00000172915	ENST00000400445	Transcript	missense_variant	probably_damaging(0.999)
chr13	49039132	49039132	*RB1*	Splice_Site	.	SNP	A	A	T	novel	gao_et_al_P3	p.X738_splice	ENSG00000139687	ENST00000267163	Transcript	splice_acceptor_variant	NA
chr13	77671811	77671811	*MYCBP2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.L3122I	ENSG00000005810	ENST00000544440	Transcript	missense_variant	probably_damaging(0.977)
chr14	104501335	104501335	*TDRD9*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.H1220Y	ENSG00000156414	ENST00000409874	Transcript	missense_variant	benign(0.141)
chr14	23889185	23889185	*MYH7*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.S1199C	ENSG00000092054	ENST00000355349	Transcript	missense_variant	probably_damaging(0.991)
chr14	31062732	31062732	*G2E3*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.R139*	ENSG00000092140	ENST00000206595	Transcript	stop_gained	NA
chr14	53119866	53119866	*ERO1L*	Missense_Mutation	.	SNP	C	C	T	rs573952507	gao_et_al_P3	p.D326N	ENSG00000197930	ENST00000395686	Transcript	missense_variant	benign(0.006)
chr14	57696555	57696555	*EXOC5*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.P398L	ENSG00000070367	ENST00000413566	Transcript	missense_variant	benign(0.063)
chr14	79432465	79432465	*NRXN3*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.F458L	ENSG00000021645	ENST00000554719	Transcript	missense_variant	probably_damaging(0.934)
chr14	88406271	88406271	*GALC*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.Y630F	ENSG00000054983	ENST00000261304	Transcript	missense_variant	probably_damaging(0.953)
chr14	94158164	94158164	*UNC79*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.E2310K	ENSG00000133958	ENST00000256339	Transcript	missense_variant	benign(0.014)
chr15	22933599	22933599	*CYFIP1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.S203F	ENSG00000068793	ENST00000313077	Transcript	missense_variant	benign(0.438)
chr15	23811915	23811915	*MKRN3*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.F329Y	ENSG00000179455	ENST00000314520	Transcript	missense_variant	probably_damaging(0.998)
chr15	43294813	43294813	*UBR1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.C1200Y	ENSG00000159459	ENST00000290650	Transcript	missense_variant	probably_damaging(0.999)
chr15	59910556	59910556	*GCNT3*	Nonsense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.L40*	ENSG00000140297	ENST00000396065	Transcript	stop_gained	NA
chr15	68446015	68446015	*PIAS1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.D306Y	ENSG00000033800	ENST00000249636	Transcript	missense_variant	probably_damaging(0.997)
chr15	69238611	69238611	*SPESP1*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.S246R	ENSG00000258484	ENST00000310673	Transcript	missense_variant	benign(0.225)
chr15	71276516	71276516	*LRRC49*	Missense_Mutation	.	SNP	A	A	T	rs139665040	gao_et_al_P3	p.E368D	ENSG00000137821	ENST00000560369	Transcript	missense_variant	benign(0.001)
chr15	79185957	79185957	*MORF4L1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.N245I	ENSG00000185787	ENST00000331268	Transcript	missense_variant	benign(0.285)
chr15	79296332	79296332	*RASGRF1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.L770Q	ENSG00000058335	ENST00000419573	Transcript	missense_variant	probably_damaging(0.997)
chr15	89453053	89453053	*MFGE8*	Nonsense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.K59*	ENSG00000140545	ENST00000268150	Transcript	stop_gained	NA
chr16	30005626	30005626	*HIRIP3*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P3	p.S280R	ENSG00000149929	ENST00000279392	Transcript	missense_variant	benign(0.03)
chr16	70415643	70415643	*ST3GAL2*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P3	p.I334M	ENSG00000157350	ENST00000393640	Transcript	missense_variant	probably_damaging(0.999)
chr16	70601440	70601440	*SF3B3*	Splice_Site	.	SNP	G	G	A	novel	gao_et_al_P3	p.X984_splice	ENSG00000189091	ENST00000302516	Transcript	splice_donor_variant	NA

chr17	16470777	16470777	*ZNF287*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P3	p.E90G	ENSG00000141040	ENST00000395824	Transcript	missense_variant	benign(0.322)
chr17	16610855	16610855	*CCDC144A*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Q246L	ENSG00000170160	ENST00000443444	Transcript	missense_variant	benign(0.403)
chr17	16612137	16612137	*CCDC144A*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.K256*	ENSG00000170160	ENST00000443444	Transcript	stop_gained	NA
chr17	34942627	34942627	*GGNBP2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.H547L	ENSG00000005955	ENST00000304718	Transcript	missense_variant	benign(0.306)
chr17	39742880	39742880	*KRT14*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Y69*	ENSG00000186847	ENST00000167586	Transcript	stop_gained	NA
chr17	45249321	45249321	*CDC27*	Nonsense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.C71*	ENSG00000004897	ENST00000531206	Transcript	stop_gained	NA
chr17	5087138	5087138	*ZNF594*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.R138S	ENSG00000180626	ENST00000399604	Transcript	missense_variant	possibly_damaging(0.607)
chr17	63186309	63186309	*RGS9*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Q234L	ENSG00000108370	ENST00000262406	Transcript	missense_variant	benign(0.049)
chr17	7573976	7573976	*TP53*	Nonsense_Mutation	.	SNP	T	T	A	rs141402957	gao_et_al_P3	p.K351*	ENSG00000141510	ENST00000269305	Transcript	stop_gained	NA
chr17	80382276	80382276	*HEXDC*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P3	p.P31Lfs*6	ENSG00000169660	ENST00000337014	Transcript	frameshift_variant	NA
chr17	9821397	9821397	*GAS7*	Missense_Mutation	.	SNP	A	A	C	rs201170646	gao_et_al_P3	p.V413G	ENSG00000007237	ENST00000432992	Transcript	missense_variant	benign(0.02)
chr18	43532506	43532506	*EPG5*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.K371I	ENSG00000152223	ENST00000282041	Transcript	missense_variant	probably_damaging(0.991)
chr19	10791740	10791740	*ILF3*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.G335C	ENSG00000129351	ENST00000449870	Transcript	missense_variant	probably_damaging(1)
chr19	12692345	12692345	*ZNF490*	Nonsense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.K182*	ENSG00000188033	ENST00000311437	Transcript	stop_gained	NA
chr19	23542311	23542311	*ZNF91*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.T1157N	ENSG00000167232	ENST00000300619	Transcript	missense_variant	benign(0.164)
chr19	42213768	42213768	*CEACAM5*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Q78H	ENSG00000105388	ENST00000221992	Transcript	missense_variant	benign(0.133)
chr19	42265952	42265952	*CEACAM6*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.H260L	ENSG00000086548	ENST00000199764	Transcript	missense_variant	possibly_damaging(0.475)
chr19	44662079	44662079	*ZNF234*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.S637*	ENSG00000263002	ENST00000426739	Transcript	stop_gained	NA
chr19	52394652	52394652	*ZNF649*	Missense_Mutation	.	SNP	C	C	T	rs200081147	gao_et_al_P3	p.R246K	ENSG00000198093	ENST00000354957	Transcript	missense_variant	benign(0)
chr19	52618370	52618370	*ZNF616*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.H683Y	ENSG00000204611	ENST00000600228	Transcript	missense_variant	probably_damaging(0.998)
chr19	53572260	53572260	*ZNF160*	Nonsense_Mutation	.	SNP	G	G	T	rs377529146	gao_et_al_P3	p.Y509*	ENSG00000170949	ENST00000429604	Transcript	stop_gained	NA
chr19	54800102	54800102	*LILRA3*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.A422S	ENSG00000170866	ENST00000251390	Transcript	missense_variant	benign(0.002)
chr19	88421688	88421688	*OR2Z1*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P3	p.M260L	ENSG00000181733	ENST00000324060	Transcript	missense_variant	probably_damaging(0.99)
chr19	94531119	94531119	*ZNF559*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.G331E	ENSG00000188321	ENST00000393883	Transcript	missense_variant	benign(0.006)
chr2	101638818	101638818	*TBC1D8*	Missense_Mutation	.	SNP	C	C	T	rs572578268	gao_et_al_P3	p.A881T	ENSG00000204634	ENST00000376840	Transcript	missense_variant	probably_damaging(0.969)
chr2	135107441	135107441	*MGAT5*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Q393L	ENSG00000152127	ENST00000409645	Transcript	missense_variant	possibly_damaging(0.723)
chr2	152402471	152402471	*NEB*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P3	p.D6836E	ENSG00000183091	ENST00000397345	Transcript	missense_variant	benign(0.336)
chr2	166152544	166152544	*SCN2A*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.P71T	ENSG00000136531	ENST00000357398	Transcript	missense_variant	benign(0.272)
chr2	168104757	168104757	*XIRP2*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.S2285R	ENSG00000163092	ENST00000409195	Transcript	missense_variant	benign(0.057)
chr2	170667383	170667383	*SSB*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.K276*	ENSG00000138385	ENST00000409333	Transcript	stop_gained	NA
chr2	178083782	178083782	*HNRNPA3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.G327R	ENSG00000170144	ENST00000392524	Transcript	missense_variant	unknown(0)
chr2	54153162	54153162	*PSME4*	Splice_Site	.	SNP	T	T	A	novel	gao_et_al_P3	p.X532_splice	ENSG00000068878	ENST00000404125	Transcript	splice_acceptor_variant	NA
chr20	17614229	17614229	*RRBP1*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.Q396L	ENSG00000125844	ENST00000377807	Transcript	missense_variant	benign(0.145)
chr20	21306936	21306937	*XRN2*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P3	p.I34Dfs*4	ENSG00000088930	ENST00000377191	Transcript	frameshift_variant	NA
chr20	49576226	49576226	*MOCS3*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.G283W	ENSG00000124217	ENST00000244051	Transcript	missense_variant	probably_damaging(0.971)
chr22	18609478	18609478	*TUBA8*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.D245Y	ENSG00000183785	ENST00000330423	Transcript	missense_variant	probably_damaging(0.993)

chr22	28503714	28503714	*TTC28*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.L707M	ENSG00000100154	ENST00000397906	Transcript	missense_variant	probably_damaging(0.98)
chr22	32112945	32112945	*PRR14L*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.N294Y	ENSG00000183530	ENST00000327423	Transcript	missense_variant	benign(0.246)
chr3	100362368	100362368	*GPR128*	Splice_Site	.	SNP	A	A	T	novel	gao_et_al_P3	p.X280_splice	ENSG00000144820	ENST00000273352	Transcript	splice_acceptor_variant	NA
chr3	109019280	109019280	*DPPA2*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P3	p.N286S	ENSG00000163530	ENST00000478945	Transcript	missense_variant	benign(0.433)
chr3	119242472	119242472	*TIMMDC1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P3	p.E244Sfs*27	ENSG00000113845	ENST00000496664	Transcript	frameshift_variant	NA
chr3	130110117	130110117	*COL6A5*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.I838F	ENSG00000172752	ENST00000265379	Transcript	missense_variant	benign(0.439)
chr3	157160236	157160236	*PTX3*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.E205V	ENSG00000163661	ENST00000295927	Transcript	missense_variant	possibly_damaging(0.555)
chr3	164754198	164754198	*SI*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.W832R	ENSG00000090402	ENST00000264382	Transcript	missense_variant	benign(0.38)
chr3	183822032	183822032	*HTR3E*	Missense_Mutation	.	SNP	T	T	A	rs150933161	gao_et_al_P3	p.S114R	ENSG00000186038	ENST00000440596	Transcript	missense_variant	possibly_damaging(0.878)
chr3	470984 63	470984 63	*SETD2*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P3	p.S2271R	ENSG00000181555	ENST00000409792	Transcript	missense_variant	benign(0.145)
chr3	484987 69	484987 69	*ATRIP*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P3	p.H261P	ENSG00000164053	ENST00000320211	Transcript	missense_variant	benign(0.367)
chr3	583769 28	583769 28	*PXK*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P3	p.E174A	ENSG00000168297	ENST00000356151	Transcript	missense_variant	benign(0.001)
chr3	692710 50	692710 50	*FRMD4B*	Nonsense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P3	p.Y230*	ENSG00000114541	ENST00000398540	Transcript	stop_gained	NA
chr4	104064466	104064466	*CENPE*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.T1748K	ENSG00000138778	ENST00000265148	Transcript	missense_variant	benign(0.272)
chr4	119952989	119952989	*SYNPO2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.Q1020L	ENSG00000172403	ENST00000307142	Transcript	missense_variant	benign(0.149)
chr4	122784410	122784410	*BBS7*	Frame_Shift_Del	.	DEL	C	C	-	rs190999071	gao_et_al_P3	p.V43*	ENSG00000138686	ENST00000264499	Transcript	frameshift_variant	NA
chr4	143129636	143129636	*INPP4B*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.E338D	ENSG00000109452	ENST00000513000	Transcript	missense_variant	possibly_damaging(0.615)
chr4	146435811	146435811	*SMAD1*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.R16*	ENSG00000170365	ENST00000515385	Transcript	stop_gained	NA
chr4	155490819	155490820	*FGB*	Frame_Shift_Ins	.	INS	-	-	A	novel	gao_et_al_P3	p.V372Sfs*10	ENSG00000171564	ENST00000302068	Transcript	frameshift_variant	NA
chr4	16587600	16587600	*LDB2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.L187Q	ENSG00000169744	ENST00000304523	Transcript	missense_variant	probably_damaging(0.989)
chr4	169157404	169157404	*DDX60*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.K1511M	ENSG00000137628	ENST00000393743	Transcript	missense_variant	possibly_damaging(0.507)
chr4	175636719	175636719	*GLRA3*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.L165*	ENSG00000145451	ENST00000274093	Transcript	stop_gained	NA
chr4	367285	367285	*ZNF141*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.K353N	ENSG00000131127	ENST00000240499	Transcript	missense_variant	benign(0.303)
chr4	68456619	68456619	*STAP1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.H226L	ENSG00000035720	ENST00000265404	Transcript	missense_variant	probably_damaging(1)
chr4	89042878	89042878	*ABCG2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.L200I	ENSG00000118777	ENST00000237612	Transcript	missense_variant	probably_damaging(0.943)
chr5	40852365	40852365	*CARD6*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.L311I	ENSG00000132357	ENST00000254691	Transcript	missense_variant	benign(0.149)
chr5	56168691	56168691	*MAP3K1*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P3	p.R516Efs*41	ENSG00000095015	ENST00000399503	Transcript	frameshift_variant	NA
chr5	77298881	77298881	*AP3B1*	Splice_Site	.	SNP	T	T	A	novel	gao_et_al_P3	p.X1044_splice	ENSG00000132842	ENST00000255194	Transcript	splice_acceptor_variant	NA
chr6	131481322	131481322	*AKAP7*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.P92Q	ENSG00000118507	ENST00000431975	Transcript	missense_variant	probably_damaging(1)
chr6	132031821	132031821	*CTAGE9*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.E113*	ENSG00000236761	ENST00000314099	Transcript	stop_gained	NA
chr6	138539396	138539396	*PBOV1*	Nonsense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.L46*	ENSG00000254440	ENST00000527246	Transcript	stop_gained	NA
chr6	168431451	168431451	*KIF25*	Splice_Site	.	SNP	A	A	T	novel	gao_et_al_P3	p.X31_splice	ENSG00000125337	ENST00000443060	Transcript	splice_acceptor_variant	NA
chr6	40697209	40697209	*FAM217A*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.F246Y	ENSG00000145975	ENST00000274673	Transcript	missense_variant	probably_damaging(0.966)
chr6	44228270	44228270	*NFKBIE*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.A372V	ENSG00000146232	ENST00000275015	Transcript	missense_variant	possibly_damaging(0.643)
chr6	45405687	45405687	*RUNX2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.K195M	ENSG00000124813	ENST00000371438	Transcript	missense_variant	probably_damaging(0.999)
chr6	75841768	75841768	*COL12A1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.V1942E	ENSG00000111799	ENST00000322507	Transcript	missense_variant	probably_damaging(0.977)

chr6	99850588	99850588	*PNISR*	Splice_Site	.	SNP	T	T	A	novel	gao_et_al_P3	p.X386_splice	ENSG00000132424	ENST00000369239	Transcript	splice_acceptor_variant	NA
chr7	106710749	106710749	*PRKAR2B*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.R111W	ENSG00000005249	ENST00000265717	Transcript	missense_variant	probably_damaging(0.969)
chr7	121650713	121650713	*PTPRZ1*	Nonsense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.L538*	ENSG00000106278	ENST00000393386	Transcript	stop_gained	NA
chr7	143772104	143772104	*OR2A25*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.E264D	ENSG00000221933	ENST00000408898	Transcript	missense_variant	benign(0.262)
chr7	151860374	151860374	*KMT2C*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.E3430K	ENSG00000055609	ENST00000262189	Transcript	missense_variant	possibly_damaging(0.648)
chr7	155473385	155473385	*RBM33*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.E117V	ENSG00000184863	ENST00000401878	Transcript	missense_variant	probably_damaging(0.988)
chr7	22651011	22651011	*MAD1L1*	Nonsense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.K79*	ENSG00000002822	ENST00000406869	Transcript	stop_gained	NA
chr7	37890011	37890011	*NME8*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.E22V	ENSG00000086288	ENST00000199447	Transcript	missense_variant	possibly_damaging(0.888)
chr7	42950096	42950096	*C7orf25*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.G193D	ENSG00000136197	ENST00000431882	Transcript	missense_variant	probably_damaging(1)
chr7	624184	624184	*PRKAR1B*	Nonsense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.K244*	ENSG00000188191	ENST00000406797	Transcript	stop_gained	NA
chr7	80439949	80439949	*SEMA3C*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P3	p.N173Tfs*6	ENSG00000075223	ENST00000265361	Transcript	frameshift_variant	NA
chr7	95625299	95625299	*DYNC1I1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.D312Y	ENSG00000158560	ENST00000324972	Transcript	missense_variant	probably_damaging(0.954)
chr8	100883091	100883091	*VPS13B*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.P3849Q	ENSG00000132549	ENST00000358544	Transcript	missense_variant	benign(0.181)
chr8	110437463	110437463	*PKHD1L1*	Splice_Site	.	SNP	T	T	A	novel	gao_et_al_P3	NA	ENSG00000205038	ENST00000378402	Transcript	splice_donor_variant	NA
chr8	17228672	17228672	*MTMR7*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P3	p.A62T	ENSG00000003987	ENST00000180173	Transcript	missense_variant	probably_damaging(0.947)
chr8	56668972	56668972	*TMEM68*	Splice_Site	.	SNP	T	T	A	novel	gao_et_al_P3	NA	ENSG00000167904	ENST00000334667	Transcript	splice_acceptor_variant	NA
chr8	70585385	70585385	*SLCO5A1*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P3	p.A756P	ENSG00000137571	ENST00000260126	Transcript	missense_variant	probably_damaging(0.954)
chr8	87755758	87755758	*CNGB3*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P3	p.P33L	ENSG00000170289	ENST00000320005	Transcript	missense_variant	benign(0.005)
chr9	10537632	10537632	*DMRT2*	Missense_Mutation	.	SNP	G	G	C	rs200011939	gao_et_al_P3	p.R189P	ENSG00000173253	ENST00000382251	Transcript	missense_variant	possibly_damaging(0.454)
chr9	125551477	125551477	*OR5C1*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.L89Q	ENSG00000148215	ENST00000373680	Transcript	missense_variant	benign(0.104)
chr9	131721347	131721347	*NUP188*	Nonsense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P3	p.Y173*	ENSG00000095319	ENST00000372577	Transcript	stop_gained	NA
chr9	138714799	138714799	*CAMSAP1*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.T570S	ENSG00000130559	ENST00000389532	Transcript	missense_variant	benign(0.012)
chr9	32634138	32634138	*TAF1L*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P3	p.D480E	ENSG00000122728	ENST00000242310	Transcript	missense_variant	benign(0.042)
chr9	33796673	33796673	*PRSS3*	Missense_Mutation	.	SNP	G	G	A	rs76740888	gao_et_al_P3	p.V82I	ENSG00000010438	ENST00000361005	Transcript	missense_variant	benign(0.153)
chr9	33797978	33797978	*PRSS3*	Missense_Mutation	.	SNP	G	G	A	rs145485932	gao_et_al_P3	p.V175I	ENSG00000010438	ENST00000361005	Transcript	missense_variant	benign(0.002)
chr9	35957983	35957983	*OR2S2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.V38E	ENSG00000122718	ENST00000341959	Transcript	missense_variant	possibly_damaging(0.675)
chr9	86518850	86518850	*KIF27*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.T195S	ENSG00000165115	ENST00000297814	Transcript	missense_variant	probably_damaging(0.999)
chr9	96392272	96392272	*PHF2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P3	p.E40V	ENSG00000197724	ENST00000359246	Transcript	missense_variant	unknown(0)
chrX	153627691	153627691	*RPL10*	Nonsense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.C12*	ENSG00000147403	ENST00000424325	Transcript	stop_gained	NA
chrX	22291150	22291150	*ZNF645*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P3	p.N14K	ENSG00000175809	ENST00000323684	Transcript	missense_variant	benign(0.124)
chrX	85386005	85386005	*KAL1*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P3	p.S333C	ENSG00000011201	ENST00000262648	Transcript	missense_variant	probably_damaging(0.94)
chrX	96684677	96684677	*DIAPH2*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P3	p.N1058K	ENSG00000147202	ENST00000324765	Transcript	missense_variant	possibly_damaging(0.872)
chrY	56057744	56057744	*PCDH11Y*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P3	p.Q1272K	ENSG00000099715	ENST00000215473	Transcript	missense_variant	probably_damaging(0.959)
chrY	69539733	69539733	*TBL1Y*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P3	p.G371V	ENSG00000092377	ENST00000383032	Transcript	missense_variant	probably_damaging(0.991)
chr1	11155555	11155555	*TTLL10*	Missense_Mutation	.	SNP	C	C	A	rs199586129	gao_et_al_P1	p.P114H	ENSG00000162571	ENST00000379290	Transcript	missense_variant	benign(0.425)
chr1	155581784	155581784	*MSTO1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.R191W	ENSG00000125459	ENST00000245564	Transcript	missense_variant	probably_damaging(0.987)

chr1	248366437	248366437	*OR2M3*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P1	p.T23S	ENSG00000228198	ENST00000456743	Transcript	missense_variant	benign(0.004)
chr1	28661177	28661177	*MED18*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P1	p.I108T	ENSG00000130772	ENST00000373842	Transcript	missense_variant	benign(0.096)
chr1	36553686	36553686	*TEKT2*	Missense_Mutation	.	SNP	A	A	G	rs200994339	gao_et_al_P1	p.T398A	ENSG00000092850	ENST00000207457	Transcript	missense_variant	benign(0.042)
chr1	45116416	45116416	*RNF220*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.A557V	ENSG00000187147	ENST00000355387	Transcript	missense_variant	benign(0.021)
chr10	102740756	102740756	*SEMA4G*	Splice_Site	.	DEL	T	T	-	novel	gao_et_al_P1	p.X548_splice	ENSG00000095539	ENST00000210633	Transcript	splice_donor_variant	NA
chr10	116335283	116335283	*ABLIM1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.R152Q	ENSG00000099204	ENST00000277895	Transcript	missense_variant	possibly_damaging(0.781)
chr11	15222437	15222437	*INSC*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P1	p.A301E	ENSG00000188487	ENST00000379554	Transcript	missense_variant	probably_damaging(0.939)
chr11	61908711	61908711	*OR52B2*	Missense_Mutation	.	SNP	C	C	T	rs201845183	gao_et_al_P1	p.R229H	ENSG00000255307	ENST00000530810	Transcript	missense_variant	benign(0.025)
chr11	67200489	67200489	*RPS6KB2*	Missense_Mutation	.	SNP	C	C	A	rs183360785	gao_et_al_P1	p.T228N	ENSG00000175634	ENST00000312629	Transcript	missense_variant	probably_damaging(0.994)
chr11	87517677	87517677	*ST5*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.S357N	ENSG00000166444	ENST00000534127	Transcript	missense_variant	benign(0.051)
chr12	123463073	123463073	*OGFOD2*	Missense_Mutation	.	SNP	C	C	T	rs199579636	gao_et_al_P1	p.S103L	ENSG00000111325	ENST00000397389	Transcript	missense_variant	possibly_damaging(0.736)
chr12	124422146	124422146	*CCDC92*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P1	p.A152V	ENSG00000119242	ENST00000238156	Transcript	missense_variant	probably_damaging(0.915)
chr14	64676760	64676760	*SYNE2*	Missense_Mutation	.	SNP	G	G	A	rs200152990	gao_et_al_P1	p.R6214K	ENSG00000054654	ENST00000358025	Transcript	missense_variant	benign(0.001)
chr14	95910934	95910934	*SYNE3*	Missense_Mutation	.	SNP	G	G	A	rs565608397	gao_et_al_P1	p.A555V	ENSG00000176438	ENST00000334258	Transcript	missense_variant	benign(0.002)
chr15	41823310	41823310	*RPAP1*	Missense_Mutation	.	SNP	G	G	A	rs567280087	gao_et_al_P1	p.P285L	ENSG00000103932	ENST00000304330	Transcript	missense_variant	benign(0.001)
chr15	42178079	42178079	*SPTBN5*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P1	p.S458R	ENSG00000137877	ENST00000320955	Transcript	missense_variant	probably_damaging(0.933)
chr15	49033856	49033856	*CEP152*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P1	p.M1345I	ENSG00000103995	ENST00000380950	Transcript	missense_variant	benign(0.2)
chr17	1198803	1198803	*TUSC5*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P1	p.Q136E	ENSG00000184811	ENST00000333813	Transcript	missense_variant	possibly_damaging(0.785)
chr17	30538164	30538164	*RHOT1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P1	p.C622F	ENSG00000126858	ENST00000358365	Transcript	missense_variant	unknown(0)
chr17	38520056	38520056	*GJD3*	Nonsense_Mutation	.	SNP	C	C	T	rs190167816	gao_et_al_P1	p.W4*	ENSG00000183153	ENST00000578689	Transcript	stop_gained	NA
chr17	45901636	45901636	*MRPL10*	Missense_Mutation	.	SNP	G	G	A	rs200394081	gao_et_al_P1	p.R251C	ENSG00000159111	ENST00000290208	Transcript	missense_variant	benign(0.007)
chr17	7216988	7216988	*GPS2*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P1	p.G178Dfs*167	ENSG00000132522	ENST00000380728	Transcript	frameshift_variant	NA
chr17	76793977	76793977	*DNAH2*	Missense_Mutation	.	SNP	G	G	A	rs530683645	gao_et_al_P1	p.R1626Q	ENSG00000183914	ENST00000572933	Transcript	missense_variant	benign(0.025)
chr19	50827192	50827192	*KCNC3*	Missense_Mutation	.	SNP	C	C	T	rs115351343	gao_et_al_P1	p.V340M	ENSG00000131398	ENST00000477616	Transcript	missense_variant	possibly_damaging(0.622)
chr2	136399306	136399306	*R3HDM1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.P474S	ENSG00000048991	ENST00000264160	Transcript	missense_variant	probably_damaging(0.979)
chr2	160269022	160269023	*BAZ2B*	In_Frame_Ins	.	INS	-	-	CAT	novel	gao_et_al_P1	p.V834_I835insD	ENSG00000123636	ENST00000392783	Transcript	inframe_insertion	NA
chr2	21232894	21232897	*APOB*	Frame_Shift_Del	.	DEL	AGCT	AGCT	-	novel	gao_et_al_P1	p.A2282Efs*3	ENSG00000084674	ENST00000232342	Transcript	frameshift_variant	NA
chr2	219870842	219870842	*CCDC108*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P1	p.S1608L	ENSG00000181378	ENST00000341552	Transcript	missense_variant	benign(0.003)
chr2	241463422	241463422	*ANKMY1*	Missense_Mutation	.	SNP	G	G	A	rs184584055	gao_et_al_P1	p.S482L	ENSG00000144504	ENST00000391987	Transcript	missense_variant	possibly_damaging(0.893)
chr22	38122252	38122252	*TRIOBP*	Missense_Mutation	.	SNP	C	C	T	rs200665858	gao_et_al_P1	p.P1230L	ENSG00000100106	ENST00000406386	Transcript	missense_variant	probably_damaging(0.999)
chr3	133835111	133835111	*NUP210*	Missense_Mutation	.	SNP	G	G	A	rs150421255	gao_et_al_P1	p.P1026L	ENSG00000132182	ENST00000254508	Transcript	missense_variant	benign(0.002)
chr3	36485033	36485033	*STAC*	Missense_Mutation	.	SNP	G	G	A	rs568735926	gao_et_al_P1	p.A97T	ENSG00000144681	ENST00000273183	Transcript	missense_variant	benign(0.001)
chr3	49698372	49698372	*BSN*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P1	p.F3032I	ENSG00000164061	ENST00000296452	Transcript	missense_variant	unknown(0)
chr3	64527574	64527574	*ADAMTS9*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P1	p.H1713N	ENSG00000163638	ENST00000498707	Transcript	missense_variant	benign(0.001)
chr3	69299222	69299222	*FRMD4B*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P1	p.I177T	ENSG00000114541	ENST00000398540	Transcript	missense_variant	benign(0.006)
chr3	96533486	96533486	*EPHA6*	Missense_Mutation	.	SNP	C	C	T	rs181119565	gao_et_al_P1	p.P7S	ENSG00000080224	ENST00000389672	Transcript	missense_variant	unknown(0)

chr4	107037487	107037487	*TBCK*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P1	p.R762W	ENSG00000145348	ENST00000273980	Transcript	missense_variant	benign(0.011)
chr5	150431801	150431801	*TNIP1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.R216Q	ENSG00000145901	ENST00000389378	Transcript	missense_variant	probably_damaging(0.996)
chr5	43245912	43245912	*NIM1K*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P1	p.V12E	ENSG00000177453	ENST00000512796	Transcript	missense_variant	benign(0.022)
chr6	159184344	159184344	*SYTL3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.T509I	ENSG00000164674	ENST00000297239	Transcript	missense_variant	benign(0.008)
chr6	7581242	7581242	*DSP*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P1	p.E1607K	ENSG00000096696	ENST00000379802	Transcript	missense_variant	benign(0.171)
chr7	124404960	124404960	*GPR37*	Missense_Mutation	.	SNP	G	G	A	rs143391902	gao_et_al_P1	p.A24V	ENSG00000170775	ENST00000303921	Transcript	missense_variant	possibly_damaging(0.739)
chr7	99711777	99711777	*TAF6*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P1	p.M56T	ENSG00000106290	ENST00000437822	Transcript	missense_variant	possibly_damaging(0.579)
chr8	41577222	41577222	*ANK1*	Missense_Mutation	.	SNP	T	T	C	rs555694301	gao_et_al_P1	p.K388R	ENSG00000029534	ENST00000265709	Transcript	missense_variant	probably_damaging(0.996)
chr9	130270384	130270384	*FAM129B*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P1	p.C512Afs*11	ENSG00000136830	ENST00000373312	Transcript	frameshift_variant	NA
chr9	15474039	15474039	*PSIP1*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P1	p.E276*	ENSG00000164985	ENST00000380733	Transcript	stop_gained	NA
chr9	43627656	43627656	*SPATA31A6*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P1	p.K344R	ENSG00000185775	ENST00000332857	Transcript	missense_variant	benign(0.094)
chr9	99582057	99582057	*ZNF782*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P1	p.D83V	ENSG00000196597	ENST00000481138	Transcript	missense_variant	benign(0.012)
chrX	103358931	103358931	*ZCCHC18*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P1	p.R43S	ENSG00000166707	ENST00000537356	Transcript	missense_variant	possibly_damaging(0.628)
chrX	140994341	140994341	*MAGEC1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P1	p.T384I	ENSG00000155495	ENST00000285879	Transcript	missense_variant	possibly_damaging(0.507)
chrX	34148967	34148967	*FAM47A*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P1	p.H477Y	ENSG00000185448	ENST00000346193	Transcript	missense_variant	possibly_damaging(0.888)
chrX	65242698	65242698	*VSIG4*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P1	p.V316A	ENSG00000155659	ENST00000374737	Transcript	missense_variant	benign(0.056)
chrX	92927886	92927886	*NAP1L3*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P1	p.N140H	ENSG00000186310	ENST00000373079	Transcript	missense_variant	probably_damaging(0.991)
chr1	1115555	1115555	*TTLL10*	Missense_Mutation	.	SNP	C	C	A	rs199586129	gao_et_al_P2	p.P114H	ENSG00000162571	ENST00000379290	Transcript	missense_variant	benign(0.425)
chr1	115393 1	115393 1	*SDF4*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P2	p.D273E	ENSG00000078808	ENST00000360001	Transcript	missense_variant	benign(0.049)
chr1	1397981	1397981	*ATAD3C*	Missense_Mutation	.	SNP	C	C	T	rs535863359	gao_et_al_P2	p.R328C	ENSG00000215915	ENST00000378785	Transcript	missense_variant	probably_damaging(0.953)
chr1	151318693	151318693	*RFX5*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R35Q	ENSG00000143390	ENST00000290524	Transcript	missense_variant	possibly_damaging(0.842)
chr1	202935085	202935085	*CYB5R1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.S92N	ENSG00000159348	ENST00000367249	Transcript	missense_variant	benign(0.009)
chr1	207930891	207930891	*CD46*	Missense_Mutation	.	SNP	C	C	T	rs116800126	gao_et_al_P2	p.T98I	ENSG00000117335	ENST00000322875	Transcript	missense_variant	benign(0.031)
chr1	247587277	247587277	*NLRP3*	Missense_Mutation	.	SNP	C	C	T	rs201867990	gao_et_al_P2	p.R178W	ENSG00000162711	ENST00000336119	Transcript	missense_variant	possibly_damaging(0.586)
chr1	28661177	28661177	*MED18*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P2	p.I108T	ENSG00000130772	ENST00000373842	Transcript	missense_variant	benign(0.096)
chr1	35915492	35915492	*KIAA0319L*	Missense_Mutation	.	SNP	G	G	A	rs144204083	gao_et_al_P2	p.R777W	ENSG00000142687	ENST00000325722	Transcript	missense_variant	possibly_damaging(0.806)
chr1	44071948	44071948	*PTPRF*	In_Frame_Del	.	DEL	GCG	GCG	-	novel	gao_et_al_P2	p.R1176del	ENSG00000142949	ENST00000359947	Transcript	inframe_deletion	NA
chr1	52881047	52881047	*PRPF38A*	Missense_Mutation	.	SNP	G	G	C	rs200048366	gao_et_al_P2	p.K295N	ENSG00000134748	ENST00000257181	Transcript	missense_variant	unknown(0)
chr1	53413744	53413744	*SCP2*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P2	p.Y64S	ENSG00000116171	ENST00000371514	Transcript	missense_variant	probably_damaging(0.984)
chr1	781135 0	781135 0	*CAMTA1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.R1594Q	ENSG00000171735	ENST00000303635	Transcript	missense_variant	probably_damaging(0.997)
chr10	100503697	100503697	*HPSE2*	Missense_Mutation	.	SNP	T	T	A	rs188784527	gao_et_al_P2	p.S243C	ENSG00000172987	ENST00000370552	Transcript	missense_variant	probably_damaging(0.923)
chr10	102740756	102740756	*SEMA4G*	Splice_Site	.	DEL	T	T	-	novel	gao_et_al_P2	p.X548_splice	ENSG00000095539	ENST00000210633	Transcript	splice_donor_variant	NA
chr10	116335283	116335283	*ABLIM1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R152Q	ENSG00000099204	ENST00000277895	Transcript	missense_variant	possibly_damaging(0.781)
chr10	95790999	95790999	*PLCE1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.G66R	ENSG00000138193	ENST00000371380	Transcript	missense_variant	benign(0.002)
chr11	118038916	118038916	*SCN2B*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.S111L	ENSG00000149575	ENST00000278947	Transcript	missense_variant	probably_damaging(0.983)
chr11	118343445	118343445	*KMT2A*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.N524S	ENSG00000118058	ENST00000534358	Transcript	missense_variant	benign(0.001)

chr11	12974385	12974385	NFRKB	Missense_Mutation	.	SNP	G	G	A	rs557840039	gao_et_al_P2	p.P803L	ENSG00000170322	ENST00000524794	Transcript	missense_variant	probably_damaging(0.958)
chr11	15222437	15222437	INSC	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P2	p.A301E	ENSG00000188487	ENST00000379554	Transcript	missense_variant	probably_damaging(0.939)
chr11	56237307	56237307	OR5M3	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P2	p.I223L	ENSG00000174937	ENST00000312240	Transcript	missense_variant	possibly_damaging(0.562)
chr11	6190871	6190871	OR52B2	Missense_Mutation	.	SNP	C	C	T	rs201845183	gao_et_al_P2	p.R229H	ENSG00000255307	ENST00000530810	Transcript	missense_variant	benign(0.025)
chr11	65674432	65674432	DNHD1	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R1755C	ENSG00000179532	ENST00000254579	Transcript	missense_variant	benign(0.391)
chr11	67200489	67200489	RPS6KB2	Missense_Mutation	.	SNP	C	C	A	rs183360785	gao_et_al_P2	p.T228N	ENSG00000175634	ENST00000312629	Transcript	missense_variant	probably_damaging(0.994)
chr12	50149484	50149484	TMBIM6	Missense_Mutation	.	SNP	C	C	G	rs186525370	gao_et_al_P2	p.H136D	ENSG00000139644	ENST00000423828	Transcript	missense_variant	benign(0.004)
chr12	58000651	58000651	DTX3	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.S2L	ENSG00000178498	ENST00000548198	Transcript	missense_variant	possibly_damaging(0.602)
chr12	72007173	72007173	ZFC3H1	Missense_Mutation	.	SNP	A	A	C	rs185254752	gao_et_al_P2	p.S1857A	ENSG00000133858	ENST00000378743	Transcript	missense_variant	benign(0.423)
chr12	80889142	80889142	PTPRQ	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P2	p.L621P	ENSG00000139304	ENST00000266688	Transcript	missense_variant	probably_damaging(0.99)
chr14	105416296	105416296	AHNAK2	Missense_Mutation	.	SNP	G	G	A	rs199536287	gao_et_al_P2	p.P1831L	ENSG00000185567	ENST00000333244	Transcript	missense_variant	probably_damaging(0.981)
chr14	24647336	24647336	REC8	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R301C	ENSG00000100918	ENST00000311457	Transcript	missense_variant	probably_damaging(0.994)
chr14	32561778	32561778	ARHGAP5	Missense_Mutation	.	SNP	C	C	T	rs115598823	gao_et_al_P2	p.R635W	ENSG00000100852	ENST00000345122	Transcript	missense_variant	possibly_damaging(0.768)
chr14	71518616	71518616	PCNX	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P2	p.F1488L	ENSG00000100731	ENST00000304743	Transcript	missense_variant	probably_damaging(0.989)
chr14	74974691	74974691	LTBP2	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P2	p.S1254G	ENSG00000119681	ENST00000261978	Transcript	missense_variant	benign(0.345)
chr14	91639696	91639696	C14orf159	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.I174V	ENSG00000133943	ENST00000518868	Transcript	missense_variant	benign(0.011)
chr14	95033456	95033456	SERPINA4	Missense_Mutation	.	SNP	C	C	T	rs369263026	gao_et_al_P2	p.R267W	ENSG00000100665	ENST00000557004	Transcript	missense_variant	benign(0.11)
chr14	95910934	95910934	SYNE3	Missense_Mutation	.	SNP	G	G	A	rs565608397	gao_et_al_P2	p.A555V	ENSG00000176438	ENST00000334258	Transcript	missense_variant	benign(0.002)
chr15	42178079	42178079	SPTBN5	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P2	p.S458R	ENSG00000137877	ENST00000320955	Transcript	missense_variant	probably_damaging(0.933)
chr15	56386433	56386433	RFX7	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.R1165W	ENSG00000181827	ENST00000423270	Transcript	missense_variant	probably_damaging(1)
chr15	68123211	68123211	SKOR1	Missense_Mutation	.	SNP	C	C	G	rs377094576	gao_et_al_P2	p.I760M	ENSG00000188779	ENST00000341418	Transcript	missense_variant	possibly_damaging(0.655)
chr15	77471385	77471385	PEAK1	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P2	p.M962V	ENSG00000173517	ENST00000560626	Transcript	missense_variant	probably_damaging(0.977)
chr15	79058391	79058391	ADAMTS7	Missense_Mutation	.	SNP	C	C	T	rs201097994	gao_et_al_P2	p.G1288R	ENSG00000136378	ENST00000388820	Transcript	missense_variant	benign(0.006)
chr16	1279347	1279347	TPSB2	Missense_Mutation	.	SNP	G	G	A	rs373095607	gao_et_al_P2	p.T115I	ENSG00000197253	ENST00000430512	Transcript	missense_variant	benign(0.004)
chr16	20481042	20481042	ACSM2A	Splice_Site	.	SNP	G	G	A	rs535053502	gao_et_al_P2	p.X199_splice	ENSG00000183747	ENST00000573854	Transcript	splice_donor_variant	NA
chr16	23646624	23646624	PALB2	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P2	p.S415R	ENSG00000083093	ENST00000261584	Transcript	missense_variant	benign(0.001)
chr16	30722105	30722105	SRCAP	Missense_Mutation	.	SNP	C	C	A	rs376370021	gao_et_al_P2	p.R389S	ENSG00000080603	ENST00000262518	Transcript	missense_variant	unknown(0)
chr16	31485214	31485214	TGFB1I1	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P2	p.S81T	ENSG00000140682	ENST00000394863	Transcript	missense_variant	probably_damaging(0.998)
chr16	56501878	56501878	OGFOD1	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P2	p.Q284Kfs*12	ENSG00000087263	ENST00000566157	Transcript	frameshift_variant	NA
chr16	87935523	87935523	CA5A	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P2	p.H205D	ENSG00000174990	ENST00000309893	Transcript	missense_variant	probably_damaging(0.956)
chr16	8905018	8905018	PMM2	Missense_Mutation	.	SNP	T	T	C	rs150719105	gao_et_al_P2	p.F144L	ENSG00000140650	ENST00000268261	Transcript	missense_variant	benign(0.31)
chr17	39186225	39186225	KRTAP1-4	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.G36R	ENSG00000204887	ENST00000377747	Transcript	missense_variant	unknown(0)
chr17	45901636	45901636	MRPL10	Missense_Mutation	.	SNP	G	G	A	rs200394081	gao_et_al_P2	p.R251C	ENSG00000159111	ENST00000290208	Transcript	missense_variant	benign(0.007)
chr17	47302197	47302197	PHOSPHO1	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.M97T	ENSG00000173868	ENST00000413580	Transcript	missense_variant	possibly_damaging(0.678)
chr17	48462517	48462517	LRRC59	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P2	p.Q213P	ENSG00000108829	ENST00000225972	Transcript	missense_variant	benign(0)
chr17	73132206	73132206	HN1	Missense_Mutation	.	SNP	G	G	T	rs202010696	gao_et_al_P2	p.S146Y	ENSG00000189159	ENST00000356033	Transcript	missense_variant	probably_damaging(0.919)

chr17	77082063	77082063	*ENGASE*	Missense_Mutation	.	SNP	G	G	A	rs199662950	gao_et_al_P2	p.V622I	ENSG00000167280	ENST00000579016	Transcript	missense_variant	benign(0.029)
chr17	78383863	78383863	*CNTROB*	Missense_Mutation	.	SNP	C	C	T	rs376598201	gao_et_al_P2	p.R173W	ENSG00000170037	ENST00000380262	Transcript	missense_variant	benign(0.05)
chr17	78405333	78405333	*CNTROB*	Missense_Mutation	.	SNP	C	C	T	rs201894732	gao_et_al_P2	p.R294C	ENSG00000170037	ENST00000380262	Transcript	missense_variant	possibly_damaging(0.685)
chr18	34289285	34289285	*FHOD3*	Missense_Mutation	.	SNP	G	G	T	rs617359998	gao_et_al_P2	p.V647F	ENSG00000134775	ENST00000257209	Transcript	missense_variant	benign(0.223)
chr19	15164601	15164601	*CASP14*	Missense_Mutation	.	SNP	G	G	C	rs143520169	gao_et_al_P2	p.V79L	ENSG00000105141	ENST00000427043	Transcript	missense_variant	possibly_damaging(0.596)
chr19	43698560	43698560	*PSG4*	Missense_Mutation	.	SNP	T	T	C	rs199876570	gao_et_al_P2	p.Y392C	ENSG00000243137	ENST00000405312	Transcript	missense_variant	probably_damaging(1)
chr19	50827192	50827192	*KCNC3*	Missense_Mutation	.	SNP	C	C	T	rs115351343	gao_et_al_P2	p.V340M	ENSG00000131398	ENST00000477616	Transcript	missense_variant	possibly_damaging(0.622)
chr19	57326397	57326397	*PEG3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R1138Q	ENSG00000198300	ENST00000326441	Transcript	missense_variant	benign(0.063)
chr19	67205533	67205533	*C3*	Missense_Mutation	.	SNP	G	G	T	rs184455094	gao_et_al_P2	p.H16Q	ENSG00000125730	ENST00000245907	Transcript	missense_variant	unknown(0)
chr2	10747350	10747350	*NOL10*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P2	p.D372Y	ENSG00000115761	ENST00000381685	Transcript	missense_variant	probably_damaging(0.986)
chr2	131520172	131520172	*AMER3*	Missense_Mutation	.	SNP	C	C	T	rs139544644	gao_et_al_P2	p.S176L	ENSG00000178171	ENST00000423981	Transcript	missense_variant	benign(0.107)
chr2	152112110	152112110	*RBM43*	Missense_Mutation	.	SNP	C	C	G	rs376270970	gao_et_al_P2	p.E51Q	ENSG00000184898	ENST00000331426	Transcript	missense_variant	probably_damaging(0.994)
chr2	152382685	152382685	*NEB*	Missense_Mutation	.	SNP	T	T	A	rs140982447	gao_et_al_P2	p.N7346I	ENSG00000183091	ENST00000397345	Transcript	missense_variant	possibly_damaging(0.47)
chr2	158977981	158977981	*UPP2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.R229Q	ENSG00000007001	ENST00000606860	Transcript	missense_variant	benign(0.006)
chr2	160269022	160269023	*BAZ2B*	In_Frame_Ins	.	INS	-	-	CAT	novel	gao_et_al_P2	p.V834_I835insD	ENSG00000123636	ENST00000392783	Transcript	inframe_insertion	NA
chr2	168105793	168105793	*XIRP2*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.T2631A	ENSG00000163092	ENST00000409195	Transcript	missense_variant	benign(0.034)
chr2	211306138	211306138	*LANCL1*	Missense_Mutation	.	SNP	T	T	G	rs202027938	gao_et_al_P2	p.H146P	ENSG00000115365	ENST00000443314	Transcript	missense_variant	benign(0.352)
chr2	219870842	219870842	*CCDC108*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.S1608L	ENSG00000181378	ENST00000341552	Transcript	missense_variant	benign(0.003)
chr2	241463303	241463303	*ANKMY1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.E522K	ENSG00000144504	ENST00000391987	Transcript	missense_variant	benign(0.272)
chr2	241463422	241463422	*ANKMY1*	Missense_Mutation	.	SNP	G	G	A	rs184584055	gao_et_al_P2	p.S482L	ENSG00000144504	ENST00000391987	Transcript	missense_variant	possibly_damaging(0.893)
chr2	28050464	28050464	*RBKS*	Frame_Shift_Del	.	DEL	G	G	-	rs372614067	gao_et_al_P2	p.T256Qfs*71	ENSG00000171174	ENST00000302188	Transcript	frameshift_variant	NA
chr2	64682795	64682795	*LGALSL*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P2	p.D61H	ENSG00000119862	ENST00000238875	Transcript	missense_variant	benign(0.03)
chr2	69002391	69002391	*ARHGAP25*	Missense_Mutation	.	SNP	G	G	A	rs551816260	gao_et_al_P2	p.A34T	ENSG00000163219	ENST00000409202	Transcript	missense_variant	benign(0.012)
chr2	73679661	73679661	*ALMS1*	Missense_Mutation	.	SNP	A	A	G	rs7587103	gao_et_al_P2	p.I2002V	ENSG00000116127	ENST00000264448	Transcript	missense_variant	benign(0.002)
chr22	19963256	19963256	*ARVCF*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R638Q	ENSG00000099889	ENST00000263207	Transcript	missense_variant	benign(0)
chr22	20106581	20106581	*RANBP1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P2	p.S21P	ENSG00000099901	ENST00000331821	Transcript	missense_variant	benign(0.005)
chr3	13383511	13383511	*NUP210*	Missense_Mutation	.	SNP	G	G	A	rs150421255	gao_et_al_P2	p.P1026L	ENSG00000132182	ENST00000254508	Transcript	missense_variant	benign(0.002)
chr3	39228788	39228788	*XIRP1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.A717T	ENSG00000168334	ENST00000340369	Transcript	missense_variant	benign(0.002)
chr3	47127765	47127765	*SETD2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.R1773C	ENSG00000181555	ENST00000409792	Transcript	missense_variant	benign(0.001)
chr3	49698372	49698372	*BSN*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P2	p.F3032I	ENSG00000164061	ENST00000296452	Transcript	missense_variant	unknown(0)
chr3	52512478	52512478	*NISCH*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.R396Q	ENSG00000010322	ENST00000345716	Transcript	missense_variant	benign(0.012)
chr3	69299222	69299222	*FRMD4B*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.I177T	ENSG00000114541	ENST00000398540	Transcript	missense_variant	benign(0.006)
chr4	184190300	184190300	*WWC2*	Missense_Mutation	.	SNP	G	G	A	rs149307334	gao_et_al_P2	p.R795Q	ENSG00000151718	ENST00000403733	Transcript	missense_variant	benign(0.004)
chr4	3432641	3432641	*RGS12*	Missense_Mutation	.	SNP	C	C	A	rs140022951	gao_et_al_P2	p.P1358Q	ENSG00000159788	ENST00000344733	Transcript	missense_variant	possibly_damaging(0.693)
chr4	84328662	84328662	*HELQ*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P2	p.L1084V	ENSG00000163312	ENST00000295488	Transcript	missense_variant	possibly_damaging(0.656)
chr4	86202177	86202177	*CPZ*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.R522Q	ENSG00000109625	ENST00000360986	Transcript	missense_variant	possibly_damaging(0.564)

chr5	140168087	140168087	*PCDHA1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P2	p.T738S	ENSG00000204970	ENST00000504120	Transcript	missense_variant	benign(0.069)
chr5	150431801	150431801	*TNIP1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R216Q	ENSG00000145901	ENST00000389378	Transcript	missense_variant	probably_damaging(0.996)
chr5	167644 09	167644 09	*MYO10*	Missense_Mutation	.	SNP	C	C	T	rs573227270	gao_et_al_P2	p.D426N	ENSG00000145555	ENST00000513610	Transcript	missense_variant	probably_damaging(0.997)
chr5	167689322	167689322	*TENM2*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.Y2611C	ENSG00000145934	ENST00000518659	Transcript	missense_variant	probably_damaging(0.928)
chr6	106267 04	106267 04	*GCNT2*	Missense_Mutation	.	SNP	T	T	G	rs200336999	gao_et_al_P2	p.V358G	ENSG00000111846	ENST00000379597	Transcript	missense_variant	benign(0.251)
chr6	139591687	139591687	*TXLNB*	Missense_Mutation	.	SNP	T	T	A	rs200899286	gao_et_al_P2	p.D198V	ENSG00000164440	ENST00000358430	Transcript	missense_variant	probably_damaging(0.992)
chr6	159184344	159184344	*SYTL3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.T509I	ENSG00000164674	ENST00000297239	Transcript	missense_variant	benign(0.008)
chr6	170627191	170627191	*FAM120B*	Missense_Mutation	.	SNP	T	T	C	rs188414778	gao_et_al_P2	p.M238T	ENSG00000112584	ENST00000476287	Transcript	missense_variant	possibly_damaging(0.583)
chr6	278397 35	278397 35	*HIST1H3I*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.I120T	ENSG00000182572	ENST00000328488	Transcript	missense_variant	benign(0.126)
chr6	758124 2	758124 2	*DSP*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.E1607K	ENSG00000096696	ENST00000379802	Transcript	missense_variant	benign(0.171)
chr7	115580652	115580652	*TFEC*	Missense_Mutation	.	SNP	T	T	C	rs575245684	gao_et_al_P2	p.S333G	ENSG00000105967	ENST00000265440	Transcript	missense_variant	probably_damaging(0.999)
chr7	141672813	141672813	*TAS2R38*	Missense_Mutation	.	SNP	G	G	T	rs185205624	gao_et_al_P2	p.T226K	ENSG00000257138	ENST00000547270	Transcript	missense_variant	probably_damaging(0.956)
chr7	430497 0	430497 0	*SDK1*	Missense_Mutation	.	SNP	G	G	A	rs531249642	gao_et_al_P2	p.G2199D	ENSG00000146555	ENST00000404826	Transcript	missense_variant	benign(0.13)
chr7	531035 10	531035 10	*POM121L12*	Missense_Mutation	.	SNP	G	G	A	rs558199586	gao_et_al_P2	p.R49H	ENSG00000221900	ENST00000408890	Transcript	missense_variant	benign(0)
chr7	997117 77	997117 77	*TAF6*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P2	p.M56T	ENSG00000106290	ENST00000437822	Transcript	missense_variant	possibly_damaging(0.579)
chr7	997969 39	997969 39	*STAG3*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.R508W	ENSG00000066923	ENST00000426455	Transcript	missense_variant	benign(0.052)
chr8	134253 93	134253 93	*C8orf48*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P2	p.S298C	ENSG00000164743	ENST00000297324	Transcript	missense_variant	benign(0.135)
chr8	143846142	143846142	*LYNX1*	Missense_Mutation	.	SNP	C	C	T	rs587717167	gao_et_al_P2	p.E93K	ENSG00000180155	ENST00000335822	Transcript	missense_variant	benign(0.023)
chr8	221719 31	221719 31	*PIWIL2*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.V694M	ENSG00000197181	ENST00000356766	Transcript	missense_variant	probably_damaging(0.954)
chr8	415772 22	415772 22	*ANK1*	Missense_Mutation	.	SNP	T	T	C	rs555694301	gao_et_al_P2	p.K388R	ENSG00000029534	ENST00000265709	Transcript	missense_variant	probably_damaging(0.996)
chr9	114136264	114136264	*KIAA0368*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P2	p.T1567S	ENSG00000136813	ENST00000259335	Transcript	missense_variant	benign(0.059)
chr9	124528784	124528784	*DAB2IP*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P2	p.R463L	ENSG00000136848	ENST00000259371	Transcript	missense_variant	probably_damaging(0.99)
chr9	130270384	130270384	*FAM129B*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P2	p.C512Afs*11	ENSG00000136830	ENST00000373312	Transcript	frameshift_variant	NA
chr9	130826116	130826116	*NAIF1*	Missense_Mutation	.	SNP	G	G	A	rs200620339	gao_et_al_P2	p.A192V	ENSG00000171169	ENST00000373078	Transcript	missense_variant	benign(0.024)
chr9	132687279	132687279	*FNBP1*	Missense_Mutation	.	SNP	T	T	C	rs199797411	gao_et_al_P2	p.K316R	ENSG00000187239	ENST00000446176	Transcript	missense_variant	benign(0.004)
chr9	136279830	136279830	*REXO4*	Missense_Mutation	.	SNP	T	T	C	rs200846181	gao_et_al_P2	p.H176R	ENSG00000148300	ENST00000371942	Transcript	missense_variant	benign(0.013)
chr9	140146231	140146231	*C9orf173*	Missense_Mutation	.	SNP	T	T	C	rs200111355	gao_et_al_P2	p.M51T	ENSG00000197768	ENST00000388931	Transcript	missense_variant	benign(0.012)
chr9	190894 77	190894 77	*HAUS6*	Missense_Mutation	.	SNP	G	G	C	rs180922782	gao_et_al_P2	p.R173G	ENSG00000147874	ENST00000380502	Transcript	missense_variant	possibly_damaging(0.565)
chr9	346490 79	346490 79	*GALT*	Splice_Site	.	SNP	G	G	T	rs367543271	gao_et_al_P2	p.X302_splice	ENSG00000213930	ENST00000378842	Transcript	splice_donor_variant	NA
chr9	356633 73	356633 73	*ARHGEF39*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P2	p.V164I	ENSG00000137135	ENST00000378387	Transcript	missense_variant	benign(0.006)
chr9	357332 11	357332 11	*CREB3*	Splice_Site	.	SNP	G	G	C	novel	gao_et_al_P2	p.X93_splice	ENSG00000107175	ENST00000353704	Transcript	splice_acceptor_variant	NA
chr9	436276 56	436276 56	*SPATA31A6*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P2	p.K344R	ENSG00000185775	ENST00000332857	Transcript	missense_variant	benign(0.094)
chr9	905017 62	905017 62	*SPATA31E1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P2	p.R787H	ENSG00000177992	ENST00000325643	Transcript	missense_variant	benign(0.005)
chrX	103358931	103358931	*ZCCHC18*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P2	p.R43S	ENSG00000166707	ENST00000537356	Transcript	missense_variant	possibly_damaging(0.628)
chrX	148037657	148037657	*AFF2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P2	p.K694N	ENSG00000155966	ENST00000370460	Transcript	missense_variant	probably_damaging(0.929)
chrX	929278 86	929278 86	*NAP1L3*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P2	p.N140H	ENSG00000186310	ENST00000373079	Transcript	missense_variant	probably_damaging(0.991)

chr1	152327665	152327670	*FLG2*	In_Frame_Del	.	DEL	CCCGAA	CCCGAA	-	novel	gao_et_al_P4	p.S865_G866del	ENSG00000143520	ENST00000388718	Transcript	inframe_deletion	NA
chr1	156876606	156876606	*PEAR1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.C193F	ENSG00000187800	ENST00000338302	Transcript	missense_variant	probably_damaging(0.999)
chr1	214816596	214816596	*CENPF*	Nonsense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.E1639*	ENSG00000117724	ENST00000366955	Transcript	stop_gained	NA
chr10	129877832	129877832	*PTPRE*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P4	p.A634G	ENSG00000132334	ENST00000254667	Transcript	missense_variant	possibly_damaging(0.543)
chr10	17203492	17203492	*TRDMT1*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P4	p.S127A	ENSG00000107614	ENST00000377799	Transcript	missense_variant	probably_damaging(0.999)
chr11	110451656	110451656	*ARHGAP20*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P4	p.D672H	ENSG00000137727	ENST00000260283	Transcript	missense_variant	possibly_damaging(0.625)
chr11	1651645	1651645	*KRTAP5-5*	Missense_Mutation	.	SNP	A	A	G	rs77039648	gao_et_al_P4	p.Y192C	ENSG00000185940	ENST00000399676	Transcript	missense_variant	unknown(0)
chr11	32953425	32953425	*QSER1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.L78F	ENSG00000060749	ENST00000399302	Transcript	missense_variant	probably_damaging(0.999)
chr11	403684	403684	*PKP3*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P4	p.V664L	ENSG00000184363	ENST00000331563	Transcript	missense_variant	benign(0.039)
chr11	6816337	6816337	*OR6A2*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P4	p.E201D	ENSG00000184933	ENST00000332601	Transcript	missense_variant	probably_damaging(0.95)
chr12	101759247	101759247	*UTP20*	Missense_Mutation	.	SNP	A	A	T	rs146367811	gao_et_al_P4	p.N1990I	ENSG00000120800	ENST00000261637	Transcript	missense_variant	benign(0.041)
chr14	101349168	101349168	*RTL1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P4	p.L653Q	ENSG00000254656	ENST00000534062	Transcript	missense_variant	probably_damaging(0.998)
chr14	39716978	39716978	*MIA2*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P4	p.R400S	ENSG00000150526	ENST00000280082	Transcript	missense_variant	benign(0.108)
chr14	58605519	58605519	*C14orf37*	Nonsense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P4	p.Y186*	ENSG00000139971	ENST00000267485	Transcript	stop_gained	NA
chr15	43027493	43027493	*CDAN1*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P4	p.K341N	ENSG00000140326	ENST00000356231	Transcript	missense_variant	benign(0.311)
chr16	15180099	15180099	*RRN3*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P4	p.N120S	ENSG00000085721	ENST00000198767	Transcript	missense_variant	benign(0.003)
chr17	1582150	1582150	*PRPF8*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P4	p.N542I	ENSG00000174231	ENST00000572621	Transcript	missense_variant	probably_damaging(1)
chr17	16664958	16664958	*CCDC144A*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P4	p.H1198N	ENSG00000170160	ENST00000443444	Transcript	missense_variant	benign(0.071)
chr17	29645357	29645357	*EVI2A*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P4	p.E248D	ENSG00000126860	ENST00000247270	Transcript	missense_variant	benign(0.039)
chr17	45216160	45216160	*CDC27*	Missense_Mutation	.	SNP	A	A	C	rs199626169	gao_et_al_P4	p.V556G	ENSG00000004897	ENST00000531206	Transcript	missense_variant	probably_damaging(0.981)
chr17	45234727	45234727	*CDC27*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P4	p.T167S	ENSG00000004897	ENST00000531206	Transcript	missense_variant	benign(0.204)
chr19	11943681	11943681	*ZNF440*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P4	p.H564N	ENSG00000171295	ENST00000304060	Transcript	missense_variant	benign(0)
chr19	2853537	2853537	*ZNF555*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P4	p.H492Y	ENSG00000186300	ENST00000334241	Transcript	missense_variant	probably_damaging(0.968)
chr19	44470300	44470300	*ZNF221*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P4	p.H216N	ENSG00000159905	ENST00000251269	Transcript	missense_variant	probably_damaging(0.94)
chr19	52034693	52034693	*SIGLEC6*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.P50T	ENSG00000105492	ENST00000425629	Transcript	missense_variant	possibly_damaging(0.858)
chr19	52826002	52826002	*ZNF480*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.R500L	ENSG00000198464	ENST00000595962	Transcript	missense_variant	benign(0.386)
chr2	153514416	153514416	*PRPF40A*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P4	p.T896S	ENSG00000196504	ENST00000410080	Transcript	missense_variant	unknown(0)
chr2	15470759	15470759	*NBAS*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P4	p.W1437L	ENSG00000151779	ENST00000281513	Transcript	missense_variant	probably_damaging(0.999)
chr2	27803505	27803505	*C2orf16*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P4	p.S1356R	ENSG00000221843	ENST00000408964	Transcript	missense_variant	possibly_damaging(0.905)
chr2	61724025	61724025	*XPO1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.Q293K	ENSG00000082898	ENST00000401558	Transcript	missense_variant	benign(0.032)
chr2	86310272	86310272	*POLR1A*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P4	p.I250M	ENSG00000068654	ENST00000263857	Transcript	missense_variant	benign(0)
chr21	33756624	33756624	*URB1*	Nonsense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P4	p.Y144*	ENSG00000142207	ENST00000382751	Transcript	stop_gained	NA
chr3	133375560	133375560	*TOPBP1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.P169T	ENSG00000163781	ENST00000260810	Transcript	missense_variant	possibly_damaging(0.827)
chr3	138762972	138762972	*PRR23C*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P4	p.P164L	ENSG00000233701	ENST00000413199	Transcript	missense_variant	benign(0.003)
chr3	39135534	39135534	*WDR48*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P4	p.I639V	ENSG00000114742	ENST00000302313	Transcript	missense_variant	benign(0.035)
chr3	97869007	97869007	*OR5H14*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P4	p.M260V	ENSG00000236032	ENST00000437310	Transcript	missense_variant	benign(0)

chr4	100826801	100826801	*DNAJB14*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P4	p.L265F	ENSG00000164031	ENST00000442697	Transcript	missense_variant	probably_damaging(0.978)
chr4	106320241	106320241	*PPA2*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P4	p.G246R	ENSG00000138777	ENST00000341695	Transcript	missense_variant	probably_damaging(1)
chr4	145635493	145635493	*HHIP*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P4	p.R514G	ENSG00000164161	ENST00000296575	Transcript	missense_variant	benign(0.098)
chr4	152024138	152024138	*RPS3A*	Missense_Mutation	.	SNP	A	A	C	rs139979828	gao_et_al_P4	p.Q157P	ENSG00000145425	ENST00000274065	Transcript	missense_variant	benign(0.162)
chr4	185689519	185689519	*ACSL1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.P360H	ENSG00000151726	ENST00000515030	Transcript	missense_variant	probably_damaging(1)
chr4	88052358	88052358	*AFF1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P4	p.V1030I	ENSG00000172493	ENST00000395146	Transcript	missense_variant	unknown(0)
chr5	137766757	137766757	*DNAH5*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.F3088L	ENSG00000039139	ENST00000265104	Transcript	missense_variant	benign(0.418)
chr5	72378599	72378599	*FCHO2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P4	p.Q731L	ENSG00000157107	ENST00000430046	Transcript	missense_variant	probably_damaging(0.997)
chr5	78975434	78975434	*PAPD4*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P4	p.A414D	ENSG00000164329	ENST00000453514	Transcript	missense_variant	probably_damaging(0.971)
chr6	139576726	139576726	*TXLNB*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P4	p.E351G	ENSG00000164440	ENST00000358430	Transcript	missense_variant	probably_damaging(0.997)
chr7	151046249	151046249	*NUB1*	Missense_Mutation	.	SNP	C	C	A	rs369312974	gao_et_al_P4	p.R94S	ENSG00000013374	ENST00000568733	Transcript	missense_variant	probably_damaging(0.956)
chr7	23306138	23306138	*GPNMB*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P4	p.P353S	ENSG00000136235	ENST00000381990	Transcript	missense_variant	benign(0.034)
chr8	134276887	134276887	*NDRG1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.D36E	ENSG00000104419	ENST00000414097	Transcript	missense_variant	probably_damaging(0.999)
chr9	103108449	103108449	*TEX10*	Missense_Mutation	.	SNP	T	T	C	rs200568844	gao_et_al_P4	p.I348V	ENSG00000136891	ENST00000374902	Transcript	missense_variant	benign(0)
chr9	79828149	79828149	*VPS13A*	Splice_Site	.	SNP	G	G	T	novel	gao_et_al_P4	NA	ENSG00000197969	ENST00000360280	Transcript	splice_acceptor_variant	NA
chrX	107978265	107978265	*IRS4*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.A437E	ENSG00000133124	ENST00000372129	Transcript	missense_variant	possibly_damaging(0.78)
chrX	109693989	109693989	*RGAG1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P4	p.L48F	ENSG00000243978	ENST00000465301	Transcript	missense_variant	probably_damaging(0.999)
chrX	79938017	79938017	*BRWD3*	Nonsense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P4	p.Y1448*	ENSG00000165288	ENST00000373275	Transcript	stop_gained	NA
chr1	151542209	151542209	*TUFT1*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P5	p.A186G	ENSG00000143367	ENST00000368849	Transcript	missense_variant	possibly_damaging(0.547)
chr1	177001859	177001859	*ASTN1*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P5	p.E200*	ENSG00000152092	ENST00000361833	Transcript	stop_gained	NA
chr1	75097539	75097539	*C1orf173*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P5	p.N226I	ENSG00000178965	ENST00000326665	Transcript	missense_variant	benign(0.099)
chr11	1651615	1651615	*KRTAP5-5*	Missense_Mutation	.	SNP	A	A	G	rs74396270	gao_et_al_P5	p.Y182C	ENSG00000185940	ENST00000399676	Transcript	missense_variant	unknown(0)
chr11	1651645	1651645	*KRTAP5-5*	Missense_Mutation	.	SNP	A	A	G	rs77039648	gao_et_al_P5	p.Y192C	ENSG00000185940	ENST00000399676	Transcript	missense_variant	unknown(0)
chr12	39973379	39973379	*ABCD2*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P5	p.G612V	ENSG00000173208	ENST00000308666	Transcript	missense_variant	possibly_damaging(0.866)
chr15	26812748	26812748	*GABRB3*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P5	p.S272Y	ENSG00000166206	ENST00000311550	Transcript	missense_variant	probably_damaging(1)
chr15	28200351	28200351	*OCA2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P5	p.Q599K	ENSG00000104044	ENST00000354638	Transcript	missense_variant	possibly_damaging(0.643)
chr15	81648918	81648918	*TMC3*	Frame_Shift_Del	.	DEL	C	C	-	novel	gao_et_al_P5	p.T255Rfs*38	ENSG00000188869	ENST00000359440	Transcript	frameshift_variant	NA
chr17	10415725	10415725	*MYH1*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P5	p.V383F	ENSG00000109061	ENST00000226207	Transcript	missense_variant	probably_damaging(0.973)
chr17	54403703	54403703	*ANKFN1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P5	p.N62Y	ENSG00000153930	ENST00000318698	Transcript	missense_variant	benign(0)
chr19	22155696	22155696	*ZNF208*	Missense_Mutation	.	SNP	T	T	C	rs201427226	gao_et_al_P5	p.I714V	ENSG00000160321	ENST00000397126	Transcript	missense_variant	benign(0.158)
chr19	37240994	37240994	*ZNF850*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P5	p.K316N	ENSG00000267041	ENST00000591344	Transcript	missense_variant	probably_damaging(0.916)
chr21	22710726	22710726	*NCAM2*	Nonsense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P5	p.Q306*	ENSG00000154654	ENST00000400546	Transcript	stop_gained	NA
chr3	13432721	13432721	*NUP210*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P5	p.N175Y	ENSG00000132182	ENST00000254508	Transcript	missense_variant	possibly_damaging(0.62)
chr3	13670509	13670509	*FBLN2*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P5	p.R892S	ENSG00000163520	ENST00000404922	Transcript	missense_variant	possibly_damaging(0.797)
chr3	49722221	49722221	*MST1*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P5	p.K573N	ENSG00000173531	ENST00000449682	Transcript	missense_variant	possibly_damaging(0.675)
chr5	140174971	140174971	*PCDHA2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P5	p.R141L	ENSG00000204969	ENST00000526136	Transcript	missense_variant	benign(0)

chr6	64395115	64395115	*PHF3*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P5	p.K498Sfs*4	ENSG00000118482	ENST00000262043	Transcript	frameshift_variant	NA
chr6	74073438	74073440	*KHDC3L*	In_Frame_Del	.	DEL	CTC	CTC	-	novel	gao_et_al_P5	p.P171del	ENSG00000203908	ENST00000370367	Transcript	inframe_deletion	NA
chrX	107977870	107977871	*IRS4*	Frame_Shift_Ins	.	INS	-	-	T	novel	gao_et_al_P5	p.G569Rfs*35	ENSG00000133124	ENST00000372129	Transcript	frameshift_variant	NA
chrX	154083006	154083006	*PIR*	Splice_Site	.	SNP	C	C	G	novel	gao_et_al_P5	p.X254_splice	ENSG00000087842	ENST00000380421	Transcript	splice_donor_variant	NA
chr1	152659495	152659495	*LCE2B*	Missense_Mutation	.	SNP	G	G	T	rs147648653	gao_et_al_P6	p.S59I	ENSG00000159455	ENST00000368780	Transcript	missense_variant	unknown(0)
chr1	154298559	154298559	*KAZN*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P6	p.L595P	ENSG00000189337	ENST00000376030	Transcript	missense_variant	probably_damaging(0.995)
chr1	222712035	222712035	*HHIPL2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P6	p.S511Y	ENSG00000143512	ENST00000343410	Transcript	missense_variant	possibly_damaging(0.669)
chr1	52854234	52854234	*ORC1*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.S421R	ENSG00000085840	ENST00000371568	Transcript	missense_variant	benign(0.043)
chr1	89448717	89448717	*RBMXL1*	Missense_Mutation	.	SNP	C	C	T	rs202218737	gao_et_al_P6	p.G265R	ENSG00000213516	ENST00000399794	Transcript	missense_variant	benign(0.213)
chr1	89449029	89449029	*RBMXL1*	Missense_Mutation	.	SNP	A	A	G	novel	gao_et_al_P6	p.S161P	ENSG00000213516	ENST00000399794	Transcript	missense_variant	benign(0.001)
chr1	89449037	89449037	*RBMXL1*	Missense_Mutation	.	SNP	C	C	A	rs200081893	gao_et_al_P6	p.G158V	ENSG00000213516	ENST00000399794	Transcript	missense_variant	benign(0.053)
chr10	129905112	129905113	*MKI67*	Frame_Shift_Del	.	DEL	TG	TG	-	rs145960091	gao_et_al_P6	p.T1664Rfs*7	ENSG00000148773	ENST00000368654	Transcript	frameshift_variant	NA
chr10	38406406	38406406	*ZNF37A*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.E109D	ENSG00000075407	ENST00000361085	Transcript	missense_variant	benign(0.007)
chr10	71977597	71977597	*PPA1*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P6	p.Y90D	ENSG00000180817	ENST00000373232	Transcript	missense_variant	probably_damaging(0.999)
chr10	89272901	89272901	*MINPP1*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P6	p.F286L	ENSG00000107789	ENST00000371996	Transcript	missense_variant	benign(0.002)
chr10	93260989	93260989	*HECTD2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.Q703L	ENSG00000165338	ENST00000298068	Transcript	missense_variant	possibly_damaging(0.787)
chr11	123601521	123601521	*ZNF202*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.D26Y	ENSG00000166261	ENST00000336139	Transcript	missense_variant	probably_damaging(0.94)
chr11	133712398	133712398	*SPATA19*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P6	p.I140R	ENSG00000166118	ENST00000299140	Transcript	missense_variant	possibly_damaging(0.891)
chr11	55033142	55033142	*TRIM48*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P6	p.V176L	ENSG00000150244	ENST00000417545	Transcript	missense_variant	benign(0.001)
chr11	93553755	93553755	*VSTM5*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P6	p.L195M	ENSG00000214376	ENST00000409977	Transcript	missense_variant	benign(0.115)
chr12	50746243	50746243	*FAM186A*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P6	p.T1458P	ENSG00000185958	ENST00000327337	Transcript	missense_variant	benign(0.001)
chr14	103342004	103342004	*TRAF3*	Missense_Mutation	.	SNP	A	A	C	rs128960018	gao_et_al_P6	p.Q114P	ENSG00000131323	ENST00000560371	Transcript	missense_variant	benign(0.002)
chr14	20010112	20010112	*POTEM*	Missense_Mutation	.	SNP	C	C	T	rs200761561	gao_et_al_P6	p.R349H	ENSG00000187537	ENST00000551509	Transcript	missense_variant	benign(0)
chr14	31185163	31185163	*SCFD1*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P6	p.M555L	ENSG00000092108	ENST00000458591	Transcript	missense_variant	benign(0.101)
chr14	55411154	55411154	*WDHD1*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P6	p.N1029H	ENSG00000198554	ENST00000360586	Transcript	missense_variant	possibly_damaging(0.838)
chr14	65008203	65008203	*HSPA2*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P6	p.I212M	ENSG00000126803	ENST00000247207	Transcript	missense_variant	probably_damaging(0.951)
chr14	68292203	68292203	*RAD51B*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P6	p.L36R	ENSG00000182185	ENST00000487270	Transcript	missense_variant	probably_damaging(0.921)
chr15	62214233	62214233	*VPS13C*	Splice_Site	.	SNP	C	C	A	novel	gao_et_al_P6	p.X2326_splice	ENSG00000129003	ENST00000261517	Transcript	splice_acceptor_variant	NA
chr16	21281117	21281117	*CRYM*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.F161L	ENSG00000103316	ENST00000219599	Transcript	missense_variant	possibly_damaging(0.906)
chr16	49671689	49671689	*ZNF423*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.E458D	ENSG00000102935	ENST00000561648	Transcript	missense_variant	possibly_damaging(0.883)
chr17	26084304	26084304	*NOS2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P6	p.Q1144K	ENSG00000007171	ENST00000313735	Transcript	missense_variant	benign(0.002)
chr17	34943627	34943627	*GGNBP2*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P6	p.L614F	ENSG00000005955	ENST00000304718	Transcript	missense_variant	benign(0.001)
chr17	45247323	45247323	*CDC27*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.S113T	ENSG00000004897	ENST00000531206	Transcript	missense_variant	benign(0.217)
chr17	79171610	79171610	*AZI1*	Missense_Mutation	.	SNP	C	C	T	rs377702390	gao_et_al_P6	p.D517N	ENSG00000141577	ENST00000450824	Transcript	missense_variant	benign(0.066)
chr18	20979558	20979558	*TMEM241*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P6	p.Y84F	ENSG00000134490	ENST00000383233	Transcript	missense_variant	possibly_damaging(0.519)
chr19	35849967	35849967	*FFAR3*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P6	p.A59S	ENSG00000185897	ENST00000327809	Transcript	missense_variant	benign(0.175)

chr19	45110994	45110994	*PLIN4*	Missense_Mutation	.	SNP	C	C	T	rs201223343	gao_et_al_P6	p.A946T	ENSG00000167676	ENST00000301286	Transcript	missense_variant	benign(0)
chr19	52034644	52034644	*SIGLEC6*	Frame_Shift_Del	.	DEL	T	T	-	novel	gao_et_al_P6	p.Y66Sfs*41	ENSG00000105492	ENST00000425629	Transcript	frameshift_variant	NA
chr19	56952721	56952721	*ZNF667*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.S548I	ENSG00000198046	ENST00000504904	Transcript	missense_variant	probably_damaging(0.999)
chr19	58773793	58773793	*ZNF544*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.N607K	ENSG00000198131	ENST00000269829	Transcript	missense_variant	benign(0.23)
chr2	191379328	191379328	*TMEM194B*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P6	p.R268S	ENSG00000189362	ENST00000409150	Transcript	missense_variant	benign(0.253)
chr2	238659876	238659876	*LRRFIP1*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P6	p.V149L	ENSG00000124831	ENST00000392000	Transcript	missense_variant	probably_damaging(0.997)
chr2	241066027	241066027	*MYEOV2*	Nonsense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.G238*	ENSG00000172428	ENST00000307266	Transcript	stop_gained	NA
chr2	42671288	42671288	*KCNG3*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.W366L	ENSG00000171126	ENST00000306078	Transcript	missense_variant	probably_damaging(0.999)
chr2	74750090	74750090	*DQX1*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P6	p.P399Q	ENSG00000144045	ENST00000404568	Transcript	missense_variant	benign(0.003)
chr2	86270233	86270233	*POLR1A*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P6	p.K1074R	ENSG00000068654	ENST00000263857	Transcript	missense_variant	benign(0.107)
chr21	37742119	37742119	*MORC3*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P6	p.D818A	ENSG00000159256	ENST00000400485	Transcript	missense_variant	benign(0.025)
chr21	45959198	45959198	*KRTAP10-1*	Missense_Mutation	.	SNP	C	C	G	novel	gao_et_al_P6	p.R279P	ENSG00000215455	ENST00000400375	Transcript	missense_variant	unknown(0)
chr21	45959763	45959763	*KRTAP10-1*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P6	p.T91P	ENSG00000215455	ENST00000400375	Transcript	missense_variant	unknown(0)
chr22	36916625	36916625	*EIF3D*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P6	p.D192E	ENSG00000100353	ENST00000216190	Transcript	missense_variant	possibly_damaging(0.768)
chr3	101219951	101219951	*SENP7*	Missense_Mutation	.	SNP	T	T	A	novel	gao_et_al_P6	p.E18V	ENSG00000138468	ENST00000394095	Transcript	missense_variant	possibly_damaging(0.719)
chr3	141535737	141535737	*GRK7*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.Q503K	ENSG00000114124	ENST00000264952	Transcript	missense_variant	benign(0)
chr4	109862552	109862552	*COL25A1*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P6	p.D178E	ENSG00000188517	ENST00000399132	Transcript	missense_variant	unknown(0)
chr4	114278766	114278766	*ANK2*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.Q2998K	ENSG00000145362	ENST00000357077	Transcript	missense_variant	benign(0.001)
chr4	126372912	126372912	*FAT4*	Missense_Mutation	.	SNP	T	T	G	novel	gao_et_al_P6	p.Y3581D	ENSG00000196159	ENST00000394329	Transcript	missense_variant	probably_damaging(0.962)
chr4	138945	138945	*CRIPAK*	Frame_Shift_Del	.	DEL	CA	CA	-	novel	gao_et_al_P6	p.T388Vfs*19	ENSG00000179979	ENST00000324803	Transcript	frameshift_variant	NA
chr4	146567150	146567150	*MMAA*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P6	p.G192D	ENSG00000151611	ENST00000281317	Transcript	missense_variant	probably_damaging(1)
chr4	166924551	166924551	*TLL1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P6	p.S214F	ENSG00000038295	ENST00000061240	Transcript	missense_variant	probably_damaging(0.988)
chr4	190878608	190878608	*FRG1*	Missense_Mutation	.	SNP	G	G	A	novel	gao_et_al_P6	p.G163E	ENSG00000109536	ENST00000226798	Transcript	missense_variant	possibly_damaging(0.642)
chr4	38829264	38829264	*TLR6*	Missense_Mutation	.	SNP	G	G	T	novel	gao_et_al_P6	p.L611M	ENSG00000174130	ENST00000436693	Transcript	missense_variant	benign(0.064)
chr4	57307895	57307895	*PAICS*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P6	p.P28L	ENSG00000128050	ENST00000399688	Transcript	missense_variant	benign(0.028)
chr5	112927718	112927718	*YTHDC2*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P6	p.I1352T	ENSG00000047188	ENST00000161863	Transcript	missense_variant	possibly_damaging(0.859)
chr5	140229002	140229002	*PCDHA9*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P6	p.M308L	ENSG00000204961	ENST00000532602	Transcript	missense_variant	benign(0.002)
chr5	180166146	180166146	*OR2Y1*	Frame_Shift_Del	.	DEL	A	A	-	novel	gao_et_al_P6	p.W305Gfs*10	ENSG00000174339	ENST00000307832	Transcript	frameshift_variant	NA
chr5	43539049	43539049	*PAIP1*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P6	p.G275R	ENSG00000172239	ENST00000306846	Transcript	missense_variant	probably_damaging(0.997)
chr5	54620032	54620032	*KIAA0947*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.T862K	ENSG00000164151	ENST00000296564	Transcript	missense_variant	possibly_damaging(0.888)
chr7	107434898	107434898	*SLC26A3*	Missense_Mutation	.	SNP	A	A	C	novel	gao_et_al_P6	p.N19K	ENSG00000091138	ENST00000340010	Transcript	missense_variant	benign(0.008)
chr7	108154969	108154969	*PNPLA8*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P6	p.E323K	ENSG00000135241	ENST00000422087	Transcript	missense_variant	benign(0.009)
chr7	155538198	155538198	*RBM33*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P6	p.P961S	ENSG00000184863	ENST00000401878	Transcript	missense_variant	unknown(0)
chr8	101287250	101287250	*RNF19A*	Missense_Mutation	.	SNP	C	C	A	novel	gao_et_al_P6	p.A272S	ENSG00000034677	ENST00000519449	Transcript	missense_variant	benign(0.018)
chr8	101624258	101624258	*SNX31*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.V194E	ENSG00000174226	ENST00000311812	Transcript	missense_variant	benign(0.005)
chr8	105509485	105509485	*LRP12*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P6	p.R432H	ENSG00000147650	ENST00000276654	Transcript	missense_variant	probably_damaging(0.998)

chr8	55537536	55537536	*RP1*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P6	p.S365T	ENSG00000104237	ENST00000220676	Transcript	missense_variant	benign(0.07)
chr8	67786810	67786810	*MCMDC2*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.T92S	ENSG00000178460	ENST00000422365	Transcript	missense_variant	possibly_damaging(0.638)
chr9	100388030	100388030	*TSTD2*	Missense_Mutation	.	SNP	G	G	C	novel	gao_et_al_P6	p.P139A	ENSG00000136925	ENST00000341170	Transcript	missense_variant	benign(0)
chrX	135956575	135956575	*RBMX*	Missense_Mutation	.	SNP	G	G	A	rs78646793	gao_et_al_P6	p.P301L	ENSG00000147274	ENST00000320676	Transcript	missense_variant	benign(0.009)
chrX	14883050	14883050	*FANCB*	Missense_Mutation	.	SNP	C	C	T	novel	gao_et_al_P6	p.E195K	ENSG00000181544	ENST00000398334	Transcript	missense_variant	benign(0.023)
chrX	23019180	23019180	*DDX53*	Missense_Mutation	.	SNP	A	A	T	novel	gao_et_al_P6	p.N336Y	ENSG00000184735	ENST00000327968	Transcript	missense_variant	benign(0.009)
chrX	46359498	46359498	*ZNF674*	Missense_Mutation	.	SNP	T	T	C	novel	gao_et_al_P6	p.K509R	ENSG00000251192	ENST00000523374	Transcript	missense_variant	probably_damaging(0.987)
chr1	1022530	1022530	*C1orf159*	Missense_Mutation	.	SNP	C	C	G	rs144168476	Patient1	p.R100P	ENSG00000131591	ENST00000421241	Transcript	missense_variant	benign(0.018)
chr1	153233460	153233460	*LOR*	Missense_Mutation	.	SNP	C	C	T	novel	Patient1	p.P12L	ENSG00000203782	ENST00000368742	Transcript	missense_variant	unknown(0)
chr1	158299840	158299840	*CD1B*	Missense_Mutation	.	SNP	C	C	T	rs358410999	Patient1	p.G137R	ENSG00000158485	ENST00000368168	Transcript	missense_variant	benign(0.005)
chr1	17257820	17257820	*CROCC*	Missense_Mutation	.	SNP	G	G	T	rs142373017	Patient1	p.R295L	ENSG00000058453	ENST00000375541	Transcript	missense_variant	probably_damaging(1)
chr1	183895326	183895326	*RGL1*	Missense_Mutation	.	SNP	T	T	C	rs377099855	Patient1	p.M771T	ENSG00000143344	ENST00000304685	Transcript	missense_variant	benign(0)
chr1	201288982	201288982	*PKP1*	Missense_Mutation	.	SNP	C	C	A	rs412699339	Patient1	p.P424Q	ENSG00000081277	ENST00000263946	Transcript	missense_variant	benign(0.022)
chr1	207235372	207235372	*PFKFB2*	Missense_Mutation	.	SNP	G	G	A	rs142450533	Patient1	p.V54M	ENSG00000123836	ENST00000367080	Transcript	missense_variant	benign(0.065)
chr1	228467095	228467095	*OBSCN*	Missense_Mutation	.	SNP	T	T	C	rs200720682	Patient1	p.V2878A	ENSG00000154358	ENST00000570156	Transcript	missense_variant	probably_damaging(0.911)
chr1	229683316	229683316	*ABCB10*	Missense_Mutation	.	SNP	C	C	T	novel	Patient1	p.R284H	ENSG00000135776	ENST00000344517	Transcript	missense_variant	benign(0.022)
chr1	24768650	24768650	*NIPAL3*	Missense_Mutation	.	SNP	G	G	A	novel	Patient1	p.V90M	ENSG00000001461	ENST00000374399	Transcript	missense_variant	probably_damaging(0.951)
chr1	57611010	57611010	*DAB1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient1	p.A54T	ENSG00000173406	ENST00000371236	Transcript	missense_variant	probably_damaging(0.93)
chr10	103454358	103454360	*FBXW4*	In_Frame_Del	.	DEL	CCT	CCT	-	novel	Patient1	p.E13del	ENSG00000107829	ENST00000331272	Transcript	inframe_deletion	NA
chr10	68139039	68139039	*CTNNA3*	Missense_Mutation	.	SNP	G	G	A	rs41274090	Patient1	p.R535C	ENSG00000183230	ENST00000433211	Transcript	missense_variant	unknown(0)
chr11	114271016	114271016	*C11orf71*	Missense_Mutation	.	SNP	T	T	C	rs374455783	Patient1	p.Q13R	ENSG00000180425	ENST00000325636	Transcript	missense_variant	benign(0.018)
chr11	17801128	17801128	*KCNC1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient1	p.G544R	ENSG00000129159	ENST00000265969	Transcript	missense_variant	benign(0.004)
chr11	397054	397054	*PKP3*	Missense_Mutation	.	SNP	C	C	T	rs151265573	Patient1	p.R185W	ENSG00000184363	ENST00000331563	Transcript	missense_variant	possibly_damaging(0.881)
chr11	45944596	45944596	*GYLTL1B*	Missense_Mutation	.	SNP	C	C	T	rs543863960	Patient1	p.R55C	ENSG00000165905	ENST00000531526	Transcript	missense_variant	benign(0.001)
chr11	56000408	56000408	*OR5T2*	Missense_Mutation	.	SNP	A	A	G	novel	Patient1	p.I85T	ENSG00000181718	ENST00000313264	Transcript	missense_variant	benign(0.269)
chr11	77815059	77815059	*ALG8*	Missense_Mutation	.	SNP	A	A	G	rs178256668	Patient1	p.I439T	ENSG00000159063	ENST00000299626	Transcript	missense_variant	benign(0.01)
chr11	82443955	82443955	*FAM181B*	Missense_Mutation	.	SNP	C	C	T	rs142346160	Patient1	p.G273S	ENSG00000182103	ENST00000329203	Transcript	missense_variant	benign(0.031)
chr12	113730816	113730816	*TPCN1*	Missense_Mutation	.	SNP	C	C	T	rs144613390	Patient1	p.R803W	ENSG00000186815	ENST00000550785	Transcript	missense_variant	benign(0.007)
chr12	47160509	47160509	*SLC38A4*	Missense_Mutation	.	SNP	T	T	C	novel	Patient1	p.D540G	ENSG00000139209	ENST00000447411	Transcript	missense_variant	benign(0)
chr13	47279258	47279258	*LRCH1*	Missense_Mutation	.	SNP	G	G	T	rs116173912	Patient1	p.A486S	ENSG00000136141	ENST00000389797	Transcript	missense_variant	benign(0.012)
chr15	73409045	73409045	*NEO1*	Missense_Mutation	.	SNP	G	G	A	rs143764154	Patient1	p.D99N	ENSG00000067141	ENST00000339362	Transcript	missense_variant	possibly_damaging(0.6)
chr15	91496233	91496233	*UNC45A*	Missense_Mutation	.	SNP	G	G	A	rs149872991	Patient1	p.R793Q	ENSG00000140553	ENST00000418476	Transcript	missense_variant	benign(0.008)
chr15	99454613	99454613	*IGF1R*	Missense_Mutation	.	SNP	G	G	A	rs339581716	Patient1	p.R511Q	ENSG00000140443	ENST00000268035	Transcript	missense_variant	benign(0.024)
chr16	22308122	22308122	*CASKIN1*	Missense_Mutation	.	SNP	G	G	A	rs185628064	Patient1	p.P853S	ENSG00000167971	ENST00000343516	Transcript	missense_variant	benign(0.004)
chr16	48232179	48232179	*ABCC11*	Missense_Mutation	.	SNP	T	T	C	rs138342031	Patient1	p.E697G	ENSG00000121270	ENST00000394747	Transcript	missense_variant	possibly_damaging(0.703)
chr16	613344	613344	*C16orf11*	Missense_Mutation	.	SNP	G	G	A	rs116903998	Patient1	p.R17Q	ENSG00000161992	ENST00000409413	Transcript	missense_variant	probably_damaging(0.926)

chr16	69377351	69377351	*TMED6*	Missense_Mutation	.	SNP	T	T	C	novel	Patient1	p.N228D	ENSG00000157315	ENST00000288025	Transcript	missense_variant	benign(0.023)
chr16	75642801	75642801	*ADAT1*	Missense_Mutation	.	SNP	G	G	A	rs77029992	Patient1	p.R377C	ENSG00000065457	ENST00000307921	Transcript	missense_variant	benign(0.212)
chr17	37822171	37822171	*TCAP*	Missense_Mutation	.	SNP	G	G	C	rs146906267	Patient1	p.E105Q	ENSG00000173991	ENST00000309889	Transcript	missense_variant	possibly_damaging(0.66)
chr17	37899280	37899280	*GRB7*	Missense_Mutation	.	SNP	G	G	T	rs147627069	Patient1	p.V169L	ENSG00000141738	ENST00000445327	Transcript	missense_variant	benign(0.188)
chr17	436105	436105	*VPS53*	Missense_Mutation	.	SNP	T	T	C	rs140376049	Patient1	p.I688V	ENSG00000141252	ENST00000437048	Transcript	missense_variant	benign(0.015)
chr17	48750485	48750485	*ABCC3*	Missense_Mutation	.	SNP	G	G	A	rs144001322	Patient1	p.V799M	ENSG00000108846	ENST00000285238	Transcript	missense_variant	benign(0.161)
chr17	7701525	7701525	*DNAH2*	Missense_Mutation	.	SNP	G	G	A	rs35295135	Patient1	p.V2761M	ENSG00000183914	ENST00000572933	Transcript	missense_variant	probably_damaging(0.983)
chr17	97608288	97608288	*GLP2R*	Missense_Mutation	.	SNP	G	G	A	rs61730822	Patient1	p.V234I	ENSG00000065325	ENST00000262441	Transcript	missense_variant	benign(0.025)
chr19	1057343	1057343	*ABCA7*	Missense_Mutation	.	SNP	G	G	A	rs117187003	Patient1	p.V1599M	ENSG00000064687	ENST00000263094	Transcript	missense_variant	probably_damaging(0.999)
chr19	1236080	1236080	*C19orf26*	Missense_Mutation	.	SNP	A	A	G	rs113298601	Patient1	p.M7T	ENSG00000099625	ENST00000590083	Transcript	missense_variant	unknown()
chr19	18701700	18701700	*C19orf60*	Missense_Mutation	.	SNP	G	G	A	rs346139611	Patient1	p.A164T	ENSG00000006015	ENST00000358607	Transcript	missense_variant	benign(0.007)
chr19	38795581	38795583	*C19orf33*	In_Frame_Del	.	DEL	AAG	AAG	-	rs201974576	Patient1	p.K100del	ENSG00000167644	ENST00000301246	Transcript	inframe_deletion	NA
chr19	40420083	40420083	*FCGBP*	Missense_Mutation	.	SNP	C	C	T	rs359228111	Patient1	p.V971M	ENSG00000090920	ENST00000221347	Transcript	missense_variant	probably_damaging(0.992)
chr19	42728658	42728658	*ZNF526*	Missense_Mutation	.	SNP	A	A	G	rs146838645	Patient1	p.T35A	ENSG00000167625	ENST00000301215	Transcript	missense_variant	benign(0)
chr19	42817572	42817572	*TMEM145*	Missense_Mutation	.	SNP	C	C	T	rs185966365	Patient1	p.P15L	ENSG00000167619	ENST00000301204	Transcript	missense_variant	benign(0.037)
chr19	58048770	58048770	*ZNF549*	Missense_Mutation	.	SNP	C	C	T	rs148639985	Patient1	p.T133M	ENSG00000121406	ENST00000376233	Transcript	missense_variant	benign(0.037)
chr19	59028208	59028208	*ZBTB45*	Nonsense_Mutation	.	SNP	G	G	C	novel	Patient1	p.S278*	ENSG00000119574	ENST00000594051	Transcript	stop_gained	NA
chr2	125405429	125405429	*CNTNAP5*	Missense_Mutation	.	SNP	C	C	G	rs182009600	Patient1	p.D656E	ENSG00000155052	ENST00000431078	Transcript	missense_variant	benign(0.066)
chr2	130877956	130877956	*POTEF*	Missense_Mutation	.	SNP	T	T	C	rs200786675	Patient1	p.T45A	ENSG00000196604	ENST00000357462	Transcript	missense_variant	benign(0.13)
chr2	167300180	167300180	*SCN7A*	Missense_Mutation	.	SNP	T	T	C	novel	Patient1	p.I545V	ENSG00000136546	ENST00000409855	Transcript	missense_variant	benign(0.023)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	C	rs121913499	Patient1	p.R132G	ENSG00000138413	ENST00000415913	Transcript	missense_variant	probably_damaging(0.998)
chr2	228771023	228771023	*DAW1*	Missense_Mutation	.	SNP	T	T	C	rs342493337	Patient1	p.I276T	ENSG00000123977	ENST00000309931	Transcript	missense_variant	possibly_damaging(0.861)
chr2	24245713	24245713	*MFSD2B*	Missense_Mutation	.	SNP	C	C	G	rs138903557	Patient1	p.P334A	ENSG00000205639	ENST00000406420	Transcript	missense_variant	probably_damaging(0.994)
chr2	67632323	67632323	*ETAA1*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient1	p.Q837*	ENSG00000143971	ENST00000272342	Transcript	stop_gained	NA
chr2	97216846	97216846	*ARID5A*	Missense_Mutation	.	SNP	G	G	A	rs150396730	Patient1	p.G194E	ENSG00000196843	ENST00000357485	Transcript	missense_variant	benign(0.014)
chr20	30408306	30408306	*MYLK2*	Missense_Mutation	.	SNP	C	C	G	rs343966614	Patient1	p.P144A	ENSG00000101306	ENST00000375994	Transcript	missense_variant	probably_damaging(0.998)
chr20	870881	870881	*ANGPT4*	Missense_Mutation	.	SNP	C	C	T	rs150123876	Patient1	p.R147H	ENSG00000101280	ENST00000381922	Transcript	missense_variant	benign(0.003)
chr21	45106786	45106786	*RRP1B*	Missense_Mutation	.	SNP	T	T	G	rs138939671	Patient1	p.L371V	ENSG00000160208	ENST00000340648	Transcript	missense_variant	benign(0.025)
chr22	22318354	22318354	*TOP3B*	Missense_Mutation	.	SNP	T	T	C	rs75602167	Patient1	p.H382R	ENSG00000100038	ENST00000398793	Transcript	missense_variant	benign(0.022)
chr22	25425357	25425357	*KIAA1671*	Missense_Mutation	.	SNP	C	C	T	novel	Patient1	p.A464V	ENSG00000197077	ENST00000358431	Transcript	missense_variant	benign(0.011)
chr22	31845370	31845370	*EIF4ENIF1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient1	p.A578T	ENSG00000184708	ENST00000397525	Transcript	missense_variant	benign(0.007)
chr22	32009392	32009392	*SFI1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient1	p.R873Q	ENSG00000198089	ENST00000400288	Transcript	missense_variant	probably_damaging(0.999)
chr3	121828181	121828181	*CD86*	Missense_Mutation	.	SNP	T	T	C	rs115021223	Patient1	p.I258T	ENSG00000114013	ENST00000330540	Transcript	missense_variant	benign(0.031)
chr3	128614248	128614248	*ACAD9*	Missense_Mutation	.	SNP	A	A	G	rs202119704	Patient1	p.I148V	ENSG00000177646	ENST00000308982	Transcript	missense_variant	possibly_damaging(0.551)
chr3	185212411	185212411	*TMEM41A*	Missense_Mutation	.	SNP	C	C	G	rs146903551	Patient1	p.G192R	ENSG00000163900	ENST00000421852	Transcript	missense_variant	probably_damaging(1)
chr3	48336219	48336219	*NME6*	Missense_Mutation	.	SNP	C	C	T	rs357846663	Patient1	p.E165K	ENSG00000172113	ENST00000421967	Transcript	missense_variant	benign(0.046)

chr3	52441470	52441470	*BAP1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient1	p.G128R	ENSG00000163930	ENST00000460680	Transcript	missense_variant	probably_damaging(1)
chr4	69682188	69682188	*UGT2B10*	Missense_Mutation	.	SNP	G	G	A	rs200419731	Patient1	p.A151T	ENSG00000109181	ENST00000265403	Transcript	missense_variant	benign(0.034)
chr4	70455164	70455164	*UGT2A1*	Missense_Mutation	.	SNP	A	A	C	rs374331982	Patient1	p.F504V	ENSG00000173610	ENST00000503640	Transcript	missense_variant	benign(0.349)
chr5	138728256	138728256	*PROB1*	Missense_Mutation	.	SNP	G	G	A	rs202094107	Patient1	p.P839S	ENSG00000228672	ENST00000434752	Transcript	missense_variant	benign(0.009)
chr5	140763906	140763906	*PCDHGA7*	Missense_Mutation	.	SNP	C	C	G	novel	Patient1	p.D480E	ENSG00000253537	ENST00000518325	Transcript	missense_variant	probably_damaging(1)
chr5	150726871	150726873	*SLC36A2*	In_Frame_Del	.	DEL	TCT	TCT	-	rs559821596	Patient1	p.K50del	ENSG00000186335	ENST00000335244	Transcript	inframe_deletion	NA
chr5	180030322	180030322	*FLT4*	Missense_Mutation	.	SNP	C	C	T	rs796200928	Patient1	p.R1321Q	ENSG00000037280	ENST00000261937	Transcript	missense_variant	benign(0.002)
chr5	23524516	23524516	*PRDM9*	Missense_Mutation	.	SNP	A	A	G	rs193211869	Patient1	p.R342G	ENSG00000164256	ENST00000296682	Transcript	missense_variant	benign(0.126)
chr5	44809525	44809525	*MRPS30*	Missense_Mutation	.	SNP	A	A	G	rs370300488	Patient1	p.H154R	ENSG00000112996	ENST00000507110	Transcript	missense_variant	benign(0.328)
chr6	119136519	119136519	*MCM9*	Missense_Mutation	.	SNP	G	G	A	novel	Patient1	p.P967L	ENSG00000111877	ENST00000316316	Transcript	missense_variant	benign(0.016)
chr6	138200353	138200353	*TNFAIP3*	Missense_Mutation	.	SNP	C	C	G	rs145392420	Patient1	p.L591V	ENSG00000118503	ENST00000237289	Transcript	missense_variant	benign(0.03)
chr6	27218515	27218515	*PRSS16*	In_Frame_Del	.	DEL	CTC	CTC	-	rs145433670	Patient1	p.S174del	ENSG00000112812	ENST00000230582	Transcript	inframe_deletion	NA
chr6	32820930	32820930	*TAP1*	Missense_Mutation	.	SNP	C	C	T	rs147255912	Patient1	p.V222M	ENSG00000168394	ENST00000354258	Transcript	missense_variant	possibly_damaging(0.641)
chr7	123672457	123672459	*TMEM229A*	In_Frame_Del	.	DEL	GCT	GCT	-	rs374529977	Patient1	p.Q201del	ENSG00000234224	ENST00000455783	Transcript	inframe_deletion	NA
chr7	135047811	135047811	*CNOT4*	Missense_Mutation	.	SNP	G	G	C	rs200460078	Patient1	p.H656Q	ENSG00000080802	ENST00000541284	Transcript	missense_variant	probably_damaging(0.962)
chr7	135123060	135123060	*CNOT4*	Missense_Mutation	.	SNP	G	G	C	rs174806116	Patient1	p.A7G	ENSG00000080802	ENST00000541284	Transcript	missense_variant	benign(0.167)
chr7	35923537	35923537	*Sep/07*	Missense_Mutation	.	SNP	A	A	C	novel	Patient1	p.I255L	ENSG00000122545	ENST00000399034	Transcript	missense_variant	benign(0.005)
chr8	70515476	70515476	*SULF1*	Missense_Mutation	.	SNP	A	A	G	rs118056333	Patient1	p.I371V	ENSG00000137573	ENST00000260128	Transcript	missense_variant	possibly_damaging(0.883)
chr9	140146560	140146560	*C9orf173*	Missense_Mutation	.	SNP	A	A	G	rs286574339	Patient1	p.S126G	ENSG00000197768	ENST00000388931	Transcript	missense_variant	probably_damaging(0.916)
chrX	132092485	132092485	*HS6ST2*	Missense_Mutation	.	SNP	G	G	A	rs181526961	Patient1	p.S49L	ENSG00000171004	ENST00000521489	Transcript	missense_variant	benign(0.253)
chrX	134294465	134294465	*CT55*	Missense_Mutation	.	SNP	G	G	A	novel	Patient1	p.R99C	ENSG00000169551	ENST00000276241	Transcript	missense_variant	benign(0)
chrX	20062561	20062561	*MAP7D2*	Missense_Mutation	.	SNP	T	T	C	novel	Patient1	p.K267R	ENSG00000184368	ENST00000379643	Transcript	missense_variant	benign(0.043)
chrX	48544153	48544153	*WAS*	Missense_Mutation	.	SNP	G	G	A	novel	Patient1	p.E131K	ENSG00000015285	ENST00000376701	Transcript	missense_variant	possibly_damaging(0.906)
chr1	109730907	109730907	*KIAA1324*	Missense_Mutation	.	SNP	C	C	G	novel	Patient2	p.P384A	ENSG00000116299	ENST00000369939	Transcript	missense_variant	probably_damaging(1)
chr1	186057125	186057125	*HMCN1*	Missense_Mutation	.	SNP	A	A	T	novel	Patient2	p.N3142I	ENSG00000143341	ENST00000271587	Transcript	missense_variant	probably_damaging(0.998)
chr12	25311419	25311419	*CASC1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient2	p.R62Q	ENSG00000118307	ENST00000395987	Transcript	missense_variant	benign(0.004)
chr12	62148806	62148806	*FAM19A2*	Splice_Site	.	SNP	C	C	A	novel	Patient2	p.X36_splice	ENSG00000198673	ENST00000416284	Transcript	splice_acceptor_variant	NA
chr13	40254162	40254162	*COG6*	Missense_Mutation	.	SNP	G	G	A	novel	Patient2	p.R225K	ENSG00000133103	ENST00000455146	Transcript	missense_variant	benign(0.15)
chr13	46543833	46543833	*ZC3H13*	Missense_Mutation	.	SNP	G	G	C	novel	Patient2	p.S949C	ENSG00000123200	ENST00000282007	Transcript	missense_variant	unknown(0)
chr14	100706238	100706238	*YY1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient2	p.F219L	ENSG00000100811	ENST00000262238	Transcript	missense_variant	benign(0.126)
chr14	20819254	20819254	*PARP2*	Missense_Mutation	.	SNP	A	A	G	novel	Patient2	p.N170S	ENSG00000129484	ENST00000250416	Transcript	missense_variant	benign(0.009)
chr14	24619838	24619838	*RNF31*	Missense_Mutation	.	SNP	G	G	C	novel	Patient2	p.S410T	ENSG00000092098	ENST00000324103	Transcript	missense_variant	benign(0)
chr14	24675757	24675757	*TSSK4*	Missense_Mutation	.	SNP	C	C	T	novel	Patient2	p.R90W	ENSG00000139908	ENST00000339917	Transcript	missense_variant	possibly_damaging(0.655)
chr14	91948224	91948224	*SMEK1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient2	p.R204L	ENSG00000100796	ENST00000554684	Transcript	missense_variant	benign(0.37)
chr17	263673	263673	*C17orf97*	Missense_Mutation	.	SNP	C	C	A	novel	Patient2	p.P347T	ENSG00000187624	ENST00000360127	Transcript	missense_variant	benign(0)
chr17	45221318	45221318	*CDC27*	Missense_Mutation	.	SNP	A	A	C	rs777392831	Patient2	p.I373M	ENSG00000004897	ENST00000531206	Transcript	missense_variant	benign(0.018)

chr17	56693569	56693569	*TEX14*	Missense_Mutation	.	SNP	G	G	C	novel	Patient2	p.S251C	ENSG00000121101	ENST00000240361	Transcript	missense_variant	probably_damaging(0.996)
chr19	44097045	44097045	*CHAF1A*	Frame_Shift_Del	.	DEL	A	A	-	novel	Patient2	p.K304Sfs*18	ENSG00000167670	ENST00000301280	Transcript	frameshift_variant	NA
chr19	47569969	47569969	*ZC3H4*	Missense_Mutation	.	SNP	T	T	C	novel	Patient2	p.K1186E	ENSG00000130749	ENST00000253048	Transcript	missense_variant	unknown(0)
chr19	52222817	52222817	*HAS1*	Missense_Mutation	.	SNP	A	A	T	novel	Patient2	p.L115Q	ENSG00000105509	ENST00000222115	Transcript	missense_variant	probably_damaging(0.999)
chr2	128631438	128631438	*AMMECR1L*	Missense_Mutation	.	SNP	G	G	T	novel	Patient2	p.P124Q	ENSG00000144233	ENST00000272647	Transcript	missense_variant	benign(0.01)
chr2	202440021	202440021	*ALS2CR11*	Missense_Mutation	.	SNP	A	A	G	novel	Patient2	p.V223A	ENSG00000155754	ENST00000439140	Transcript	missense_variant	benign(0.037)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	C	rs121913499	Patient2	p.R132G	ENSG00000138413	ENST00000415913	Transcript	missense_variant	probably_damaging(0.998)
chr2	27606350	27606350	*PPM1G*	Missense_Mutation	.	SNP	T	T	C	novel	Patient2	p.M362V	ENSG00000115241	ENST00000344034	Transcript	missense_variant	possibly_damaging(0.699)
chr3	178952085	178952085	*PIK3CA*	Missense_Mutation	.	SNP	A	A	G	rs121913279	Patient2	p.H1047R	ENSG00000121879	ENST00000263967	Transcript	missense_variant	possibly_damaging(0.529)
chr3	52441470	52441470	*BAP1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient2	p.G128R	ENSG00000163930	ENST00000460680	Transcript	missense_variant	probably_damaging(1)
chr4	191003234	191003234	*DUX4L4*	Missense_Mutation	.	SNP	C	C	A	novel	Patient2	p.A382E	ENSG00000258834	ENST00000538692	Transcript	missense_variant	possibly_damaging(0.52)
chr5	157182096	157182096	*LSM11*	Missense_Mutation	.	SNP	C	C	T	novel	Patient2	p.R303W	ENSG00000155858	ENST00000286307	Transcript	missense_variant	possibly_damaging(0.825)
chr6	136600949	136600949	*BCLAF1*	Missense_Mutation	.	SNP	G	G	A	rs149618892	Patient2	p.S19F	ENSG00000029363	ENST00000531224	Transcript	missense_variant	unknown(0)
chr6	84913722	84913722	*KIAA1009*	Missense_Mutation	.	SNP	C	C	G	novel	Patient2	p.E222Q	ENSG00000135315	ENST00000403245	Transcript	missense_variant	possibly_damaging(0.597)
chr7	52677769	52677769	*WIPI2*	Missense_Mutation	.	SNP	G	G	A	novel	Patient2	p.A350T	ENSG00000157954	ENST00000288828	Transcript	missense_variant	benign(0.003)
chr7	92163841	92163841	*RBM48*	Missense_Mutation	.	SNP	A	A	G	rs187507005	Patient2	p.N192D	ENSG00000127993	ENST00000265732	Transcript	missense_variant	benign(0.001)
chr8	30702067	30702067	*TEX15*	Nonsense_Mutation	.	SNP	G	G	T	novel	Patient2	p.Y1489*	ENSG00000133863	ENST00000256246	Transcript	stop_gained	NA
chr1	248308467	248308467	*OR2M5*	Missense_Mutation	.	SNP	G	G	T	novel	Patient3	p.Q6H	ENSG00000162727	ENST00000366476	Transcript	missense_variant	benign(0.012)
chr1	27106829	27106830	*ARID1A*	Frame_Shift_Ins	.	INS	-	-	G	novel	Patient3	p.Y2148Vfs*2	ENSG00000117713	ENST00000324856	Transcript	frameshift_variant	NA
chr1	52827234	52827234	*CC2D1B*	Missense_Mutation	.	SNP	A	A	C	novel	Patient3	p.V90G	ENSG00000154222	ENST00000371586	Transcript	missense_variant	benign(0.075)
chr10	71139638	71139638	*HK1*	Missense_Mutation	.	SNP	A	A	T	novel	Patient3	p.N355I	ENSG00000156515	ENST00000404387	Transcript	missense_variant	possibly_damaging(0.822)
chr10	75864959	75864959	*VCL*	Missense_Mutation	.	SNP	A	A	G	novel	Patient3	p.N761S	ENSG00000035403	ENST00000211998	Transcript	missense_variant	probably_damaging(0.996)
chr11	7984901	7984901	*NLRP10*	Missense_Mutation	.	SNP	C	C	G	novel	Patient3	p.E48Q	ENSG00000182261	ENST00000328600	Transcript	missense_variant	benign(0.061)
chr15	90190916	90190916	*KIF7*	Missense_Mutation	.	SNP	T	T	A	novel	Patient3	p.T491S	ENSG00000166813	ENST00000394412	Transcript	missense_variant	benign(0.001)
chr17	38955250	38955250	*KRT28*	Missense_Mutation	.	SNP	A	A	T	novel	Patient3	p.I151N	ENSG00000173908	ENST00000306658	Transcript	missense_variant	possibly_damaging(0.615)
chr17	39383172	39383172	*KRTAP9-2*	Missense_Mutation	.	SNP	C	C	T	rs143324960	Patient3	p.T89I	ENSG00000239886	ENST00000377721	Transcript	missense_variant	unknown(0)
chr17	45216124	45216124	*CDC27*	Missense_Mutation	.	SNP	A	A	G	novel	Patient3	p.M568T	ENSG00000004897	ENST00000531206	Transcript	missense_variant	benign(0.009)
chr17	48549880	48549880	*ACSF2*	Missense_Mutation	.	SNP	A	A	T	novel	Patient3	p.Y472F	ENSG00000167107	ENST00000300441	Transcript	missense_variant	probably_damaging(0.999)
chr17	72943109	72943109	*OTOP3*	Missense_Mutation	.	SNP	A	A	G	novel	Patient3	p.S387G	ENSG00000182938	ENST00000328801	Transcript	missense_variant	possibly_damaging(0.509)
chr19	17362492	17362492	*USHBP1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient3	p.Q607H	ENSG00000130307	ENST00000259257	Transcript	missense_variant	probably_damaging(0.947)
chr19	18538766	18538766	*SSBP4*	Missense_Mutation	.	SNP	G	G	A	novel	Patient3	p.G85S	ENSG00000130511	ENST00000270061	Transcript	missense_variant	benign(0.002)
chr19	42740855	42740855	*GSK3A*	Missense_Mutation	.	SNP	T	T	A	novel	Patient3	p.Y190F	ENSG00000105723	ENST00000222330	Transcript	missense_variant	possibly_damaging(0.57)
chr2	111921764	111921764	*BCL2L11*	Nonsense_Mutation	.	SNP	C	C	T	rs138706378	Patient3	p.R185*	ENSG00000153094	ENST00000393256	Transcript	stop_gained	NA
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	Patient3	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	95539307	95539307	*TEKT4*	Missense_Mutation	.	SNP	A	A	G	rs769341115	Patient3	p.T181A	ENSG00000163060	ENST00000295201	Transcript	missense_variant	possibly_damaging(0.859)
chr20	35521385	35521385	*SAMHD1*	Nonsense_Mutation	.	SNP	G	G	A	novel	Patient3	p.R611*	ENSG00000101347	ENST00000262878	Transcript	stop_gained	NA

chr22	19171079	19171079	*CLTCL1*	Frame_Shift_Del	.	DEL	G	G	-	novel	Patient3	p.Q1551Rfs*52	ENSG00000070371	ENST00000263200	Transcript	frameshift_variant	NA
chr3	52439921	52439922	*BAP1*	Frame_Shift_Ins	.	INS	-	-	T	novel	Patient3	p.R264Kfs*20	ENSG00000163930	ENST00000460680	Transcript	frameshift_variant	NA
chr3	55108223	55108223	*CACNA2D3*	Missense_Mutation	.	SNP	T	T	C	novel	Patient3	p.F1089S	ENSG00000157445	ENST00000474759	Transcript	missense_variant	possibly_damaging(0.665)
chr4	19088426	19088426	*FRG1*	Missense_Mutation	.	SNP	G	G	A	rs373037319	Patient3	p.D254N	ENSG00000109536	ENST00000226798	Transcript	missense_variant	probably_damaging(0.993)
chr7	57187872	57187872	*ZNF479*	Missense_Mutation	.	SNP	A	A	G	novel	Patient3	p.V417A	ENSG00000185177	ENST00000331162	Transcript	missense_variant	benign(0.001)
chr7	66397579	66397579	*C7orf26*	Missense_Mutation	.	SNP	G	G	A	novel	Patient3	p.V294I	ENSG00000146576	ENST00000344417	Transcript	missense_variant	benign(0.208)
chr8	52732958	52732958	*PCMTD1*	Missense_Mutation	.	SNP	G	G	A	rs200497338	Patient3	p.L343F	ENSG00000168300	ENST00000360540	Transcript	missense_variant	probably_damaging(0.986)
chr9	125563230	125563230	*OR1K1*	Missense_Mutation	.	SNP	G	G	T	novel	Patient3	p.V277F	ENSG00000165204	ENST00000277309	Transcript	missense_variant	possibly_damaging(0.58)
chrX	123518579	123518579	*TENM1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient3	p.P2068S	ENSG00000009694	ENST00000422452	Transcript	missense_variant	possibly_damaging(0.636)
chrX	70354222	70354222	*MED12*	Missense_Mutation	.	SNP	G	G	T	novel	Patient3	p.D1545Y	ENSG00000184634	ENST00000374080	Transcript	missense_variant	probably_damaging(0.99)
chrX	98628766	98628766	*SHROOM2*	Missense_Mutation	.	SNP	G	G	A	novel	Patient3	p.A310T	ENSG00000146950	ENST00000380913	Transcript	missense_variant	possibly_damaging(0.892)
chr1	151395941	151395941	*POGZ*	Missense_Mutation	.	SNP	C	C	T	novel	Patient4	p.R537H	ENSG00000143442	ENST00000271715	Transcript	missense_variant	probably_damaging(0.999)
chr1	161010060	161010060	*USF1*	Frame_Shift_Del	.	DEL	G	G	-	novel	Patient4	p.H259Tfs*43	ENSG00000158773	ENST00000368021	Transcript	frameshift_variant	NA
chr1	47157601	47157602	*EFCAB14*	Frame_Shift_Del	.	DEL	AG	AG	-	novel	Patient4	p.A196Vfs*22	ENSG00000159658	ENST00000371933	Transcript	frameshift_variant	NA
chr12	11286702	11286702	*TAS2R30*	Missense_Mutation	.	SNP	G	G	C	novel	Patient4	p.L48V	ENSG00000256188	ENST00000539585	Transcript	missense_variant	benign(0.159)
chr13	72440658	72440658	*DACH1*	Missense_Mutation	.	SNP	t	t	C	novel	Patient4	p.S84G	ENSG00000165659	ENST00000305425	Transcript	missense_variant	unknown(0)
chr14	68249673	68249673	*ZFYVE26*	Missense_Mutation	.	SNP	G	G	T	novel	Patient4	p.T1399N	ENSG00000072121	ENST00000347230	Transcript	missense_variant	benign(0.277)
chr15	22743249	22743249	*GOLGA6L1*	Missense_Mutation	.	SNP	T	T	A	novel	Patient4	p.M545K	ENSG00000197414	ENST00000316397	Transcript	missense_variant	unknown(0)
chr15	52439671	52439671	*GNB5*	Missense_Mutation	.	SNP	C	C	T	novel	Patient4	p.C160Y	ENSG00000069966	ENST00000261837	Transcript	missense_variant	probably_damaging(0.992)
chr15	82530841	82530841	*EFTUD1*	Missense_Mutation	.	SNP	G	G	T	novel	Patient4	p.L180I	ENSG00000140598	ENST00000268206	Transcript	missense_variant	possibly_damaging(0.649)
chr17	26943438	26943438	*KIAA0100*	Missense_Mutation	.	SNP	G	G	A	novel	Patient4	p.R2083W	ENSG00000007202	ENST00000528896	Transcript	missense_variant	probably_damaging(0.993)
chr17	39221816	39221816	*KRTAP2-4*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient4	p.W94*	ENSG00000213417	ENST00000394015	Transcript	stop_gained	NA
chr17	44091670	44091670	*MAPT*	Missense_Mutation	.	SNP	G	G	A	novel	Patient4	p.G661D	ENSG00000186868	ENST00000344290	Transcript	missense_variant	benign(0.307)
chr17	72346628	72346628	*KIF19*	Missense_Mutation	.	SNP	G	G	A	novel	Patient4	p.M434I	ENSG00000196169	ENST00000389916	Transcript	missense_variant	benign(0.091)
chr19	36004372	36004372	*DMKN*	Missense_Mutation	.	SNP	C	C	A	novel	Patient4	p.K2N	ENSG00000161249	ENST00000339686	Transcript	missense_variant	probably_damaging(0.985)
chr19	55286836	55286836	*KIR2DL1*	Missense_Mutation	.	SNP	G	G	C	novel	Patient4	p.R197T	ENSG00000125498	ENST00000336077	Transcript	missense_variant	benign(0.045)
chr2	197157288	197157288	*HECW2*	Splice_Site	.	SNP	C	C	T	novel	Patient4	NA	ENSG00000138411	ENST00000260983	Transcript	splice_donor_variant	NA
chr2	20911311	20911311	*IDH1*	Missense_Mutation	.	SNP	G	G	C	rs121913499	Patient4	p.R132G	ENSG00000138413	ENST00000415913	Transcript	missense_variant	probably_damaging(0.998)
chr20	36150802	36150802	*NNAT*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient4	p.R39*	ENSG00000053438	ENST00000062104	Transcript	stop_gained	NA
chr21	47423734	47423734	*COL6A1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient4	p.A965E	ENSG00000142156	ENST00000361866	Transcript	missense_variant	probably_damaging(0.979)
chr3	38151691	38151691	*DLEC1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient4	p.R1121H	ENSG00000008226	ENST00000308059	Transcript	missense_variant	benign(0)
chr3	75788230	75788230	*ZNF717*	Missense_Mutation	.	SNP	C	C	T	novel	Patient4	p.V182I	ENSG00000227124	ENST00000422325	Transcript	missense_variant	benign(0.027)
chr4	88732765	88732765	*IBSP*	Missense_Mutation	.	SNP	G	G	T	novel	Patient4	p.R219S	ENSG00000029559	ENST00000226284	Transcript	missense_variant	benign(0.034)
chr5	140052227	140052227	*DND1*	Missense_Mutation	.	SNP	T	T	C	rs200604559	Patient4	p.E136G	ENSG00000256453	ENST00000542735	Transcript	missense_variant	probably_damaging(0.948)
chr5	82834433	82834433	*VCAN*	Missense_Mutation	.	SNP	T	T	C	novel	Patient4	p.S1871P	ENSG00000038427	ENST00000265077	Transcript	missense_variant	benign(0.015)
chr6	136594292	136594292	*BCLAF1*	Missense_Mutation	.	SNP	T	T	C	rs7381749	Patient4	p.N629S	ENSG00000029363	ENST00000531224	Transcript	missense_variant	possibly_damaging(0.486)

chr6	145051577	145051577	*UTRN*	Missense_Mutation	.	SNP	A	A	G	rs115190750	Patient4	p.I2632V	ENSG00000152818	ENST00000367545	Transcript	missense_variant	benign(0.02)
chr6	32487344	32487344	*HLA-DRB5*	Missense_Mutation	.	SNP	T	T	C	rs201863832	Patient4	p.Y152C	ENSG00000198502	ENST00000374975	Transcript	missense_variant	probably_damaging(1)
chr6	93965643	93965643	*EPHA7*	Missense_Mutation	.	SNP	C	C	T	novel	Patient4	p.R762H	ENSG00000135333	ENST00000369303	Transcript	missense_variant	benign(0.005)
chr7	123303016	123303016	*LMOD2*	Missense_Mutation	.	SNP	T	T	G	novel	Patient4	p.I459S	ENSG00000170807	ENST00000458573	Transcript	missense_variant	probably_damaging(0.996)
chr7	75028393	75028393	*TRIM73*	Missense_Mutation	.	SNP	T	T	C	novel	Patient4	p.V59A	ENSG00000178809	ENST00000323819	Transcript	missense_variant	benign(0)
chr8	67935533	67935533	*DEFA4*	Missense_Mutation	.	SNP	G	G	A	rs559546450	Patient4	p.R95C	ENSG00000164821	ENST00000297435	Transcript	missense_variant	benign(0.001)
chr9	34521596	34521596	*ENHO*	Missense_Mutation	.	SNP	G	G	A	novel	Patient4	p.A33V	ENSG00000168913	ENST00000399775	Transcript	missense_variant	possibly_damaging(0.682)
chr1	151553512	151553512	*TUFT1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient5	p.P368L	ENSG00000143367	ENST00000368849	Transcript	missense_variant	benign(0.002)
chr1	158605703	158605703	*SPTA1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient5	p.R1811Q	ENSG00000163554	ENST00000368147	Transcript	missense_variant	probably_damaging(1)
chr1	164621676	164621676	*EPHA2*	Nonsense_Mutation	.	SNP	T	T	A	novel	Patient5	p.K468*	ENSG00000142627	ENST00000358432	Transcript	stop_gained	NA
chr1	171535854	171535854	*PRRC2C*	Missense_Mutation	.	SNP	C	C	A	novel	Patient5	p.P2142T	ENSG00000117523	ENST00000338920	Transcript	missense_variant	benign(0.14)
chr1	201180409	201180409	*IGFN1*	Missense_Mutation	.	SNP	A	A	G	novel	Patient5	p.S2130G	ENSG00000163395	ENST00000335211	Transcript	missense_variant	unknown(0)
chr1	205027755	205027755	*CNTN2*	Missense_Mutation	.	SNP	G	G	T	novel	Patient5	p.V151L	ENSG00000184144	ENST00000331830	Transcript	missense_variant	benign(0.07)
chr1	35824927	35824927	*ZMYM4*	Missense_Mutation	.	SNP	A	A	C	novel	Patient5	p.K163Q	ENSG00000146463	ENST00000314607	Transcript	missense_variant	benign(0.03)
chr1	92441876	92441876	*BRDT*	Missense_Mutation	.	SNP	G	G	A	rs112246679	Patient5	p.A167T	ENSG00000137948	ENST00000362005	Transcript	missense_variant	benign(0.004)
chr10	37430895	37430895	*ANKRD30A*	Missense_Mutation	.	SNP	C	C	T	novel	Patient5	p.T301I	ENSG00000148513	ENST00000361713	Transcript	missense_variant	possibly_damaging(0.86)
chr12	95416118	95416118	*NR2C1*	Nonsense_Mutation	.	SNP	C	C	A	novel	Patient5	p.E567*	ENSG00000120798	ENST00000333003	Transcript	stop_gained	NA
chr15	33795931	33795931	*RYR3*	Missense_Mutation	.	SNP	G	G	A	novel	Patient5	p.G91S	ENSG00000198838	ENST00000389232	Transcript	missense_variant	benign(0.01)
chr16	53967898	53967898	*FTO*	Missense_Mutation	.	SNP	C	C	G	novel	Patient5	p.T414R	ENSG00000140718	ENST00000471389	Transcript	missense_variant	possibly_damaging(0.873)
chr16	71884890	71884890	*ATXN1L*	Missense_Mutation	.	SNP	C	C	A	novel	Patient5	p.A416D	ENSG00000224470	ENST00000427980	Transcript	missense_variant	probably_damaging(0.997)
chr17	19645434	19645434	*ALDH3A1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient5	p.G191A	ENSG00000108602	ENST00000457500	Transcript	missense_variant	benign(0.02)
chr17	38128387	38128387	*GSDMA*	Missense_Mutation	.	SNP	C	C	A	novel	Patient5	p.P221T	ENSG00000167914	ENST00000301659	Transcript	missense_variant	probably_damaging(0.989)
chr17	40344493	40344493	*GHDC*	Nonsense_Mutation	.	SNP	C	C	A	novel	Patient5	p.E219*	ENSG00000167925	ENST00000301671	Transcript	stop_gained	NA
chr17	42294007	42294007	*UBTF*	Missense_Mutation	.	SNP	C	C	A	novel	Patient5	p.D42Y	ENSG00000108312	ENST00000302904	Transcript	missense_variant	probably_damaging(0.999)
chr19	16060302	16060302	*OR10H4*	Missense_Mutation	.	SNP	C	C	T	novel	Patient5	p.T162M	ENSG00000176231	ENST00000322107	Transcript	missense_variant	benign(0.009)
chr19	17010309	17010309	*CPAMD8*	Nonsense_Mutation	.	SNP	G	G	A	novel	Patient5	p.R1656*	ENSG00000160111	ENST00000443236	Transcript	stop_gained	NA
chr19	41354538	41354538	*CYP2A6*	Missense_Mutation	.	SNP	G	G	C	rs60605885	Patient5	p.D158E	ENSG00000255974	ENST00000301141	Transcript	missense_variant	benign(0)
chr19	55263700	55263700	*KIR2DL3*	Missense_Mutation	.	SNP	A	A	G	novel	Patient5	p.N285D	ENSG00000243772	ENST00000342376	Transcript	missense_variant	benign(0.001)
chr19	55285082	55285082	*KIR2DL1*	Missense_Mutation	.	SNP	T	T	C	novel	Patient5	p.I123T	ENSG00000125498	ENST00000336077	Transcript	missense_variant	benign(0.001)
chr19	55340875	55340875	*KIR3DL1*	Missense_Mutation	.	SNP	c	c	A	novel	Patient5	p.L354I	ENSG00000167633	ENST00000391728	Transcript	missense_variant	benign(0.001)
chr2	170103393	170103393	*LRP2*	Missense_Mutation	.	SNP	C	C	A	novel	Patient5	p.M1004I	ENSG00000081479	ENST00000263816	Transcript	missense_variant	possibly_damaging(0.871)
chr2	204022462	204022462	*NBEAL1*	Frame_Shift_Del	.	DEL	G	G	-	novel	Patient5	p.E1848Kfs*2	ENSG00000144426	ENST00000449802	Transcript	frameshift_variant	NA
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	Patient5	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	85570849	85570849	*RETSAT*	Missense_Mutation	.	SNP	C	C	T	rs4832168	Patient5	p.G536R	ENSG00000042445	ENST00000295802	Transcript	missense_variant	probably_damaging(0.998)
chr3	52437565	52437565	*BAP1*	Frame_Shift_Del	.	DEL	A	A	-	novel	Patient5	p.F532Lfs*39	ENSG00000163930	ENST00000460680	Transcript	frameshift_variant	NA
chr4	146824256	146824256	*ZNF827*	Missense_Mutation	.	SNP	T	T	C	novel	Patient5	p.Y52C	ENSG00000151612	ENST00000379448	Transcript	missense_variant	possibly_damaging(0.771)

chr4	191003213	191003213	*DUX4L4*	Missense_Mutation	.	SNP	G	G	C	novel	Patient5	p.R375P	ENSG00000258834	ENST00000538692	Transcript	missense_variant	benign(0.415)
chr4	42282423	42282423	*OTOP1*	Missense_Mutation	.	SNP	G	G	T	rs200057225	Patient5	p.H117N	ENSG00000163982	ENST00000296358	Transcript	missense_variant	benign(0.009)
chr5	127610310	127610310	*FBN2*	Missense_Mutation	.	SNP	A	A	C	novel	Patient5	p.F2554V	ENSG00000138829	ENST00000508053	Transcript	missense_variant	probably_damaging(1)
chr5	140048015	140048015	*WDR55*	Missense_Mutation	.	SNP	C	C	T	novel	Patient5	p.S103F	ENSG00000120314	ENST00000358337	Transcript	missense_variant	probably_damaging(0.999)
chr5	140347642	140347642	*PCDHAC2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient5	p.R431W	ENSG00000243232	ENST00000289269	Transcript	missense_variant	possibly_damaging(0.846)
chr5	53814341	53814341	*SNX18*	Missense_Mutation	.	SNP	G	G	A	novel	Patient5	p.V187M	ENSG00000178996	ENST00000326277	Transcript	missense_variant	benign(0.007)
chr6	111636540	111636540	*REV3L*	Missense_Mutation	.	SNP	T	T	G	novel	Patient5	p.K2799T	ENSG00000009413	ENST00000358835	Transcript	missense_variant	probably_damaging(0.997)
chr6	11191369	11191369	*NEDD9*	Missense_Mutation	.	SNP	G	G	A	novel	Patient5	p.P245S	ENSG00000111859	ENST00000379446	Transcript	missense_variant	benign(0.007)
chr6	136594292	136594292	*BCLAF1*	Missense_Mutation	.	SNP	T	T	C	rs7381749	Patient5	p.N629S	ENSG00000029363	ENST00000531224	Transcript	missense_variant	possibly_damaging(0.486)
chr6	35911932	35911932	*SLC26A8*	Missense_Mutation	.	SNP	C	C	T	novel	Patient5	p.M886I	ENSG00000112053	ENST00000490799	Transcript	missense_variant	benign(0)
chr6	70964698	70964698	*COL9A1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient5	p.R545C	ENSG00000112280	ENST00000357250	Transcript	missense_variant	probably_damaging(0.935)
chr7	154863304	154863304	*HTR5A*	Missense_Mutation	.	SNP	G	G	T	novel	Patient5	p.G232V	ENSG00000157219	ENST00000287907	Transcript	missense_variant	possibly_damaging(0.904)
chr7	20824970	20824970	*SP8*	Missense_Mutation	.	SNP	c	c	T	novel	Patient5	p.G156S	ENSG00000164651	ENST00000418710	Transcript	missense_variant	benign(0.007)
chr7	73030463	73030463	*MLXIPL*	Frame_Shift_Ins	.	INS	-	-	T	novel	Patient5	p.L114Afs*40	ENSG00000009950	ENST00000313375	Transcript	frameshift_variant	NA
chr8	133816130	133816130	*PHF20L1*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient5	p.R192*	ENSG00000129292	ENST00000395386	Transcript	stop_gained	NA
chr1	89735096	89735096	*GBP5*	Missense_Mutation	.	SNP	C	C	T	rs61735237	Patient6	p.R48H	ENSG00000154451	ENST00000343435	Transcript	missense_variant	benign(0.311)
chr10	126691579	126691579	*CTBP2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient6	p.R643Q	ENSG00000175029	ENST00000309035	Transcript	missense_variant	probably_damaging(1)
chr10	152553099	152553099	*FAM171A1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient6	p.A730S	ENSG00000148468	ENST00000378116	Transcript	missense_variant	probably_damaging(0.999)
chr10	29811469	29811469	*SVIL*	Missense_Mutation	.	SNP	C	C	T	novel	Patient6	p.D1087N	ENSG00000197321	ENST00000375398	Transcript	missense_variant	benign(0.258)
chr11	57585549	57585549	*OR56B1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient6	p.S268L	ENSG00000181023	ENST00000317121	Transcript	missense_variant	possibly_damaging(0.864)
chr11	63885724	63885724	*FLRT1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient6	p.R662Q	ENSG00000126500	ENST00000246841	Transcript	missense_variant	probably_damaging(1)
chr12	10584728	10584728	*KLRC2*	Missense_Mutation	.	SNP	T	T	C	rs373433059	Patient6	p.I187M	ENSG00000205809	ENST00000381902	Transcript	missense_variant	benign(0.132)
chr12	11507480	11507480	*PRB1*	Nonsense_Mutation	.	SNP	G	G	A	novel	Patient6	p.Q25*	ENSG00000251655	ENST00000500254	Transcript	stop_gained	NA
chr12	118533556	118533556	*VSIG10*	Missense_Mutation	.	SNP	G	G	A	novel	Patient6	p.S48L	ENSG00000176834	ENST00000359236	Transcript	missense_variant	benign(0.077)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	Patient6	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr12	29936562	29936562	*TMTC1*	Nonsense_Mutation	.	SNP	G	G	T	novel	Patient6	p.Y41*	ENSG00000133687	ENST00000539277	Transcript	stop_gained	NA
chr14	105421308	105421308	*AHNAK2*	Missense_Mutation	.	SNP	C	C	G	novel	Patient6	p.G213R	ENSG00000185567	ENST00000333244	Transcript	missense_variant	probably_damaging(0.952)
chr15	74364639	74364639	*GOLGA6A*	Missense_Mutation	.	SNP	G	G	C	rs200350318	Patient6	p.Q505E	ENSG00000159289	ENST00000290438	Transcript	missense_variant	benign(0)
chr16	66730332	66730332	*CMTM4*	Missense_Mutation	.	SNP	G	G	A	novel	Patient6	p.P33S	ENSG00000183723	ENST00000330687	Transcript	missense_variant	probably_damaging(0.996)
chr17	42103944	42103944	*UBE2G1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient6	p.G24D	ENSG00000132388	ENST00000396981	Transcript	missense_variant	probably_damaging(0.996)
chr17	45258951	45258951	*CDC27*	Missense_Mutation	.	SNP	A	A	G	rs62077275	Patient6	p.L27P	ENSG00000004897	ENST00000531206	Transcript	missense_variant	probably_damaging(0.932)
chr17	7592025	7592025	*WRAP53*	Missense_Mutation	.	SNP	C	C	T	novel	Patient6	p.P20L	ENSG00000141499	ENST00000316024	Transcript	missense_variant	benign(0.028)
chr19	12219933	12219933	*STK11*	Missense_Mutation	.	SNP	T	T	G	novel	Patient6	p.I303S	ENSG00000118046	ENST00000326873	Transcript	missense_variant	probably_damaging(0.998)
chr19	36348062	36348062	*KIRREL2*	Missense_Mutation	.	SNP	T	T	G	novel	Patient6	p.F14C	ENSG00000126259	ENST00000360202	Transcript	missense_variant	benign(0.001)
chr19	45412367	45412367	*APOE*	Missense_Mutation	.	SNP	G	G	T	novel	Patient6	p.A272S	ENSG00000130203	ENST00000252486	Transcript	missense_variant	probably_damaging(0.991)
chr2	130832598	130832598	*POTEF*	Missense_Mutation	.	SNP	C	C	T	rs3948036	Patient6	p.R816H	ENSG00000196604	ENST00000357462	Transcript	missense_variant	benign(0.005)

chr3	122287478	122287478	*DTX3L*	Missense_Mutation	.	SNP	T	T	C	novel	Patient6	p.I181T	ENSG00000163840	ENST00000296161	Transcript	missense_variant	possibly_damaging(0.573)
chr5	121187794	121187794	*FTMT*	Missense_Mutation	.	SNP	C	C	T	novel	Patient6	p.R46C	ENSG00000181867	ENST00000321339	Transcript	missense_variant	benign(0)
chr5	37052579	37052579	*NIPBL*	Missense_Mutation	.	SNP	T	T	C	novel	Patient6	p.C2392R	ENSG00000164190	ENST00000282516	Transcript	missense_variant	probably_damaging(0.993)
chr6	32632706	32632706	*HLA-DQB1*	Missense_Mutation	.	SNP	G	G	C	rs200780973	Patient6	p.T83R	ENSG00000179344	ENST00000374943	Transcript	missense_variant	probably_damaging(0.996)
chr7	127014813	127014813	*ZNF800*	Missense_Mutation	.	SNP	G	G	A	novel	Patient6	p.P193S	ENSG00000048405	ENST00000393313	Transcript	missense_variant	benign(0.001)
chr12	11183340	111833340	*TAS2R31*	Missense_Mutation	.	SNP	T	T	C	novel	Patient7	p.I199V	ENSG00000256436	ENST00000390675	Transcript	missense_variant	benign(0.248)
chr12	11214752	112147452	*TAS2R46*	Missense_Mutation	.	SNP	G	G	C	novel	Patient7	p.L48V	ENSG00000226761	ENST00000533467	Transcript	missense_variant	benign(0.319)
chr12	20968704	209687004	*SLCO1B3*	Missense_Mutation	.	SNP	C	C	A	novel	Patient7	p.A11E	ENSG00000111700	ENST00000381545	Transcript	missense_variant	benign(0.002)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	Patient7	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr19	22836805	22836805	*ZNF492*	Missense_Mutation	.	SNP	G	G	A	rs200144130	Patient7	p.A40T	ENSG00000229676	ENST00000456783	Transcript	missense_variant	possibly_damaging(0.811)
chr4	191003234	191003234	*DUX4L4*	Missense_Mutation	.	SNP	C	C	T	novel	Patient7	p.A382V	ENSG00000258834	ENST00000538692	Transcript	missense_variant	benign(0.004)
chr4	26737075	26737075	*TBC1D19*	Splice_Site	.	SNP	A	A	T	novel	Patient7	p.X362_splice	ENSG00000109680	ENST00000264866	Transcript	splice_acceptor_variant	NA
chr6	29798157	29798157	*HLA-G*	Nonstop_Mutation	.	SNP	T	T	A	rs376635255	Patient7	p.*339Rext*11	ENSG00000204632	ENST00000428701	Transcript	stop_lost	NA
chr1	109792751	109792751	*CELSR2*	Missense_Mutation	.	SNP	t	t	C	rs200277265	Patient8	p.L17P	ENSG00000143126	ENST00000271332	Transcript	missense_variant	unknown(0)
chr1	154842196	154842196	*KCNN3*	Missense_Mutation	.	SNP	G	G	T	novel	Patient8	p.P82Q	ENSG00000143603	ENST00000271915	Transcript	missense_variant	unknown(0)
chr1	161596072	161596072	*FCGR3B*	Missense_Mutation	.	SNP	T	T	C	novel	Patient8	p.D183G	ENSG00000162747	ENST00000531221	Transcript	missense_variant	benign(0)
chr1	17272075	172720075	*CROCC*	Missense_Mutation	.	SNP	G	G	A	rs2781608	Patient8	p.A704T	ENSG00000058453	ENST00000375541	Transcript	missense_variant	benign(0.26)
chr1	24288284	242882842	*PNRC2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient8	p.H113Y	ENSG00000189266	ENST00000334351	Transcript	missense_variant	possibly_damaging(0.813)
chr1	32377354	323773754	*PTP4A2*	Missense_Mutation	.	SNP	T	T	A	novel	Patient8	p.K88I	ENSG00000184007	ENST00000344035	Transcript	missense_variant	probably_damaging(0.942)
chr10	123263395	123263395	*FGFR2*	Missense_Mutation	.	SNP	G	G	A	rs536181987	Patient8	p.R451C	ENSG00000066468	ENST00000457416	Transcript	missense_variant	probably_damaging(0.961)
chr11	63175629	63175629	*SLC22A9*	Missense_Mutation	.	SNP	C	C	T	rs138350283	Patient8	p.A445V	ENSG00000149742	ENST00000279178	Transcript	missense_variant	benign(0.022)
chr12	25398281	25398281	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	Patient8	p.G13D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.506)
chr14	21109808	21109808	*OR6S1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient8	p.V15I	ENSG00000181803	ENST00000320704	Transcript	missense_variant	benign(0.002)
chr14	70924335	70924335	*ADAM21*	Missense_Mutation	.	SNP	C	C	T	rs199920662	Patient8	p.P40L	ENSG00000139985	ENST00000603540	Transcript	missense_variant	benign(0.262)
chr17	35988709	35988709	*DDX52*	Missense_Mutation	.	SNP	C	C	T	novel	Patient8	p.R252K	ENSG00000141141	ENST00000349699	Transcript	missense_variant	possibly_damaging(0.718)
chr17	46924003	46924003	*GLTPD2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient8	p.R33W	ENSG00000182327	ENST00000331264	Transcript	missense_variant	benign(0.002)
chr18	51750584	51750585	*MBD2*	In_Frame_Ins	.	INS	-	-	GCC	novel	Patient8	p.G115dup	ENSG00000134046	ENST00000256429	Transcript	inframe_insertion	NA
chr19	22497993	22497993	*ZNF729*	Missense_Mutation	.	SNP	G	G	A	novel	Patient8	p.V592I	ENSG00000196350	ENST00000601693	Transcript	missense_variant	benign(0.009)
chr20	39830851	39830851	*ZHX3*	Missense_Mutation	.	SNP	C	C	A	novel	Patient8	p.Q902H	ENSG00000174306	ENST00000309060	Transcript	missense_variant	benign(0.004)
chr3	45817302	45817302	*SLC6A20*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient8	p.W178*	ENSG00000163817	ENST00000358525	Transcript	stop_gained	NA
chr4	367169	367169	*ZNF141*	Missense_Mutation	.	SNP	G	G	A	novel	Patient8	p.E315K	ENSG00000131127	ENST00000240499	Transcript	missense_variant	probably_damaging(0.966)
chr5	134010747	134010747	*SEC24A*	Missense_Mutation	.	SNP	G	G	T	novel	Patient8	p.A331S	ENSG00000113615	ENST00000398844	Transcript	missense_variant	benign(0.009)
chr7	127222146	127222146	*GCC1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient8	p.L750F	ENSG00000179562	ENST00000321407	Transcript	missense_variant	probably_damaging(1)
chr8	104933932	104933932	*RIMS2*	Missense_Mutation	.	SNP	C	C	T	rs530250614	Patient8	p.R706C	ENSG00000176406	ENST00000406091	Transcript	missense_variant	probably_damaging(0.997)
chr9	35906601	35906601	*HRCT1*	Missense_Mutation	.	SNP	c	c	A	rs112212538	Patient8	p.P106H	ENSG00000196196	ENST00000354323	Transcript	missense_variant	unknown(0)
chrX	64959036	64959036	*MSN*	Missense_Mutation	.	SNP	C	C	T	novel	Patient8	p.R517C	ENSG00000147065	ENST00000360270	Transcript	missense_variant	probably_damaging(0.988)

chr1	152192345	152192345	*HRNR*	Missense_Mutation	.	SNP	T	T	C	rs201037339	Patient9	p.Q587R	ENSG00000197915	ENST00000368801	Transcript	missense_variant	unknown(0)
chr1	201179521	201179521	*IGFN1*	Missense_Mutation	.	SNP	G	G	A	rs373128981	Patient9	p.A1834T	ENSG00000163395	ENST00000335211	Transcript	missense_variant	benign(0.144)
chr10	135439804	135439804	*FRG2B*	Missense_Mutation	.	SNP	G	G	C	novel	Patient9	p.S61W	ENSG00000225899	ENST00000425520	Transcript	missense_variant	possibly_damaging(0.809)
chr12	11461427	11461427	*PRB4*	Missense_Mutation	.	SNP	C	C	T	rs200289411	Patient9	p.G164R	ENSG00000230657	ENST00000279575	Transcript	missense_variant	unknown(0)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	Patient9	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr12	72023388	72023388	*ZFC3H1*	Splice_Site	.	SNP	C	C	T	novel	Patient9	NA	ENSG00000133858	ENST00000378743	Transcript	splice_donor_variant	NA
chr19	44891010	44891010	*ZNF285*	Missense_Mutation	.	SNP	G	G	C	rs150792548	Patient9	p.A466G	ENSG00000267508	ENST00000330997	Transcript	missense_variant	benign(0.003)
chr19	53770747	53770747	*VN1R4*	Missense_Mutation	.	SNP	G	G	A	rs145154362	Patient9	p.R58C	ENSG00000228567	ENST00000311170	Transcript	missense_variant	benign(0.018)
chr19	55086927	55086927	*LILRA2*	Missense_Mutation	.	SNP	C	C	G	novel	Patient9	p.P287R	ENSG00000239998	ENST00000251377	Transcript	missense_variant	benign(0.001)
chr19	55250953	55250953	*KIR2DL3*	Missense_Mutation	.	SNP	G	G	C	novel	Patient9	p.G12A	ENSG00000243772	ENST00000342376	Transcript	missense_variant	benign(0.024)
chr7	57188007	57188007	*ZNF479*	Missense_Mutation	.	SNP	C	C	T	novel	Patient9	p.R372K	ENSG00000185177	ENST00000331162	Transcript	missense_variant	benign(0)
chr8	124382158	124382158	*ATAD2*	Missense_Mutation	.	SNP	t	t	A	rs373069275	Patient9	p.E278D	ENSG00000156802	ENST00000287394	Transcript	missense_variant	benign(0.002)
chr1	152192345	152192345	*HRNR*	Missense_Mutation	.	SNP	T	T	C	rs201037339	Patient10	p.Q587R	ENSG00000197915	ENST00000368801	Transcript	missense_variant	unknown(0)
chr1	53925343	53925343	*DMRTB1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient10	p.G73R	ENSG00000143006	ENST00000371445	Transcript	missense_variant	probably_damaging(0.946)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	Patient10	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr17	39394539	39394539	*KRTAP9-8*	Missense_Mutation	.	SNP	C	C	T	rs201444580	Patient10	p.T79I	ENSG00000187272	ENST00000254072	Transcript	missense_variant	unknown(0)
chr17	65822269	65822269	*BPTF*	In_Frame_Del	.	DEL	GAG	GAG	-	rs369989246	Patient10	p.E143del	ENSG00000171634	ENST00000306378	Transcript	inframe_deletion	NA
chr19	41595958	41595958	*CYP2A13*	Missense_Mutation	.	SNP	C	C	T	rs757030709	Patient10	p.A117V	ENSG00000197838	ENST00000330436	Transcript	missense_variant	benign(0.019)
chr3	75790820	75790820	*ZNF717*	Missense_Mutation	.	SNP	G	G	A	rs747789223	Patient10	p.A42V	ENSG00000227124	ENST00000422325	Transcript	missense_variant	probably_damaging(0.918)
chr7	75028249	75028249	*TRIM73*	Missense_Mutation	.	SNP	A	A	G	novel	Patient10	p.E11G	ENSG00000178809	ENST00000323819	Transcript	missense_variant	possibly_damaging(0.493)
chr1	109824461	109824461	*PSRC1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.G100D	ENSG00000134222	ENST00000369909	Transcript	missense_variant	probably_damaging(0.929)
chr1	115258747	115258747	*NRAS*	Missense_Mutation	.	SNP	C	C	A	novel	Patient11	p.G12V	ENSG00000213281	ENST00000369535	Transcript	missense_variant	possibly_damaging(0.902)
chr1	158368443	158368443	*OR10T2*	Nonsense_Mutation	.	SNP	G	G	A	novel	Patient11	p.Q272*	ENSG00000186306	ENST00000334438	Transcript	stop_gained	NA
chr1	164749	164749	*EPHA2*	Frame_Shift_Ins	.	INS	-	-	C	novel	Patient11	p.E241*	ENSG00000142627	ENST00000358432	Transcript	frameshift_variant	NA
chr1	216138706	216138706	*USH2A*	Missense_Mutation	.	SNP	A	A	T	novel	Patient11	p.L2358H	ENSG00000042781	ENST00000307340	Transcript	missense_variant	benign(0)
chr1	237666726	237666726	*RYR2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.T845I	ENSG00000198626	ENST00000366574	Transcript	missense_variant	benign(0.013)
chr1	24496029	24496029	*PANK4*	Splice_Site	.	SNP	C	C	T	novel	Patient11	p.X406_splice	ENSG00000157881	ENST00000378466	Transcript	splice_donor_variant	NA
chr1	29475717	29475717	*SRSF4*	Missense_Mutation	.	SNP	G	G	C	novel	Patient11	p.S230R	ENSG00000116350	ENST00000373795	Transcript	missense_variant	benign(0.307)
chr11	33123810	33123810	*CSTF3*	Nonsense_Mutation	.	SNP	G	G	A	novel	Patient11	p.Q247*	ENSG00000176102	ENST00000323959	Transcript	stop_gained	NA
chr11	66061833	66061833	*TMEM151A*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.R39H	ENSG00000179292	ENST00000327259	Transcript	missense_variant	probably_damaging(0.998)
chr11	68331829	68331829	*PPP6R3*	Missense_Mutation	.	SNP	A	A	G	novel	Patient11	p.N302D	ENSG00000110075	ENST00000393801	Transcript	missense_variant	benign(0.025)
chr12	108006587	108006587	*BTBD11*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.R614C	ENSG00000151136	ENST00000280758	Transcript	missense_variant	probably_damaging(0.991)
chr12	14766128	14766128	*GUCY2C*	Missense_Mutation	.	SNP	G	G	A	rs140551603	Patient11	p.R1049W	ENSG00000070019	ENST00000261170	Transcript	missense_variant	possibly_damaging(0.88)
chr12	53691828	53691828	*PFDN5*	Splice_Site	.	SNP	G	G	A	novel	Patient11	NA	ENSG00000123349	ENST00000551018	Transcript	splice_acceptor_variant	NA
chr12	56481922	56481922	*ERBB3*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.G284R	ENSG00000065361	ENST00000267101	Transcript	missense_variant	probably_damaging(0.981)
chr12	58217774	58217774	*CTDSP2*	Missense_Mutation	.	SNP	C	C	A	rs113792624	Patient11	p.K201N	ENSG00000175215	ENST00000398073	Transcript	missense_variant	probably_damaging(1)

chr12	67699246	67699246	*CAND1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient11	p.L600V	ENSG00000111530	ENST00000545606	Transcript	missense_variant	benign(0.114)
chr12	6777112	6777112	*ZNF384*	Missense_Mutation	.	SNP	t	t	G	novel	Patient11	p.Q501P	ENSG00000126746	ENST00000396801	Transcript	missense_variant	benign(0.153)
chr13	114138359	114138359	*DCUN1D2*	Missense_Mutation	.	SNP	A	A	T	novel	Patient11	p.S6T	ENSG00000150401	ENST00000478244	Transcript	missense_variant	benign(0.099)
chr13	38320090	38320090	*TRPC4*	Missense_Mutation	.	SNP	T	T	G	novel	Patient11	p.K294T	ENSG00000133107	ENST00000379681	Transcript	missense_variant	probably_damaging(0.996)
chr13	41766767	41766767	*KBTBD7*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.E543K	ENSG00000120696	ENST00000379483	Transcript	missense_variant	benign(0.025)
chr15	43270095	43270095	*UBR1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient11	p.D1401Y	ENSG00000159459	ENST00000290650	Transcript	missense_variant	probably_damaging(1)
chr15	66610933	66610933	*DIS3L*	Missense_Mutation	.	SNP	A	A	G	novel	Patient11	p.T381A	ENSG00000166938	ENST00000319212	Transcript	missense_variant	benign(0.049)
chr15	74473699	74473699	*STRA6*	Missense_Mutation	.	SNP	C	C	T	rs375362287	Patient11	p.A580T	ENSG00000137868	ENST00000563965	Transcript	missense_variant	benign(0.005)
chr15	84592666	84592666	*ADAMTSL3*	Missense_Mutation	.	SNP	A	A	C	novel	Patient11	p.E666D	ENSG00000156218	ENST00000286744	Transcript	missense_variant	probably_damaging(0.916)
chr15	86312993	86312993	*KLHL25*	Missense_Mutation	.	SNP	A	A	G	novel	Patient11	p.S17P	ENSG00000183655	ENST00000337975	Transcript	missense_variant	benign(0.174)
chr17	39274364	39274364	*KRTAP4-11*	Missense_Mutation	.	SNP	T	T	G	novel	Patient11	p.R68S	ENSG00000212721	ENST00000391413	Transcript	missense_variant	unknown(0)
chr17	39324237	39324237	*KRTAP4-3*	Missense_Mutation	.	SNP	c	c	G	novel	Patient11	p.S63T	ENSG00000196156	ENST00000391356	Transcript	missense_variant	unknown(0)
chr17	7577121	7577121	*TP53*	Missense_Mutation	.	SNP	G	G	A	rs121913343	Patient11	p.R273C	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.998)
chr17	80577005	80577005	*WDR45B*	Splice_Site	.	SNP	C	C	G	novel	Patient11	p.X207_splice	ENSG00000141580	ENST00000392325	Transcript	splice_acceptor_variant	NA
chr18	29444634	29444634	*TRAPPC8*	Nonsense_Mutation	.	SNP	G	G	A	novel	Patient11	p.R901*	ENSG00000153339	ENST00000283351	Transcript	stop_gained	NA
chr19	45161107	45161107	*PVR*	Missense_Mutation	.	SNP	A	A	T	novel	Patient11	p.N307I	ENSG00000073008	ENST00000425690	Transcript	missense_variant	probably_damaging(1)
chr2	125521340	125521340	*CNTNAP5*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.A775T	ENSG00000155052	ENST00000431078	Transcript	missense_variant	possibly_damaging(0.604)
chr2	141232842	141232842	*LRP1B*	Missense_Mutation	.	SNP	T	T	A	novel	Patient11	p.N3164Y	ENSG00000168702	ENST00000389484	Transcript	missense_variant	possibly_damaging(0.703)
chr2	153575538	153575538	*ARL6IP6*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.E134K	ENSG00000177917	ENST00000326446	Transcript	missense_variant	benign(0.438)
chr2	166909454	166909454	*SCN1A*	Splice_Site	.	SNP	C	C	T	novel	Patient11	p.X201_splice	ENSG00000144285	ENST00000303395	Transcript	splice_acceptor_variant	NA
chr2	17898161	17898161	*SMC6*	Missense_Mutation	.	SNP	G	G	C	novel	Patient11	p.S398C	ENSG00000163029	ENST00000448223	Transcript	missense_variant	benign(0.021)
chr2	196834773	196834773	*DNAH7*	Missense_Mutation	.	SNP	G	G	T	novel	Patient11	p.Q702K	ENSG00000118997	ENST00000312428	Transcript	missense_variant	possibly_damaging(0.573)
chr2	237489664	237489664	*ACKR3*	Missense_Mutation	.	SNP	G	G	A	rs143561143	Patient11	p.V186I	ENSG00000144476	ENST00000272928	Transcript	missense_variant	benign(0.056)
chr2	27604495	27604495	*PPM1G*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.D538N	ENSG00000115241	ENST00000344034	Transcript	missense_variant	benign(0.081)
chr2	54886387	54886387	*SPTBN1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.E2114K	ENSG00000115306	ENST00000356805	Transcript	missense_variant	benign(0.002)
chr20	2795865	2795865	*TMEM239*	Missense_Mutation	.	SNP	G	G	A	rs143838675	Patient11	p.R12H	ENSG00000241690	ENST00000380593	Transcript	missense_variant	benign(0.068)
chr20	33026428	33026428	*ITCH*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.R265H	ENSG00000078747	ENST00000262650	Transcript	missense_variant	probably_damaging(0.999)
chr20	368812	368812	*TRIB3*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.P53L	ENSG00000101255	ENST00000217233	Transcript	missense_variant	benign(0.007)
chr20	44641960	44641960	*MMP9*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.T466M	ENSG00000100985	ENST00000372330	Transcript	missense_variant	benign(0.049)
chr20	95104422	95104422	*LAMP5*	Missense_Mutation	.	SNP	G	G	C	novel	Patient11	p.R273T	ENSG00000125869	ENST00000246070	Transcript	missense_variant	benign(0.326)
chr21	27423421	27423421	*APP*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.C186Y	ENSG00000142192	ENST00000346798	Transcript	missense_variant	benign(0.424)
chr21	45507715	45507715	*TRAPPC10*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.G892E	ENSG00000160218	ENST00000291574	Transcript	missense_variant	benign(0.005)
chr22	39355683	39355683	*APOBEC3A*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.H56Y	ENSG00000128383	ENST00000402255	Transcript	missense_variant	benign(0.021)
chr3	190159264	190159264	*TMEM207*	Missense_Mutation	.	SNP	T	T	G	novel	Patient11	p.N41H	ENSG00000198398	ENST00000354905	Transcript	missense_variant	benign(0.33)
chr3	53910736	53910736	*ACTR8*	Missense_Mutation	.	SNP	T	T	C	novel	Patient11	p.Y230C	ENSG00000113812	ENST00000335754	Transcript	missense_variant	probably_damaging(1)
chr4	166405714	166405714	*CPE*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.D311N	ENSG00000109472	ENST00000402744	Transcript	missense_variant	possibly_damaging(0.844)

chr5	151777675	151777675	*NMUR2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.E253K	ENSG00000132911	ENST00000255262	Transcript	missense_variant	benign(0.058)
chr6	157469898	157469898	*ARID1B*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient11	p.R898*	ENSG00000049618	ENST00000346085	Transcript	stop_gained	NA
chr6	30682828	30682828	*MDC1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.G42E	ENSG00000137337	ENST00000376406	Transcript	missense_variant	probably_damaging(0.998)
chr6	33053655	33053655	*HLA-DPB1*	Missense_Mutation	.	SNP	G	G	T	novel	Patient11	p.R249M	ENSG00000223865	ENST00000418931	Transcript	missense_variant	possibly_damaging(0.896)
chr7	48413084	48413084	*RADIL*	Missense_Mutation	.	SNP	C	C	T	rs199808263	Patient11	p.G940S	ENSG00000157927	ENST00000399583	Transcript	missense_variant	benign(0.01)
chr7	70239016	70239017	*AUTS2*	Frame_Shift_Ins	.	INS	-	-	T	novel	Patient11	p.S612Ffs*66	ENSG00000158321	ENST00000342771	Transcript	frameshift_variant	NA
chr7	72848627	72848627	*FZD9*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.A97V	ENSG00000188763	ENST00000344575	Transcript	missense_variant	benign(0.072)
chr8	105361055	105361055	*DCSTAMP*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.R92H	ENSG00000164935	ENST00000297581	Transcript	missense_variant	benign(0.019)
chr8	134024233	134024233	*TG*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.T2117I	ENSG00000042832	ENST00000220616	Transcript	missense_variant	benign(0.002)
chr8	144946763	144946763	*EPPK1*	Missense_Mutation	.	SNP	C	C	T	rs200639583	Patient11	p.R220H	ENSG00000227184	ENST00000525985	Transcript	missense_variant	benign(0.302)
chr8	28320800	28320800	*CSMD1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient11	p.G2878V	ENSG00000183117	ENST00000537824	Transcript	missense_variant	possibly_damaging(0.743)
chr8	56436511	56436511	*XKR4*	Missense_Mutation	.	SNP	G	G	A	novel	Patient11	p.D560N	ENSG00000206579	ENST00000327381	Transcript	missense_variant	benign(0.41)
chr8	82441695	82441695	*FABP12*	Missense_Mutation	.	SNP	G	G	A	rs536105592	Patient11	p.T75M	ENSG00000197416	ENST00000360464	Transcript	missense_variant	probably_damaging(0.996)
chr9	101900171	101900171	*TGFBR1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient11	p.A202V	ENSG00000106799	ENST00000374994	Transcript	missense_variant	probably_damaging(0.997)
chr9	138441166	138441166	*OBP2A*	Missense_Mutation	.	SNP	T	T	C	rs117518871	Patient11	p.L168P	ENSG00000122136	ENST00000539850	Transcript	missense_variant	benign(0)
chr9	18908505	18908505	*ADAMTSL1*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient11	p.Q1750*	ENSG00000178031	ENST00000380548	Transcript	stop_gained	NA
chr9	33796758	33796758	*PRSS3*	Missense_Mutation	.	SNP	T	T	A	novel	Patient11	p.I110N	ENSG00000010438	ENST00000361005	Transcript	missense_variant	probably_damaging(1)
chr9	8486263	8486263	*PTPRD*	Missense_Mutation	.	SNP	G	G	T	novel	Patient11	p.P852T	ENSG00000153707	ENST00000381196	Transcript	missense_variant	probably_damaging(0.998)
chr9	95277436	95277436	*ECM2*	Missense_Mutation	.	SNP	A	A	C	novel	Patient11	p.F177L	ENSG00000106823	ENST00000344604	Transcript	missense_variant	benign(0.002)
chr9	95277477	95277477	*ECM2*	Missense_Mutation	.	SNP	A	A	C	novel	Patient11	p.S164A	ENSG00000106823	ENST00000344604	Transcript	missense_variant	benign(0.001)
chr1	183616945	183616945	*APOBEC4*	Missense_Mutation	.	SNP	T	T	A	novel	Patient12	p.Q324H	ENSG00000173627	ENST00000308641	Transcript	missense_variant	benign(0.057)
chr1	210411339	210411339	*SERTAD4*	Missense_Mutation	.	SNP	G	G	A	rs146773666	Patient12	p.E12K	ENSG00000082497	ENST00000367012	Transcript	missense_variant	probably_damaging(0.986)
chr1	245765981	245765981	*KIF26B*	Missense_Mutation	.	SNP	G	G	A	novel	Patient12	p.D485N	ENSG00000162849	ENST00000407071	Transcript	missense_variant	unknown(0)
chr1	248525923	248525923	*OR2T4*	Missense_Mutation	.	SNP	G	G	A	rs138713748	Patient12	p.M347I	ENSG00000196944	ENST00000366475	Transcript	missense_variant	benign(0)
chr1	27057937	27057937	*ARID1A*	Frame_Shift_Del	.	DEL	C	C	-	novel	Patient12	p.Y551Tfs*68	ENSG00000117713	ENST00000324856	Transcript	frameshift_variant	NA
chr1	9790744	9790744	*CLSTN1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient12	p.S923I	ENSG00000171603	ENST00000377298	Transcript	missense_variant	possibly_damaging(0.677)
chr11	123901182	123901182	*OR10G8*	Missense_Mutation	.	SNP	G	G	T	novel	Patient12	p.V285F	ENSG00000234560	ENST00000431524	Transcript	missense_variant	possibly_damaging(0.563)
chr12	104324309	104324309	*HSP90B1*	Missense_Mutation	.	SNP	G	G	T	rs149528402	Patient12	p.V6L	ENSG00000166598	ENST00000299767	Transcript	missense_variant	benign(0)
chr12	55688653	55688653	*OR6C6*	Missense_Mutation	.	SNP	C	C	T	rs201844969	Patient12	p.V122I	ENSG00000188324	ENST00000358433	Transcript	missense_variant	benign(0.035)
chr12	71966655	71966655	*LGR5*	Missense_Mutation	.	SNP	G	G	A	rs148289646	Patient12	p.E388K	ENSG00000139292	ENST00000266674	Transcript	missense_variant	benign(0.408)
chr12	76424711	76424712	*PHLDA1*	In_Frame_Ins	.	INS	-	-	CCA	novel	Patient12	p.Q270_G271insW	ENSG00000139289	ENST00000266671	Transcript	inframe_insertion	NA
chr12	94654603	94654603	*PLXNC1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient12	p.S1146F	ENSG00000136040	ENST00000258526	Transcript	missense_variant	probably_damaging(0.942)
chr15	23048908	23048908	*NIPA1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient12	p.G304V	ENSG00000170113	ENST00000337435	Transcript	missense_variant	probably_damaging(1)
chr17	10547913	10547913	*MYH3*	Missense_Mutation	.	SNP	T	T	A	novel	Patient12	p.Q416H	ENSG00000109063	ENST00000583535	Transcript	missense_variant	probably_damaging(0.992)
chr19	4714275	4714275	*DPP9*	Missense_Mutation	.	SNP	G	G	A	rs147966989	Patient12	p.A44V	ENSG00000142002	ENST00000262960	Transcript	missense_variant	benign(0.001)
chr2	131403314	131403314	*POTEJ*	Missense_Mutation	.	SNP	G	G	T	novel	Patient12	p.R482I	ENSG00000222038	ENST00000409602	Transcript	missense_variant	unknown(0)

chr2	44502719	44502719	*SLC3A1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient12	p.M15I	ENSG00000138079	ENST00000260649	Transcript	missense_variant	benign(0.002)
chr2	95539334	95539334	*TEKT4*	Nonsense_Mutation	.	SNP	C	C	T	novel	Patient12	p.R190*	ENSG00000163060	ENST00000295201	Transcript	stop_gained	NA
chr20	30497598	30497598	*TTLL9*	Missense_Mutation	.	SNP	G	G	A	rs559511299	Patient12	p.R126H	ENSG00000131044	ENST00000375938	Transcript	missense_variant	probably_damaging(0.993)
chr20	36851978	36851978	*KIAA1755*	Missense_Mutation	.	SNP	C	C	T	rs139388351	Patient12	p.E744K	ENSG00000149633	ENST00000279024	Transcript	missense_variant	benign(0.001)
chr22	42042982	42042982	*XRCC6*	Missense_Mutation	.	SNP	A	A	G	novel	Patient12	p.I286V	ENSG00000196419	ENST00000359308	Transcript	missense_variant	benign(0.001)
chr3	105404264	105404264	*CBLB*	Missense_Mutation	.	SNP	G	G	C	novel	Patient12	p.P701A	ENSG00000114423	ENST00000264122	Transcript	missense_variant	benign(0)
chr3	133783121	133783121	*NUP210*	Missense_Mutation	.	SNP	C	C	A	novel	Patient12	p.R1217L	ENSG00000132182	ENST00000254508	Transcript	missense_variant	possibly_damaging(0.805)
chr3	75787321	75787321	*ZNF717*	Missense_Mutation	.	SNP	C	C	T	rs202223162	Patient12	p.G485R	ENSG00000227124	ENST00000422325	Transcript	missense_variant	probably_damaging(0.997)
chr6	56323889	56323889	*DST*	Missense_Mutation	.	SNP	G	G	A	novel	Patient12	p.R5144W	ENSG00000151914	ENST00000244364	Transcript	missense_variant	probably_damaging(1)
chr7	48285587	48285587	*ABCA13*	Missense_Mutation	.	SNP	C	C	T	rs199762385	Patient12	p.T540M	ENSG00000179869	ENST00000435803	Transcript	missense_variant	possibly_damaging(0.615)
chr7	64269068	64269068	*RAC1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient12	p.P34R	ENSG00000136238	ENST00000356142	Transcript	missense_variant	probably_damaging(0.998)
chr9	33395119	33395119	*AQP7*	Missense_Mutation	.	SNP	A	A	T	rs2381004	Patient12	p.V34E	ENSG00000165269	ENST00000539936	Transcript	missense_variant	possibly_damaging(0.609)
chr9	33799086	33799086	*PRSS3*	Missense_Mutation	.	SNP	C	C	T	rs150624305	Patient12	p.H275Y	ENSG00000010438	ENST00000361005	Transcript	missense_variant	benign(0.002)
chr9	84609683	84609683	*SPATA31D1*	Missense_Mutation	.	SNP	C	C	A	novel	Patient12	p.S1433Y	ENSG00000214929	ENST00000344803	Transcript	missense_variant	possibly_damaging(0.563)
chr1	27057919	27057919	*ARID1A*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.Q543K	ENSG00000117713	ENST00000324856	Transcript	missense_variant	benign(0.001)
chr10	106970946	106970946	*SORCS3*	Nonsense_Mutation	.	SNP	G	G	A	novel	Patient13	p.W771*	ENSG00000156395	ENST00000369701	Transcript	stop_gained	NA
chr10	125805375	125805375	*CHST15*	Missense_Mutation	.	SNP	G	G	T	novel	Patient13	p.S118R	ENSG00000182022	ENST00000346248	Transcript	missense_variant	benign(0.068)
chr10	126691634	126691634	*CTBP2*	Missense_Mutation	.	SNP	T	T	A	rs757947878	Patient13	p.I625F	ENSG00000175029	ENST00000309035	Transcript	missense_variant	probably_damaging(0.997)
chr10	21414904	21414904	*C10orf113*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.A106S	ENSG00000204683	ENST00000534331	Transcript	missense_variant	possibly_damaging(0.567)
chr10	89720833	89720833	*PTEN*	Frame_Shift_Del	.	DEL	A	A	-	novel	Patient13	p.N329Ifs*15	ENSG00000171862	ENST00000371953	Transcript	frameshift_variant	NA
chr11	67896644	67896644	*OR2AG2*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.R175S	ENSG00000188124	ENST00000338569	Transcript	missense_variant	benign(0.034)
chr12	109889420	109889420	*KCTD10*	Missense_Mutation	.	SNP	G	G	A	novel	Patient13	p.R308W	ENSG00000110906	ENST00000228495	Transcript	missense_variant	possibly_damaging(0.876)
chr12	11371111	11371111	*ERC1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient13	p.S14R	ENSG00000082805	ENST00000397203	Transcript	missense_variant	possibly_damaging(0.649)
chr12	54383018	54383018	*HOXC10*	Missense_Mutation	.	SNP	T	T	C	novel	Patient13	p.C273R	ENSG00000180818	ENST00000303460	Transcript	missense_variant	probably_damaging(0.976)
chr12	99640382	99640382	*ANKS1B*	Missense_Mutation	.	SNP	T	T	G	novel	Patient13	p.I673L	ENSG00000185046	ENST00000547776	Transcript	missense_variant	benign(0.017)
chr14	65252594	65252594	*SPTB*	Missense_Mutation	.	SNP	A	A	G	novel	Patient13	p.F1213L	ENSG00000070182	ENST00000389722	Transcript	missense_variant	probably_damaging(0.983)
chr15	45456052	45456052	*DUOX1*	Missense_Mutation	.	SNP	T	T	C	novel	Patient13	p.I1490T	ENSG00000137857	ENST00000321429	Transcript	missense_variant	benign(0.004)
chr15	90320111	90320111	*MESP2*	Missense_Mutation	.	SNP	A	A	G	novel	Patient13	p.T175A	ENSG00000188095	ENST00000341735	Transcript	missense_variant	benign(0.004)
chr15	90631837	90631837	*IDH2*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.R172S	ENSG00000182054	ENST00000330062	Transcript	missense_variant	probably_damaging(1)
chr16	28914210	28914210	*ATP2A1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient13	p.E908K	ENSG00000196296	ENST00000357084	Transcript	missense_variant	probably_damaging(1)
chr16	55727960	55727960	*SLC6A2*	Missense_Mutation	.	SNP	G	G	T	novel	Patient13	p.L319F	ENSG00000103546	ENST00000219833	Transcript	missense_variant	probably_damaging(0.997)
chr16	70986374	70986374	*HYDIN*	Missense_Mutation	.	SNP	C	C	T	novel	Patient13	p.G2161S	ENSG00000157423	ENST00000393567	Transcript	missense_variant	benign(0.345)
chr16	71026024	71026024	*HYDIN*	Missense_Mutation	.	SNP	G	G	T	novel	Patient13	p.A1245E	ENSG00000157423	ENST00000393567	Transcript	missense_variant	probably_damaging(0.986)
chr17	27031735	27031735	*PROCA1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient13	p.C73Y	ENSG00000167525	ENST00000301039	Transcript	missense_variant	probably_damaging(1)
chr18	20572852	20572853	*RBBP8*	Frame_Shift_Ins	.	INS	-	-	A	novel	Patient13	p.H358Tfs*8	ENSG00000101773	ENST00000399722	Transcript	frameshift_variant	NA
chr18	72223610	72223610	*CNDP1*	Missense_Mutation	.	SNP	A	A	T	novel	Patient13	p.E21V	ENSG00000150656	ENST00000358821	Transcript	missense_variant	possibly_damaging(0.505)

chr19	33490500	33490500	*RHPN2*	Missense_Mutation	.	SNP	C	C	T	rs201438314	Patient13	p.R406Q	ENSG00000131941	ENST00000254260	Transcript	missense_variant	benign(0.009)
chr2	240982213	240982213	*PRR21*	Missense_Mutation	.	SNP	C	C	G	rs113855430	Patient13	p.A63P	ENSG00000221961	ENST00000408934	Transcript	missense_variant	benign(0.004)
chr2	26534066	26534066	*GPR113*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.A844S	ENSG00000173567	ENST00000311519	Transcript	missense_variant	benign(0.281)
chr2	63540412	63540412	*WDPCP*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.V595F	ENSG00000143951	ENST00000272321	Transcript	missense_variant	possibly_damaging(0.879)
chr22	32548075	32548075	*C22orf42*	Missense_Mutation	.	SNP	G	G	A	novel	Patient13	p.P127S	ENSG00000205856	ENST00000382097	Transcript	missense_variant	benign(0)
chr3	100961534	100961534	*IMPG2*	Missense_Mutation	.	SNP	G	G	A	novel	Patient13	p.S1007L	ENSG00000081148	ENST00000193391	Transcript	missense_variant	possibly_damaging(0.871)
chr3	149238743	149238743	*WWTR1*	Missense_Mutation	.	SNP	T	T	C	novel	Patient13	p.N351S	ENSG00000018408	ENST00000465804	Transcript	missense_variant	benign(0.003)
chr3	63638431	63638431	*SNTN*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.A23E	ENSG00000188817	ENST00000343837	Transcript	missense_variant	benign(0.022)
chr4	151199148	151199148	*LRBA*	Missense_Mutation	.	SNP	C	C	G	novel	Patient13	p.Q2786H	ENSG00000198589	ENST00000357115	Transcript	missense_variant	benign(0.007)
chr4	42282 43	42282 43	*OTOP1*	Missense_Mutation	.	SNP	G	G	T	rs200057225	Patient13	p.H117N	ENSG00000163982	ENST00000296358	Transcript	missense_variant	benign(0.009)
chr4	68441165	68441165	*STAP1*	Missense_Mutation	.	SNP	G	G	T	novel	Patient13	p.K85N	ENSG00000035720	ENST00000265404	Transcript	missense_variant	benign(0.011)
chr4	941613	941613	*TMEM175*	Missense_Mutation	.	SNP	G	G	A	novel	Patient13	p.G29E	ENSG00000127419	ENST00000264771	Transcript	missense_variant	possibly_damaging(0.616)
chr6	32713625	32713625	*HLA-DQA2*	Missense_Mutation	.	SNP	C	C	T	rs116163401	Patient13	p.T130I	ENSG00000237541	ENST00000374940	Transcript	missense_variant	benign(0.027)
chr7	144096158	144096158	*NOBOX*	Missense_Mutation	.	SNP	C	C	T	rs112190116	Patient13	p.D452N	ENSG00000106410	ENST00000467773	Transcript	missense_variant	benign(0)
chr8	18258329	18258329	*NAT2*	Missense_Mutation	.	SNP	G	G	T	novel	Patient13	p.K272N	ENSG00000156006	ENST00000286479	Transcript	missense_variant	benign(0.001)
chr8	32655 06	32655 06	*CSMD1*	Missense_Mutation	.	SNP	C	C	A	rs559348370	Patient13	p.Q662H	ENSG00000183117	ENST00000537824	Transcript	missense_variant	probably_damaging(0.983)
chr8	33247088	33247088	*FUT10*	Missense_Mutation	.	SNP	T	T	C	novel	Patient13	p.Q202R	ENSG00000172728	ENST00000327671	Transcript	missense_variant	benign(0.008)
chr9	13183527	13183527	*MPDZ*	Missense_Mutation	.	SNP	G	G	A	novel	Patient13	p.P847S	ENSG00000107186	ENST00000541718	Transcript	missense_variant	benign(0.041)
chrX	134991902	134991902	*SAGE1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient13	p.V563I	ENSG00000181433	ENST00000535938	Transcript	missense_variant	benign(0.015)
chrX	36385158	36385158	*CXorf30*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.P480H	ENSG00000205081	ENST00000378657	Transcript	missense_variant	probably_damaging(1)
chrX	49227317	49227318	*GAGE2C*	In_Frame_Ins	.	INS	-	-	TAT	novel	Patient13	p.Y9dup	ENSG00000236249	ENST00000381708	Transcript	inframe_insertion	NA
chrX	79286071	79286071	*TBX22*	Missense_Mutation	.	SNP	C	C	A	novel	Patient13	p.L342I	ENSG00000122145	ENST00000373294	Transcript	missense_variant	benign(0.035)
chrX	82764049	82764049	*POU3F4*	Missense_Mutation	.	SNP	G	G	T	novel	Patient13	p.Q239H	ENSG00000196767	ENST00000373200	Transcript	missense_variant	probably_damaging(1)
chr1	109441560	109441560	*GPSM2*	Frame_Shift_Del	.	DEL	C	C	-	rs528069912	Patient14	p.G249Efs*32	ENSG00000121957	ENST00000406462	Transcript	frameshift_variant	NA
chr1	12342990	12342990	*VPS13D*	Missense_Mutation	.	SNP	G	G	A	rs41279452	Patient14	p.E1611K	ENSG00000048707	ENST00000358136	Transcript	missense_variant	benign(0.058)
chr1	228496066	228496066	*OBSCN*	Missense_Mutation	.	SNP	G	G	T	rs55704206	Patient14	p.A5198S	ENSG00000154358	ENST00000570156	Transcript	missense_variant	probably_damaging(0.999)
chr1	22987340	22987340	*C1QB*	Missense_Mutation	.	SNP	G	G	A	rs35477594	Patient14	p.G75R	ENSG00000173369	ENST00000314933	Transcript	missense_variant	probably_damaging(1)
chr1	31754270	31754270	*SNRNP40*	Missense_Mutation	.	SNP	T	T	C	rs188008327	Patient14	p.N202S	ENSG00000060688	ENST00000263694	Transcript	missense_variant	benign(0.37)
chr1	43772828	43772828	*TIE1*	Missense_Mutation	.	SNP	G	G	A	rs368249010	Patient14	p.R219H	ENSG00000066056	ENST00000372476	Transcript	missense_variant	benign(0.003)
chr1	43897496	43897496	*SZT2*	Missense_Mutation	.	SNP	G	G	A	rs147797700	Patient14	p.R1676H	ENSG00000198198	ENST00000562955	Transcript	missense_variant	probably_damaging(0.996)
chr1	89250482	89250484	*PKN2*	In_Frame_Del	.	DEL	TCT	TCT	-	rs201679232	Patient14	p.L383del	ENSG00000065243	ENST00000370521	Transcript	inframe_deletion	NA
chr10	103543141	103543141	*NPM3*	Missense_Mutation	.	SNP	C	C	T	rs146931276	Patient14	p.A3T	ENSG00000107833	ENST00000370110	Transcript	missense_variant	unknown(0)
chr10	59997515	59997515	*IPMK*	Frame_Shift_Del	.	DEL	G	G	-	novel	Patient14	p.P84Qfs*21	ENSG00000151151	ENST00000373935	Transcript	frameshift_variant	NA
chr10	61552763	61552763	*CCDC6*	Missense_Mutation	.	SNP	G	G	A	rs61740504	Patient14	p.P446L	ENSG00000108091	ENST00000263102	Transcript	missense_variant	unknown(0)
chr10	91520368	91520368	*KIF20B*	Missense_Mutation	.	SNP	T	T	A	rs117258675	Patient14	p.F1549Y	ENSG00000138182	ENST00000260753	Transcript	missense_variant	benign(0.017)
chr11	101832689	101832689	*KIAA1377*	Missense_Mutation	.	SNP	A	A	T	rs61742172	Patient14	p.H308L	ENSG00000110318	ENST00000263468	Transcript	missense_variant	possibly_damaging(0.804)

chr11	111747587	111747587	*FDXACB1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.D160N	ENSG00000255561	ENST00000260257	Transcript	missense_variant	benign(0.034)
chr11	111753246	111753246	*C11orf1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient14	p.R67H	ENSG00000137720	ENST00000260276	Transcript	missense_variant	benign(0.059)
chr11	111896251	111896251	*DLAT*	Missense_Mutation	.	SNP	G	G	C	novel	Patient14	p.E19Q	ENSG00000150768	ENST00000280346	Transcript	missense_variant	benign(0.017)
chr11	111942362	111942362	*PIH1D2*	Missense_Mutation	.	SNP	A	A	G	novel	Patient14	p.S100P	ENSG00000150773	ENST00000280350	Transcript	missense_variant	benign(0.033)
chr11	111957665	111957665	*SDHD*	Missense_Mutation	.	SNP	G	G	A	rs34677591	Patient14	p.G12S	ENSG00000204370	ENST00000375549	Transcript	missense_variant	benign(0.003)
chr11	130011907	130011907	*APLP2*	Missense_Mutation	.	SNP	G	G	A	rs367626362	Patient14	p.V710I	ENSG00000084234	ENST00000263574	Transcript	missense_variant	probably_damaging(0.998)
chr11	132205008	132205008	*NTM*	Missense_Mutation	.	SNP	C	C	T	rs138401779	Patient14	p.L346F	ENSG00000182667	ENST00000425719	Transcript	missense_variant	benign(0.005)
chr11	48267442	48267442	*OR4X2*	Missense_Mutation	.	SNP	G	G	T	rs137858399	Patient14	p.V263L	ENSG00000172208	ENST00000302329	Transcript	missense_variant	benign(0.047)
chr11	55340387	55340387	*OR4C16*	Missense_Mutation	.	SNP	G	G	A	rs141913559	Patient14	p.V262I	ENSG00000181935	ENST00000314634	Transcript	missense_variant	benign(0.005)
chr11	62286666	62286666	*AHNAK*	Missense_Mutation	.	SNP	C	C	T	rs114515655	Patient14	p.V5075M	ENSG00000124942	ENST00000378024	Transcript	missense_variant	benign(0.187)
chr11	62543398	62543398	*TAF6L*	Missense_Mutation	.	SNP	C	C	T	rs144825291	Patient14	p.T48M	ENSG00000162227	ENST00000294168	Transcript	missense_variant	benign(0.322)
chr11	63987971	63987971	*FERMT3*	Missense_Mutation	.	SNP	G	G	A	rs374091426	Patient14	p.D463N	ENSG00000149781	ENST00000279227	Transcript	missense_variant	probably_damaging(0.945)
chr11	64811900	64811900	*SAC3D1*	Missense_Mutation	.	SNP	C	C	T	rs193165731	Patient14	p.R260C	ENSG00000168061	ENST00000398846	Transcript	missense_variant	benign(0.147)
chr11	68191036	68191036	*LRP5*	Missense_Mutation	.	SNP	G	G	A	rs61889560	Patient14	p.R1036Q	ENSG00000162337	ENST00000294304	Transcript	missense_variant	benign(0.257)
chr11	73748732	73748732	*C2CD3*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.S1891N	ENSG00000168014	ENST00000313663	Transcript	missense_variant	benign(0.012)
chr12	104408832	104408832	*GLT8D2*	Missense_Mutation	.	SNP	T	T	C	rs117801489	Patient14	p.Y24C	ENSG00000120820	ENST00000360814	Transcript	missense_variant	probably_damaging(0.963)
chr12	120499628	120499628	*CCDC64*	Missense_Mutation	.	SNP	G	G	A	novel	Patient14	p.E254K	ENSG00000135127	ENST00000397558	Transcript	missense_variant	probably_damaging(0.961)
chr13	39585591	39585591	*PROSER1*	Missense_Mutation	.	SNP	C	C	A	rs731694601	Patient14	p.A916S	ENSG00000120685	ENST00000352251	Transcript	missense_variant	benign(0.269)
chr13	46544544	46544544	*ZC3H13*	Missense_Mutation	.	SNP	C	C	T	rs144621814	Patient14	p.R842H	ENSG00000123200	ENST00000282007	Transcript	missense_variant	unknown(0)
chr13	52971517	52971517	*THSD1*	Missense_Mutation	.	SNP	C	C	T	rs41292808	Patient14	p.E291K	ENSG00000136114	ENST00000258613	Transcript	missense_variant	benign(0.26)
chr14	105965215	105965215	*C14orf80*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.R405W	ENSG00000185347	ENST00000392522	Transcript	missense_variant	benign(0.003)
chr14	23312603	23312603	*MMP14*	Missense_Mutation	.	SNP	C	C	T	rs145239346	Patient14	p.R276C	ENSG00000157227	ENST00000311852	Transcript	missense_variant	probably_damaging(0.959)
chr14	62204978	62204978	*HIF1A*	Missense_Mutation	.	SNP	G	G	T	rs138451482	Patient14	p.A499S	ENSG00000100644	ENST00000539097	Transcript	missense_variant	benign(0.011)
chr14	93118790	93118790	*RIN3*	Missense_Mutation	.	SNP	A	A	C	rs139248637	Patient14	p.I466L	ENSG00000100599	ENST00000216487	Transcript	missense_variant	benign(0.01)
chr14	95675791	95675791	*CLMN*	Missense_Mutation	.	SNP	C	C	T	rs118150470	Patient14	p.E276K	ENSG00000165959	ENST00000298912	Transcript	missense_variant	probably_damaging(1)
chr14	96769517	96769517	*ATG2B*	Missense_Mutation	.	SNP	G	G	A	novel	Patient14	p.R1640W	ENSG00000066739	ENST00000359933	Transcript	missense_variant	probably_damaging(0.963)
chr15	100537693	100537693	*ADAMTS17*	Missense_Mutation	.	SNP	A	A	G	rs202099735	Patient14	p.V898A	ENSG00000140470	ENST00000268070	Transcript	missense_variant	possibly_damaging(0.578)
chr15	23006299	23006300	*NIPA2*	In_Frame_Ins	.	INS	-	-	TCA	rs576755299	Patient14	p.E335_E336insD	ENSG00000140157	ENST00000337451	Transcript	inframe_insertion	NA
chr15	29416890	29416890	*FAM189A1*	Missense_Mutation	.	SNP	C	C	G	rs61736885	Patient14	p.A435P	ENSG00000104059	ENST00000261275	Transcript	missense_variant	benign(0.038)
chr15	44038756	44038756	*PDIA3*	Missense_Mutation	.	SNP	G	G	T	rs201549098	Patient14	p.A7S	ENSG00000167004	ENST00000300289	Transcript	missense_variant	benign(0.01)
chr15	48431282	48431282	*SLC24A5*	Missense_Mutation	.	SNP	T	T	C	rs200031114	Patient14	p.W330R	ENSG00000188467	ENST00000345149	Transcript	missense_variant	benign(0.358)
chr15	60741825	60741825	*NARG2*	Frame_Shift_Del	.	DEL	T	T	-	novel	Patient14	p.D448Afs*13	ENSG00000128915	ENST00000261520	Transcript	frameshift_variant	NA
chr16	16342411	16342411	*IFT140*	Missense_Mutation	.	SNP	T	T	C	rs139619013	Patient14	p.I446V	ENSG00000187535	ENST00000426508	Transcript	missense_variant	benign(0.004)
chr16	17062755	17062755	*CRAMP1L*	Missense_Mutation	.	SNP	C	C	T	rs200270407	Patient14	p.P506L	ENSG00000007545	ENST00000397412	Transcript	missense_variant	benign(0.006)
chr16	20974740	20974740	*DNAH3*	Missense_Mutation	.	SNP	C	C	T	rs111539520	Patient14	p.R3489Q	ENSG00000158486	ENST00000261383	Transcript	missense_variant	benign(0.003)
chr16	28619816	28619816	*SULT1A1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient14	p.A86V	ENSG00000196502	ENST00000395609	Transcript	missense_variant	benign(0)

chr16	3085326	3085326	*CCDC64B*	Missense_Mutation	.	SNP	C	C	T	rs71386699	Patient14	p.E58K	ENSG00000162069	ENST00000572449	Transcript	missense_variant	probably_damaging(0.995)
chr16	347063	347063	*AXIN1*	Missense_Mutation	.	SNP	C	C	T	rs117208012	Patient14	p.G650S	ENSG00000103126	ENST00000262320	Transcript	missense_variant	benign(0.003)
chr16	613344	613344	*C16orf11*	Missense_Mutation	.	SNP	G	G	A	rs116903998	Patient14	p.R17Q	ENSG00000161992	ENST00000409413	Transcript	missense_variant	probably_damaging(0.926)
chr16	68056400	68056400	*DDX28*	Missense_Mutation	.	SNP	C	C	G	rs116447313	Patient14	p.D236H	ENSG00000182810	ENST00000332395	Transcript	missense_variant	benign(0.174)
chr16	70503095	70503095	*FUK*	Missense_Mutation	.	SNP	A	A	G	rs113497209	Patient14	p.N275S	ENSG00000157353	ENST00000288078	Transcript	missense_variant	benign(0.027)
chr16	70590898	70590898	*SF3B3*	Missense_Mutation	.	SNP	C	C	T	rs116924445	Patient14	p.S659L	ENSG00000189091	ENST00000302516	Transcript	missense_variant	benign(0.001)
chr16	72822645	72822645	*ZFHX3*	Missense_Mutation	.	SNP	G	G	A	rs149133285	Patient14	p.S3177L	ENSG00000140836	ENST00000268489	Transcript	missense_variant	unknown(0)
chr16	84030873	84030873	*NECAB2*	Missense_Mutation	.	SNP	T	T	G	rs139863929	Patient14	p.M283R	ENSG00000103154	ENST00000305202	Transcript	missense_variant	benign(0.367)
chr16	89735891	89735892	*SPATA33*	Frame_Shift_Ins	.	INS	-	-	TG	rs147716338	Patient14	p.H136Lfs*19	ENSG00000167523	ENST00000301031	Transcript	frameshift_variant	NA
chr17	19702831	19702831	*ULK2*	Missense_Mutation	.	SNP	T	T	G	rs142840164	Patient14	p.D500A	ENSG00000083290	ENST00000395544	Transcript	missense_variant	benign(0.021)
chr17	27238135	27238135	*PHF12*	Missense_Mutation	.	SNP	T	T	C	rs148347485	Patient14	p.N737S	ENSG00000109118	ENST00000332830	Transcript	missense_variant	benign(0.002)
chr17	39593672	39593672	*KRT38*	Nonsense_Mutation	.	SNP	G	G	A	rs201381536	Patient14	p.R455*	ENSG00000171360	ENST00000246646	Transcript	stop_gained	NA
chr17	39642658	39642660	*KRT36*	In_Frame_Del	.	DEL	GGA	GGA	-	rs565828637	Patient14	p.S458del	ENSG00000126337	ENST00000328119	Transcript	inframe_deletion	NA
chr17	61278229	61278229	*TANC2*	Missense_Mutation	.	SNP	T	T	G	rs117690040	Patient14	p.I153S	ENSG00000170921	ENST00000424789	Transcript	missense_variant	benign(0)
chr17	76823418	76823418	*USP36*	Missense_Mutation	.	SNP	G	G	T	rs150547254	Patient14	p.H200N	ENSG00000055483	ENST00000542802	Transcript	missense_variant	benign(0.188)
chr17	77926526	77926526	*TBC1D16*	Missense_Mutation	.	SNP	C	C	T	rs150604803	Patient14	p.A291T	ENSG00000167291	ENST00000310924	Transcript	missense_variant	benign(0.295)
chr18	28647999	28648000	*DSC2*	Frame_Shift_Ins	.	INS	-	-	TC	rs200056085	Patient14	p.A897Kfs*4	ENSG00000134755	ENST00000280904	Transcript	frameshift_variant	NA
chr19	14991881	14991881	*OR7A17*	Missense_Mutation	.	SNP	C	C	T	rs139004201	Patient14	p.G96D	ENSG00000185385	ENST00000327462	Transcript	missense_variant	benign(0.157)
chr19	16799058	16799060	*TMEM38A*	In_Frame_Del	.	DEL	ACG	ACG	-	rs538628487	Patient14	p.D260del	ENSG00000072954	ENST00000187762	Transcript	inframe_deletion	NA
chr19	3179517	3179517	*S1PR4*	Missense_Mutation	.	SNP	C	C	T	rs617311111	Patient14	p.R243C	ENSG00000125910	ENST00000246115	Transcript	missense_variant	probably_damaging(0.99)
chr19	37368535	37368535	*ZNF345*	Missense_Mutation	.	SNP	G	G	C	rs112729744	Patient14	p.S268T	ENSG00000251247	ENST00000529555	Transcript	missense_variant	benign(0.006)
chr19	42880062	42880062	*MEGF8*	Missense_Mutation	.	SNP	C	C	T	rs147216997	Patient14	p.P2491L	ENSG00000105429	ENST00000334370	Transcript	missense_variant	benign(0.001)
chr19	46202131	46202131	*QPCTL*	Missense_Mutation	.	SNP	C	C	T	rs145016874	Patient14	p.R287C	ENSG00000011478	ENST00000012049	Transcript	missense_variant	probably_damaging(0.92)
chr19	7687302	7687302	*XAB2*	Missense_Mutation	.	SNP	A	A	G	novel	Patient14	p.L511P	ENSG00000076924	ENST00000358368	Transcript	missense_variant	possibly_damaging(0.691)
chr19	8434123	8434123	*ANGPTL4*	Missense_Mutation	.	SNP	G	G	C	rs77938377	Patient14	p.E190Q	ENSG00000167772	ENST00000301455	Transcript	missense_variant	benign(0.422)
chr19	9578370	9578370	*ZNF560*	Missense_Mutation	.	SNP	C	C	T	rs111436709	Patient14	p.G418D	ENSG00000198028	ENST00000301480	Transcript	missense_variant	probably_damaging(0.989)
chr2	112722801	112722801	*MERTK*	Missense_Mutation	.	SNP	C	C	G	rs199779970	Patient14	p.A264G	ENSG00000153208	ENST00000295408	Transcript	missense_variant	probably_damaging(0.985)
chr2	113138525	113138525	*RGPD8*	Missense_Mutation	.	SNP	T	T	C	novel	Patient14	p.H1646R	ENSG00000169629	ENST00000302558	Transcript	missense_variant	benign(0.003)
chr2	219755011	219755011	*WNT10A*	Missense_Mutation	.	SNP	T	T	A	rs121908120	Patient14	p.F228I	ENSG00000135925	ENST00000258411	Transcript	missense_variant	probably_damaging(0.994)
chr2	242695399	242695399	*D2HGDH*	Missense_Mutation	.	SNP	G	G	A	rs146578303	Patient14	p.A426T	ENSG00000180902	ENST00000321264	Transcript	missense_variant	benign(0.059)
chr2	27730169	27730170	*GCKR*	Frame_Shift_Ins	.	INS	-	-	A	rs573498430	Patient14	p.T379Nfs*36	ENSG00000084734	ENST00000264717	Transcript	frameshift_variant	NA
chr2	71043462	71043462	*CLEC4F*	Missense_Mutation	.	SNP	G	G	A	novel	Patient14	p.R351C	ENSG00000152672	ENST00000272367	Transcript	missense_variant	benign(0.004)
chr2	74907227	74907227	*SEMA4F*	Missense_Mutation	.	SNP	G	G	A	rs113159774	Patient14	p.S735N	ENSG00000135622	ENST00000357877	Transcript	missense_variant	benign(0.018)
chr20	2846052	2846052	*VPS16*	Missense_Mutation	.	SNP	T	T	C	rs617292229	Patient14	p.W728R	ENSG00000215305	ENST00000380445	Transcript	missense_variant	possibly_damaging(0.727)
chr20	37198582	37198582	*RALGAPB*	Missense_Mutation	.	SNP	C	C	T	rs142678293	Patient14	p.P1336S	ENSG00000170471	ENST00000262879	Transcript	missense_variant	benign(0.061)
chr20	62608492	62608492	*SAMD10*	Missense_Mutation	.	SNP	G	G	A	rs199900212	Patient14	p.R93W	ENSG00000130590	ENST00000369886	Transcript	missense_variant	possibly_damaging(0.582)

chr21	32493056	32493056	*TIAM1*	Missense_Mutation	.	SNP	T	T	C	rs111536576	Patient14	p.K1469R	ENSG00000156299	ENST00000286827	Transcript	missense_variant	benign(0.001)
chr21	47542052	47542052	*COL6A2*	Missense_Mutation	.	SNP	C	C	T	rs141166141	Patient14	p.P518S	ENSG00000142173	ENST00000300527	Transcript	missense_variant	benign(0.37)
chr22	26239789	26239789	*MYO18B*	Missense_Mutation	.	SNP	C	C	T	rs147821283	Patient14	p.T1099M	ENSG00000133454	ENST00000335473	Transcript	missense_variant	probably_damaging(0.91)
chr22	32894494	32894494	*FBXO7*	Missense_Mutation	.	SNP	G	G	C	rs343164445	Patient14	p.D516H	ENSG00000100225	ENST00000266087	Transcript	missense_variant	benign(0.4)
chr3	10219567	102195767	*IRAK2*	Missense_Mutation	.	SNP	C	C	A	rs114658614	Patient14	p.S47Y	ENSG00000134070	ENST00000256458	Transcript	missense_variant	probably_damaging(0.983)
chr3	145917773	145917773	*PLSCR4*	Missense_Mutation	.	SNP	G	G	T	rs114444125	Patient14	p.Q151K	ENSG00000114698	ENST00000354952	Transcript	missense_variant	probably_damaging(0.999)
chr3	44488293	44488293	*ZNF445*	Missense_Mutation	.	SNP	T	T	C	rs143141433	Patient14	p.E957G	ENSG00000185219	ENST00000425708	Transcript	missense_variant	benign(0.403)
chr3	50005916	50005916	*RBM6*	Missense_Mutation	.	SNP	C	C	T	rs61731329	Patient14	p.S353F	ENSG00000004534	ENST00000266022	Transcript	missense_variant	benign(0.318)
chr3	52383001	52383001	*DNAH1*	Missense_Mutation	.	SNP	G	G	A	rs187636110	Patient14	p.S735N	ENSG00000114841	ENST00000420323	Transcript	missense_variant	benign(0)
chr3	52836533	52836533	*ITIH3*	Missense_Mutation	.	SNP	G	G	A	rs74320783	Patient14	p.G523R	ENSG00000162267	ENST00000449956	Transcript	missense_variant	possibly_damaging(0.762)
chr4	10445207	104452007	*ZNF518B*	Missense_Mutation	.	SNP	T	T	C	rs754877988	Patient14	p.I916V	ENSG00000178163	ENST00000326756	Transcript	missense_variant	benign(0.003)
chr4	113351611	113351611	*ALPK1*	Missense_Mutation	.	SNP	G	G	A	rs142200712	Patient14	p.R303H	ENSG00000073331	ENST00000458497	Transcript	missense_variant	probably_damaging(0.921)
chr4	129792810	129792810	*JADE1*	Missense_Mutation	.	SNP	G	G	A	rs141808337	Patient14	p.R641H	ENSG00000077684	ENST00000226319	Transcript	missense_variant	benign(0.004)
chr4	129891542	129891542	*SCLT1*	Missense_Mutation	.	SNP	C	C	A	rs141863899	Patient14	p.M256I	ENSG00000151466	ENST00000281142	Transcript	missense_variant	benign(0.005)
chr4	184334	184334	*LETM1*	Missense_Mutation	.	SNP	T	T	C	rs626233389	Patient14	p.H109R	ENSG00000168924	ENST00000302787	Transcript	missense_variant	possibly_damaging(0.864)
chr4	38775747	38775747	*TLR10*	Missense_Mutation	.	SNP	T	T	C	rs142566451	Patient14	p.R489G	ENSG00000174123	ENST00000308973	Transcript	missense_variant	benign(0.002)
chr4	77677759	77677759	*SHROOM3*	Missense_Mutation	.	SNP	C	C	A	rs143947261	Patient14	p.Q1623K	ENSG00000138771	ENST00000296043	Transcript	missense_variant	benign(0.445)
chr4	78528928	78528928	*CXCL13*	Missense_Mutation	.	SNP	C	C	T	rs371680233	Patient14	p.R46C	ENSG00000156234	ENST00000286758	Transcript	missense_variant	possibly_damaging(0.862)
chr5	178310934	178310934	*ZNF354B*	Missense_Mutation	.	SNP	A	A	G	rs141410132	Patient14	p.Y494C	ENSG00000178338	ENST00000322434	Transcript	missense_variant	probably_damaging(1)
chr5	180166677	180166677	*OR2Y1*	Missense_Mutation	.	SNP	G	G	A	rs11960429	Patient14	p.R128C	ENSG00000174339	ENST00000307832	Transcript	missense_variant	probably_damaging(0.932)
chr5	31799522	31799522	*PDZD2*	Missense_Mutation	.	SNP	C	C	T	rs145138976	Patient14	p.T56M	ENSG00000133401	ENST00000438447	Transcript	missense_variant	benign(0.386)
chr5	52393093	52393093	*ADAMTS16*	Missense_Mutation	.	SNP	G	G	A	rs68077031	Patient14	p.V734I	ENSG00000145536	ENST00000274181	Transcript	missense_variant	benign(0.002)
chr5	80408670	80408670	*RASGRF2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.P694S	ENSG00000113319	ENST00000265080	Transcript	missense_variant	possibly_damaging(0.882)
chr6	110620177	110620177	*METTL24*	Missense_Mutation	.	SNP	T	T	C	rs41288584	Patient14	p.H245R	ENSG00000053328	ENST00000338882	Transcript	missense_variant	benign(0.002)
chr6	112460365	112460365	*LAMA4*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.R1080Q	ENSG00000112769	ENST00000230538	Transcript	missense_variant	probably_damaging(0.999)
chr6	112508755	112508755	*LAMA4*	Missense_Mutation	.	SNP	G	G	C	novel	Patient14	p.A288G	ENSG00000112769	ENST00000230538	Transcript	missense_variant	benign(0.063)
chr6	131191206	131191206	*EPB41L2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.E702K	ENSG00000079819	ENST00000337057	Transcript	missense_variant	benign(0.053)
chr6	131996316	131996316	*ENPP3*	Missense_Mutation	.	SNP	A	A	G	rs141662829	Patient14	p.M287V	ENSG00000154269	ENST00000414305	Transcript	missense_variant	benign(0.001)
chr6	150267688	150267688	*ULBP2*	Missense_Mutation	.	SNP	T	T	A	rs537356181	Patient14	p.V177D	ENSG00000131015	ENST00000367351	Transcript	missense_variant	benign(0)
chr6	35840349	35840349	*SRPK1*	Missense_Mutation	.	SNP	C	C	T	rs184806596	Patient14	p.G248R	ENSG00000096063	ENST00000373825	Transcript	missense_variant	possibly_damaging(0.73)
chr6	45882039	45882039	*CLIC5*	Missense_Mutation	.	SNP	G	G	A	rs138254725	Patient14	p.R331W	ENSG00000112782	ENST00000185206	Transcript	missense_variant	possibly_damaging(0.817)
chr6	70972993	70972993	*COL9A1*	Missense_Mutation	.	SNP	T	T	C	rs777068588	Patient14	p.E450G	ENSG00000112280	ENST00000357250	Transcript	missense_variant	probably_damaging(0.999)
chr7	107596043	107596043	*LAMB1*	Missense_Mutation	.	SNP	A	A	G	rs139487685	Patient14	p.I908T	ENSG00000091136	ENST00000222399	Transcript	missense_variant	benign(0.201)
chr7	10978113	10978113	*GPR146*	Missense_Mutation	.	SNP	A	A	G	rs140289241	Patient14	p.D221G	ENSG00000164849	ENST00000397095	Transcript	missense_variant	benign(0.186)
chr7	43830880	43830880	*BLVRA*	Missense_Mutation	.	SNP	A	A	G	rs1050916	Patient14	p.Q56R	ENSG00000106605	ENST00000402924	Transcript	missense_variant	probably_damaging(0.999)
chr8	10583616	10583616	*SOX7*	Missense_Mutation	.	SNP	C	C	T	rs180762782	Patient14	p.G267S	ENSG00000171056	ENST00000304501	Transcript	missense_variant	benign(0.001)

chr8	65517322	65517322	*CYP7B1*	Frame_Shift_Del	.	DEL	C	C	-	novel	Patient14	p.D384Tfs*10	ENSG00000172817	ENST00000310193	Transcript	frameshift_variant	NA
chr8	74706352	74706352	*UBE2W*	Splice_Site	.	DEL	T	T	-	rs144174398	Patient14	p.X188_splice	ENSG00000104343	ENST00000419880	Transcript	splice_acceptor_variant	NA
chr8	77768498	77768498	*ZFHX4*	Missense_Mutation	.	SNP	G	G	A	rs142555710	Patient14	p.G3114D	ENSG00000091656	ENST00000521891	Transcript	missense_variant	probably_damaging(0.964)
chr8	87560606	87560608	*CPNE3*	In_Frame_Del	.	DEL	TAA	TAA	-	novel	Patient14	p.N320del	ENSG00000085719	ENST00000521271	Transcript	inframe_deletion	NA
chr9	116191187	116191187	*C9orf43*	Missense_Mutation	.	SNP	C	C	T	rs143283507	Patient14	p.T372M	ENSG00000157653	ENST00000288462	Transcript	missense_variant	possibly_damaging(0.775)
chr9	136501756	136501756	*DBH*	Missense_Mutation	.	SNP	G	G	C	rs3025380	Patient14	p.G88A	ENSG00000123454	ENST00000393056	Transcript	missense_variant	probably_damaging(1)
chr9	140146560	140146560	*C9orf173*	Missense_Mutation	.	SNP	A	A	G	rs28657439	Patient14	p.S126G	ENSG00000197768	ENST00000388931	Transcript	missense_variant	probably_damaging(0.916)
chr9	147759706	147759706	*FREM1*	Missense_Mutation	.	SNP	G	G	A	rs375476655	Patient14	p.R1580W	ENSG00000164946	ENST00000422223	Transcript	missense_variant	possibly_damaging(0.776)
chrX	127185638	127185639	*ACTRT1*	Frame_Shift_Ins	.	INS	-	-	T	novel	Patient14	p.M183Nfs*17	ENSG00000123165	ENST00000371124	Transcript	frameshift_variant	NA
chrX	149937538	149937538	*CD99L2*	Missense_Mutation	.	SNP	G	G	A	novel	Patient14	p.P253L	ENSG00000102181	ENST00000370377	Transcript	missense_variant	probably_damaging(0.913)
chrX	153409801	153409801	*OPN1LW*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.P15L	ENSG00000102076	ENST00000369951	Transcript	missense_variant	benign(0.002)
chrX	49047959	49047959	*SYP*	Missense_Mutation	.	SNP	C	C	T	novel	Patient14	p.G293S	ENSG00000102003	ENST00000263233	Transcript	missense_variant	unknown(0)
chrX	67652730	67652730	*OPHN1*	Missense_Mutation	.	SNP	C	C	T	rs148262378	Patient14	p.A45T	ENSG00000079482	ENST00000355520	Transcript	missense_variant	benign(0.002)
chr1	233511718	233511718	*MLK4*	Nonsense_Mutation	.	SNP	G	G	T	novel	Patient15	p.E578*	ENSG00000143674	ENST00000366624	Transcript	stop_gained	NA
chr1	27105756	27105757	*ARID1A*	Frame_Shift_Ins	.	INS	-	-	T	novel	Patient15	p.S1791Ffs*11	ENSG00000117713	ENST00000324856	Transcript	frameshift_variant	NA
chr1	47882511	47882511	*FOXE3*	Missense_Mutation	.	SNP	A	A	C	novel	Patient15	p.H175P	ENSG00000186790	ENST00000335071	Transcript	missense_variant	benign(0.009)
chr10	126686680	126686680	*CTBP2*	Missense_Mutation	.	SNP	A	A	C	novel	Patient15	p.C680G	ENSG00000175029	ENST00000309035	Transcript	missense_variant	benign(0.011)
chr10	17146456	17146456	*CUBN*	Missense_Mutation	.	SNP	C	C	T	rs376051685	Patient15	p.R460H	ENSG00000107611	ENST00000377833	Transcript	missense_variant	benign(0.017)
chr10	24889718	24889718	*ARHGAP21*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.D997N	ENSG00000107863	ENST00000396432	Transcript	missense_variant	probably_damaging(1)
chr10	85984164	85984164	*LRIT2*	Nonsense_Mutation	.	SNP	G	G	A	rs139197166	Patient15	p.R273*	ENSG00000204033	ENST00000372113	Transcript	stop_gained	NA
chr11	12554856	12554856	*ACRV1*	Missense_Mutation	.	SNP	A	A	G	novel	Patient15	p.I30T	ENSG00000134940	ENST00000533904	Transcript	missense_variant	benign(0.333)
chr11	43889006	43889006	*OR52B4*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.S207L	ENSG00000221996	ENST00000408920	Transcript	missense_variant	benign(0.013)
chr12	32902874	32902874	*YARS2*	Missense_Mutation	.	SNP	C	C	T	rs372406231	Patient15	p.R424Q	ENSG00000139131	ENST00000324868	Transcript	missense_variant	benign(0.02)
chr12	49460445	49460445	*RHEBL1*	Missense_Mutation	.	SNP	C	C	G	novel	Patient15	p.V78L	ENSG00000167550	ENST00000301068	Transcript	missense_variant	benign(0.007)
chr12	72167781	72167781	*RAB21*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.E124K	ENSG00000080371	ENST00000261263	Transcript	missense_variant	benign(0.028)
chr14	24003276	24003276	*ZFHX2*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.R420H	ENSG00000136367	ENST00000419474	Transcript	missense_variant	probably_damaging(0.998)
chr14	64675639	64675639	*SYNE2*	Missense_Mutation	.	SNP	C	C	A	novel	Patient15	p.A6122D	ENSG00000054654	ENST00000358025	Transcript	missense_variant	probably_damaging(0.972)
chr14	76638281	76638282	*GPATCH2L*	Frame_Shift_Del	.	DEL	TC	TC	-	novel	Patient15	p.S275*	ENSG00000089916	ENST00000261530	Transcript	frameshift_variant	NA
chr15	29996456	29996456	*TJP1*	Missense_Mutation	.	SNP	G	G	T	novel	Patient15	p.L1708M	ENSG00000104067	ENST00000346128	Transcript	missense_variant	probably_damaging(0.958)
chr16	14819869	14819869	*NPIPA3*	Missense_Mutation	.	SNP	G	G	T	novel	Patient15	p.D258Y	ENSG00000224712	ENST00000552140	Transcript	missense_variant	probably_damaging(0.952)
chr17	33501307	33501307	*UNC45B*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.A628V	ENSG00000141161	ENST00000268876	Transcript	missense_variant	possibly_damaging(0.588)
chr17	61771015	61771015	*MAP3K3*	Missense_Mutation	.	SNP	C	C	G	novel	Patient15	p.Q618E	ENSG00000198909	ENST00000361357	Transcript	missense_variant	benign(0.012)
chr17	72309978	72309978	*NEURL4*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.R170W	ENSG00000215041	ENST00000399464	Transcript	missense_variant	possibly_damaging(0.773)
chr17	82163722	82163722	*ARHGEF15*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.R245Q	ENSG00000198844	ENST00000361926	Transcript	missense_variant	benign(0.131)
chr19	19349163	19349163	*NCAN*	Missense_Mutation	.	SNP	C	C	T	rs375854561	Patient15	p.R1118C	ENSG00000130287	ENST00000252575	Transcript	missense_variant	probably_damaging(0.938)
chr19	31768045	31768045	*TSHZ3*	Missense_Mutation	.	SNP	G	G	A	rs369979777	Patient15	p.S885L	ENSG00000121297	ENST00000240587	Transcript	missense_variant	benign(0.013)

chr19	31770175	31770175	*TSHZ3*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.T175M	ENSG00000121297	ENST00000240587	Transcript	missense_variant	probably_damaging(0.999)
chr19	49422470	49422470	*NUCB1*	Missense_Mutation	.	SNP	G	G	T	novel	Patient15	p.R310L	ENSG00000104805	ENST00000405315	Transcript	missense_variant	probably_damaging(0.961)
chr19	52715982	52715982	*PPP2R1A*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.R183W	ENSG00000105568	ENST00000322088	Transcript	missense_variant	probably_damaging(1)
chr19	57050469	57050469	*ZFP28*	Missense_Mutation	.	SNP	G	G	T	novel	Patient15	p.G28C	ENSG00000196867	ENST00000301318	Transcript	missense_variant	possibly_damaging(0.575)
chr19	6213094	6213094	*MLLT1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.V547M	ENSG00000130382	ENST00000252674	Transcript	missense_variant	possibly_damaging(0.623)
chr19	746399	746399	*PALM*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.T250M	ENSG00000099864	ENST00000338448	Transcript	missense_variant	benign(0.16)
chr2	113348 7	113348 7	*SNTG2*	Missense_Mutation	.	SNP	G	G	A	rs367999966	Patient15	p.E135K	ENSG00000172554	ENST00000308624	Transcript	missense_variant	benign(0.032)
chr2	160602295	160602295	*Mar/07*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.H121Y	ENSG00000136536	ENST00000259050	Transcript	missense_variant	benign(0.424)
chr2	26417473	26417473	*HADHA*	Missense_Mutation	.	SNP	G	G	A	rs369588406	Patient15	p.A552V	ENSG00000084754	ENST00000380649	Transcript	missense_variant	possibly_damaging(0.624)
chr2	39187125	39187125	*ARHGEF33*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.A560V	ENSG00000214694	ENST00000409978	Transcript	missense_variant	benign(0.058)
chr20	62065255	62065255	*KCNQ2*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.S342L	ENSG00000075043	ENST00000359125	Transcript	missense_variant	benign(0.003)
chr21	45941923	45941923	*TSPEAR*	Missense_Mutation	.	SNP	G	G	T	novel	Patient15	p.T470N	ENSG00000175894	ENST00000323084	Transcript	missense_variant	benign(0.027)
chr22	41523593	41523593	*EP300*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.L337F	ENSG00000100393	ENST00000263253	Transcript	missense_variant	unknown(0)
chr3	30732969	30732969	*TGFBR2*	Missense_Mutation	.	SNP	C	C	T	rs104893810	Patient15	p.R553C	ENSG00000163513	ENST00000359013	Transcript	missense_variant	probably_damaging(1)
chr3	75786501	75786501	*ZNF717*	Missense_Mutation	.	SNP	T	T	A	rs372539402	Patient15	p.Y758F	ENSG00000227124	ENST00000422325	Transcript	missense_variant	possibly_damaging(0.741)
chr4	153245377	153245377	*FBXW7*	Missense_Mutation	.	SNP	A	A	T	novel	Patient15	p.I605N	ENSG00000109670	ENST00000281708	Transcript	missense_variant	probably_damaging(0.999)
chr5	101592891	101592891	*SLCO4C1*	Missense_Mutation	.	SNP	G	G	A	rs145600550	Patient15	p.T466M	ENSG00000173930	ENST00000310954	Transcript	missense_variant	benign(0.005)
chr5	109103262	109103262	*MAN2A1*	Missense_Mutation	.	SNP	A	A	G	novel	Patient15	p.I288V	ENSG00000112893	ENST00000261483	Transcript	missense_variant	benign(0.058)
chr5	112321627	112321627	*DCP2*	Missense_Mutation	.	SNP	A	A	G	novel	Patient15	p.Y50C	ENSG00000172795	ENST00000389063	Transcript	missense_variant	benign(0.034)
chr5	150029164	150029164	*SYNPO*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.A687T	ENSG00000171992	ENST00000394243	Transcript	missense_variant	benign(0.033)
chr6	117706985	117706985	*ROS1*	Missense_Mutation	.	SNP	G	G	A	rs372637439	Patient15	p.T722M	ENSG00000047936	ENST00000368508	Transcript	missense_variant	benign(0.005)
chr6	75950957	75950957	*COX7A2*	Missense_Mutation	.	SNP	T	T	C	novel	Patient15	p.T47A	ENSG00000112695	ENST00000370081	Transcript	missense_variant	benign(0.402)
chr7	140481411	140481411	*BRAF*	Missense_Mutation	.	SNP	C	C	A	novel	Patient15	p.G466V	ENSG00000157764	ENST00000288602	Transcript	missense_variant	probably_damaging(0.936)
chr7	43548590	43548590	*HECW1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.R1297W	ENSG00000002746	ENST00000395891	Transcript	missense_variant	probably_damaging(1)
chr8	28320705	28320705	*CSMD1*	Missense_Mutation	.	SNP	C	C	T	rs199997360	Patient15	p.V2880I	ENSG00000183117	ENST00000537824	Transcript	missense_variant	benign(0.003)
chr8	28555933	28555933	*CSMD1*	Missense_Mutation	.	SNP	C	C	T	rs371234513	Patient15	p.V2773M	ENSG00000183117	ENST00000537824	Transcript	missense_variant	benign(0.282)
chr9	137726835	137726835	*COL5A1*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.E1719K	ENSG00000130635	ENST00000371817	Transcript	missense_variant	unknown(0)
chr9	69423330	69423330	*ANKRD20A4*	Nonsense_Mutation	.	SNP	T	T	A	rs200425688	Patient15	p.Y542*	ENSG00000172014	ENST00000357336	Transcript	stop_gained	NA
chr9	95378254	95378254	*IPPK*	Missense_Mutation	.	SNP	C	C	T	rs146410819	Patient15	p.E446K	ENSG00000127080	ENST00000287996	Transcript	missense_variant	probably_damaging(0.984)
chrX	107811995	107811995	*COL4A5*	Missense_Mutation	.	SNP	C	C	G	novel	Patient15	p.P110A	ENSG00000188153	ENST00000328300	Transcript	missense_variant	unknown(0)
chrX	114413997	114413997	*LRCH2*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.P286L	ENSG00000130224	ENST00000317135	Transcript	missense_variant	possibly_damaging(0.69)
chrX	148037958	148037958	*AFF2*	Missense_Mutation	.	SNP	C	C	A	novel	Patient15	p.H795N	ENSG00000155966	ENST00000370460	Transcript	missense_variant	benign(0.061)
chrX	153036958	153036958	*PLXNB3*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.A812T	ENSG00000198753	ENST00000538966	Transcript	missense_variant	benign(0.019)
chrX	153633169	153633169	*DNASE1L1*	Missense_Mutation	.	SNP	C	C	T	novel	Patient15	p.R104Q	ENSG00000013563	ENST00000369809	Transcript	missense_variant	probably_damaging(0.982)
chrX	153696236	153696236	*PLXNA3*	Missense_Mutation	.	SNP	G	G	A	novel	Patient15	p.V1238M	ENSG00000130827	ENST00000369682	Transcript	missense_variant	probably_damaging(0.998)
chrX	64737866	64737866	*LAS1L*	Splice_Site	.	SNP	C	C	T	novel	Patient15	p.X643_splice	ENSG00000001497	ENST00000374811	Transcript	splice_donor_variant	NA

chr1	115217380	115217380	*AMPD1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P122	p.L631S	ENSG00000116748	ENST00000520113	Transcript	missense_variant	probably_damaging(0.995)
chr1	167088659	167088659	*DUSP27*	Missense_Mutation	.	SNP	G	G	A	rs149727025	shanshan_et_al_P122	p.R204Q	ENSG00000198842	ENST00000361200	Transcript	missense_variant	probably_damaging(0.988)
chr1	179504040	179504040	*AXDND1*	Missense_Mutation	.	SNP	c	c	G	novel	shanshan_et_al_P122	p.Q992E	ENSG00000162779	ENST00000367618	Transcript	missense_variant	unknown(0)
chr1	214542866	214542866	*PTPN14*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P122	p.V1069L	ENSG00000152104	ENST00000366956	Transcript	missense_variant	probably_damaging(0.996)
chr1	40701888	40701889	*RLF*	Frame_Shift_Del	.	DEL	AT	AT	-	novel	shanshan_et_al_P122	p.D505Gfs*8	ENSG00000117000	ENST00000372771	Transcript	frameshift_variant	NA
chr11	118065080	118065080	*AMICA1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P122	p.K382T	ENSG00000160593	ENST00000356289	Transcript	missense_variant	benign(0.005)
chr11	2950237	2950238	*PHLDA2*	Frame_Shift_Ins	.	INS	-	-	G	novel	shanshan_et_al_P122	p.A121Rfs*75	ENSG00000181649	ENST00000314222	Transcript	frameshift_variant	NA
chr11	56000281	56000281	*OR5T2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P122	p.K127N	ENSG00000181718	ENST00000313264	Transcript	missense_variant	benign(0.013)
chr11	57296320	57296320	*TIMM10*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P122	p.S48F	ENSG00000134809	ENST00000257245	Transcript	missense_variant	probably_damaging(0.938)
chr11	67191096	67191096	*CARNS1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P122	p.Q626R	ENSG00000172508	ENST00000445895	Transcript	missense_variant	benign(0.056)
chr11	82705139	82705139	*RAB30*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P122	p.A40D	ENSG00000137502	ENST00000535486	Transcript	missense_variant	probably_damaging(0.991)
chr12	113728805	113728805	*TPCN1*	Splice_Site	.	SNP	T	T	C	novel	shanshan_et_al_P122	p.X725_splice	ENSG00000186815	ENST00000550785	Transcript	splice_donor_variant	NA
chr12	22063144	22063144	*ABCC9*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P122	p.Q423K	ENSG00000069431	ENST00000261200	Transcript	missense_variant	benign(0.193)
chr15	33928584	33928584	*RYR3*	Missense_Mutation	.	SNP	G	G	A	rs558475472	shanshan_et_al_P122	p.R1130H	ENSG00000198838	ENST00000389232	Transcript	missense_variant	possibly_damaging(0.906)
chr17	11833381	11833381	*DNAH9*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P122	p.L4026M	ENSG00000007174	ENST00000262442	Transcript	missense_variant	probably_damaging(0.98)
chr17	17380384	17380384	*MED9*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P122	p.R10Q	ENSG00000141026	ENST00000268711	Transcript	missense_variant	probably_damaging(0.992)
chr17	29685499	29685499	*NF1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P122	p.H2658Y	ENSG00000196712	ENST00000358273	Transcript	missense_variant	benign(0.001)
chr17	37903122	37903122	*GRB7*	Missense_Mutation	.	SNP	G	G	A	rs547219172	shanshan_et_al_P122	p.R547H	ENSG00000141738	ENST00000445327	Transcript	missense_variant	possibly_damaging(0.775)
chr19	36293942	36293942	*PRODH2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P122	p.A423V	ENSG00000250799	ENST00000301175	Transcript	missense_variant	benign(0.405)
chr19	38382377	38382377	*WDR87*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P122	p.E1031A	ENSG00000171804	ENST00000303868	Transcript	missense_variant	benign(0.056)
chr2	209113112	209113112	*IDH1*	Missense_Mutation	.	SNP	C	C	A	rs121913500	shanshan_et_al_P122	p.R132L	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.833)
chr22	37906338	37906338	*CARD10*	Missense_Mutation	.	SNP	t	t	C	novel	shanshan_et_al_P122	p.K264E	ENSG00000100065	ENST00000403299	Transcript	missense_variant	possibly_damaging(0.483)
chr3	108780897	108780897	*MORC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P122	p.I302L	ENSG00000114487	ENST00000232603	Transcript	missense_variant	benign(0)
chr3	134322812	134322812	*KY*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P122	p.K532R	ENSG00000174611	ENST00000423778	Transcript	missense_variant	possibly_damaging(0.572)
chr3	52437861	52437865	*BAP1*	Frame_Shift_Del	.	DEL	CAGCA	CAGCA	-	novel	shanshan_et_al_P122	p.A433Wfs*16	ENSG00000163930	ENST00000460680	Transcript	frameshift_variant	NA
chr4	3076662	3076662	*HTT*	Missense_Mutation	.	SNP	a	a	C	rs61792465	shanshan_et_al_P122	p.Q37P	ENSG00000197386	ENST00000355072	Transcript	missense_variant	benign(0)
chr5	101815958	101815958	*SLCO6A1*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P122	p.L180*	ENSG00000205359	ENST00000506729	Transcript	frameshift_variant	NA
chr5	121356358	121356358	*SRFBP1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P122	p.L310V	ENSG00000151304	ENST00000339397	Transcript	missense_variant	benign(0.118)
chr5	140167440	140167440	*PCDHA1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P122	p.P522H	ENSG00000204970	ENST00000504120	Transcript	missense_variant	probably_damaging(0.912)
chr5	64748604	64748604	*ADAMTS6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P122	p.A258V	ENSG00000049192	ENST00000536360	Transcript	missense_variant	probably_damaging(0.999)
chr6	51720720	51720720	*PKHD1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P122	p.E2628K	ENSG00000170927	ENST00000371117	Transcript	missense_variant	benign(0.005)
chr7	77268018	77268018	*PTPN12*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P122	p.S751P	ENSG00000127947	ENST00000248594	Transcript	missense_variant	benign(0.002)
chr9	35616234	35616234	*CD72*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P122	p.L132M	ENSG00000137101	ENST00000396757	Transcript	missense_variant	probably_damaging(0.996)
chrX	12736297	12736297	*FRMPD4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P122	p.A1118S	ENSG00000169933	ENST00000380682	Transcript	missense_variant	benign(0.027)
chrX	138633418	138633418	*F9*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P122	p.W240R	ENSG00000101981	ENST00000218099	Transcript	missense_variant	probably_damaging(1)
chrX	149678287	149678287	*MAMLD1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P122	p.Y633C	ENSG00000013619	ENST00000432680	Transcript	missense_variant	possibly_damaging(0.823)

chr1	13670952	13670952	*PRAMEF14*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P132	p.E110G	ENSG00000204481	ENST00000334600	Transcript	missense_variant	benign(0.234)
chr1	247836117	247836117	*OR13G1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P132	p.P76L	ENSG00000197437	ENST00000359688	Transcript	missense_variant	probably_damaging(0.998)
chr1	248487170	248487170	*OR2M7*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P132	p.R234H	ENSG00000177186	ENST00000317965	Transcript	missense_variant	benign(0.013)
chr1	33960027	33960027	*ZSCAN20*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P132	p.E695K	ENSG00000121903	ENST00000361328	Transcript	missense_variant	possibly_damaging(0.872)
chr1	77966000	77966000	*CAMTA1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P132	p.R1088H	ENSG00000171735	ENST00000303635	Transcript	missense_variant	probably_damaging(0.996)
chr1	92508402	92508402	*EPHX4*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P132	p.R114*	ENSG00000172031	ENST00000370383	Transcript	stop_gained	NA
chr10	103789503	103789503	*C10orf76*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P132	NA	ENSG00000120029	ENST00000370033	Transcript	splice_acceptor_variant	NA
chr11	89450816	89450816	*TRIM77*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P132	p.L377V	ENSG00000214414	ENST00000398290	Transcript	missense_variant	probably_damaging(0.93)
chr12	51127954	51127954	*DIP2B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P132	p.D1340N	ENSG00000066084	ENST00000301180	Transcript	missense_variant	probably_damaging(1)
chr17	45216160	45216160	*CDC27*	Missense_Mutation	.	SNP	A	A	C	rs199626169	shanshan_et_al_P132	p.V556G	ENSG00000004897	ENST00000531206	Transcript	missense_variant	probably_damaging(0.981)
chr17	45216182	45216182	*CDC27*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P132	p.L549F	ENSG00000004897	ENST00000531206	Transcript	missense_variant	probably_damaging(1)
chr17	53068211	53068211	*STXBP4*	Missense_Mutation	.	SNP	A	A	G	rs372904801	shanshan_et_al_P132	p.I25V	ENSG00000166263	ENST00000376352	Transcript	missense_variant	benign(0.002)
chr17	76117181	76117181	*TMC6*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P132	p.N483S	ENSG00000141524	ENST00000590602	Transcript	missense_variant	probably_damaging(0.913)
chr18	9122638	9122638	*NDUFV2*	Missense_Mutation	.	SNP	G	G	C	rs148158107	shanshan_et_al_P132	p.R143P	ENSG00000178127	ENST00000318388	Transcript	missense_variant	probably_damaging(0.964)
chr19	22155783	22155783	*ZNF208*	Missense_Mutation	.	SNP	C	C	T	rs199604702	shanshan_et_al_P132	p.V685I	ENSG00000160321	ENST00000397176	Transcript	missense_variant	benign(0.008)
chr19	39125730	39125730	*EIF3K*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P132	p.K199N	ENSG00000178982	ENST00000248342	Transcript	missense_variant	possibly_damaging(0.88)
chr2	209113112	209113112	*IDH1*	Missense_Mutation	.	SNP	C	C	A	rs121913500	shanshan_et_al_P132	p.R132L	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.833)
chr2	241835330	241835330	*C2orf54*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P132	p.E29K	ENSG00000172478	ENST00000388934	Transcript	missense_variant	benign(0.039)
chr3	119222460	119222460	*TIMMDC1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P132	p.I148V	ENSG00000113845	ENST00000494664	Transcript	missense_variant	benign(0.21)
chr3	124527879	124527879	*ITGB5*	Missense_Mutation	.	SNP	A	A	G	rs369922990	shanshan_et_al_P132	p.I418T	ENSG00000082781	ENST00000296181	Transcript	missense_variant	benign(0.233)
chr3	183994711	183994711	*ECE2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P132	p.L171S	ENSG00000145194	ENST00000402825	Transcript	missense_variant	benign(0.367)
chr6	150005276	150005276	*LATS1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P132	p.Q317*	ENSG00000131023	ENST00000543571	Transcript	stop_gained	NA
chr8	145106271	145106271	*OPLAH*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P132	p.H1275N	ENSG00000178814	ENST00000426825	Transcript	missense_variant	benign(0)
chr8	90777638	90777638	*RIPK2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P132	p.N133H	ENSG00000104312	ENST00000220751	Transcript	missense_variant	probably_damaging(1)
chrX	148062316	148062316	*AFF2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P132	p.G1207R	ENSG00000155966	ENST00000370460	Transcript	missense_variant	possibly_damaging(0.859)
chrX	32388828	32388828	*MXRA5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P132	p.F1633Y	ENSG00000101825	ENST00000217939	Transcript	missense_variant	possibly_damaging(0.719)
chr1	63999835	63999835	*EFCAB7*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P42	p.M251T	ENSG00000203965	ENST00000371088	Transcript	missense_variant	benign(0.097)
chr17	62498297	62498297	*DDX5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P42	p.R380H	ENSG00000108654	ENST00000225792	Transcript	missense_variant	probably_damaging(0.982)
chr17	78914348	78914348	*RPTOR*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P42	p.R991Q	ENSG00000141564	ENST00000306801	Transcript	missense_variant	benign(0.308)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	shanshan_et_al_P42	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	21231975	21231975	*APOB*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P42	p.E2589K	ENSG00000084674	ENST00000233242	Transcript	missense_variant	benign(0.006)
chr4	152096848	152096848	*SH3D19*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P42	NA	ENSG00000109686	ENST00000304527	Transcript	splice_acceptor_variant	NA
chr5	140812739	140812739	*PCDHGA12*	Missense_Mutation	.	SNP	G	G	A	rs147848043	shanshan_et_al_P42	p.G805R	ENSG00000253159	ENST00000252085	Transcript	missense_variant	benign(0.001)
chr12	11992223	11992223	*ETV6*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P46	p.R105G	ENSG00000139083	ENST00000396373	Transcript	missense_variant	probably_damaging(0.999)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P46	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr17	62122727	62122727	*ERN1*	Missense_Mutation	.	SNP	A	A	G	rs530279351	shanshan_et_al_P46	p.L882P	ENSG00000178607	ENST00000433197	Transcript	missense_variant	probably_damaging(1)

chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	shanshan_et_al_P46	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	95336400	95336400	*ASAP2*	Missense_Mutation	.	SNP	G	G	A	rs113489643	shanshan_et_al_P46	p.V850I	ENSG00000151693	ENST00000281419	Transcript	missense_variant	benign(0.066)
chr5	140564296	140564296	*PCDHB16*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P46	p.S721L	ENSG00000196963	ENST00000361016	Transcript	missense_variant	benign(0.005)
chrX	37431496	37431496	*LANCL3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P46	p.A125T	ENSG00000147036	ENST00000378619	Transcript	missense_variant	possibly_damaging(0.851)
chr1	118165494	118165494	*FAM46C*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_6	p.A2S	ENSG00000183508	ENST00000369448	Transcript	missense_variant	benign(0.025)
chr1	12464004	12464004	*VPS13D*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.N4003S	ENSG00000048707	ENST00000358136	Transcript	missense_variant	benign(0.002)
chr1	209799240	209799240	*LAMB3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_6	p.V577L	ENSG00000196878	ENST00000391911	Transcript	missense_variant	benign(0.005)
chr1	45481105	45481105	*UROD*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.P347S	ENSG00000126088	ENST00000246337	Transcript	missense_variant	probably_damaging(1)
chr1	57044678	57044678	*PPAP2B*	Nonsense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P8_6	p.Y4*	ENSG00000162407	ENST00000371250	Transcript	stop_gained	NA
chr1	62041300	62041300	*CHD5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.D630N	ENSG00000116254	ENST00000262450	Transcript	missense_variant	benign(0.142)
chr1	89264522	89264522	*ENO1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.G185R	ENSG00000074800	ENST00000234590	Transcript	missense_variant	possibly_damaging(0.89)
chr10	55626440	55626440	*PCDH15*	Missense_Mutation	.	SNP	C	C	T	rs368127988	shanshan_et_al_P8_6	p.D1227N	ENSG00000150275	ENST00000361849	Transcript	missense_variant	benign(0.037)
chr11	128842695	128842695	*ARHGAP32*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_6	p.D1222Y	ENSG00000134909	ENST00000310343	Transcript	missense_variant	possibly_damaging(0.855)
chr12	70459339	70459339	*ATN1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P8_6	p.H503Q	ENSG00000111676	ENST00000356654	Transcript	missense_variant	benign(0.008)
chr12	90905300	90905300	*PHC1*	Missense_Mutation	.	SNP	G	G	T	rs199586201	shanshan_et_al_P8_6	p.D912Y	ENSG00000111752	ENST00000543824	Transcript	missense_variant	unknown(0)
chr14	24000822	24000822	*ZFHX2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_6	p.R890S	ENSG00000136367	ENST00000419474	Transcript	missense_variant	probably_damaging(0.936)
chr15	75646791	75646791	*NEIL1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P8_6	p.K298N	ENSG00000140398	ENST00000564784	Transcript	missense_variant	possibly_damaging(0.779)
chr17	34892214	34892214	*TRPV1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_6	p.H411N	ENSG00000196689	ENST00000571088	Transcript	missense_variant	possibly_damaging(0.493)
chr17	39471753	39471767	*KRTAP17-1*	In_Frame_Del	.	DEL	GCCCCCGCAGCCAGA	GCCCCCGCAGCCAGA	-	rs572148015	shanshan_et_al_P8_6	p.G47_S51del	ENSG00000186860	ENST00000334202	Transcript	inframe_deletion	NA
chr17	57752083	57752083	*CLTC*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_6	p.V814I	ENSG00000141367	ENST00000269122	Transcript	missense_variant	benign(0.265)
chr17	65907635	65907636	*BPTF*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P8_6	p.I1215Hfs*3	ENSG00000171634	ENST00000306378	Transcript	frameshift_variant	NA
chr17	72840546	72840546	*GRIN2C*	Missense_Mutation	.	SNP	C	C	T	rs140182608	shanshan_et_al_P8_6	p.V818I	ENSG00000161509	ENST00000293190	Transcript	missense_variant	probably_damaging(0.999)
chr19	14952245	14952245	*OR7A10*	Missense_Mutation	.	SNP	A	A	C	rs372948454	shanshan_et_al_P8_6	p.W149G	ENSG00000127515	ENST00000248058	Transcript	missense_variant	probably_damaging(1)
chr19	22363737	22363737	*ZNF676*	Missense_Mutation	.	SNP	C	C	G	rs572031376	shanshan_et_al_P8_6	p.G261A	ENSG00000196109	ENST00000397121	Transcript	missense_variant	benign(0.001)
chr19	41019419	41019419	*SPTBN4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_6	p.R908H	ENSG00000160460	ENST00000352632	Transcript	missense_variant	benign(0.035)
chr2	112786383	112786383	*MERTK*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P8_6	p.L981*	ENSG00000153208	ENST00000295408	Transcript	stop_gained	NA
chr2	152446470	152446470	*NEB*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P8_6	p.H5060R	ENSG00000183091	ENST00000397345	Transcript	missense_variant	possibly_damaging(0.781)
chr2	209113113	209113113	*IDH1*	Missense_Mutation	.	SNP	G	G	A	rs121913499	shanshan_et_al_P8_6	p.R132C	ENSG00000138413	ENST00000415913	Transcript	missense_variant	possibly_damaging(0.907)
chr2	210560213	210560217	*MAP2*	Frame_Shift_Del	.	DEL	GAGAC	GAGAC	-	novel	shanshan_et_al_P8_6	p.E1107Rfs*10	ENSG00000078018	ENST00000360351	Transcript	frameshift_variant	NA
chr2	228566900	228566901	*SLC19A3*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P8_6	p.N45Kfs*10	ENSG00000135917	ENST00000258403	Transcript	frameshift_variant	NA
chr2	74392405	74392405	*MOB1A*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P8_6	p.Y117D	ENSG00000114978	ENST00000396049	Transcript	missense_variant	possibly_damaging(0.802)
chr2	74751409	74751409	*DQX1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P8_6	p.Q153E	ENSG00000144045	ENST00000404568	Transcript	missense_variant	benign(0.026)
chr22	25627640	25627640	*CRYBB2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P8_6	p.D173E	ENSG00000244752	ENST00000398215	Transcript	missense_variant	benign(0.005)
chr22	27003902	27003902	*CRYBB1*	Missense_Mutation	.	SNP	G	G	A	rs201327237	shanshan_et_al_P8_6	p.S128L	ENSG00000100122	ENST00000215939	Transcript	missense_variant	probably_damaging(0.964)
chr22	39710690	39710690	*RPL3*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P8_6	NA	ENSG00000100316	ENST00000216146	Transcript	splice_donor_variant	NA
chr3	48789026	48789026	*PRKAR2A*	Missense_Mutation	.	SNP	C	C	T	rs374377380	shanshan_et_al_P8_6	p.G403R	ENSG00000114302	ENST00000265563	Transcript	missense_variant	probably_damaging(0.921)

chr5	159368 28	159 368 28	*FBXL7*	Missense _Mutatio n	.	SN P	G	G	A	novel	shansha n_et_al_ P8_6	p.V337I	ENSG00 000183 580	ENST000 0050459 5	Transcr ipt	missense_ variant	benign(0.0 01)
chr5	963418 13	963 418 13	*LNPEP*	Nonsens e_Mutati on	.	SN P	A	A	T	novel	shansha n_et_al_ P8_6	p.K608*	ENSG00 000113 441	ENST000 0023136 8	Transcr ipt	stop_gain ed	NA
chr6	411661 19	411 661 19	*TREML2*	Missense _Mutatio n	.	SN P	T	T	C	novel	shansha n_et_al_ P8_6	p.E35G	ENSG00 000112 195	ENST000 0048372 2	Transcr ipt	missense_ variant	benign(0.0 24)
chr9	212020 73	212 020 73	*IFNA7*	Missense _Mutatio n	.	SN P	C	C	G	rs7690386 3	shansha n_et_al_ P8_6	p.S31T	ENSG00 000214 042	ENST000 0023934 7	Transcr ipt	missense_ variant	benign(0.0 94)
chr9	212021 05	212 021 05	*IFNA7*	Nonsens e_Mutati on	.	SN P	G	G	T	rs7517418 9	shansha n_et_al_ P8_6	p.C20*	ENSG00 000214 042	ENST000 0023934 7	Transcr ipt	stop_gain ed	NA
chrX	100911 641	100 911 641	*ARMCX 2*	Missense _Mutatio n	.	SN P	G	G	A	novel	shansha n_et_al_ P8_6	p.R312C	ENSG00 000184 867	ENST000 0032876 6	Transcr ipt	missense_ variant	benign(0.0 14)
chrX	118147 047	118 147 047	*LONRF3*	Missense _Mutatio n	.	SN P	C	C	A	novel	shansha n_et_al_ P8_6	p.F619L	ENSG00 000175 556	ENST000 0037162 8	Transcr ipt	missense_ variant	probably_d amaging(0. 999)
chrX	122616 713	122 616 713	*GRIA3*	Missense _Mutatio n	.	SN P	C	C	A	novel	shansha n_et_al_ P8_6	p.L835 M	ENSG00 000125 675	ENST000 0026435 7	Transcr ipt	missense_ variant	probably_d amaging(1)
chrX	130408 103	130 408 103	*IGSF1*	Missense _Mutatio n	.	SN P	C	C	A	novel	shansha n_et_al_ P8_6	p.V1282 L	ENSG00 000147 255	ENST000 0037090 3	Transcr ipt	missense_ variant	benign(0.2 75)
chr1	156941 572	156 941 572	*ARHGEF 11*	Missense _Mutatio n	.	SN P	G	G	T	novel	shansha n_et_al_ P03	p.L207I	ENSG00 000132 694	ENST000 0036819 4	Transcr ipt	missense_ variant	benign(0.0 56)
chr1 0	117093 839	117 093 839	*ATRNL1*	Missense _Mutatio n	.	SN P	G	G	A	novel	shansha n_et_al_ P03	p.E1029 K	ENSG00 000107 518	ENST000 0035504 4	Transcr ipt	missense_ variant	benign(0.3 55)
chr1 0	932521 75	932 521 75	*HECTD2*	Missense _Mutatio n	.	SN P	G	G	A	novel	shansha n_et_al_ P03	p.D456 N	ENSG00 000165 338	ENST000 0029806 8	Transcr ipt	missense_ variant	probably_d amaging(0. 998)
chr1 1	168632 09	168 632 09	*PLEKHA 7*	Missense _Mutatio n	.	SN P	C	C	T	rs2019819 94	shansha n_et_al_ P03	p.E253K	ENSG00 000166 689	ENST000 0035566 1	Transcr ipt	missense_ variant	benign(0.1 91)
chr1 1	582754 54	582 754 54	*OR5B21*	Missense _Mutatio n	.	SN P	C	C	T	novel	shansha n_et_al_ P03	p.G42E	ENSG00 000198 283	ENST000 0036037 4	Transcr ipt	missense_ variant	possibly_d amaging(0. 82)
chr1 1	663316 12	663 316 12	*CTSF*	Missense _Mutatio n	.	SN P	C	C	A	novel	shansha n_et_al_ P03	p.D443Y	ENSG00 000174 080	ENST000 0031032 5	Transcr ipt	missense_ variant	possibly_d amaging(0. 718)
chr1 2	111885 491	111 885 491	*SH2B3*	Missense _Mutatio n	.	SN P	A	A	G	novel	shansha n_et_al_ P03	p.Q423R	ENSG00 000111 252	ENST000 0034125 9	Transcr ipt	missense_ variant	possibly_d amaging(0. 837)
chr1 2	133795 930	133 795 930	*ANHX*	Missense _Mutatio n	.	SN P	G	G	A	rs5677134 75	shansha n_et_al_ P03	p.P331L	ENSG00 000227 059	ENST000 0054594 0	Transcr ipt	missense_ variant	benign(0.0 01)
chr1 2	213777 11	213 777 11	*SLCO1B 1*	Missense _Mutatio n	.	SN P	G	G	T	novel	shansha n_et_al_ P03	p.K601N	ENSG00 000134 538	ENST000 0025695 8	Transcr ipt	missense_ variant	probably_d amaging(0. 99)
chr1 2	253982 84	253 982 84	*KRAS*	Missense _Mutatio n	.	SN P	C	C	T	novel	shansha n_et_al_ P03	p.G12D	ENSG00 000133 703	ENST000 0025607 8	Transcr ipt	missense_ variant	benign(0.3 61)
chr1 4	682496 14	682 496 14	*ZFYVE2 6*	Missense _Mutatio n	.	SN P	C	C	T	novel	shansha n_et_al_ P03	p.E1419 K	ENSG00 000072 121	ENST000 0034723 0	Transcr ipt	missense_ variant	benign(0.2 04)
chr1 5	656218 37	656 218 37	*IGDCC3*	Missense _Mutatio n	.	SN P	C	C	T	novel	shansha n_et_al_ P03	p.R699Q	ENSG00 000174 498	ENST000 0032798 7	Transcr ipt	missense_ variant	benign(0.0 01)
chr1 6	130652 3	130 652 3	*TPSD1*	Missense _Mutatio n	.	SN P	G	G	T	rs2401937	shansha n_et_al_ P03	p.G30V	ENSG00 000095 917	ENST000 0021107 6	Transcr ipt	missense_ variant	probably_d amaging(0. 989)
chr1 6	887935 58	887 935 58	*PIEZO1*	Missense _Mutatio n	.	SN P	A	A	C	novel	shansha n_et_al_ P03	p.V1115 G	ENSG00 000103 335	ENST000 0030101 5	Transcr ipt	missense_ variant	probably_d amaging(0. 999)
chr1 7	389767 85	389 767 85	*KRT10*	Missense _Mutatio n	.	SN P	T	T	A	novel	shansha n_et_al_ P03	p.Y282F	ENSG00 000186 395	ENST000 0026957 6	Transcr ipt	missense_ variant	benign(0.0 55)
chr1 7	411700 51	411 700 51	*VAT1*	Splice_Si te	.	SN P	A	A	C	novel	shansha n_et_al_ P03	p.X256_ splice	ENSG00 000108 828	ENST000 0035565 3	Transcr ipt	splice_do nor_varia nt	NA
chr1 7	480468 60	480 468 60	*DLX4*	Missense _Mutatio n	.	SN P	G	G	C	novel	shansha n_et_al_ P03	p.G10R	ENSG00 000108 813	ENST000 0024030 6	Transcr ipt	missense_ variant	probably_d amaging(0. 956)
chr1 8	485919 30	485 919 30	*SMAD4*	Missense _Mutatio n	.	SN P	G	G	A	novel	shansha n_et_al_ P03	p.G365S	ENSG00 000141 646	ENST000 0034298 8	Transcr ipt	missense_ variant	probably_d amaging(1)
chr1 8	562054 55	562 054 55	*ALPK2*	Missense _Mutatio n	.	SN P	A	A	C	novel	shansha n_et_al_ P03	p.V655G	ENSG00 000198 796	ENST000 0036167 3	Transcr ipt	missense_ variant	benign(0.0 99)
chr1 9	104439 68	104 439 68	*RAVER1*	Missense _Mutatio n	.	SN P	G	G	T	novel	shansha n_et_al_ P03	p.N89K	ENSG00 000161 847	ENST000 0029367 7	Transcr ipt	missense_ variant	probably_d amaging(0. 972)
chr1 9	407177	407 177	*C2CD4C*	Frame_S hift_Del	.	DEL	C	C	-	novel	shansha n_et_al_ P03	p.N396T fs*19	ENSG00 000183 186	ENST000 0033223 5	Transcr ipt	frameshift _variant	NA
chr2	159433 886	159 433 886	*PKP4*	Missense _Mutatio n	.	SN P	C	C	G	novel	shansha n_et_al_ P03	p.A79G	ENSG00 000144 283	ENST000 0038975 9	Transcr ipt	missense_ variant	benign(0)
chr2 0	354220 73	354 220 73	*SOGA1*	Nonsens e_Mutati on	.	SN P	G	G	T	novel	shansha n_et_al_ P03	p.S1471 *	ENSG00 000149 639	ENST000 0023753 6	Transcr ipt	stop_gain ed	NA
chr2 0	551084 48	551 084 48	*FAM209 B*	Missense _Mutatio n	.	SN P	C	C	G	novel	shansha n_et_al_ P03	p.S17R	ENSG00 000213 714	ENST000 0037132 5	Transcr ipt	missense_ variant	possibly_d amaging(0. 883)
chr2 2	377691 89	377 691 89	*ELFN2*	Missense _Mutatio n	.	SN P	C	C	A	novel	shansha n_et_al_ P03	p.V796F	ENSG00 000166 897	ENST000 0040291 8	Transcr ipt	missense_ variant	probably_d amaging(0. 999)
chr5	137921 15	137 921 15	*DNAH5*	Missense _Mutatio n	.	SN P	G	G	C	novel	shansha n_et_al_ P03	p.I2812 M	ENSG00 000039 139	ENST000 0026510 4	Transcr ipt	missense_ variant	possibly_d amaging(0. 639)
chr5	180057 783	180 057 783	*FLT4*	Missense _Mutatio n	.	SN P	C	C	T	rs1481269 51	shansha n_et_al_ P03	p.E58K	ENSG00 000037 280	ENST000 0026193 7	Transcr ipt	missense_ variant	benign(0.0 37)

chr5	26881414	26881414	*CDH9*	Nonsense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P03	p.S734*	ENSG00000113100	ENST00000231021	Transcript	stop_gained	NA
chr6	116600530	116600530	*TSPYL1*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P03	p.V155G	ENSG00000189241	ENST00000368608	Transcript	missense_variant	benign(0.007)
chr6	116914199	116914199	*RWDD1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P03	p.L223M	ENSG00000111832	ENST00000466444	Transcript	missense_variant	unknown(0)
chr7	140434567	140434567	*BRAF*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P03	p.L711F	ENSG00000157764	ENST00000288602	Transcript	missense_variant	possibly_damaging(0.703)
chrX	38664390	38664390	*MID1IP1*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P03	p.E64G	ENSG00000165175	ENST00000336949	Transcript	missense_variant	benign(0.019)
chr1	1266786	1266786	*TAS1R3*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P07	p.A21S	ENSG00000169962	ENST00000339381	Transcript	missense_variant	benign(0.014)
chr12	120884072	120884072	*TRIAP1*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P07	p.D35A	ENSG00000170855	ENST00000546954	Transcript	missense_variant	benign(0.446)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P07	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr12	27924017	27924017	*MANSC4*	Frame_Shift_Del	.	DEL	G	G	-	novel	shansha n_et_al_P07	p.Q65Rfs*44	ENSG00000205693	ENST00000381273	Transcript	frameshift_variant	NA
chr14	73729186	73729186	*PAPLN*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P07	p.N765H	ENSG00000100767	ENST00000340738	Transcript	missense_variant	probably_damaging(1)
chr15	49031479	49031479	*CEP152*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P07	p.P1367R	ENSG00000103995	ENST00000380950	Transcript	missense_variant	probably_damaging(0.951)
chr16	36146044	36146044	*NLRC3*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P07	p.T159P	ENSG00000167984	ENST00000448023	Transcript	missense_variant	benign(0.265)
chr17	17726904	17726904	*SREBF1*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P07	p.R37G	ENSG00000072310	ENST00000355815	Transcript	missense_variant	benign(0)
chr19	51871824	51871824	*CLDND2*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P07	p.V3G	ENSG00000160318	ENST00000291715	Transcript	missense_variant	possibly_damaging(0.713)
chr2	27481626	27481626	*SLC30A3*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P07	p.V91G	ENSG00000115194	ENST00000235335	Transcript	missense_variant	benign(0.16)
chr22	50946091	50946091	*LMF2*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P07	p.R5P	ENSG00000100258	ENST00000474879	Transcript	missense_variant	possibly_damaging(0.503)
chr7	27224121	27224121	*HOXA11*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P07	p.R215G	ENSG00000005073	ENST00000060015	Transcript	missense_variant	benign(0.079)
chr9	130269558	130269558	*FAM129B*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P07	p.S603R	ENSG00000136830	ENST00000373312	Transcript	missense_variant	benign(0.001)
chr1	151678722	151678723	*CELF3*	In_Frame_Ins	.	INS	-	-	TGC	novel	shansha n_et_al_P107	p.Q368dup	ENSG00000159409	ENST00000290583	Transcript	inframe_insertion	NA
chr1	202287524	202287524	*LGR6*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P107	p.G698E	ENSG00000133067	ENST00000367278	Transcript	missense_variant	benign(0.356)
chr10	121203161	121203161	*GRK5*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P107	p.R388L	ENSG00000198873	ENST00000392870	Transcript	missense_variant	probably_damaging(0.913)
chr10	135053221	135053221	*VENTX*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P107	p.R95C	ENSG00000151650	ENST00000325980	Transcript	missense_variant	possibly_damaging(0.808)
chr11	22398184	22398184	*SLC17A6*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P107	p.C460F	ENSG00000091664	ENST00000263160	Transcript	missense_variant	probably_damaging(0.979)
chr12	125396804	125396804	*UBC*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P107	p.Q505P	ENSG00000150991	ENST00000536769	Transcript	missense_variant	benign(0.343)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P107	p.G12V	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.479)
chr13	61141657	61141657	*TDRD3*	Splice_Site	.	SNP	A	A	G	novel	shansha n_et_al_P107	p.X707_splice	ENSG00000083544	ENST00000535286	Transcript	splice_acceptor_variant	NA
chr15	25223587	25223587	*SNRPN*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P107	p.P240R	ENSG00000128739	ENST00000400100	Transcript	missense_variant	unknown(0)
chr16	81969881	81969881	*PLCG2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P107	p.R984C	ENSG00000197943	ENST00000359376	Transcript	missense_variant	probably_damaging(1)
chr17	12901792	12901792	*ELAC2*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P107	p.L486R	ENSG00000006744	ENST00000338034	Transcript	missense_variant	probably_damaging(0.999)
chr17	79496251	79496251	*FSCN2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P107	p.V232M	ENSG00000186765	ENST00000334850	Transcript	missense_variant	benign(0.027)
chr18	13741678	13741678	*RNMT*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P107	p.S321N	ENSG00000101654	ENST00000383314	Transcript	missense_variant	possibly_damaging(0.906)
chr19	11559785	11559785	*PRKCSH*	Missense_Mutation	.	SNP	G	G	A	rs201614230	shansha n_et_al_P107	p.G441D	ENSG00000130175	ENST00000252455	Transcript	missense_variant	probably_damaging(0.987)
chr19	12874492	12874492	*HOOK2*	Missense_Mutation	.	SNP	C	C	G	rs374381452	shansha n_et_al_P107	p.R643P	ENSG00000095066	ENST00000397668	Transcript	missense_variant	possibly_damaging(0.665)
chr2	60995638	60995638	*PAPOLG*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P107	p.G94C	ENSG00000115421	ENST00000238714	Transcript	missense_variant	probably_damaging(0.981)
chr20	45353935	45353935	*SLC2A10*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P107	p.A87V	ENSG00000197496	ENST00000359271	Transcript	missense_variant	benign(0.004)
chr3	16419576	16419576	*RFTN1*	Missense_Mutation	.	SNP	C	C	T	rs151244908	shansha n_et_al_P107	p.V159I	ENSG00000131378	ENST00000334133	Transcript	missense_variant	benign(0.197)

chr5	127450319	127450319	*SLC12A2*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P107	p.T332A	ENSG00000064651	ENST00000262461	Transcript	missense_variant	probably_damaging(0.932)
chr5	57753033	57753033	*PLK2*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P107	p.I328S	ENSG00000145632	ENST00000274289	Transcript	missense_variant	possibly_damaging(0.867)
chr6	42897358	42897360	*CNPY3*	In_Frame_Del	.	DEL	TGC	TGC	-	novel	shansha n_et_al_P107	p.L20del	ENSG00000137161	ENST00000372836	Transcript	inframe_deletion	NA
chr7	75197514	75197514	*HIP1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P107	p.E264D	ENSG00000127946	ENST00000336926	Transcript	missense_variant	benign(0.351)
chr8	106573623	106573623	*ZFPM2*	Nonsense_Mutation	.	SNP	C	C	T	rs121908602	shansha n_et_al_P107	p.R112*	ENSG00000169946	ENST00000407775	Transcript	stop_gained	NA
chrX	114425149	114425149	*RBMXL3*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P107	p.R382H	ENSG00000175718	ENST00000424776	Transcript	missense_variant	possibly_damaging(0.522)
chrX	114541292	114541292	*LUZP4*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P107	p.N289H	ENSG00000102021	ENST00000371920	Transcript	missense_variant	benign(0.044)
chr1	109369841	109369841	*AKNAD1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P108	p.S641*	ENSG00000162641	ENST00000370001	Transcript	stop_gained	NA
chr1	27003112	27003112	*TTC34*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P108	p.A177T	ENSG00000215912	ENST00000401095	Transcript	missense_variant	probably_damaging(0.959)
chr1	27100082	27100082	*ARID1A*	Missense_Mutation	.	SNP	G	G	A	rs538431643	shansha n_et_al_P108	p.G1293E	ENSG00000117713	ENST00000324856	Transcript	missense_variant	unknown(0)
chr1	67559216	67559217	*C1orf141*	Frame_Shift_Ins	.	INS	-	-	T	novel	shansha n_et_al_P108	NA	ENSG00000203963	ENST00000371007	Transcript	frameshift_variant	NA
chr11	111904162	111904162	*DLAT*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P108	p.M232T	ENSG00000150768	ENST00000280346	Transcript	missense_variant	benign(0.332)
chr11	494979	494979	*RNH1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P108	p.R401H	ENSG00000023191	ENST00000534797	Transcript	missense_variant	probably_damaging(0.959)
chr11	51412298	51412298	*OR4A5*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P108	p.Y33C	ENSG00000221840	ENST00000319760	Transcript	missense_variant	possibly_damaging(0.5)
chr12	20885887	20885887	*SLCO1C1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P108	p.G411R	ENSG00000139155	ENST00000381552	Transcript	missense_variant	probably_damaging(0.996)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P108	p.G12V	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.479)
chr12	41967137	41967137	*PDZRN4*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P108	p.S852R	ENSG00000165966	ENST00000406825	Transcript	missense_variant	probably_damaging(0.997)
chr12	48596381	48596381	*OR10AD1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P108	p.S232F	ENSG00000172640	ENST00000310248	Transcript	missense_variant	benign(0.026)
chr12	52864372	52864372	*KRT6C*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P108	p.L374V	ENSG00000170465	ENST00000252250	Transcript	missense_variant	probably_damaging(0.999)
chr12	58131354	58131354	*AGAP2*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P108	p.S226C	ENSG00000135439	ENST00000547588	Transcript	missense_variant	possibly_damaging(0.843)
chr12	67075500	67075500	*CHD4*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P108	p.W508*	ENSG00000111642	ENST00000357008	Transcript	stop_gained	NA
chr13	110438120	110438120	*IRS2*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P108	p.A94G	ENSG00000185950	ENST00000375856	Transcript	missense_variant	benign(0.155)
chr13	114083332	114083332	*ADPRHL1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P108	p.R194K	ENSG00000153531	ENST00000375418	Transcript	missense_variant	probably_damaging(0.973)
chr13	84455240	84455240	*SLITRK1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P108	p.L135I	ENSG00000178235	ENST00000377084	Transcript	missense_variant	probably_damaging(1)
chr14	20502659	20502659	*OR4K13*	Nonsense_Mutation	.	SNP	G	G	A	rs202200696	shansha n_et_al_P108	p.R87*	ENSG00000176253	ENST00000315693	Transcript	stop_gained	NA
chr14	21961267	21961267	*TOX4*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P108	p.L498V	ENSG00000092203	ENST00000405508	Transcript	missense_variant	benign(0.005)
chr14	93412799	93412799	*ITPK1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P108	p.E260K	ENSG00000100605	ENST00000267615	Transcript	missense_variant	benign(0.283)
chr15	29415586	29415586	*FAM189A1*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P108	p.E526Q	ENSG00000104059	ENST00000261275	Transcript	missense_variant	benign(0.007)
chr16	88951511	88951511	*CBFA2T3*	Nonsense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P108	p.R354*	ENSG00000129993	ENST00000268679	Transcript	stop_gained	NA
chr17	10222426	10222426	*MYH13*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P108	p.R1140H	ENSG00000006788	ENST00000418404	Transcript	missense_variant	probably_damaging(0.963)
chr17	42152809	42152809	*G6PC3*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P108	p.D223H	ENSG00000141349	ENST00000269097	Transcript	missense_variant	probably_damaging(0.969)
chr17	7577559	7577559	*TP53*	Missense_Mutation	.	SNP	G	G	A	rs28934573	shansha n_et_al_P108	p.S241F	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(1)
chr19	49164950	49164950	*NTN5*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P108	p.P485L	ENSG00000142233	ENST00000270235	Transcript	missense_variant	probably_damaging(0.996)
chr19	50247521	50247521	*TSKS*	Missense_Mutation	.	SNP	C	C	T	rs374085678	shansha n_et_al_P108	p.R443Q	ENSG00000126467	ENST00000246801	Transcript	missense_variant	probably_damaging(0.996)
chr19	52869634	52869634	*ZNF610*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P108	p.Q335*	ENSG00000167554	ENST00000403906	Transcript	stop_gained	NA
chr19	56274176	56274176	*RFPL4A*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P108	p.V167M	ENSG00000223638	ENST00000434937	Transcript	missense_variant	probably_damaging(0.953)

chr2	141625299	141625299	*LRP1B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P108	p.S1480N	ENSG00000168702	ENST00000389484	Transcript	missense_variant	benign(0.009)
chr22	26176157	26176157	*MYO18B*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P108	p.Q735*	ENSG00000133454	ENST00000335473	Transcript	stop_gained	NA
chr22	39710716	39710716	*RPL3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P108	p.H275R	ENSG00000100316	ENST00000216146	Transcript	missense_variant	possibly_damaging(0.807)
chr3	10976725	10976727	*SLC6A11*	In_Frame_Del	.	DEL	TCT	TCT	-	novel	shanshan_et_al_P108	p.F531del	ENSG00000132164	ENST00000254488	Transcript	inframe_deletion	NA
chr3	178952085	178952085	*PIK3CA*	Missense_Mutation	.	SNP	A	A	G	rs121913279	shanshan_et_al_P108	p.H1047R	ENSG00000121879	ENST00000263967	Transcript	missense_variant	possibly_damaging(0.529)
chr3	182941958	182941958	*MCF2L2*	Nonsense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P108	p.Y712*	ENSG00000053524	ENST00000328913	Transcript	stop_gained	NA
chr3	52360159	52360159	*DNAH1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P108	p.G137E	ENSG00000114841	ENST00000420323	Transcript	missense_variant	benign(0.001)
chr3	52545756	52545756	*STAB1*	Missense_Mutation	.	SNP	G	G	A	rs201709604	shanshan_et_al_P108	p.G960S	ENSG00000010327	ENST00000321725	Transcript	missense_variant	benign(0.041)
chr3	77607107	77607107	*ROBO2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P108	p.R431I	ENSG00000185008	ENST00000487694	Transcript	missense_variant	benign(0.308)
chr4	145038018	145038018	*GYPA*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P108	p.R116*	ENSG00000170180	ENST00000360771	Transcript	stop_gained	NA
chr5	132160905	132160905	*SHROOM1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P108	p.E310K	ENSG00000164403	ENST00000378679	Transcript	missense_variant	benign(0.011)
chr5	43174972	43174972	*ZNF131*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P108	p.E503K	ENSG00000172262	ENST00000509634	Transcript	missense_variant	possibly_damaging(0.54)
chr6	152265535	152265535	*ESR1*	Missense_Mutation	.	SNP	G	G	A	rs571716552	shanshan_et_al_P108	p.E330K	ENSG00000091831	ENST00000440973	Transcript	missense_variant	benign(0.007)
chr6	26452100	26452100	*BTN3A3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P108	p.E406Q	ENSG00000111801	ENST00000244519	Transcript	missense_variant	benign(0.079)
chr7	127954977	127954977	*RBM28*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P108	p.E629K	ENSG00000106344	ENST00000223073	Transcript	missense_variant	benign(0)
chr7	158424395	158424395	*NCAPG2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P108	p.S1132L	ENSG00000146918	ENST00000409423	Transcript	missense_variant	benign(0.176)
chr8	100654571	100654571	*VPS13B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P108	p.R1943Q	ENSG00000132549	ENST00000358544	Transcript	missense_variant	possibly_damaging(0.885)
chr8	110416854	110416854	*PKHD1L1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P108	p.R482Q	ENSG00000205038	ENST00000378402	Transcript	missense_variant	benign(0.034)
chr8	55542151	55542151	*RP1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P108	p.E1903D	ENSG00000104237	ENST00000220676	Transcript	missense_variant	probably_damaging(0.998)
chr8	93004034	93004034	*RUNX1T1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P108	p.R286Q	ENSG00000079102	ENST00000436581	Transcript	missense_variant	probably_damaging(0.98)
chr9	125424476	125424476	*OR1L1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P108	p.L161H	ENSG00000173679	ENST00000309623	Transcript	missense_variant	possibly_damaging(0.634)
chrX	24844692	24844692	*POLA1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P108	p.D1231V	ENSG00000101868	ENST00000379059	Transcript	missense_variant	probably_damaging(0.999)
chrX	66765158	66765158	*AR*	Missense_Mutation	.	SNP	T	T	A	rs786867937	shanshan_et_al_P108	p.L57Q	ENSG00000169083	ENST00000374690	Transcript	missense_variant	unknown(0)
chr1	103381209	103381209	*COL11A1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.P1265L	ENSG00000060718	ENST00000370096	Transcript	missense_variant	unknown(0)
chr1	110581320	110581320	*STRIP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P111	p.T89M	ENSG00000143093	ENST00000369795	Transcript	missense_variant	probably_damaging(0.966)
chr1	156449559	156449559	*MEF2D*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P111	p.M142I	ENSG00000116604	ENST00000348159	Transcript	missense_variant	benign(0.174)
chr1	17657625	17657625	*PADI4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P111	p.G85V	ENSG00000159339	ENST00000375448	Transcript	missense_variant	benign(0.004)
chr1	27106504	27106504	*ARID1A*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P111	p.Q2039*	ENSG00000117713	ENST00000324856	Transcript	stop_gained	NA
chr1	68942629	68942629	*DEPDC1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.R808C	ENSG00000024526	ENST00000456315	Transcript	missense_variant	benign(0.028)
chr1	74507219	74507220	*LRRIQ3*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P111	p.Y466*	ENSG00000162620	ENST00000354431	Transcript	frameshift_variant	NA
chr10	102275937	102275937	*SEC31B*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P111	p.N40S	ENSG00000075826	ENST00000370345	Transcript	missense_variant	benign(0.004)
chr10	108357142	108357142	*SORCS1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.R1078*	ENSG00000108018	ENST00000344440	Transcript	stop_gained	NA
chr10	61834572	61834572	*ANK3*	Missense_Mutation	.	SNP	C	C	T	rs146929899	shanshan_et_al_P111	p.A2023T	ENSG00000151150	ENST00000280772	Transcript	missense_variant	benign(0.001)
chr11	92715229	92715229	*MTNR1B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P111	p.E280D	ENSG00000134640	ENST00000257068	Transcript	missense_variant	benign(0.008)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P111	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr14	94088174	94088174	*UNC79*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P111	p.P1355L	ENSG00000133958	ENST00000256339	Transcript	missense_variant	benign(0.007)

chr16	19620328	19620328	*C16orf62*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P111	p.K394R	ENSG00000103544	ENST00000438132	Transcript	missense_variant	benign(0.004)
chr17	20914573	20914573	*USP22*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.P332S	ENSG00000124422	ENST00000261497	Transcript	missense_variant	benign(0.41)
chr2	159033054	159033055	*CCDC148*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P111	p.L536Ffs*6	ENSG00000153237	ENST00000283233	Transcript	frameshift_variant	NA
chr2	201436744	201436744	*SGOL2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P111	p.Y559H	ENSG00000163535	ENST00000357799	Transcript	missense_variant	benign(0.212)
chr2	27857793	27857793	*GPN1*	Splice_Site	.	SNP	T	T	G	novel	shanshan_et_al_P111	p.X157_splice	ENSG00000198522	ENST00000264718	Transcript	splice_donor_variant	NA
chr2	68882553	68882553	*PROKR1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.V343M	ENSG00000169618	ENST00000303786	Transcript	missense_variant	benign(0.133)
chr2	74741944	74741944	*TLX2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P111	p.G4A	ENSG00000115297	ENST00000233638	Transcript	missense_variant	benign(0)
chr22	17445711	17445711	*GAB4*	Missense_Mutation	.	SNP	G	G	A	rs141562718	shanshan_et_al_P111	p.T474M	ENSG00000215568	ENST00000400588	Transcript	missense_variant	benign(0)
chr3	148896286	148896286	*CP*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P111	p.D932H	ENSG00000047457	ENST00000264613	Transcript	missense_variant	probably_damaging(0.975)
chr3	30713853	30713853	*TGFBR2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.C418Y	ENSG00000163513	ENST00000359013	Transcript	missense_variant	probably_damaging(0.998)
chr3	54933813	54933813	*CACNA2D3*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P111	p.X790_splice	ENSG00000157445	ENST00000474759	Transcript	splice_acceptor_variant	NA
chr6	160174638	160174638	*WTAP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.S200N	ENSG00000146457	ENST00000358372	Transcript	missense_variant	benign(0.107)
chr7	144345911	144345911	*TPK1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P111	p.Y83N	ENSG00000196511	ENST00000360057	Transcript	missense_variant	probably_damaging(0.994)
chr8	134042167	134042167	*TG*	Missense_Mutation	.	SNP	G	G	A	rs369236885	shanshan_et_al_P111	p.V2380M	ENSG00000042832	ENST00000220616	Transcript	missense_variant	probably_damaging(0.999)
chr8	89209488	89209488	*MMP16*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P111	p.M60I	ENSG00000156103	ENST00000286614	Transcript	missense_variant	benign(0.159)
chr9	41505636	41505636	*SPATA31A5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P111	p.L970F	ENSG00000233788	ENST00000377621	Transcript	missense_variant	NA
chr9	86468653	86468653	*KIF27*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P111	p.L1083R	ENSG00000165115	ENST00000297814	Transcript	missense_variant	possibly_damaging(0.894)
chrX	37587545	37587545	*XK*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P111	p.Q389*	ENSG00000047597	ENST00000378616	Transcript	stop_gained	NA
chrX	47032597	47032597	*RBM10*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P111	p.X168_splice	ENSG00000182872	ENST00000377604	Transcript	splice_donor_variant	NA
chr1	200377084	200377084	*ZNF281*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P120	p.I584L	ENSG00000162702	ENST00000294740	Transcript	missense_variant	benign(0.018)
chr11	18878133	18878133	*LSP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P120	p.L37F	ENSG00000130592	ENST00000381775	Transcript	missense_variant	unknown(0)
chr12	117768481	117768481	*NOS1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P120	p.A132T	ENSG00000089250	ENST00000338101	Transcript	missense_variant	benign(0.017)
chr12	25398285	25398285	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P120	p.G12C	ENSG00000133703	ENST00000256078	Transcript	missense_variant	probably_damaging(0.993)
chr13	33629207	33629207	*KL*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P120	p.V452F	ENSG00000133116	ENST00000380099	Transcript	missense_variant	probably_damaging(0.954)
chr16	58287944	58287944	*CCDC113*	Missense_Mutation	.	SNP	C	C	T	rs375219394	shanshan_et_al_P120	p.R91C	ENSG00000103021	ENST00000219299	Transcript	missense_variant	benign(0.028)
chr2	42867369	42867369	*MTA3*	Missense_Mutation	.	SNP	A	A	T	rs370642232	shanshan_et_al_P120	p.D125V	ENSG00000057935	ENST00000407270	Transcript	missense_variant	benign(0.008)
chr3	105400433	105400433	*CBLB*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P120	p.S773C	ENSG00000114423	ENST00000264122	Transcript	missense_variant	possibly_damaging(0.667)
chr3	52550752	52550752	*STAB1*	Missense_Mutation	.	SNP	C	C	T	rs377337830	shanshan_et_al_P120	p.A1444V	ENSG00000010327	ENST00000321725	Transcript	missense_variant	possibly_damaging(0.84)
chr3	54958999	54958999	*LRTM1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P120	p.N84I	ENSG00000144771	ENST00000273286	Transcript	missense_variant	probably_damaging(1)
chr4	23816104	23816104	*PPARGC1A*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P120	p.S334R	ENSG00000109819	ENST00000264867	Transcript	missense_variant	possibly_damaging(0.677)
chr7	148947266	148947266	*ZNF212*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P120	p.R14H	ENSG00000170260	ENST00000335870	Transcript	missense_variant	benign(0.012)
chr8	143993984	143993984	*CYP11B2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P120	p.R454C	ENSG00000179142	ENST00000323110	Transcript	missense_variant	probably_damaging(1)
chr9	114820772	114820772	*SUSD1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P120	p.N682I	ENSG00000106868	ENST00000374270	Transcript	missense_variant	probably_damaging(0.999)
chr9	128347883	128347883	*MAPKAP1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P120	p.G208W	ENSG00000119487	ENST00000265960	Transcript	missense_variant	probably_damaging(1)
chr9	69423807	69423807	*ANKRD20A4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P120	p.Q701H	ENSG00000172014	ENST00000357336	Transcript	missense_variant	probably_damaging(0.929)
chr1	12907358	12907358	*HNRNPCL1*	Missense_Mutation	.	SNP	T	T	C	rs74587302,rs559905244	shanshan_et_al_P129	p.Q262R	ENSG00000179172	ENST00000317869	Transcript	missense_variant	benign(0.001)

chr1	12919574	12919574	*PRAMEF2*	Nonsense_Mutation	.	SNP	T	T	A	rs78738981	shanshan_et_al_P129	p.L105*	ENSG00000120952	ENST00000240189	Transcript	stop_gained	NA
chr1	158911819	158911819	*PYHIN1*	Missense_Mutation	.	SNP	G	G	A	rs140327432	shanshan_et_al_P129	p.R211Q	ENSG00000163564	ENST00000368140	Transcript	missense_variant	benign(0.003)
chr1	185931768	185931768	*HMCN1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P129	p.D649E	ENSG00000143341	ENST00000271588	Transcript	missense_variant	probably_damaging(0.977)
chr1	46874779	46874779	*FAAH*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.P362S	ENSG00000117480	ENST00000243167	Transcript	missense_variant	possibly_damaging(0.684)
chr1	53543382	53543383	*PODN*	Frame_Shift_Ins	.	INS	-	-	G	novel	shanshan_et_al_P129	p.A305Gfs*20	ENSG00000174348	ENST00000312553	Transcript	frameshift_variant	NA
chr1	60314179	60314179	*HOOK1*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P129	p.Y374*	ENSG00000134709	ENST00000371208	Transcript	stop_gained	NA
chr10	101961894	101961895	*CHUK*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P129	p.M507Nfs*17	ENSG00000213341	ENST00000370397	Transcript	frameshift_variant	NA
chr10	27313408	27313408	*ANKRD26*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P129	p.K1351N	ENSG00000107890	ENST00000376087	Transcript	missense_variant	probably_damaging(0.962)
chr11	116798030	116798030	*SIK3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.T116I	ENSG00000160584	ENST00000292055	Transcript	missense_variant	benign(0.201)
chr11	123886958	123886958	*OR10G4*	Missense_Mutation	.	SNP	G	G	A	rs112194008	shanshan_et_al_P129	p.R226Q	ENSG00000254737	ENST00000320891	Transcript	missense_variant	benign(0.034)
chr11	59225149	59225149	*OR4D6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.T239M	ENSG00000166884	ENST00000300127	Transcript	missense_variant	probably_damaging(1)
chr11	62380940	62380940	*ROM1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.P63S	ENSG00000149489	ENST00000278833	Transcript	missense_variant	probably_damaging(0.986)
chr11	62931321	62931321	*SLC22A25*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.A540V	ENSG00000196600	ENST00000306494	Transcript	missense_variant	benign(0.01)
chr11	92523203	92523203	*FAT3*	Missense_Mutation	.	SNP	C	C	A	rs375548582	shanshan_et_al_P129	p.T1477K	ENSG00000165323	ENST00000298047	Transcript	missense_variant	possibly_damaging(0.901)
chr12	123276583	123276583	*CCDC62*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P129	p.K229N	ENSG00000130783	ENST00000253079	Transcript	missense_variant	probably_damaging(0.997)
chr12	15130986	15130986	*PDE6H*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.Q14*	ENSG00000139053	ENST00000266395	Transcript	stop_gained	NA
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr12	45822933	45822933	*ANO6*	Missense_Mutation	.	SNP	G	G	C	rs140463382	shanshan_et_al_P129	p.D879H	ENSG00000177119	ENST00000423947	Transcript	missense_variant	probably_damaging(1)
chr12	52374954	52374954	*ACVR1B*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P129	p.I261S	ENSG00000135503	ENST00000541224	Transcript	missense_variant	probably_damaging(0.999)
chr12	54394208	54394208	*HOXC9*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.P79L	ENSG00000180806	ENST00000303450	Transcript	missense_variant	probably_damaging(0.999)
chr12	70975011	70975011	*PTPRB*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.Q795*	ENSG00000127329	ENST00000334414	Transcript	stop_gained	NA
chr12	88512305	88512305	*CEP290*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P129	p.I556Nfs*20	ENSG00000198707	ENST00000552810	Transcript	frameshift_variant	NA
chr14	105413795	105413795	*AHNAK2*	Missense_Mutation	.	SNP	C	C	T	rs369787479	shanshan_et_al_P129	p.E2665K	ENSG00000185567	ENST00000333244	Transcript	missense_variant	benign(0)
chr14	23549113	23549113	*ACIN1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P129	p.E535D	ENSG00000100813	ENST00000262710	Transcript	missense_variant	benign(0.302)
chr14	32562545	32562545	*ARHGAP5*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P129	p.E893*	ENSG00000100852	ENST00000345122	Transcript	frameshift_variant	NA
chr15	30385155	30385155	*GOLGA8J*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.G511R	ENSG00000179938	ENST00000567927	Transcript	missense_variant	possibly_damaging(0.457)
chr15	32688530	32688530	*GOLGA8K*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P129	p.S363R	ENSG00000249931	ENST00000512626	Transcript	missense_variant	benign(0.001)
chr15	64422138	64422138	*SNX1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P129	p.Q277H	ENSG00000028528	ENST00000261889	Transcript	missense_variant	possibly_damaging(0.601)
chr15	79227355	79227355	*CTSH*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P129	p.K124E	ENSG00000103811	ENST00000220166	Transcript	missense_variant	benign(0.008)
chr16	24581635	24581635	*RBBP6*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P129	p.K1208N	ENSG00000122257	ENST00000319715	Transcript	missense_variant	unknown(0)
chr17	15532029	15532029	*TRIM16*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.A532V	ENSG00000221926	ENST00000578237	Transcript	missense_variant	possibly_damaging(0.515)
chr17	34171885	34171886	*TAF15*	Frame_Shift_Ins	.	INS	-	-	G	novel	shanshan_et_al_P129	p.Y531Lfs*56	ENSG00000172660	ENST00000588240	Transcript	frameshift_variant	NA
chr17	39643395	39643395	*KRT36*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.E339K	ENSG00000126337	ENST00000328119	Transcript	missense_variant	probably_damaging(0.996)
chr17	66039357	66039357	*KPNA2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P129	p.D270Y	ENSG00000182481	ENST00000537025	Transcript	missense_variant	probably_damaging(0.977)
chr17	7578406	7578406	*TP53*	Missense_Mutation	.	SNP	C	C	T	rs28934578	shanshan_et_al_P129	p.R175H	ENSG00000141510	ENST00000269305	Transcript	missense_variant	benign(0.308)
chr19	11833852	11833852	*ZNF823*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P129	p.C166F	ENSG00000197933	ENST00000341191	Transcript	missense_variant	probably_damaging(0.971)

chr19	40411763	40411764	*FCGBP*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P129	p.H1289Qfs*14	ENSG00000090920	ENST00000221347	Transcript	frameshift_variant	NA
chr19	41289949	41289949	*RAB4B*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P129	p.F133L	ENSG00000167578	ENST00000594800	Transcript	missense_variant	possibly_damaging(0.608)
chr19	54140051	54140051	*DPRX*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P129	p.F129I	ENSG00000204595	ENST00000376650	Transcript	missense_variant	benign(0.007)
chr2	22042315 4	22042315 4	*OBSL1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P129	p.A1085E	ENSG00000124006	ENST00000404537	Transcript	missense_variant	benign(0.013)
chr2	73679160	73679160	*ALMS1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P129	p.P1835T	ENSG00000116127	ENST00000264448	Transcript	missense_variant	possibly_damaging(0.511)
chr20	36868058	36868058	*KIAA1755*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P129	p.A540D	ENSG00000149633	ENST00000279024	Transcript	missense_variant	benign(0.006)
chr22	29885644	29885644	*NEFH*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P129	p.A672E	ENSG00000100285	ENST00000310624	Transcript	missense_variant	benign(0.001)
chr3	121345679	121345679	*FBXO40*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.M684I	ENSG00000163833	ENST00000338040	Transcript	missense_variant	possibly_damaging(0.805)
chr3	158254895	158254895	*RSRC1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.V223I	ENSG00000174891	ENST00000295930	Transcript	missense_variant	benign(0.382)
chr3	75788394	75788394	*ZNF717*	Missense_Mutation	.	SNP	C	C	G	rs201974353	shanshan_et_al_P129	p.R127T	ENSG00000227124	ENST00000423225	Transcript	missense_variant	possibly_damaging(0.587)
chr3	97194294	97194294	*EPHA6*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P129	p.I665F	ENSG00000080224	ENST00000389672	Transcript	missense_variant	probably_damaging(0.998)
chr4	154626161	154626161	*TLR2*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P129	p.F701C	ENSG00000137462	ENST00000260010	Transcript	missense_variant	probably_damaging(1)
chr4	94006296	94006296	*GRID2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.G132E	ENSG00000152208	ENST00000282020	Transcript	missense_variant	benign(0.103)
chr5	132534816	132534816	*FSTL4*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P129	p.T834A	ENSG00000053108	ENST00000265342	Transcript	missense_variant	benign(0.002)
chr5	41058274	41058274	*MROH2B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P129	p.T216K	ENSG00000171495	ENST00000399564	Transcript	missense_variant	benign(0.168)
chr6	118015332	118015332	*NUS1*	Missense_Mutation	.	SNP	C	C	G	rs76776814	shanshan_et_al_P129	p.A227G	ENSG00000153989	ENST00000368494	Transcript	missense_variant	benign(0)
chr6	33284572	33284572	*ZBTB22*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.S41N	ENSG00000236104	ENST00000431845	Transcript	missense_variant	possibly_damaging(0.614)
chr6	75865405	75865405	*COL12A1*	Missense_Mutation	.	SNP	T	T	C	rs192171030	shanshan_et_al_P129	p.D1139G	ENSG00000111799	ENST00000322507	Transcript	missense_variant	probably_damaging(0.992)
chr7	117188877	117188877	*CFTR*	Missense_Mutation	.	SNP	G	G	T	rs397508198	shanshan_et_al_P129	p.K464N	ENSG00000001626	ENST00000003084	Transcript	missense_variant	probably_damaging(0.997)
chr7	77797412	77797412	*MAGI2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.A806V	ENSG00000187391	ENST00000354212	Transcript	missense_variant	probably_damaging(0.926)
chr8	24207486	24207486	*ADAM28*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.X700_splice	ENSG00000042980	ENST00000265769	Transcript	splice_donor_variant	NA
chr9	118949636	118949636	*PAPPA*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P129	p.F207L	ENSG00000182752	ENST00000328252	Transcript	missense_variant	benign(0.001)
chrX	132161989	132161989	*USP26*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P129	p.S87F	ENSG00000134588	ENST00000511190	Transcript	missense_variant	probably_damaging(0.911)
chrX	153457315	153457315	*OPN1MW*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P129	p.Y239H	ENSG00000147380	ENST00000369935	Transcript	missense_variant	probably_damaging(0.997)
chrX	153494433	153494433	*OPN1MW2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P129	p.Y239H	ENSG00000166160	ENST00000369929	Transcript	missense_variant	probably_damaging(0.997)
chrX	41333619	41333619	*NYX*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P129	p.L305F	ENSG00000188937	ENST00000342595	Transcript	missense_variant	possibly_damaging(0.791)
chr1	155221641	155221641	*FAM189B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.P226L	ENSG00000160767	ENST00000361361	Transcript	missense_variant	benign(0)
chr1	160192555	160192555	*DCAF8*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P133	p.F442L	ENSG00000132716	ENST00000368073	Transcript	missense_variant	benign(0.327)
chr1	173526502	173526502	*SLC9C2*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R398*	ENSG00000162753	ENST00000367714	Transcript	stop_gained	NA
chr1	216850804	216850804	*ESRRG*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P133	p.R34P	ENSG00000196482	ENST00000366937	Transcript	missense_variant	probably_damaging(0.998)
chr1	248487703	248487703	*OR2M7*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.H56Q	ENSG00000177186	ENST00000317965	Transcript	missense_variant	probably_damaging(0.95)
chr1	26230211	26230211	*STMN1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.P36L	ENSG00000117632	ENST00000426559	Transcript	missense_variant	benign(0.076)
chr1	29606044	29606044	*PTPRU*	Missense_Mutation	.	SNP	G	G	A	rs370694990	shanshan_et_al_P133	p.R547H	ENSG00000060656	ENST00000345512	Transcript	missense_variant	benign(0.284)
chr1	39823347	39823347	*MACF1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P133	p.S1847G	ENSG00000127603	ENST00000545844	Transcript	missense_variant	benign(0)
chr1	49193587	49193587	*BEND5*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R413*	ENSG00000162373	ENST00000371833	Transcript	stop_gained	NA
chr1	55559732	55559732	*USP24*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.P2078S	ENSG00000162402	ENST00000294383	Transcript	missense_variant	benign(0.029)

chr1	874822	874822	*SAMD11*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.H230N	ENSG00000187634	ENST00000342066	Transcript	missense_variant	benign(0.003)
chr1	91182581	91182581	*BARHL2*	Missense_Mutation	.	SNP	C	C	T	rs150916366	shanshan_et_al_P133	p.V58I	ENSG00000143032	ENST00000370445	Transcript	missense_variant	probably_damaging(0.959)
chr1	92944306	92944306	*GFI1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.R310Q	ENSG00000162676	ENST00000370332	Transcript	missense_variant	possibly_damaging(0.877)
chr10	129536928	129536928	*FOXI2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.A219E	ENSG00000186766	ENST00000388920	Transcript	missense_variant	benign(0.008)
chr11	124489462	124489462	*PANX3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P133	p.Q270H	ENSG00000154143	ENST00000284288	Transcript	missense_variant	possibly_damaging(0.802)
chr11	124495747	124495747	*TBRG1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.K134N	ENSG00000154144	ENST00000441174	Transcript	missense_variant	probably_damaging(0.981)
chr11	1977498	1977498	*MRPL23*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P133	p.T104A	ENSG00000214026	ENST00000397298	Transcript	missense_variant	probably_damaging(0.994)
chr11	33565454	33565454	*KIAA1549L*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.S485I	ENSG00000110427	ENST00000321505	Transcript	missense_variant	possibly_damaging(0.58)
chr11	755975	755975	*TALDO1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.A65V	ENSG00000177156	ENST00000319006	Transcript	missense_variant	benign(0.267)
chr12	109637326	109637326	*ACACB*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P133	p.V916D	ENSG00000076555	ENST00000338432	Transcript	missense_variant	probably_damaging(0.918)
chr12	132837669	132837669	*GALNT9*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.R209Q	ENSG00000182870	ENST00000328957	Transcript	missense_variant	probably_damaging(0.916)
chr12	1755069	1755069	*WNT5B*	Missense_Mutation	.	SNP	G	G	A	rs150533323	shanshan_et_al_P133	p.R244Q	ENSG00000111186	ENST00000397196	Transcript	missense_variant	benign(0.001)
chr12	18234370	18234370	*RERGL*	Nonsense_Mutation	.	SNP	G	G	A	rs200801104	shanshan_et_al_P133	p.R125*	ENSG00000111404	ENST00000229002	Transcript	stop_gained	NA
chr12	25398285	25398285	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.G12C	ENSG00000133703	ENST00000256078	Transcript	missense_variant	probably_damaging(0.993)
chr12	27126968	27126968	*TM7SF3*	Missense_Mutation	.	SNP	C	C	T	rs354435766	shanshan_et_al_P133	p.R548Q	ENSG00000064115	ENST00000343028	Transcript	missense_variant	benign(0.007)
chr12	56481627	56481627	*ERBB3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.P221H	ENSG00000065361	ENST00000267101	Transcript	missense_variant	probably_damaging(0.93)
chr12	81647354	81647354	*ACSS3*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.R634*	ENSG00000111058	ENST00000548058	Transcript	stop_gained	NA
chr12	85460577	85460577	*LRRIQ1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.V866F	ENSG00000133640	ENST00000393217	Transcript	missense_variant	possibly_damaging(0.747)
chr13	101890116	101890116	*NALCN*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.T475M	ENSG00000102452	ENST00000251127	Transcript	missense_variant	possibly_damaging(0.906)
chr13	38357230	38357230	*TRPC4*	Nonsense_Mutation	.	SNP	c	c	A	novel	shanshan_et_al_P133	p.E81*	ENSG00000133107	ENST00000379681	Transcript	stop_gained	NA
chr13	49281758	49281758	*CYSLTR2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.V269I	ENSG00000152207	ENST00000282018	Transcript	missense_variant	benign(0.001)
chr15	45398328	45398328	*DUOX2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.D715N	ENSG00000140279	ENST00000603300	Transcript	missense_variant	probably_damaging(0.998)
chr15	75975220	75975220	*CSPG4*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.Q1538*	ENSG00000173546	ENST00000308508	Transcript	stop_gained	NA
chr15	79265694	79265694	*RASGRF1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.T1204M	ENSG00000058335	ENST00000419573	Transcript	missense_variant	probably_damaging(0.995)
chr15	88576096	88576096	*NTRK3*	Missense_Mutation	.	SNP	G	G	A	rs371590703	shanshan_et_al_P133	p.P526L	ENSG00000140538	ENST00000360948	Transcript	missense_variant	possibly_damaging(0.641)
chr16	597732	597734	*CAPN15*	In_Frame_Del	.	DEL	GGA	GGA	-	novel	shanshan_et_al_P133	p.E301del	ENSG00000103326	ENST00000219611	Transcript	inframe_deletion	NA
chr17	10543537	10543537	*MYH3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R820C	ENSG00000109063	ENST00000583535	Transcript	missense_variant	probably_damaging(0.988)
chr17	10549104	10549104	*MYH3*	Missense_Mutation	.	SNP	G	G	A	rs367706009	shanshan_et_al_P133	p.T354M	ENSG00000109063	ENST00000583535	Transcript	missense_variant	probably_damaging(0.999)
chr17	33267585	33267585	*CCT6B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.R314H	ENSG00000132141	ENST00000314144	Transcript	missense_variant	possibly_damaging(0.524)
chr17	48823081	48823081	*LUC7L3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.E232K	ENSG00000108848	ENST00000505658	Transcript	missense_variant	unknown(0)
chr18	48591919	48591919	*SMAD4*	Missense_Mutation	.	SNP	G	G	A	rs377767347	shanshan_et_al_P133	p.R361H	ENSG00000141646	ENST00000342988	Transcript	missense_variant	probably_damaging(1)
chr19	11327936	11327936	*DOCK6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R1228W	ENSG00000130158	ENST00000294618	Transcript	missense_variant	possibly_damaging(0.453)
chr19	35557171	35557171	*HPN*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.G412S	ENSG00000105707	ENST00000262626	Transcript	missense_variant	probably_damaging(0.956)
chr19	37382567	37382567	*ZNF829*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.D457Y	ENSG00000185869	ENST00000520965	Transcript	missense_variant	possibly_damaging(0.874)
chr19	46733629	46733629	*IGFL1*	Missense_Mutation	.	SNP	G	G	A	rs373596301	shanshan_et_al_P133	p.V60I	ENSG00000188293	ENST00000437936	Transcript	missense_variant	possibly_damaging(0.472)
chr19	47228739	47228739	*STRN4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.T479M	ENSG00000090372	ENST00000391910	Transcript	missense_variant	possibly_damaging(0.629)

chr19	49686413	49686415	*TRPM4*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	shanshan_et_al_P133	p.L563del	ENSG00000130529	ENST00000252826	Transcript	inframe_deletion	NA
chr19	54559955	54559955	*ZNRF4*	Missense_Mutation	.	SNP	G	G	A	rs377472519	shanshan_et_al_P133	p.D165N	ENSG00000105428	ENST00000222033	Transcript	missense_variant	benign(0.056)
chr19	57286598	57286598	*ZIM2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R348W	ENSG00000269699	ENST00000391708	Transcript	missense_variant	possibly_damaging(0.545)
chr2	136873083	136873083	*CXCR4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.V143I	ENSG00000121966	ENST00000409817	Transcript	missense_variant	possibly_damaging(0.529)
chr2	160043530	160043530	*TANC1*	Missense_Mutation	.	SNP	G	G	A	rs374465130	shanshan_et_al_P133	p.V913M	ENSG00000115183	ENST00000263635	Transcript	missense_variant	probably_damaging(1)
chr2	166895977	166895977	*SCN1A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.L849I	ENSG00000144285	ENST00000303395	Transcript	missense_variant	possibly_damaging(0.845)
chr2	166898844	166898844	*SCN1A*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R712*	ENSG00000144285	ENST00000303395	Transcript	stop_gained	NA
chr2	179260240	179260240	*OSBPL6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R945Q	ENSG00000079156	ENST00000392505	Transcript	missense_variant	probably_damaging(0.999)
chr2	200137047	200137047	*SATB2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.E697K	ENSG00000119042	ENST00000417098	Transcript	missense_variant	possibly_damaging(0.534)
chr2	210681640	210681640	*UNC80*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.S448I	ENSG00000144406	ENST00000439458	Transcript	missense_variant	possibly_damaging(0.451)
chr2	220357468	220357468	*SPEG*	Missense_Mutation	.	SNP	G	G	A	rs558216115	shanshan_et_al_P133	p.R3255H	ENSG00000072195	ENST00000312358	Transcript	missense_variant	benign(0.254)
chr2	27601343	27601343	*ZNF513*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R264*	ENSG00000163795	ENST00000323703	Transcript	stop_gained	NA
chr2	43452831	43452832	*ZFP36L2*	Frame_Shift_Ins	.	INS	-	-	C	novel	shanshan_et_al_P133	p.T38Dfs*46	ENSG00000152518	ENST00000282388	Transcript	frameshift_variant	NA
chr2	54849543	54849543	*SPTBN1*	Missense_Mutation	.	SNP	G	G	A	rs187892511	shanshan_et_al_P133	p.R328H	ENSG00000115306	ENST00000356805	Transcript	missense_variant	probably_damaging(0.979)
chr2	84777081	84777081	*DNAH6*	Missense_Mutation	.	SNP	C	C	T	rs116693971	shanshan_et_al_P133	p.S462L	ENSG00000115423	ENST00000389394	Transcript	missense_variant	benign(0.004)
chr2	98273619	98273619	*ACTR1B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P133	p.I342F	ENSG00000115073	ENST00000289228	Transcript	missense_variant	probably_damaging(0.94)
chr21	32526647	32526647	*TIAM1*	Missense_Mutation	.	SNP	G	G	A	rs138288728	shanshan_et_al_P133	p.A1030V	ENSG00000156299	ENST00000286827	Transcript	missense_variant	benign(0.006)
chr22	43603587	43603587	*SCUBE1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R923C	ENSG00000159307	ENST00000360835	Transcript	missense_variant	probably_damaging(0.999)
chr22	43831108	43831108	*MPPED1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.E127K	ENSG00000186732	ENST00000417669	Transcript	missense_variant	probably_damaging(0.945)
chr22	43933407	43933407	*EFCAB6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.V1300M	ENSG00000186976	ENST00000262726	Transcript	missense_variant	benign(0.11)
chr3	141497220	141497220	*GRK7*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.R32W	ENSG00000114124	ENST00000264952	Transcript	missense_variant	possibly_damaging(0.852)
chr3	148894115	148894115	*CP*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P133	p.I1035L	ENSG00000047457	ENST00000264613	Transcript	missense_variant	benign(0.099)
chr3	178921553	178921553	*PIK3CA*	Missense_Mutation	.	SNP	T	T	A	rs121913284	shanshan_et_al_P133	p.N345K	ENSG00000121879	ENST00000263967	Transcript	missense_variant	probably_damaging(1)
chr3	35729276	35729276	*ARPP21*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P133	p.E103Q	ENSG00000172995	ENST00000458225	Transcript	missense_variant	benign(0.025)
chr3	36763045	36763045	*DCLK3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.V520I	ENSG00000163673	ENST00000416516	Transcript	missense_variant	probably_damaging(0.978)
chr3	49698778	49698778	*BSN*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.P3167H	ENSG00000164061	ENST00000296452	Transcript	missense_variant	unknown(0)
chr3	49831352	49831352	*CDHR4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.A456V	ENSG00000187492	ENST00000412678	Transcript	missense_variant	benign(0.22)
chr4	144545333	144545333	*FREM3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.L1861M	ENSG00000183090	ENST00000329798	Transcript	missense_variant	probably_damaging(0.931)
chr4	183267884	183267884	*TENM3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.L105I	ENSG00000218336	ENST00000511685	Transcript	missense_variant	possibly_damaging(0.694)
chr4	184426521	184426521	*ING2*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.X58_splice	ENSG00000168556	ENST00000302327	Transcript	splice_donor_variant	NA
chr4	40099049	40099049	*N4BP2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R30H	ENSG00000078177	ENST00000261435	Transcript	missense_variant	benign(0.001)
chr4	62936438	62936438	*LPHN3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.G1408S	ENSG00000150471	ENST00000514591	Transcript	missense_variant	benign(0.005)
chr4	77324344	77324344	*CCDC158*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.W6L	ENSG00000163749	ENST00000388914	Transcript	missense_variant	benign(0)
chr5	112175752	112175752	*APC*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P133	p.L1488Yfs*19	ENSG00000134982	ENST00000457016	Transcript	frameshift_variant	NA
chr5	118969858	118969858	*FAM170A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.V139M	ENSG00000164334	ENST00000515256	Transcript	missense_variant	possibly_damaging(0.799)
chr5	135692538	135692538	*TRPC7*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.V180M	ENSG00000069018	ENST00000513104	Transcript	missense_variant	probably_damaging(0.96)

chr5	140215137	140215137	*PCDHA7*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.T390M	ENSG00000204963	ENST00000525929	Transcript	missense_variant	benign(0.059)
chr5	140431404	140431404	*PCDHB1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P133	p.F117L	ENSG00000171815	ENST00000306549	Transcript	missense_variant	benign(0.122)
chr5	140764210	140764210	*PCDHGA7*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.A582T	ENSG00000253537	ENST00000518325	Transcript	missense_variant	probably_damaging(0.918)
chr5	140773552	140773552	*PCDHGA8*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.P391L	ENSG00000253767	ENST00000398604	Transcript	missense_variant	probably_damaging(0.958)
chr5	158140014	158140014	*EBF1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.V445M	ENSG00000164330	ENST00000313708	Transcript	missense_variant	possibly_damaging(0.907)
chr5	335770	335770	*ADAMTS12*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P133	p.L1019V	ENSG00000151388	ENST00000504830	Transcript	missense_variant	benign(0.003)
chr6	152674520	152674520	*SYNE1*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.E3711*	ENSG00000131018	ENST00000367255	Transcript	stop_gained	NA
chr6	26123757	26123758	*HIST1H2BC*	Frame_Shift_Ins	.	INS	-	-	G	novel	shanshan_et_al_P133	p.K126Qfs*12	ENSG00000180596	ENST00000314332	Transcript	frameshift_variant	NA
chr6	49439006	49439006	*CDYL*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.W416*	ENSG00000153046	ENST00000397588	Transcript	stop_gained	NA
chr6	50791450	50791450	*TFAP2B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.R138W	ENSG00000008196	ENST00000393655	Transcript	missense_variant	probably_damaging(0.991)
chr6	83905381	83905381	*RWDD2A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R90Q	ENSG00000013392	ENST00000369724	Transcript	missense_variant	possibly_damaging(0.706)
chr6	88853781	88853781	*CNR1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R405*	ENSG00000118432	ENST00000537554	Transcript	stop_gained	NA
chr7	100282761	100282761	*GIGYF1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.R401W	ENSG00000146830	ENST00000275732	Transcript	missense_variant	unknown(0)
chr7	126173278	126173278	*GRM8*	Missense_Mutation	.	SNP	G	G	T	rs77499554	shanshan_et_al_P133	p.H720N	ENSG00000179603	ENST00000339582	Transcript	missense_variant	probably_damaging(0.998)
chr7	28848874	28848874	*CREB5*	Missense_Mutation	.	SNP	G	G	A	rs376502932	shanshan_et_al_P133	p.R366Q	ENSG00000146592	ENST00000357727	Transcript	missense_variant	unknown(0)
chr7	30962227	30962227	*AQP1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.A200T	ENSG00000240583	ENST00000311813	Transcript	missense_variant	possibly_damaging(0.559)
chr7	75694258	75694258	*MDH2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.P291L	ENSG00000146701	ENST00000315758	Transcript	missense_variant	probably_damaging(0.997)
chr8	104928737	104928737	*RIMS2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.V670I	ENSG00000176406	ENST00000406091	Transcript	missense_variant	benign(0.344)
chr8	125080023	125080023	*FER1L6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P133	p.P1232T	ENSG00000214814	ENST00000522917	Transcript	missense_variant	benign(0.001)
chr8	134034311	134034311	*TG*	Missense_Mutation	.	SNP	G	G	A	rs201930579	shanshan_et_al_P133	p.D2318N	ENSG00000042832	ENST00000220616	Transcript	missense_variant	possibly_damaging(0.556)
chr8	25766040	25766040	*EBF2*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.Q195*	ENSG00000221818	ENST00000520164	Transcript	stop_gained	NA
chr8	41122786	41122786	*SFRP1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.T282M	ENSG00000104332	ENST00000220772	Transcript	missense_variant	benign(0.392)
chr8	66659975	66659975	*PDE7A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P133	p.R116Q	ENSG00000205268	ENST00000401827	Transcript	missense_variant	possibly_damaging(0.556)
chr9	65504652	65504652	*SPATA31A7*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P133	p.L970F	ENSG00000234734	ENST00000355045	Transcript	missense_variant	probably_damaging(0.998)
chrX	140785800	140785800	*SPANXD*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P133	p.P39Q	ENSG00000196406	ENST00000370515	Transcript	missense_variant	probably_damaging(0.999)
chr1	111957781	111957781	*OVGP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P134	p.G448S	ENSG00000085465	ENST00000369732	Transcript	missense_variant	benign(0.024)
chr10	102739956	102739958	*SEMA4G*	In_Frame_Del	.	DEL	GTT	GTT	-	novel	shanshan_et_al_P134	p.L403del	ENSG00000095539	ENST00000210633	Transcript	inframe_deletion	NA
chr10	43606853	43606853	*RET*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P134	p.T488S	ENSG00000165731	ENST00000355710	Transcript	missense_variant	benign(0.007)
chr10	89711966	89711966	*PTEN*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P134	p.F195S	ENSG00000171862	ENST00000371953	Transcript	missense_variant	benign(0.193)
chr11	66033568	66033568	*KLC2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P134	p.G536D	ENSG00000174996	ENST00000417856	Transcript	missense_variant	possibly_damaging(0.703)
chr11	71208554	71208554	*NADSYN1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P134	p.E597G	ENSG00000172890	ENST00000319023	Transcript	missense_variant	probably_damaging(0.981)
chr11	78177001	78177001	*NARS2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P134	p.I362K	ENSG00000137513	ENST00000281038	Transcript	missense_variant	benign(0.091)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P134	p.G12A	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.773)
chr12	72022795	72022795	*ZFC3H1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P134	p.K1283N	ENSG00000133858	ENST00000378743	Transcript	missense_variant	benign(0.365)
chr14	44974303	44974303	*FSCB*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P134	p.A630T	ENSG00000189139	ENST00000340446	Transcript	missense_variant	unknown(0)
chr14	75330206	75330206	*PROX2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P134	p.P111L	ENSG00000119608	ENST00000556084	Transcript	missense_variant	benign(0)

chr15	52506866	52506866	*MYO5C*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P134	p.M1326V	ENSG00000128833	ENST00000261839	Transcript	missense_variant	benign(0.01)
chr15	90125922	90125922	*TICRR*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P134	p.W220*	ENSG00000140534	ENST00000268138	Transcript	stop_gained	NA
chr15	90347207	90347207	*ANPEP*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P134	p.E402D	ENSG00000166825	ENST00000300600	Transcript	missense_variant	benign(0.008)
chr16	20944736	20944736	*DNAH3*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P134	NA	ENSG00000158486	ENST00000261383	Transcript	frameshift_variant	NA
chr17	17928015	17928015	*ATPAF2*	Nonsense_Mutation	.	SNP	G	G	C	rs377476973	shanshan_et_al_P134	p.Y142*	ENSG00000171953	ENST00000474627	Transcript	stop_gained	NA
chr17	40950129	40950129	*COA3*	Missense_Mutation	.	SNP	C	C	T	rs61757404	shanshan_et_al_P134	p.E91K	ENSG00000183978	ENST00000328434	Transcript	missense_variant	unknown(0)
chr17	7574017	7574017	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs121912664	shanshan_et_al_P134	p.R337L	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.914)
chr17	7577547	7577547	*TP53*	Missense_Mutation	.	SNP	C	C	T	rs121912656	shanshan_et_al_P134	p.G245D	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(1)
chr19	17756595	17756595	*UNC13A*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P134	p.D748E	ENSG00000130477	ENST00000519716	Transcript	missense_variant	probably_damaging(0.988)
chr19	53619609	53619609	*ZNF415*	Nonsense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P134	p.Y31*	ENSG00000170954	ENST00000500605	Transcript	stop_gained	NA
chr19	54802050	54802050	*LILRA3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P134	p.A380T	ENSG00000170866	ENST00000251390	Transcript	missense_variant	possibly_damaging(0.872)
chr2	131130445	131130445	*PTPN18*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P134	p.X414_splice	ENSG00000072135	ENST00000175756	Transcript	splice_acceptor_variant	NA
chr20	30915452	30915452	*KIF3B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P134	p.E652D	ENSG00000101350	ENST00000375712	Transcript	missense_variant	benign(0)
chr20	35459953	35459953	*ATRN*	Splice_Site	.	SNP	A	A	G	novel	shanshan_et_al_P134	p.X596_splice	ENSG00000088812	ENST00000262919	Transcript	splice_acceptor_variant	NA
chr5	33576822	33576822	*ADAMTS12*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P134	p.E1103D	ENSG00000151388	ENST00000504830	Transcript	missense_variant	benign(0)
chr6	116967057	116967057	*ZUFSP*	Missense_Mutation	.	SNP	G	G	T	rs141299898	shanshan_et_al_P134	p.N503K	ENSG00000153975	ENST00000368576	Transcript	missense_variant	probably_damaging(0.913)
chr6	26205128	26205128	*HIST1H4E*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P134	p.D86N	ENSG00000198518	ENST00000360441	Transcript	missense_variant	probably_damaging(0.933)
chr6	46659271	46659271	*TDRD6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P134	p.T1136A	ENSG00000180113	ENST00000316081	Transcript	missense_variant	benign(0.028)
chr6	73332234	73332234	*KCNQ5*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P134	p.V106A	ENSG00000185760	ENST00000342056	Transcript	missense_variant	benign(0.001)
chr7	23293812	23293812	*GPNMB*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P134	p.T83S	ENSG00000136235	ENST00000381990	Transcript	missense_variant	probably_damaging(0.983)
chr7	23353246	23353246	*IGF2BP3*	Missense_Mutation	.	SNP	A	A	C	rs199812608	shanshan_et_al_P134	p.I474M	ENSG00000136231	ENST00000258729	Transcript	missense_variant	benign(0.036)
chr9	104171708	104171708	*ZNF189*	Missense_Mutation	.	SNP	C	C	T	rs146407899	shanshan_et_al_P134	p.S553L	ENSG00000136870	ENST00000339664	Transcript	missense_variant	possibly_damaging(0.885)
chr9	107599377	107599377	*ABCA1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P134	p.V399M	ENSG00000165029	ENST00000374736	Transcript	missense_variant	probably_damaging(0.984)
chrX	114400852	114400852	*LRCH2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P134	p.S351I	ENSG00000130224	ENST00000317135	Transcript	missense_variant	probably_damaging(0.998)
chrX	129299554	129299554	*AIFM1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P134	p.R26Q	ENSG00000156709	ENST00000287295	Transcript	missense_variant	benign(0.001)
chrX	69366580	69366580	*IGBP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P134	p.L194F	ENSG00000089289	ENST00000342206	Transcript	missense_variant	probably_damaging(0.967)
chr11	108203492	108203492	*ATM*	Nonsense_Mutation	.	SNP	C	C	T	rs138941496	shanshan_et_al_P137	p.R2598*	ENSG00000149311	ENST00000278616	Transcript	stop_gained	NA
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P137	p.G12V	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.479)
chr12	51540601	51540601	*KCNA5*	Missense_Mutation	.	SNP	C	C	T	rs559584338	shanshan_et_al_P137	p.R250W	ENSG00000130037	ENST00000252321	Transcript	missense_variant	probably_damaging(0.999)
chr12	79456377	79456377	*NANOG*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P137	p.E81D	ENSG00000111704	ENST00000229307	Transcript	missense_variant	benign(0.071)
chr13	44411548	44411548	*CCDC122*	Nonsense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P137	p.Y230*	ENSG00000151773	ENST00000446144	Transcript	stop_gained	NA
chr16	24166004	24166004	*PRKCB*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P137	NA	ENSG00000166501	ENST00000303531	Transcript	splice_acceptor_variant	NA
chr17	38152515	38152515	*PSMD3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P137	p.Y467C	ENSG00000108344	ENST00000264639	Transcript	missense_variant	probably_damaging(1)
chr17	76803645	76803645	*USP36*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P137	p.S494F	ENSG00000055483	ENST00000542802	Transcript	missense_variant	benign(0.007)
chr19	10908058	10908058	*DNM2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P137	p.T400M	ENSG00000079805	ENST00000389253	Transcript	missense_variant	probably_damaging(0.996)
chr19	36034295	36034295	*GAPDHS*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P137	p.R265S	ENSG00000105679	ENST00000222286	Transcript	missense_variant	benign(0.011)

chr19	39395873	39395873	*NFKBIB*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P137	p.E106G	ENSG00000104825	ENST00000313582	Transcript	missense_variant	possibly_damaging(0.882)
chr19	40363914	40363914	*FCGBP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P137	p.L4910F	ENSG00000090920	ENST00000221347	Transcript	missense_variant	probably_damaging(0.969)
chr2	167019 8	167019 8	*PXDN*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P137	p.T360M	ENSG00000130508	ENST00000252804	Transcript	missense_variant	probably_damaging(0.982)
chr20	32266101	32266101	*E2F1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P137	p.R211*	ENSG00000101412	ENST00000343380	Transcript	stop_gained	NA
chr20	44048180	44048180	*PIGT*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P137	p.F211L	ENSG00000124155	ENST00000279036	Transcript	missense_variant	possibly_damaging(0.588)
chr3	101212769	101212769	*SENP7*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P137	p.Q45R	ENSG00000138468	ENST00000394095	Transcript	missense_variant	benign(0.219)
chr4	367169	367169	*ZNF141*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P137	p.E315K	ENSG00000131127	ENST00000240499	Transcript	missense_variant	probably_damaging(0.966)
chr5	33576343	33576343	*ADAMTS12*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P137	p.T1263M	ENSG00000151388	ENST00000504830	Transcript	missense_variant	benign(0.008)
chr6	76731925	76731925	*IMPG1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P137	p.V192I	ENSG00000112706	ENST00000369950	Transcript	missense_variant	benign(0.003)
chr7	74197350	74197350	*NCF1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P137	p.E174K	ENSG00000158517	ENST00000289473	Transcript	missense_variant	possibly_damaging(0.883)
chrX	48558900	48558900	*SUV39H1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P137	p.C195F	ENSG00000101945	ENST00000376687	Transcript	missense_variant	probably_damaging(0.997)
chr1	22532843 8	22532843 8	*DNAH14*	Missense_Mutation	.	SNP	G	G	T	rs202118490	shanshan_et_al_P144	p.R1391I	ENSG00000185842	ENST00000430092	Transcript	missense_variant	benign(0)
chr1	43317003	43317003	*ZNF691*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P144	p.S156F	ENSG00000164011	ENST00000397044	Transcript	missense_variant	probably_damaging(1)
chr10	101165535	101165535	*GOT1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P144	p.K207M	ENSG00000120053	ENST00000370508	Transcript	missense_variant	benign(0.177)
chr11	56321026	56321026	*TRIM6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P144	p.S362F	ENSG00000121236	ENST00000380097	Transcript	missense_variant	benign(0.049)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P144	p.G12V	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.479)
chr12	26755978	26755978	*CACNA1C*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P144	p.R507C	ENSG00000151067	ENST00000347598	Transcript	missense_variant	possibly_damaging(0.737)
chr12	29936501	29936501	*TMTC1*	Missense_Mutation	.	SNP	C	C	T	rs764243334	shanshan_et_al_P144	p.D62N	ENSG00000133687	ENST00000539277	Transcript	missense_variant	benign(0.298)
chr12	29936515	29936515	*TMTC1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P144	p.I57T	ENSG00000133687	ENST00000539277	Transcript	missense_variant	possibly_damaging(0.733)
chr12	95927629	95927629	*USP44*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P144	p.G135D	ENSG00000136014	ENST00000258499	Transcript	missense_variant	benign(0.002)
chr15	29346119	29346119	*APBA2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P144	p.S11N	ENSG00000034053	ENST00000558402	Transcript	missense_variant	benign(0.003)
chr15	86076959	86076959	*AKAP13*	Missense_Mutation	.	SNP	A	A	G	rs148518787	shanshan_et_al_P144	p.N109S	ENSG00000170776	ENST00000361243	Transcript	missense_variant	probably_damaging(0.994)
chr16	56969335	56969335	*HERPUD1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P144	p.H83R	ENSG00000051108	ENST00000439977	Transcript	missense_variant	probably_damaging(1)
chr17	10352233	10352233	*MYH4*	Missense_Mutation	.	SNP	C	C	T	rs139449510	shanshan_et_al_P144	p.R1438Q	ENSG00000264424	ENST00000255381	Transcript	missense_variant	probably_damaging(0.999)
chr17	39168011	39168011	*ZZEF1*	Missense_Mutation	.	SNP	G	G	A	rs112497098	shanshan_et_al_P144	p.H2841Y	ENSG00000074755	ENST00000381638	Transcript	missense_variant	benign(0.038)
chr17	48605584	48605584	*MYCBPAP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P144	p.G830D	ENSG00000136449	ENST00000323776	Transcript	missense_variant	benign(0.251)
chr21	47558507	47558507	*FTCD*	Missense_Mutation	.	SNP	G	G	A	rs200283734	shanshan_et_al_P144	p.T453M	ENSG00000160282	ENST00000291670	Transcript	missense_variant	possibly_damaging(0.553)
chr22	45574529	45574529	*NUP50*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P144	p.M251V	ENSG00000093000	ENST00000347635	Transcript	missense_variant	benign(0)
chr4	90170826	90170826	*GPRIN3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P144	p.I146V	ENSG00000185477	ENST00000609438	Transcript	missense_variant	benign(0)
chr5	140182649	140182649	*PCDHA3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P144	p.R623C	ENSG00000255408	ENST00000522353	Transcript	missense_variant	possibly_damaging(0.662)
chr5	140256484	140256484	*PCDHA12*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P144	p.T476R	ENSG00000251664	ENST00000398631	Transcript	missense_variant	probably_damaging(0.912)
chr6	101173474	101173474	*ASCC3*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P144	p.L615V	ENSG00000112249	ENST00000369162	Transcript	missense_variant	probably_damaging(0.957)
chr6	131829 15	131829 15	*PHACTR1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P144	p.P221S	ENSG00000112137	ENST00000379350	Transcript	missense_variant	benign(0.057)
chr6	46977694	46977694	*GPR110*	Missense_Mutation	.	SNP	C	C	T	rs377139714	shanshan_et_al_P144	p.V493I	ENSG00000153292	ENST00000371253	Transcript	missense_variant	benign(0)
chr9	34996576	34996576	*DNAJB5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P144	p.R290W	ENSG00000137094	ENST00000453597	Transcript	missense_variant	benign(0.003)
chrX	27998532	27998532	*DCAF8L1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P144	p.E307G	ENSG00000226372	ENST00000441525	Transcript	missense_variant	probably_damaging(0.933)

chrX	79985517	79985517	*BRWD3*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P144	p.L377S	ENSG00000165288	ENST00000373275	Transcript	missense_variant	probably_damaging(0.998)
chr1	186084057	186084057	*HMCN1*	Nonsense_Mutation	.	SNP	C	C	T	rs150673369	shansha n_et_al_P17	p.R3795*	ENSG00000143341	ENST00000271588	Transcript	stop_gained	NA
chr11	71105127	71105127	*RBMXL2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P17	p.P59L	ENSG00000170748	ENST00000306904	Transcript	missense_variant	benign(0.161)
chr12	29936501	29936501	*TMTC1*	Missense_Mutation	.	SNP	C	C	T	rs76424334	shansha n_et_al_P17	p.D62N	ENSG00000133687	ENST00000539277	Transcript	missense_variant	benign(0.298)
chr14	105995475	105995475	*TMEM121*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P17	p.R102C	ENSG00000184986	ENST00000392519	Transcript	missense_variant	possibly_damaging(0.736)
chr17	75784044	75784044	*TP53*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P17	p.C176S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	benign(0.377)
chr19	31040147	31040147	*ZNF536*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P17	p.D1207E	ENSG00000198597	ENST00000355537	Transcript	missense_variant	benign(0.009)
chr2	61275882	61275882	*PEX13*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P17	p.D397H	ENSG00000162928	ENST00000295030	Transcript	missense_variant	benign(0)
chr20	37826111	37826111	*CDC25B*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P17	p.S321F	ENSG00000101224	ENST00000245960	Transcript	missense_variant	probably_damaging(0.981)
chr20	39800857	39800857	*PLCG1*	Missense_Mutation	.	SNP	C	C	T	rs557681742	shansha n_et_al_P17	p.R945W	ENSG00000124181	ENST00000373272	Transcript	missense_variant	probably_damaging(1)
chr22	35947894	35947894	*RASD2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P17	p.V206M	ENSG00000100302	ENST00000216127	Transcript	missense_variant	benign(0.042)
chr22	46319073	46319073	*WNT7B*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P17	p.V238G	ENSG00000188064	ENST00000339464	Transcript	missense_variant	probably_damaging(0.996)
chr4	166915607	166915607	*TLL1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P17	p.P146T	ENSG00000038295	ENST00000061240	Transcript	missense_variant	benign(0.006)
chr6	152673313	152673313	*SYNE1*	Missense_Mutation	.	SNP	G	G	A	rs375577011	shansha n_et_al_P17	p.T3810M	ENSG00000131018	ENST00000367255	Transcript	missense_variant	benign(0.256)
chr6	25726439	25726439	*HIST1H2AA*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P17	p.G106D	ENSG00000164508	ENST00000297012	Transcript	missense_variant	probably_damaging(0.999)
chrX	53619395	53619395	*HUWE1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P17	p.R1312H	ENSG00000086758	ENST00000342160	Transcript	missense_variant	benign(0.024)
chr12	25398285	25398285	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P17	p.G12C	ENSG00000133703	ENST00000256078	Transcript	missense_variant	probably_damaging(0.993)
chr1	227842678	227842678	*ZNF678*	Missense_Mutation	.	SNP	T	T	G	rs138082142	shansha n_et_al_P29	p.C243G	ENSG00000181450	ENST00000343776	Transcript	missense_variant	benign(0)
chr1	247150500	247150500	*ZNF695*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P29	p.D439E	ENSG00000197472	ENST00000339986	Transcript	missense_variant	benign(0.081)
chr10	46322021	46322021	*AGAP4*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P29	p.Q445R	ENSG00000188234	ENST00000448048	Transcript	missense_variant	possibly_damaging(0.855)
chr12	24970965	24970965	*BCAT1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P29	p.D392N	ENSG00000060982	ENST00000539282	Transcript	missense_variant	benign(0.004)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P29	p.G12V	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.479)
chr15	92459523	92459523	*SLCO3A1*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P29	p.P161A	ENSG00000176463	ENST00000318445	Transcript	missense_variant	benign(0.088)
chr16	15122780	15122780	*PDXDC1*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P29	p.G417A	ENSG00000179889	ENST00000396410	Transcript	missense_variant	benign(0)
chr16	22546778	22546778	*NPIPB5*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P29	p.G825E	ENSG00000243716	ENST00000424340	Transcript	missense_variant	benign(0.254)
chr16	31927011	31927011	*ZNF267*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P29	p.M481V	ENSG00000185947	ENST00000300870	Transcript	missense_variant	benign(0.009)
chr16	58756052	58756052	*GOT2*	Splice_Site	.	SNP	A	A	C	novel	shansha n_et_al_P29	p.X125_splice	ENSG00000125166	ENST00000245206	Transcript	splice_donor_variant	NA
chr17	41003601	41003601	*AOC3*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P29	p.P81A	ENSG00000131471	ENST00000308423	Transcript	missense_variant	benign(0.006)
chr19	20229964	20229964	*ZNF90*	Missense_Mutation	.	SNP	C	C	A	rs186928119	shansha n_et_al_P29	p.A534E	ENSG00000213988	ENST00000418063	Transcript	missense_variant	benign(0.003)
chr19	20308256	20308256	*ZNF486*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P29	p.V246A	ENSG00000256229	ENST00000335117	Transcript	missense_variant	benign(0)
chr19	21240552	21240552	*ZNF430*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P29	p.S480T	ENSG00000118620	ENST00000261560	Transcript	missense_variant	benign(0.001)
chr19	21606987	21606987	*ZNF493*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P29	p.I509R	ENSG00000196268	ENST00000392288	Transcript	missense_variant	benign(0.002)
chr19	21607311	21607311	*ZNF493*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P29	p.S617T	ENSG00000196268	ENST00000392288	Transcript	missense_variant	benign(0.023)
chr19	21607323	21607323	*ZNF493*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P29	p.K621R	ENSG00000196268	ENST00000392288	Transcript	missense_variant	benign(0.02)
chr19	21912311	21912311	*DOT1L*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P29	p.L162W	ENSG00000104885	ENST00000398665	Transcript	missense_variant	probably_damaging(0.998)
chr19	21992058	21992058	*ZNF43*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P29	p.E261K	ENSG00000198521	ENST00000354959	Transcript	missense_variant	possibly_damaging(0.717)

chr19	22497013	22497013	*ZNF729*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P29	p.R265K	ENSG00000196350	ENST00000601693	Transcript	missense_variant	benign(0.011)
chr19	22499682	22499682	*ZNF729*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P29	p.S1155T	ENSG00000196350	ENST00000601693	Transcript	missense_variant	benign(0.001)
chr19	23926748	23926748	*ZNF681*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P29	p.T535K	ENSG00000196172	ENST00000402377	Transcript	missense_variant	probably_damaging(0.937)
chr19	36211993	36211993	*KMT2B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P29	p.S582T	ENSG00000272333	ENST00000222270	Transcript	missense_variant	benign(0.264)
chr3	12633228	12633228	*RAF1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P29	p.R391K	ENSG00000132155	ENST00000251849	Transcript	missense_variant	benign(0.009)
chr3	25665842	25665842	*TOP2B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P29	p.R809Q	ENSG00000077097	ENST00000435706	Transcript	missense_variant	probably_damaging(0.996)
chr3	44763346	44763346	*ZNF502*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P29	p.S346T	ENSG00000196653	ENST00000296091	Transcript	missense_variant	benign(0.001)
chr3	48612861	48612861	*COL7A1*	Missense_Mutation	.	SNP	C	C	T	rs121912838	shanshan_et_al_P29	p.G2031S	ENSG00000114270	ENST00000328333	Transcript	missense_variant	unknown(0)
chr4	43733030	43733030	*ZNF721*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P29	p.V309E	ENSG00000182903	ENST00000511833	Transcript	missense_variant	benign(0.002)
chr5	154214417	154214417	*FAXDC2*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P29	p.W42*	ENSG00000170271	ENST00000326080	Transcript	stop_gained	NA
chr5	36051979	36051979	*UGT3A2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P29	p.G102C	ENSG00000168671	ENST00000282507	Transcript	missense_variant	benign(0.008)
chr6	74190727	74190727	*MTO1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P29	p.C423F	ENSG00000135297	ENST00000415954	Transcript	missense_variant	unknown(0)
chr6	74190738	74190739	*MTO1*	Frame_Shift_Ins	.	INS	-	-	C	novel	shanshan_et_al_P29	p.R428Qfs*6	ENSG00000135297	ENST00000415954	Transcript	frameshift_variant	NA
chr7	63808905	63808905	*ZNF736*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P29	p.V222I	ENSG00000234444	ENST00000423484	Transcript	missense_variant	benign(0.08)
chr7	64167716	64167716	*ZNF107*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P29	p.R345K	ENSG00000196247	ENST00000395391	Transcript	missense_variant	benign(0.007)
chr7	64864143	64864143	*ZNF92*	Missense_Mutation	.	SNP	T	T	A	rs200450265	shanshan_et_al_P29	p.D372E	ENSG00000146757	ENST00000328747	Transcript	missense_variant	benign(0.002)
chr9	43915540	43915540	*CNTNAP3B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P29	p.A1208V	ENSG00000154529	ENST00000377564	Transcript	missense_variant	benign(0.007)
chrX	83128895	83128895	*CYLC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P29	p.N393K	ENSG00000183035	ENST00000329312	Transcript	missense_variant	unknown(0)
chr1	153905343	153905343	*DENND4B*	Missense_Mutation	.	SNP	C	C	T	rs375597225	shanshan_et_al_P33	p.R1206Q	ENSG00000198837	ENST00000361217	Transcript	missense_variant	probably_damaging(0.978)
chr10	68940163	68940163	*CTNNA3*	Missense_Mutation	.	SNP	G	G	A	rs139460414	shanshan_et_al_P33	p.T320M	ENSG00000183230	ENST00000433211	Transcript	missense_variant	probably_damaging(0.938)
chr11	121430301	121430301	*SORL1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P33	p.E995A	ENSG00000137642	ENST00000260197	Transcript	missense_variant	benign(0.004)
chr12	113726026	113726026	*TPCN1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P33	p.P637S	ENSG00000186815	ENST00000550785	Transcript	missense_variant	probably_damaging(1)
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P33	p.G12V	ENSG00000133703	ENST00000256078	Transcript	missense_variant	possibly_damaging(0.479)
chr16	449461	449461	*NME4*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P33	p.S103C	ENSG00000103202	ENST00000219479	Transcript	missense_variant	probably_damaging(0.996)
chr2	125192246	125192246	*CNTNAP5*	Missense_Mutation	.	SNP	G	G	T	rs377138572	shanshan_et_al_P33	p.A239S	ENSG00000155052	ENST00000431078	Transcript	missense_variant	benign(0.014)
chr2	220505520	220505520	*SLC4A3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P33	p.W1180R	ENSG00000114923	ENST00000373762	Transcript	missense_variant	probably_damaging(1)
chr6	32007133	32007133	*CYP21A2*	Missense_Mutation	.	SNP	C	C	T	rs577450124	shanshan_et_al_P33	p.R150C	ENSG00000231852	ENST00000418967	Transcript	missense_variant	probably_damaging(0.953)
chr7	146805424	146805424	*CNTNAP2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P33	p.V246F	ENSG00000174469	ENST00000361727	Transcript	missense_variant	benign(0.021)
chr7	27238939	27238939	*HOXA13*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P33	p.P253L	ENSG00000106031	ENST00000222753	Transcript	missense_variant	probably_damaging(0.998)
chr7	44185219	44185219	*GCK*	Missense_Mutation	.	SNP	C	C	T	rs193922264	shanshan_et_al_P33	p.R378H	ENSG00000106633	ENST00000345378	Transcript	missense_variant	probably_damaging(1)
chrX	100745657	100745657	*ARMCX4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P33	p.A694D	ENSG00000196440	ENST00000423738	Transcript	missense_variant	possibly_damaging(0.826)
chrX	49114840	49114840	*FOXP3*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P33	p.G43Efs*19	ENSG00000049768	ENST00000376207	Transcript	frameshift_variant	NA
chr1	186303541	186303541	*TPR*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P59	p.M1700V	ENSG00000047410	ENST00000367478	Transcript	missense_variant	benign(0.019)
chr1	200613582	200613582	*DDX59*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P59	p.K554*	ENSG00000118197	ENST00000331314	Transcript	stop_gained	NA
chr12	25398284	25398284	*KRAS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P59	p.G12D	ENSG00000133703	ENST00000256078	Transcript	missense_variant	benign(0.361)
chr12	6080796	6080796	*VWF*	Missense_Mutation	.	SNP	G	G	A	rs181094101	shanshan_et_al_P59	p.P2506L	ENSG00000110799	ENST00000261405	Transcript	missense_variant	benign(0)

chr13	101881754	101881754	*NALCN*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P59	p.T539M	ENSG00000102452	ENST00000251127	Transcript	missense_variant	probably_damaging(0.998)
chr14	105418360	105418360	*AHNAK2*	Missense_Mutation	.	SNP	G	G	A	rs199546516	shanshan_et_al_P59	p.A1143V	ENSG00000185567	ENST00000333244	Transcript	missense_variant	benign(0.247)
chr15	68609602	68609602	*ITGA11*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P59	p.X905_splice	ENSG00000137809	ENST00000315757	Transcript	splice_donor_variant	NA
chr15	75684622	75684622	*SIN3A*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P59	p.S938G	ENSG00000169375	ENST00000394947	Transcript	missense_variant	benign(0.015)
chr16	24268113	24268113	*CACNG3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P59	p.T13N	ENSG00000006116	ENST00000005284	Transcript	missense_variant	probably_damaging(0.999)
chr17	75785555	75785555	*TP53*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P59	p.X126_splice	ENSG00000141510	ENST00000269305	Transcript	splice_acceptor_variant	NA
chr18	21044196	21044196	*RIOK3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P59	p.K118E	ENSG00000101782	ENST00000339486	Transcript	missense_variant	benign(0.032)
chr19	36592216	36592216	*WDR62*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P59	p.E990Q	ENSG00000075702	ENST00000401500	Transcript	missense_variant	possibly_damaging(0.848)
chr19	43697534	43697534	*PSG4*	Missense_Mutation	.	SNP	A	A	G	rs147632606	shanshan_et_al_P59	p.I417T	ENSG00000243137	ENST00000405312	Transcript	missense_variant	benign(0.002)
chr19	46828400	46828400	*DPP9*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P59	p.A781V	ENSG00000142002	ENST00000262960	Transcript	missense_variant	probably_damaging(0.976)
chr2	172950481	172950481	*DLX1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P59	p.P26A	ENSG00000144355	ENST00000361725	Transcript	missense_variant	benign(0.024)
chr2	220434967	220434967	*OBSL1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P59	p.S330C	ENSG00000124006	ENST00000404537	Transcript	missense_variant	probably_damaging(0.999)
chr2	242189388	242189388	*HDLBP*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P59	p.R460S	ENSG00000115677	ENST00000391975	Transcript	missense_variant	possibly_damaging(0.864)
chr2	67630425	67630425	*ETAA1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P59	p.E204V	ENSG00000143971	ENST00000272342	Transcript	missense_variant	probably_damaging(0.995)
chr3	47035468	47035469	*NBEAL2*	Frame_Shift_Ins	.	INS	-	-	AA	novel	shanshan_et_al_P59	p.R386Kfs*4	ENSG00000160796	ENST00000450053	Transcript	frameshift_variant	NA
chr3	53684912	53684912	*CACNA1D*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P59	p.W197*	ENSG00000157388	ENST00000288139	Transcript	stop_gained	NA
chr4	39077684	39077685	*KLHL5*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P59	p.M210Nfs*8	ENSG00000109790	ENST00000504108	Transcript	frameshift_variant	NA
chr7	124387076	124387076	*GPR37*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P59	p.C449S	ENSG00000170775	ENST00000303921	Transcript	missense_variant	probably_damaging(1)
chr8	10467547	10467547	*RP1L1*	Missense_Mutation	.	SNP	G	G	A	rs201532540	shanshan_et_al_P59	p.A1354V	ENSG00000183638	ENST00000382483	Transcript	missense_variant	unknown(0)
chr8	144940706	144940706	*EPPK1*	Missense_Mutation	.	SNP	C	C	T	rs112377501	shanshan_et_al_P59	p.R2239H	ENSG00000227184	ENST00000525985	Transcript	missense_variant	possibly_damaging(0.832)
chr8	65494020	65494020	*BHLHE22*	Missense_Mutation	.	SNP	g	g	A	rs62519836	shanshan_et_al_P59	p.G225S	ENSG00000180828	ENST00000321870	Transcript	missense_variant	unknown(0)
chr9	116779055	116779055	*ZNF618*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P59	p.A267T	ENSG00000157657	ENST00000288466	Transcript	missense_variant	benign(0.23)
chrX	47045027	47045027	*RBM10*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P59	p.K785*	ENSG00000182872	ENST00000377604	Transcript	stop_gained	NA
chrX	70349261	70349261	*MED12*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P59	p.K1225Q	ENSG00000184634	ENST00000374080	Transcript	missense_variant	probably_damaging(0.999)
chr1	215901617	215901617	*USH2A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P66	p.R3941W	ENSG00000042781	ENST00000307340	Transcript	missense_variant	probably_damaging(0.959)
chr11	26529800	26529800	*ANO3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P66	p.L194F	ENSG00000134343	ENST00000256737	Transcript	missense_variant	probably_damaging(0.999)
chr12	6094770	6094770	*VWF*	Missense_Mutation	.	SNP	C	C	T	rs563856279	shanshan_et_al_P66	p.R2287Q	ENSG00000110799	ENST00000261405	Transcript	missense_variant	possibly_damaging(0.857)
chr19	56223796	56223796	*NLRP9*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P66	p.E888*	ENSG00000185792	ENST00000332836	Transcript	stop_gained	NA
chr22	19124841	19124841	*DGCR14*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P66	p.F344V	ENSG00000100056	ENST00000252137	Transcript	missense_variant	possibly_damaging(0.665)
chr22	43986044	43986044	*EFCAB6*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P66	p.T981S	ENSG00000186976	ENST00000262726	Transcript	missense_variant	benign(0.002)
chr3	39307666	39307666	*CX3CR1*	Missense_Mutation	.	SNP	C	C	G	rs201442030	shanshan_et_al_P66	p.G144A	ENSG00000168329	ENST00000358309	Transcript	missense_variant	probably_damaging(0.954)
chr8	23115951	23115951	*CHMP7*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P66	p.T317A	ENSG00000147457	ENST00000397677	Transcript	missense_variant	benign(0.164)
chrX	48650841	48650841	*GATA1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P66	p.Q237P	ENSG00000102145	ENST00000376670	Transcript	missense_variant	probably_damaging(0.934)
chr12	25398285	25398285	*KRAS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P66	p.G12C	ENSG00000133703	ENST00000256078	Transcript	missense_variant	probably_damaging(0.993)
chr1	12907358	12907358	*HNRNPCL1*	Missense_Mutation	.	SNP	T	T	C	rs745873052,rs559905244	shanshan_et_al_P05	p.Q262R	ENSG00000179172	ENST00000317869	Transcript	missense_variant	benign(0.001)
chr1	156714141	156714141	*HDGF*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P05	p.X118_splice	ENSG00000143321	ENST00000368206	Transcript	splice_acceptor_variant	NA

chr1	15970017	15970017	*DDI2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P05	p.G254V	ENSG00000197312	ENST00000480945	Transcript	missense_variant	probably_damaging(1)
chr1	29644413	29644413	*PTPRU*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P05	p.I1233V	ENSG00000060656	ENST00000345512	Transcript	missense_variant	possibly_damaging(0.701)
chr1	38230653	38230653	*EPHA10*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P05	p.R29Q	ENSG00000183317	ENST00000373048	Transcript	missense_variant	probably_damaging(0.986)
chr10	11894194	11894194	*PROSER2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P05	p.R40C	ENSG00000148426	ENST00000277570	Transcript	missense_variant	probably_damaging(1)
chr10	135053697	135053697	*VENTX*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P05	p.G222W	ENSG00000151650	ENST00000325980	Transcript	missense_variant	benign(0.366)
chr10	18187106	18187106	*MRC1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P05	p.S1132C	ENSG00000120586	ENST00000239761	Transcript	missense_variant	probably_damaging(1)
chr11	111946333	111946333	*C11orf57*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P05	p.R12K	ENSG00000150776	ENST00000393047	Transcript	missense_variant	probably_damaging(0.99)
chr11	40137154	40137154	*LRRC4C*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P05	p.H230R	ENSG00000148948	ENST00000278198	Transcript	missense_variant	benign(0)
chr12	48701677	48701677	*GALNT8*	Missense_Mutation	.	SNP	G	G	A	rs373711782	shanshan_et_al_P05	p.R406Q	ENSG00000130035	ENST00000252318	Transcript	missense_variant	possibly_damaging(0.758)
chr12	79738777	79738777	*SLC2A14*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P05	p.Q326H	ENSG00000173262	ENST00000543909	Transcript	missense_variant	possibly_damaging(0.762)
chr12	98909791	98909791	*TMPO*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P05	p.N49T	ENSG00000120802	ENST00000266732	Transcript	missense_variant	probably_damaging(0.992)
chr14	75200807	75200807	*FCF1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P05	p.D161V	ENSG00000119616	ENST00000341162	Transcript	missense_variant	probably_damaging(0.986)
chr14	88654388	88654388	*KCNK10*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P05	p.G312S	ENSG00000100433	ENST00000319231	Transcript	missense_variant	probably_damaging(1)
chr16	14947821	14947821	*NOMO1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P05	p.T301A	ENSG00000103512	ENST00000287667	Transcript	missense_variant	possibly_damaging(0.558)
chr16	28944772	28944772	*CD19*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P05	p.Y260Ifs*7	ENSG00000177455	ENST00000538922	Transcript	frameshift_variant	NA
chr16	31090262	31090262	*ZNF646*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P05	p.G873W	ENSG00000167395	ENST00000300850	Transcript	missense_variant	probably_damaging(1)
chr17	16346993	16346993	*FAM211A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P05	p.T315K	ENSG00000181350	ENST00000470794	Transcript	missense_variant	benign(0.083)
chr17	37566082	37566082	*MED1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P05	p.D798N	ENSG00000125686	ENST00000300651	Transcript	missense_variant	possibly_damaging(0.663)
chr17	7577568	7577568	*TP53*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P05	p.C238F	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(1)
chr19	14000475	14000475	*C19orf57*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P05	p.S398R	ENSG00000132016	ENST00000346736	Transcript	missense_variant	benign(0)
chr19	36134262	36134262	*ETV2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P05	p.T108P	ENSG00000105672	ENST00000402764	Transcript	missense_variant	benign(0.002)
chr19	46119129	46119129	*EML2*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P05	p.T711P	ENSG00000125746	ENST00000587152	Transcript	missense_variant	probably_damaging(0.988)
chr19	51334742	51334742	*KLK15*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P05	p.L3I	ENSG00000174562	ENST00000598239	Transcript	missense_variant	possibly_damaging(0.794)
chr20	36940313	36940313	*BPI*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P05	p.A196S	ENSG00000101425	ENST00000262865	Transcript	missense_variant	benign(0.002)
chr22	50722627	50722634	*PLXNB2*	Frame_Shift_Del	.	DEL	TGGCATCG	TGGCATCG	-	novel	shanshan_et_al_P05	p.D731Rfs*41	ENSG00000196576	ENST00000449103	Transcript	frameshift_variant	NA
chr4	15689990	15689990	*FAM200B*	Nonsense_Mutation	.	SNP	c	c	T	novel	shanshan_et_al_P05	p.R464*	ENSG00000237765	ENST00000422728	Transcript	stop_gained	NA
chr5	15339087	15339087	*FAM114A2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P05	p.D306Y	ENSG00000055147	ENST00000351797	Transcript	missense_variant	possibly_damaging(0.821)
chr8	28210808	28210808	*ZNF395*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P05	p.H234P	ENSG00000186918	ENST00000344423	Transcript	missense_variant	benign(0.006)
chr8	59409434	59409434	*CYP7A1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P05	p.D213N	ENSG00000167910	ENST00000301645	Transcript	missense_variant	probably_damaging(1)
chr9	131762032	131762032	*NUP188*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P05	p.S1264N	ENSG00000095319	ENST00000372577	Transcript	missense_variant	probably_damaging(0.918)
chr9	41505983	41505983	*SPATA31A5*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P05	p.H1085Q	ENSG00000233788	ENST00000377621	Transcript	missense_variant	NA
chr9	65504305	65504305	*SPATA31A7*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P05	p.H1085Q	ENSG00000234734	ENST00000355045	Transcript	missense_variant	possibly_damaging(0.714)
chrX	51637751	51637751	*MAGED1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P05	p.H25P	ENSG00000179222	ENST00000375695	Transcript	missense_variant	unknown(0)
chrX	98662722	98662722	*SHROOM2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P05	p.E945*	ENSG00000146950	ENST00000380913	Transcript	stop_gained	NA
chr1	179414280	179414280	*AXDND1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P08	p.I580S	ENSG00000162779	ENST00000367618	Transcript	missense_variant	possibly_damaging(0.507)
chr1	205180417	205180417	*DSTYK*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P08	p.E83K	ENSG00000133059	ENST00000367162	Transcript	missense_variant	benign(0)

chr1	248129634	248129634	*OR2AK2*	Missense_Mutation	.	SNP	T	T	A	rs529638198	shansha n_et_al_ P08	p.L334Q	ENSG00000187080	ENST00000366480	Transcript	missense_variant	possibly_damaging(0.766)
chr1	26152814	26152815	*MTFR1L*	Frame_Shift_Ins	.	INS	-	-	TG	novel	shansha n_et_al_ P08	p.L53Vfs*2	ENSG00000117640	ENST00000374301	Transcript	frameshift_variant	NA
chr1	27432470	27432470	*SLC9A1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_ P08	p.S464Y	ENSG00000090020	ENST00000263980	Transcript	missense_variant	probably_damaging(0.934)
chr1	29185574	29185574	*OPRD1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_ P08	p.E112D	ENSG00000116329	ENST00000234961	Transcript	missense_variant	benign(0.027)
chr1	34667819	34667819	*C1orf94*	Missense_Mutation	.	SNP	C	C	G	rs531268354	shansha n_et_al_ P08	p.P469A	ENSG00000142698	ENST00000488417	Transcript	missense_variant	benign(0.199)
chr1	68947861	68947861	*DEPDC1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_ P08	p.S544C	ENSG00000024526	ENST00000456315	Transcript	missense_variant	possibly_damaging(0.599)
chr1	94940756	94940756	*ABCD3*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_ P08	p.R155*	ENSG00000117528	ENST00000370214	Transcript	stop_gained	NA
chr10	123767762	123767762	*DMBT1*	Missense_Mutation	.	SNP	G	G	A	rs148891350	shansha n_et_al_ P08	p.R1497H	ENSG00000187908	ENST00000368909	Transcript	missense_variant	benign(0.004)
chr10	17730130	17730130	*STAM*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_ P08	p.N134K	ENSG00000136738	ENST00000377524	Transcript	missense_variant	benign(0.036)
chr10	49459621	49459621	*FRMPD2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_ P08	p.D47Y	ENSG00000170324	ENST00000374201	Transcript	missense_variant	probably_damaging(1)
chr10	89720857	89720857	*PTEN*	Nonsense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_ P08	p.Y336*	ENSG00000171862	ENST00000371953	Transcript	stop_gained	NA
chr11	18332304	18332304	*HPS5*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_ P08	p.T154N	ENSG00000110756	ENST00000349215	Transcript	missense_variant	possibly_damaging(0.543)
chr11	4144502	4144502	*RRM1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_ P08	p.P403L	ENSG00000167325	ENST00000300738	Transcript	missense_variant	probably_damaging(1)
chr11	47200762	47200762	*PACSIN3*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_ P08	p.W283*	ENSG00000165912	ENST00000539589	Transcript	stop_gained	NA
chr11	47906334	47906334	*OR51F1*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P08	p.R172G	ENSG00000188069	ENST00000343430	Transcript	missense_variant	benign(0.004)
chr11	49974335	49974335	*OR4C13*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_ P08	p.Y121N	ENSG00000258817	ENST00000555099	Transcript	missense_variant	probably_damaging(0.948)
chr11	55102223	55102223	*OR52D1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_ P08	p.S96F	ENSG00000181609	ENST00000322641	Transcript	missense_variant	possibly_damaging(0.83)
chr11	62744331	62744331	*SLC22A6*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_ P08	p.Q543K	ENSG00000197901	ENST00000377871	Transcript	missense_variant	benign(0.011)
chr11	77937513	77937513	*GAB2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_ P08	p.R402Q	ENSG00000033327	ENST00000361507	Transcript	missense_variant	benign(0.426)
chr12	123419855	123419855	*ABCB9*	Missense_Mutation	.	SNP	C	C	G	rs147328787	shansha n_et_al_ P08	p.G623R	ENSG00000150967	ENST00000542678	Transcript	missense_variant	benign(0.161)
chr12	53693715	53693715	*C12orf10*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P08	p.L65P	ENSG00000139637	ENST00000267103	Transcript	missense_variant	probably_damaging(1)
chr12	58001248	58001249	*DTX3*	Frame_Shift_Del	.	DEL	TG	TG	-	novel	shansha n_et_al_ P08	p.C202Rfs*21	ENSG00000178498	ENST00000548198	Transcript	frameshift_variant	NA
chr12	62785633	62785634	*USP15*	Frame_Shift_Ins	.	INS	-	-	A	novel	shansha n_et_al_ P08	p.R760Kfs*4	ENSG00000135655	ENST00000280377	Transcript	frameshift_variant	NA
chr14	45711538	45711538	*MIS18BP1*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P08	p.Q281R	ENSG00000129534	ENST00000310806	Transcript	missense_variant	benign(0.005)
chr14	60903744	60903744	*C14orf39*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P08	p.E528G	ENSG00000179008	ENST00000321731	Transcript	missense_variant	possibly_damaging(0.859)
chr17	14013339	14013339	*INPP5K*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_ P08	p.T285S	ENSG00000132376	ENST00000421807	Transcript	missense_variant	benign(0.032)
chr17	39197512	39197512	*KRTAP1-1*	Frame_Shift_Del	.	DEL	C	C	-	novel	shansha n_et_al_ P08	p.P47Qfs*66	ENSG00000188581	ENST00000306271	Transcript	frameshift_variant	NA
chr17	39580600	39580600	*KRT37*	Nonsense_Mutation	.	SNP	G	G	T	rs369515531	shansha n_et_al_ P08	p.S59*	ENSG00000108417	ENST00000225550	Transcript	stop_gained	NA
chr18	25990750	25990750	*NDC80*	Nonsense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_ P08	p.K427*	ENSG00000080986	ENST00000261597	Transcript	stop_gained	NA
chr18	33234695	33234695	*GALNT1*	Frame_Shift_Del	.	DEL	C	C	-	novel	shansha n_et_al_ P08	p.L24Cfs*25	ENSG00000141429	ENST00000269195	Transcript	frameshift_variant	NA
chr18	63476982	63476982	*CDH7*	Missense_Mutation	.	SNP	A	A	T	rs114235038	shansha n_et_al_ P08	p.I85F	ENSG00000081138	ENST00000397968	Transcript	missense_variant	benign(0.04)
chr19	19822669	19822669	*ZNF14*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_ P08	p.P474H	ENSG00000105708	ENST00000344099	Transcript	missense_variant	probably_damaging(1)
chr19	39898509	39898509	*ZFP36*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_ P08	p.T57P	ENSG00000128016	ENST00000597629	Transcript	missense_variant	benign(0.004)
chr19	53086139	53086139	*ZNF701*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_ P08	p.G342V	ENSG00000167562	ENST00000540331	Transcript	missense_variant	probably_damaging(0.999)
chr2	152426737	152426737	*NEB*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_ P08	p.D5763V	ENSG00000183091	ENST00000397345	Transcript	missense_variant	probably_damaging(1)
chr2	225750429	225750429	*DOCK10*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P08	p.K236E	ENSG00000135905	ENST00000258390	Transcript	missense_variant	possibly_damaging(0.804)

chr2	55812299	55812299	*SMEK2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P08	p.M374T	ENSG00000138041	ENST00000345102	Transcript	missense_variant	benign(0.028)
chr20	30556342	30556342	*XKR7*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P08	p.S122P	ENSG00000260903	ENST00000562532	Transcript	missense_variant	benign(0.01)
chr20	31374381	31374381	*DNMT3B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P08	p.R127L	ENSG00000088305	ENST00000328111	Transcript	missense_variant	probably_damaging(0.985)
chr20	57768383	57768383	*ZNF831*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P08	p.G770V	ENSG00000124203	ENST00000371030	Transcript	missense_variant	possibly_damaging(0.844)
chr22	20103591	20103591	*TRMT2A*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P08	p.E190G	ENSG00000099899	ENST00000252136	Transcript	missense_variant	benign(0.299)
chr22	29083962	29083962	*CHEK2*	Missense_Mutation	.	SNP	G	G	C	rs200432447	shanshan_et_al_P08	p.R562G	ENSG00000183765	ENST00000382580	Transcript	missense_variant	benign(0.061)
chr3	121438521	121438521	*GOLGB1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P08	p.Q248L	ENSG00000173230	ENST00000393667	Transcript	missense_variant	possibly_damaging(0.858)
chr3	132408027	132408027	*NPHP3*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P08	p.S925*	ENSG00000113971	ENST00000333731	Transcript	stop_gained	NA
chr3	40231397	40231397	*MYRIP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P08	p.A370T	ENSG00000170011	ENST00000302541	Transcript	missense_variant	benign(0.009)
chr3	75788394	75788394	*ZNF717*	Missense_Mutation	.	SNP	C	C	G	rs201974353	shanshan_et_al_P08	p.R127T	ENSG00000227124	ENST00000422325	Transcript	missense_variant	possibly_damaging(0.587)
chr4	144618702	144618702	*FREM3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P08	p.S1043T	ENSG00000183090	ENST00000329798	Transcript	missense_variant	benign(0.348)
chr4	15826591	15826591	*CD38*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P08	p.G151C	ENSG00000004468	ENST00000226279	Transcript	missense_variant	probably_damaging(1)
chr4	985445	985445	*SLC26A1*	Missense_Mutation	.	SNP	G	G	A	rs199532422	shanshan_et_al_P08	p.P16L	ENSG00000145217	ENST00000361661	Transcript	missense_variant	benign(0)
chr5	140176744	140176744	*PCDHA2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P08	p.R732H	ENSG00000204969	ENST00000526136	Transcript	missense_variant	benign(0.001)
chr5	140515207	140515207	*PCDHB5*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P08	p.A64E	ENSG00000113209	ENST00000231134	Transcript	missense_variant	probably_damaging(0.983)
chr5	166802469	166802469	*TENM2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P08	p.D165Y	ENSG00000145934	ENST00000518659	Transcript	missense_variant	benign(0.146)
chr5	86659222	86659222	*RASA1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P08	p.L504P	ENSG00000145715	ENST00000274376	Transcript	missense_variant	probably_damaging(0.996)
chr6	147106755	147106755	*ADGB*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P08	p.A1408P	ENSG00000118492	ENST00000397944	Transcript	missense_variant	probably_damaging(0.949)
chr6	64776342	64776342	*EYS*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P08	p.L2205H	ENSG00000188107	ENST00000503581	Transcript	missense_variant	probably_damaging(0.928)
chr6	88144699	88144700	*C6ORF165*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P08	p.N477Kfs*15	ENSG00000272514	ENST00000369562	Transcript	frameshift_variant	NA
chr7	102743935	102743935	*NAPEPLD*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P08	p.F375L	ENSG00000161048	ENST00000417955	Transcript	missense_variant	probably_damaging(0.977)
chr7	117876942	117876942	*ANKRD7*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P08	p.S225*	ENSG00000106013	ENST00000265224	Transcript	stop_gained	NA
chr7	148725 1	148725 1	*MICALL2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P08	p.Q162R	ENSG00000164877	ENST00000297508	Transcript	missense_variant	benign(0.046)
chr7	16298559	16298559	*ISPD*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P08	p.F338V	ENSG00000214960	ENST00000407010	Transcript	missense_variant	possibly_damaging(0.721)
chr7	66569000	66569000	*ZNF853*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P08	p.C31F	ENSG00000236609	ENST00000457543	Transcript	missense_variant	unknown(0)
chr7	97861273	97861273	*TECPR1*	Splice_Site	.	SNP	T	T	G	novel	shanshan_et_al_P08	p.X607_splice	ENSG00000205356	ENST00000447648	Transcript	splice_acceptor_variant	NA
chr7	98248953	98248953	*NPTX2*	Splice_Site	.	SNP	A	A	C	novel	shanshan_et_al_P08	p.X143_splice	ENSG00000106236	ENST00000265634	Transcript	splice_acceptor_variant	NA
chr8	144773829	144773829	*ZNF707*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P08	p.V68I	ENSG00000181135	ENST00000532205	Transcript	missense_variant	benign(0.007)
chr9	39889013	39889013	*SPATA31A2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P08	p.P667L	ENSG00000204848	ENST00000456183	Transcript	missense_variant	benign(0.002)
chr9	70427767	70427767	*FOXD4L4*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P08	p.L378P	ENSG00000184659	ENST00000377413	Transcript	missense_variant	benign(0)
chrX	105125700	105125700	*NRK*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P08	NA	ENSG00000123572	ENST00000428173	Transcript	splice_acceptor_variant	NA
chrX	138870360	138870360	*ATP11C*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P08	p.G507V	ENSG00000101974	ENST00000327569	Transcript	missense_variant	probably_damaging(0.982)
chrX	47271854	47271854	*ZNF157*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P08	p.Q128*	ENSG00000147117	ENST00000377073	Transcript	stop_gained	NA
chrX	49071670	49071671	*CACNA1F*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P08	p.P1169T	ENSG00000102001	ENST00000376265	Transcript	missense_variant	benign(0.29)
chr17	75784933	75784933	*TP53*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P08	p.R146H	ENSG00000141510	ENST00000269305	Transcript	stop_gained	probably_damaging(0.831)
chr1	120930078	120930078	*FCGR1B*	Missense_Mutation	.	SNP	G	G	A	rs372170772	shanshan_et_al_P09	p.R175C	ENSG00000198019	ENST00000369384	Transcript	missense_variant	probably_damaging(0.987)

chr1	159889583	159889583	*TAGLN2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P09	p.A75S	ENSG00000158710	ENST00000368097	Transcript	missense_variant	benign(0.019)
chr1	17313629	17313629	*ATP13A2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P09	p.V999M	ENSG00000159363	ENST00000326735	Transcript	missense_variant	benign(0.042)
chr1	179783089	179783089	*FAM163A*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P09	p.V90G	ENSG00000143340	ENST00000341785	Transcript	missense_variant	benign(0)
chr1	22179228	22179228	*HSPG2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P09	p.S2230L	ENSG00000142798	ENST00000374695	Transcript	missense_variant	probably_damaging(0.999)
chr11	93494817	93494817	*C11orf54*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P09	p.D254V	ENSG00000182919	ENST00000528288	Transcript	missense_variant	probably_damaging(1)
chr12	56721355	56721355	*PAN2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P09	p.S238R	ENSG00000135473	ENST00000425394	Transcript	missense_variant	possibly_damaging(0.811)
chr15	27128339	27128339	*GABRA5*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P09	p.I79V	ENSG00000186297	ENST00000335625	Transcript	missense_variant	probably_damaging(0.994)
chr15	62205536	62205536	*VPS13C*	Missense_Mutation	.	SNP	A	A	C	rs542996658	shansha n_et_al_P09	p.C2842G	ENSG00000129003	ENST00000261517	Transcript	missense_variant	probably_damaging(1)
chr15	85341693	85341693	*ZNF592*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P09	p.M908I	ENSG00000166716	ENST00000299927	Transcript	missense_variant	probably_damaging(0.981)
chr17	37313184	37313184	*ARL5C*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P09	p.R168I	ENSG00000141748	ENST00000445555	Transcript	missense_variant	benign(0.079)
chr17	7577106	7577106	*TP53*	Missense_Mutation	.	SNP	G	G	A	rs1784978 1	shansha n_et_al_P09	p.P278S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(1)
chr19	1043372	1043372	*ABCA7*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P09	p.H277P	ENSG00000064687	ENST00000263094	Transcript	missense_variant	possibly_damaging(0.649)
chr19	39086595	39086595	*MAP4K1*	Frame_Shift_Del	.	DEL	C	C	-	novel	shansha n_et_al_P09	p.M722Wfs*3	ENSG00000104814	ENST00000591517	Transcript	frameshift_variant	NA
chr19	56029381	56029381	*SSC5D*	Missense_Mutation	.	SNP	T	T	A	rs561891391	shansha n_et_al_P09	p.H1246Q	ENSG00000179954	ENST00000389623	Transcript	missense_variant	unknown(0)
chr19	56029595	56029595	*SSC5D*	Missense_Mutation	.	SNP	G	G	C	rs201516796	shansha n_et_al_P09	p.D1318H	ENSG00000179954	ENST00000389623	Transcript	missense_variant	unknown(0)
chr2	95537734	95537734	*TEKT4*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P09	p.F137C	ENSG00000163060	ENST00000295201	Transcript	missense_variant	possibly_damaging(0.895)
chr20	34430626	34430626	*PHF20*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P09	p.Q72L	ENSG00000025293	ENST00000374012	Transcript	missense_variant	probably_damaging(0.995)
chr20	39831609	39831609	*ZHX3*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P09	p.K650Q	ENSG00000174306	ENST00000309060	Transcript	missense_variant	probably_damaging(1)
chr22	38119902	38119902	*TRIOBP*	Missense_Mutation	.	SNP	A	A	G	rs537300122	shansha n_et_al_P09	p.T447A	ENSG00000100106	ENST00000406386	Transcript	missense_variant	benign(0)
chr4	95191958	95191958	*SMARCAD1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P09	p.A521T	ENSG00000163104	ENST00000354268	Transcript	missense_variant	probably_damaging(1)
chr5	102342538	102342538	*PAM*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P09	p.P613S	ENSG00000145730	ENST00000304400	Transcript	missense_variant	probably_damaging(0.994)
chr7	97487714	97487714	*ASNS*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P09	p.G260V	ENSG00000070669	ENST00000175506	Transcript	missense_variant	probably_damaging(0.996)
chr8	125076714	125076714	*FER1L6*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P09	p.A1152D	ENSG00000214814	ENST00000522917	Transcript	missense_variant	benign(0.013)
chr8	141874481	141874481	*PTK2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P09	p.R127L	ENSG00000169398	ENST00000340930	Transcript	missense_variant	probably_damaging(0.954)
chr8	59515912	59515912	*NSMAF*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P09	p.Y332C	ENSG00000035681	ENST00000427130	Transcript	missense_variant	probably_damaging(0.994)
chr9	19378450	19378450	*RPS6*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P09	p.A138S	ENSG00000137154	ENST00000380394	Transcript	missense_variant	benign(0.134)
chrX	15833867	15833867	*ZRSR2*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P09	p.F209L	ENSG00000169249	ENST00000307771	Transcript	missense_variant	possibly_damaging(0.826)
chr1	43773103	43773103	*TIE1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P113	p.A258D	ENSG00000066056	ENST00000372476	Transcript	missense_variant	probably_damaging(0.998)
chr10	119003551	119003551	*SLC18A2*	Missense_Mutation	.	SNP	G	G	A	rs186416980	shansha n_et_al_P113	p.R64K	ENSG00000165646	ENST00000298472	Transcript	missense_variant	benign(0.001)
chr10	132891516	132891516	*TCERG1L*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P113	p.R557I	ENSG00000176769	ENST00000368642	Transcript	missense_variant	probably_damaging(0.953)
chr11	126391275	126391275	*KIRREL3*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P113	p.A123V	ENSG00000149571	ENST00000525144	Transcript	missense_variant	possibly_damaging(0.69)
chr11	55872934	55872934	*OR8H2*	Missense_Mutation	.	SNP	G	G	T	rs191786486	shansha n_et_al_P113	p.R139M	ENSG00000181767	ENST00000313503	Transcript	missense_variant	possibly_damaging(0.737)
chr13	80911668	80911668	*SPRY2*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P113	p.G58A	ENSG00000136158	ENST00000377102	Transcript	missense_variant	benign(0.004)
chr14	21991956	21991956	*SALL2*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P113	p.C636S	ENSG00000165821	ENST00000327430	Transcript	missense_variant	probably_damaging(0.989)
chr17	10227575	10227575	*MYH13*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P113	p.E900K	ENSG00000006788	ENST00000418404	Transcript	missense_variant	probably_damaging(0.98)
chr17	18675736	18675736	*FBXW10*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P113	p.N673T	ENSG00000171931	ENST00000395665	Transcript	missense_variant	probably_damaging(0.91)

chr17	36719592	36719592	*SRCIN1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P113	p.A236V	ENSG00000017373	ENST00000264659	Transcript	missense_variant	possibly_damaging(0.628)
chr17	40937397	40937397	*WNK4*	Missense_Mutation	.	SNP	G	G	T	rs368869602	shanshan_et_al_P113	p.R458L	ENSG00000126562	ENST00000246914	Transcript	missense_variant	unknown(0)
chr17	55917213	55917213	*MRPS23*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P113	p.Q168H	ENSG00000181610	ENST00000313608	Transcript	missense_variant	possibly_damaging(0.45)
chr17	7579406	7579406	*TP53*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P113	p.S94*	ENSG00000141510	ENST00000269305	Transcript	stop_gained	NA
chr18	61006117	61006117	*KDSR*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P113	p.X232_splice	ENSG00000119537	ENST00000406396	Transcript	splice_acceptor_variant	NA
chr19	17837708	17837708	*MAP1S*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P113	p.E505D	ENSG00000130479	ENST00000324096	Transcript	missense_variant	benign(0.016)
chr19	53269289	53269289	*ZNF600*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P113	p.R574G	ENSG00000189190	ENST00000338230	Transcript	missense_variant	possibly_damaging(0.866)
chr22	30000081	30000081	*NF2*	Nonsense_Mutation	.	SNP	G	G	T	rs373337083	shanshan_et_al_P113	p.E32*	ENSG00000186575	ENST00000338641	Transcript	stop_gained	NA
chr4	55973998	55973998	*KDR*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P113	p.T440A	ENSG00000128052	ENST00000263923	Transcript	missense_variant	benign(0.007)
chr4	68380089	68380089	*CENPC*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P113	p.T383A	ENSG00000145241	ENST00000273853	Transcript	missense_variant	benign(0.037)
chr4	956312	956312	*DGKQ*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P113	p.A709S	ENSG00000145214	ENST00000273814	Transcript	missense_variant	benign(0.062)
chr5	41149466	41149466	*C6*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P113	p.I834V	ENSG00000039537	ENST00000263413	Transcript	missense_variant	benign(0.006)
chr6	170865969	170865969	*TBP*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P113	NA	ENSG00000112592	ENST00000392092	Transcript	splice_acceptor_variant	NA
chr8	107773510	107773510	*ABRA*	Missense_Mutation	.	SNP	G	G	A	rs182944429	shanshan_et_al_P113	p.R301C	ENSG00000174429	ENST00000311955	Transcript	missense_variant	possibly_damaging(0.857)
chr9	35802548	35802548	*NPR2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P113	p.I587V	ENSG00000159899	ENST00000342694	Transcript	missense_variant	benign(0.123)
chrX	114358553	114358553	*LRCH2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P113	p.T602A	ENSG00000130224	ENST00000317135	Transcript	missense_variant	benign(0.001)
chrX	134481082	134481082	*ZNF449*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P113	p.L13F	ENSG00000173275	ENST00000339249	Transcript	missense_variant	probably_damaging(0.941)
chrX	80370392	80370392	*HMGN5*	Missense_Mutation	.	SNP	c	c	T	novel	shanshan_et_al_P113	p.R202K	ENSG00000198157	ENST00000358130	Transcript	missense_variant	unknown(0)
chr1	109803859	109803859	*CELSR2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q1385L	ENSG00000143126	ENST00000271332	Transcript	missense_variant	probably_damaging(0.947)
chr1	110034238	110034238	*ATXN7L2*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K685*	ENSG00000162650	ENST00000369870	Transcript	stop_gained	NA
chr1	11827056	11827056	*C1orf167*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P119	p.G466R	ENSG00000215910	ENST00000433342	Transcript	missense_variant	unknown(0)
chr1	13330623	13330623	*PRAMEF3*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.C221*	ENSG00000204503	ENST00000376173	Transcript	stop_gained	NA
chr1	151774931	151774931	*LINGO4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S84C	ENSG00000213171	ENST00000368820	Transcript	missense_variant	benign(0.023)
chr1	155230223	155230223	*SCAMP3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.T96S	ENSG00000116521	ENST00000302631	Transcript	missense_variant	benign(0.184)
chr1	156846831	156846831	*FHAD1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E841V	ENSG00000142621	ENST00000358897	Transcript	missense_variant	probably_damaging(0.965)
chr1	157067737	157067737	*ETV3L*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q177L	ENSG00000253831	ENST00000454449	Transcript	missense_variant	benign(0.147)
chr1	171504565	171504565	*PRRC2C*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.X623_splice	ENSG00000117523	ENST00000338920	Transcript	splice_acceptor_variant	NA
chr1	19018446	19018446	*PAX7*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q262L	ENSG00000009709	ENST00000375375	Transcript	missense_variant	benign(0.41)
chr1	197890658	197890658	*LHX9*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Y201F	ENSG00000143355	ENST00000367387	Transcript	missense_variant	benign(0.001)
chr1	223285741	223285741	*TLR5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.R211S	ENSG00000187554	ENST00000540964	Transcript	missense_variant	benign(0.155)
chr1	228525739	228525739	*OBSCN*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L6589Q	ENSG00000154358	ENST00000570156	Transcript	missense_variant	probably_damaging(1)
chr1	26515998	26515998	*CNKSR1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P119	p.P701S	ENSG00000142675	ENST00000361530	Transcript	missense_variant	benign(0.043)
chr1	29383338	29383338	*ACTRT2*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P119	p.G30Dfs*13	ENSG00000169717	ENST00000378404	Transcript	frameshift_variant	NA
chr1	43890069	43890069	*SZT2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S813C	ENSG00000198198	ENST00000562955	Transcript	missense_variant	probably_damaging(0.982)
chr1	44433083	44433083	*IPO13*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I904F	ENSG00000117408	ENST00000372343	Transcript	missense_variant	benign(0.002)
chr1	55565544	55565544	*USP24*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X1758_splice	ENSG00000162402	ENST00000294383	Transcript	splice_acceptor_variant	NA

chr1	6214762	6214762	*CHD5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P119	p.Q235K	ENSG00000116254	ENST00000262450	Transcript	missense_variant	benign(0.002)
chr1	95294069	95294069	*SLC44A3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S146C	ENSG00000143036	ENST00000271227	Transcript	missense_variant	possibly_damaging(0.806)
chr10	23326397	23326397	*ARMC3*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.R870*	ENSG00000165309	ENST00000298032	Transcript	stop_gained	NA
chr10	69651251	69651251	*SIRT1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q294L	ENSG00000096717	ENST00000212015	Transcript	missense_variant	probably_damaging(0.998)
chr10	77637379	77637379	*ITIH2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E289V	ENSG00000151655	ENST00000358415	Transcript	missense_variant	possibly_damaging(0.623)
chr11	100999800	100999800	*PGR*	Translation_Start_Site	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.M1?	ENSG00000082175	ENST00000325455	Transcript	initiator_codon_variant	possibly_damaging(0.855)
chr11	103070122	103070122	*DYNC2H1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S2669C	ENSG00000187240	ENST00000398093	Transcript	missense_variant	benign(0.049)
chr11	108593923	108593923	*DDX10*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P119	p.E567K	ENSG00000178105	ENST00000322536	Transcript	missense_variant	benign(0.004)
chr11	113628549	113628549	*ZW10*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.R254W	ENSG00000086827	ENST00000200135	Transcript	missense_variant	possibly_damaging(0.656)
chr11	116827770	116827770	*SIK3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K37M	ENSG00000160584	ENST00000292055	Transcript	missense_variant	probably_damaging(1)
chr11	118498962	118498962	*PHLDB1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P119	p.R475W	ENSG00000019144	ENST00000361417	Transcript	missense_variant	probably_damaging(0.973)
chr11	124761432	124761432	*ROBO4*	Missense_Mutation	.	SNP	C	C	T	rs369179467	shanshan_et_al_P119	p.G571S	ENSG00000154133	ENST00000306534	Transcript	missense_variant	probably_damaging(0.999)
chr11	134238601	134238601	*GLB1L2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H318L	ENSG00000149328	ENST00000535456	Transcript	missense_variant	probably_damaging(0.99)
chr11	2593278	2593278	*KCNQ1*	Missense_Mutation	.	SNP	A	A	T	rs533669726	shanshan_et_al_P119	p.H240L	ENSG00000053918	ENST00000155840	Transcript	missense_variant	probably_damaging(0.958)
chr11	43427103	43427103	*TTC17*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T507S	ENSG00000052841	ENST00000039989	Transcript	missense_variant	benign(0.001)
chr11	46388867	46388867	*DGKZ*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q252L	ENSG00000149091	ENST00000454345	Transcript	missense_variant	benign(0.003)
chr11	62613977	62613977	*CNGA4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T125S	ENSG00000132259	ENST00000379936	Transcript	missense_variant	probably_damaging(0.989)
chr11	64022882	64022882	*PLCB3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K161M	ENSG00000149782	ENST00000540288	Transcript	missense_variant	possibly_damaging(0.798)
chr11	73941339	73941339	*PPME1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I150F	ENSG00000214517	ENST00000328257	Transcript	missense_variant	benign(0.248)
chr11	84622466	84622466	*STK33*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I309K	ENSG00000130413	ENST00000447869	Transcript	missense_variant	probably_damaging(0.995)
chr11	88911873	88911873	*TYR*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Y251F	ENSG00000077498	ENST00000263321	Transcript	missense_variant	benign(0.068)
chr12	109968357	109968357	*UBE3B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H939L	ENSG00000151148	ENST00000342494	Transcript	missense_variant	possibly_damaging(0.772)
chr12	122818637	122818637	*CLIP1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P119	p.Q883*	ENSG00000130779	ENST00000540338	Transcript	stop_gained	NA
chr12	122825457	122825457	*CLIP1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q765L	ENSG00000130779	ENST00000540338	Transcript	missense_variant	probably_damaging(0.943)
chr12	125441289	125441289	*DHX37*	Missense_Mutation	.	SNP	T	T	A	rs145434272	shanshan_et_al_P119	p.I801F	ENSG00000150990	ENST00000308736	Transcript	missense_variant	probably_damaging(0.965)
chr12	14976470	14976470	*C12orf60*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.K201E	ENSG00000182993	ENST00000330828	Transcript	missense_variant	benign(0.001)
chr12	22627686	22627686	*C2CD5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E681V	ENSG00000111731	ENST00000333957	Transcript	missense_variant	benign(0.016)
chr12	2760876	2760876	*CACNA1C*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L1387Q	ENSG00000151067	ENST00000347598	Transcript	missense_variant	probably_damaging(0.996)
chr12	46592528	46592528	*SLC38A1*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X335_splice	ENSG00000111371	ENST00000398637	Transcript	splice_acceptor_variant	NA
chr12	49959442	49959442	*MCRS1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K66M	ENSG00000187778	ENST00000357123	Transcript	missense_variant	probably_damaging(0.988)
chr12	52758779	52758779	*KRT85*	Frame_Shift_Del	.	DEL	AT	AT	-	novel	shanshan_et_al_P119	p.V200Afs*12	ENSG00000135443	ENST00000257901	Transcript	frameshift_variant	NA
chr12	53686114	53686114	*ESPL1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.Y1950C	ENSG00000135476	ENST00000257934	Transcript	missense_variant	probably_damaging(1)
chr12	55846616	55846616	*OR6C2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I207F	ENSG00000179695	ENST00000322678	Transcript	missense_variant	benign(0.153)
chr12	57009268	57009268	*BAZ2A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Y89F	ENSG00000076108	ENST00000551812	Transcript	missense_variant	probably_damaging(0.98)
chr12	57422980	57422980	*MYO1A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.T981S	ENSG00000166866	ENST00000442789	Transcript	missense_variant	possibly_damaging(0.71)
chr12	58024298	58024298	*B4GALNT1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.L165Q	ENSG00000135454	ENST00000341156	Transcript	missense_variant	possibly_damaging(0.671)

chr12	66715758	66715758	*HELB*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q729L	ENSG00000127311	ENST00000247815	Transcript	missense_variant	benign(0.25)
chr12	85446008	85446008	*LRRIQ1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K244N	ENSG00000133640	ENST00000393217	Transcript	missense_variant	benign(0.086)
chr12	970386	970386	*WNK1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S610C	ENSG00000060237	ENST00000315939	Transcript	missense_variant	unknown(0)
chr13	108861215	108861215	*LIG4*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P119	p.Y801C	ENSG00000174405	ENST00000356922	Transcript	missense_variant	benign(0.001)
chr13	111102119	111102119	*COL4A2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L391H	ENSG00000134871	ENST00000360467	Transcript	missense_variant	probably_damaging(0.939)
chr13	25399879	25399879	*RNF17*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E738D	ENSG00000132972	ENST00000255324	Transcript	missense_variant	probably_damaging(0.973)
chr13	26620876	26620876	*SHISA2*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P119	p.T222Rfs*6	ENSG00000180730	ENST00000319420	Transcript	frameshift_variant	NA
chr14	21547147	21547147	*ARHGEF40*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q784L	ENSG00000165801	ENST00000298694	Transcript	missense_variant	benign(0.304)
chr14	64542703	64542703	*SYNE2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E3636V	ENSG00000054654	ENST00000358025	Transcript	missense_variant	possibly_damaging(0.809)
chr14	65208994	65208994	*PLEKHG3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E864V	ENSG00000126822	ENST00000247226	Transcript	missense_variant	probably_damaging(0.962)
chr14	71109177	71109177	*TTC9*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K111*	ENSG00000133985	ENST00000256367	Transcript	stop_gained	NA
chr14	74824304	74824304	*VRTN*	Missense_Mutation	.	SNP	T	T	A	rs140227220	shanshan_et_al_P119	p.L273Q	ENSG00000133980	ENST00000256362	Transcript	missense_variant	probably_damaging(0.933)
chr15	43307939	43307940	*UBR1*	Frame_Shift_Del	.	DEL	AT	AT	-	novel	shanshan_et_al_P119	p.Y1052*	ENSG00000159459	ENST00000290650	Transcript	frameshift_variant	NA
chr15	43446997	43446997	*TMEM62*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S384C	ENSG00000137842	ENST00000260403	Transcript	missense_variant	possibly_damaging(0.753)
chr15	45399031	45399031	*DUOX2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L610F	ENSG00000140279	ENST00000603300	Transcript	missense_variant	possibly_damaging(0.776)
chr15	50154546	50154546	*ATP8B4*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K1065*	ENSG00000104043	ENST00000284509	Transcript	stop_gained	NA
chr15	79183829	79183829	*MORF4L1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P119	p.P157H	ENSG00000185787	ENST00000331268	Transcript	missense_variant	possibly_damaging(0.664)
chr15	89424819	89424819	*HAPLN3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.W88R	ENSG00000140511	ENST00000359555	Transcript	missense_variant	probably_damaging(1)
chr15	99478246	99478246	*IGF1R*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E1050D	ENSG00000140443	ENST00000268035	Transcript	missense_variant	probably_damaging(0.983)
chr16	11001439	11001439	*CIITA*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H697L	ENSG00000179583	ENST00000328428	Transcript	missense_variant	benign(0.002)
chr16	12625300	12625300	*CACNA1H*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X1593_splice	ENSG00000196557	ENST00000348261	Transcript	splice_donor_variant	NA
chr16	21262133	21262133	*ANKS4B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S416C	ENSG00000175311	ENST00000311620	Transcript	missense_variant	possibly_damaging(0.807)
chr16	22926576	22926576	*HS3ST2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L266Q	ENSG00000122254	ENST00000261374	Transcript	missense_variant	possibly_damaging(0.481)
chr16	24135213	24135213	*PRKCB*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S326T	ENSG00000166501	ENST00000303531	Transcript	missense_variant	benign(0.009)
chr16	29909302	29909302	*SEZ6L2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.L28Q	ENSG00000174938	ENST00000308713	Transcript	missense_variant	benign(0.44)
chr16	396776	396776	*AXIN1*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K84*	ENSG00000103126	ENST00000262320	Transcript	stop_gained	NA
chr16	46508243	46508243	*ANKRD26P1*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	NA	ENSG00000261239	ENST00000571006	Transcript	splice_acceptor_variant	NA
chr16	46771662	46771662	*MYLK3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q321L	ENSG00000140795	ENST00000394809	Transcript	missense_variant	benign(0.001)
chr16	47514749	47514749	*ANKS3*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.R359*	ENSG00000168096	ENST00000304283	Transcript	stop_gained	NA
chr16	56704477	56704477	*MT1H*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K30*	ENSG00000205358	ENST00000332374	Transcript	stop_gained	NA
chr16	57758742	57758742	*CCDC135*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I585F	ENSG00000159625	ENST00000360716	Transcript	missense_variant	possibly_damaging(0.747)
chr16	67229816	67229816	*E2F4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S314C	ENSG00000205250	ENST00000379378	Transcript	missense_variant	possibly_damaging(0.846)
chr16	67404918	67404918	*LRRC36*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S423C	ENSG00000159708	ENST00000329956	Transcript	missense_variant	possibly_damaging(0.905)
chr16	69602396	69602396	*NFAT5*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.X25_splice	ENSG00000102908	ENST00000432919	Transcript	splice_acceptor_variant	NA
chr16	69680984	69680984	*NFAT5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T103S	ENSG00000102908	ENST00000432919	Transcript	missense_variant	probably_damaging(0.952)
chr16	75276951	75276951	*BCAR1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E63V	ENSG00000050820	ENST00000418647	Transcript	missense_variant	probably_damaging(0.999)

chr16	88495850	88495850	*ZNF469*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P119	p.P658S	ENSG00000225614	ENST00000437464	Transcript	missense_variant	benign(0.016)
chr16	89713675	89713675	*CHMP1A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q106L	ENSG00000131165	ENST00000397901	Transcript	missense_variant	possibly_damaging(0.787)
chr17	20135564	20135564	*SPECC1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P119	p.V733L	ENSG00000128487	ENST00000261503	Transcript	missense_variant	possibly_damaging(0.905)
chr17	26668457	26668457	*TNFAIP1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S165C	ENSG00000109079	ENST00000226225	Transcript	missense_variant	probably_damaging(0.91)
chr17	36623567	36623567	*ARHGAP23*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.F548Y	ENSG00000225485	ENST00000431231	Transcript	missense_variant	probably_damaging(0.997)
chr17	39619260	39619260	*KRT32*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.Y347H	ENSG00000108759	ENST00000225899	Transcript	missense_variant	possibly_damaging(0.876)
chr17	39871824	39871824	*GAST*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.W46R	ENSG00000184502	ENST00000329402	Transcript	missense_variant	probably_damaging(0.961)
chr17	42739769	42739769	*C17orf104*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.C97S	ENSG00000180336	ENST00000409122	Transcript	missense_variant	benign(0.054)
chr17	64938366	64938366	*KIAA0753*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.N852I	ENSG00000198920	ENST00000361413	Transcript	missense_variant	possibly_damaging(0.775)
chr17	66614443	66614443	*XAF1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H23L	ENSG00000132530	ENST00000361842	Transcript	missense_variant	probably_damaging(0.997)
chr17	66638766	66638766	*XAF1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q126L	ENSG00000132530	ENST00000361842	Transcript	missense_variant	benign(0.258)
chr17	67226668	67226668	*TEKT1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.L67H	ENSG00000167858	ENST00000338694	Transcript	missense_variant	probably_damaging(0.989)
chr17	75784555	75784555	*TP53*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P119	p.A159P	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.991)
chr17	76816055	76816055	*DNAH2*	Missense_Mutation	.	SNP	A	A	T	rs374078452	shanshan_et_al_P119	p.M1787L	ENSG00000183914	ENST00000572933	Transcript	missense_variant	benign(0.199)
chr17	80154655	80154655	*ALOXE3*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K376*	ENSG00000179148	ENST00000318227	Transcript	stop_gained	NA
chr18	12122314	12122314	*ANKRD62*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L418Q	ENSG00000181626	ENST00000587848	Transcript	missense_variant	possibly_damaging(0.902)
chr18	20596798	20596798	*RBBP8*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S789C	ENSG00000101773	ENST00000399722	Transcript	missense_variant	possibly_damaging(0.619)
chr18	70092339	70092339	*LAMA1*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.R1334*	ENSG00000101680	ENST00000389658	Transcript	stop_gained	NA
chr19	14910228	14910228	*OR7C1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.C241S	ENSG00000127530	ENST00000248073	Transcript	missense_variant	probably_damaging(1)
chr19	16855259	16855259	*NWD1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.C76S	ENSG00000188039	ENST00000524140	Transcript	missense_variant	possibly_damaging(0.738)
chr19	23328191	23328191	*ZNF730*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K115N	ENSG00000183850	ENST00000597761	Transcript	missense_variant	probably_damaging(0.952)
chr19	30017525	30017525	*VSTM2B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Y12F	ENSG00000187135	ENST00000335523	Transcript	missense_variant	benign(0.153)
chr19	33355184	33355184	*SLC7A9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Y99F	ENSG00000021488	ENST00000230624	Transcript	missense_variant	probably_damaging(1)
chr19	38318100	38318100	*ZFR2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q149L	ENSG00000105278	ENST00000262961	Transcript	missense_variant	benign(0.001)
chr19	38689034	38689034	*SIPA1L3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I1616F	ENSG00000105738	ENST00000222345	Transcript	missense_variant	benign(0.208)
chr19	39976413	39976413	*TIMM50*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E256V	ENSG00000105197	ENST00000314349	Transcript	missense_variant	probably_damaging(0.999)
chr19	45315801	45315801	*BCAM*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q167L	ENSG00000187244	ENST00000270233	Transcript	missense_variant	possibly_damaging(0.707)
chr19	50154500	50154500	*SCAF1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P119	p.E285A	ENSG00000126461	ENST00000360565	Transcript	missense_variant	unknown(0)
chr19	51526433	51526433	*KLK11*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q204L	ENSG00000167757	ENST00000594768	Transcript	missense_variant	benign(0.068)
chr19	52034690	52034690	*SIGLEC6*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.C51S	ENSG00000105492	ENST00000425629	Transcript	missense_variant	probably_damaging(0.994)
chr19	53208806	53208806	*ZNF611*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K501M	ENSG00000213020	ENST00000543227	Transcript	missense_variant	possibly_damaging(0.907)
chr19	55237662	55237662	*KIR3DL3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Y72N	ENSG00000242019	ENST00000291860	Transcript	missense_variant	possibly_damaging(0.449)
chr19	56329362	56329362	*NLRP11*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Y60F	ENSG00000179873	ENST00000443188	Transcript	missense_variant	probably_damaging(0.998)
chr19	58118585	58118585	*ZNF530*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q564H	ENSG00000183647	ENST00000332854	Transcript	missense_variant	benign(0.346)
chr2	105961828	105961828	*C2orf49*	Nonstop_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P119	p.*233Cext*11	ENSG00000135974	ENST00000258457	Transcript	stop_lost	NA
chr2	113780356	113780356	*IL36B*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X131_splice	ENSG00000136696	ENST00000259213	Transcript	splice_acceptor_variant	NA

chr2	11767202	11767202	GREB1	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q1474L	ENSG00000196208	ENST00000381486	Transcript	missense_variant	benign(0.258)
chr2	120438997	120438997	TMEM177	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T190S	ENSG00000144120	ENST00000424086	Transcript	missense_variant	benign(0.01)
chr2	120640187	120640187	PTPN4	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H192L	ENSG00000088179	ENST00000263708	Transcript	missense_variant	probably_damaging(0.999)
chr2	128855116	128855116	UGGT1	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T58S	ENSG00000136731	ENST00000259253	Transcript	missense_variant	benign(0.031)
chr2	141143540	141143540	LRP1B	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.N3485Y	ENSG00000168702	ENST00000389484	Transcript	missense_variant	possibly_damaging(0.904)
chr2	165552311	165552311	COBLL1	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.T569S	ENSG00000082438	ENST00000342193	Transcript	missense_variant	benign(0.293)
chr2	166183470	166183470	SCN2A	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S709C	ENSG00000136531	ENST00000357398	Transcript	missense_variant	possibly_damaging(0.804)
chr2	166764192	166764192	TTC21B	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q855L	ENSG00000123607	ENST00000243344	Transcript	missense_variant	benign(0.206)
chr2	168103327	168103327	XIRP2	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I1809F	ENSG00000163092	ENST00000409195	Transcript	missense_variant	probably_damaging(0.962)
chr2	168105079	168105079	XIRP2	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.M2393L	ENSG00000163092	ENST00000409195	Transcript	missense_variant	benign(0.001)
chr2	175326222	175326222	GPR155	Splice_Site	.	SNP	T	T	C	novel	shanshan_et_al_P119	NA	ENSG00000163328	ENST00000395552	Transcript	splice_acceptor_variant	NA
chr2	18113513	18113513	KCNS3	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Y413F	ENSG00000170745	ENST00000403915	Transcript	missense_variant	benign(0.18)
chr2	185802969	185802969	ZNF804A	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q949L	ENSG00000170396	ENST00000302277	Transcript	missense_variant	benign(0.076)
chr2	187516707	187516707	ITGAV	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.X466_splice	ENSG00000138448	ENST00000261023	Transcript	splice_acceptor_variant	NA
chr2	188223952	188223952	CALCRL	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.Y277H	ENSG00000064989	ENST00000409998	Transcript	missense_variant	probably_damaging(0.971)
chr2	206659775	206659775	NRP2	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.E930V	ENSG00000118257	ENST00000360409	Transcript	missense_variant	possibly_damaging(0.773)
chr2	209201588	209201588	PIKFYVE	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K1516M	ENSG00000115020	ENST00000264380	Transcript	missense_variant	probably_damaging(0.933)
chr2	220348946	220348946	SPEG	Missense_Mutation	.	SNP	T	T	A	rs567855380	shanshan_et_al_P119	p.L2254Q	ENSG00000072195	ENST00000312358	Transcript	missense_variant	benign(0.013)
chr2	220353787	220353787	SPEG	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.W2721R	ENSG00000072195	ENST00000312358	Transcript	missense_variant	probably_damaging(0.998)
chr2	226447431	226447431	NYAP2	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H433L	ENSG00000144460	ENST00000272907	Transcript	missense_variant	probably_damaging(0.998)
chr2	228884824	228884824	SPHKAP	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.L249Q	ENSG00000153820	ENST00000392056	Transcript	missense_variant	benign(0.002)
chr2	237395519	237395519	IQCA1	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K225*	ENSG00000132321	ENST00000409907	Transcript	stop_gained	NA
chr2	239237565	239237565	TRAF3IP1	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.X167_splice	ENSG00000204104	ENST00000373327	Transcript	splice_acceptor_variant	NA
chr2	241700261	241700261	KIF1A	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P119	p.X756_splice	ENSG00000130294	ENST00000498729	Transcript	splice_acceptor_variant	NA
chr2	25754369	25754369	DTNB	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E325V	ENSG00000138101	ENST00000406818	Transcript	missense_variant	probably_damaging(0.95)
chr2	26667182	26667182	DRC1	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K374I	ENSG00000157856	ENST00000288710	Transcript	missense_variant	benign(0.093)
chr2	29356607	29356607	CLIP4	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.N152Y	ENSG00000115295	ENST00000320081	Transcript	missense_variant	probably_damaging(0.992)
chr2	31410672	31410672	CAPN14	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E513D	ENSG00000214711	ENST00000403897	Transcript	missense_variant	benign(0.002)
chr2	31600003	31600003	XDH	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E448V	ENSG00000158125	ENST00000379416	Transcript	missense_variant	benign(0.002)
chr2	42720536	42720536	KCNG3	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S36C	ENSG00000171126	ENST00000306078	Transcript	missense_variant	probably_damaging(0.999)
chr2	46605841	46605841	EPAS1	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K497*	ENSG00000116016	ENST00000263734	Transcript	stop_gained	NA
chr2	74135834	74135834	ACTG2	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.V97E	ENSG00000163017	ENST00000409624	Transcript	missense_variant	possibly_damaging(0.885)
chr2	80529404	80529404	LRRTM1	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q514L	ENSG00000162951	ENST00000295057	Transcript	missense_variant	probably_damaging(0.932)
chr2	90488826	90488826	MBOAT2	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.L107Q	ENSG00000143797	ENST00000305997	Transcript	missense_variant	probably_damaging(0.988)
chr2	96680389	96680389	ADAM17	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L165F	ENSG00000151694	ENST00000310823	Transcript	missense_variant	probably_damaging(0.996)
chr2	97026404	97026404	NCAPH	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.N515Y	ENSG00000121152	ENST00000240423	Transcript	missense_variant	benign(0.389)

chr20	21687214	21687214	*PAX1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.V142E	ENSG00000125813	ENST00000398485	Transcript	missense_variant	probably_damaging(0.999)
chr20	23966809	23966809	*GGTLC1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P119	p.G70R	ENSG00000149435	ENST00000335694	Transcript	missense_variant	probably_damaging(0.987)
chr20	37659445	37659445	*CENPB*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.T396S	ENSG00000125817	ENST00000379751	Transcript	missense_variant	unknown(0)
chr20	58453085	58453085	*SYCP2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K986M	ENSG00000196074	ENST00000355752	Transcript	missense_variant	benign(0.331)
chr20	62737376	62737376	*NPBWR2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.L270H	ENSG00000125522	ENST00000369768	Transcript	missense_variant	probably_damaging(0.993)
chr21	36164700	36164700	*RUNX1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q392L	ENSG00000159216	ENST00000300305	Transcript	missense_variant	benign(0.017)
chr21	43413159	43413159	*ZBTB21*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q349L	ENSG00000173276	ENST00000310826	Transcript	missense_variant	possibly_damaging(0.65)
chr21	44841919	44841919	*SIK1*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X92_splice	ENSG00000142178	ENST00000270162	Transcript	splice_acceptor_variant	NA
chr21	45774583	45774583	*TRPM2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.V73E	ENSG00000142185	ENST00000397928	Transcript	missense_variant	possibly_damaging(0.501)
chr21	46066653	46066653	*KRTAP10-11*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P119	p.C95Afs*213	ENSG00000243489	ENST00000334670	Transcript	frameshift_variant	NA
chr21	46086493	46086493	*KRTAP12-2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.L104Q	ENSG00000221864	ENST00000360770	Transcript	missense_variant	possibly_damaging(0.773)
chr22	20024365	20024365	*TANGO2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.K15I	ENSG00000183597	ENST00000327374	Transcript	missense_variant	benign(0.303)
chr22	28492398	28492398	*TTC28*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	NA	ENSG00000100154	ENST00000397906	Transcript	splice_acceptor_variant	NA
chr22	31013440	31013440	*TCN2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.V355E	ENSG00000185339	ENST00000215838	Transcript	missense_variant	possibly_damaging(0.657)
chr22	38882323	38882323	*DDX17*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P119	p.R605W	ENSG00000100201	ENST00000396821	Transcript	missense_variant	possibly_damaging(0.804)
chr3	124103755	124103755	*KALRN*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.C610S	ENSG00000160145	ENST00000240874	Transcript	missense_variant	unknown(0)
chr3	126229580	126229580	*UROC1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P119	p.P62S	ENSG00000159650	ENST00000383579	Transcript	missense_variant	benign(0.018)
chr3	127390284	127390284	*PODXL2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.I478N	ENSG00000114631	ENST00000342480	Transcript	missense_variant	probably_damaging(0.981)
chr3	128077070	128077070	*EEFSEC*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.D485V	ENSG00000132394	ENST00000254730	Transcript	missense_variant	benign(0.04)
chr3	128623244	128623244	*ACAD9*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.M349L	ENSG00000177646	ENST00000308982	Transcript	missense_variant	benign(0.113)
chr3	129769 61	129769 61	*IQSEC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.N533Y	ENSG00000144711	ENST00000273221	Transcript	missense_variant	probably_damaging(1)
chr3	132360859	132360859	*ACAD11*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q165L	ENSG00000240303	ENST00000264990	Transcript	missense_variant	benign(0.21)
chr3	138121086	138121086	*MRAS*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H201L	ENSG00000158186	ENST00000289104	Transcript	missense_variant	benign(0.001)
chr3	150911419	150911419	*MED12L*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H704L	ENSG00000144893	ENST00000474524	Transcript	missense_variant	benign(0.007)
chr3	151196 51	151196 51	*ZFYVE20*	Missense_Mutation	.	SNP	T	T	C	rs372379857	shanshan_et_al_P119	p.Y310C	ENSG00000131381	ENST00000253699	Transcript	missense_variant	probably_damaging(0.998)
chr3	155210644	155210644	*PLCH1*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X716_splice	ENSG00000114805	ENST00000340059	Transcript	splice_acceptor_variant	NA
chr3	158384162	158384162	*GFM1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T530S	ENSG00000168827	ENST00000486715	Transcript	missense_variant	benign(0.021)
chr3	158523163	158523163	*MFSD1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.N126D	ENSG00000118855	ENST00000415822	Transcript	missense_variant	benign(0.007)
chr3	168845708	168845708	*MECOM*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S128C	ENSG00000085276	ENST00000264674	Transcript	missense_variant	possibly_damaging(0.649)
chr3	185304301	185304301	*SENP2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S34C	ENSG00000163904	ENST00000296257	Transcript	missense_variant	possibly_damaging(0.759)
chr3	185990076	185990076	*DGKG*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K323*	ENSG00000058866	ENST00000265022	Transcript	stop_gained	NA
chr3	187388070	187388070	*SST*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.C4S	ENSG00000157005	ENST00000287641	Transcript	missense_variant	benign(0.005)
chr3	194407887	194407887	*FAM43A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L111Q	ENSG00000185112	ENST00000329759	Transcript	missense_variant	probably_damaging(0.999)
chr3	215524 16	215524 16	*ZNF385D*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S126C	ENSG00000151789	ENST00000281523	Transcript	missense_variant	benign(0.174)
chr3	443289 23	443289 23	*TOPAZ1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.V1160E	ENSG00000173769	ENST00000309765	Transcript	missense_variant	possibly_damaging(0.635)
chr3	448679 45	448679 45	*KIF15*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.S927C	ENSG00000163808	ENST00000326047	Transcript	missense_variant	possibly_damaging(0.838)

chr3	45965182	45965182	*FYCO1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.I1443F	ENSG00000163820	ENST00000296137	Transcript	missense_variant	possibly_damaging(0.779)
chr3	48629432	48629432	*COL7A1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.Q419L	ENSG00000114270	ENST00000328333	Transcript	missense_variant	unknown(0)
chr3	49570051	49570051	*DAG1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.T703S	ENSG00000173402	ENST00000545947	Transcript	missense_variant	benign(0.068)
chr3	52027799	52027799	*RPL29*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.K149I	ENSG00000162244	ENST00000466397	Transcript	missense_variant	probably_damaging(0.993)
chr3	52485850	52485850	*TNNC1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.E76V	ENSG00000114854	ENST00000232975	Transcript	missense_variant	probably_damaging(0.999)
chr3	53217135	53217135	*PRKCD*	Splice_Site	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.X191_splice	ENSG00000163932	ENST00000394729	Transcript	splice_acceptor_variant	NA
chr3	54661900	54661900	*CACNA2D3*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.S350R	ENSG00000157445	ENST00000474759	Transcript	missense_variant	benign(0.006)
chr3	62543149	62543149	*CADPS*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P119	p.K562E	ENSG00000163618	ENST00000383710	Transcript	missense_variant	benign(0.187)
chr3	87039772	87039772	*VGLL3*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.Q41L	ENSG00000206538	ENST00000398399	Transcript	missense_variant	possibly_damaging(0.733)
chr3	97686259	97686259	*MINA*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.E60V	ENSG00000170854	ENST00000333396	Transcript	missense_variant	probably_damaging(1)
chr4	101109222	101109222	*DDIT4L*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.L65Q	ENSG00000145358	ENST00000273990	Transcript	missense_variant	probably_damaging(1)
chr4	123246471	123246471	*KIAA1109*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.D3664V	ENSG00000138688	ENST00000264501	Transcript	missense_variant	benign(0.295)
chr4	141868808	141868808	*RNF150*	Missense_Mutation	.	SNP	C	C	T	rs200661337	shansha n_et_al_P119	p.R297Q	ENSG00000170153	ENST00000515673	Transcript	missense_variant	benign(0.162)
chr4	151773675	151773675	*LRBA*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.N1063Y	ENSG00000198589	ENST00000357115	Transcript	missense_variant	benign(0.109)
chr4	154702659	154702659	*SFRP2*	Nonsense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.K278*	ENSG00000145423	ENST00000274063	Transcript	stop_gained	NA
chr4	164394868	164394868	*TKTL2*	Nonsense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.K7*	ENSG00000151005	ENST00000280605	Transcript	stop_gained	NA
chr4	187510324	187510324	*FAT1*	Missense_Mutation	.	SNP	T	T	A	rs535317218	shansha n_et_al_P119	p.I4397L	ENSG00000083857	ENST00000441802	Transcript	missense_variant	probably_damaging(0.992)
chr4	256777 61	256777 61	*SLC34A2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P119	p.A488V	ENSG00000157765	ENST00000382051	Transcript	missense_variant	probably_damaging(0.992)
chr4	392555 64	392555 64	*WDR19*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.Q972L	ENSG00000157796	ENST00000399820	Transcript	missense_variant	possibly_damaging(0.726)
chr4	421221 36	421221 36	*BEND4*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.V441E	ENSG00000188848	ENST00000502486	Transcript	missense_variant	probably_damaging(0.988)
chr4	425928 67	425928 67	*ATP8A1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P119	p.G162E	ENSG00000124406	ENST00000381668	Transcript	missense_variant	benign(0.081)
chr4	638272 5	638272 5	*PPP2R2C*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.E56V	ENSG00000074211	ENST00000335585	Transcript	missense_variant	benign(0.013)
chr4	74276073	74276073	*ALB*	Frame_Shift_Del	.	DEL	AG	AG	-	novel	shansha n_et_al_P119	p.R221Tfs*30	ENSG00000163631	ENST00000295897	Transcript	frameshift_variant	NA
chr4	84191035	84191035	*COQ2*	Missense_Mutation	.	SNP	T	T	A	rs121918230	shansha n_et_al_P119	p.Y297F	ENSG00000173085	ENST00000311469	Transcript	missense_variant	possibly_damaging(0.873)
chr4	89199642	89199642	*PPM1K*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.R32W	ENSG00000163644	ENST00000608933	Transcript	missense_variant	possibly_damaging(0.604)
chr5	126738327	126738327	*MEGF10*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.D290E	ENSG00000145794	ENST00000274473	Transcript	missense_variant	benign(0.015)
chr5	140482146	140482146	*PCDHB3*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.H638L	ENSG00000113205	ENST00000231130	Transcript	missense_variant	benign(0.287)
chr5	141041681	141041681	*ARAP3*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.K981I	ENSG00000120318	ENST00000239440	Transcript	missense_variant	probably_damaging(1)
chr5	141244731	141244731	*PCDH1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.I389F	ENSG00000156453	ENST00000287008	Transcript	missense_variant	probably_damaging(0.999)
chr5	153855379	153855379	*HAND1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.E212V	ENSG00000113196	ENST00000231121	Transcript	missense_variant	probably_damaging(0.973)
chr5	156753269	156753269	*CYFIP2*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P119	p.E665D	ENSG00000055163	ENST00000521420	Transcript	missense_variant	probably_damaging(1)
chr5	171523540	171523540	*STK10*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.S299C	ENSG00000072786	ENST00000176763	Transcript	missense_variant	possibly_damaging(0.563)
chr5	178139478	178139478	*ZNF354A*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.K467N	ENSG00000169131	ENST00000335815	Transcript	missense_variant	probably_damaging(0.99)
chr5	35010157	35010157	*AGXT2*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P119	p.G429A	ENSG00000113492	ENST00000231420	Transcript	missense_variant	probably_damaging(1)
chr5	37815958	37815958	*GDNF*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P119	p.Y161F	ENSG00000168621	ENST00000427982	Transcript	missense_variant	probably_damaging(0.993)
chr5	39130690	39130690	*FYB*	Splice_Site	.	SNP	A	A	T	rs201476585	shansha n_et_al_P119	p.X624_splice	ENSG00000082074	ENST00000540520	Transcript	splice_donor_variant	NA

chr5	72853467	72853467	*ANKRA2*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X150_splice	ENSG00000164331	ENST00000296785	Transcript	splice_acceptor_variant	NA
chr6	106634428	106634428	*ATG5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q272L	ENSG00000057663	ENST00000369076	Transcript	missense_variant	benign(0.001)
chr6	109935621	109935621	*AK9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.M488L	ENSG00000155085	ENST00000424296	Transcript	missense_variant	benign(0.001)
chr6	117662737	117662737	*ROS1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P119	p.I1576M	ENSG00000047936	ENST00000368508	Transcript	missense_variant	possibly_damaging(0.739)
chr6	125569430	125569430	*TPD52L1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P119	p.Y96S	ENSG00000111907	ENST00000534000	Transcript	missense_variant	probably_damaging(0.997)
chr6	137519389	137519389	*IFNGR1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S417C	ENSG00000027697	ENST00000367739	Transcript	missense_variant	possibly_damaging(0.808)
chr6	138576598	138576598	*KIAA1244*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P119	p.V266L	ENSG00000112379	ENST00000251691	Transcript	missense_variant	benign(0.177)
chr6	138628511	138628511	*KIAA1244*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Y1317F	ENSG00000112379	ENST00000251691	Transcript	missense_variant	probably_damaging(0.963)
chr6	149833385	149833385	*PPIL4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.H378L	ENSG00000131013	ENST00000253329	Transcript	missense_variant	benign(0.205)
chr6	165712993	165712993	*C6orf118*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	NA	ENSG00000112539	ENST00000230301	Transcript	splice_acceptor_variant	NA
chr6	30671957	30671957	*MDC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q1668L	ENSG00000137337	ENST00000376406	Transcript	missense_variant	benign(0.085)
chr6	49962155	49962155	*RPP40*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E288V	ENSG00000124787	ENST00000380051	Transcript	missense_variant	possibly_damaging(0.772)
chr6	49976862	49976862	*DEFB110*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.C60R	ENSG00000203970	ENST00000396630	Transcript	missense_variant	probably_damaging(0.955)
chr6	73902359	73902359	*KCNQ5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H613L	ENSG00000185760	ENST00000342056	Transcript	missense_variant	benign(0)
chr6	75743177	75743177	*DSP*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.X711_splice	ENSG00000096696	ENST00000379802	Transcript	splice_acceptor_variant	NA
chr6	82935195	82935195	*IBTK*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q275L	ENSG00000005700	ENST00000306270	Transcript	missense_variant	benign(0.063)
chr6	84859375	84859375	*KIAA1009*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.H1226L	ENSG00000135315	ENST00000403245	Transcript	missense_variant	probably_damaging(0.999)
chr7	127544860	127544860	*SND1*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P119	p.D506Ifs*164	ENSG00000197157	ENST00000354725	Transcript	frameshift_variant	NA
chr7	130368449	130368449	*TSGA13*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P119	p.V29Lfs*18	ENSG00000213265	ENST00000456951	Transcript	frameshift_variant	NA
chr7	141450153	141450153	*SSBP1*	Nonstop_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.*149Lext*3	ENSG00000106028	ENST00000481508	Transcript	stop_lost	NA
chr7	157903543	157903543	*PTPRN2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S541C	ENSG00000155093	ENST00000389418	Transcript	missense_variant	possibly_damaging(0.756)
chr7	20418782	20418782	*ITGB8*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L166*	ENSG00000105855	ENST00000222573	Transcript	stop_gained	NA
chr7	45123806	45123806	*NACAD*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K658M	ENSG00000136274	ENST00000490531	Transcript	missense_variant	benign(0.19)
chr7	47967933	47967933	*FOXK1*	Missense_Mutation	.	SNP	A	A	T	rs199578801	shanshan_et_al_P119	p.T407S	ENSG00000164916	ENST00000328914	Transcript	missense_variant	benign(0.424)
chr7	56142414	56142414	*SUMF2*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P119	p.R193*	ENSG00000129103	ENST00000342190	Transcript	stop_gained	NA
chr7	72873940	72873940	*BAZ1B*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.R1120*	ENSG00000009954	ENST00000339594	Transcript	stop_gained	NA
chr7	76228600	76228600	*MIOS*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.K502R	ENSG00000164654	ENST00000340080	Transcript	missense_variant	benign(0.005)
chr7	82545753	82545753	*PCLO*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q3850L	ENSG00000186472	ENST00000333891	Transcript	missense_variant	unknown(0)
chr7	97493810	97493810	*ASNS*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X84_splice	ENSG00000070669	ENST00000175506	Transcript	splice_acceptor_variant	NA
chr7	99631564	99631564	*ZKSCAN1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.H479L	ENSG00000106261	ENST00000324306	Transcript	missense_variant	probably_damaging(0.999)
chr8	100836129	100836129	*VPS13B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T3110S	ENSG00000132549	ENST00000358544	Transcript	missense_variant	benign(0.292)
chr8	11687801	11687801	*FDFT1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.N251Y	ENSG00000079459	ENST00000220584	Transcript	missense_variant	probably_damaging(0.956)
chr8	139164223	139164223	*FAM135B*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P119	p.I832T	ENSG00000147724	ENST00000395297	Transcript	missense_variant	benign(0)
chr8	145439602	145439602	*FAM203B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q371L	ENSG00000230567	ENST00000377406	Transcript	missense_variant	benign(0.003)
chr8	20107310	20107310	*LZTS1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S572C	ENSG00000061337	ENST00000381569	Transcript	missense_variant	benign(0.155)
chr8	37696501	37696501	*GPR124*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P119	p.G763R	ENSG00000020181	ENST00000412232	Transcript	missense_variant	benign(0.005)

chr8	77745615	77745615	*ZFHX4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T1123S	ENSG00000091656	ENST00000521891	Transcript	missense_variant	benign(0.006)
chr8	80950452	80950452	*TPD52*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K192*	ENSG00000076554	ENST00000379097	Transcript	stop_gained	NA
chr8	90995053	90995053	*NBN*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E23V	ENSG00000104320	ENST00000265433	Transcript	missense_variant	possibly_damaging(0.905)
chr9	101814676	101814676	*COL15A1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T971S	ENSG00000204291	ENST00000375001	Transcript	missense_variant	benign(0.004)
chr9	113538138	113538138	*MUSK*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.R419*	ENSG00000030304	ENST00000374448	Transcript	stop_gained	NA
chr9	130477837	130477837	*PTRH1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P119	p.G28W	ENSG00000187024	ENST00000419060	Transcript	missense_variant	probably_damaging(0.998)
chr9	135772727	135772727	*TSC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Q940L	ENSG00000165699	ENST00000298552	Transcript	missense_variant	possibly_damaging(0.87)
chr9	135864542	135864542	*GFI1B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P119	p.G202D	ENSG00000165702	ENST00000339463	Transcript	missense_variant	probably_damaging(0.976)
chr9	26996313	26996313	*LRRC19*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.N260K	ENSG00000184434	ENST00000380055	Transcript	missense_variant	benign(0.019)
chr9	38596345	38596345	*ANKRD18A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K331M	ENSG00000180071	ENST00000399703	Transcript	missense_variant	probably_damaging(0.926)
chr9	98669432	98669432	*ERCC6L2*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.R234*	ENSG00000182150	ENST00000288985	Transcript	stop_gained	NA
chrX	100809225	100809225	*ARMCX1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P119	p.N438H	ENSG00000126947	ENST00000372829	Transcript	missense_variant	benign(0.003)
chrX	10180535	10180535	*CLCN4*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P119	p.M473Ifs*24	ENSG00000073464	ENST00000380833	Transcript	frameshift_variant	NA
chrX	108906543	108906543	*ACSL4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E534D	ENSG00000068366	ENST00000340800	Transcript	missense_variant	benign(0.086)
chrX	118222291	118222291	*KIAA1210*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K968*	ENSG00000250423	ENST00000402510	Transcript	stop_gained	NA
chrX	118223259	118223259	*KIAA1210*	Missense_Mutation	.	SNP	A	A	T	rs182751561	shanshan_et_al_P119	p.M645K	ENSG00000250423	ENST00000402510	Transcript	missense_variant	possibly_damaging(0.849)
chrX	129354456	129354456	*ZNF280C*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	NA	ENSG00000056277	ENST00000370978	Transcript	splice_acceptor_variant	NA
chrX	133119345	133119345	*GPC3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.R44S	ENSG00000147257	ENST00000394299	Transcript	missense_variant	possibly_damaging(0.507)
chrX	135126797	135126797	*SLC9A6*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.I674F	ENSG00000198689	ENST00000370695	Transcript	missense_variant	possibly_damaging(0.517)
chrX	135431670	135431670	*GPR112*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P119	p.A1936Qfs*26	ENSG00000156920	ENST00000394143	Transcript	frameshift_variant	NA
chrX	13621529	13621529	*EGFL6*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L165Q	ENSG00000198759	ENST00000380602	Transcript	missense_variant	probably_damaging(1)
chrX	138667339	138667339	*MCF2*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X954_splice	ENSG00000101977	ENST00000519895	Transcript	splice_acceptor_variant	NA
chrX	152770193	152770193	*BGN*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.M35K	ENSG00000182492	ENST00000331595	Transcript	missense_variant	benign(0.085)
chrX	47272277	47272277	*ZNF157*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.T269S	ENSG00000147117	ENST00000377073	Transcript	missense_variant	probably_damaging(0.985)
chrX	47426129	47426129	*ARAF*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.N217Y	ENSG00000078061	ENST00000377045	Transcript	missense_variant	possibly_damaging(0.713)
chrX	50378391	50378391	*SHROOM4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.S228C	ENSG00000158352	ENST00000376020	Transcript	missense_variant	benign(0.009)
chrX	54048758	54048758	*PHF8*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.K112M	ENSG00000172943	ENST00000357988	Transcript	missense_variant	benign(0.219)
chrX	65409598	65409598	*HEPH*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.L348*	ENSG00000089472	ENST00000519389	Transcript	stop_gained	NA
chrX	65413410	65413410	*HEPH*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.Y487*	ENSG00000089472	ENST00000519389	Transcript	stop_gained	NA
chrX	70331299	70331299	*IL2RG*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.N31Y	ENSG00000147168	ENST00000374202	Transcript	missense_variant	possibly_damaging(0.564)
chrX	70361081	70361081	*MED12*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P119	p.Q2090L	ENSG00000184634	ENST00000374080	Transcript	missense_variant	unknown(0)
chrX	71522096	71522096	*CITED1*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.X21_splice	ENSG00000125931	ENST00000246139	Transcript	splice_acceptor_variant	NA
chrY	21883052	21883052	*KDM5D*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P119	p.E506V	ENSG00000012817	ENST00000317961	Transcript	missense_variant	probably_damaging(0.996)
chr1	156177730	156177730	*SLC25A44*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P121	p.V227L	ENSG00000160785	ENST00000359511	Transcript	missense_variant	benign(0.006)
chr1	156202181	156202181	*PMF1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P121	p.D78N	ENSG00000160783	ENST00000567140	Transcript	missense_variant	possibly_damaging(0.481)
chr1	204588236	204588236	*LRRN2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P121	p.M295I	ENSG00000170382	ENST00000367175	Transcript	missense_variant	probably_damaging(0.991)

chr10	37508335	37508335	*ANKRD30A*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P121	p.Q1176R	ENSG00000148513	ENST00000361713	Transcript	missense_variant	benign(0.403)
chr10	71154858	71154858	*HK1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P121	p.E795V	ENSG00000156515	ENST00000404387	Transcript	missense_variant	probably_damaging(0.975)
chr11	4790976	4790976	*OR51F1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P121	p.H58N	ENSG00000188069	ENST00000343430	Transcript	missense_variant	possibly_damaging(0.753)
chr11	60073583	60073583	*MS4A4A*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P121	p.G186A	ENSG00000110079	ENST00000337908	Transcript	missense_variant	benign(0.04)
chr12	112227632	112227632	*ALDH2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P121	p.Y149C	ENSG00000111275	ENST00000261733	Transcript	missense_variant	probably_damaging(0.966)
chr12	130921814	130921814	*RIMBP2*	Missense_Mutation	.	SNP	G	G	A	rs530744461	shanshan_et_al_P121	p.T543M	ENSG00000060709	ENST00000261655	Transcript	missense_variant	benign(0.013)
chr12	53186577	53186577	*KRT3*	Missense_Mutation	.	SNP	G	G	T	rs199614200	shanshan_et_al_P121	p.A314D	ENSG00000186442	ENST00000417996	Transcript	missense_variant	probably_damaging(0.975)
chr12	60169172	60169172	*SLC16A7*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P121	p.V366M	ENSG00000118596	ENST00000261187	Transcript	missense_variant	probably_damaging(1)
chr16	19722744	19722744	*KNOP1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P121	p.E313Q	ENSG00000103550	ENST00000219837	Transcript	missense_variant	probably_damaging(0.996)
chr16	70590870	70590870	*SF3B3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P121	p.K650E	ENSG00000189091	ENST00000302516	Transcript	missense_variant	benign(0.001)
chr17	65144710	65144710	*HELZ*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P121	p.Y866N	ENSG00000198265	ENST00000358691	Transcript	missense_variant	probably_damaging(1)
chr17	7578440	7578440	*TP53*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P121	p.K164*	ENSG00000141510	ENST00000269305	Transcript	stop_gained	NA
chr17	9615381	9615381	*USP43*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P121	p.P756R	ENSG00000154914	ENST00000285199	Transcript	missense_variant	benign(0.05)
chr19	13006842	13006842	*GCDH*	Missense_Mutation	.	SNP	A	A	C	rs398123194	shanshan_et_al_P121	p.E181A	ENSG00000105607	ENST00000222214	Transcript	missense_variant	probably_damaging(1)
chr19	49963051	49963051	*ALDH16A1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P121	p.H149N	ENSG00000161618	ENST00000293350	Transcript	missense_variant	possibly_damaging(0.845)
chr2	189434045	189434045	*GULP1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P121	p.V160A	ENSG00000144366	ENST00000409580	Transcript	missense_variant	probably_damaging(0.99)
chr2	232325429	232325429	*NCL*	Missense_Mutation	.	SNP	t	t	A	rs144444417	shanshan_et_al_P121	p.E254D	ENSG00000115053	ENST00000322723	Transcript	missense_variant	benign(0.004)
chr21	45877031	45877031	*LRRC3*	Missense_Mutation	.	SNP	C	C	G	rs145333607	shanshan_et_al_P121	p.D168E	ENSG00000160233	ENST00000291592	Transcript	missense_variant	benign(0.018)
chr22	32233080	32233080	*DEPDC5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P121	p.G756C	ENSG00000100150	ENST00000382112	Transcript	missense_variant	benign(0.443)
chr22	38119988	38119988	*TRIOBP*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P121	p.D475E	ENSG00000100106	ENST00000406386	Transcript	missense_variant	benign(0)
chr3	42305116	42305116	*CCK*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P121	p.S3G	ENSG00000187094	ENST00000396169	Transcript	missense_variant	benign(0.003)
chr3	57131806	57131806	*IL17RD*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P121	p.A642D	ENSG00000144730	ENST00000296318	Transcript	missense_variant	benign(0.031)
chr4	37831635	37831635	*PGM2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P121	p.K44T	ENSG00000169299	ENST00000381967	Transcript	missense_variant	benign(0)
chr5	136964010	136964010	*KLHL3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P121	p.M523V	ENSG00000146021	ENST00000309755	Transcript	missense_variant	benign(0.352)
chr5	169535349	169535349	*FOXI1*	Missense_Mutation	.	SNP	G	G	A	rs148265639	shanshan_et_al_P121	p.G291R	ENSG00000168269	ENST00000306268	Transcript	missense_variant	possibly_damaging(0.816)
chr6	132201090	132201092	*ENPP1*	In_Frame_Del	.	DEL	TCT	TCT	-	novel	shanshan_et_al_P121	p.L674del	ENSG00000197594	ENST00000360971	Transcript	inframe_deletion	NA
chr6	24843737	24843737	*FAM65B*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P121	p.E425*	ENSG00000111913	ENST00000259698	Transcript	stop_gained	NA
chr6	46135309	46135309	*ENPP5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P121	p.L231M	ENSG00000112796	ENST00000371383	Transcript	missense_variant	benign(0.071)
chr8	106815608	106815608	*ZFPM2*	Missense_Mutation	.	SNP	C	C	G	rs199678497	shanshan_et_al_P121	p.Q1100E	ENSG00000169946	ENST00000407775	Transcript	missense_variant	benign(0.304)
chr8	130789776	130789776	*GSDMC*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P121	p.D20Y	ENSG00000147697	ENST00000276708	Transcript	missense_variant	probably_damaging(0.997)
chr9	113166647	113166647	*SVEP1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P121	p.E3209G	ENSG00000165124	ENST00000401783	Transcript	missense_variant	possibly_damaging(0.861)
chrX	142967292	142967292	*UBE2NL*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P121	p.S30R	ENSG00000102069	ENST00000370494	Transcript	missense_variant	benign(0.021)
chr1	100155038	100155041	*PALMD*	Frame_Shift_Del	.	DEL	AATG	AATG	-	novel	shanshan_et_al_P123	p.N408Ifs*5	ENSG00000099260	ENST00000263174	Transcript	frameshift_variant	NA
chr1	110022069	110022069	*SYPL2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.H240Y	ENSG00000143028	ENST00000369872	Transcript	missense_variant	benign(0.001)
chr1	160326909	160326909	*NCSTN*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P123	p.A625S	ENSG00000162736	ENST00000294785	Transcript	missense_variant	benign(0.028)
chr1	19981627	19981627	*NBL1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.C70Y	ENSG00000158747	ENST00000289749	Transcript	missense_variant	probably_damaging(0.996)

chr1	6314094	6314094	*GPR153*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P123	p.Y157C	ENSG00000158292	ENST00000378933	Transcript	missense_variant	probably_damaging(1)
chr1	78433858	78433858	*FUBP1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P123	p.Q81E	ENSG00000162613	ENST00000370768	Transcript	missense_variant	benign(0.061)
chr10	102048164	102048164	*PKD2L1*	Missense_Mutation	.	SNP	G	G	T	rs199789744	shanshan_et_al_P123	p.Q803K	ENSG00000107593	ENST00000318222	Transcript	missense_variant	benign(0.042)
chr10	115981204	115981204	*TDRD1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.N953K	ENSG00000095627	ENST00000251864	Transcript	missense_variant	probably_damaging(0.969)
chr10	135085055	135085055	*ADAM8*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.Q421*	ENSG00000151651	ENST00000445355	Transcript	stop_gained	NA
chr10	30918597	30918597	*LYZL2*	Missense_Mutation	.	SNP	T	T	C	rs74551644	shanshan_et_al_P123	p.K13R	ENSG00000151033	ENST00000375318	Transcript	missense_variant	benign(0.007)
chr11	123994485	123994485	*VWA5A*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.P380A	ENSG00000110002	ENST00000456829	Transcript	missense_variant	benign(0.393)
chr11	32118719	32118719	*RCN1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P123	p.G95A	ENSG00000049449	ENST00000054950	Transcript	missense_variant	benign(0.033)
chr11	4608632	4608632	*OR52I2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P123	p.P197H	ENSG00000226288	ENST00000312614	Transcript	missense_variant	probably_damaging(0.996)
chr11	57993345	57993345	*OR52N5*	Missense_Mutation	.	SNP	G	G	A	rs563908927	shanshan_et_al_P123	p.R174C	ENSG00000181009	ENST00000317093	Transcript	missense_variant	benign(0.052)
chr11	67401704	67401704	*TBX10*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.D169H	ENSG00000167800	ENST00000335385	Transcript	missense_variant	probably_damaging(0.975)
chr11	687999	687999	*DEAF1*	Nonsense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P123	p.Y192*	ENSG00000177030	ENST00000382409	Transcript	stop_gained	NA
chr11	77594962	77594962	*INTS4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.P877S	ENSG00000149262	ENST00000534064	Transcript	missense_variant	possibly_damaging(0.743)
chr12	109182506	109182506	*SSH1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P123	p.N803S	ENSG00000084112	ENST00000326495	Transcript	missense_variant	benign(0.003)
chr12	15262150	15262150	*RERG*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.R165Q	ENSG00000134533	ENST00000256953	Transcript	missense_variant	possibly_damaging(0.778)
chr12	56568456	56568456	*SMARCC2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.G492D	ENSG00000139613	ENST00000267064	Transcript	missense_variant	probably_damaging(0.982)
chr12	62929421	62929421	*MON2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.G611D	ENSG00000061987	ENST00000393632	Transcript	missense_variant	benign(0.242)
chr13	46099156	46099156	*COG3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P123	p.T734A	ENSG00000136152	ENST00000349995	Transcript	missense_variant	benign(0.02)
chr14	95669906	95669906	*CLMN*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.D594N	ENSG00000165959	ENST00000298912	Transcript	missense_variant	benign(0.01)
chr14	96768405	96768405	*ATG2B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.R1693K	ENSG00000066739	ENST00000359933	Transcript	missense_variant	possibly_damaging(0.838)
chr15	45386807	45386807	*DUOX2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P123	p.P1493R	ENSG00000140279	ENST00000603300	Transcript	missense_variant	probably_damaging(1)
chr16	86601102	86601102	*FOXC2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.R54H	ENSG00000176692	ENST00000320354	Transcript	missense_variant	probably_damaging(0.991)
chr16	89016665	89016665	*RP11-830F9.6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.V47I	ENSG00000205018	ENST00000378347	Transcript	missense_variant	benign(0.205)
chr17	18075575	18075575	*MYO15A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P123	p.G3441C	ENSG00000091536	ENST00000205890	Transcript	missense_variant	unknown()
chr17	38079462	38079462	*ORMDL3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P123	p.Q77E	ENSG00000172057	ENST00000394169	Transcript	missense_variant	possibly_damaging(0.791)
chr17	39777943	39777943	*KRT17*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.G246S	ENSG00000128422	ENST00000311208	Transcript	missense_variant	possibly_damaging(0.859)
chr17	61621609	61621609	*KCNH6*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.X781_splice	ENSG00000173826	ENST00000583023	Transcript	splice_acceptor_variant	NA
chr17	7573976	7573976	*TP53*	Missense_Mutation	.	SNP	T	T	C	rs141402957	shanshan_et_al_P123	p.K351E	ENSG00000141510	ENST00000269305	Transcript	missense_variant	possibly_damaging(0.734)
chr18	14772192	14772192	*ANKRD30B*	Missense_Mutation	.	SNP	A	A	G	rs369533372	shanshan_et_al_P123	p.T432A	ENSG00000180777	ENST00000358984	Transcript	missense_variant	benign(0.136)
chr19	19762593	19762593	*ATP13A1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.T747M	ENSG00000105726	ENST00000357324	Transcript	missense_variant	probably_damaging(1)
chr19	41269577	41269577	*SNRPA*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P123	p.N229S	ENSG00000077312	ENST00000243563	Transcript	missense_variant	benign(0.152)
chr19	41509955	41509955	*CYP2B6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P123	p.P74H	ENSG00000197408	ENST00000324071	Transcript	missense_variant	probably_damaging(0.978)
chr19	49392831	49392831	*TULP2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.P191L	ENSG00000104804	ENST00000221399	Transcript	missense_variant	benign(0.025)
chr2	135884178	135884178	*RAB3GAP1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.H309D	ENSG00000115839	ENST00000442034	Transcript	missense_variant	benign(0.028)
chr2	196689151	196689151	*DNAH7*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.G3040A	ENSG00000118997	ENST00000312428	Transcript	missense_variant	benign(0.443)
chr2	234681191	234681191	*UGT1A6*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P123	NA	ENSG00000167165	ENST00000305139	Transcript	frameshift_variant	NA

chr21	35468920	35468920	*SLCSA3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P123	p.M475V	ENSG00000272962	ENST00000608209	Transcript	missense_variant	benign(0.002)
chr22	18300641	18300641	*MICAL3*	Missense_Mutation	.	SNP	G	G	A	rs199559753	shanshan_et_al_P123	p.R1596C	ENSG00000243156	ENST00000441493	Transcript	missense_variant	probably_damaging(0.997)
chr22	18371802	18371802	*MICAL3*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.S630T	ENSG00000243156	ENST00000441493	Transcript	missense_variant	benign(0.001)
chr22	40760365	40760365	*ADSL*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.R396H	ENSG00000239900	ENST00000216194	Transcript	missense_variant	possibly_damaging(0.669)
chr22	46611071	46611071	*PPARA*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P123	p.D70E	ENSG00000186951	ENST00000396000	Transcript	missense_variant	benign(0.002)
chr3	147096037	147096038	*CCDC174*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P123	p.M304Dfs*14	ENSG00000154781	ENST00000383794	Transcript	frameshift_variant	NA
chr3	156867308	156867308	*CCNL1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.D367H	ENSG00000163660	ENST00000295926	Transcript	missense_variant	possibly_damaging(0.501)
chr3	172070600	172070600	*FNDC3B*	Missense_Mutation	.	SNP	A	A	G	rs117207991	shanshan_et_al_P123	p.N841S	ENSG00000075420	ENST00000336824	Transcript	missense_variant	probably_damaging(0.984)
chr3	38156521	38156521	*DLEC1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.R1278H	ENSG00000008226	ENST00000308059	Transcript	missense_variant	possibly_damaging(0.602)
chr3	49765618	49765618	*IP6K1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.S237L	ENSG00000176095	ENST00000321599	Transcript	missense_variant	probably_damaging(0.999)
chr3	52547244	52547244	*STAB1*	Missense_Mutation	.	SNP	G	G	A	rs373744584	shanshan_et_al_P123	p.R1086H	ENSG00000010327	ENST00000321725	Transcript	missense_variant	benign(0.009)
chr3	74411186	74411186	*CNTN3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P123	p.A407S	ENSG00000113805	ENST00000263665	Transcript	missense_variant	possibly_damaging(0.762)
chr4	100273815	100273815	*ADH1C*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P123	p.V7*	ENSG00000248144	ENST00000515683	Transcript	frameshift_variant	NA
chr4	23816006	23816006	*PPARGC1A*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.G367A	ENSG00000109819	ENST00000264867	Transcript	missense_variant	benign(0.387)
chr4	52895026	52895026	*SGCB*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.S164N	ENSG00000163069	ENST00000381431	Transcript	missense_variant	benign(0.194)
chr4	54186088	54186088	*STK32B*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P123	p.V170A	ENSG00000152953	ENST00000282908	Transcript	missense_variant	benign(0.332)
chr4	56337503	56337503	*EVC2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.E494Q	ENSG00000173040	ENST00000344408	Transcript	missense_variant	benign(0.372)
chr4	73935213	73935213	*COX18*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P123	p.N52D	ENSG00000163626	ENST00000295890	Transcript	missense_variant	benign(0.002)
chr4	92460401	92460401	*USP17L17*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P123	p.S146*	ENSG00000249104	ENST00000511568	Transcript	stop_gained	NA
chr5	70754420	70754420	*BDP1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.G76D	ENSG00000145734	ENST00000358731	Transcript	missense_variant	benign(0.009)
chr6	12813503	12813503	*THEMIS*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P123	p.E251G	ENSG00000172673	ENST00000543064	Transcript	missense_variant	probably_damaging(0.999)
chr6	69666596	69666596	*BAI3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.G474S	ENSG00000135298	ENST00000370598	Transcript	missense_variant	probably_damaging(1)
chr6	90660516	90660516	*BACH2*	Missense_Mutation	.	SNP	C	C	T	rs147349828	shanshan_et_al_P123	p.A437T	ENSG00000112182	ENST00000257749	Transcript	missense_variant	benign(0.003)
chr7	100490833	100490833	*ACHE*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.D341H	ENSG00000087085	ENST00000302913	Transcript	missense_variant	probably_damaging(0.98)
chr7	103969292	103969306	*LHFPL3*	In_Frame_Del	.	DEL	CCAAGCTGTACCACA	CCAAGCTGTACCACA	-	novel	shanshan_et_al_P123	p.K23_T27del	ENSG00000187416	ENST00000535008	Transcript	inframe_deletion	NA
chr8	116599439	116599439	*TRPS1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P123	p.V830G	ENSG00000104447	ENST00000395715	Transcript	missense_variant	benign(0.007)
chr8	27905024	27905024	*NUGGC*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P123	p.E438*	ENSG00000189233	ENST00000413272	Transcript	stop_gained	NA
chr8	57079730	57079730	*PLAG1*	Missense_Mutation	.	SNP	C	C	T	rs367971972	shanshan_et_al_P123	p.R192H	ENSG00000181690	ENST00000316981	Transcript	missense_variant	probably_damaging(0.991)
chr9	103271385	103271385	*TMEFF1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P123	p.I135M	ENSG00000241697	ENST00000374879	Transcript	missense_variant	benign(0.351)
chr9	13176348	13176348	*MPDZ*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P123	p.Q906H	ENSG00000107186	ENST00000541718	Transcript	missense_variant	possibly_damaging(0.693)
chr9	86421324	86421324	*GKAP1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P123	p.R37*	ENSG00000165113	ENST00000376371	Transcript	stop_gained	NA
chrX	107381045	107381045	*ATG4A*	Missense_Mutation	.	SNP	C	C	T	rs140831275	shanshan_et_al_P123	p.R187C	ENSG00000101844	ENST00000372232	Transcript	missense_variant	benign(0)
chrX	32410277	32410277	*MXRA5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P123	p.S900Y	ENSG00000101825	ENST00000217939	Transcript	missense_variant	benign(0.254)
chrX	71753811	71753811	*STS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P123	p.T84I	ENSG00000101846	ENST00000217961	Transcript	missense_variant	probably_damaging(1)
chr1	19491299	19491299	*UBR4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P125	p.E1502V	ENSG00000127481	ENST00000375254	Transcript	missense_variant	benign(0.432)
chr1	205273506	205273506	*NUAK2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P125	p.G320V	ENSG00000163545	ENST00000367157	Transcript	missense_variant	benign(0.101)

chr1	3415312	3415312	*MEGF6*	Nonsense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P125	p.S1058*	ENSG00000162591	ENST00000356575	Transcript	stop_gained	NA
chr10	125516776	125516776	*CPXM2*	Nonsense_Mutation	.	SNP	C	C	A	rs145812368	shanshan_et_al_P125	p.E624*	ENSG00000121898	ENST00000241305	Transcript	stop_gained	NA
chr10	72195275	72195275	*NODAL*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P125	p.W220R	ENSG00000156574	ENST00000287139	Transcript	missense_variant	probably_damaging(0.999)
chr12	32138837	32138837	*KIAA1551*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P125	p.E1650K	ENSG00000174718	ENST00000312561	Transcript	missense_variant	benign(0.111)
chr15	40212157	40212157	*GPR176*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.A24E	ENSG00000166073	ENST00000561100	Transcript	missense_variant	benign(0)
chr15	48052552	48052552	*SEMA6D*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P125	p.Q54L	ENSG00000137872	ENST00000316364	Transcript	missense_variant	probably_damaging(0.992)
chr15	89836213	89836214	*FANCI*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P125	p.N739Kfs*2	ENSG00000140525	ENST00000310775	Transcript	frameshift_variant	NA
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P125	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr17	77755496	77755496	*CBX2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.E62*	ENSG00000173894	ENST00000310942	Transcript	stop_gained	NA
chr19	40704404	40704404	*MAP3K10*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P125	p.W269R	ENSG00000130758	ENST00000253055	Transcript	missense_variant	probably_damaging(0.999)
chr19	53612744	53612744	*ZNF415*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P125	p.I185T	ENSG00000170954	ENST00000500065	Transcript	missense_variant	benign(0.01)
chr19	55284899	55284899	*KIR2DL1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P125	p.R62K	ENSG00000125498	ENST00000336077	Transcript	missense_variant	probably_damaging(1)
chr2	183960177	183960177	*DUSP19*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P125	p.H149Y	ENSG00000162999	ENST00000354221	Transcript	missense_variant	probably_damaging(0.999)
chr20	25597079	25597079	*NANP*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P125	p.E77K	ENSG00000170191	ENST00000304788	Transcript	missense_variant	possibly_damaging(0.482)
chr21	32007769	32007769	*KRTAP20-2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.G63C	ENSG00000184032	ENST00000330798	Transcript	missense_variant	unknown(0)
chr21	36259172	36259172	*RUNX1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P125	p.R107C	ENSG00000159216	ENST00000300305	Transcript	missense_variant	probably_damaging(0.999)
chr21	47965164	47965164	*DIP2A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.G764V	ENSG00000160305	ENST00000417564	Transcript	missense_variant	benign(0.017)
chr22	18299497	18299497	*MICAL3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P125	p.D1802N	ENSG00000243156	ENST00000441493	Transcript	missense_variant	probably_damaging(0.998)
chr3	142277598	142277598	*ATR*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.H585N	ENSG00000175054	ENST00000350721	Transcript	missense_variant	benign(0)
chr3	183824093	183824093	*HTR3E*	Missense_Mutation	.	SNP	A	A	G	rs192364815	shanshan_et_al_P125	p.E394G	ENSG00000186038	ENST00000440596	Transcript	missense_variant	benign(0)
chr3	194152498	194152498	*ATP13A3*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P125	p.H790P	ENSG00000133657	ENST00000439040	Transcript	missense_variant	possibly_damaging(0.611)
chr3	45077180	45077180	*CLEC3B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P125	p.V125M	ENSG00000163815	ENST00000296130	Transcript	missense_variant	benign(0.041)
chr5	37138912	37138912	*C5orf42*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P125	p.D2847G	ENSG00000197603	ENST00000425232	Transcript	missense_variant	benign(0.39)
chr5	86685261	86685261	*RASA1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P125	p.R993C	ENSG00000145715	ENST00000274376	Transcript	missense_variant	probably_damaging(0.946)
chr6	108214859	108214859	*SEC63*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P125	p.Q501*	ENSG00000025796	ENST00000369002	Transcript	stop_gained	NA
chr6	138584341	138584341	*KIAA1244*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P125	p.I574K	ENSG00000112379	ENST00000251691	Transcript	missense_variant	probably_damaging(0.998)
chr6	168273023	168273023	*MLLT4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.D182Y	ENSG00000130396	ENST00000392108	Transcript	missense_variant	probably_damaging(0.947)
chr6	43139653	43139653	*SRF*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P125	p.E87K	ENSG00000112658	ENST00000265354	Transcript	missense_variant	unknown(0)
chr6	46847555	46847555	*GPR116*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P125	p.G346S	ENSG00000069122	ENST00000283296	Transcript	missense_variant	probably_damaging(0.962)
chr6	65301096	65301096	*EYS*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P125	p.T1555I	ENSG00000188107	ENST00000503581	Transcript	missense_variant	benign(0.001)
chr7	100806669	100806669	*VGF*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P125	p.A486S	ENSG00000128564	ENST00000249330	Transcript	missense_variant	unknown(0)
chr7	104751254	104751254	*KMT2E*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P125	p.N1336T	ENSG00000005483	ENST00000311117	Transcript	missense_variant	benign(0.001)
chr7	106509350	106509350	*PIK3CG*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.E448D	ENSG00000105851	ENST00000359195	Transcript	missense_variant	benign(0.002)
chr7	138719380	138719380	*ZC3HAV1L*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P125	p.M137K	ENSG00000146858	ENST00000275766	Transcript	missense_variant	benign(0)
chr7	143747693	143747693	*OR2A5*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P125	p.I67V	ENSG00000221836	ENST00000408906	Transcript	missense_variant	benign(0.007)
chr7	150752866	150752866	*CDK5*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P125	p.K128Q	ENSG00000164885	ENST00000485972	Transcript	missense_variant	probably_damaging(0.929)

chr7	73973346	73973346	*GTF2IRD1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P125	p.A787S	ENSG00000006704	ENST00000455841	Transcript	missense_variant	probably_damaging(0.953)
chrX	100601518	100601518	*TIMM8A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P125	p.K88M	ENSG00000126953	ENST00000372902	Transcript	missense_variant	possibly_damaging(0.789)
chrX	127185710	127185710	*ACTRT1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P125	p.G159A	ENSG00000123165	ENST00000371124	Transcript	missense_variant	probably_damaging(0.976)
chr1	150241131	150241134	*APH1A*	Frame_Shift_Del	.	DEL	CCAG	CCAG	-	novel	shanshan_et_al_P127	p.A26Gfs*33	ENSG00000117362	ENST00000369109	Transcript	frameshift_variant	NA
chr1	24212577	24212577	*PLCH2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P127	p.E462V	ENSG00000149527	ENST00000449969	Transcript	missense_variant	probably_damaging(1)
chr12	10958930	10958930	*TAS2R8*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P127	p.L217P	ENSG00000121314	ENST00000240615	Transcript	missense_variant	possibly_damaging(0.568)
chr14	36987136	36987136	*NKX2-1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P127	p.P185T	ENSG00000136352	ENST00000354822	Transcript	missense_variant	possibly_damaging(0.492)
chr14	52985913	52985913	*TXNDC16*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P127	p.Y164F	ENSG00000087301	ENST00000281741	Transcript	missense_variant	probably_damaging(0.927)
chr15	74564066	74564066	*CCDC33*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P127	p.E190V	ENSG00000140481	ENST00000398814	Transcript	missense_variant	possibly_damaging(0.895)
chr16	21217054	21217054	*ZP2*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P127	p.K176*	ENSG00000103310	ENST00000574002	Transcript	stop_gained	NA
chr16	74729555	74729555	*MLKL*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P127	p.R34H	ENSG00000168404	ENST00000308807	Transcript	missense_variant	possibly_damaging(0.818)
chr17	40010454	40010454	*KLHL11*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P127	p.N555K	ENSG00000178502	ENST00000319121	Transcript	missense_variant	benign(0.013)
chr17	50867055	50867055	*ZNF594*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P127	p.V283I	ENSG00000180626	ENST00000399604	Transcript	missense_variant	possibly_damaging(0.891)
chr17	60522287	60522287	*METTL2A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P127	p.Q300L	ENSG00000087995	ENST00000311506	Transcript	missense_variant	probably_damaging(0.967)
chr17	7577498	7577498	*TP53*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P127	p.X261_splice	ENSG00000141510	ENST00000269305	Transcript	splice_donor_variant	NA
chr19	38692562	38692562	*SIPA1L3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P127	p.P1682L	ENSG00000105738	ENST00000222345	Transcript	missense_variant	possibly_damaging(0.568)
chr19	55325303	55325303	*KIR2DL4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P127	p.D256N	ENSG00000189013	ENST00000345540	Transcript	missense_variant	possibly_damaging(0.738)
chr2	162805701	162805701	*SLC4A10*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P127	p.L770R	ENSG00000144290	ENST00000446997	Transcript	missense_variant	possibly_damaging(0.895)
chr22	30035078	30035078	*NF2*	Splice_Site	.	SNP	G	G	C	novel	shanshan_et_al_P127	NA	ENSG00000186575	ENST00000338641	Transcript	splice_acceptor_variant	NA
chr22	36013222	36013222	*MB*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P127	p.E28G	ENSG00000198125	ENST00000397326	Transcript	missense_variant	benign(0.348)
chr3	161214760	161214760	*OTOL1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P127	p.E55D	ENSG00000182447	ENST00000327928	Transcript	missense_variant	unknown(0)
chr7	148544398	148544398	*EZH2*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P127	NA	ENSG00000106462	ENST00000320356	Transcript	splice_acceptor_variant	NA
chr9	40705856	40705856	*SPATA31A3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P127	p.F1171L	ENSG00000147926	ENST00000356699	Transcript	missense_variant	benign(0.002)
chrX	101396249	101396249	*TCEAL6*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P127	p.E19Q	ENSG00000204071	ENST00000372774	Transcript	missense_variant	possibly_damaging(0.878)
chrX	102632614	102632614	*NGFRAP1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P127	p.D65E	ENSG00000166681	ENST00000372645	Transcript	missense_variant	probably_damaging(0.918)
chrX	107930868	107930868	*COL4A5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P127	p.E1491V	ENSG00000188153	ENST00000328300	Transcript	missense_variant	possibly_damaging(0.6)
chrX	110395646	110395646	*PAK3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P127	p.A183S	ENSG00000077264	ENST00000360648	Transcript	missense_variant	benign(0.008)
chrX	51806109	51806109	*MAGED4B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P127	p.M603L	ENSG00000187243	ENST00000431659	Transcript	missense_variant	probably_damaging(0.988)
chrX	51934178	51934178	*MAGED4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P127	p.M587L	ENSG00000154545	ENST00000375626	Transcript	missense_variant	probably_damaging(0.98)
chr1	186008949	186008949	*HMCN1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P128	p.A2040S	ENSG00000143341	ENST00000271588	Transcript	missense_variant	probably_damaging(0.996)
chr1	201061111	201061111	*CACNA1S*	Missense_Mutation	.	SNP	G	G	C	rs141204958	shanshan_et_al_P128	p.S177W	ENSG00000081248	ENST00000362061	Transcript	missense_variant	probably_damaging(0.999)
chr1	215813980	215813981	*USH2A*	Frame_Shift_Ins	.	INS	-	-	C	novel	shanshan_et_al_P128	p.E4963Gfs*38	ENSG00000042781	ENST00000307340	Transcript	frameshift_variant	NA
chr1	234040855	234040855	*SLC35F3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P128	p.P11L	ENSG00000183780	ENST00000366618	Transcript	missense_variant	benign(0.056)
chr1	37948355	37948355	*ZC3H12A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P128	p.G315R	ENSG00000163874	ENST00000373087	Transcript	missense_variant	probably_damaging(1)
chr1	7798224	7798224	*CAMTA1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P128	p.S1288R	ENSG00000171735	ENST00000303635	Transcript	missense_variant	benign(0.157)
chr10	50531843	50531843	*C10orf71*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P128	p.Q418R	ENSG00000177354	ENST00000374144	Transcript	missense_variant	probably_damaging(0.999)

chr10	89622183	89622183	*KLLN*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P128	p.R21Q	ENSG00000227268	ENST00000445946	Transcript	missense_variant	benign(0)
chr11	124487256	124487256	*PANX3*	Missense_Mutation	.	SNP	C	C	A	rs144166888	shansha n_et_al_P128	p.S137R	ENSG00000154143	ENST00000284288	Transcript	missense_variant	possibly_damaging(0.459)
chr11	21250965	21250965	*NELL1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P128	p.K505I	ENSG00000165973	ENST00000357134	Transcript	missense_variant	possibly_damaging(0.649)
chr11	40136849	40136849	*LRRC4C*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P128	p.T332S	ENSG00000148948	ENST00000278198	Transcript	missense_variant	benign(0)
chr11	62288510	62288510	*AHNAK*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P128	p.S4460C	ENSG00000124942	ENST00000378024	Transcript	missense_variant	probably_damaging(0.987)
chr11	68700868	68700868	*IGHMBP2*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P128	p.Q446L	ENSG00000132740	ENST00000255078	Transcript	missense_variant	benign(0.315)
chr11	68854064	68854064	*TPCN2*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P128	p.I693V	ENSG00000162341	ENST00000294309	Transcript	missense_variant	benign(0.19)
chr11	76825287	76825287	*CAPN5*	Splice_Site	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.X169_splice	ENSG00000149260	ENST00000278559	Transcript	splice_acceptor_variant	NA
chr11	88911458	88911458	*TYR*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P128	p.T113A	ENSG00000077498	ENST00000263321	Transcript	missense_variant	benign(0.003)
chr12	123678991	123678991	*MPHOSPH9*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P128	p.Y576F	ENSG00000051825	ENST00000392425	Transcript	missense_variant	probably_damaging(0.998)
chr12	51236851	51236851	*TMPRSS12*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P128	p.P35L	ENSG00000186452	ENST00000398458	Transcript	missense_variant	benign(0)
chr12	54379492	54379492	*HOXC10*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.R150L	ENSG00000180818	ENST00000303460	Transcript	missense_variant	probably_damaging(0.97)
chr12	661265	661265	*B4GALNT3*	Missense_Mutation	.	SNP	C	C	A	rs200173452	shansha n_et_al_P128	p.R382S	ENSG00000139044	ENST00000266383	Transcript	missense_variant	probably_damaging(1)
chr12	9070332	9070332	*PHC1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.G20V	ENSG00000111752	ENST00000543824	Transcript	missense_variant	unknown(0)
chr13	99947324	99947324	*GPR183*	Frame_Shift_Del	.	DEL	T	T	-	novel	shansha n_et_al_P128	p.N359Mfs*26	ENSG00000169508	ENST00000376414	Transcript	frameshift_variant	NA
chr14	102904496	102904496	*TECPR2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.W844C	ENSG00000196663	ENST00000359520	Transcript	missense_variant	probably_damaging(0.998)
chr14	70245218	70245218	*SLC10A1*	Missense_Mutation	.	SNP	C	C	T	rs200425043	shansha n_et_al_P128	p.G259R	ENSG00000100652	ENST00000216540	Transcript	missense_variant	possibly_damaging(0.875)
chr14	74489809	74489809	*CCDC176*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P128	p.S83R	ENSG00000119636	ENST00000394009	Transcript	missense_variant	possibly_damaging(0.807)
chr14	77844536	77844544	*SAMD15*	In_Frame_Del	.	DEL	CAGGCTAGA	CAGGCTAGA	-	novel	shansha n_et_al_P128	p.Q259_R261del	ENSG00000100583	ENST00000216471	Transcript	inframe_deletion	NA
chr14	94039067	94039067	*UNC79*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P128	p.L482V	ENSG00000133958	ENST00000256339	Transcript	missense_variant	probably_damaging(0.995)
chr14	99969294	99969294	*CCNK*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P128	p.S328R	ENSG00000090061	ENST00000389879	Transcript	missense_variant	benign(0.184)
chr15	74003483	74003483	*CD276*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.Q518H	ENSG00000103855	ENST00000318443	Transcript	missense_variant	benign(0.109)
chr15	74481552	74481552	*STRA6*	Frame_Shift_Del	.	DEL	C	C	-	novel	shansha n_et_al_P128	p.D371Mfs*24	ENSG00000137868	ENST00000563965	Transcript	frameshift_variant	NA
chr15	78780991	78780991	*IREB2*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P128	p.T652S	ENSG00000136381	ENST00000258886	Transcript	missense_variant	benign(0.004)
chr15	79382726	79382726	*RASGRF1*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P128	p.W39R	ENSG00000058335	ENST00000419573	Transcript	missense_variant	probably_damaging(1)
chr15	79382755	79382755	*RASGRF1*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P128	p.L29R	ENSG00000058335	ENST00000419573	Transcript	missense_variant	possibly_damaging(0.761)
chr16	28328771	28328771	*SBK1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P128	p.G20E	ENSG00000188322	ENST00000341901	Transcript	missense_variant	probably_damaging(0.931)
chr17	72937869	72937869	*OTOP3*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P128	p.Y152C	ENSG00000182938	ENST00000328801	Transcript	missense_variant	possibly_damaging(0.789)
chr17	74774288	74774288	*MFSD11*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.A402S	ENSG00000092931	ENST00000588460	Transcript	missense_variant	probably_damaging(0.971)
chr17	75739966	75739966	*TP53*	Missense_Mutation	.	SNP	A	A	C	rs121912662	shansha n_et_al_P128	p.L344R	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.979)
chr17	77811696	77811697	*CBX4*	Frame_Shift_Ins	.	INS	-	-	TA	novel	shansha n_et_al_P128	p.N40Ifs*16	ENSG00000141582	ENST00000269397	Transcript	frameshift_variant	NA
chr18	14105152	14105152	*ZNF519*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.E463*	ENSG00000175322	ENST00000590202	Transcript	stop_gained	NA
chr18	44284595	44284595	*ST8SIA5*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P128	p.Y55C	ENSG00000101638	ENST00000315087	Transcript	missense_variant	benign(0.002)
chr19	42473645	42473645	*ATP1A3*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P128	p.R890Q	ENSG00000105409	ENST00000545399	Transcript	missense_variant	probably_damaging(0.999)
chr19	54485526	54485526	*CACNG8*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P128	p.A234V	ENSG00000142408	ENST00000270458	Transcript	missense_variant	benign(0.055)
chr19	55592170	55592170	*EPS8L1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P128	p.A154T	ENSG00000131037	ENST00000201647	Transcript	missense_variant	probably_damaging(0.979)

chr19	57327999	57327999	*PEG3*	Missense_Mutation	.	SNP	C	C	T	rs200022665	shansha n_et_al_P128	p.R604H	ENSG00000198300	ENST00000326441	Transcript	missense_variant	benign(0.039)
chr2	109384034	109384034	*RANBP2*	Missense_Mutation	.	SNP	G	G	A	rs151064332	shansha n_et_al_P128	p.G2347S	ENSG00000153201	ENST00000283195	Transcript	missense_variant	benign(0.074)
chr2	152496949	152496949	*NEB*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P128	p.N2869H	ENSG00000183091	ENST00000397345	Transcript	missense_variant	benign(0.01)
chr2	162251685	162251685	*PSMD14*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P128	p.M248V	ENSG00000115233	ENST00000409682	Transcript	missense_variant	benign(0.042)
chr2	166468 2	166468 2	*PXDN*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.A603D	ENSG00000130508	ENST00000252804	Transcript	missense_variant	possibly_damaging(0.493)
chr2	176995 86	176995 86	*RAD51AP2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P128	p.S33R	ENSG00000214842	ENST00000399080	Transcript	missense_variant	possibly_damaging(0.641)
chr2	202558641	202558641	*MPP4*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P128	p.K13E	ENSG00000082126	ENST00000409474	Transcript	missense_variant	benign(0.002)
chr2	207171802	207171802	*ZDBF2*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P128	p.E850D	ENSG00000204186	ENST00000374423	Transcript	missense_variant	possibly_damaging(0.585)
chr2	215890488	215890488	*ABCA12*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P128	p.L399R	ENSG00000144452	ENST00000272895	Transcript	missense_variant	probably_damaging(0.986)
chr2	231775073	231775073	*GPR55*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P128	p.S202F	ENSG00000135898	ENST00000392040	Transcript	missense_variant	benign(0.008)
chr2	241715334	241715334	*KIF1A*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P128	p.K298E	ENSG00000130294	ENST00000498729	Transcript	missense_variant	probably_damaging(0.96)
chr2	63272303	63272303	*EHBP1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P128	p.A1198V	ENSG00000115504	ENST00000263991	Transcript	missense_variant	probably_damaging(1)
chr2	97637875	97637875	*FAM178B*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.D109E	ENSG00000168754	ENST00000490605	Transcript	missense_variant	probably_damaging(0.932)
chr20	20020291	20020291	*CRNKL1*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.E664*	ENSG00000101343	ENST00000377340	Transcript	stop_gained	NA
chr21	41143098	41143098	*IGSF5*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.R225L	ENSG00000183067	ENST00000380588	Transcript	missense_variant	benign(0.053)
chr22	50688063	50688063	*HDAC10*	Splice_Site	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.X188_splice	ENSG00000100429	ENST00000216271	Transcript	splice_donor_variant	NA
chr3	101578168	101578168	*NFKBIZ*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P128	p.R704G	ENSG00000144802	ENST00000326172	Transcript	missense_variant	benign(0.418)
chr3	128758582	128758582	*EFCC1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P128	p.L563Q	ENSG00000114654	ENST00000480450	Transcript	missense_variant	probably_damaging(0.999)
chr3	129252533	129252533	*RHO*	Missense_Mutation	.	SNP	C	C	G	rs148748781	shansha n_et_al_P128	p.T340R	ENSG00000163914	ENST00000296271	Transcript	missense_variant	possibly_damaging(0.611)
chr3	154145382	154145382	*GPR149*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P128	p.R366P	ENSG00000174948	ENST00000389740	Transcript	missense_variant	possibly_damaging(0.847)
chr3	170585827	170585827	*RPL22L1*	Missense_Mutation	.	SNP	C	C	A	rs139790884	shansha n_et_al_P128	p.V67F	ENSG00000163584	ENST00000295830	Transcript	missense_variant	benign(0.078)
chr3	25665866	25665866	*TOP2B*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P128	p.Q801L	ENSG00000077097	ENST00000435706	Transcript	missense_variant	benign(0.006)
chr3	47165258	47165258	*SETD2*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.E290*	ENSG00000181555	ENST00000409792	Transcript	stop_gained	NA
chr3	87294880	87294880	*CHMP2B*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P128	p.K48T	ENSG00000083937	ENST00000263780	Transcript	missense_variant	probably_damaging(0.922)
chr4	68441149	68441149	*STAP1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P128	p.Q80L	ENSG00000035720	ENST00000265404	Transcript	missense_variant	benign(0.007)
chr4	79400873	79400873	*FRAS1*	Splice_Site	.	SNP	G	G	T	novel	shansha n_et_al_P128	p.X2815_splice	ENSG00000138759	ENST00000264895	Transcript	splice_donor_variant	NA
chr5	132087754	132087754	*Sep/08*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.C469F	ENSG00000164402	ENST00000378719	Transcript	missense_variant	probably_damaging(0.991)
chr5	13751352	13751352	*DNAH5*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.K3682N	ENSG00000039139	ENST00000265104	Transcript	missense_variant	possibly_damaging(0.728)
chr5	140870391	140870391	*PCDHGC5*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P128	p.Q528H	ENSG00000240764	ENST00000252087	Transcript	missense_variant	probably_damaging(0.998)
chr5	14280489	14280489	*TRIO*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P128	p.D97E	ENSG00000038382	ENST00000344204	Transcript	missense_variant	probably_damaging(0.992)
chr5	23527660	23527660	*PRDM9*	Missense_Mutation	.	SNP	A	A	T	rs185636293	shansha n_et_al_P128	p.R821S	ENSG00000164256	ENST00000296682	Transcript	missense_variant	benign(0.006)
chr5	74651259	74651259	*HMGCR*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P128	p.R598C	ENSG00000113161	ENST00000287936	Transcript	missense_variant	benign(0.005)
chr6	133100511	133100511	*SLC18B1*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P128	p.L231V	ENSG00000146409	ENST00000275227	Transcript	missense_variant	probably_damaging(0.951)
chr6	13872628 3	13872628 3	*HEBP2*	Missense_Mutation	.	SNP	C	C	G	rs148433984	shansha n_et_al_P128	p.P35R	ENSG00000051620	ENST00000607197	Transcript	missense_variant	possibly_damaging(0.745)
chr6	41059275	41059275	*NFYA*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.P186T	ENSG00000001167	ENST00000341376	Transcript	missense_variant	benign(0.044)
chr6	64404493	64404493	*PHF3*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P128	p.S840*	ENSG00000118482	ENST00000262043	Transcript	stop_gained	NA

chr6	75912486	75912486	*COL12A1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P128	p.A8E	ENSG00000111799	ENST00000322507	Transcript	missense_variant	benign(0.156)
chr6	84303452	84303452	*SNAP91*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P128	p.A481S	ENSG00000065609	ENST00000439399	Transcript	missense_variant	benign(0.364)
chr7	106710735	106710735	*PRKAR2B*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P128	p.I106T	ENSG00000005249	ENST00000265717	Transcript	missense_variant	benign(0.002)
chr8	48647870	48647870	*SPIDR*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P128	p.S869I	ENSG00000164808	ENST00000297423	Transcript	missense_variant	benign(0.015)
chr9	101751487	101751487	*COL15A1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P128	p.E251K	ENSG00000204291	ENST00000375001	Transcript	missense_variant	benign(0.081)
chr9	116224120	116224120	*RGS3*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P128	p.W73Gfs*22	ENSG00000138835	ENST00000374140	Transcript	frameshift_variant	NA
chr9	123780066	123780066	*C5*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P128	p.Q524R	ENSG00000106804	ENST00000223642	Transcript	missense_variant	probably_damaging(0.944)
chr9	32251555	32251555	*RFX3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P128	p.E713K	ENSG00000080298	ENST00000382004	Transcript	missense_variant	benign(0.062)
chr9	34724376	34724376	*FAM205A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P128	p.P954L	ENSG00000205108	ENST00000378788	Transcript	missense_variant	benign(0.002)
chr9	99521410	99521410	*ZNF510*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P128	p.G568*	ENSG00000081386	ENST00000375231	Transcript	stop_gained	NA
chrX	115588781	115588781	*SLC6A14*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P128	p.F541V	ENSG00000087916	ENST00000371900	Transcript	missense_variant	benign(0.099)
chrX	129519343	129519343	*GPR119*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P128	p.V27M	ENSG00000147262	ENST00000276218	Transcript	missense_variant	benign(0.301)
chrX	24078209	24078209	*EIF2S3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P128	p.V130F	ENSG00000130741	ENST00000253039	Transcript	missense_variant	benign(0.107)
chr1	151787427	151787427	*RORC*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.S258I	ENSG00000143365	ENST00000318247	Transcript	missense_variant	benign(0.089)
chr1	152193463	152193463	*HRNR*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.Q214H	ENSG00000197915	ENST00000368801	Transcript	missense_variant	unknown(0)
chr1	158735911	158735911	*OR6N1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.A188S	ENSG00000197403	ENST00000335094	Transcript	missense_variant	possibly_damaging(0.589)
chr1	160970824	160970824	*F11R*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P13	p.N76S	ENSG00000158769	ENST00000368026	Transcript	missense_variant	benign(0.017)
chr1	228407193	228407193	*OBSCN*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P13	p.V941E	ENSG00000154358	ENST00000570156	Transcript	missense_variant	benign(0.409)
chr1	27942356	27942356	*FGR*	Splice_Site	.	SNP	C	C	G	novel	shanshan_et_al_P13	p.X228_splice	ENSG00000000938	ENST00000374005	Transcript	splice_acceptor_variant	NA
chr1	40777742	40777742	*COL9A2*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.R136*	ENSG00000049089	ENST00000372748	Transcript	stop_gained	NA
chr1	52499024	52499024	*KTI12*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.R137L	ENSG00000198841	ENST00000371614	Transcript	missense_variant	benign(0.03)
chr1	85486790	85486790	*MCOLN3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.F497S	ENSG00000055732	ENST00000370589	Transcript	missense_variant	probably_damaging(0.999)
chr1	86851217	86851217	*ODF2L*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.A57V	ENSG00000122417	ENST00000359242	Transcript	missense_variant	possibly_damaging(0.778)
chr10	102053117	102053117	*PKD2L1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P13	p.I560N	ENSG00000107593	ENST00000318222	Transcript	missense_variant	probably_damaging(1)
chr10	104678298	104678298	*CNNM2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.A21S	ENSG00000148842	ENST00000369878	Transcript	missense_variant	possibly_damaging(0.515)
chr10	105184975	105184975	*PDCD11*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.K1000E	ENSG00000148843	ENST00000369797	Transcript	missense_variant	benign(0.097)
chr10	121203077	121203077	*GRK5*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.Q360R	ENSG00000198873	ENST00000392870	Transcript	missense_variant	benign(0.253)
chr10	50533075	50533075	*C10orf71*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.E829*	ENSG00000177354	ENST00000374144	Transcript	stop_gained	NA
chr10	50819670	50819670	*SLC18A3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P13	p.A295V	ENSG00000187714	ENST00000374115	Transcript	missense_variant	probably_damaging(0.996)
chr10	74684272	74684272	*OIT3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.R413S	ENSG00000138315	ENST00000334011	Transcript	missense_variant	benign(0.109)
chr10	89653867	89653867	*PTEN*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P13	NA	ENSG00000171862	ENST00000371953	Transcript	splice_donor_variant	NA
chr11	113221975	113221975	*TTC12*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P13	p.F421C	ENSG00000149292	ENST00000529221	Transcript	missense_variant	benign(0.003)
chr11	47189716	47189716	*ARFGAP2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P13	p.D343V	ENSG00000149182	ENST00000524782	Transcript	missense_variant	probably_damaging(0.955)
chr11	50203804	50203804	*OR51L1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P13	p.H58Y	ENSG00000176798	ENST00000321543	Transcript	missense_variant	benign(0.34)
chr12	119594412	119594412	*SRRM4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P13	p.Y549N	ENSG00000139767	ENST00000267260	Transcript	missense_variant	unknown(0)
chr12	69600908	69600908	*CDCA3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P13	p.V7I	ENSG00000111665	ENST00000538862	Transcript	missense_variant	benign(0.012)

chr13	111130443	111130443	*COL4A2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P13	p.L840Q	ENSG00000134871	ENST00000360467	Transcript	missense_variant	possibly_damaging(0.788)
chr13	57729807	57729807	*PRR20C*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P13	p.P70Lfs*38	ENSG00000229665	ENST00000544357	Transcript	frameshift_variant	NA
chr14	105420665	105420665	*AHNAK2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P13	p.S375C	ENSG00000185567	ENST00000333244	Transcript	missense_variant	possibly_damaging(0.892)
chr14	23299285	23299285	*MRPL52*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.V19L	ENSG00000172590	ENST00000355151	Transcript	missense_variant	benign(0)
chr14	23826721	23826721	*EFS*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.P467L	ENSG00000100842	ENST00000216733	Transcript	missense_variant	probably_damaging(1)
chr16	11369982	11369982	*PRM2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.C82*	ENSG00000122304	ENST00000241808	Transcript	stop_gained	NA
chr16	68057083	68057083	*DDX28*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.R8L	ENSG00000182810	ENST00000332395	Transcript	missense_variant	benign(0.001)
chr17	18221145	18221145	*SMCR8*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P13	p.V681A	ENSG00000176994	ENST00000406438	Transcript	missense_variant	benign(0.001)
chr17	34074884	34074884	*GAS2L2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.C272*	ENSG00000132139	ENST00000254466	Transcript	stop_gained	NA
chr17	3970502	3970502	*ZZEF1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.E1370D	ENSG00000074755	ENST00000381638	Transcript	missense_variant	benign(0.002)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P13	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr17	76134461	76134461	*TMC8*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P13	p.S522W	ENSG00000167895	ENST00000318430	Transcript	missense_variant	possibly_damaging(0.818)
chr18	22806113	22806113	*ZNF521*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.L590S	ENSG00000198795	ENST00000361524	Transcript	missense_variant	probably_damaging(0.999)
chr18	29171935	29171935	*TTR*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.X23_splice	ENSG00000118271	ENST00000237014	Transcript	splice_donor_variant	NA
chr18	33744438	33744438	*ELP2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.A653T	ENSG00000134759	ENST00000442325	Transcript	missense_variant	probably_damaging(0.988)
chr19	21132956	21132956	*ZNF85*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.A546S	ENSG00000105750	ENST00000328178	Transcript	missense_variant	possibly_damaging(0.543)
chr19	2834374	2834374	*ZNF554*	Missense_Mutation	.	SNP	G	G	A	rs372864879	shanshan_et_al_P13	p.G381R	ENSG00000172006	ENST00000317243	Transcript	missense_variant	benign(0)
chr19	40411969	40411969	*FCGBP*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.G1220V	ENSG00000090920	ENST00000221347	Transcript	missense_variant	probably_damaging(1)
chr19	42482130	42482130	*ATP1A3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P13	p.I647N	ENSG00000105409	ENST00000545399	Transcript	missense_variant	probably_damaging(1)
chr19	52469327	52469327	*ZNF350*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.D127Y	ENSG00000256683	ENST00000246364	Transcript	missense_variant	benign(0.01)
chr19	55743321	55743321	*PPP6R1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.V719L	ENSG00000105063	ENST00000412770	Transcript	missense_variant	benign(0.04)
chr19	56052671	56052671	*SBK3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.E207D	ENSG00000231274	ENST00000420723	Transcript	missense_variant	probably_damaging(0.992)
chr19	56223303	56223303	*NLRP9*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P13	p.C902W	ENSG00000185792	ENST00000332836	Transcript	missense_variant	probably_damaging(0.928)
chr19	56600085	56600085	*ZNF787*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.C152*	ENSG00000142409	ENST00000270459	Transcript	stop_gained	NA
chr19	57647140	57647140	*ZIM3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.H189Y	ENSG00000141946	ENST00000269834	Transcript	missense_variant	benign(0.378)
chr19	57793939	57793939	*BSG*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.R78L	ENSG00000172270	ENST00000333511	Transcript	missense_variant	probably_damaging(0.982)
chr19	9204243	9204243	*OR1M1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.G108D	ENSG00000170929	ENST00000429566	Transcript	missense_variant	probably_damaging(1)
chr2	109087175	109087175	*GCC2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.E464*	ENSG00000135968	ENST00000309863	Transcript	stop_gained	NA
chr2	175337915	175337915	*GPR155*	Missense_Mutation	.	SNP	C	C	A	rs144639457	shanshan_et_al_P13	p.R213L	ENSG00000163328	ENST00000392552	Transcript	missense_variant	possibly_damaging(0.704)
chr2	71360152	71360152	*MPHOSPH10*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.D72N	ENSG00000124383	ENST00000244230	Transcript	missense_variant	probably_damaging(1)
chr2	72725596	72725596	*EXOC6B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.A442S	ENSG00000144036	ENST00000272427	Transcript	missense_variant	benign(0)
chr2	85581589	85581590	*RETSAT*	Frame_Shift_Ins	.	INS	-	-	TG	novel	shanshan_et_al_P13	p.A15Rfs*32	ENSG00000042445	ENST00000295802	Transcript	frameshift_variant	NA
chr2	96690390	96690390	*GPAT2*	Missense_Mutation	.	SNP	G	G	T	rs370280326	shanshan_et_al_P13	p.T485K	ENSG00000186281	ENST00000434632	Transcript	missense_variant	possibly_damaging(0.742)
chr2	97217749	97217749	*ARID5A*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P13	p.V495A	ENSG00000196843	ENST00000357485	Transcript	missense_variant	benign(0)
chr20	40033858	40033858	*CHD6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.G2508V	ENSG00000124177	ENST00000373233	Transcript	missense_variant	probably_damaging(0.963)
chr20	57769084	57769084	*ZNF831*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.I1004V	ENSG00000124203	ENST00000371030	Transcript	missense_variant	benign(0.006)

chr20	61542712	61542712	*DIDO1*	Missense_Mutation	.	SNP	C	C	A	rs138139875	shanshan_et_al_P13	p.G85C	ENSG00000101191	ENST00000266070	Transcript	missense_variant	probably_damaging(1)
chr20	62124632	62124632	*EEF1A2*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P13	p.W210*	ENSG00000101210	ENST00000217182	Transcript	stop_gained	NA
chr21	45502786	45502786	*TRAPPC10*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.S614N	ENSG00000160218	ENST00000291574	Transcript	missense_variant	benign(0.157)
chr22	20907437	20907437	*MED15*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.K72E	ENSG00000099917	ENST00000263205	Transcript	missense_variant	unknown(0)
chr22	40054956	40054956	*CACNA1I*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.Q722R	ENSG00000100346	ENST00000402142	Transcript	missense_variant	benign(0.227)
chr22	50217161	50217161	*BRD1*	Missense_Mutation	.	SNP	C	C	A	rs555085765	shanshan_et_al_P13	p.A269S	ENSG00000100425	ENST00000216267	Transcript	missense_variant	possibly_damaging(0.894)
chr3	11300845	11300845	*HRH1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.T41K	ENSG00000196639	ENST00000397056	Transcript	missense_variant	probably_damaging(1)
chr3	124732832	124732832	*HEG1*	Missense_Mutation	.	SNP	C	C	A	rs371922838	shanshan_et_al_P13	p.A531S	ENSG00000173706	ENST00000311127	Transcript	missense_variant	benign(0.002)
chr3	50412208	50412208	*CACNA2D2*	Nonsense_Mutation	.	SNP	G	G	T	rs199862239	shanshan_et_al_P13	p.Y648*	ENSG00000007402	ENST00000479441	Transcript	stop_gained	NA
chr4	135121249	135121249	*PABPC4L*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P13	p.L367R	ENSG00000254535	ENST00000529122	Transcript	missense_variant	probably_damaging(0.999)
chr5	131398462	131398462	*IL3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.T146N	ENSG00000164399	ENST00000296870	Transcript	missense_variant	benign(0.403)
chr5	70751716	70751716	*BDP1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.R4S	ENSG00000145734	ENST00000358731	Transcript	missense_variant	probably_damaging(0.999)
chr6	102266269	102266269	*GRIK2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.G410C	ENSG00000164418	ENST00000421544	Transcript	missense_variant	probably_damaging(1)
chr6	132892350	132892350	*TAAR6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.C297Y	ENSG00000146383	ENST00000275198	Transcript	missense_variant	benign(0.021)
chr6	42612073	42612073	*UBR2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P13	p.K740T	ENSG00000024048	ENST00000372899	Transcript	missense_variant	benign(0.088)
chr6	46047610	46047610	*CLIC5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.L124F	ENSG00000112782	ENST00000185206	Transcript	missense_variant	benign(0.02)
chr6	47681849	47681849	*GPR115*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.A290T	ENSG00000153294	ENST00000283303	Transcript	missense_variant	possibly_damaging(0.798)
chr6	65301109	65301109	*EYS*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.E1551*	ENSG00000188107	ENST00000503581	Transcript	stop_gained	NA
chr7	107696124	107696124	*LAMB4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.F1236L	ENSG00000091128	ENST00000388781	Transcript	missense_variant	benign(0.009)
chr7	116502696	116502696	*CAPZA2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.E11*	ENSG00000198898	ENST00000361183	Transcript	stop_gained	NA
chr7	123593779	123593779	*SPAM1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.A52D	ENSG00000106304	ENST00000340011	Transcript	missense_variant	probably_damaging(0.936)
chr7	141618961	141618961	*OR9A4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.A96S	ENSG00000258083	ENST00000548136	Transcript	missense_variant	benign(0.14)
chr7	81579718	81579718	*CACNA2D1*	Missense_Mutation	.	SNP	C	C	T	rs143631985	shanshan_et_al_P13	p.R1089H	ENSG00000153956	ENST00000356860	Transcript	missense_variant	benign(0)
chr7	99032823	99032823	*PTCD1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.P64T	ENSG00000106246	ENST00000555673	Transcript	missense_variant	benign(0.311)
chr8	29761077	29761077	*CSMD1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P13	p.Y2082N	ENSG00000183117	ENST00000537824	Transcript	missense_variant	possibly_damaging(0.617)
chr8	95508665	95508665	*KIAA1429*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P13	p.A1425V	ENSG00000164944	ENST00000297591	Transcript	missense_variant	benign(0.009)
chr9	101748165	101748165	*COL15A1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.E140G	ENSG00000204291	ENST00000375001	Transcript	missense_variant	probably_damaging(0.985)
chr9	138589362	138589362	*SOHLH1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P13	p.S153G	ENSG00000165643	ENST00000425225	Transcript	missense_variant	benign(0)
chr9	96030136	96030136	*WNK2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P13	p.R1269G	ENSG00000165238	ENST00000297954	Transcript	missense_variant	unknown(0)
chrX	114418979	114418979	*LRCH2*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.E206*	ENSG00000130224	ENST00000317135	Transcript	stop_gained	NA
chrX	134990759	134990759	*SAGE1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P13	p.M475T	ENSG00000181433	ENST00000535938	Transcript	missense_variant	benign(0.061)
chrX	141943	141943	*CSF2RA*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P13	p.R289*	ENSG00000198223	ENST00000417535	Transcript	stop_gained	NA
chrX	148664241	148664241	*MAGEA9B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.A199S	ENSG00000123584	ENST00000243314	Transcript	missense_variant	benign(0.149)
chrX	148868467	148868467	*MAGEA9*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P13	p.A199S	ENSG00000166008	ENST00000298974	Transcript	missense_variant	benign(0.149)
chrX	49066496	49066496	*CACNA1F*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P13	p.L1543P	ENSG00000102001	ENST00000376265	Transcript	missense_variant	benign(0.429)
chrX	52786937	52786937	*SSX2B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P13	p.P113T	ENSG00000157950	ENST00000375515	Transcript	missense_variant	possibly_damaging(0.833)

chr1	12854098	12854098	*PRAMEF1*	Missense_Mutation	.	SNP	G	G	T	rs569213907	shansha n_et_al_P130	p.V108F	ENSG00000116721	ENST00000332296	Transcript	missense_variant	probably_damaging(0.998)
chr1	168007624	168007624	*DCAF6*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P130	p.K542R	ENSG00000143164	ENST00000367840	Transcript	missense_variant	benign(0.015)
chr1	180044231	180044231	*CEP350*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.R1881L	ENSG00000135837	ENST00000367607	Transcript	missense_variant	probably_damaging(0.999)
chr1	211910118	211910118	*EIF4G3*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.C936F	ENSG00000075151	ENST00000602326	Transcript	missense_variant	probably_damaging(1)
chr1	237824130	237824130	*RYR2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.W2773C	ENSG00000198626	ENST00000366574	Transcript	missense_variant	probably_damaging(0.973)
chr1	45473170	45473170	*HECTD3*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.R473L	ENSG00000126107	ENST00000372172	Transcript	missense_variant	benign(0.241)
chr10	101590191	101590191	*ABCC2*	Splice_Site	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.X916_splice	ENSG00000023839	ENST00000370449	Transcript	splice_donor_variant	NA
chr10	115357747	115357747	*NRAP*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P130	p.A1438V	ENSG00000197893	ENST00000359988	Transcript	missense_variant	probably_damaging(0.998)
chr10	125805589	125805589	*CHST15*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P130	p.V47E	ENSG00000182022	ENST00000346248	Transcript	missense_variant	benign(0.398)
chr10	135126297	135126297	*ZNF511*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.P229H	ENSG00000198546	ENST00000361518	Transcript	missense_variant	probably_damaging(0.997)
chr10	226061	226061	*ZMYND11*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P130	p.I37V	ENSG00000015171	ENST00000397962	Transcript	missense_variant	benign(0.038)
chr10	50666905	50666905	*ERCC6*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P130	p.S1480P	ENSG00000225830	ENST00000355832	Transcript	missense_variant	benign(0.001)
chr10	52588005	52588005	*A1CF*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.E227*	ENSG00000148584	ENST00000373995	Transcript	stop_gained	NA
chr10	70764800	70764800	*KIAA1279*	Splice_Site	.	SNP	A	A	G	novel	shansha n_et_al_P130	p.X176_splice	ENSG00000198954	ENST00000361983	Transcript	splice_acceptor_variant	NA
chr11	111594376	111594376	*SIK2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.F768L	ENSG00000170145	ENST00000304987	Transcript	missense_variant	possibly_damaging(0.64)
chr11	118827115	118827115	*UPK2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.L19M	ENSG00000110375	ENST00000264031	Transcript	missense_variant	unknown(0)
chr11	123909020	123909020	*OR10G7*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P130	p.S230L	ENSG00000182634	ENST00000330487	Transcript	missense_variant	possibly_damaging(0.555)
chr11	64323775	64323775	*SLC22A11*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P130	p.A102T	ENSG00000168065	ENST00000301891	Transcript	missense_variant	probably_damaging(0.969)
chr11	64367893	64367893	*SLC22A12*	Missense_Mutation	.	SNP	C	C	T	rs572933684	shansha n_et_al_P130	p.A447V	ENSG00000197891	ENST00000377574	Transcript	missense_variant	benign(0.393)
chr12	104461804	104461804	*HCFC2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.S131I	ENSG00000111727	ENST00000229330	Transcript	missense_variant	probably_damaging(0.974)
chr12	70698733	70698733	*PTPN6*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P130	p.R574P	ENSG00000111679	ENST00000456013	Transcript	missense_variant	unknown(0)
chr12	88568497	88568497	*TMTC3*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P130	p.A438V	ENSG00000139324	ENST00000267112	Transcript	missense_variant	possibly_damaging(0.761)
chr13	48947539	48947539	*RB1*	Splice_Site	.	SNP	A	A	G	novel	shansha n_et_al_P130	p.X376_splice	ENSG00000139687	ENST00000267163	Transcript	splice_acceptor_variant	NA
chr13	61103227	61103227	*TDRD3*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.G623V	ENSG00000083544	ENST00000535286	Transcript	missense_variant	benign(0.331)
chr14	53619451	53619451	*DDHD1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.Q122H	ENSG00000100523	ENST00000323669	Transcript	missense_variant	benign(0.229)
chr14	64628920	64628920	*SYNE2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.Q5409K	ENSG00000054654	ENST00000358025	Transcript	missense_variant	benign(0.238)
chr14	74876302	74876302	*SYNDIG1L*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P130	p.A49V	ENSG00000183379	ENST00000331628	Transcript	missense_variant	benign(0.073)
chr15	40708323	40708323	*IVD*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.C339F	ENSG00000128928	ENST00000487418	Transcript	missense_variant	possibly_damaging(0.846)
chr15	57837794	57837794	*CGNL1*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P130	p.R1169G	ENSG00000128849	ENST00000281282	Transcript	missense_variant	probably_damaging(0.996)
chr15	72454657	72454657	*GRAMD2*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P130	p.Q340E	ENSG00000175318	ENST00000309731	Transcript	missense_variant	possibly_damaging(0.701)
chr16	11369763	11369763	*PRM2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.R101S	ENSG00000122304	ENST00000241808	Transcript	missense_variant	unknown(0)
chr16	50816304	50816304	*CYLD*	Nonsense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.E585*	ENSG00000083799	ENST00000427738	Transcript	stop_gained	NA
chr16	53501036	53501036	*RBL2*	Nonsense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P130	p.R644*	ENSG00000103479	ENST00000262133	Transcript	stop_gained	NA
chr16	89789814	89789814	*ZNF276*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P130	p.D235Y	ENSG00000158805	ENST00000443381	Transcript	missense_variant	possibly_damaging(0.834)
chr17	10300214	10300214	*MYH8*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P130	p.R1423L	ENSG00000133020	ENST00000403437	Transcript	missense_variant	probably_damaging(0.976)
chr17	3301340	3301340	*OR1E1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P130	p.R122H	ENSG00000180016	ENST00000322608	Transcript	missense_variant	benign(0.253)

chr17	37599809	37599809	*MED1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P130	p.L69V	ENSG00000125686	ENST00000300651	Transcript	missense_variant	probably_damaging(0.969)
chr17	42161198	42161198	*HDAC5*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P130	p.A778G	ENSG00000108840	ENST00000225983	Transcript	missense_variant	probably_damaging(0.987)
chr17	60024327	60024327	*MED13*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P130	p.S2115G	ENSG00000108510	ENST00000397786	Transcript	missense_variant	probably_damaging(0.966)
chr17	71394212	71394212	*SDK2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.R1106S	ENSG00000069188	ENST00000392650	Transcript	missense_variant	possibly_damaging(0.813)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P130	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr18	34297875	34297875	*FHOD3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.D697Y	ENSG00000134775	ENST00000257209	Transcript	missense_variant	probably_damaging(0.999)
chr18	34335264	34335264	*FHOD3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P130	p.M1297T	ENSG00000134775	ENST00000257209	Transcript	missense_variant	possibly_damaging(0.882)
chr19	15132468	15132470	*CCDC105*	In_Frame_Del	.	DEL	TCC	TCC	-	novel	shanshan_et_al_P130	p.L362del	ENSG00000160994	ENST00000295744	Transcript	inframe_deletion	NA
chr19	18965991	18965991	*UPF1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.G495V	ENSG00000005007	ENST00000262803	Transcript	missense_variant	probably_damaging(1)
chr19	47933653	47933653	*SLC8A2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.G820V	ENSG00000118160	ENST00000236877	Transcript	missense_variant	probably_damaging(1)
chr19	49165272	49165272	*NTN5*	Missense_Mutation	.	SNP	C	C	T	rs375834403	shanshan_et_al_P130	p.E378K	ENSG00000142233	ENST00000270235	Transcript	missense_variant	possibly_damaging(0.899)
chr19	51768646	51768646	*SIGLECL1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.S16Y	ENSG00000179213	ENST00000316401	Transcript	missense_variant	probably_damaging(0.955)
chr19	56466968	56466968	*NLRP8*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.A515E	ENSG00000179709	ENST00000291971	Transcript	missense_variant	probably_damaging(0.98)
chr2	101023110	101023110	*CHST10*	Missense_Mutation	.	SNP	C	C	T	rs150069978	shanshan_et_al_P130	p.A10T	ENSG00000115526	ENST00000264249	Transcript	missense_variant	benign(0.008)
chr2	153519583	153519583	*PRPF40A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.A731D	ENSG00000196504	ENST00000410080	Transcript	missense_variant	benign(0.086)
chr2	49195955	49195955	*FSHR*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.A246S	ENSG00000170820	ENST00000406846	Transcript	missense_variant	probably_damaging(0.995)
chr2	74684885	74684885	*INO80B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.C322F	ENSG00000115274	ENST00000233331	Transcript	missense_variant	probably_damaging(0.993)
chr20	32255577	32255577	*ACTL10*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.E92*	ENSG00000182584	ENST00000330271	Transcript	stop_gained	NA
chr21	42778915	42778915	*MX2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.A632D	ENSG00000183486	ENST00000330714	Transcript	missense_variant	probably_damaging(0.955)
chr21	47545900	47545901	*COL6A2*	Frame_Shift_Del	.	DEL	GT	GT	-	novel	shanshan_et_al_P130	p.F726Cfs*15	ENSG00000142173	ENST00000300527	Transcript	frameshift_variant	NA
chr22	22313604	22313604	*TOP3B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.G602V	ENSG00000100038	ENST00000398793	Transcript	missense_variant	benign(0.007)
chr22	38038582	38038582	*SH3BP1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P130	p.A82T	ENSG00000100092	ENST00000357436	Transcript	missense_variant	probably_damaging(1)
chr22	40676044	40676044	*TNRC6B*	Missense_Mutation	.	SNP	A	A	G	rs201343353	shanshan_et_al_P130	p.N1103S	ENSG00000100354	ENST00000454349	Transcript	missense_variant	probably_damaging(0.989)
chr3	101390190	101390190	*ZBTB11*	Missense_Mutation	.	SNP	C	C	T	rs368388126	shanshan_et_al_P130	p.V188M	ENSG00000066422	ENST00000312938	Transcript	missense_variant	possibly_damaging(0.595)
chr3	133495987	133495987	*TF*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.C656F	ENSG00000091513	ENST00000402696	Transcript	missense_variant	probably_damaging(0.999)
chr3	133547664	133547664	*RAB6B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.P199T	ENSG00000154917	ENST00000285208	Transcript	missense_variant	benign(0.001)
chr3	33481280	33481280	*UBP1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.A21S	ENSG00000153560	ENST00000283629	Transcript	missense_variant	benign(0.142)
chr3	47142965	47142965	*SETD2*	Nonsense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P130	p.Y1666*	ENSG00000181555	ENST00000409792	Transcript	stop_gained	NA
chr4	1018917	1018917	*FGFRL1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P130	p.P433S	ENSG00000127418	ENST00000398484	Transcript	missense_variant	benign(0.009)
chr4	156274410	156274410	*MAP9*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.A488D	ENSG00000164114	ENST00000311277	Transcript	missense_variant	probably_damaging(1)
chr4	156294512	156294512	*MAP9*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P130	p.P86L	ENSG00000164114	ENST00000311277	Transcript	missense_variant	benign(0.007)
chr4	44638032	44638032	*YIPF7*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P130	p.A87T	ENSG00000177752	ENST00000332990	Transcript	missense_variant	benign(0)
chr4	92520063	92520063	*CCSER1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P130	p.A853G	ENSG00000184305	ENST00000509176	Transcript	missense_variant	benign(0.081)
chr4	93328938	93328938	*USP17L25*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P130	p.D421G	ENSG00000230430	ENST00000509271	Transcript	missense_variant	benign(0)
chr5	138758421	138758421	*DNAJC18*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.P252H	ENSG00000170464	ENST00000302060	Transcript	missense_variant	probably_damaging(0.99)
chr5	140263706	140263706	*PCDHA13*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P130	p.A618V	ENSG00000239389	ENST00000289272	Transcript	missense_variant	benign(0.007)

chr5	140554686	140554686	*PCDHB7*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.S757Y	ENSG00000113212	ENST00000231137	Transcript	missense_variant	benign(0.185)
chr5	166750524	166750524	*MYO10*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.C1634*	ENSG00000145555	ENST00000513610	Transcript	stop_gained	NA
chr5	391351107	391351107	*FYB*	Missense_Mutation	.	SNP	G	G	T	rs193074720	shanshan_et_al_P130	p.P519T	ENSG00000082074	ENST00000540520	Transcript	missense_variant	probably_damaging(0.996)
chr5	393827768	393827768	*DAB2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P130	p.I431M	ENSG00000153071	ENST00000320816	Transcript	missense_variant	possibly_damaging(0.781)
chr6	125550371	125550371	*TPD52L1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.Q81H	ENSG00000111907	ENST00000534000	Transcript	missense_variant	benign(0.049)
chr6	125550393	125550393	*TPD52L1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.D89Y	ENSG00000111907	ENST00000534000	Transcript	missense_variant	probably_damaging(0.995)
chr6	146673473	146673473	*GRM1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P130	p.Q425R	ENSG00000152822	ENST00000361719	Transcript	missense_variant	benign(0.281)
chr6	160968906	160968906	*LPA*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.P1740Q	ENSG00000198670	ENST00000447678	Transcript	missense_variant	possibly_damaging(0.549)
chr6	427137 84	427137 84	*TBCC*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P130	p.A10T	ENSG00000124659	ENST00000246625	Transcript	missense_variant	benign(0.154)
chr6	781720 48	781720 48	*HTR1B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.G358V	ENSG00000135312	ENST00000369947	Transcript	missense_variant	probably_damaging(1)
chr6	830751 66	830751 66	*TPBG*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.S163*	ENSG00000146242	ENST00000369750	Transcript	stop_gained	NA
chr7	150763 726	150763 726	*SLC4A2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P130	p.N234I	ENSG00000164889	ENST00000485713	Transcript	missense_variant	probably_damaging(0.929)
chr7	156799 271	156799 271	*MNX1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P130	p.Q252*	ENSG00000130675	ENST00000252971	Transcript	stop_gained	NA
chr7	201989 86	201989 86	*MACC1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P130	p.I333T	ENSG00000183742	ENST00000400331	Transcript	missense_variant	possibly_damaging(0.548)
chr7	552292 63	552292 63	*EGFR*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.V524F	ENSG00000146648	ENST00000275493	Transcript	missense_variant	benign(0.003)
chr7	992604 71	992604 71	*CYP3A5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.S278Y	ENSG00000106258	ENST00000222982	Transcript	missense_variant	possibly_damaging(0.679)
chr8	104427 611	104427 611	*DCAF13*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P130	p.R131S	ENSG00000164934	ENST00000297579	Transcript	missense_variant	benign(0)
chr8	105361 442	105361 442	*DCSTAMP*	Nonsense_Mutation	.	SNP	C	C	A	rs144238227	shanshan_et_al_P130	p.S221*	ENSG00000164935	ENST00000297581	Transcript	stop_gained	NA
chr8	143566 123	143566 123	*BAI1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P130	p.L769Q	ENSG00000181790	ENST00000517894	Transcript	missense_variant	probably_damaging(0.928)
chr8	665995	665995	*ERICH1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P130	p.K12T	ENSG00000104714	ENST00000262109	Transcript	missense_variant	probably_damaging(0.996)
chr8	727560 27	727560 27	*MSC*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.R129S	ENSG00000178860	ENST00000325509	Transcript	missense_variant	probably_damaging(0.966)
chr9	140948 389	140948 389	*CACNA1B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P130	p.A1300E	ENSG00000148408	ENST00000371372	Transcript	missense_variant	probably_damaging(0.996)
chrX	101093 763	101093 763	*NXF5*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P130	p.L245P	ENSG00000126952	ENST00000537026	Transcript	missense_variant	possibly_damaging(0.666)
chrX	101575 974	101575 974	*NXF2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P130	p.L356P	ENSG00000185554	ENST00000395088	Transcript	missense_variant	possibly_damaging(0.897)
chrX	101620 976	101620 976	*NXF2B*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P130	p.L356P	ENSG00000185945	ENST00000457521	Transcript	missense_variant	possibly_damaging(0.897)
chr1	124603 35	124603 35	*VPS13D*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Q3911L	ENSG00000048707	ENST00000358136	Transcript	missense_variant	probably_damaging(0.954)
chr1	160604 625	160604 625	*SLAMF1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.L160M	ENSG00000117090	ENST00000302035	Transcript	missense_variant	benign(0.194)
chr1	179623 487	179623 487	*TDRD5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.E771V	ENSG00000162782	ENST00000444136	Transcript	missense_variant	possibly_damaging(0.597)
chr1	196392 233	196392 233	*KCNT2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.A378S	ENSG00000162687	ENST00000294725	Transcript	missense_variant	probably_damaging(0.996)
chr1	203830 821	203830 821	*SNRPE*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.K12*	ENSG00000182004	ENST00000414487	Transcript	stop_gained	NA
chr1	215820 908	215820 908	*USH2A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.G4916D	ENSG00000042781	ENST00000307340	Transcript	missense_variant	probably_damaging(1)
chr1	215901 593	215901 593	*USH2A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.G3949S	ENSG00000042781	ENST00000307340	Transcript	missense_variant	possibly_damaging(0.671)
chr1	243716 053	243716 053	*AKT3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.L381M	ENSG00000117020	ENST00000366539	Transcript	missense_variant	possibly_damaging(0.844)
chr1	276210 03	276210 03	*WDTC1*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.X253_splice	ENSG00000142784	ENST00000361771	Transcript	splice_acceptor_variant	NA
chr1	384884 01	384884 01	*UTP11L*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.N200Y	ENSG00000183520	ENST00000373014	Transcript	missense_variant	benign(0.167)
chr1	705047 36	705047 36	*LRRC7*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.S1039T	ENSG00000033122	ENST00000353833	Transcript	missense_variant	benign(0.004)

chr1	75693538	75693538	*SLC44A5*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P131	p.I286M	ENSG00000137968	ENST00000370855	Transcript	missense_variant	probably_damaging(0.954)
chr10	134722047	134722047	*TTC40*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.R950L	ENSG00000171811	ENST00000368586	Transcript	missense_variant	possibly_damaging(0.827)
chr10	47193284	47193284	*AGAP10*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.G324S	ENSG00000204172	ENST00000413193	Transcript	missense_variant	unknown(0)
chr10	78608233	78608233	*TAF3*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P131	p.R51Gfs*22	ENSG00000165632	ENST00000344293	Transcript	frameshift_variant	NA
chr11	10821805	10821805	*EIF4G2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P131	p.I651V	ENSG00000110321	ENST00000526148	Transcript	missense_variant	benign(0.016)
chr11	17190708	17190708	*PIK3C2A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P131	p.P194L	ENSG00000011405	ENST00000265970	Transcript	missense_variant	benign(0.188)
chr11	30032819	30032819	*KCNA4*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P131	p.H469Q	ENSG00000182255	ENST00000328224	Transcript	missense_variant	benign(0.078)
chr11	57561528	57561528	*CTNND1*	Missense_Mutation	.	SNP	c	c	T	rs374173249	shanshan_et_al_P131	p.S81L	ENSG00000198561	ENST00000399050	Transcript	missense_variant	benign(0.035)
chr12	107080718	107080718	*RFX4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Y154F	ENSG00000111783	ENST00000357881	Transcript	missense_variant	benign(0.205)
chr12	11506787	11506787	*PRB1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.G84R	ENSG00000251655	ENST00000500254	Transcript	missense_variant	unknown(0)
chr12	29648281	29648281	*OVCH1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.N131Y	ENSG00000187950	ENST00000318184	Transcript	missense_variant	probably_damaging(0.962)
chr12	29945677	29945677	*RHNO1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Q12L	ENSG00000171792	ENST00000489288	Transcript	missense_variant	benign(0.022)
chr12	39967595	39967595	*ABCD2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.D642E	ENSG00000173208	ENST00000308666	Transcript	missense_variant	probably_damaging(0.926)
chr12	50452758	50452758	*ASIC1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.H70L	ENSG00000110881	ENST00000228468	Transcript	missense_variant	benign(0)
chr12	53237959	53237959	*KRT78*	Missense_Mutation	.	SNP	A	A	T	rs138924880	shanshan_et_al_P131	p.M322K	ENSG00000170423	ENST00000304620	Transcript	missense_variant	benign(0.362)
chr12	78481489	78481489	*GDF3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.E59V	ENSG00000184344	ENST00000329913	Transcript	missense_variant	possibly_damaging(0.623)
chr12	95479603	95479603	*FGD6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.W1354R	ENSG00000180263	ENST00000343958	Transcript	missense_variant	probably_damaging(1)
chr13	108518427	108518427	*FAM155A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P131	p.P173H	ENSG00000204442	ENST00000375915	Transcript	missense_variant	probably_damaging(0.999)
chr13	21562330	21562330	*LATS2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q530L	ENSG00000150457	ENST00000382592	Transcript	missense_variant	benign(0.205)
chr13	24797806	24797806	*SPATA13*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.M247L	ENSG00000182957	ENST00000424834	Transcript	missense_variant	benign(0.001)
chr13	36767864	36767864	*SOHLH2*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.X186_splice	ENSG00000120669	ENST00000554962	Transcript	splice_acceptor_variant	NA
chr13	53035553	53035553	*CKAP2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P131	p.D199H	ENSG00000136108	ENST00000378037	Transcript	missense_variant	possibly_damaging(0.835)
chr13	98673301	98673301	*IPO5*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.I1059V	ENSG00000065150	ENST00000261574	Transcript	missense_variant	benign(0.101)
chr14	21789464	21789464	*RPGRIP1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.L505Q	ENSG00000092200	ENST00000400017	Transcript	missense_variant	probably_damaging(0.977)
chr14	31420109	31420109	*STRN3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.S168C	ENSG00000196792	ENST00000357479	Transcript	missense_variant	probably_damaging(0.998)
chr14	62542072	62542072	*SYT16*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.S319F	ENSG00000139973	ENST00000430451	Transcript	missense_variant	benign(0.289)
chr14	69814679	69814679	*GALNT16*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.P500Q	ENSG00000100626	ENST00000337827	Transcript	missense_variant	benign(0.002)
chr14	94395463	94395463	*FAM181A*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.K340*	ENSG00000140067	ENST00000267594	Transcript	stop_gained	NA
chr15	45968456	45968456	*SQRDL*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.Q271R	ENSG00000137767	ENST00000260324	Transcript	missense_variant	benign(0.033)
chr15	49776595	49776595	*FGF7*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P131	p.G160V	ENSG00000140285	ENST00000267843	Transcript	missense_variant	probably_damaging(1)
chr15	55664086	55664086	*CCPG1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.K204M	ENSG00000260916	ENST00000442196	Transcript	missense_variant	possibly_damaging(0.847)
chr15	73635865	73635865	*HCN4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.L357H	ENSG00000138622	ENST00000261917	Transcript	missense_variant	possibly_damaging(0.472)
chr15	74166078	74166078	*TBC1D21*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P131	p.L10V	ENSG00000167139	ENST00000300504	Transcript	missense_variant	benign(0.015)
chr15	79068662	79068662	*ADAMTS7*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.G525V	ENSG00000136378	ENST00000388820	Transcript	missense_variant	probably_damaging(1)
chr16	22114849	22114849	*VWA3A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.K161M	ENSG00000175267	ENST00000389398	Transcript	missense_variant	probably_damaging(0.966)
chr16	3779361	3779361	*CREBBP*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q1896L	ENSG00000005339	ENST00000262367	Transcript	missense_variant	unknown(0)

chr17	15609773	15609773	*ZNF286A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.R67W	ENSG00000187607	ENST00000464847	Transcript	missense_variant	possibly_damaging(0.807)
chr17	26861836	26861836	*FOXN1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.P416Q	ENSG00000109101	ENST00000226247	Transcript	missense_variant	benign(0.323)
chr17	39203302	39203302	*KRTAP2-1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.C73Y	ENSG00000212725	ENST00000391419	Transcript	missense_variant	probably_damaging(0.99)
chr17	56060741	56060741	*VEZF1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P131	p.S16F	ENSG00000136451	ENST00000581208	Transcript	missense_variant	benign(0.205)
chr17	63923809	63923809	*CEP112*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.X625_splice	ENSG00000154240	ENST00000392769	Transcript	splice_acceptor_variant	NA
chr17	7578239	7578239	*TP53*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.E204*	ENSG00000141510	ENST00000269305	Transcript	stop_gained	NA
chr18	21427601	21427601	*LAMA3*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P131	p.P1369A	ENSG00000053747	ENST00000313654	Transcript	missense_variant	benign(0.039)
chr19	15783833	15783833	*MBD3*	Missense_Mutation	.	SNP	c	c	T	novel	shanshan_et_al_P131	p.E278K	ENSG00000071655	ENST00000156825	Transcript	missense_variant	benign(0.292)
chr19	23836228	23836228	*ZNF675*	Missense_Mutation	.	SNP	T	T	A	rs562318908	shanshan_et_al_P131	p.T503S	ENSG00000197372	ENST00000359788	Transcript	missense_variant	benign(0.012)
chr19	28345100	28345100	*ZNF554*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.H426L	ENSG00000172006	ENST00000317243	Transcript	missense_variant	probably_damaging(0.999)
chr19	36213507	36213507	*KMT2B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.H870L	ENSG00000272333	ENST00000222270	Transcript	missense_variant	possibly_damaging(0.84)
chr19	37117073	37117073	*ZNF382*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P131	p.E92*	ENSG00000161298	ENST00000292928	Transcript	stop_gained	NA
chr19	38160851	38160851	*ZNF781*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.G67R	ENSG00000196381	ENST00000358582	Transcript	missense_variant	probably_damaging(0.968)
chr19	45296780	45296780	*CBLC*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P131	p.W396L	ENSG00000142273	ENST00000270279	Transcript	missense_variant	benign(0.021)
chr19	50370454	50370454	*PNKP*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.E3V	ENSG00000039650	ENST00000322344	Transcript	missense_variant	benign(0.051)
chr19	56244066	56244066	*NLRP9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.K377N	ENSG00000185792	ENST00000332836	Transcript	missense_variant	benign(0.384)
chr19	57036779	57036779	*ZNF471*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Q448L	ENSG00000196263	ENST00000308031	Transcript	missense_variant	probably_damaging(0.988)
chr19	58199438	58199438	*ZNF551*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.S599C	ENSG00000204519	ENST00000282296	Transcript	missense_variant	probably_damaging(0.996)
chr2	166165177	166165177	*SCN2A*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P131	p.Y160H	ENSG00000136531	ENST00000357398	Transcript	missense_variant	probably_damaging(0.999)
chr2	179247810	179247810	*OSBPL6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P131	p.A586T	ENSG00000079156	ENST00000392505	Transcript	missense_variant	possibly_damaging(0.686)
chr2	209198037	209198037	*PIKFYVE*	Splice_Site	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.X1322_splice	ENSG00000115020	ENST00000264380	Transcript	splice_acceptor_variant	NA
chr2	219486194	219486194	*PLCD4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.W138R	ENSG00000115556	ENST00000450993	Transcript	missense_variant	possibly_damaging(0.534)
chr2	220149603	220149603	*DNAJB2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Q290L	ENSG00000135924	ENST00000336576	Transcript	missense_variant	benign(0.002)
chr2	236659018	236659018	*AGAP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.P187S	ENSG00000157985	ENST00000304032	Transcript	missense_variant	probably_damaging(0.974)
chr2	47273501	47273501	*TTC7A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.E617V	ENSG00000068724	ENST00000319190	Transcript	missense_variant	benign(0.424)
chr2	70906095	70906095	*ADD2*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.X376_splice	ENSG00000075340	ENST00000264436	Transcript	splice_acceptor_variant	NA
chr2	99909019	99909019	*LYG1*	Frame_Shift_Del	.	DEL	C	C	-	rs147183942	shanshan_et_al_P131	p.R43Lfs*4	ENSG00000144214	ENST00000409448	Transcript	frameshift_variant	NA
chr20	4705585	4705585	*PRND*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.Q130K	ENSG00000171864	ENST00000305817	Transcript	missense_variant	benign(0)
chr21	40665751	40665751	*BRWD1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P131	p.I273L	ENSG00000185658	ENST00000333229	Transcript	missense_variant	possibly_damaging(0.881)
chr22	25282591	25282591	*SGSM1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P131	p.R611C	ENSG00000167037	ENST00000400359	Transcript	missense_variant	probably_damaging(0.991)
chr22	32482268	32482268	*SLC5A1*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.C361*	ENSG00000100170	ENST00000266088	Transcript	stop_gained	NA
chr22	40075796	40075796	*CACNA1I*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P131	p.D1822N	ENSG00000100346	ENST00000402142	Transcript	missense_variant	possibly_damaging(0.555)
chr22	43995979	43995979	*EFCAB6*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q949L	ENSG00000186976	ENST00000267726	Transcript	missense_variant	possibly_damaging(0.71)
chr22	50502577	50502577	*MLC1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.Q315H	ENSG00000100427	ENST00000311597	Transcript	missense_variant	benign(0.439)
chr3	115395178	115395178	*GAP43*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P131	p.D153Mfs*93	ENSG00000172020	ENST00000393780	Transcript	frameshift_variant	NA
chr3	123010209	123010209	*ADCY5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.K1026N	ENSG00000173175	ENST00000462833	Transcript	missense_variant	probably_damaging(0.992)

chr3	129023648	129023648	*HMCES*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.K349*	ENSG00000183624	ENST00000383463	Transcript	stop_gained	NA
chr3	170625534	170625534	*EIF5A2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q21L	ENSG00000163577	ENST00000295822	Transcript	missense_variant	possibly_damaging(0.51)
chr3	176755903	176755903	*TBL1XR1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.D369Y	ENSG00000177565	ENST00000430069	Transcript	missense_variant	probably_damaging(0.996)
chr3	32586594	32586594	*DYNC1LI1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q114H	ENSG00000144635	ENST00000273130	Transcript	missense_variant	benign(0.012)
chr3	383699	383699	*CHL1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.F205I	ENSG00000134121	ENST00000256509	Transcript	missense_variant	probably_damaging(0.975)
chr3	38946723	38946723	*SCN11A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.R521S	ENSG00000168356	ENST00000302328	Transcript	missense_variant	probably_damaging(0.982)
chr3	46775694	46775694	*PRSS46*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.C41S	ENSG00000261603	ENST00000463091	Transcript	missense_variant	probably_damaging(0.913)
chr3	51749744	51749744	*GRM2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.T652N	ENSG00000164082	ENST00000395052	Transcript	missense_variant	probably_damaging(1)
chr3	51750100	51750100	*GRM2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.I771V	ENSG00000164082	ENST00000395052	Transcript	missense_variant	benign(0.361)
chr4	188924520	188924520	*ZFP42*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P131	p.A187T	ENSG00000179059	ENST00000326866	Transcript	missense_variant	benign(0.001)
chr4	22529600	22529600	*MXD4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q108L	ENSG00000123933	ENST00000337190	Transcript	missense_variant	benign(0.042)
chr4	48993572	48993572	*CWH43*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.S113T	ENSG00000109182	ENST00000226432	Transcript	missense_variant	benign(0.019)
chr4	84358198	84358198	*HELQ*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.K621*	ENSG00000163312	ENST00000295488	Transcript	stop_gained	NA
chr5	101834523	101834523	*SLCO6A1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P131	p.S9Y	ENSG00000205359	ENST00000506729	Transcript	missense_variant	benign(0.174)
chr5	132535320	132535320	*FSTL4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P131	p.A666S	ENSG00000053108	ENST00000265342	Transcript	missense_variant	benign(0.007)
chr5	133643968	133643968	*CDKL3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P131	p.I409V	ENSG00000006837	ENST00000265334	Transcript	missense_variant	benign(0.001)
chr5	137420325	137420325	*WNT8A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P131	p.A81T	ENSG00000061492	ENST00000398754	Transcript	missense_variant	probably_damaging(0.994)
chr5	156346517	156346517	*TIMD4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.N363I	ENSG00000145850	ENST00000274532	Transcript	missense_variant	possibly_damaging(0.809)
chr5	178311177	178311177	*ZNF354B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.E575V	ENSG00000178338	ENST00000322434	Transcript	missense_variant	probably_damaging(0.993)
chr5	24487809	24487809	*CDH10*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P131	p.E777G	ENSG00000040731	ENST00000264463	Transcript	missense_variant	benign(0.327)
chr5	78915873	78915873	*PAPD4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Q65L	ENSG00000164329	ENST00000453514	Transcript	missense_variant	benign(0.021)
chr6	109980447	109980447	*AK9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.E205V	ENSG00000155085	ENST00000424296	Transcript	missense_variant	benign(0.173)
chr6	136709537	136709537	*MAP7*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.S196C	ENSG00000135525	ENST00000454590	Transcript	missense_variant	probably_damaging(0.94)
chr6	152532640	152532640	*SYNE1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q7526H	ENSG00000131018	ENST00000367255	Transcript	missense_variant	benign(0.396)
chr6	159657345	159657345	*FNDC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.W1356R	ENSG00000164694	ENST00000297267	Transcript	missense_variant	unknown(0)
chr6	42928567	42928567	*GNMT*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.Q21R	ENSG00000124713	ENST00000372808	Transcript	missense_variant	probably_damaging(0.993)
chr6	65301088	65301088	*EYS*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.T1558S	ENSG00000188107	ENST00000503581	Transcript	missense_variant	possibly_damaging(0.866)
chr6	88120348	88120348	*C6ORF165*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.R52G	ENSG00000272514	ENST00000369562	Transcript	missense_variant	benign(0.119)
chr6	88125402	88125402	*C6ORF165*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P131	NA	ENSG00000272514	ENST00000369562	Transcript	splice_acceptor_variant	NA
chr7	100087151	100087151	*NYAP1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.I603F	ENSG00000166924	ENST00000300179	Transcript	missense_variant	benign(0.17)
chr7	103243800	103243800	*RELN*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.E1095V	ENSG00000189056	ENST00000428762	Transcript	missense_variant	probably_damaging(0.997)
chr7	140374503	140374503	*ADCK2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P131	p.K342N	ENSG00000133597	ENST00000072869	Transcript	missense_variant	probably_damaging(0.924)
chr7	147815235	147815235	*CNTNAP2*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P131	p.P804Qfs*27	ENSG00000174469	ENST00000361727	Transcript	frameshift_variant	NA
chr7	150831646	150831654	*AGAP3*	In_Frame_Del	.	DEL	GGGGGCACA	GGGGGCACA	-	novel	shanshan_et_al_P131	p.G496_T498del	ENSG00000133612	ENST00000397238	Transcript	inframe_deletion	NA
chr7	20438523	20438523	*ITGB8*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.V396E	ENSG00000105855	ENST00000222573	Transcript	missense_variant	benign(0.201)
chr7	26297366	26297366	*IQCE*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.R414*	ENSG00000106012	ENST00000402050	Transcript	stop_gained	NA

chr7	27148292	27148292	*HOXA3*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.K192*	ENSG00000105997	ENST00000396352	Transcript	stop_gained	NA
chr7	38457432	38457432	*AMPH*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.E464V	ENSG00000078053	ENST00000356264	Transcript	missense_variant	benign(0.024)
chr7	42005003	42005003	*GLI3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Y1223F	ENSG00000106571	ENST00000395925	Transcript	missense_variant	benign(0.004)
chr7	44279206	44279206	*CAMK2B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.M335L	ENSG00000058404	ENST00000395749	Transcript	missense_variant	benign(0.039)
chr7	45115444	45115444	*CCM2*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.K396*	ENSG00000136280	ENST00000381112	Transcript	stop_gained	NA
chr7	63982251	63982251	*ZNF680*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Y294F	ENSG00000173041	ENST00000309683	Transcript	missense_variant	benign(0.026)
chr7	74212526	74212526	*GTF2IRD2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.Q442L	ENSG00000196275	ENST00000405086	Transcript	missense_variant	benign(0.432)
chr7	97863051	97863051	*TECPR1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.R452W	ENSG00000205356	ENST00000447648	Transcript	missense_variant	benign(0.325)
chr8	116616395	116616395	*TRPS1*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.R601*	ENSG00000104447	ENST00000395715	Transcript	stop_gained	NA
chr8	124382158	124382158	*ATAD2*	Missense_Mutation	.	SNP	t	t	A	rs373069275	shanshan_et_al_P131	p.E278D	ENSG00000156802	ENST00000287394	Transcript	missense_variant	benign(0.002)
chr8	65494083	65494083	*BHLHE22*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P131	p.N246D	ENSG00000180828	ENST00000321870	Transcript	missense_variant	benign(0.044)
chr9	138660691	138660691	*KCNT1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.L473Q	ENSG00000107147	ENST00000371757	Transcript	missense_variant	probably_damaging(0.996)
chr9	139903308	139903308	*ABCA2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P131	p.T2315S	ENSG00000107331	ENST00000341511	Transcript	missense_variant	benign(0.002)
chr9	27455195	27455195	*MOB3B*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P131	p.M118I	ENSG00000120162	ENST00000262244	Transcript	missense_variant	benign(0.006)
chr9	96439033	96439033	*PHF2*	Missense_Mutation	.	SNP	G	G	C	rs109928557	shanshan_et_al_P131	p.S997T	ENSG00000197724	ENST00000359246	Transcript	missense_variant	unknown()
chr9	96439035	96439035	*PHF2*	Missense_Mutation	.	SNP	A	A	C	rs109928558	shanshan_et_al_P131	p.T998P	ENSG00000197724	ENST00000359246	Transcript	missense_variant	unknown()
chrX	110951488	110951488	*ALG13*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.K206I	ENSG00000101901	ENST00000394780	Transcript	missense_variant	possibly_damaging(0.897)
chrX	47867271	47867271	*SPACA5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Y24F	ENSG00000171489	ENST00000304355	Transcript	missense_variant	benign(0.063)
chrX	47990140	47990140	*SPACA5B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.Y24F	ENSG00000171478	ENST00000304270	Transcript	missense_variant	benign(0.063)
chrX	70341616	70341616	*MED12*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P131	p.M351L	ENSG00000184634	ENST00000374080	Transcript	missense_variant	benign(0)
chr1	111217163	111217163	*KCNA3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.P90Q	ENSG00000177272	ENST00000369769	Transcript	missense_variant	benign(0.175)
chr1	118491040	118491040	*WDR3*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.Q479*	ENSG00000065183	ENST00000349139	Transcript	stop_gained	NA
chr1	11883785	11883785	*CLCN6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P135	p.I159V	ENSG00000011021	ENST00000346436	Transcript	missense_variant	possibly_damaging(0.573)
chr1	156018394	156018394	*UBQLN4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.D266E	ENSG00000160803	ENST00000368309	Transcript	missense_variant	probably_damaging(0.999)
chr1	161496265	161496265	*HSPA6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.R606H	ENSG00000173110	ENST00000309758	Transcript	missense_variant	benign(0.003)
chr1	196303097	196303097	*KCNT2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.R626T	ENSG00000162687	ENST00000294725	Transcript	missense_variant	benign(0.002)
chr1	196759303	196759303	*CFHR3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P135	p.S248T	ENSG00000116785	ENST00000367425	Transcript	missense_variant	probably_damaging(0.995)
chr1	200881146	200881146	*C1orf106*	Missense_Mutation	.	SNP	G	G	A	rs552392029	shanshan_et_al_P135	p.E509K	ENSG00000163362	ENST00000413687	Transcript	missense_variant	benign(0.106)
chr1	206328960	206328960	*CTSE*	Splice_Site	.	SNP	A	A	C	novel	shanshan_et_al_P135	p.X310_splice	ENSG00000196188	ENST00000358184	Transcript	splice_acceptor_variant	NA
chr1	21900187	21900187	*ALPL*	Missense_Mutation	.	SNP	G	G	A	rs121918017	shanshan_et_al_P135	p.E298K	ENSG00000162551	ENST00000374840	Transcript	missense_variant	possibly_damaging(0.652)
chr1	223976872	223976872	*TP53BP2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P135	p.P1001A	ENSG00000143514	ENST00000343537	Transcript	missense_variant	probably_damaging(0.999)
chr1	231830517	231830517	*DISC1*	Missense_Mutation	.	SNP	G	G	C	rs530661133	shanshan_et_al_P135	p.R338P	ENSG00000162946	ENST00000366633	Transcript	missense_variant	possibly_damaging(0.769)
chr1	237774219	237774219	*RYR2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.R1614H	ENSG00000198626	ENST00000366574	Transcript	missense_variant	benign(0.18)
chr1	247492768	247492768	*ZNF496*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.P38H	ENSG00000162714	ENST00000294753	Transcript	missense_variant	probably_damaging(1)
chr1	33502357	33502357	*AK2*	Missense_Mutation	.	SNP	C	C	T	rs199641857	shanshan_et_al_P135	p.G25R	ENSG00000004455	ENST00000354858	Transcript	missense_variant	benign(0.148)
chr1	47610279	47610279	*CYP4A22*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P135	p.M319V	ENSG00000162365	ENST00000371891	Transcript	missense_variant	probably_damaging(0.92)

chr1	52264057	52264057	*NRD1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P135	p.Y891C	ENSG00000078618	ENST00000354831	Transcript	missense_variant	possibly_damaging(0.775)
chr1	76384798	76384798	*ASB17*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.D243H	ENSG00000154007	ENST00000284142	Transcript	missense_variant	probably_damaging(0.953)
chr1	86622024	86622024	*COL24A1*	Missense_Mutation	.	SNP	G	G	C	rs200244344	shanshan_et_al_P135	p.T19R	ENSG00000171502	ENST00000370571	Transcript	missense_variant	benign(0.013)
chr10	104181184	104181184	*FBXL15*	Missense_Mutation	.	SNP	C	C	T	rs376935734	shanshan_et_al_P135	p.R43W	ENSG00000107872	ENST00000224862	Transcript	missense_variant	benign(0.001)
chr10	65210611	65210611	*PRKCQ*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.V416L	ENSG00000065675	ENST00000263125	Transcript	missense_variant	probably_damaging(0.963)
chr11	113934729	113934729	*ZBTB16*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.P236R	ENSG00000109906	ENST00000335953	Transcript	missense_variant	benign(0.007)
chr11	118955769	118955769	*HMBS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.A9V	ENSG00000256269	ENST00000278715	Transcript	missense_variant	benign(0.008)
chr11	17653705	17653705	*OTOG*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P135	p.T2348Lfs*36	ENSG00000188162	ENST00000399391	Transcript	frameshift_variant	NA
chr11	96092240	96092240	*CCDC82*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P135	p.T495A	ENSG00000149231	ENST00000278520	Transcript	missense_variant	benign(0.112)
chr12	6135127	6135127	*VWF*	Missense_Mutation	.	SNP	G	G	T	rs534377998	shanshan_et_al_P135	p.P1018H	ENSG00000110799	ENST00000261405	Transcript	missense_variant	benign(0.329)
chr12	66924599	66924599	*CHD4*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P135	p.Y1322C	ENSG00000111642	ENST00000357008	Transcript	missense_variant	probably_damaging(0.998)
chr13	102030983	102030983	*NALCN*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.D105N	ENSG00000102452	ENST00000251127	Transcript	missense_variant	possibly_damaging(0.836)
chr13	114088137	114088137	*ADPRHL1*	Missense_Mutation	.	SNP	C	C	T	rs376266488	shanshan_et_al_P135	p.R142Q	ENSG00000153531	ENST00000375418	Transcript	missense_variant	possibly_damaging(0.722)
chr13	114782808	114782808	*RASA3*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.R371*	ENSG00000185989	ENST00000334062	Transcript	stop_gained	NA
chr13	28794407	28794407	*PAN3*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.G298*	ENSG00000152520	ENST00000380958	Transcript	stop_gained	NA
chr13	38266351	38266351	*TRPC4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P135	p.F340Y	ENSG00000133107	ENST00000379681	Transcript	missense_variant	benign(0.105)
chr13	99948153	99948153	*GPR183*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.A83T	ENSG00000169508	ENST00000376414	Transcript	missense_variant	probably_damaging(0.996)
chr14	105408107	105408107	*AHNAK2*	Missense_Mutation	.	SNP	G	G	T	rs200549975	shanshan_et_al_P135	p.L4561I	ENSG00000185567	ENST00000332434	Transcript	missense_variant	benign(0.413)
chr14	20924154	20924155	*APEX1*	Frame_Shift_Ins	.	INS	-	-	C	novel	shanshan_et_al_P135	p.D50Rfs*28	ENSG00000100823	ENST00000216714	Transcript	frameshift_variant	NA
chr14	37737996	37737996	*MIPOL1*	Nonsense_Mutation	.	SNP	A	A	T	rs111708093	shanshan_et_al_P135	p.K129*	ENSG00000151338	ENST00000327441	Transcript	stop_gained	NA
chr14	45496625	45496625	*FAM179B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.R1151I	ENSG00000198718	ENST00000361577	Transcript	missense_variant	benign(0.078)
chr14	81950704	81950704	*SEL1L*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P135	p.H637Q	ENSG00000071537	ENST00000336735	Transcript	missense_variant	probably_damaging(0.997)
chr15	100252738	100252738	*MEF2A*	Missense_Mutation	.	SNP	A	A	C	rs201861701	shanshan_et_al_P135	p.Q421P	ENSG00000068305	ENST00000354410	Transcript	missense_variant	benign(0)
chr15	24921280	24921280	*NPAP1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.G89V	ENSG00000185823	ENST00000329468	Transcript	missense_variant	probably_damaging(0.979)
chr15	25220642	25220642	*SNRPN*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.E47D	ENSG00000128739	ENST00000400100	Transcript	missense_variant	probably_damaging(0.992)
chr15	41071483	41071483	*DNAJC17*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.A78V	ENSG00000104129	ENST00000220496	Transcript	missense_variant	probably_damaging(0.959)
chr15	45427385	45427385	*DUOX1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.D131N	ENSG00000137857	ENST00000321429	Transcript	missense_variant	probably_damaging(0.927)
chr16	10274007	10274012	*GRIN2A*	In_Frame_Del	.	DEL	CGCACA	CGCACA	-	novel	shanshan_et_al_P135	p.C87_V88del	ENSG00000183454	ENST00000396573	Transcript	inframe_deletion	NA
chr16	10274016	10274017	*GRIN2A*	Frame_Shift_Del	.	DEL	GC	GC	-	novel	shanshan_et_al_P135	p.H85Rfs*52	ENSG00000183454	ENST00000396573	Transcript	frameshift_variant	NA
chr16	11940401	11940401	*RSL1D1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P135	p.I198V	ENSG00000171490	ENST00000571133	Transcript	missense_variant	benign(0.075)
chr16	22546169	22546169	*NPIPB5*	Missense_Mutation	.	SNP	C	C	G	rs370469653	shanshan_et_al_P135	p.P622R	ENSG00000243716	ENST00000424340	Transcript	missense_variant	benign(0.001)
chr16	53532400	53532400	*AKTIP*	Missense_Mutation	.	SNP	T	T	C	rs199669647	shanshan_et_al_P135	p.T51A	ENSG00000166971	ENST00000394657	Transcript	missense_variant	benign(0.001)
chr16	89764086	89764087	*SPATA2L*	Frame_Shift_Ins	.	INS	-	-	AG	novel	shanshan_et_al_P135	p.S311Lfs*7	ENSG00000158792	ENST00000289805	Transcript	frameshift_variant	NA
chr16	89764088	89764088	*SPATA2L*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P135	p.L310R	ENSG00000158792	ENST00000289805	Transcript	missense_variant	probably_damaging(0.938)
chr17	38289323	38289323	*MSL1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.R243Q	ENSG00000188895	ENST00000579565	Transcript	missense_variant	probably_damaging(0.994)
chr17	65732794	65732794	*NOL11*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P135	p.V356A	ENSG00000130935	ENST00000253247	Transcript	missense_variant	benign(0.075)

chr17	73664598	73664598	*SAP30BP*	Missense_Mutation	.	SNP	G	G	C	rs367727956	shansha n_et_al_P135	p.E37Q	ENSG00000161526	ENST00000584667	Transcript	missense_variant	benign(0.115)
chr17	7577018	7577018	*TP53*	Splice_Site	.	SNP	C	C	A	novel	shansha n_et_al_P135	p.X307_splice	ENSG00000141510	ENST00000269305	Transcript	splice_donor_variant	NA
chr17	76411040	76411040	*PGS1*	Missense_Mutation	.	SNP	C	C	G	rs372097158	shansha n_et_al_P135	p.H495D	ENSG00000087157	ENST00000262764	Transcript	missense_variant	benign(0.082)
chr18	31709893	31709893	*NOL4*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P135	p.T119M	ENSG00000101746	ENST00000261592	Transcript	missense_variant	benign(0.062)
chr18	48591888	48591888	*SMAD4*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P135	p.D351Y	ENSG00000141646	ENST00000342988	Transcript	missense_variant	probably_damaging(1)
chr18	61306469	61306469	*SERPINB4*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P135	p.D240Y	ENSG00000206073	ENST00000341074	Transcript	missense_variant	probably_damaging(0.97)
chr18	658196	658196	*C18orf56*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P135	p.P18A	ENSG00000176912	ENST00000323813	Transcript	missense_variant	possibly_damaging(0.728)
chr19	10463703	10463703	*TYK2*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P135	p.N1033K	ENSG00000105397	ENST00000525621	Transcript	missense_variant	possibly_damaging(0.652)
chr19	11979192	11979192	*ZNF439*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P135	p.K436N	ENSG00000171291	ENST00000304030	Transcript	missense_variant	probably_damaging(0.999)
chr19	14717866	14717866	*CLEC17A*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P135	p.A319D	ENSG00000187912	ENST00000417570	Transcript	missense_variant	benign(0.001)
chr19	38125896	38125896	*ZFP30*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P135	p.H516Y	ENSG00000120784	ENST00000351218	Transcript	missense_variant	probably_damaging(0.963)
chr19	38125976	38125976	*ZFP30*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P135	p.S489F	ENSG00000120784	ENST00000351218	Transcript	missense_variant	probably_damaging(0.999)
chr19	38126002	38126002	*ZFP30*	Frame_Shift_Del	.	DEL	T	T	-	novel	shansha n_et_al_P135	p.L481*	ENSG00000120784	ENST00000351218	Transcript	frameshift_variant	NA
chr19	44934469	44934469	*ZNF229*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P135	p.D163H	ENSG00000167383	ENST00000588931	Transcript	missense_variant	benign(0.011)
chr19	57641791	57641791	*USP29*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P135	p.L583R	ENSG00000131864	ENST00000254181	Transcript	missense_variant	benign(0.276)
chr2	101624549	101624549	*TBC1D8*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P135	p.P1053S	ENSG00000204634	ENST00000376840	Transcript	missense_variant	benign(0.001)
chr2	102984428	102984428	*IL18R1*	Missense_Mutation	.	SNP	C	C	A	rs367800541	shansha n_et_al_P135	p.L68M	ENSG00000115604	ENST00000409599	Transcript	missense_variant	possibly_damaging(0.687)
chr2	198363515	198363515	*HSPD1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P135	p.P20S	ENSG00000144381	ENST00000388968	Transcript	missense_variant	possibly_damaging(0.664)
chr2	203848307	203848308	*CARF*	Frame_Shift_Ins	.	INS	-	-	A	rs201520695	shansha n_et_al_P135	p.T716Nfs*5	ENSG00000138380	ENST00000402905	Transcript	frameshift_variant	NA
chr2	242373687	242373687	*FARP2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P135	p.P328S	ENSG00000006607	ENST00000264042	Transcript	missense_variant	probably_damaging(0.933)
chr20	35414983	35414983	*SOGA1*	Missense_Mutation	.	SNP	G	G	A	rs553477162	shansha n_et_al_P135	p.R1631C	ENSG00000149639	ENST00000237536	Transcript	missense_variant	probably_damaging(0.978)
chr20	60318773	60318773	*CDH4*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P135	p.Q108H	ENSG00000179242	ENST00000360469	Transcript	missense_variant	possibly_damaging(0.811)
chr21	27326987	27326987	*APP*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P135	p.R535L	ENSG00000142192	ENST00000346798	Transcript	missense_variant	probably_damaging(0.994)
chr21	31802902	31802902	*KRTAP13-4*	Nonsense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P135	p.Y103*	ENSG00000186971	ENST00000334068	Transcript	stop_gained	NA
chr21	31971156	31971156	*KRTAP6-2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P135	p.H13P	ENSG00000186930	ENST00000334897	Transcript	missense_variant	unknown(0)
chr21	34954302	34954302	*DONSON*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P135	p.G369D	ENSG00000159147	ENST00000303071	Transcript	missense_variant	probably_damaging(0.999)
chr22	38897182	38897183	*DDX17*	Frame_Shift_Ins	.	INS	-	-	A	novel	shansha n_et_al_P135	p.E131*	ENSG00000100201	ENST00000396821	Transcript	frameshift_variant	NA
chr22	40661931	40661931	*TNRC6B*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P135	p.G566V	ENSG00000100354	ENST00000454349	Transcript	missense_variant	probably_damaging(1)
chr3	101284835	101284835	*TRMT10C*	Nonstop_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P135	p.*404Eext*17	ENSG00000174173	ENST00000309922	Transcript	stop_lost	NA
chr3	122646768	122646768	*SEMA5B*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P135	p.V294A	ENSG00000082684	ENST00000451055	Transcript	missense_variant	possibly_damaging(0.778)
chr3	123456371	123456371	*MYLK*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P135	p.P203L	ENSG00000065534	ENST00000360304	Transcript	missense_variant	benign(0.018)
chr3	157820626	157820626	*SHOX2*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P135	p.D156E	ENSG00000168779	ENST00000389589	Transcript	missense_variant	benign(0.036)
chr3	165548484	165548484	*BCHE*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P135	p.N113T	ENSG00000114200	ENST00000264381	Transcript	missense_variant	possibly_damaging(0.831)
chr3	173998882	173998882	*NLGN1*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P135	p.L754P	ENSG00000169760	ENST00000457714	Transcript	missense_variant	probably_damaging(0.996)
chr3	63594966	63594966	*SYNPR*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P135	p.V192L	ENSG00000163630	ENST00000478300	Transcript	missense_variant	benign(0.001)
chr3	63824177	63824177	*THOC7*	Splice_Site	.	SNP	T	T	A	novel	shansha n_et_al_P135	p.X46_splice	ENSG00000163634	ENST00000295899	Transcript	splice_acceptor_variant	NA

chr3	7456852	7456852	*GRM7*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P135	NA	ENSG00000196277	ENST00000357716	Transcript	splice_donor_variant	NA
chr3	77638054	77638054	*ROBO2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P135	p.K901Q	ENSG00000185008	ENST00000487694	Transcript	missense_variant	benign(0.403)
chr4	155395 86	155395 86	*CC2D2A*	Missense_Mutation	.	SNP	C	C	T	rs376457814	shanshan_et_al_P135	p.P610L	ENSG00000048342	ENST00000424120	Transcript	missense_variant	benign(0.003)
chr4	685279 36	685279 36	*UBA6*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P135	p.T359A	ENSG00000033178	ENST00000322244	Transcript	missense_variant	benign(0)
chr4	687039 95	687039 95	*TMPRSS11D*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P135	p.R124G	ENSG00000153802	ENST00000283916	Transcript	missense_variant	benign(0.046)
chr4	802467 96	802467 96	*NAA11*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.R79P	ENSG00000156269	ENST00000286794	Transcript	missense_variant	possibly_damaging(0.836)
chr4	869384 33	869384 33	*MAPK10*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P135	p.D448V	ENSG00000109339	ENST00000359221	Transcript	missense_variant	possibly_damaging(0.873)
chr4	940320 12	940320 12	*GRID2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P135	p.M215L	ENSG00000152208	ENST00000282020	Transcript	missense_variant	benign(0.003)
chr5	121786 780	121786 780	*SNCAIP*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P135	p.H746Q	ENSG00000064692	ENST00000261368	Transcript	missense_variant	probably_damaging(0.997)
chr5	137626 366	137626 366	*CDC25C*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.D276N	ENSG00000158402	ENST00000323760	Transcript	missense_variant	benign(0.029)
chr5	139486 9	139486 9	*SLC6A3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.R615H	ENSG00000142319	ENST00000270349	Transcript	missense_variant	benign(0.004)
chr5	140530 319	140530 319	*PCDHB6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P135	p.T161A	ENSG00000113211	ENST00000231136	Transcript	missense_variant	benign(0.001)
chr5	142678 231	142678 231	*NR3C1*	Splice_Site	.	SNP	A	A	C	novel	shanshan_et_al_P135	p.X632_splice	ENSG00000113580	ENST00000231509	Transcript	splice_donor_variant	NA
chr5	389625 88	389625 88	*RICTOR*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P135	p.K556T	ENSG00000164327	ENST00000357387	Transcript	missense_variant	probably_damaging(0.999)
chr5	537518 07	537518 07	*HSPB3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.P63L	ENSG00000169271	ENST00000302005	Transcript	missense_variant	benign(0)
chr5	804097 24	804097 24	*RASGRF2*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.R819*	ENSG00000113319	ENST00000265080	Transcript	stop_gained	NA
chr6	109767 486	109767 486	*MICAL1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.E812K	ENSG00000135596	ENST00000358807	Transcript	missense_variant	possibly_damaging(0.611)
chr6	133271 29	133271 29	*TBC1D7*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P135	p.M1?	ENSG00000145979	ENST00000607658	Transcript	frameshift_variant	NA
chr6	393255	393255	*IRF4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.G35C	ENSG00000137265	ENST00000380956	Transcript	missense_variant	possibly_damaging(0.553)
chr6	696464 25	696464 25	*BAI3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P135	p.E295Q	ENSG00000135298	ENST00000370598	Transcript	missense_variant	possibly_damaging(0.904)
chr6	784553 1	784553 1	*BMP6*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P135	p.S275R	ENSG00000153162	ENST00000283147	Transcript	missense_variant	possibly_damaging(0.791)
chr6	837677 34	837677 34	*UBE3D*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P135	p.K29*	ENSG00000118420	ENST00000369747	Transcript	stop_gained	NA
chr7	150068 604	150068 604	*REPIN1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.R149G	ENSG00000214022	ENST00000489432	Transcript	missense_variant	benign(0.44)
chr7	151945 256	151945 256	*KMT2C*	Nonsense_Mutation	.	SNP	G	G	A	rs201234598	shanshan_et_al_P135	p.Q755*	ENSG00000055609	ENST00000262189	Transcript	stop_gained	NA
chr7	151962 290	151962 290	*KMT2C*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.K339N	ENSG00000055609	ENST00000262189	Transcript	missense_variant	probably_damaging(0.998)
chr7	416712 3	416712 3	*SDK1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P135	p.Y1312D	ENSG00000146555	ENST00000404826	Transcript	missense_variant	probably_damaging(0.999)
chr7	417398 63	417398 63	*INHBA*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P135	p.S37C	ENSG00000122641	ENST00000242208	Transcript	missense_variant	possibly_damaging(0.701)
chr7	531036 83	531036 83	*POM121L12*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.A107T	ENSG00000221900	ENST00000408890	Transcript	missense_variant	probably_damaging(0.913)
chr7	940390 78	940390 78	*COL1A2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.R327H	ENSG00000164692	ENST00000297268	Transcript	missense_variant	unknown(0)
chr7	944699	944699	*ADAP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.D167N	ENSG00000105963	ENST00000265846	Transcript	missense_variant	possibly_damaging(0.732)
chr8	139701 164	139701 164	*COL22A1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P135	p.E953A	ENSG00000169436	ENST00000303045	Transcript	missense_variant	unknown(0)
chr9	131255 075	131255 075	*ODF2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P135	p.E581D	ENSG00000136811	ENST00000434106	Transcript	missense_variant	possibly_damaging(0.779)
chr9	132481 528	132481 528	*PRRX2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.G93E	ENSG00000167157	ENST00000372469	Transcript	missense_variant	benign(0.244)
chr9	136277 538	136277 538	*REXO4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.R264H	ENSG00000148300	ENST00000371942	Transcript	missense_variant	probably_damaging(1)
chr9	137591 754	137591 754	*COL5A1*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P135	NA	ENSG00000130635	ENST00000371817	Transcript	splice_acceptor_variant	NA
chr9	137990 304	137990 304	*OLFM1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P135	p.R192T	ENSG00000130558	ENST00000252854	Transcript	missense_variant	possibly_damaging(0.587)

chr9	140110380	140110380	*NDOR1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.R489W	ENSG00000188566	ENST00000371521	Transcript	missense_variant	possibly_damaging(0.888)
chr9	140387525	140387525	*PNPLA7*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P135	p.R713G	ENSG00000130653	ENST00000406427	Transcript	missense_variant	possibly_damaging(0.758)
chr9	17464512	17464512	*CNTLN*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.R1141M	ENSG00000044459	ENST00000380647	Transcript	missense_variant	probably_damaging(0.999)
chr9	39358276	39358276	*SPATA31A1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.G172C	ENSG00000204849	ENST00000377647	Transcript	missense_variant	probably_damaging(0.999)
chr9	41503242	41503242	*SPATA31A5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.G172C	ENSG00000233788	ENST00000377621	Transcript	missense_variant	NA
chr9	43625463	43625463	*SPATA31A6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.R1075K	ENSG00000185775	ENST00000332857	Transcript	missense_variant	possibly_damaging(0.671)
chr9	43628173	43628173	*SPATA31A6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P135	p.G172C	ENSG00000185775	ENST00000332857	Transcript	missense_variant	probably_damaging(0.997)
chr9	82333783	82333783	*TLE4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P135	p.S496N	ENSG00000106829	ENST00000376552	Transcript	missense_variant	possibly_damaging(0.737)
chr9	86468591	86468591	*KIF27*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P135	p.L1104M	ENSG00000165115	ENST00000297814	Transcript	missense_variant	probably_damaging(1)
chr9	86518654	86518654	*KIF27*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.R260Q	ENSG00000165115	ENST00000297814	Transcript	missense_variant	probably_damaging(1)
chrX	111019981	111019981	*TRPC5*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P135	p.K828Q	ENSG00000072315	ENST00000262839	Transcript	missense_variant	benign(0.173)
chrX	149638411	149638411	*MAMLD1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P135	p.P164H	ENSG00000013619	ENST00000432680	Transcript	missense_variant	probably_damaging(0.973)
chrX	155003673	155003673	*SPRY3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P135	p.Q47R	ENSG00000168939	ENST00000302805	Transcript	missense_variant	benign(0.01)
chrX	47044992	47044992	*RBM10*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P135	p.A773V	ENSG00000182872	ENST00000377604	Transcript	missense_variant	probably_damaging(0.994)
chrX	69502174	69502174	*RAB41*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P135	p.F36C	ENSG00000147127	ENST00000276066	Transcript	missense_variant	probably_damaging(0.997)
chrX	71495426	71495426	*RPS4X*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P135	p.R77P	ENSG00000198034	ENST00000316084	Transcript	missense_variant	probably_damaging(0.977)
chr1	12321179	12321179	*VPS13D*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P140	p.E463K	ENSG00000048707	ENST00000358136	Transcript	missense_variant	benign(0.015)
chr1	232002303	232002303	*DISC1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.Q672H	ENSG00000162946	ENST00000366636	Transcript	missense_variant	unknown(0)
chr1	36212367	36212367	*CLSPN*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P140	p.D952H	ENSG00000092853	ENST00000318121	Transcript	missense_variant	possibly_damaging(0.854)
chr10	25885616	25885616	*GPR158*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P140	p.E681D	ENSG00000151025	ENST00000376351	Transcript	missense_variant	possibly_damaging(0.772)
chr10	47086937	47086937	*NPY4R*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P140	p.T52A	ENSG00000204174	ENST00000374312	Transcript	missense_variant	benign(0.146)
chr11	122929771	122929771	*HSPA8*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P140	p.I440T	ENSG00000109971	ENST00000534624	Transcript	missense_variant	benign(0.045)
chr11	133814242	133814242	*IGSF9B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P140	p.D94E	ENSG00000080854	ENST00000538871	Transcript	missense_variant	benign(0.442)
chr11	57995536	57995536	*OR10Q1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.T271N	ENSG00000180475	ENST00000316770	Transcript	missense_variant	possibly_damaging(0.864)
chr11	62290722	62290722	*AHNAK*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P140	p.G3723R	ENSG00000124942	ENST00000378024	Transcript	missense_variant	probably_damaging(0.999)
chr12	132393680	132393680	*ULK1*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P140	NA	ENSG00000177169	ENST00000321867	Transcript	splice_acceptor_variant	NA
chr12	30877346	30877346	*CAPRIN2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P140	p.P649A	ENSG00000110888	ENST00000298892	Transcript	missense_variant	benign(0.072)
chr12	56740622	56740622	*STAT2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.W614C	ENSG00000170581	ENST00000314128	Transcript	missense_variant	probably_damaging(1)
chr12	67330336	67330336	*LPAR5*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P140	p.V27L	ENSG00000184574	ENST00000329858	Transcript	missense_variant	possibly_damaging(0.629)
chr12	99640564	99640564	*ANKS1B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P140	p.S612F	ENSG00000185046	ENST00000547776	Transcript	missense_variant	possibly_damaging(0.878)
chr13	32954039	32954039	*BRCA2*	Nonsense_Mutation	.	SNP	C	C	T	rs202155613	shanshan_et_al_P140	p.Q3036*	ENSG00000139618	ENST00000544455	Transcript	stop_gained	NA
chr13	48942667	48942667	*RB1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.E352*	ENSG00000139687	ENST00000267163	Transcript	stop_gained	NA
chr13	53421633	53421633	*PCDH8*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.D313E	ENSG00000136099	ENST00000377942	Transcript	missense_variant	probably_damaging(0.993)
chr14	103406408	103406408	*CDC42BPB*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.L1522F	ENSG00000198752	ENST00000361246	Transcript	missense_variant	possibly_damaging(0.553)
chr14	55422414	55422414	*WDHD1*	Splice_Site	.	SNP	T	T	C	novel	shanshan_et_al_P140	p.X973_splice	ENSG00000198554	ENST00000360586	Transcript	splice_acceptor_variant	NA
chr15	28483290	28483290	*HERC2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.M1274I	ENSG00000128731	ENST00000261609	Transcript	missense_variant	benign(0.159)

chr15	88690602	88690602	*NTRK3*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.S143*	ENSG00000140538	ENST00000360948	Transcript	stop_gained	NA
chr15	94841562	94841562	*MCTP2*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P140	p.L23*	ENSG00000140563	ENST00000357742	Transcript	stop_gained	NA
chr16	10864187	10864187	*TVP23A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.A195D	ENSG00000166676	ENST00000299866	Transcript	missense_variant	benign(0.002)
chr16	20432723	20432723	*ACSM5*	Missense_Mutation	.	SNP	G	G	A	rs374265273	shanshan_et_al_P140	p.R256K	ENSG00000183549	ENST00000331849	Transcript	missense_variant	possibly_damaging(0.571)
chr16	49080007	49080007	*UBN1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P140	p.D89G	ENSG00000118900	ENST00000396658	Transcript	missense_variant	benign(0.339)
chr16	71317747	71317747	*CMTR2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.D693Y	ENSG00000180917	ENST00000338099	Transcript	missense_variant	benign(0.17)
chr16	82891983	82891983	*CDH13*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P140	p.S68F	ENSG00000140945	ENST00000268613	Transcript	missense_variant	benign(0.004)
chr17	30376157	30376157	*LRRC37B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.R807L	ENSG00000185158	ENST00000341671	Transcript	missense_variant	possibly_damaging(0.726)
chr17	41566882	41566882	*DHX8*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P140	p.N73Kfs*11	ENSG00000067596	ENST00000262415	Transcript	frameshift_variant	NA
chr17	56572598	56572598	*MTMR4*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P140	p.N969H	ENSG00000108389	ENST00000323456	Transcript	missense_variant	benign(0.281)
chr17	75793111	75793111	*TP53*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.X125_splice	ENSG00000141510	ENST00000269305	Transcript	splice_donor_variant	NA
chr18	55103488	55103488	*ONECUT2*	Missense_Mutation	.	SNP	c	c	G	novel	shanshan_et_al_P140	p.H180Q	ENSG00000119547	ENST00000491143	Transcript	missense_variant	benign(0.26)
chr19	11553282	11553282	*PRKCSH*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P140	p.E184Q	ENSG00000130175	ENST00000252455	Transcript	missense_variant	probably_damaging(0.99)
chr19	46886706	46886706	*PPP5C*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.S224R	ENSG00000011485	ENST00000012443	Transcript	missense_variant	benign(0.068)
chr19	57334150	57334150	*PEG3*	Missense_Mutation	.	SNP	C	C	T	rs531986471	shanshan_et_al_P140	p.R179H	ENSG00000198300	ENST00000326441	Transcript	missense_variant	benign(0.037)
chr19	84359600	84359600	*ANGPTL4*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P140	p.Q228E	ENSG00000167772	ENST00000301455	Transcript	missense_variant	probably_damaging(0.997)
chr2	10008515	10008515	*TAF1B*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P140	p.I170M	ENSG00000115750	ENST00000266363	Transcript	missense_variant	benign(0.129)
chr2	109381472	109381472	*RANBP2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.E1493*	ENSG00000153201	ENST00000283195	Transcript	stop_gained	NA
chr2	161052067	161052067	*ITGB6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P140	p.Y136H	ENSG00000115221	ENST00000283249	Transcript	missense_variant	probably_damaging(1)
chr2	220480797	220480797	*STK11IP*	Missense_Mutation	.	SNP	G	G	T	rs531254740	shanshan_et_al_P140	p.R1061L	ENSG00000144589	ENST00000295641	Transcript	missense_variant	possibly_damaging(0.6)
chr21	15537680	15537680	*LIPI*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P140	p.R276S	ENSG00000188992	ENST00000344577	Transcript	missense_variant	probably_damaging(0.999)
chr21	16337081	16337081	*NRIP1*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.G1145*	ENSG00000180530	ENST00000400202	Transcript	stop_gained	NA
chr22	30975186	30975186	*PES1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.G487C	ENSG00000100029	ENST00000354694	Transcript	missense_variant	benign(0.04)
chr3	148563264	148563264	*CPB1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P140	p.E278K	ENSG00000153002	ENST00000491148	Transcript	missense_variant	probably_damaging(1)
chr3	73433915	73433915	*PDZRN3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.A601E	ENSG00000121440	ENST00000263666	Transcript	missense_variant	benign(0.008)
chr4	25146671	25146671	*SEPSECS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.G297C	ENSG00000109618	ENST00000382103	Transcript	missense_variant	probably_damaging(0.995)
chr5	150897269	150897269	*FAT2*	Missense_Mutation	.	SNP	C	C	T	rs200068080	shanshan_et_al_P140	p.R3792Q	ENSG00000086570	ENST00000261800	Transcript	missense_variant	benign(0.001)
chr6	170871052	170871053	*TBP*	Frame_Shift_Del	.	DEL	GC	GC	-	novel	shanshan_et_al_P140	p.Q77Afs*100	ENSG00000112592	ENST00000392092	Transcript	frameshift_variant	NA
chr6	41303637	41303637	*NCR2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.P8Q	ENSG00000096264	ENST00000373089	Transcript	missense_variant	possibly_damaging(0.507)
chr7	138258270	138258270	*TRIM24*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P140	p.I633L	ENSG00000122779	ENST00000343526	Transcript	missense_variant	benign(0.089)
chr7	35288451	35288451	*TBX20*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.R128M	ENSG00000164532	ENST00000408931	Transcript	missense_variant	probably_damaging(0.937)
chr7	42497271	42497271	*SDK1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.W1822C	ENSG00000146555	ENST00000404826	Transcript	missense_variant	probably_damaging(1)
chr7	44268439	44268439	*CAMK2B*	Frame_Shift_Ins	.	INS	-	-	G	novel	shanshan_et_al_P140	p.P476Afs*20	ENSG00000058404	ENST00000395749	Transcript	frameshift_variant	NA
chr7	73011829	73011829	*MLXIPL*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.P429H	ENSG00000009950	ENST00000313375	Transcript	missense_variant	possibly_damaging(0.754)
chr8	117950619	117950619	*AARD*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P140	p.Q46L	ENSG00000205002	ENST00000378279	Transcript	missense_variant	possibly_damaging(0.607)
chr8	81760074	81760074	*SGK223*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.A1271S	ENSG00000182319	ENST00000520004	Transcript	missense_variant	probably_damaging(0.997)

chr9	104312898	104312898	*RNF20*	Missense_Mutation	.	SNP	G	G	T	rs368721473	shanshan_et_al_P140	p.R368L	ENSG00000155827	ENST00000389120	Transcript	missense_variant	benign(0.25)
chr9	35077350	35077350	*FANCG*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P140	p.P186L	ENSG00000221829	ENST00000378643	Transcript	missense_variant	benign(0.162)
chrX	109693883	109693883	*RGAG1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.T13K	ENSG00000243978	ENST00000465301	Transcript	missense_variant	benign(0.212)
chrX	151900607	151900607	*MAGEA12*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P140	p.P65H	ENSG00000213401	ENST00000393900	Transcript	missense_variant	probably_damaging(0.986)
chrX	158471719	158471719	*P2RY8*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.A245S	ENSG00000182162	ENST00000381297	Transcript	missense_variant	benign(0.063)
chrX	19021224	19021224	*GPR64*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P140	p.R657P	ENSG00000173698	ENST00000379869	Transcript	missense_variant	probably_damaging(1)
chrX	31645909	31645909	*DMD*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P140	p.K2700*	ENSG00000198947	ENST00000357033	Transcript	stop_gained	NA
chrX	43655116	43655116	*MAOB*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P140	p.G213V	ENSG00000069535	ENST00000378069	Transcript	missense_variant	probably_damaging(1)
chrX	48341392	48341392	*FTSJ1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P140	p.S326C	ENSG00000068438	ENST00000348411	Transcript	missense_variant	benign(0.258)
chr1	114340440	114340440	*RSBN1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P141	p.S308A	ENSG00000081019	ENST00000261441	Transcript	missense_variant	possibly_damaging(0.57)
chr1	17350557	17350557	*SDHB*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P141	p.E185*	ENSG00000117118	ENST00000375499	Transcript	stop_gained	NA
chr1	202278196	202278196	*LGR6*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P141	p.Q433P	ENSG00000133067	ENST00000367278	Transcript	missense_variant	possibly_damaging(0.811)
chr1	26212309	26212309	*STMN1*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P141	p.E144*	ENSG00000117632	ENST00000426559	Transcript	stop_gained	NA
chr1	26629322	26629322	*UBXN11*	Missense_Mutation	.	SNP	G	G	A	rs201437983	shanshan_et_al_P141	p.S18L	ENSG00000158062	ENST00000374222	Transcript	missense_variant	benign(0.015)
chr1	32207722	32207722	*BAI2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P141	p.G450D	ENSG00000121753	ENST00000373658	Transcript	missense_variant	benign(0.405)
chr1	95609561	95609561	*TMEM56*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P141	p.S35F	ENSG00000152078	ENST00000370203	Transcript	missense_variant	benign(0.019)
chr1	98112 4	98112 4	*AGRN*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.D850Y	ENSG00000188157	ENST00000379370	Transcript	missense_variant	probably_damaging(0.961)
chr10	135020810	135020810	*KNDC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P141	p.L1250Q	ENSG00000171798	ENST00000304613	Transcript	missense_variant	probably_damaging(0.998)
chr10	16806507	16806507	*RSU1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P141	p.V55M	ENSG00000148484	ENST00000377921	Transcript	missense_variant	probably_damaging(0.98)
chr10	38121463	38121463	*ZNF248*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P141	p.I274V	ENSG00000198105	ENST00000395867	Transcript	missense_variant	benign(0.007)
chr10	73434879	73434879	*CDH23*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P141	p.N492S	ENSG00000107736	ENST00000224721	Transcript	missense_variant	probably_damaging(0.937)
chr10	75673516	75673516	*PLAU*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P141	p.I227N	ENSG00000122861	ENST00000372764	Transcript	missense_variant	possibly_damaging(0.851)
chr11	125542520	125542520	*ACRV1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P141	p.C256G	ENSG00000134940	ENST00000533904	Transcript	missense_variant	probably_damaging(1)
chr11	17333656	17333656	*NUCB2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.V301I	ENSG00000070081	ENST00000529010	Transcript	missense_variant	probably_damaging(0.999)
chr11	56409209	56409209	*OR5AP2*	Missense_Mutation	.	SNP	G	G	A	rs140197428	shanshan_et_al_P141	p.S236L	ENSG00000172464	ENST00000302981	Transcript	missense_variant	possibly_damaging(0.871)
chr12	100453202	100453202	*UHRF1BP1L*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P141	p.C618F	ENSG00000111647	ENST00000279907	Transcript	missense_variant	probably_damaging(0.999)
chr12	100691850	100691850	*SCYL2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P141	p.L126S	ENSG00000136021	ENST00000360820	Transcript	missense_variant	probably_damaging(0.986)
chr12	42503494	42503494	*GXYLT1*	Splice_Site	.	SNP	C	C	G	novel	shanshan_et_al_P141	p.X163_splice	ENSG00000151233	ENST00000398675	Transcript	splice_acceptor_variant	NA
chr12	51453144	51453144	*LETMD1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P141	p.E351V	ENSG00000050426	ENST00000418425	Transcript	missense_variant	benign(0.213)
chr12	80730301	80730301	*OTOGL*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P141	p.I1561R	ENSG00000165899	ENST00000458043	Transcript	missense_variant	probably_damaging(0.927)
chr13	23928670	23928670	*SACS*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.A694V	ENSG00000151835	ENST00000382298	Transcript	missense_variant	benign(0.001)
chr15	40655855	40655855	*DISP2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P141	p.A50V	ENSG00000140323	ENST00000267889	Transcript	missense_variant	benign(0.389)
chr15	65450936	65450936	*CLPX*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P141	p.L290*	ENSG00000166855	ENST00000300107	Transcript	stop_gained	NA
chr16	50136303	50136303	*HEATR3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P141	p.L626S	ENSG00000155393	ENST00000299192	Transcript	missense_variant	probably_damaging(0.995)
chr16	72110310	72110310	*HPR*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P141	p.N126I	ENSG00000261701	ENST00000540303	Transcript	missense_variant	possibly_damaging(0.908)
chr16	89349639	89349639	*ANKRD11*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P141	p.D1104G	ENSG00000167522	ENST00000301030	Transcript	missense_variant	benign(0.213)

chr17	39186251	39186251	*KRTAP1-4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.P27Q	ENSG00000204887	ENST00000377747	Transcript	missense_variant	unknown(0)
chr17	65720186	65720186	*NOL11*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.V181L	ENSG00000130935	ENST00000253247	Transcript	missense_variant	benign(0.275)
chr17	72939718	72939718	*OTOP3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P141	p.T235N	ENSG00000182938	ENST00000328801	Transcript	missense_variant	possibly_damaging(0.827)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P141	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr18	35343337	35343337	*DLGAP1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P141	p.E778D	ENSG00000170579	ENST00000315677	Transcript	missense_variant	benign(0.083)
chr19	1220391	1220391	*STK11*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.D162Y	ENSG00000118046	ENST00000326873	Transcript	missense_variant	probably_damaging(0.974)
chr19	33493767	33493767	*RHPN2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P141	p.I300M	ENSG00000131941	ENST00000254260	Transcript	missense_variant	possibly_damaging(0.806)
chr2	198363406	198363406	*HSPD1*	Missense_Mutation	.	SNP	C	C	T	rs200514123	shanshan_et_al_P141	p.G56E	ENSG00000144381	ENST00000388968	Transcript	missense_variant	benign(0.327)
chr2	230875533	230875533	*FBXO36*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P141	p.L167H	ENSG00000153832	ENST00000283946	Transcript	missense_variant	possibly_damaging(0.766)
chr2	28828736	28828736	*PLB1*	Missense_Mutation	.	SNP	C	C	T	rs371058996	shanshan_et_al_P141	p.T993M	ENSG00000163803	ENST00000327757	Transcript	missense_variant	benign(0.045)
chr2	74184338	74184338	*DGUOK*	Missense_Mutation	.	SNP	C	C	G	rs372217661	shanshan_et_al_P141	p.H226Q	ENSG00000114956	ENST00000264093	Transcript	missense_variant	probably_damaging(1)
chr20	23731467	23731467	*CST1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P141	p.A13T	ENSG00000170373	ENST00000304749	Transcript	missense_variant	unknown(0)
chr20	25656194	25656194	*ZNF337*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P141	p.C577Y	ENSG00000130684	ENST00000376436	Transcript	missense_variant	unknown(0)
chr22	17601380	17601380	*CECR6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P141	p.G213V	ENSG00000183307	ENST00000331437	Transcript	missense_variant	unknown(0)
chr22	42609849	42609849	*TCF20*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P141	p.R488T	ENSG00000100207	ENST00000359486	Transcript	missense_variant	probably_damaging(0.997)
chr3	17052813	17052813	*PLCL2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.E533*	ENSG00000154822	ENST00000418129	Transcript	stop_gained	NA
chr3	97888085	97888085	*OR5H15*	Missense_Mutation	.	SNP	C	C	T	rs62266800	shanshan_et_al_P141	p.T181I	ENSG00000233412	ENST00000356526	Transcript	missense_variant	benign(0)
chr4	183721176	183721176	*TENM3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.R2591H	ENSG00000218336	ENST00000511685	Transcript	missense_variant	possibly_damaging(0.84)
chr4	186423611	186423611	*PDLIM3*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P141	p.K311T	ENSG00000154553	ENST00000284770	Transcript	missense_variant	probably_damaging(0.997)
chr5	118832280	118832280	*HSD17B4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P141	p.S329L	ENSG00000133835	ENST00000504811	Transcript	missense_variant	benign(0.018)
chr5	141243441	141243441	*PCDH1*	Missense_Mutation	.	SNP	G	G	A	rs576196969	shanshan_et_al_P141	p.R819C	ENSG00000156453	ENST00000287008	Transcript	missense_variant	possibly_damaging(0.729)
chr5	41018003	41018003	*MROH2B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P141	p.T945S	ENSG00000171495	ENST00000399564	Transcript	missense_variant	benign(0.013)
chr7	102604079	102604079	*FBXL13*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P141	p.D209H	ENSG00000161040	ENST00000313221	Transcript	missense_variant	probably_damaging(0.98)
chr7	140082295	140082295	*SLC37A3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.S11F	ENSG00000157800	ENST00000326232	Transcript	missense_variant	benign(0.165)
chr7	146825878	146825878	*CNTNAP2*	Missense_Mutation	.	SNP	G	G	T	rs145832489	shanshan_et_al_P141	p.V345F	ENSG00000174469	ENST00000361727	Transcript	missense_variant	benign(0.319)
chr7	30825394	30825394	*FAM188B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.G150D	ENSG00000106125	ENST00000265299	Transcript	missense_variant	benign(0.005)
chr8	113323333	113323333	*CSMD3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.Q2587K	ENSG00000164796	ENST00000297405	Transcript	missense_variant	possibly_damaging(0.484)
chr8	144940706	144940706	*EPPK1*	Missense_Mutation	.	SNP	C	C	T	rs112377501	shanshan_et_al_P141	p.R2239H	ENSG00000227184	ENST00000529985	Transcript	missense_variant	possibly_damaging(0.832)
chr8	24192998	24192998	*ADAM28*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.E471K	ENSG00000042980	ENST00000265769	Transcript	missense_variant	probably_damaging(0.997)
chr9	33548311	33548311	*ANKRD18B*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.E447*	ENSG00000230453	ENST00000290943	Transcript	stop_gained	NA
chr9	96019387	96019387	*WNK2*	Missense_Mutation	.	SNP	C	C	T	rs370579014	shanshan_et_al_P141	p.A783V	ENSG00000165238	ENST00000297954	Transcript	missense_variant	unknown(0)
chrX	120094583	120094583	*CT47A6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.P167L	ENSG00000226023	ENST00000440360	Transcript	missense_variant	benign(0)
chrX	152686391	152686391	*ZFP92*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.G186S	ENSG00000189420	ENST00000338647	Transcript	missense_variant	probably_damaging(0.997)
chrX	154009536	154009536	*MPP1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P141	p.A401V	ENSG00000130830	ENST00000369534	Transcript	missense_variant	possibly_damaging(0.494)
chrX	78618924	78618924	*ITM2A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P141	p.P80H	ENSG00000078596	ENST00000373298	Transcript	missense_variant	possibly_damaging(0.907)
chr11	124764163	124764163	*ROBO4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P143	p.V418L	ENSG00000154133	ENST00000306534	Transcript	missense_variant	possibly_damaging(0.733)

chr11	66114676	66114676	*B3GNT1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P143	p.E114V	ENSG00000174684	ENST00000311181	Transcript	missense_variant	benign(0.238)
chr15	23812278	23812278	*MKRN3*	Missense_Mutation	.	SNP	G	G	T	rs370444185	shanshan_et_al_P143	p.R450L	ENSG00000179455	ENST00000314520	Transcript	missense_variant	benign(0.095)
chr15	42110250	42110250	*MAPKBP1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P143	p.G656W	ENSG00000137802	ENST00000456763	Transcript	missense_variant	probably_damaging(0.999)
chr16	90095558	90095558	*C16orf3*	Missense_Mutation	.	SNP	c	c	T	rs76646627	shanshan_et_al_P143	p.G65S	ENSG00000221819	ENST00000408886	Transcript	missense_variant	probably_damaging(0.931)
chr17	29554566	29554566	*NF1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P143	p.W784*	ENSG00000196712	ENST00000358273	Transcript	stop_gained	NA
chr17	74944059	74944059	*MGAT5B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P143	p.A700S	ENSG00000167889	ENST00000428789	Transcript	missense_variant	benign(0.287)
chr2	86255777	86255777	*POLR1A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P143	p.G1613S	ENSG00000068654	ENST00000263857	Transcript	missense_variant	probably_damaging(1)
chr3	148727077	148727077	*GYG1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.I166V	ENSG00000163754	ENST00000345003	Transcript	missense_variant	benign(0.012)
chr3	89521634	89521634	*EPHA3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.D904G	ENSG00000044524	ENST00000336596	Transcript	missense_variant	probably_damaging(0.977)
chr4	56820414	56820414	*CEP135*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P143	p.E113*	ENSG00000174799	ENST00000257287	Transcript	stop_gained	NA
chr4	92136444	92136444	*USP17L10*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.D421G	ENSG00000231396	ENST00000417945	Transcript	missense_variant	benign(0)
chr5	14609126	14609126	*FAM105A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P143	p.Q299H	ENSG00000145569	ENST00000274217	Transcript	missense_variant	possibly_damaging(0.857)
chr5	176918896	176918896	*PDLIM7*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P143	p.Y104N	ENSG00000196923	ENST00000355841	Transcript	missense_variant	benign(0.001)
chr5	71490897	71490897	*MAP1B*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.N572S	ENSG00000131711	ENST00000296755	Transcript	missense_variant	unknown(0)
chr6	46846033	46846033	*GPR116*	Nonsense_Mutation	.	SNP	G	G	T	rs372082410	shanshan_et_al_P143	p.C382*	ENSG00000069122	ENST00000283296	Transcript	stop_gained	NA
chr6	64694495	64694495	*EYS*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P143	p.A2279E	ENSG00000188107	ENST00000503581	Transcript	missense_variant	benign(0.131)
chr7	43503278	43503278	*HECW1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.T891A	ENSG00000002746	ENST00000395891	Transcript	missense_variant	probably_damaging(0.989)
chr8	144895892	144895892	*SCRIB*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P143	p.P121A	ENSG00000180900	ENST00000356994	Transcript	missense_variant	possibly_damaging(0.775)
chr8	146076454	146076454	*COMMD5*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P143	p.H90Q	ENSG00000170619	ENST00000450361	Transcript	missense_variant	possibly_damaging(0.588)
chr9	97321230	97321230	*FBP2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P143	p.A337V	ENSG00000130957	ENST00000375337	Transcript	missense_variant	benign(0.004)
chrX	128701285	128701285	*OCRL*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.I471V	ENSG00000122126	ENST00000371113	Transcript	missense_variant	probably_damaging(0.999)
chrX	140993421	140993421	*MAGEC1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P143	p.Q77H	ENSG00000155495	ENST00000285879	Transcript	missense_variant	benign(0.216)
chrX	151869767	151869767	*MAGEA6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.K153E	ENSG00000197172	ENST00000329342	Transcript	missense_variant	benign(0.009)
chrX	53655552	53655552	*HUWE1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P143	p.Y378*	ENSG00000086758	ENST00000342160	Transcript	stop_gained	NA
chrX	69353826	69353826	*IGBP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P143	p.P10L	ENSG00000089289	ENST00000342206	Transcript	missense_variant	benign(0.035)
chrX	86873115	86873115	*KLHL4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P143	p.A303E	ENSG00000102271	ENST00000373114	Transcript	missense_variant	benign(0.301)
chr17	75785290	75785300	*TP53*	*Missense_Mutation*	.	SNP	A	A	G	novel	shanshan_et_al_P143	p.F134L	ENSG00000141510	ENST00000269305	Transcript	missense_variant	1
chr1	118535140	118535140	*SPAG17*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P145	p.Q1770H	ENSG00000155761	ENST00000336338	Transcript	missense_variant	possibly_damaging(0.902)
chr1	155837791	155837791	*SYT11*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P145	p.S24P	ENSG00000132718	ENST00000368324	Transcript	missense_variant	benign(0.115)
chr1	160851835	160851835	*ITLN1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P145	p.S106I	ENSG00000179914	ENST00000326245	Transcript	missense_variant	possibly_damaging(0.888)
chr1	169576261	169576261	*SELP*	Nonsense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P145	p.L482*	ENSG00000174175	ENST00000263686	Transcript	stop_gained	NA
chr1	174418054	174418054	*GPR52*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P145	p.R269W	ENSG00000203737	ENST00000367685	Transcript	missense_variant	possibly_damaging(0.908)
chr1	181480505	181480505	*CACNA1E*	Splice_Site	.	SNP	A	A	T	novel	shansha n_et_al_P145	p.X125_splice	ENSG00000198216	ENST00000367573	Transcript	splice_acceptor_variant	NA
chr1	185970850	185970850	*HMCN1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P145	p.K1442M	ENSG00000143341	ENST00000271588	Transcript	missense_variant	probably_damaging(0.999)
chr1	192993015	192993015	*UCHL5*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P145	p.Y231H	ENSG00000116750	ENST00000367455	Transcript	missense_variant	benign(0.182)
chr1	205027066	205027066	*CNTN2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P145	p.G30*	ENSG00000184144	ENST00000331830	Transcript	stop_gained	NA

chr1	20680449	20680449	*VWA5B1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.S1119I	ENSG00000158816	ENST00000375079	Transcript	missense_variant	benign(0.014)
chr1	229773268	229773268	*URB2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P145	p.I970V	ENSG00000135763	ENST00000258243	Transcript	missense_variant	benign(0.007)
chr1	71513120	71513120	*PTGER3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P145	p.C47W	ENSG00000050628	ENST00000356595	Transcript	missense_variant	probably_damaging(0.95)
chr10	105376985	105376985	*SH3PXD2A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P145	p.R269W	ENSG00000107957	ENST00000355946	Transcript	missense_variant	probably_damaging(0.921)
chr10	17865099	17865099	*MRC1L1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P145	p.E30K	ENSG00000183748	ENST00000331429	Transcript	missense_variant	benign(0.116)
chr10	21435406	21435406	*C10orf113*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.M11K	ENSG00000204683	ENST00000533431	Transcript	missense_variant	benign(0.092)
chr10	43016577	43016577	*ZNF37BP*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P145	NA	ENSG00000234420	ENST00000452075	Transcript	splice_acceptor_variant	NA
chr10	48371261	48371261	*ZNF488*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.H243Q	ENSG00000165388	ENST00000395702	Transcript	missense_variant	benign(0.208)
chr10	80063115	80063115	*TAF3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.Q281L	ENSG00000165632	ENST00000344293	Transcript	missense_variant	probably_damaging(0.969)
chr10	85991969	85991969	*LRIT1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P145	p.N529S	ENSG00000148602	ENST00000372105	Transcript	missense_variant	probably_damaging(0.999)
chr10	89692794	89692794	*PTEN*	Missense_Mutation	.	SNP	A	A	G	rs121909238	shanshan_et_al_P145	p.H93R	ENSG00000171862	ENST00000371953	Transcript	missense_variant	probably_damaging(0.92)
chr10	98742244	98742244	*C10orf12*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P145	p.S366T	ENSG00000155640	ENST00000286067	Transcript	missense_variant	possibly_damaging(0.547)
chr11	53448333	53448333	*OR51B2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.R232I	ENSG00000184881	ENST00000328813	Transcript	missense_variant	possibly_damaging(0.865)
chr11	59271301	59271301	*OR4D11*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P145	p.L85F	ENSG00000176200	ENST00000313253	Transcript	missense_variant	probably_damaging(0.928)
chr12	130648454	130648454	*FZD10*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.S323C	ENSG00000111432	ENST00000229030	Transcript	missense_variant	probably_damaging(0.999)
chr12	50747029	50747029	*FAM186A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.T1196S	ENSG00000185958	ENST00000327337	Transcript	missense_variant	benign(0.301)
chr12	52884703	52884703	*KRT6A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.L284Q	ENSG00000205420	ENST00000330722	Transcript	missense_variant	probably_damaging(0.999)
chr12	53293558	53293558	*KRT8*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P145	p.X355_splice	ENSG00000170421	ENST00000552150	Transcript	splice_donor_variant	NA
chr12	53682059	53682059	*ESPL1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.T1494S	ENSG00000135476	ENST00000257934	Transcript	missense_variant	benign(0.071)
chr12	63454116	63454116	*CD9*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P145	p.V199A	ENSG00000010278	ENST00000382518	Transcript	missense_variant	possibly_damaging(0.768)
chr12	78522584	78522584	*NAV3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.P1460H	ENSG00000067798	ENST00000536525	Transcript	missense_variant	probably_damaging(1)
chr13	103309468	103309468	*TPP2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P145	p.K1005N	ENSG00000134900	ENST00000376065	Transcript	missense_variant	benign(0.18)
chr15	48726812	48726812	*FBN1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.G2199C	ENSG00000166147	ENST00000316623	Transcript	missense_variant	probably_damaging(0.999)
chr15	55790430	55790430	*DYX1C1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.V33E	ENSG00000256061	ENST00000321149	Transcript	missense_variant	probably_damaging(0.982)
chr15	73996212	73996212	*CD276*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.D316Y	ENSG00000103855	ENST00000318443	Transcript	missense_variant	possibly_damaging(0.633)
chr15	79092535	79092535	*ADAMTS7*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P145	p.L152R	ENSG00000136378	ENST00000388820	Transcript	missense_variant	possibly_damaging(0.521)
chr16	21215715	21215715	*TSC2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.D635V	ENSG00000103197	ENST00000219476	Transcript	missense_variant	probably_damaging(0.944)
chr16	34060304	34060304	*OR2C1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P145	p.L32V	ENSG00000168158	ENST00000304936	Transcript	missense_variant	benign(0.025)
chr17	25981611	25981611	*CLUH*	Missense_Mutation	.	SNP	C	C	A	rs374551796	shanshan_et_al_P145	p.D909Y	ENSG00000132361	ENST00000570628	Transcript	missense_variant	benign(0.212)
chr17	65105777	65105777	*HELZ*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P145	p.N1315S	ENSG00000198265	ENST00000358691	Transcript	missense_variant	benign(0.023)
chr17	75782355	75782355	*TP53*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P145	p.Y205C	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.99)
chr18	12454436	12454436	*SPIRE1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.E562V	ENSG00000134278	ENST00000409402	Transcript	missense_variant	probably_damaging(0.999)
chr18	51851169	51851169	*STARD6*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P145	p.K186Q	ENSG00000174448	ENST00000581310	Transcript	missense_variant	possibly_damaging(0.48)
chr19	33498970	33498970	*RHPN2*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P145	p.Q237P	ENSG00000131941	ENST00000254260	Transcript	missense_variant	benign(0.098)
chr19	36362233	36362233	*APLP1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.R173S	ENSG00000105290	ENST00000221891	Transcript	missense_variant	possibly_damaging(0.896)
chr19	45165071	45165071	*PVR*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.T416K	ENSG00000073008	ENST00000425690	Transcript	missense_variant	probably_damaging(0.94)

chr19	46891698	46891698	*PPP5C*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.Q390L	ENSG00000011485	ENST00000012443	Transcript	missense_variant	probably_damaging(0.923)
chr19	54782777	54782777	*LILRB2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.T282N	ENSG00000131042	ENST00000391749	Transcript	missense_variant	possibly_damaging(0.901)
chr19	57133274	57133274	*ZNF71*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.T207S	ENSG00000197951	ENST00000328070	Transcript	missense_variant	probably_damaging(0.958)
chr2	220494351	220494351	*SLC4A3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.A182D	ENSG00000114923	ENST00000373762	Transcript	missense_variant	benign(0.022)
chr2	55252372	55252372	*RTN4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P145	p.V955I	ENSG00000115310	ENST00000337526	Transcript	missense_variant	benign(0.004)
chr2	74782298	74782298	*DOK1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.W26C	ENSG00000115325	ENST00000236668	Transcript	missense_variant	probably_damaging(0.997)
chr20	18574465	18574465	*DTD1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.M45K	ENSG00000125821	ENST00000377452	Transcript	missense_variant	possibly_damaging(0.603)
chr20	25729999	25729999	*TMC2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.V293E	ENSG00000149488	ENST00000358864	Transcript	missense_variant	probably_damaging(0.994)
chr3	122642525	122642525	*SEMA5B*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P145	p.R458P	ENSG00000082684	ENST00000451055	Transcript	missense_variant	probably_damaging(0.976)
chr3	134343927	134343927	*KY*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.Q151K	ENSG00000174611	ENST00000423778	Transcript	missense_variant	benign(0.005)
chr3	47445222	47445222	*ITPR1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.Q1500H	ENSG00000150995	ENST00000302640	Transcript	missense_variant	probably_damaging(0.993)
chr3	52555914	52555914	*STAB1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.G2073V	ENSG00000010327	ENST00000321725	Transcript	missense_variant	benign(0.126)
chr4	106816811	106816811	*NPNT*	Translation_Start_Site	.	SNP	T	T	C	novel	shanshan_et_al_P145	p.M1?	ENSG00000168743	ENST00000427316	Transcript	initiator_codon_variant	possibly_damaging(0.904)
chr4	110687953	110687953	*CFI*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.V29L	ENSG00000205403	ENST00000394634	Transcript	missense_variant	benign(0.003)
chr5	101726706	101726706	*SLCO6A1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.Y620N	ENSG00000205359	ENST00000506729	Transcript	missense_variant	probably_damaging(0.984)
chr5	13919298	13919298	*DNAH5*	Missense_Mutation	.	SNP	G	G	A	rs201077964	shanshan_et_al_P145	p.S321L	ENSG00000039139	ENST00000265104	Transcript	missense_variant	possibly_damaging(0.651)
chr6	129470177	129470177	*LAMA2*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.C321*	ENSG00000196569	ENST00000421865	Transcript	stop_gained	NA
chr6	151673209	151673209	*AKAP12*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.V1228E	ENSG00000131016	ENST00000406766	Transcript	missense_variant	benign(0.001)
chr6	155632457	155632457	*TFB1M*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.K50N	ENSG00000029639	ENST00000367166	Transcript	missense_variant	benign(0.049)
chr6	46826312	46826312	*GPR116*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.M1110L	ENSG00000069122	ENST00000283296	Transcript	missense_variant	possibly_damaging(0.842)
chr7	143701371	143701371	*OR6B1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P145	p.F94L	ENSG00000221813	ENST00000408922	Transcript	missense_variant	benign(0.039)
chr7	20198675	20198675	*MACC1*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P145	p.S439Pfs*8	ENSG00000183742	ENST00000400331	Transcript	frameshift_variant	NA
chr7	48318466	48318466	*ABCA13*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P145	p.Y2559H	ENSG00000179869	ENST00000435803	Transcript	missense_variant	probably_damaging(0.987)
chr7	99445852	99445852	*CYP3A43*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.N166Y	ENSG00000021461	ENST00000222382	Transcript	missense_variant	possibly_damaging(0.722)
chr8	72977790	72977790	*TRPA1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.L150M	ENSG00000104321	ENST00000262209	Transcript	missense_variant	probably_damaging(0.999)
chr8	92201769	92201769	*LRRC69*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P145	p.R224M	ENSG00000214954	ENST00000448384	Transcript	missense_variant	benign(0.232)
chr8	99039847	99039847	*MATN2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P145	p.K716E	ENSG00000132561	ENST00000520016	Transcript	missense_variant	possibly_damaging(0.472)
chr9	131198053	131198053	*CERCAM*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P145	p.S553T	ENSG00000167123	ENST00000372838	Transcript	missense_variant	benign(0.009)
chr9	35555684	35555684	*RUSC2*	Missense_Mutation	.	SNP	C	C	G	rs200605865	shanshan_et_al_P145	p.T881S	ENSG00000198853	ENST00000455600	Transcript	missense_variant	benign(0.001)
chrX	10535418	10535418	*MID1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P145	p.P57L	ENSG00000101871	ENST00000317552	Transcript	missense_variant	probably_damaging(1)
chrX	12735700	12735700	*FRMPD4*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P145	p.S919R	ENSG00000169933	ENST00000380682	Transcript	missense_variant	benign(0.318)
chrX	84362818	84362818	*SATL1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P145	p.M386K	ENSG00000184788	ENST00000509231	Transcript	missense_variant	benign(0.004)
chr1	183602267	183602267	*ARPC5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P16	p.Q59K	ENSG00000162704	ENST00000294742	Transcript	missense_variant	benign(0.003)
chr1	201180607	201180607	*IGFN1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P16	p.F2196I	ENSG00000163395	ENST00000335211	Transcript	missense_variant	unknown(0)
chr1	24076378	24076378	*TCEB3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P16	p.H86R	ENSG00000011007	ENST00000418390	Transcript	missense_variant	benign(0.049)
chr1	39768605	39768605	*MACF1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P16	p.C887S	ENSG00000127603	ENST00000545844	Transcript	missense_variant	benign(0.039)

chr1	87025963	87025963	*CLCA4*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P16	p.C124S	ENSG00000160602	ENST00000370563	Transcript	missense_variant	possibly_damaging(0.855)
chr10	50943383	50943383	*OGDHL*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P16	p.D975A	ENSG00000197444	ENST00000374103	Transcript	missense_variant	benign(0.001)
chr11	46666923	46666923	*ATG13*	Frame_Shift_Del	.	DEL	A	A	-	novel	shansha n_et_al_P16	p.I37Ffs*17	ENSG00000175224	ENST00000528494	Transcript	frameshift_variant	NA
chr11	93460493	93460493	*KIAA1731*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P16	p.L2284R	ENSG00000166004	ENST00000325212	Transcript	missense_variant	probably_damaging(0.973)
chr12	132529477	132529477	*EP400*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P16	p.R2255*	ENSG00000183495	ENST00000389561	Transcript	stop_gained	NA
chr12	46761074	46761074	*SLC38A2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.L122I	ENSG00000134294	ENST00000256689	Transcript	missense_variant	probably_damaging(0.971)
chr12	72523022	72523022	*C1RL*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P16	p.E224G	ENSG00000139178	ENST00000266542	Transcript	missense_variant	benign(0.412)
chr13	110434985	110434985	*IRS2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P16	p.D1139A	ENSG00000185950	ENST00000375856	Transcript	missense_variant	probably_damaging(0.986)
chr13	25044054	25044054	*PARP4*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P16	p.N675S	ENSG00000102699	ENST00000381989	Transcript	missense_variant	probably_damaging(0.995)
chr14	32561340	32561340	*ARHGAP5*	Missense_Mutation	.	SNP	G	G	A	rs78337553	shansha n_et_al_P16	p.E489K	ENSG00000100852	ENST00000345122	Transcript	missense_variant	possibly_damaging(0.811)
chr14	56104500	56104500	*KTN1*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P16	p.I574V	ENSG00000126777	ENST00000395314	Transcript	missense_variant	benign(0.007)
chr14	81728269	81728269	*STON2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P16	p.E874K	ENSG00000140022	ENST00000555447	Transcript	missense_variant	benign(0.116)
chr16	22268109	22268109	*EEF2K*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.R220I	ENSG00000103319	ENST00000263026	Transcript	missense_variant	probably_damaging(0.996)
chr16	71509288	71509288	*ZNF19*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P16	p.D388N	ENSG00000157429	ENST00000288177	Transcript	missense_variant	benign(0.005)
chr16	79245590	79245590	*WWOX*	Missense_Mutation	.	SNP	G	G	T	rs202002431	shansha n_et_al_P16	p.R381L	ENSG00000186153	ENST00000566780	Transcript	missense_variant	benign(0.018)
chr17	7574035	7574035	*TP53*	Splice_Site	.	SNP	T	T	A	novel	shansha n_et_al_P16	p.X332_splice	ENSG00000141510	ENST00000269305	Transcript	splice_acceptor_variant	NA
chr18	12449677	12449677	*SPIRE1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P16	p.S744L	ENSG00000134278	ENST00000409402	Transcript	missense_variant	possibly_damaging(0.491)
chr18	63547948	63547948	*CDH7*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P16	p.P726T	ENSG00000081138	ENST00000397968	Transcript	missense_variant	probably_damaging(1)
chr19	13063762	13063762	*RAD23A*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.G331C	ENSG00000179262	ENST00000586534	Transcript	missense_variant	probably_damaging(0.999)
chr19	14034145	14034145	*CC2D1A*	Splice_Site	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.X548_splice	ENSG00000132024	ENST00000318003	Transcript	splice_acceptor_variant	NA
chr19	17892111	17892111	*FCHO1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P16	p.R567W	ENSG00000130475	ENST00000594202	Transcript	missense_variant	possibly_damaging(0.878)
chr19	18004561	18004561	*SLC5A5*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P16	p.G603S	ENSG00000105641	ENST00000222248	Transcript	missense_variant	benign(0.004)
chr19	50774726	50774726	*MYH14*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.V1032L	ENSG00000105357	ENST00000601313	Transcript	missense_variant	possibly_damaging(0.693)
chr2	100210039	100210039	*AFF3*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.T720N	ENSG00000144218	ENST00000356421	Transcript	missense_variant	benign(0.124)
chr2	23106560 9	23106560 9	*SP110*	Missense_Mutation	.	SNP	A	A	G	rs200263454	shansha n_et_al_P16	p.V374A	ENSG00000135899	ENST00000258381	Transcript	missense_variant	benign(0.294)
chr2	23873794 5	23873794 5	*RBM44*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.V897L	ENSG00000177483	ENST00000316997	Transcript	missense_variant	probably_damaging(0.973)
chr2	26437363	26437363	*HADHA*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P16	p.K289N	ENSG00000084754	ENST00000380649	Transcript	missense_variant	possibly_damaging(0.598)
chr20	35651078	35651078	*RBL1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P16	p.L845H	ENSG00000080839	ENST00000373664	Transcript	missense_variant	probably_damaging(1)
chr20	9353722	9353722	*PLCB4*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.V239L	ENSG00000101333	ENST00000378501	Transcript	missense_variant	benign(0.061)
chr3	111870794	111870794	*SLC9C1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.A1145D	ENSG00000172139	ENST00000305815	Transcript	missense_variant	benign(0)
chr4	175899102	175899102	*ADAM29*	Missense_Mutation	.	SNP	T	T	C	rs200731905	shansha n_et_al_P16	p.M809T	ENSG00000168594	ENST00000359240	Transcript	missense_variant	unknown(0)
chr4	9270563	9270563	*USP17L22*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P16	p.E407Q	ENSG00000248933	ENST00000511280	Transcript	missense_variant	benign(0.104)
chr5	108233386	108233386	*FER*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P16	p.Q358L	ENSG00000151422	ENST00000281092	Transcript	missense_variant	benign(0.004)
chr5	140745785	140745785	*PCDHGA5*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P16	p.R630*	ENSG00000253485	ENST00000518069	Transcript	stop_gained	NA
chr5	150660593	150660593	*SLC36A3*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P16	p.A417T	ENSG00000186334	ENST00000377713	Transcript	missense_variant	benign(0.055)
chr6	112397659	112397659	*TUBE1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P16	p.P168T	ENSG00000074935	ENST00000368662	Transcript	missense_variant	probably_damaging(0.989)

chr6	31376822	31376822	*BPHL*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P16	p.E207K	ENSG00000137274	ENST00000380379	Transcript	missense_variant	benign(0.003)
chr6	56135233	56135233	*FARS2*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P16	p.D397Ifs*3	ENSG00000145982	ENST00000324331	Transcript	frameshift_variant	NA
chr6	75887648	75887648	*COL12A1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P16	p.K723I	ENSG00000111799	ENST00000322507	Transcript	missense_variant	benign(0.004)
chr7	11514106	11514106	*THSD7A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P16	p.P703S	ENSG00000005108	ENST00000423059	Transcript	missense_variant	benign(0.045)
chr8	110131553	110131553	*TRHR*	Missense_Mutation	.	SNP	G	G	A	rs147019235	shanshan_et_al_P16	p.V356I	ENSG00000174417	ENST00000518632	Transcript	missense_variant	benign(0.021)
chr8	35624493	35624493	*UNC5D*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P16	p.T796K	ENSG00000156687	ENST00000404895	Transcript	missense_variant	benign(0.14)
chr9	130479917	130479917	*TTC16*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P16	p.Y98N	ENSG00000167094	ENST00000373289	Transcript	missense_variant	probably_damaging(1)
chr9	140328750	140328750	*NOXA1*	Missense_Mutation	.	SNP	G	G	T	rs144777481	shanshan_et_al_P16	p.G464C	ENSG00000188747	ENST00000341349	Transcript	missense_variant	benign(0.05)
chr9	27172744	27172744	*TEK*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P16	p.K253N	ENSG00000120156	ENST00000380036	Transcript	missense_variant	benign(0.196)
chr9	33467459	33467459	*NOL6*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P16	p.L554Sfs*8	ENSG00000165271	ENST00000379471	Transcript	frameshift_variant	NA
chr9	79441582	79441582	*PRUNE2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P16	p.L192R	ENSG00000106772	ENST00000376718	Transcript	missense_variant	probably_damaging(0.999)
chrX	72900790	72900790	*CHIC1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P16	p.V209I	ENSG00000204116	ENST00000373502	Transcript	missense_variant	probably_damaging(0.942)
chr1	145248876	145248876	*NOTCH2NL*	Missense_Mutation	.	SNP	A	A	G	rs200866084	shanshan_et_al_P20	p.N7S	ENSG00000213240	ENST00000369340	Transcript	missense_variant	probably_damaging(0.978)
chr1	228346166	228346166	*GJC2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P20	p.G236V	ENSG00000198835	ENST00000366714	Transcript	missense_variant	probably_damaging(1)
chr1	248343535	248343535	*OR2M2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P20	p.F83S	ENSG00000198601	ENST00000359682	Transcript	missense_variant	benign(0.266)
chr1	75708631	75708631	*SLC44A5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P20	p.K137N	ENSG00000137968	ENST00000370855	Transcript	missense_variant	benign(0.002)
chr10	33218859	33218859	*ITGB1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P20	p.I89M	ENSG00000150093	ENST00000396033	Transcript	missense_variant	benign(0.089)
chr10	65271515	65271515	*PRKCQ*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P20	p.N326I	ENSG00000065675	ENST00000263125	Transcript	missense_variant	benign(0.019)
chr11	66466367	66466367	*DCHS1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P20	p.L2313Q	ENSG00000166341	ENST00000299441	Transcript	missense_variant	probably_damaging(1)
chr12	10962248	10962248	*TAS2R9*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P20	p.I143Lfs*29	ENSG00000121381	ENST00000240691	Transcript	frameshift_variant	NA
chr12	11420773	11420773	*PRB3*	Missense_Mutation	.	SNP	C	C	T	rs200940772	shanshan_et_al_P20	p.R137H	ENSG00000197870	ENST00000381842	Transcript	missense_variant	unknown(0)
chr12	16115749	16115749	*DERA*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P20	p.A126S	ENSG00000023697	ENST00000428559	Transcript	missense_variant	probably_damaging(0.96)
chr12	41337931	41337931	*CNTN1*	Frame_Shift_Ins	.	INS	-	-	GA	novel	shanshan_et_al_P20	p.D548Efs*23	ENSG00000018236	ENST00000551295	Transcript	frameshift_variant	NA
chr12	78401198	78401198	*NAV3*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P20	p.T627S	ENSG00000067798	ENST00000536525	Transcript	missense_variant	probably_damaging(0.997)
chr12	93245003	93245003	*EEA1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P20	p.K228E	ENSG00000102189	ENST00000322349	Transcript	missense_variant	possibly_damaging(0.566)
chr13	28964068	28964068	*FLT1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P20	p.T612A	ENSG00000102755	ENST00000282397	Transcript	missense_variant	benign(0.013)
chr15	48063497	48063497	*SEMA6D*	Missense_Mutation	.	SNP	G	G	A	rs374871367	shanshan_et_al_P20	p.G913R	ENSG00000137872	ENST00000316364	Transcript	missense_variant	benign(0.097)
chr17	10397888	10397888	*MYH1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P20	p.Q1857K	ENSG00000109061	ENST00000226207	Transcript	missense_variant	probably_damaging(0.996)
chr17	55194225	55194225	*AKAP1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P20	p.D813Y	ENSG00000121057	ENST00000337714	Transcript	missense_variant	probably_damaging(1)
chr17	61457161	61457161	*TANC2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P20	p.H815Y	ENSG00000170921	ENST00000424789	Transcript	missense_variant	possibly_damaging(0.677)
chr17	62891049	62891049	*LRRC37A3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P20	p.R776H	ENSG00000176809	ENST00000584306	Transcript	missense_variant	benign(0)
chr19	45110941	45110941	*PLIN4*	Missense_Mutation	.	SNP	C	C	T	rs201223343	shanshan_et_al_P20	p.A946T	ENSG00000167676	ENST00000301286	Transcript	missense_variant	benign(0)
chr19	51647676	51647676	*SIGLEC7*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P20	p.R149S	ENSG00000168995	ENST00000317643	Transcript	missense_variant	benign(0.046)
chr19	55677780	55677780	*DNAAF3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P20	p.M48K	ENSG00000167646	ENST00000527223	Transcript	missense_variant	probably_damaging(0.998)
chr19	56423938	56423938	*NLRP13*	Missense_Mutation	.	SNP	G	G	T	rs561112842	shanshan_et_al_P20	p.N415K	ENSG00000173572	ENST00000342929	Transcript	missense_variant	possibly_damaging(0.694)
chr2	24507714	24507714	*ITSN2*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P20	p.X622_splice	ENSG00000198399	ENST00000355123	Transcript	splice_acceptor_variant	NA

chr2	9599739	9599739	*CPSF3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P20	p.I593K	ENSG00000119203	ENST00000238112	Transcript	missense_variant	benign(0)
chr2	9599742	9599742	*CPSF3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P20	p.R594K	ENSG00000119203	ENST00000238112	Transcript	missense_variant	benign(0)
chr3	111923246	111923246	*SLC9C1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P20	p.A664V	ENSG00000172139	ENST00000305815	Transcript	missense_variant	benign(0.047)
chr3	113169364	113169364	*SPICE1*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P20	p.X715_splice	ENSG00000163611	ENST00000295872	Transcript	splice_acceptor_variant	NA
chr3	44763513	44763513	*ZNF502*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P20	p.T402S	ENSG00000196653	ENST00000296091	Transcript	missense_variant	possibly_damaging(0.886)
chr3	48784662	48784662	*ITPR1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P20	p.R2663K	ENSG00000150995	ENST00000302640	Transcript	missense_variant	benign(0.005)
chr3	74350606	74350606	*CNTN3*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P20	p.K680*	ENSG00000113805	ENST00000263665	Transcript	stop_gained	NA
chr4	107845802	107845802	*DKK2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P20	p.D143E	ENSG00000155011	ENST00000285311	Transcript	missense_variant	benign(0.001)
chr5	154299544	154299544	*GEMIN5*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P20	p.D528Y	ENSG00000082516	ENST00000285873	Transcript	missense_variant	probably_damaging(0.95)
chr5	175535641	175535641	*FAM153B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P20	p.G222E	ENSG00000182230	ENST00000515817	Transcript	missense_variant	benign(0)
chr5	251503	251503	*SDHA*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P20	p.M572V	ENSG00000073578	ENST00000264932	Transcript	missense_variant	benign(0.148)
chr5	96503349	96503349	*RIOK2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P20	p.V407F	ENSG00000058729	ENST00000283109	Transcript	missense_variant	benign(0.001)
chr6	26091275	26091275	*HFE*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P20	p.D95N	ENSG00000010704	ENST00000357618	Transcript	missense_variant	probably_damaging(0.986)
chr7	103969264	103969264	*LHFPL3*	Missense_Mutation	.	SNP	g	g	A	novel	shanshan_et_al_P20	p.A13T	ENSG00000187416	ENST00000535008	Transcript	missense_variant	possibly_damaging(0.695)
chr7	114619638	114619638	*MDFIC*	Missense_Mutation	.	SNP	G	G	C	rs548881845	shanshan_et_al_P20	p.G208R	ENSG00000135272	ENST00000257724	Transcript	missense_variant	probably_damaging(0.984)
chr7	116593724	116593724	*ST7*	Missense_Mutation	.	SNP	A	A	G	rs376240267	shanshan_et_al_P20	p.I44V	ENSG00000004866	ENST00000265437	Transcript	missense_variant	benign(0.001)
chr7	131829986	131829986	*PLXNA4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P20	p.G1706V	ENSG00000221866	ENST00000359827	Transcript	missense_variant	probably_damaging(1)
chr7	54610501	54610501	*VSTM2A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P20	p.Q26H	ENSG00000170419	ENST00000407838	Transcript	missense_variant	benign(0.026)
chr8	87423940	87423940	*WWP1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P20	p.S300C	ENSG00000123124	ENST00000517970	Transcript	missense_variant	benign(0.001)
chr9	67935957	67935957	*ANKRD20A1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P20	p.Q228K	ENSG00000196774	ENST00000377477	Transcript	missense_variant	benign(0.001)
chrX	147018025	147018025	*FMR1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P20	p.K295E	ENSG00000102081	ENST00000370475	Transcript	missense_variant	probably_damaging(0.995)
chrX	48372651	48372651	*PORCN*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P20	p.A248G	ENSG00000102312	ENST00000326194	Transcript	missense_variant	probably_damaging(0.954)
chrX	54265342	54265342	*WNK3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P20	p.R1281L	ENSG00000196632	ENST00000354646	Transcript	missense_variant	possibly_damaging(0.843)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P20	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.997)
chr1	166818721	166818721	*POGK*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P26	p.G302V	ENSG00000143157	ENST00000367875	Transcript	missense_variant	probably_damaging(0.999)
chr1	186034441	186034441	*HMCN1*	Missense_Mutation	.	SNP	A	A	G	rs145591176	shanshan_et_al_P26	p.I2529V	ENSG00000143341	ENST00000271588	Transcript	missense_variant	benign(0.001)
chr10	124343863	124343863	*DMBT1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P26	p.S472R	ENSG00000187908	ENST00000368909	Transcript	missense_variant	benign(0)
chr10	50947853	50947853	*OGDHL*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P26	p.N725Y	ENSG00000197444	ENST00000374103	Transcript	missense_variant	benign(0.176)
chr11	19256369	19256369	*E2F8*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P26	p.I230V	ENSG00000129173	ENST00000527884	Transcript	missense_variant	benign(0.001)
chr11	93530772	93530772	*MED17*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P26	p.M405I	ENSG00000042429	ENST00000251871	Transcript	missense_variant	benign(0.002)
chr12	112186983	112186983	*ACAD10*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P26	p.H915L	ENSG00000111271	ENST00000455480	Transcript	missense_variant	benign(0.09)
chr12	128900032	128900032	*TMEM132C*	Missense_Mutation	.	SNP	G	G	A	rs200249610	shanshan_et_al_P26	p.A281T	ENSG00000181234	ENST00000435159	Transcript	missense_variant	benign(0.014)
chr12	32977098	32977098	*PKP2*	Splice_Site	.	SNP	T	T	C	novel	shanshan_et_al_P26	p.X563_splice	ENSG00000057294	ENST00000070846	Transcript	splice_acceptor_variant	NA
chr12	46328012	46328012	*SCAF11*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P26	p.M193I	ENSG00000139218	ENST00000369367	Transcript	missense_variant	benign(0.001)
chr15	22383092	22383092	*OR4N4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P26	p.T207I	ENSG00000183706	ENST00000328795	Transcript	missense_variant	possibly_damaging(0.864)
chr17	3195014	3195014	*OR3A1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P26	p.L288R	ENSG00000180090	ENST00000323404	Transcript	missense_variant	probably_damaging(0.96)

chr20	4229177	4229177	*ADRA1D*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P26	p.L143Q	ENSG00000171873	ENST00000379453	Transcript	missense_variant	probably_damaging(0.998)
chr3	178952085	178952085	*PIK3CA*	Missense_Mutation	.	SNP	A	A	G	rs121913279	shansha n_et_al_P26	p.H1047R	ENSG00000121879	ENST00000263967	Transcript	missense_variant	possibly_damaging(0.529)
chr4	71201811	71201811	*CABS1*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P26	p.V352A	ENSG00000145309	ENST00000273936	Transcript	missense_variant	benign(0)
chr5	180582271	180582271	*OR2V2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P26	p.G110V	ENSG00000182613	ENST00000328275	Transcript	missense_variant	probably_damaging(1)
chr5	34821954	34821954	*RAI14*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P26	p.Q374L	ENSG00000039560	ENST00000515799	Transcript	missense_variant	possibly_damaging(0.46)
chr6	72467223	72467223	*RREB1*	Frame_Shift_Del	.	DEL	AG	AG	-	novel	shansha n_et_al_P26	p.E1348Afs*8	ENSG00000124782	ENST00000379938	Transcript	frameshift_variant	NA
chr7	151071182	151071182	*NUB1*	Splice_Site	.	SNP	G	G	C	novel	shansha n_et_al_P26	NA	ENSG00000013374	ENST00000568733	Transcript	splice_acceptor_variant	NA
chr9	105767083	105767083	*CYLC2*	Missense_Mutation	.	SNP	G	G	A	rs113473315	shansha n_et_al_P26	p.R96K	ENSG00000155833	ENST00000374798	Transcript	missense_variant	possibly_damaging(0.554)
chrX	103041425	103041425	*PLP1*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P26	p.T75A	ENSG00000123560	ENST00000418604	Transcript	missense_variant	benign(0.114)
chrX	75395318	75395318	*PBDC1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P26	p.S56L	ENSG00000102390	ENST00000373358	Transcript	missense_variant	probably_damaging(0.992)
chr17	75781777	75781777	*TP53*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P26	p.E224D	ENSG00000141510	ENST00000269305	Transcript	missense_variant	benign(0.001)
chr1	111957125	111957125	*OVGP1*	Frame_Shift_Del	.	DEL	T	T	-	novel	shansha n_et_al_P28	p.E667Kfs*30	ENSG00000085465	ENST00000369732	Transcript	frameshift_variant	NA
chr1	114916 0	114916 0	*TNFRSF4*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P28	p.G51R	ENSG00000186827	ENST00000379236	Transcript	missense_variant	probably_damaging(0.966)
chr1	189627 97	189627 97	*PAX7*	Missense_Mutation	.	SNP	c	c	T	novel	shansha n_et_al_P28	p.A173V	ENSG00000009709	ENST00000375375	Transcript	missense_variant	benign(0.075)
chr1	205740755	205740755	*RAB7L1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P28	p.R75*	ENSG00000117280	ENST00000367139	Transcript	stop_gained	NA
chr1	207245668	207245668	*PFKFB2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P28	p.K490N	ENSG00000123836	ENST00000367080	Transcript	missense_variant	benign(0)
chr1	228461210	228461211	*OBSCN*	Frame_Shift_Ins	.	INS	-	-	G	novel	shansha n_et_al_P28	p.Q2078Pfs*32	ENSG00000154358	ENST00000570156	Transcript	frameshift_variant	NA
chr1	48267215	48267215	*TRABD2B*	Missense_Mutation	.	SNP	G	G	A	rs541790975	shansha n_et_al_P28	p.T248M	ENSG00000269113	ENST00000606738	Transcript	missense_variant	possibly_damaging(0.518)
chr1	52878217	52878217	*PRPF38A*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P28	p.L177Q	ENSG00000134748	ENST00000257181	Transcript	missense_variant	probably_damaging(0.999)
chr1	70504220	70504220	*LRRC7*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P28	p.T867A	ENSG00000033122	ENST00000353833	Transcript	missense_variant	benign(0.164)
chr10	6259131	6259131	*PFKFB3*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P28	p.T159A	ENSG00000170525	ENST00000379775	Transcript	missense_variant	benign(0)
chr12	112600213	112600213	*HECTD4*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P28	p.R4266H	ENSG00000173064	ENST00000550722	Transcript	missense_variant	probably_damaging(0.996)
chr12	52574326	52574326	*KRT80*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P28	p.V213M	ENSG00000167767	ENST00000394815	Transcript	missense_variant	benign(0.047)
chr12	52758834	52758834	*KRT85*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P28	p.R181W	ENSG00000135443	ENST00000257901	Transcript	missense_variant	probably_damaging(0.998)
chr12	54063678	54063678	*ATP5G2*	Nonsense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P28	p.R89*	ENSG00000135390	ENST00000394349	Transcript	stop_gained	NA
chr12	6125705	6125705	*VWF*	Missense_Mutation	.	SNP	C	C	A	rs373074982	shansha n_et_al_P28	p.R1763L	ENSG00000110799	ENST00000261405	Transcript	missense_variant	benign(0.026)
chr12	75592633	75592633	*CD163L1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P28	p.Q318K	ENSG00000177675	ENST00000313599	Transcript	missense_variant	benign(0.004)
chr12	8085704	8085704	*SLC2A3*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P28	p.G50R	ENSG00000059804	ENST00000075120	Transcript	missense_variant	benign(0.003)
chr12	81924900	81924900	*FOXJ2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P28	p.R21L	ENSG00000065970	ENST00000162391	Transcript	missense_variant	probably_damaging(0.968)
chr13	21562382	21562382	*LATS2*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P28	p.C513G	ENSG00000150457	ENST00000382592	Transcript	missense_variant	benign(0.015)
chr13	60545096	60545096	*DIAPH3*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P28	p.G617*	ENSG00000139734	ENST00000400324	Transcript	stop_gained	NA
chr14	101347303	101347303	*RTL1*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P28	p.T1275P	ENSG00000254656	ENST00000534062	Transcript	missense_variant	benign(0.012)
chr14	64691257	64691257	*SYNE2*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P28	p.R6821*	ENSG00000054654	ENST00000358025	Transcript	stop_gained	NA
chr14	75265092	75265092	*YLPM1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P28	p.T1031K	ENSG00000119596	ENST00000325680	Transcript	missense_variant	benign(0.342)
chr14	94394887	94394887	*FAM181A*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P28	p.D148Y	ENSG00000140067	ENST00000267594	Transcript	missense_variant	possibly_damaging(0.521)
chr15	34113005	34113005	*RYR3*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P28	p.T3603A	ENSG00000198838	ENST00000389232	Transcript	missense_variant	benign(0.05)

chr15	52876997	52876997	*FAM214A*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P28	p.K1008Q	ENSG00000047346	ENST00000261844	Transcript	missense_variant	benign(0.057)
chr15	52901184	52901184	*FAM214A*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P28	p.N643D	ENSG00000047346	ENST00000261844	Transcript	missense_variant	benign(0.001)
chr15	55613506	55613506	*PIGB*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P28	p.L112P	ENSG00000069943	ENST00000164305	Transcript	missense_variant	probably_damaging(0.967)
chr15	64972962	64972962	*ZNF609*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P28	p.R1355C	ENSG00000180357	ENST00000326648	Transcript	missense_variant	probably_damaging(0.944)
chr15	74640322	74640322	*CYP11A1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P28	p.G115A	ENSG00000140459	ENST00000268053	Transcript	missense_variant	probably_damaging(1)
chr15	91035863	91035863	*IQGAP1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P28	p.K1516N	ENSG00000140575	ENST00000268182	Transcript	missense_variant	probably_damaging(1)
chr16	3253053	3253053	*RGS11*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P28	p.Q63H	ENSG00000076344	ENST00000397770	Transcript	missense_variant	benign(0.01)
chr17	45198352	45198352	*CDC27*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P28	p.M814I	ENSG00000004897	ENST00000531206	Transcript	missense_variant	benign(0.21)
chr17	5304777	5304777	*VPS53*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P28	p.R304H	ENSG00000141252	ENST00000437048	Transcript	missense_variant	benign(0.013)
chr17	73487140	73487140	*KIAA0195*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P28	p.R380L	ENSG00000177728	ENST00000314256	Transcript	missense_variant	benign(0.031)
chr17	7407007	7407007	*POLR2A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.R1046Q	ENSG00000181222	ENST00000322644	Transcript	missense_variant	probably_damaging(0.999)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P28	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr17	76446412	76446412	*DNAH17*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.A3641V	ENSG00000187775	ENST00000389840	Transcript	missense_variant	probably_damaging(0.997)
chr17	8171937	8171937	*PFAS*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.V1157M	ENSG00000178921	ENST00000314666	Transcript	missense_variant	probably_damaging(0.963)
chr18	47511148	47511148	*MYO5B*	Missense_Mutation	.	SNP	T	T	C	rs79714279	shanshan_et_al_P28	p.I296V	ENSG00000167306	ENST00000285039	Transcript	missense_variant	possibly_damaging(0.812)
chr19	1109717	1109717	*SBNO2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P28	p.G1030R	ENSG00000064932	ENST00000361757	Transcript	missense_variant	possibly_damaging(0.902)
chr19	11123688	11123688	*SMARCA4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.E780K	ENSG00000127616	ENST00000429416	Transcript	missense_variant	probably_damaging(0.999)
chr19	19257143	19257143	*MEF2B*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P28	p.T274P	ENSG00000213999	ENST00000162023	Transcript	missense_variant	benign(0.094)
chr19	2115334	2115334	*AP3D1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P28	p.K745E	ENSG00000065000	ENST00000355272	Transcript	missense_variant	possibly_damaging(0.688)
chr19	2987200	2987200	*TLE6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.G169S	ENSG00000104953	ENST00000246112	Transcript	missense_variant	benign(0.29)
chr19	38881004	38881004	*SPRED3*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P28	p.V21G	ENSG00000188766	ENST00000338502	Transcript	missense_variant	possibly_damaging(0.637)
chr19	42914611	42914611	*LIPE*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.R423C	ENSG00000079435	ENST00000244289	Transcript	missense_variant	probably_damaging(0.989)
chr19	45543487	45543487	*CLASRP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.R6Q	ENSG00000104859	ENST00000221455	Transcript	missense_variant	probably_damaging(1)
chr19	53385106	53385106	*ZNF320*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P28	p.E91D	ENSG00000182986	ENST00000595635	Transcript	missense_variant	possibly_damaging(0.629)
chr19	6719407	6719407	*C3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P28	p.I28V	ENSG00000125730	ENST00000245907	Transcript	missense_variant	benign(0.004)
chr2	128467270	128467270	*WDR33*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.R1157*	ENSG00000136709	ENST00000322313	Transcript	stop_gained	NA
chr20	61597917	61597917	*SLC17A9*	Missense_Mutation	.	SNP	G	G	T	rs570848200	shanshan_et_al_P28	p.A368S	ENSG00000101194	ENST00000370351	Transcript	missense_variant	probably_damaging(0.985)
chr3	119336894	119336894	*PLA1A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.M261I	ENSG00000144837	ENST00000273371	Transcript	missense_variant	probably_damaging(0.929)
chr3	186450291	186450291	*KNG1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P28	p.G253V	ENSG00000113889	ENST00000265023	Transcript	missense_variant	benign(0.02)
chr3	42727523	42727523	*KLHL40*	Missense_Mutation	.	SNP	G	G	A	rs142285083	shanshan_et_al_P28	p.R138H	ENSG00000157119	ENST00000287777	Transcript	missense_variant	probably_damaging(0.996)
chr3	48455317	48455318	*PLXNB1*	Frame_Shift_Del	.	DEL	AA	AA	-	novel	shanshan_et_al_P28	p.L1458Afs*2	ENSG00000164050	ENST00000358536	Transcript	frameshift_variant	NA
chr4	111543439	111543439	*PITX2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P28	p.S60T	ENSG00000164093	ENST00000306732	Transcript	missense_variant	benign(0.004)
chr4	150678616	150678616	*CPEB2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.D973N	ENSG00000137449	ENST00000538197	Transcript	missense_variant	probably_damaging(1)
chr4	152571525	152571525	*FAM160A1*	Missense_Mutation	.	SNP	G	G	T	rs11940735	shanshan_et_al_P28	p.D778Y	ENSG00000164142	ENST00000435205	Transcript	missense_variant	benign(0.429)
chr4	16014957	16014957	*PROM1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P28	p.Y361C	ENSG00000007062	ENST00000510224	Transcript	missense_variant	probably_damaging(0.996)
chr5	140347554	140347554	*PCDHAC2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P28	p.S401R	ENSG00000243232	ENST00000289269	Transcript	missense_variant	benign(0.092)

chr5	14751349	14751349	*ANKH*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P28	p.X173_splice	ENSG00000154122	ENST00000284268	Transcript	splice_acceptor_variant	NA
chr5	153674473	153674473	*GALNT10*	Missense_Mutation	.	SNP	G	G	A	rs200653755	shanshan_et_al_P28	p.R86H	ENSG00000164574	ENST00000297107	Transcript	missense_variant	possibly_damaging(0.778)
chr6	42936227	42936227	*PEX6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P28	p.S497P	ENSG00000124587	ENST00000304611	Transcript	missense_variant	benign(0.319)
chr6	46801209	46801209	*MEP1A*	Missense_Mutation	.	SNP	C	C	A	rs539407668	shanshan_et_al_P28	p.P515T	ENSG00000112818	ENST00000230588	Transcript	missense_variant	benign(0.248)
chr6	7583347	7583347	*DSP*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P28	p.R1951L	ENSG00000096696	ENST00000379802	Transcript	missense_variant	probably_damaging(0.994)
chr6	90422360	90422360	*MDN1*	Missense_Mutation	.	SNP	C	C	T	rs62417304	shanshan_et_al_P28	p.R2455Q	ENSG00000112159	ENST00000369393	Transcript	missense_variant	benign(0.009)
chr7	107542817	107542817	*DLD*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P28	p.N82K	ENSG00000091140	ENST00000205402	Transcript	missense_variant	possibly_damaging(0.487)
chr7	138602210	138602210	*KIAA1549*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P28	p.S721I	ENSG00000122778	ENST00000422774	Transcript	missense_variant	benign(0.003)
chr7	150649858	150649858	*KCNH2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P28	p.S404R	ENSG00000055118	ENST00000262186	Transcript	missense_variant	probably_damaging(0.998)
chr8	101733663	101733663	*PABPC1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P28	p.R50L	ENSG00000070756	ENST00000318607	Transcript	missense_variant	benign(0.25)
chr8	82371557	82371557	*FABP9*	Missense_Mutation	.	SNP	G	G	T	rs188083853	shanshan_et_al_P28	p.A30D	ENSG00000205186	ENST00000379071	Transcript	missense_variant	benign(0.016)
chr9	140510636	140510636	*C9orf37*	Missense_Mutation	.	SNP	C	C	A	rs532085749	shanshan_et_al_P28	p.V6F	ENSG00000203993	ENST00000371417	Transcript	missense_variant	benign(0.035)
chrX	17156978	17156978	*REPS2*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P28	p.X603_splice	ENSG00000169891	ENST00000357277	Transcript	splice_acceptor_variant	NA
chr1	11014114	11014114	*C1orf127*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P34	p.P354L	ENSG00000175262	ENST00000377004	Transcript	missense_variant	probably_damaging(0.992)
chr1	117158899	117158899	*IGSF3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P34	p.M75T	ENSG00000143061	ENST00000369483	Transcript	missense_variant	benign(0.001)
chr1	124891898	124891898	*CPSF3L*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P34	p.R344W	ENSG00000127054	ENST00000540437	Transcript	missense_variant	possibly_damaging(0.877)
chr1	163782820	163782820	*CLCNKB*	Missense_Mutation	.	SNP	G	G	A	rs201540273	shanshan_et_al_P34	p.R438H	ENSG00000184908	ENST00000375679	Transcript	missense_variant	probably_damaging(1)
chr1	26665812	26665812	*AIM1L*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P34	p.Q231*	ENSG00000176092	ENST00000527815	Transcript	stop_gained	NA
chr10	93242780	93242780	*HECTD2*	Missense_Mutation	.	SNP	G	G	C	rs532704320	shanshan_et_al_P34	p.Q256H	ENSG00000165338	ENST00000298068	Transcript	missense_variant	possibly_damaging(0.54)
chr11	108121439	108121439	*ATM*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P34	p.A416V	ENSG00000149311	ENST00000278616	Transcript	missense_variant	benign(0.002)
chr11	108121588	108121588	*ATM*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P34	p.Q466*	ENSG00000149311	ENST00000278616	Transcript	stop_gained	NA
chr11	108121601	108121601	*ATM*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P34	p.S470L	ENSG00000149311	ENST00000278616	Transcript	missense_variant	benign(0.002)
chr11	32118715	32118715	*RCN1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P34	p.D94N	ENSG00000049449	ENST00000549500	Transcript	missense_variant	benign(0.109)
chr11	52210933	52210933	*OR51V1*	Missense_Mutation	.	SNP	C	C	T	rs182727082	shanshan_et_al_P34	p.V280M	ENSG00000176742	ENST00000321255	Transcript	missense_variant	benign(0.072)
chr11	64004663	64004663	*VEGFB*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P34	p.K129Rfs*5	ENSG00000173511	ENST00000309422	Transcript	frameshift_variant	NA
chr11	65403125	65403127	*PCNXL3*	In_Frame_Del	.	DEL	CTC	CTC	-	novel	shanshan_et_al_P34	p.S1772del	ENSG00000197136	ENST00000355703	Transcript	inframe_deletion	NA
chr11	65658585	65658585	*CCDC85B*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P34	p.E111*	ENSG00000175602	ENST00000312579	Transcript	stop_gained	NA
chr17	7577509	7577509	*TP53*	Missense_Mutation	.	SNP	C	C	G	rs121912652	shanshan_et_al_P34	p.E258Q	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.96)
chr19	54760357	54760357	*LILRB5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P34	p.A117V	ENSG00000105609	ENST00000449561	Transcript	missense_variant	benign(0)
chr2	100167958	100167958	*AFF3*	Missense_Mutation	.	SNP	C	C	T	rs150108936	shanshan_et_al_P34	p.R1245Q	ENSG00000144218	ENST00000356421	Transcript	missense_variant	probably_damaging(0.935)
chr20	60791510	60791510	*HRH3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P34	p.G297D	ENSG00000101180	ENST00000340177	Transcript	missense_variant	possibly_damaging(0.613)
chr20	61461004	61461004	*COL9A3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P34	p.A360S	ENSG00000092758	ENST00000343916	Transcript	missense_variant	probably_damaging(0.951)
chr20	62076690	62076690	*KCNQ2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P34	p.V139M	ENSG00000075043	ENST00000359125	Transcript	missense_variant	probably_damaging(0.999)
chr21	27840860	27840860	*CYYR1*	Missense_Mutation	.	SNP	C	C	T	rs373162538	shanshan_et_al_P34	p.R142H	ENSG00000166265	ENST00000299340	Transcript	missense_variant	probably_damaging(0.991)
chr22	22990089	22990089	*GGTLC2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P34	p.R179W	ENSG00000100121	ENST00000480559	Transcript	missense_variant	probably_damaging(0.978)
chr22	32588955	32588955	*RFPL2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P34	p.I164V	ENSG00000128253	ENST00000400237	Transcript	missense_variant	benign(0.023)

chr3	39108051	39108052	*WDR48*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P34	p.S95Ffs*2	ENSG00000114742	ENST00000302313	Transcript	frameshift_variant	NA
chr3	53857864	53857864	*CHDH*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P34	p.R58G	ENSG00000016391	ENST00000315251	Transcript	missense_variant	probably_damaging(1)
chr4	92130116	92130116	*USP17L10*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P34	p.G212R	ENSG00000231396	ENST00000417945	Transcript	missense_variant	probably_damaging(0.999)
chr6	126080670	126080670	*HEY2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P34	p.V246I	ENSG00000135547	ENST00000368364	Transcript	missense_variant	benign(0.003)
chr8	11189402	11189402	*SLC35G5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P34	p.A263T	ENSG00000177710	ENST00000382435	Transcript	missense_variant	benign(0.038)
chr9	136857354	136857354	*VAV2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P34	p.V16G	ENSG00000160293	ENST00000371850	Transcript	missense_variant	probably_damaging(0.999)
chr9	65504710	65504710	*SPATA31A7*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P34	p.E950D	ENSG00000234734	ENST00000355045	Transcript	missense_variant	possibly_damaging(0.555)
chrX	37961664	37961664	*SYTL5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P34	p.R378C	ENSG00000147041	ENST00000456733	Transcript	missense_variant	benign(0.001)
chr1	19282240	19282240	*IFFO2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P41	p.D196V	ENSG00000169991	ENST00000455833	Transcript	missense_variant	probably_damaging(0.994)
chr1	228290219	228290219	*C1orf35*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P41	p.E112K	ENSG00000143793	ENST00000272139	Transcript	missense_variant	benign(0.007)
chr1	39332598	39332598	*MYCBP*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P41	p.E74G	ENSG00000214114	ENST00000397572	Transcript	missense_variant	benign(0.178)
chr1	40768806	40768806	*COL9A2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.Q534K	ENSG00000049089	ENST00000372748	Transcript	missense_variant	possibly_damaging(0.688)
chr1	44134910	44134910	*KDM4A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.A435S	ENSG00000066135	ENST00000372396	Transcript	missense_variant	benign(0.049)
chr10	89717672	89717672	*PTEN*	Nonsense_Mutation	.	SNP	C	C	T	rs121909219	shanshan_et_al_P41	p.R233*	ENSG00000171862	ENST00000371953	Transcript	stop_gained	NA
chr11	31312387	31312387	*DCDC1*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P41	p.L256*	ENSG00000170959	ENST00000452803	Transcript	frameshift_variant	NA
chr11	45307574	45307574	*SYT13*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P41	p.X61_splice	ENSG00000019505	ENST00000209226	Transcript	splice_donor_variant	NA
chr11	55653674	55653674	*TRIM51*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P41	p.T163P	ENSG00000124900	ENST00000449290	Transcript	missense_variant	possibly_damaging(0.775)
chr11	55735542	55735542	*OR10AG1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P41	p.I133N	ENSG00000174970	ENST00000312345	Transcript	missense_variant	benign(0.162)
chr12	51584328	51584328	*POU6F1*	Missense_Mutation	.	SNP	G	G	A	rs375633440	shanshan_et_al_P41	p.P203L	ENSG00000184271	ENST00000389243	Transcript	missense_variant	probably_damaging(0.982)
chr12	57596242	57596242	*LRP1*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P41	p.N3545Tfs*238	ENSG00000123384	ENST00000240737	Transcript	frameshift_variant	NA
chr12	58190116	58190116	*TSFM*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P41	p.S264Y	ENSG00000123297	ENST00000323833	Transcript	missense_variant	possibly_damaging(0.785)
chr13	21563060	21563060	*LATS2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P41	p.A287S	ENSG00000150457	ENST00000382592	Transcript	missense_variant	benign(0.005)
chr13	49050852	49050852	*RB1*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P41	p.Q846*	ENSG00000139687	ENST00000267163	Transcript	stop_gained	NA
chr14	105406645	105406645	*AHNAK2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P41	p.S5048F	ENSG00000185567	ENST00000332434	Transcript	missense_variant	possibly_damaging(0.78)
chr15	28483324	28483324	*HERC2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.A1263D	ENSG00000128731	ENST00000261609	Transcript	missense_variant	benign(0.1)
chr15	66727451	66727451	*MAP2K1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P41	p.Q56P	ENSG00000169032	ENST00000307102	Transcript	missense_variant	possibly_damaging(0.52)
chr17	39620685	39620685	*KRT32*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.S240Y	ENSG00000108759	ENST00000225899	Transcript	missense_variant	benign(0.273)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P41	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr19	17547396	17547396	*TMEM221*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.S249R	ENSG00000188051	ENST00000341130	Transcript	missense_variant	benign(0.003)
chr19	58325300	58325300	*FUT6*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P41	p.L17V	ENSG00000156413	ENST00000318336	Transcript	missense_variant	probably_damaging(0.999)
chr2	143742720	143742720	*KYNU*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.G266V	ENSG00000115919	ENST00000264170	Transcript	missense_variant	probably_damaging(0.973)
chr2	150327236	150327236	*LYPD6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P41	p.P130T	ENSG00000187123	ENST00000334166	Transcript	missense_variant	possibly_damaging(0.711)
chr2	152236004	152236004	*TNFAIP6*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P41	p.T264S	ENSG00000123610	ENST00000243347	Transcript	missense_variant	benign(0.001)
chr2	189867729	189867729	*COL3A1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P41	p.E832K	ENSG00000168542	ENST00000304636	Transcript	missense_variant	unknown(0)
chr2	210882233	210882233	*RPE*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P41	p.I172V	ENSG00000197713	ENST00000359429	Transcript	missense_variant	possibly_damaging(0.686)
chr2	219487457	219487457	*PLCD4*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P41	p.E210Q	ENSG00000115556	ENST00000450993	Transcript	missense_variant	benign(0.153)

chr2	219487489	219487489	*PLCD4*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P41	p.Q220H	ENSG00000115556	ENST00000450993	Transcript	missense_variant	probably_damaging(0.946)
chr2	228881815	228881815	*SPHKAP*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P41	p.N1252S	ENSG00000153820	ENST00000392056	Transcript	missense_variant	possibly_damaging(0.618)
chr2	37500086	37500086	*ALLC*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P41	p.I370T	ENSG00000151360	ENST00000252505	Transcript	missense_variant	benign(0.159)
chr3	142422812	142422812	*PLS1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P41	p.T492S	ENSG00000120756	ENST00000337737	Transcript	missense_variant	possibly_damaging(0.87)
chr3	167254745	167254745	*WDR49*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P41	p.I271V	ENSG00000174776	ENST00000308378	Transcript	missense_variant	benign(0.015)
chr3	183975398	183975398	*ECE2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P41	p.M112V	ENSG00000145194	ENST00000402825	Transcript	missense_variant	possibly_damaging(0.787)
chr4	134073216	134073216	*PCDH10*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.A641S	ENSG00000138650	ENST00000264360	Transcript	missense_variant	probably_damaging(0.998)
chr4	144614283	144614283	*FREM3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P41	p.F1753S	ENSG00000183090	ENST00000329798	Transcript	missense_variant	possibly_damaging(0.793)
chr4	92655266	92655266	*USP17L21*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P41	p.P310L	ENSG00000249811	ENST00000506414	Transcript	missense_variant	benign(0.02)
chr5	127610310	127610310	*FBN2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P41	p.F2554V	ENSG00000138829	ENST00000508053	Transcript	missense_variant	probably_damaging(1)
chr5	149927871	149927871	*NDST1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P41	p.A746V	ENSG00000070614	ENST00000261797	Transcript	missense_variant	benign(0)
chr5	45645361	45645361	*HCN1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P41	p.F259I	ENSG00000164588	ENST00000303230	Transcript	missense_variant	probably_damaging(0.994)
chr8	145140994	145140994	*GPAA1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.W611L	ENSG00000197858	ENST00000355091	Transcript	missense_variant	probably_damaging(1)
chr8	23386532	23386532	*SLC25A37*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P41	p.G6E	ENSG00000147454	ENST00000519973	Transcript	missense_variant	benign(0.076)
chr9	35725689	35725689	*TLN1*	Translation_Start_Site	.	SNP	C	C	G	novel	shanshan_et_al_P41	p.M1?	ENSG00000137076	ENST00000314888	Transcript	initiator_codon_variant	possibly_damaging(0.577)
chr9	70918720	70918720	*FOXD4L3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P41	p.A285S	ENSG00000187559	ENST00000342833	Transcript	missense_variant	benign(0.092)
chr9	71534600	71534600	*PIP5K1B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P41	p.L357F	ENSG00000107242	ENST00000265382	Transcript	missense_variant	benign(0.083)
chrX	28359995	28359995	*ARSD*	Missense_Mutation	.	SNP	C	C	A	rs150899882	shanshan_et_al_P41	p.C238F	ENSG00000006756	ENST00000381154	Transcript	missense_variant	benign(0)
chrX	28360002	28360002	*ARSD*	Missense_Mutation	.	SNP	C	C	T	rs190767292	shanshan_et_al_P41	p.V236M	ENSG00000006756	ENST00000381154	Transcript	missense_variant	benign(0.067)
chrX	54955222	54955222	*TRO*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P41	p.T689P	ENSG00000067445	ENST00000173898	Transcript	missense_variant	unknown(0)
chr1	10238798	10238798	*UBE4B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.A1208T	ENSG00000130939	ENST00000343090	Transcript	missense_variant	possibly_damaging(0.727)
chr1	152785137	152785137	*LCE1B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P44	p.G72V	ENSG00000196734	ENST00000360090	Transcript	missense_variant	unknown(0)
chr1	201981144	201981144	*ELF3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P44	p.W75R	ENSG00000163435	ENST00000359651	Transcript	missense_variant	probably_damaging(1)
chr1	231411243	231411243	*GNPAT*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P44	p.I646V	ENSG00000116906	ENST00000366647	Transcript	missense_variant	benign(0.001)
chr1	35996644	35996644	*TP73*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.R36W	ENSG00000078900	ENST00000378295	Transcript	missense_variant	possibly_damaging(0.462)
chr1	43812535	43812535	*MPL*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P44	p.P413R	ENSG00000117400	ENST00000372470	Transcript	missense_variant	possibly_damaging(0.879)
chr10	89690847	89690847	*PTEN*	Splice_Site	.	SNP	G	G	A	rs587776667	shanshan_et_al_P44	NA	ENSG00000171862	ENST00000371953	Transcript	splice_donor_variant	NA
chr11	133816111	133816111	*IGSF9B*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P44	p.R36T	ENSG00000080854	ENST00000538871	Transcript	missense_variant	probably_damaging(0.997)
chr11	64419617	64419617	*NRXN2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P44	p.P809R	ENSG00000110076	ENST00000265459	Transcript	missense_variant	benign(0.045)
chr11	66834221	66834221	*RHOD*	Missense_Mutation	.	SNP	A	A	G	rs200747179	shanshan_et_al_P44	p.Y78C	ENSG00000173156	ENST00000308831	Transcript	missense_variant	probably_damaging(1)
chr12	56661034	56661034	*COQ10A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.M44I	ENSG00000135469	ENST00000308197	Transcript	missense_variant	benign(0)
chr14	102816331	102816331	*CINP*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.E136K	ENSG00000100865	ENST00000536961	Transcript	missense_variant	possibly_damaging(0.574)
chr16	30776762	30776762	*RNF40*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P44	p.Y312C	ENSG00000103549	ENST00000324685	Transcript	missense_variant	possibly_damaging(0.706)
chr16	70989370	70989370	*HYDIN*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P44	p.V2075E	ENSG00000157423	ENST00000393567	Transcript	missense_variant	possibly_damaging(0.469)
chr17	40043958	40043958	*ACLY*	Splice_Site	.	SNP	T	T	C	novel	shanshan_et_al_P44	p.X591_splice	ENSG00000131473	ENST00000352035	Transcript	splice_acceptor_variant	NA
chr17	40937447	40937447	*WNK4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.E475K	ENSG00000126562	ENST00000246914	Transcript	missense_variant	unknown(0)

chr17	41180652	41180652	*RND2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P44	p.E213D	ENSG00000108830	ENST00000587250	Transcript	missense_variant	benign(0)
chr17	49073373	49073373	*KIF1C*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P44	p.D302A	ENSG00000129250	ENST00000320785	Transcript	missense_variant	probably_damaging(0.926)
chr19	1220449	1220449	*STK11*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P44	p.N181S	ENSG00000118046	ENST00000326873	Transcript	missense_variant	probably_damaging(0.999)
chr19	38055687	38055687	*ZNF571*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P44	p.H548R	ENSG00000180479	ENST00000328550	Transcript	missense_variant	probably_damaging(0.96)
chr19	50910345	50910345	*POLD1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P44	p.E534*	ENSG00000062822	ENST00000440232	Transcript	stop_gained	NA
chr19	50946761	50946761	*MYBPC2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P44	p.E305Q	ENSG00000086967	ENST00000357701	Transcript	missense_variant	probably_damaging(0.976)
chr19	55317424	55317424	*KIR2DL4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.S127L	ENSG00000189013	ENST00000345540	Transcript	missense_variant	possibly_damaging(0.466)
chr19	58868892	58868892	*ZNF497*	Missense_Mutation	.	SNP	C	C	T	rs370174117	shanshan_et_al_P44	p.G37D	ENSG00000174586	ENST00000311044	Transcript	missense_variant	probably_damaging(0.959)
chr19	7976372	7976372	*MAP2K7*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.E330K	ENSG00000076984	ENST00000399799	Transcript	missense_variant	probably_damaging(0.933)
chr2	207634902	207634902	*FASTKD2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P44	p.L289V	ENSG00000118246	ENST00000236980	Transcript	missense_variant	benign(0.181)
chr2	23980572	23980572	*ATAD2B*	Missense_Mutation	.	SNP	C	C	A	rs369011855	shanshan_et_al_P44	p.G1265V	ENSG00000119778	ENST00000238789	Transcript	missense_variant	benign(0.107)
chr2	69759291	69759291	*AAK1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P44	p.E180Q	ENSG00000115977	ENST00000409085	Transcript	missense_variant	unknown(0)
chr20	40877335	40877335	*PTPRT*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P44	p.I768M	ENSG00000196090	ENST00000373187	Transcript	missense_variant	benign(0.01)
chr20	60419757	60419757	*CDH4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.R204W	ENSG00000179242	ENST00000360469	Transcript	missense_variant	probably_damaging(0.948)
chr21	33296847	33296847	*HUNK*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.R110Q	ENSG00000142149	ENST00000270112	Transcript	missense_variant	probably_damaging(1)
chr21	45107921	45107921	*RRP1B*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P44	p.E556Q	ENSG00000160208	ENST00000340648	Transcript	missense_variant	possibly_damaging(0.782)
chr22	19435022	19435022	*C22orf39*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P44	p.R61L	ENSG00000242259	ENST00000399562	Transcript	missense_variant	probably_damaging(0.963)
chr22	41360075	41360075	*RBX1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.A61V	ENSG00000100387	ENST00000216225	Transcript	missense_variant	probably_damaging(0.923)
chr3	130871234	130871234	*NEK11*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P44	p.S217*	ENSG00000114670	ENST00000383366	Transcript	stop_gained	NA
chr3	132153463	132153463	*DNAJC13*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.X23_splice	ENSG00000138246	ENST00000260818	Transcript	splice_donor_variant	NA
chr3	13649565	13649565	*FBLN2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.S437F	ENSG00000163520	ENST00000404922	Transcript	missense_variant	probably_damaging(0.996)
chr3	148599357	148599357	*CPA3*	Nonsense_Mutation	.	SNP	C	C	T	rs141357361	shanshan_et_al_P44	p.R209*	ENSG00000163751	ENST00000296046	Transcript	stop_gained	NA
chr3	170110200	170110200	*SKIL*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.E684K	ENSG00000136603	ENST00000458537	Transcript	missense_variant	benign(0.297)
chr3	47039145	47039145	*ITPR1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P44	p.Q452H	ENSG00000150995	ENST00000302640	Transcript	missense_variant	probably_damaging(0.993)
chr3	48700025	48700025	*CELSR3*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P44	p.S15A	ENSG00000008300	ENST00000164024	Transcript	missense_variant	benign(0.006)
chr3	56597721	56597721	*CCDC66*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P44	p.K38E	ENSG00000180376	ENST00000394672	Transcript	missense_variant	probably_damaging(0.999)
chr4	123267913	123267913	*KIAA1109*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.P4290L	ENSG00000138688	ENST00000264501	Transcript	missense_variant	possibly_damaging(0.518)
chr4	169325132	169325133	*DDX60L*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P44	p.L1113Ffs*3	ENSG00000181381	ENST00000260184	Transcript	frameshift_variant	NA
chr5	31532521	31532521	*C5orf22*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.R8C	ENSG00000082213	ENST00000325366	Transcript	missense_variant	benign(0.002)
chr5	41917285	41917285	*C5orf51*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P44	p.G257R	ENSG00000205765	ENST00000381647	Transcript	missense_variant	probably_damaging(1)
chr6	12120575	12120575	*HIVEP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.H183Y	ENSG00000095951	ENST00000379388	Transcript	missense_variant	benign(0.222)
chr6	28359202	28359202	*ZSCAN12*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P44	p.L289V	ENSG00000158691	ENST00000361028	Transcript	missense_variant	benign(0.02)
chr7	39905900	39905900	*SDK1*	Missense_Mutation	.	SNP	A	A	G	rs147733079	shanshan_et_al_P44	p.I295V	ENSG00000146555	ENST00000404826	Transcript	missense_variant	benign(0.12)
chr7	74197947	74197947	*NCF1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P44	p.E218D	ENSG00000158517	ENST00000289473	Transcript	missense_variant	probably_damaging(0.957)
chr8	28360629	28360629	*FZD3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P44	p.L33F	ENSG00000104290	ENST00000240093	Transcript	missense_variant	probably_damaging(0.998)
chr8	39080673	39080673	*ADAM32*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.L481F	ENSG00000197140	ENST00000379907	Transcript	missense_variant	benign(0.178)

chr9	112189399	112189399	*PTPN3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P44	p.E278K	ENSG00000070159	ENST00000374541	Transcript	missense_variant	possibly_damaging(0.697)
chrX	153042370	153042370	*PLXNB3*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P44	p.V1644G	ENSG00000198753	ENST00000538966	Transcript	missense_variant	possibly_damaging(0.806)
chrX	82764358	82764359	*POU3F4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P44	p.Q343K	ENSG00000196767	ENST00000373200	Transcript	missense_variant	benign(0.024)
chr1	157509008	157509008	*FCRL5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P51	p.R424W	ENSG00000143297	ENST00000361835	Transcript	missense_variant	probably_damaging(0.932)
chr1	162470036	162470036	*UHMK1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P51	p.Q187R	ENSG00000152332	ENST00000489294	Transcript	missense_variant	probably_damaging(0.977)
chr1	171688329	171688329	*VAMP4*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P51	p.R49T	ENSG00000117533	ENST00000236192	Transcript	missense_variant	benign(0.033)
chr1	186008081	186008081	*HMCN1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P51	p.C1991F	ENSG00000143341	ENST00000271588	Transcript	missense_variant	probably_damaging(0.998)
chr1	36437789	36437789	*TP73*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P51	p.X281_splice	ENSG00000078900	ENST00000378295	Transcript	splice_donor_variant	NA
chr10	114057904	114057904	*TECTB*	Missense_Mutation	.	SNP	G	G	A	rs142767041	shanshan_et_al_P51	p.R250Q	ENSG00000119913	ENST00000369422	Transcript	missense_variant	probably_damaging(0.999)
chr10	1405722	1405722	*ADARB2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P51	p.P193R	ENSG00000185736	ENST00000381312	Transcript	missense_variant	probably_damaging(0.999)
chr10	75006808	75006808	*DNAJC9*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P51	p.V47G	ENSG00000213551	ENST00000372950	Transcript	missense_variant	possibly_damaging(0.672)
chr11	61917614	61917614	*INCENP*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P51	p.L826R	ENSG00000149503	ENST00000394818	Transcript	missense_variant	probably_damaging(0.999)
chr11	65161845	65161845	*FRMD8*	Missense_Mutation	.	SNP	G	G	A	rs150610909	shanshan_et_al_P51	p.R177H	ENSG00000126391	ENST00000317568	Transcript	missense_variant	probably_damaging(0.97)
chr12	105557961	105557961	*KIAA1033*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P51	p.R1077T	ENSG00000136051	ENST00000332180	Transcript	missense_variant	benign(0.441)
chr12	117768256	117768256	*NOS1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P51	p.K207E	ENSG00000089250	ENST00000338101	Transcript	missense_variant	benign(0.019)
chr12	121712173	121712173	*CAMKK2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P51	p.I53V	ENSG00000110931	ENST00000324774	Transcript	missense_variant	benign(0.008)
chr12	53069146	53069151	*KRT1*	In_Frame_Del	.	DEL	CCTCTG	CCTCTG	-	novel	shanshan_et_al_P51	p.R588_G589del	ENSG00000167768	ENST00000252244	Transcript	inframe_deletion	NA
chr13	36158140	36158140	*NBEA*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P51	p.T2381A	ENSG00000172915	ENST00000400445	Transcript	missense_variant	benign(0.17)
chr14	50251689	50251689	*NEMF*	Missense_Mutation	.	SNP	G	G	T	rs367709510	shanshan_et_al_P51	p.S1036Y	ENSG00000165525	ENST00000298310	Transcript	missense_variant	benign(0.021)
chr14	75590874	75590874	*NEK9*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P51	p.K91R	ENSG00000119638	ENST00000238616	Transcript	missense_variant	benign(0.336)
chr15	56736697	56736697	*MNS1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P51	p.K211E	ENSG00000138587	ENST00000260453	Transcript	missense_variant	possibly_damaging(0.559)
chr15	74483188	74483188	*STRA6*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P51	p.I346T	ENSG00000137868	ENST00000563965	Transcript	missense_variant	benign(0.023)
chr15	80452129	80452129	*FAH*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P51	p.Q75L	ENSG00000103876	ENST00000407106	Transcript	missense_variant	benign(0.001)
chr15	85165000	85165000	*ZSCAN2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P51	p.T525K	ENSG00000176371	ENST00000448803	Transcript	missense_variant	probably_damaging(0.996)
chr16	72832225	72832225	*ZFHX3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P51	p.H1452Q	ENSG00000140836	ENST00000268489	Transcript	missense_variant	probably_damaging(0.986)
chr16	84214936	84214936	*TAF1C*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P51	p.Q414E	ENSG00000103168	ENST00000567759	Transcript	missense_variant	possibly_damaging(0.607)
chr17	67252332	67252332	*ABCA5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P51	p.V1275D	ENSG00000154265	ENST00000392676	Transcript	missense_variant	probably_damaging(0.999)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P51	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr18	67231798	67231798	*DOK6*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P51	p.E48*	ENSG00000206052	ENST00000382713	Transcript	stop_gained	NA
chr19	13445238	13445238	*CACNA1A*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P51	p.Q384H	ENSG00000141837	ENST00000360228	Transcript	missense_variant	possibly_damaging(0.891)
chr19	20045089	20045089	*ZNF93*	Missense_Mutation	.	SNP	A	A	G	rs199672648	shanshan_et_al_P51	p.K442R	ENSG00000184635	ENST00000343769	Transcript	missense_variant	benign(0.004)
chr2	207174459	207174459	*ZDBF2*	Missense_Mutation	.	SNP	A	A	T	rs374837095	shanshan_et_al_P51	p.D1736V	ENSG00000204186	ENST00000374423	Transcript	missense_variant	possibly_damaging(0.804)
chr2	230724031	230724031	*TRIP12*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P51	p.Q120*	ENSG00000153827	ENST00000283943	Transcript	stop_gained	NA
chr2	99012744	99012744	*CNGA3*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P51	p.V373*	ENSG00000144191	ENST00000393504	Transcript	frameshift_variant	NA
chr20	53208187	53208187	*DOK5*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P51	p.N148H	ENSG00000101134	ENST00000262593	Transcript	missense_variant	possibly_damaging(0.89)
chr20	62323101	62323101	*RTEL1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P51	p.S879C	ENSG00000258366	ENST00000508582	Transcript	missense_variant	benign(0.003)

chr21	19770215	19770215	*TMPRSS15*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P51	p.S109P	ENSG00000154646	ENST00000288485	Transcript	missense_variant	probably_damaging(0.981)
chr22	37695340	37695340	*CYTH4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P51	p.A143S	ENSG00000100055	ENST00000248901	Transcript	missense_variant	probably_damaging(1)
chr3	138724374	138724374	*PRR23A*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P51	p.H246P	ENSG00000206260	ENST00000383163	Transcript	missense_variant	unknown(0)
chr4	155489625	155489625	*FGB*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P51	p.D271N	ENSG00000171564	ENST00000302068	Transcript	missense_variant	probably_damaging(1)
chr4	48073630	48073630	*TXK*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P51	p.L473F	ENSG00000074966	ENST00000264316	Transcript	missense_variant	benign(0.023)
chr6	144095241	144095241	*PHACTR2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P51	p.K493T	ENSG00000112419	ENST00000440869	Transcript	missense_variant	probably_damaging(0.998)
chr6	158873184	158873184	*TULP4*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P51	p.P248R	ENSG00000130338	ENST00000367097	Transcript	missense_variant	probably_damaging(0.99)
chr6	46107340	46107340	*ENPP4*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P51	p.L7R	ENSG00000001561	ENST00000321037	Transcript	missense_variant	possibly_damaging(0.534)
chr7	146825887	146825887	*CNTNAP2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P51	p.T348A	ENSG00000174469	ENST00000361727	Transcript	missense_variant	benign(0.148)
chr7	151904477	151904477	*KMT2C*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P51	p.S1250C	ENSG00000055609	ENST00000262189	Transcript	missense_variant	probably_damaging(0.968)
chr7	44797630	44797630	*ZMIZ2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P51	p.L246M	ENSG00000122515	ENST00000309315	Transcript	missense_variant	benign(0.024)
chr7	69599520	69599520	*AUTS2*	Splice_Site	.	SNP	A	A	G	novel	shanshan_et_al_P51	p.X209_splice	ENSG00000158321	ENST00000342771	Transcript	splice_acceptor_variant	NA
chr8	103297980	103297980	*UBR5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P51	p.P1749T	ENSG00000104517	ENST00000520539	Transcript	missense_variant	probably_damaging(0.991)
chr8	14978087	14978087	*DLGAP2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P51	p.H316Q	ENSG00000198010	ENST00000421627	Transcript	missense_variant	benign(0.13)
chr9	10826879	10826879	*FSD1L*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P51	p.X196_splice	ENSG00000106701	ENST00000481272	Transcript	splice_acceptor_variant	NA
chr9	138712974	138712974	*CAMSAP1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P51	p.R1178L	ENSG00000130559	ENST00000389532	Transcript	missense_variant	benign(0.312)
chr1	110587495	110587495	*STRIP1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P58	p.S440R	ENSG00000143093	ENST00000369795	Transcript	missense_variant	possibly_damaging(0.875)
chr1	145562056	145562056	*ANKRD35*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P58	p.E582K	ENSG00000198483	ENST00000355594	Transcript	missense_variant	possibly_damaging(0.636)
chr1	160916767	160916767	*FBLIM1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P58	p.W63C	ENSG00000162458	ENST00000441801	Transcript	missense_variant	probably_damaging(0.988)
chr1	167409971	167409971	*CD247*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P58	p.L31H	ENSG00000198821	ENST00000362089	Transcript	missense_variant	probably_damaging(0.993)
chr1	22033256	22033256	*USP48*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P58	p.E690G	ENSG00000090686	ENST00000308271	Transcript	missense_variant	benign(0.196)
chr1	226175617	226175617	*SDE2*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P58	p.E372*	ENSG00000143751	ENST00000272091	Transcript	stop_gained	NA
chr1	52947569	52947569	*ZCCHC11*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P58	p.D514E	ENSG00000134744	ENST00000257177	Transcript	missense_variant	benign(0.303)
chr10	125528200	125528200	*CPXM2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P58	p.N381D	ENSG00000121898	ENST00000241305	Transcript	missense_variant	probably_damaging(0.999)
chr10	18199245	18199245	*MRC1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.Y1408N	ENSG00000120586	ENST00000239761	Transcript	missense_variant	probably_damaging(0.956)
chr10	70156583	70156583	*RUFY2*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P58	p.M153Wfs*8	ENSG00000204130	ENST00000388768	Transcript	frameshift_variant	NA
chr11	119206919	119206919	*RNF26*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P58	p.G363S	ENSG00000173456	ENST00000311413	Transcript	missense_variant	benign(0.004)
chr11	28116225	28116225	*KIF18A*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P58	p.E150*	ENSG00000121621	ENST00000263181	Transcript	stop_gained	NA
chr11	66838987	66838987	*RHOD*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.F183I	ENSG00000173156	ENST00000308831	Transcript	missense_variant	probably_damaging(0.999)
chr12	11149831	11149831	*TAS2R20*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P58	p.G215E	ENSG00000255837	ENST00000538986	Transcript	missense_variant	probably_damaging(0.996)
chr12	124840118	124840118	*NCOR2*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P58	NA	ENSG00000196498	ENST00000405201	Transcript	splice_acceptor_variant	NA
chr12	52886456	52886456	*KRT6A*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.K173*	ENSG00000205420	ENST00000330722	Transcript	stop_gained	NA
chr14	44975880	44975880	*FSCB*	Missense_Mutation	.	SNP	G	G	A	rs374018207	shanshan_et_al_P58	p.A104V	ENSG00000189139	ENST00000340446	Transcript	missense_variant	benign(0.383)
chr15	25953373	25953373	*ATP10A*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P58	p.G807C	ENSG00000206190	ENST00000356865	Transcript	missense_variant	probably_damaging(0.992)
chr16	28113251	28113251	*XPO6*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P58	p.F988V	ENSG00000169180	ENST00000304658	Transcript	missense_variant	probably_damaging(0.977)
chr17	26938585	26938585	*SGK494*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P58	p.A271S	ENSG00000167524	ENST00000301037	Transcript	missense_variant	probably_damaging(0.932)

chr17	27001380	27001380	*SUPT6H*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.D63E	ENSG00000109111	ENST00000314616	Transcript	missense_variant	unknown(0)
chr17	27936012	27936012	*ANKRD13B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P58	p.D189Y	ENSG00000198720	ENST00000394859	Transcript	missense_variant	probably_damaging(0.975)
chr17	37783716	37783716	*PPP1R1B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P58	p.Q24L	ENSG00000131771	ENST00000254079	Transcript	missense_variant	benign(0.001)
chr17	40061912	40061912	*ACLY*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P58	NA	ENSG00000131473	ENST00000352035	Transcript	splice_acceptor_variant	NA
chr17	61511848	61511848	*CYB561*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P58	p.W224*	ENSG00000008283	ENST00000392976	Transcript	stop_gained	NA
chr17	7578224	7578224	*TP53*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.R209*	ENSG00000141510	ENST00000269305	Transcript	stop_gained	NA
chr17	76456070	76456070	*DNAH17*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.E3136V	ENSG00000187775	ENST00000389840	Transcript	missense_variant	probably_damaging(0.913)
chr19	19035081	19035081	*DDX49*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P58	p.S272R	ENSG00000105671	ENST00000247003	Transcript	missense_variant	benign(0.094)
chr19	22575732	22575732	*ZNF98*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P58	p.F104S	ENSG00000197360	ENST00000357774	Transcript	frameshift_variant	NA
chr19	36394686	36394686	*HCST*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P58	p.G41V	ENSG00000126264	ENST00000246551	Transcript	missense_variant	probably_damaging(0.988)
chr19	41645044	41645044	*CREB3L3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P58	p.Q194L	ENSG00000060566	ENST00000078445	Transcript	missense_variant	benign(0.198)
chr19	44981055	44981055	*ZNF180*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P58	p.P548L	ENSG00000167384	ENST00000221327	Transcript	missense_variant	probably_damaging(1)
chr2	160139338	160139338	*WDSUB1*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P58	p.W81*	ENSG00000196151	ENST00000409990	Transcript	frameshift_variant	NA
chr2	179997145	179997145	*SESTD1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P58	p.N286K	ENSG00000187231	ENST00000428443	Transcript	missense_variant	benign(0.036)
chr2	96781498	96781498	*ADRA2B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P58	p.C131S	ENSG00000222040	ENST00000409345	Transcript	missense_variant	benign(0.008)
chr2	97784158	97784158	*ANKRD36*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.F130L	ENSG00000135976	ENST00000420699	Transcript	missense_variant	possibly_damaging(0.786)
chr2	98458319	98458319	*TMEM131*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P58	p.P228T	ENSG00000075568	ENST00000186436	Transcript	missense_variant	probably_damaging(1)
chr20	37603330	37603330	*SPEF1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.N68Y	ENSG00000101222	ENST00000379756	Transcript	missense_variant	probably_damaging(0.991)
chr20	60991294	60991294	*RBBP8NL*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P58	NA	ENSG00000130701	ENST00000252998	Transcript	splice_acceptor_variant	NA
chr21	33065634	33065634	*SCAF4*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P58	p.P496A	ENSG00000156304	ENST00000286835	Transcript	missense_variant	possibly_damaging(0.857)
chr22	30189610	30189610	*ASCC2*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P58	p.A582Hfs*67	ENSG00000100325	ENST00000397771	Transcript	frameshift_variant	NA
chr22	35480473	35480473	*ISX*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P58	p.P160H	ENSG00000175329	ENST00000308700	Transcript	missense_variant	possibly_damaging(0.701)
chr3	130187749	130187749	*COL6A5*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P58	p.R2301*	ENSG00000172752	ENST00000265379	Transcript	stop_gained	NA
chr3	184910636	184910636	*EHHADH*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P58	p.G517V	ENSG00000113790	ENST00000231887	Transcript	missense_variant	probably_damaging(1)
chr5	180477298	180477298	*BTNL9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.L222H	ENSG00000165810	ENST00000327705	Transcript	missense_variant	benign(0)
chr5	71479618	71479618	*MAP1B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.L112Q	ENSG00000131711	ENST00000296755	Transcript	missense_variant	unknown(0)
chr7	115580744	115580744	*TFEC*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.Q302L	ENSG00000105967	ENST00000265440	Transcript	missense_variant	possibly_damaging(0.785)
chr7	20406662	20406662	*ITGB8*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P58	p.E81*	ENSG00000105855	ENST00000222573	Transcript	stop_gained	NA
chr7	79818405	79818405	*GNAI1*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P58	NA	ENSG00000127955	ENST00000351004	Transcript	splice_acceptor_variant	NA
chr8	10465152	10465152	*RP1L1*	Missense_Mutation	.	SNP	A	A	C	rs192863038	shanshan_et_al_P58	p.D2152E	ENSG00000183638	ENST00000382483	Transcript	missense_variant	unknown(0)
chr8	61654710	61654710	*CHD7*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P58	p.Q240L	ENSG00000171316	ENST00000423902	Transcript	missense_variant	benign(0)
chr9	130487160	130487160	*TTC16*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.C415S	ENSG00000167094	ENST00000373289	Transcript	missense_variant	benign(0.2)
chr9	19516234	19516234	*SLC24A2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.I635F	ENSG00000155886	ENST00000341998	Transcript	missense_variant	benign(0.063)
chrX	144905208	144905208	*SLITRK2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P58	p.L422Q	ENSG00000185985	ENST00000370490	Transcript	missense_variant	probably_damaging(1)
chr1	152280133	152280133	*FLG*	Missense_Mutation	.	SNP	C	C	T	rs201701803	shanshan_et_al_P63	p.R2410H	ENSG00000143631	ENST00000368799	Transcript	missense_variant	benign(0.246)
chr1	152280540	152280540	*FLG*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P63	p.Q2274H	ENSG00000143631	ENST00000368799	Transcript	missense_variant	benign(0.216)

chr1	154543934	154543934	*CHRNB2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P63	p.R212H	ENSG00000160716	ENST00000368476	Transcript	missense_variant	probably_damaging(0.993)
chr1	89521775	89521775	*GBP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P63	p.G431E	ENSG00000117228	ENST00000370473	Transcript	missense_variant	probably_damaging(0.978)
chr10	127349670	127349670	*TEX36*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P63	p.Q62K	ENSG00000175018	ENST00000368821	Transcript	missense_variant	possibly_damaging(0.544)
chr10	73544798	73544798	*CDH23*	Missense_Mutation	.	SNP	C	C	T	rs368848049	shanshan_et_al_P63	p.R1890C	ENSG00000107736	ENST00000224721	Transcript	missense_variant	benign(0.368)
chr11	118764729	118764729	*CXCR5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P63	p.R159H	ENSG00000160683	ENST00000292174	Transcript	missense_variant	probably_damaging(0.993)
chr11	17653759	17653759	*OTOG*	Missense_Mutation	.	SNP	G	G	A	rs560725852	shanshan_et_al_P63	p.R2365H	ENSG00000188162	ENST00000399391	Transcript	missense_variant	probably_damaging(0.956)
chr12	112843815	112843815	*RPL6*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P63	p.L186V	ENSG00000089009	ENST00000424576	Transcript	missense_variant	possibly_damaging(0.536)
chr13	20797280	20797280	*GJB6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P63	p.D114N	ENSG00000121742	ENST00000356192	Transcript	missense_variant	benign(0.001)
chr15	85341942	85341942	*ZNF592*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P63	p.R954W	ENSG00000166716	ENST00000299927	Transcript	missense_variant	probably_damaging(0.949)
chr16	31434958	31434958	*ITGAD*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P63	p.S1012C	ENSG00000156886	ENST00000389202	Transcript	missense_variant	possibly_damaging(0.905)
chr16	89971655	89971655	*USP7*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P63	p.S600C	ENSG00000187555	ENST00000344836	Transcript	missense_variant	benign(0.002)
chr17	29585521	29585521	*NF1*	Splice_Site	.	SNP	G	G	C	novel	shanshan_et_al_P63	p.X1444_splice	ENSG00000196712	ENST00000358273	Transcript	splice_donor_variant	NA
chr17	7577538	7577538	*TP53*	Missense_Mutation	.	SNP	C	C	T	rs11540652	shanshan_et_al_P63	p.R248Q	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(1)
chr19	1506160	1506160	*ADAMTSL5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P63	p.R424W	ENSG00000185761	ENST00000330475	Transcript	missense_variant	probably_damaging(0.954)
chr19	38860665	38860665	*CATSPERG*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P63	p.F1025S	ENSG00000099338	ENST00000409235	Transcript	missense_variant	benign(0.008)
chr2	167060926	167060926	*SCN9A*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P63	p.N1472H	ENSG00000169432	ENST00000409672	Transcript	missense_variant	probably_damaging(0.984)
chr2	190530907	190530907	*ASNSD1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P63	p.Q17E	ENSG00000138381	ENST00000260952	Transcript	missense_variant	benign(0.001)
chr2	85262234	85262234	*KCMF1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P63	p.Q94E	ENSG00000176407	ENST00000409785	Transcript	missense_variant	benign(0.18)
chr20	18461131	18461131	*POLR3F*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P63	p.I220T	ENSG00000132664	ENST00000377603	Transcript	missense_variant	probably_damaging(0.986)
chr20	20140084	20140084	*C20orf26*	Missense_Mutation	.	SNP	C	C	T	rs201733475	shanshan_et_al_P63	p.P341L	ENSG00000089101	ENST00000245957	Transcript	missense_variant	benign(0.002)
chr22	21988836	21988836	*CCDC116*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P63	p.L200M	ENSG00000161180	ENST00000292779	Transcript	missense_variant	probably_damaging(0.998)
chr22	37771192	37771192	*ELFN2*	Missense_Mutation	.	SNP	C	C	T	rs531505355	shanshan_et_al_P63	p.R128H	ENSG00000166897	ENST00000409178	Transcript	missense_variant	benign(0.329)
chr3	183957181	183957181	*VWA5B2*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P63	NA	ENSG00000145198	ENST00000426955	Transcript	splice_acceptor_variant	NA
chr4	77055327	77055327	*NUP54*	Splice_Site	.	SNP	C	C	T	novel	shanshan_et_al_P63	NA	ENSG00000138750	ENST00000264883	Transcript	splice_donor_variant	NA
chr5	140720660	140720660	*PCDHGA2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P63	p.V708I	ENSG00000081853	ENST00000394576	Transcript	missense_variant	benign(0.263)
chr5	65458332	65458332	*SREK1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P63	p.R223W	ENSG00000153914	ENST00000334121	Transcript	missense_variant	probably_damaging(0.983)
chr5	92923847	92923847	*NR2F1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P63	p.A230T	ENSG00000175745	ENST00000327111	Transcript	missense_variant	probably_damaging(0.977)
chr6	112041037	112041037	*FYN*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P63	p.T73M	ENSG00000010810	ENST00000354650	Transcript	missense_variant	benign(0.294)
chr6	46135305	46135305	*ENPP5*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P63	p.N232S	ENSG00000112796	ENST00000371383	Transcript	missense_variant	probably_damaging(0.999)
chr6	47681774	47681774	*GPR115*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P63	p.T265S	ENSG00000153294	ENST00000283303	Transcript	missense_variant	benign(0.001)
chr6	64472524	64472524	*EYS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P63	p.C2634Y	ENSG00000188107	ENST00000503581	Transcript	missense_variant	probably_damaging(0.999)
chr7	141750579	141750579	*MGAM*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P63	p.T907M	ENSG00000257335	ENST00000549489	Transcript	missense_variant	probably_damaging(0.92)
chr8	121344387	121344387	*COL14A1*	Missense_Mutation	.	SNP	C	C	T	rs199850589	shanshan_et_al_P63	p.P1556L	ENSG00000187955	ENST00000297848	Transcript	missense_variant	probably_damaging(1)
chr8	2806872	2806872	*CSMD1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P63	p.Q3451K	ENSG00000183117	ENST00000537824	Transcript	missense_variant	possibly_damaging(0.897)
chr9	103035322	103035322	*INVS*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P63	p.M583K	ENSG00000119509	ENST00000262457	Transcript	missense_variant	probably_damaging(0.997)
chrX	151303861	151303861	*MAGEA10*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P63	p.D78N	ENSG00000124260	ENST00000370323	Transcript	missense_variant	benign(0.139)

chr1	12726141	12726141	*AADACL4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P71	p.V207M	ENSG00000204518	ENST00000376221	Transcript	missense_variant	possibly_damaging(0.692)
chr1	160147404	160147404	*ATP1A4*	Missense_Mutation	.	SNP	T	T	A	rs201686010	shanshan_et_al_P71	p.W896R	ENSG00000132681	ENST00000368081	Transcript	missense_variant	probably_damaging(1)
chr1	161476312	161476312	*FCGR2A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.S99C	ENSG00000143226	ENST00000271450	Transcript	missense_variant	probably_damaging(0.998)
chr1	171482230	171482230	*PRRC2C*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.K68I	ENSG00000117523	ENST00000338920	Transcript	missense_variant	unknown(0)
chr1	181701903	181701903	*CACNA1E*	Missense_Mutation	.	SNP	C	C	A	rs200322209	shanshan_et_al_P71	p.P894Q	ENSG00000198216	ENST00000367573	Transcript	missense_variant	possibly_damaging(0.884)
chr1	19430716	19430716	*UBR4*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.K4255*	ENSG00000127481	ENST00000375254	Transcript	stop_gained	NA
chr1	21031285	21031285	*KIF17*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P71	p.A260S	ENSG00000117245	ENST00000247986	Transcript	missense_variant	probably_damaging(0.994)
chr1	241753378	241753378	*KMO*	Missense_Mutation	.	SNP	C	C	T	rs139031464	shanshan_et_al_P71	p.A388V	ENSG00000117009	ENST00000366559	Transcript	missense_variant	benign(0.014)
chr1	247031021	247031021	*AHCTF1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P71	p.K1070E	ENSG00000153207	ENST00000326225	Transcript	missense_variant	possibly_damaging(0.767)
chr1	248031306	248031306	*TRIM58*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.M271K	ENSG00000162722	ENST00000366481	Transcript	missense_variant	benign(0.122)
chr1	28354311	28354311	*EYA3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.Y163F	ENSG00000158161	ENST00000373871	Transcript	missense_variant	possibly_damaging(0.722)
chr1	51584376	51584376	*C1orf185*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.E54V	ENSG00000204006	ENST00000371759	Transcript	missense_variant	benign(0.011)
chr1	90484250	90484250	*ZNF326*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.M361L	ENSG00000162664	ENST00000340281	Transcript	missense_variant	possibly_damaging(0.59)
chr11	123465446	123465446	*GRAMD1B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Y115F	ENSG00000023171	ENST00000529750	Transcript	missense_variant	probably_damaging(0.998)
chr12	111160390	111160390	*PPP1CC*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P71	p.D212Y	ENSG00000186298	ENST00000340766	Transcript	missense_variant	possibly_damaging(0.455)
chr12	15654750	15654750	*PTPRO*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.F286L	ENSG00000151490	ENST00000281171	Transcript	missense_variant	benign(0.003)
chr12	48539363	48539363	*PFKM*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P71	p.E810K	ENSG00000152556	ENST00000340802	Transcript	missense_variant	benign(0.004)
chr12	52992743	52992743	*KRT72*	Missense_Mutation	.	SNP	C	C	T	rs142970524	shanshan_et_al_P71	p.G194R	ENSG00000170486	ENST00000293745	Transcript	missense_variant	benign(0.003)
chr12	56346183	56346183	*DGKA*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.C571S	ENSG00000065357	ENST00000331886	Transcript	missense_variant	probably_damaging(1)
chr12	66757756	66757756	*NOP2*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.K53*	ENSG00000111641	ENST00000382421	Transcript	stop_gained	NA
chr12	80866029	80866029	*PTPRQ*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.D391E	ENSG00000139304	ENST00000266688	Transcript	missense_variant	benign(0.005)
chr12	85255635	85255635	*SLC6A15*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Y657N	ENSG00000072041	ENST00000266682	Transcript	missense_variant	probably_damaging(0.981)
chr12	91502374	91502374	*LUM*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.L128Q	ENSG00000139329	ENST00000266718	Transcript	missense_variant	possibly_damaging(0.739)
chr13	45149121	45149121	*TSC22D1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.L364M	ENSG00000102804	ENST00000458659	Transcript	missense_variant	probably_damaging(0.998)
chr14	45716394	45716394	*MIS18BP1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P71	p.D32E	ENSG00000129534	ENST00000310806	Transcript	missense_variant	probably_damaging(0.991)
chr15	35166184	35166184	*AQR*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.N1148Y	ENSG00000021776	ENST00000156471	Transcript	missense_variant	probably_damaging(0.981)
chr15	40915356	40915356	*CASC5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Q991L	ENSG00000137812	ENST00000346991	Transcript	missense_variant	possibly_damaging(0.65)
chr15	42170543	42170543	*SPTBN5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.E1156V	ENSG00000137877	ENST00000320955	Transcript	missense_variant	probably_damaging(0.909)
chr15	43281059	43281059	*UBR1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.M1319L	ENSG00000159459	ENST00000290650	Transcript	missense_variant	benign(0)
chr15	55972250	55972250	*PRTG*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.X325_splice	ENSG00000166450	ENST00000389286	Transcript	splice_donor_variant	NA
chr15	56387737	56387737	*RFX7*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.Q730L	ENSG00000181827	ENST00000423270	Transcript	missense_variant	benign(0.001)
chr15	56723693	56723693	*MNS1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P71	p.R425C	ENSG00000138587	ENST00000260453	Transcript	missense_variant	probably_damaging(0.976)
chr15	94942235	94942235	*MCTP2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.L612I	ENSG00000140563	ENST00000357742	Transcript	missense_variant	probably_damaging(0.989)
chr16	12093152	12093152	*SNX29*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P71	NA	ENSG00000048471	ENST00000566228	Transcript	splice_acceptor_variant	NA
chr16	48396197	48396197	*SIAH1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.V79E	ENSG00000196470	ENST00000356721	Transcript	missense_variant	possibly_damaging(0.887)
chr16	597967	597967	*CAPN15*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P71	p.P377A	ENSG00000103326	ENST00000219611	Transcript	missense_variant	benign(0.003)

chr16	67911472	67911472	EDC4	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P71	p.R234S	ENSG00000038358	ENST00000358933	Transcript	missense_variant	possibly_damaging(0.776)
chr16	69727852	69727852	NFAT5	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Q1375L	ENSG00000102908	ENST00000432919	Transcript	missense_variant	probably_damaging(0.978)
chr17	10362659	10362659	MYH4	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.L499Q	ENSG00000264424	ENST00000255381	Transcript	missense_variant	benign(0.233)
chr17	11778498	11778498	DNAH9	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.K3492I	ENSG00000007174	ENST00000262442	Transcript	missense_variant	possibly_damaging(0.806)
chr17	36717733	36717733	SRCIN1	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P71	p.G556R	ENSG00000017373	ENST00000264659	Transcript	missense_variant	probably_damaging(0.985)
chr17	42856594	42856594	ADAM11	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.I761F	ENSG00000073670	ENST00000200557	Transcript	missense_variant	possibly_damaging(0.492)
chr17	74041349	74041349	POLR2A	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Y618F	ENSG00000181222	ENST00000322644	Transcript	missense_variant	possibly_damaging(0.464)
chr17	75775688	75775688	TP53	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P71	p.C238F	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(1)
chr18	25750578	25750578	NDC80	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P71	p.G58C	ENSG00000080986	ENST00000261597	Transcript	missense_variant	probably_damaging(0.964)
chr18	50866104	50866104	DCC	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P71	p.P729R	ENSG00000187323	ENST00000442544	Transcript	missense_variant	probably_damaging(1)
chr19	57327876	57327876	PEG3	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.H645L	ENSG00000198300	ENST00000326441	Transcript	missense_variant	probably_damaging(1)
chr2	113081919	113081919	ZC3H6	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P71	p.P511S	ENSG00000188177	ENST00000409871	Transcript	missense_variant	benign(0.029)
chr2	149679720	149679720	KIF5C	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.Y47*	ENSG00000168280	ENST00000435030	Transcript	stop_gained	NA
chr2	162061188	162061188	TANK	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.N71Y	ENSG00000136560	ENST00000392749	Transcript	missense_variant	possibly_damaging(0.594)
chr2	167297907	167297907	SCN7A	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.L719Q	ENSG00000136546	ENST00000409855	Transcript	missense_variant	probably_damaging(1)
chr2	209113365	209113365	IDH1	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.N48Y	ENSG00000138413	ENST00000415913	Transcript	missense_variant	benign(0.016)
chr2	239003074	239003074	SCLY	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Q348L	ENSG00000132330	ENST00000254663	Transcript	missense_variant	benign(0.006)
chr2	242076617	242076617	PASK	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.L313F	ENSG00000115687	ENST00000358649	Transcript	missense_variant	probably_damaging(0.999)
chr2	86292580	86292580	POLR1A	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.Q625H	ENSG00000068654	ENST00000263857	Transcript	missense_variant	possibly_damaging(0.903)
chr20	31021622	31021622	UBOX5	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.S375C	ENSG00000185019	ENST00000217173	Transcript	missense_variant	benign(0.013)
chr20	44669966	44669966	SLC12A5	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.X308_splice	ENSG00000124140	ENST00000454036	Transcript	splice_acceptor_variant	NA
chr21	15870838	15870838	SAMSN1	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.I350F	ENSG00000155307	ENST00000285670	Transcript	missense_variant	probably_damaging(0.913)
chr22	30927942	30927942	SEC14L6	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.E156V	ENSG00000214491	ENST00000402034	Transcript	missense_variant	probably_damaging(0.938)
chr22	50684783	50684783	HDAC10	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P71	p.R532G	ENSG00000100429	ENST00000216271	Transcript	missense_variant	benign(0)
chr3	125179630	125179630	SNX4	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.Y310F	ENSG00000114520	ENST00000251775	Transcript	missense_variant	benign(0.016)
chr3	193080428	193080428	ATP13A5	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.X129_splice	ENSG00000187527	ENST00000342358	Transcript	splice_acceptor_variant	NA
chr3	44345505	44345505	TOPAZ1	Splice_Site	.	SNP	A	A	C	novel	shanshan_et_al_P71	p.X1266_splice	ENSG00000173769	ENST00000309765	Transcript	splice_acceptor_variant	NA
chr4	106510453	106510453	ARHGEF38	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P71	p.P82L	ENSG00000236699	ENST00000420470	Transcript	missense_variant	benign(0)
chr4	138451703	138451703	PCDH18	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.I514L	ENSG00000189184	ENST00000344876	Transcript	missense_variant	benign(0.394)
chr4	159756593	159756593	FNIP2	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Q231L	ENSG00000052795	ENST00000264433	Transcript	missense_variant	benign(0.219)
chr4	43735555	43735555	ZNF721	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P71	p.G301*	ENSG00000182903	ENST00000511833	Transcript	stop_gained	NA
chr5	137289904	137289904	FAM13B	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P71	p.H535Y	ENSG00000031003	ENST00000330379	Transcript	missense_variant	possibly_damaging(0.597)
chr5	52942144	52942144	NDUFS4	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.M87L	ENSG00000164258	ENST00000296684	Transcript	missense_variant	probably_damaging(0.944)
chr6	137815010	137815010	OLIG3	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.N100Y	ENSG00000177468	ENST00000367734	Transcript	missense_variant	possibly_damaging(0.9)
chr6	152722287	152722287	SYNE1	Missense_Mutation	.	SNP	A	A	T	rs568512911	shanshan_et_al_P71	p.L2339M	ENSG00000131018	ENST00000367255	Transcript	missense_variant	possibly_damaging(0.497)
chr6	25966883	25966883	TRIM38	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P71	p.K45E	ENSG00000112343	ENST00000357085	Transcript	missense_variant	benign(0.006)

chr6	35604817	35604817	*FKBP5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.E75V	ENSG00000096060	ENST00000536438	Transcript	missense_variant	benign(0.119)
chr6	70642754	70642754	*COL19A1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.K249M	ENSG00000082293	ENST00000322773	Transcript	missense_variant	unknown(0)
chr6	88769271	88769271	*SPACA1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.V192E	ENSG00000118434	ENST00000237201	Transcript	missense_variant	probably_damaging(0.943)
chr6	89977435	89977435	*GABRR2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.F233L	ENSG00000111886	ENST00000402938	Transcript	missense_variant	probably_damaging(0.996)
chr7	117176611	117176611	*CFTR*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P71	p.R251S	ENSG00000001626	ENST00000030804	Transcript	missense_variant	benign(0.039)
chr7	36461510	36461510	*ANLN*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Q736H	ENSG00000011426	ENST00000265748	Transcript	missense_variant	probably_damaging(0.983)
chr7	82580537	82580537	*PCLO*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.T3123S	ENSG00000186472	ENST00000333891	Transcript	missense_variant	unknown(0)
chr8	110587828	110587828	*SYBU*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.D433E	ENSG00000147642	ENST00000422135	Transcript	missense_variant	benign(0.045)
chr8	36766896	36766896	*KCNU1*	Missense_Mutation	.	SNP	A	A	T	rs561315246	shanshan_et_al_P71	p.H725L	ENSG00000215262	ENST00000398881	Transcript	missense_variant	benign(0.063)
chr8	70967630	70967630	*PRDM14*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.T465S	ENSG00000147596	ENST00000276594	Transcript	missense_variant	probably_damaging(0.985)
chr9	139904475	139904475	*ABCA2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.Y2152F	ENSG00000107331	ENST00000341511	Transcript	missense_variant	probably_damaging(0.924)
chr9	21333634	21333634	*KLHL9*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P71	p.A409S	ENSG00000198642	ENST00000359039	Transcript	missense_variant	benign(0.377)
chr9	33338526	33338526	*NFX1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.D685V	ENSG00000086102	ENST00000379540	Transcript	missense_variant	benign(0.129)
chr9	60142778	60142778	*RANBP6*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.K444*	ENSG00000137040	ENST00000259569	Transcript	stop_gained	NA
chr9	84609680	84609680	*SPATA31D1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.L1432H	ENSG00000214929	ENST00000344803	Transcript	missense_variant	probably_damaging(0.98)
chrX	110507163	110507163	*CAPN6*	Translation_Start_Site	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.M1?	ENSG00000077274	ENST00000324068	Transcript	initiator_codon_variant	benign(0.227)
chrX	117676887	117676887	*DOCK11*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.X74_splice	ENSG00000147251	ENST00000276202	Transcript	splice_acceptor_variant	NA
chrX	131219616	131219616	*FRMD7*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.V213E	ENSG00000165694	ENST00000298542	Transcript	missense_variant	probably_damaging(0.999)
chrX	154319075	154319075	*BRCC3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.Y170F	ENSG00000185515	ENST00000369462	Transcript	missense_variant	probably_damaging(0.989)
chrX	30578009	30578009	*CXorf21*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.L155*	ENSG00000120280	ENST00000378962	Transcript	stop_gained	NA
chrX	34148324	34148324	*FAM47A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P71	p.V691E	ENSG00000185448	ENST00000346193	Transcript	missense_variant	probably_damaging(0.98)
chrX	53430585	53430585	*SMC1A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.E778V	ENSG00000072501	ENST00000322213	Transcript	missense_variant	benign(0.005)
chrX	75003796	75003796	*MAGEE2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P71	p.Y364F	ENSG00000186675	ENST00000373359	Transcript	missense_variant	probably_damaging(0.989)
chr1	158299402	158299402	*CD1B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P85	p.P215L	ENSG00000158485	ENST00000368168	Transcript	missense_variant	possibly_damaging(0.858)
chr1	158746718	158746718	*OR6N2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P85	p.K236N	ENSG00000188340	ENST00000339258	Transcript	missense_variant	probably_damaging(0.998)
chr1	220369733	220369733	*RAB3GAP2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P85	p.M273I	ENSG00000118873	ENST00000358951	Transcript	missense_variant	benign(0.007)
chr1	368157	368157	*OR4F29*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P85	p.A167P	ENSG00000235249	ENST00000426406	Transcript	missense_variant	benign(0)
chr1	75097523	75097523	*C1orf173*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P85	p.M231I	ENSG00000178965	ENST00000326665	Transcript	missense_variant	benign(0.02)
chr10	50819847	50819847	*SLC18A3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P85	p.H354R	ENSG00000187714	ENST00000374115	Transcript	missense_variant	benign(0.034)
chr10	99656674	99656674	*CRTAC1*	Missense_Mutation	.	SNP	C	C	T	rs550794669	shanshan_et_al_P85	p.R403Q	ENSG00000095713	ENST00000370597	Transcript	missense_variant	possibly_damaging(0.564)
chr11	76062600	76062600	*PRKRIR*	Missense_Mutation	.	SNP	G	G	T	rs9666739	shanshan_et_al_P85	p.H532N	ENSG00000137492	ENST00000260045	Transcript	missense_variant	benign(0.147)
chr11	76915134	76915134	*MYO7A*	Nonsense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P85	p.Y1780*	ENSG00000137474	ENST00000409709	Transcript	stop_gained	NA
chr12	118651840	118651840	*TAOK3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P85	p.T240R	ENSG00000135090	ENST00000392533	Transcript	missense_variant	benign(0.014)
chr12	118651845	118651855	*TAOK3*	Frame_Shift_Del	.	DEL	GGAGTCATTCT	GGAGTCATTCT	-	novel	shanshan_et_al_P85	p.Q235Pfs*6	ENSG00000135090	ENST00000392533	Transcript	frameshift_variant	NA
chr12	29936515	29936515	*TMTC1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P85	p.I57T	ENSG00000133687	ENST00000539277	Transcript	missense_variant	possibly_damaging(0.733)
chr12	46316272	46316272	*SCAF11*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P85	p.E1407Q	ENSG00000139218	ENST00000369367	Transcript	missense_variant	probably_damaging(0.92)

chr14	24706305	24706305	GMPR2	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P85	p.V183A	ENSG00000100938	ENST00000420554	Transcript	missense_variant	benign(0.439)
chr14	47324319	47324322	MDGA2	Frame_Shift_Del	.	DEL	TTGT	TTGT	-	novel	shanshan_et_al_P85	p.T632Qfs*2	ENSG00000139915	ENST00000426342	Transcript	frameshift_variant	NA
chr15	24921631	24921631	NPAP1	Missense_Mutation	.	SNP	G	G	C	rs375083307	shanshan_et_al_P85	p.G206A	ENSG00000185823	ENST00000329468	Transcript	missense_variant	benign(0.228)
chr15	41819471	41819471	RPAP1	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P85	p.R547Q	ENSG00000103932	ENST00000300330	Transcript	missense_variant	probably_damaging(0.999)
chr15	48722919	48722919	FBN1	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P85	p.C2274R	ENSG00000166147	ENST00000316623	Transcript	missense_variant	probably_damaging(0.999)
chr15	65621333	65621333	IGDCC3	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P85	p.D787N	ENSG00000174498	ENST00000327987	Transcript	missense_variant	benign(0.021)
chr16	16232307	16232307	ABCC1	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P85	p.V1460E	ENSG00000103222	ENST00000399410	Transcript	missense_variant	probably_damaging(0.982)
chr16	22546169	22546169	NPIPB5	Missense_Mutation	.	SNP	C	C	G	rs370469653	shanshan_et_al_P85	p.P622R	ENSG00000243716	ENST00000424340	Transcript	missense_variant	benign(0.001)
chr16	44323348	44323348	VASN	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P85	p.Q490H	ENSG00000168140	ENST00000304735	Transcript	missense_variant	benign(0.003)
chr17	36829625	36829625	C17orf96	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P85	p.N375S	ENSG00000179294	ENST00000325814	Transcript	missense_variant	possibly_damaging(0.486)
chr17	7577121	7577121	TP53	Missense_Mutation	.	SNP	G	G	T	rs121913343	shanshan_et_al_P85	p.R273S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.996)
chr17	77507300	77507300	KDM6B	Missense_Mutation	.	SNP	g	g	A	novel	shanshan_et_al_P85	p.S406N	ENSG00000132510	ENST00000254846	Transcript	missense_variant	unknown(0)
chr17	80151895	80151895	CCDC57	Missense_Mutation	.	SNP	C	C	G	rs376571892	shanshan_et_al_P85	p.G247R	ENSG00000176155	ENST00000392343	Transcript	missense_variant	benign(0)
chr18	29340201	29340201	SLC25A52	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P85	p.Q152*	ENSG00000141437	ENST00000269205	Transcript	stop_gained	NA
chr18	43420200	43420200	SIGLEC15	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P85	p.P300R	ENSG00000197046	ENST00000389474	Transcript	missense_variant	benign(0.014)
chr19	14071278	14071278	DCAF15	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P85	p.G545S	ENSG00000132017	ENST00000254337	Transcript	missense_variant	benign(0.197)
chr19	15566961	15566961	RASAL3	Missense_Mutation	.	SNP	G	G	C	rs577646736	shanshan_et_al_P85	p.R559G	ENSG00000105122	ENST00000343625	Transcript	missense_variant	possibly_damaging(0.66)
chr19	21607526	21607526	ZNF493	Missense_Mutation	.	SNP	A	A	G	rs202237831	shanshan_et_al_P85	p.K689E	ENSG00000196268	ENST00000392288	Transcript	missense_variant	benign(0.004)
chr19	47572471	47572471	ZC3H4	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P85	p.P759R	ENSG00000130749	ENST00000253048	Transcript	missense_variant	unknown(0)
chr2	109382106	109382106	RANBP2	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P85	p.P1704L	ENSG00000153201	ENST00000283195	Transcript	missense_variant	benign(0.164)
chr2	158114635	158114635	GALNT5	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P85	p.V14D	ENSG00000136542	ENST00000259056	Transcript	missense_variant	possibly_damaging(0.878)
chr2	165551248	165551248	COBLL1	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P85	p.A923G	ENSG00000082438	ENST00000342193	Transcript	missense_variant	possibly_damaging(0.76)
chr2	181925392	181925392	UBE2E3	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P85	p.V127I	ENSG00000170035	ENST00000410062	Transcript	missense_variant	benign(0.388)
chr2	222298897	222298897	EPHA4	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P85	p.G821W	ENSG00000116106	ENST00000281821	Transcript	missense_variant	probably_damaging(0.999)
chr20	39980503	39980503	LPIN3	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P85	p.Y382C	ENSG00000132793	ENST00000373257	Transcript	missense_variant	probably_damaging(0.989)
chr3	52668814	52668814	PBRM1	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P85	p.G369*	ENSG00000163939	ENST00000394830	Transcript	stop_gained	NA
chr5	433010	433010	AHRR	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P85	p.L376M	ENSG00000063438	ENST00000316418	Transcript	missense_variant	probably_damaging(0.94)
chr5	76249961	76249961	CRHBP	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P85	p.I95V	ENSG00000145708	ENST00000274368	Transcript	missense_variant	benign(0.036)
chr6	41655744	41655744	TFEB	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P85	p.L191P	ENSG00000112561	ENST00000230323	Transcript	missense_variant	probably_damaging(0.914)
chr6	52617677	52617677	GSTA2	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P85	p.N130S	ENSG00000244067	ENST00000493422	Transcript	missense_variant	benign(0.001)
chr7	73938437	73938437	GTF2IRD1	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P85	p.I380T	ENSG00000006704	ENST00000455841	Transcript	missense_variant	possibly_damaging(0.709)
chr8	11189402	11189402	SLC35G5	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P85	p.A263T	ENSG00000177710	ENST00000382435	Transcript	missense_variant	benign(0.038)
chr9	124535523	124535523	DAB2IP	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P85	p.P878T	ENSG00000136848	ENST00000259371	Transcript	missense_variant	probably_damaging(0.999)
chr9	93375718	93375718	DIRAS2	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P85	p.V131A	ENSG00000165023	ENST00000375765	Transcript	missense_variant	possibly_damaging(0.614)
chrX	102586465	102586465	TCEAL7	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P85	p.L45Pfs*8	ENSG00000182916	ENST00000332431	Transcript	frameshift_variant	NA
chr1	25784930	25784930	TMEM57	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P87	p.N234S	ENSG00000204178	ENST00000374343	Transcript	missense_variant	probably_damaging(0.983)

chr1	55470789	55470789	*BSND*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P87	p.S91T	ENSG00000162399	ENST00000371265	Transcript	missense_variant	benign(0.094)
chr1	59042418	59042418	*TACSTD2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P87	p.D137E	ENSG00000184292	ENST00000371225	Transcript	missense_variant	benign(0.136)
chr10	129868571	129868571	*PTPRE*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P87	p.Y384N	ENSG00000132334	ENST00000254667	Transcript	missense_variant	probably_damaging(0.999)
chr10	37506805	37506805	*ANKRD30A*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P87	p.Q1033R	ENSG00000148513	ENST00000361713	Transcript	missense_variant	benign(0.403)
chr11	118392772	118392772	*KMT2A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P87	p.R3935L	ENSG00000118058	ENST00000534358	Transcript	missense_variant	probably_damaging(0.997)
chr11	4936623	4936623	*OR51G2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P87	p.W91R	ENSG00000176893	ENST00000322013	Transcript	missense_variant	benign(0.444)
chr11	79819655	79819655	*NLRP10*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P87	p.D398E	ENSG00000182261	ENST00000328600	Transcript	missense_variant	benign(0.038)
chr12	12006491	12006491	*ETV6*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P87	p.E153D	ENSG00000139083	ENST00000396373	Transcript	missense_variant	benign(0.001)
chr13	109704736	109704736	*MYO16*	Missense_Mutation	.	SNP	C	C	G	rs561599115	shanshan_et_al_P87	p.F965L	ENSG00000041515	ENST00000356711	Transcript	missense_variant	benign(0.009)
chr15	64017691	64017691	*HERC1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P87	p.P1123H	ENSG00000103657	ENST00000443617	Transcript	missense_variant	possibly_damaging(0.843)
chr16	30545610	30545610	*ZNF747*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P87	p.R131C	ENSG00000169955	ENST00000252799	Transcript	missense_variant	possibly_damaging(0.531)
chr17	7578226	7578226	*TP53*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P87	p.D208V	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(1)
chr19	1789501	1789501	*ATP8B3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P87	p.L902M	ENSG00000130270	ENST00000310127	Transcript	missense_variant	probably_damaging(0.998)
chr2	32602801	32602801	*BIRC6*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P87	p.Q157H	ENSG00000115760	ENST00000421745	Transcript	missense_variant	benign(0.254)
chr2	37414560	37414560	*SULT6B1*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P87	p.K46*	ENSG00000138068	ENST00000260637	Transcript	stop_gained	NA
chr3	91464641	91464641	*SRGAP3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P87	p.E109G	ENSG00000196220	ENST00000383836	Transcript	missense_variant	probably_damaging(0.997)
chr4	173961241	173961241	*GALNTL6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P87	p.A599V	ENSG00000174473	ENST00000506823	Transcript	missense_variant	benign(0.001)
chr4	42042226	42042226	*OTOP1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P87	p.N227Y	ENSG00000163982	ENST00000296358	Transcript	missense_variant	probably_damaging(0.972)
chr5	163276	163276	*PLEKHG4B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P87	p.L674Q	ENSG00000153404	ENST00000283426	Transcript	missense_variant	possibly_damaging(0.598)
chr8	18730245	18730245	*PSD3*	Splice_Site	.	SNP	T	T	G	novel	shanshan_et_al_P87	p.X44_splice	ENSG00000156011	ENST00000327040	Transcript	splice_acceptor_variant	NA
chr9	135798860	135798862	*TSC1*	In_Frame_Del	.	DEL	ACA	ACA	-	rs118203379	shanshan_et_al_P87	p.V128del	ENSG00000165699	ENST00000298552	Transcript	inframe_deletion	NA
chr1	145474529	145474529	*ANKRD34A*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.P401T	ENSG00000181039	ENST00000323397	Transcript	missense_variant	benign(0.093)
chr1	156593325	156593325	*HAPLN2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_2	p.L15F	ENSG00000132702	ENST00000255039	Transcript	missense_variant	benign(0.003)
chr1	201179716	201179716	*IGFN1*	Missense_Mutation	.	SNP	G	G	A	rs376205662	shanshan_et_al_P8_2	p.G1899R	ENSG00000163395	ENST00000335211	Transcript	missense_variant	unknown(0)
chr1	228594190	228594190	*TRIM11*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.D25Y	ENSG00000154370	ENST00000284551	Transcript	missense_variant	probably_damaging(1)
chr1	235972644	235972644	*LYST*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.H492N	ENSG00000143669	ENST00000389794	Transcript	missense_variant	probably_damaging(0.979)
chr1	240370964	240370965	*FMN2*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P8_2	p.A952Sfs*301	ENSG00000155816	ENST00000319653	Transcript	frameshift_variant	NA
chr1	87043708	87043708	*CLCA4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.R692L	ENSG00000016602	ENST00000370563	Transcript	missense_variant	benign(0.004)
chr10	127585221	127585221	*FANK1*	Nonsense_Mutation	.	SNP	C	C	T	rs202109621	shanshan_et_al_P8_2	p.Q4*	ENSG00000203780	ENST00000368693	Transcript	stop_gained	NA
chr10	135084557	135084557	*ADAM8*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.E464D	ENSG00000151651	ENST00000445355	Transcript	missense_variant	probably_damaging(0.918)
chr10	46568147	46568147	*PTPN20A*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P8_2	p.I226V	ENSG00000204179	ENST00000374339	Transcript	missense_variant	probably_damaging(0.998)
chr10	72520345	72520345	*ADAMTS14*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.K1139N	ENSG00000138316	ENST00000373208	Transcript	missense_variant	benign(0.021)
chr11	104879687	104879687	*CASP5*	Frame_Shift_Del	.	DEL	T	T	-	rs372526393	shanshan_et_al_P8_2	p.R23Gfs*21	ENSG00000137757	ENST00000393141	Transcript	frameshift_variant	NA
chr11	65349726	65349726	*EHBP1L1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.S528Y	ENSG00000173442	ENST00000309295	Transcript	missense_variant	probably_damaging(0.987)
chr11	66114908	66114908	*B3GNT1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.H37N	ENSG00000174684	ENST00000311181	Transcript	missense_variant	probably_damaging(0.977)
chr12	110206804	110206804	*FAM222A*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.T357N	ENSG00000139438	ENST00000538780	Transcript	missense_variant	probably_damaging(0.99)

chr12	120593176	120593176	GCN1L1	Missense_Mutation	.	SNP	C	C	A	rs199974268	shansha n_et_al_P8_2	p.D1167Y	ENSG00000089154	ENST00000300648	Transcript	missense_variant	probably_damaging(1)
chr12	132445234	132445234	EP400	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_2	p.E24K	ENSG00000183495	ENST00000389561	Transcript	missense_variant	unknown(0)
chr12	50749920	50749920	FAM186A	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_2	p.T232I	ENSG00000185958	ENST00000327337	Transcript	missense_variant	benign(0.093)
chr12	64636026	64636033	SCNN1A	Splice_Site	.	INS	-	-	C	novel	shansha n_et_al_P8_2	p.X513_splice	ENSG00000111319	ENST00000360168	Transcript	splice_donor_variant	NA
chr13	31850845	31850845	B3GALTL	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_2	p.P263T	ENSG00000187676	ENST00000343307	Transcript	missense_variant	probably_damaging(0.93)
chr14	105419314	105419314	AHNAK2	Missense_Mutation	.	SNP	T	T	G	rs557538603	shansha n_et_al_P8_2	p.E825A	ENSG00000185567	ENST00000333244	Transcript	missense_variant	benign(0.159)
chr14	50101087	50101087	DNAAF2	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.H261N	ENSG00000165506	ENST00000298292	Transcript	missense_variant	possibly_damaging(0.649)
chr14	89220861	89220861	EML5	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_2	p.G118*	ENSG00000165521	ENST00000554922	Transcript	stop_gained	NA
chr16	14645893	14645893	PARN	Nonsense_Mutation	.	SNP	C	C	A	rs576638299	shansha n_et_al_P8_2	p.E489*	ENSG00000140694	ENST00000437198	Transcript	stop_gained	NA
chr16	67262969	67262969	TMEM208	Nonsense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.E159*	ENSG00000168701	ENST00000304800	Transcript	stop_gained	NA
chr16	72821704	72821704	ZFHX3	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P8_2	p.G3491S	ENSG00000140836	ENST00000268489	Transcript	missense_variant	unknown(0)
chr17	19642877	19642877	ALDH3A1	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P8_2	p.F354I	ENSG00000108602	ENST00000457500	Transcript	missense_variant	possibly_damaging(0.61)
chr17	263122	263122	C17orf97	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_2	p.A163E	ENSG00000187624	ENST00000360127	Transcript	missense_variant	possibly_damaging(0.858)
chr17	7640469	7640469	DNAH2	Missense_Mutation	.	SNP	A	A	C	rs140967246	shansha n_et_al_P8_2	p.K355Q	ENSG00000183914	ENST00000572933	Transcript	missense_variant	benign(0.261)
chr19	11577593	11577593	ELAVL3	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.P20Q	ENSG00000196361	ENST00000359227	Transcript	missense_variant	benign(0.025)
chr19	12501281	12501281	ZNF799	Nonstop_Mutation	.	SNP	T	T	A	rs2006651	shansha n_et_al_P8_2	p.*644Lext*4	ENSG00000196466	ENST00000430385	Transcript	stop_lost	NA
chr19	1490279	1490279	PCSK4	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_2	p.A23S	ENSG00000115257	ENST00000300954	Transcript	missense_variant	possibly_damaging(0.739)
chr19	38384612	38384612	WDR87	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.N538K	ENSG00000171804	ENST00000303868	Transcript	missense_variant	probably_damaging(0.947)
chr19	40978541	40978541	SPTBN4	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P8_2	p.P5S	ENSG00000160460	ENST00000352632	Transcript	missense_variant	benign(0.001)
chr19	46973008	46973008	PNMAL1	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.P429T	ENSG00000182013	ENST00000313683	Transcript	missense_variant	possibly_damaging(0.803)
chr19	7927287	7927287	EVI5L	Missense_Mutation	.	SNP	G	G	T	rs376230554	shansha n_et_al_P8_2	p.R605L	ENSG00000142459	ENST00000538904	Transcript	missense_variant	benign(0.006)
chr2	130912789	130912789	SMPD4	Missense_Mutation	.	SNP	A	A	C	rs148027738	shansha n_et_al_P8_2	p.F484V	ENSG00000136699	ENST00000409031	Transcript	missense_variant	possibly_damaging(0.765)
chr2	224824660	224824660	MRPL44	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.A197S	ENSG00000135900	ENST00000258383	Transcript	missense_variant	probably_damaging(0.986)
chr2	233351335	233351335	ECEL1	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P8_2	p.H10P	ENSG00000171551	ENST00000304546	Transcript	missense_variant	probably_damaging(0.991)
chr2	99438690	99438690	KIAA1211L	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.F682L	ENSG00000196872	ENST00000397899	Transcript	missense_variant	probably_damaging(0.923)
chr2	99779172	99779172	LIPT1	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P8_2	p.T251M	ENSG00000144182	ENST00000393477	Transcript	missense_variant	benign(0.009)
chr20	55108522	55108522	FAM209B	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P8_2	p.F42Y	ENSG00000213714	ENST00000371325	Transcript	missense_variant	probably_damaging(0.953)
chr20	62421195	62421195	ZBTB46	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_2	p.P306S	ENSG00000130584	ENST00000245663	Transcript	missense_variant	benign(0.059)
chr21	33684279	33684279	MRAP	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.G164V	ENSG00000170262	ENST00000399784	Transcript	missense_variant	possibly_damaging(0.866)
chr22	23974044	23974044	C22orf43	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P8_2	p.G56A	ENSG00000189269	ENST00000317749	Transcript	missense_variant	probably_damaging(0.996)
chr22	31591456	31591456	RNF185	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.W66L	ENSG00000138942	ENST00000326132	Transcript	missense_variant	probably_damaging(0.995)
chr22	41967972	41967972	CSDC2	Translation_Start_Site	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.M1?	ENSG00000172346	ENST00000306149	Transcript	initiator_codon_variant	possibly_damaging(0.775)
chr22	51065644	51065644	ARSA	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.P139T	ENSG00000100299	ENST00000216124	Transcript	missense_variant	benign(0.004)
chr3	124045018	124045018	KALRN	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.Q426H	ENSG00000160145	ENST00000240874	Transcript	missense_variant	benign(0.295)
chr3	169710427	169710427	SEC62	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_2	p.R259M	ENSG00000008952	ENST00000337002	Transcript	missense_variant	unknown(0)
chr3	46751098	46751098	TMIE	Missense_Mutation	.	SNP	a	a	G	rs201683042	shansha n_et_al_P8_2	p.K131E	ENSG00000181585	ENST00000326431	Transcript	missense_variant	possibly_damaging(0.801)

chr3	47890253	47890253	*DHX30*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.C905*	ENSG00000132153	ENST00000445061	Transcript	stop_gained	NA
chr4	128949741	128949741	*C4orf29*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.Q271K	ENSG00000164074	ENST00000398965	Transcript	missense_variant	benign(0.001)
chr4	77660607	77660607	*SHROOM3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.F427L	ENSG00000138771	ENST00000296043	Transcript	missense_variant	benign(0.006)
chr4	84191047	84191047	*COQ2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.W293L	ENSG00000173085	ENST00000311469	Transcript	missense_variant	probably_damaging(0.99)
chr4	84457873	84457873	*AGPAT9*	Missense_Mutation	.	SNP	G	G	A	rs372747571	shanshan_et_al_P8_2	p.G33D	ENSG00000138678	ENST00000395226	Transcript	missense_variant	probably_damaging(0.999)
chr5	167894969	167894969	*WWC1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.R1098M	ENSG00000113645	ENST00000521089	Transcript	missense_variant	probably_damaging(0.967)
chr5	55195924	55195924	*IL31RA*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.V345L	ENSG00000164509	ENST00000447346	Transcript	missense_variant	benign(0.012)
chr6	159654872	159654872	*FNDC1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.H1110N	ENSG00000164694	ENST00000297267	Transcript	missense_variant	unknown(0)
chr7	101918628	101918628	*CUX1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.A519S	ENSG00000257923	ENST00000437600	Transcript	missense_variant	benign(0.188)
chr7	102292888	102292888	*SPDYE2B*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P8_2	p.S31R	ENSG00000173678	ENST00000507450	Transcript	missense_variant	probably_damaging(0.993)
chr7	23552631	23552631	*TRA2A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_2	p.R136H	ENSG00000164548	ENST00000297071	Transcript	missense_variant	possibly_damaging(0.765)
chr7	75050957	75050957	*POM121C*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_2	p.A860T	ENSG00000135213	ENST00000453279	Transcript	missense_variant	benign(0)
chr8	145665844	145665844	*TONSL*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.L394M	ENSG00000160949	ENST00000409379	Transcript	missense_variant	probably_damaging(0.928)
chr8	146015206	146015206	*RPL8*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_2	p.Q253*	ENSG00000161016	ENST00000262584	Transcript	stop_gained	NA
chr8	27634635	27634635	*ESCO2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P8_2	p.L270F	ENSG00000171320	ENST00000305188	Transcript	missense_variant	benign(0.395)
chr9	127975694	127975694	*RABEPK*	Missense_Mutation	.	SNP	G	G	T	rs368079784	shanshan_et_al_P8_2	p.R86L	ENSG00000136933	ENST00000373538	Transcript	missense_variant	probably_damaging(0.999)
chr9	140450001	140450001	*DPH7*	Missense_Mutation	.	SNP	C	C	T	rs149407940	shanshan_et_al_P8_2	p.R350Q	ENSG00000148399	ENST00000277540	Transcript	missense_variant	benign(0.003)
chrX	129148574	129148574	*BCORL1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.R609L	ENSG00000085185	ENST00000540052	Transcript	missense_variant	probably_damaging(0.998)
chrX	18616725	18616725	*CDKL5*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_2	p.L323F	ENSG00000008086	ENST00000379989	Transcript	missense_variant	possibly_damaging(0.587)
chr17	7577610	7577610	*TP53*	Splice_Site	.	SNP	T	T	A	novel	shanshan_et_al_P8_2	NA	ENSG00000141510	ENST00000269305	Transcript	splice_acceptor_variant	probably_damaging(0.831)
chr1	103405915	103405915	*COL11A1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.P1118T	ENSG00000060718	ENST00000370096	Transcript	missense_variant	unknown(0)
chr1	155209740	155209740	*GBA*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.T82A	ENSG00000177628	ENST00000327247	Transcript	missense_variant	benign(0.047)
chr1	158736024	158736024	*OR6N1*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P8_4	p.L150*	ENSG00000197403	ENST00000335094	Transcript	stop_gained	NA
chr1	176054920	176054920	*RFWD2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.R378H	ENSG00000143207	ENST00000367669	Transcript	missense_variant	benign(0.003)
chr1	220160597	220160597	*EPRS*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.Q975H	ENSG00000136628	ENST00000366923	Transcript	missense_variant	possibly_damaging(0.593)
chr1	224612233	224612233	*WDR26*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.H251N	ENSG00000162923	ENST00000414423	Transcript	missense_variant	benign(0.222)
chr1	240256392	240256392	*FMN2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P8_4	p.A328G	ENSG00000155816	ENST00000319653	Transcript	missense_variant	unknown(0)
chr1	24181001	24181001	*FUCA1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.H273R	ENSG00000179163	ENST00000374479	Transcript	missense_variant	probably_damaging(0.928)
chr1	247875618	247875618	*OR6F1*	Missense_Mutation	.	SNP	C	C	T	rs190994496	shanshan_et_al_P8_4	p.G147D	ENSG00000169214	ENST00000302084	Transcript	missense_variant	possibly_damaging(0.756)
chr1	94032982	94032983	*BCAR3*	Frame_Shift_Ins	.	INS	-	-	C	novel	shanshan_et_al_P8_4	p.E718Gfs*8	ENSG00000137936	ENST00000370244	Transcript	frameshift_variant	NA
chr1	94032985	94032986	*BCAR3*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P8_4	p.M717Ifs*9	ENSG00000137936	ENST00000370244	Transcript	frameshift_variant	NA
chr10	22498136	22498136	*EBLN1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.L259F	ENSG00000223601	ENST00000422359	Transcript	missense_variant	benign(0)
chr10	24886483	24886483	*ARHGAP21*	Missense_Mutation	.	SNP	C	C	T	rs372140665	shanshan_et_al_P8_4	p.R1076H	ENSG00000107863	ENST00000396432	Transcript	missense_variant	probably_damaging(1)
chr10	46322588	46322588	*AGAP4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.G256V	ENSG00000188234	ENST00000448048	Transcript	missense_variant	possibly_damaging(0.892)
chr11	102575310	102575310	*MMP27*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.G100V	ENSG00000137675	ENST00000260229	Transcript	missense_variant	possibly_damaging(0.9)
chr11	118919082	118919082	*HYOU1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P8_4	p.D752H	ENSG00000149428	ENST00000404233	Transcript	missense_variant	probably_damaging(0.996)

chr11	34473671	34473671	*CAT*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.A133S	ENSG00000121691	ENST00000241052	Transcript	missense_variant	possibly_damaging(0.632)
chr11	89645245	89645245	*TRIM49D1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.T290I	ENSG00000223417	ENST00000530311	Transcript	missense_variant	benign(0.289)
chr12	112185123	112185123	*ACAD10*	Missense_Mutation	.	SNP	A	A	G	rs138769725	shanshan_et_al_P8_4	p.I838V	ENSG00000111271	ENST00000455480	Transcript	missense_variant	benign(0.007)
chr12	46245473	46245473	*ARID2*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P8_4	p.G1190Efs*14	ENSG00000189079	ENST00000334344	Transcript	frameshift_variant	NA
chr12	51122384	51122405	*DIP2B*	Frame_Shift_Del	.	DEL	GTTGTACTCTTCTCGGCAGATC	GTTGTACTCTTCTCGGCAGATC	-	novel	shanshan_et_al_P8_4	p.L1189Pfs*28	ENSG00000066084	ENST00000301180	Transcript	frameshift_variant	NA
chr12	56091812	56091812	*ITGA7*	Splice_Site	.	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.X402_splice	ENSG00000135424	ENST00000553804	Transcript	splice_acceptor_variant	NA
chr12	79802504	79802504	*SLC2A14*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P8_4	p.Q257L	ENSG00000173262	ENST00000543909	Transcript	missense_variant	benign(0.016)
chr12	995180	995180	*WNK1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.P1737L	ENSG00000060237	ENST00000315939	Transcript	missense_variant	probably_damaging(0.99)
chr14	31118742	31118742	*SCFD1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.P208T	ENSG00000092108	ENST00000458591	Transcript	missense_variant	probably_damaging(1)
chr14	93460311	93460311	*ITPK1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P8_4	p.V93A	ENSG00000100605	ENST00000267615	Transcript	missense_variant	possibly_damaging(0.474)
chr15	31360207	31360207	*TRPM1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P8_4	p.I140T	ENSG00000134160	ENST00000542188	Transcript	missense_variant	possibly_damaging(0.77)
chr15	32988773	32988773	*SCG5*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.V201A	ENSG00000166922	ENST00000300175	Transcript	missense_variant	benign(0.014)
chr15	43307938	43307938	*UBR1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.D1053Y	ENSG00000159459	ENST00000290650	Transcript	missense_variant	probably_damaging(0.94)
chr16	23382775	23382775	*SCNN1B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.V346I	ENSG00000168447	ENST00000343070	Transcript	missense_variant	benign(0.268)
chr16	84432201	84432201	*ATP2C2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.A66T	ENSG00000064270	ENST00000262429	Transcript	missense_variant	benign(0.052)
chr17	18673308	18673308	*FBXW10*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.I639T	ENSG00000171931	ENST00000395665	Transcript	missense_variant	possibly_damaging(0.844)
chr17	42636335	42636335	*FZD2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.G427C	ENSG00000180340	ENST00000315323	Transcript	missense_variant	probably_damaging(1)
chr17	7578410	7578410	*TP53*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P8_4	p.R174W	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.997)
chr18	64211245	64211245	*CDH19*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P8_4	p.S393P	ENSG00000071991	ENST00000262150	Transcript	missense_variant	probably_damaging(0.939)
chr18	70526102	70526102	*NETO1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P8_4	p.L143R	ENSG00000166342	ENST00000327305	Transcript	missense_variant	probably_damaging(1)
chr18	7231789	7231789	*LRRC30*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.G218V	ENSG00000206422	ENST00000383467	Transcript	missense_variant	benign(0.021)
chr19	22154197	22154197	*ZNF208*	Missense_Mutation	.	SNP	T	T	A	rs560585093	shanshan_et_al_P8_4	p.R1213S	ENSG00000160321	ENST00000397126	Transcript	missense_variant	benign(0.001)
chr19	22155725	22155725	*ZNF208*	Missense_Mutation	.	SNP	C	C	G	rs200459967	shanshan_et_al_P8_4	p.W704S	ENSG00000160321	ENST00000397126	Transcript	missense_variant	benign(0.013)
chr19	4816725	4816725	*TICAM1*	Missense_Mutation	.	SNP	G	G	T	rs550630185	shanshan_et_al_P8_4	p.H555Q	ENSG00000127666	ENST00000248244	Transcript	missense_variant	benign(0.01)
chr19	52447417	52447417	*ZNF613*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P8_4	p.Q94L	ENSG00000176024	ENST00000293471	Transcript	missense_variant	benign(0.001)
chr19	9296676	9296676	*OR7D2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P8_4	p.F73L	ENSG00000188000	ENST00000344248	Transcript	missense_variant	benign(0.076)
chr2	155566280	155566280	*KCNJ3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P8_4	p.T290S	ENSG00000162989	ENST00000295101	Transcript	missense_variant	benign(0.003)
chr2	167433325	167433325	*FAM49A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.A128E	ENSG00000197872	ENST00000381323	Transcript	missense_variant	probably_damaging(0.99)
chr2	220341633	220341633	*SPEG*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.G1497W	ENSG00000072195	ENST00000312358	Transcript	missense_variant	possibly_damaging(0.755)
chr2	39281778	39281778	*SOS1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P8_4	p.N233Y	ENSG00000115904	ENST00000426016	Transcript	missense_variant	possibly_damaging(0.621)
chr20	10620244	10620244	*JAG1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P8_4	p.N1187H	ENSG00000101384	ENST00000254958	Transcript	missense_variant	benign(0.003)
chr20	42159033	42159033	*L3MBTL1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.T367M	ENSG00000185513	ENST00000427442	Transcript	missense_variant	possibly_damaging(0.684)
chr20	44637690	44637690	*MMP9*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.R42M	ENSG00000100985	ENST00000372330	Transcript	missense_variant	benign(0.007)
chr20	46262302	46262302	*NCOA3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P8_4	p.I296V	ENSG00000124151	ENST00000371998	Transcript	missense_variant	benign(0.006)
chr20	57769410	57769410	*ZNF831*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P8_4	p.E1112D	ENSG00000124203	ENST00000371030	Transcript	missense_variant	benign(0.307)
chr22	29025627	29025627	*TTC28*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P8_4	p.R98S	ENSG00000100154	ENST00000397906	Transcript	missense_variant	probably_damaging(0.998)

chr22	51018460	51018460	*CHKB*	Missense_Mutation	.	SNP	G	G	T	rs140020889	shanshan_et_al_P8_4	p.H290Q	ENSG00000100288	ENST00000406938	Transcript	missense_variant	benign(0.012)
chr3	130427249	130427249	*PIK3R4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.Q807K	ENSG00000196455	ENST00000356763	Transcript	missense_variant	benign(0)
chr3	42916381	42916381	*CYP8B1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.E310K	ENSG00000180432	ENST00000316161	Transcript	missense_variant	benign(0.021)
chr3	44762397	44762397	*ZNF502*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.Q30K	ENSG00000196653	ENST00000296091	Transcript	missense_variant	benign(0.011)
chr3	64133309	64133309	*PRICKLE2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.A286D	ENSG00000163637	ENST00000295902	Transcript	missense_variant	benign(0.439)
chr3	74350696	74350696	*CNTN3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.P650S	ENSG00000113805	ENST00000266365	Transcript	missense_variant	probably_damaging(1)
chr4	110920932	110920932	*EGF*	Missense_Mutation	.	SNP	G	G	C	rs138528000	shanshan_et_al_P8_4	p.V1035L	ENSG00000138798	ENST00000265171	Transcript	missense_variant	benign(0.019)
chr4	77069490	77069490	*NUP54*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P8_4	p.G13A	ENSG00000138750	ENST00000264883	Transcript	missense_variant	unknown(0)
chr4	77746066	77746066	*AFAP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.A732T	ENSG00000196526	ENST00000420658	Transcript	missense_variant	probably_damaging(0.973)
chr4	88356332	88356332	*NUDT9*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P8_4	p.S103A	ENSG00000170502	ENST00000302174	Transcript	missense_variant	benign(0.006)
chr5	108679931	108679931	*PJA2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.H654R	ENSG00000198961	ENST00000361189	Transcript	missense_variant	probably_damaging(0.999)
chr5	138269761	138269761	*CTNNA1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.A902S	ENSG00000044115	ENST00000302763	Transcript	missense_variant	benign(0.011)
chr5	149998001	149998001	*SYNPO*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.Q24H	ENSG00000171992	ENST00000394243	Transcript	missense_variant	benign(0.264)
chr5	154173154	154173154	*LARP1*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.X170_splice	ENSG00000155506	ENST00000336314	Transcript	splice_acceptor_variant	NA
chr5	179665373	179665373	*MAPK9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P8_4	p.E364V	ENSG00000050748	ENST00000452135	Transcript	missense_variant	benign(0.259)
chr5	180278392	180278392	*ZFP62*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.P35S	ENSG00000196670	ENST00000502412	Transcript	missense_variant	benign(0.008)
chr5	37016210	37016210	*NIPBL*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P8_4	p.T1572A	ENSG00000164190	ENST00000282516	Transcript	missense_variant	benign(0.194)
chr5	66118412	66118412	*NSUN2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.W364L	ENSG00000037474	ENST00000264670	Transcript	missense_variant	probably_damaging(0.997)
chr5	72354261	72354261	*FCHO2*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P8_4	p.K419*	ENSG00000157107	ENST00000430046	Transcript	stop_gained	NA
chr5	73931761	73931761	*ENC1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.D184Y	ENSG00000171617	ENST00000302351	Transcript	missense_variant	probably_damaging(0.97)
chr6	147556405	147556405	*STXBP5*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.E90*	ENSG00000164506	ENST00000321680	Transcript	stop_gained	NA
chr6	43005568	43005568	*CUL7*	Missense_Mutation	.	SNP	A	A	T	rs369627224	shanshan_et_al_P8_4	p.V1736D	ENSG00000044090	ENST00000535468	Transcript	missense_variant	possibly_damaging(0.812)
chr7	12412713	12412713	*VWDE*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.D493Y	ENSG00000146530	ENST00000275358	Transcript	missense_variant	probably_damaging(1)
chr7	142723412	142723412	*OR9A2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.V270I	ENSG00000179468	ENST00000350513	Transcript	missense_variant	benign(0.113)
chr7	37927884	37927884	*NME8*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.C418F	ENSG00000086288	ENST00000199447	Transcript	missense_variant	probably_damaging(0.961)
chr7	38505802	38505802	*AMPH*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.E213K	ENSG00000078053	ENST00000356264	Transcript	missense_variant	probably_damaging(0.999)
chr7	92247499	92247499	*CDK6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.E241K	ENSG00000105810	ENST00000265734	Transcript	missense_variant	benign(0.445)
chr7	94057757	94057757	*COL1A2*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P8_4	p.W1227G	ENSG00000164692	ENST00000297268	Transcript	missense_variant	unknown(0)
chr8	101542040	101542040	*ANKRD46*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.D8Y	ENSG00000186106	ENST00000520552	Transcript	missense_variant	possibly_damaging(0.861)
chr8	121256212	121256212	*COL14A1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.G815V	ENSG00000187955	ENST00000297848	Transcript	missense_variant	probably_damaging(0.977)
chr8	144589967	144589967	*ZC3H3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.P555L	ENSG00000014164	ENST00000262577	Transcript	missense_variant	benign(0.002)
chr8	28208857	28208857	*CSMD1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.R3114L	ENSG00000183117	ENST00000537824	Transcript	missense_variant	benign(0.109)
chr8	30472220	30472220	*GTF2E2*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.R91*	ENSG00000197265	ENST00000355904	Transcript	stop_gained	NA
chr9	114456105	114456105	*C9orf84*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.P1083T	ENSG00000165181	ENST00000374287	Transcript	missense_variant	probably_damaging(1)
chr9	117124782	117124782	*AKNA*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.A607D	ENSG00000106948	ENST00000307564	Transcript	missense_variant	probably_damaging(0.997)
chr9	86414198	86414198	*GKAP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.A88T	ENSG00000165113	ENST00000376371	Transcript	missense_variant	benign(0.012)

chrX	118223419	118223419	*KIAA1210*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.D592Y	ENSG00000250423	ENST00000402510	Transcript	missense_variant	benign(0.346)
chrX	123181356	123181356	*STAG2*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.X273_splice	ENSG00000101972	ENST00000218089	Transcript	splice_donor_variant	NA
chrX	37850405	37850405	*CXorf27*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P8_4	p.L106Cfs*20	ENSG00000187516	ENST00000340116	Transcript	frameshift_variant	NA
chrX	48771756	48771756	*PIM2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P8_4	p.D230H	ENSG00000102096	ENST00000376509	Transcript	missense_variant	probably_damaging(1)
chrX	67751762	67751762	*YIPF6*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.R211L	ENSG00000181704	ENST00000462683	Transcript	missense_variant	probably_damaging(0.996)
chr1	109198321	109198321	*HENMT1*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P90	NA	ENSG00000162639	ENST00000370032	Transcript	splice_acceptor_variant	NA
chr1	109810543	109810543	*CELSR2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.R2060L	ENSG00000143126	ENST00000271332	Transcript	missense_variant	benign(0.059)
chr1	109953700	109953700	*PSMA5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.C165Y	ENSG00000143106	ENST00000271308	Transcript	missense_variant	benign(0.015)
chr1	110085864	110085864	*GPR61*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.R74*	ENSG00000156097	ENST00000527748	Transcript	stop_gained	NA
chr1	138398 50	138398 50	*LRRC38*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.G80V	ENSG00000162494	ENST00000376085	Transcript	missense_variant	possibly_damaging(0.892)
chr1	145791072	145791072	*GPR89A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.S239L	ENSG00000117262	ENST00000313835	Transcript	missense_variant	benign(0.013)
chr1	147438884	147438884	*GPR89B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.S239L	ENSG00000188092	ENST00000314163	Transcript	missense_variant	benign(0.013)
chr1	155796708	155796708	*GON4L*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P90	p.S206C	ENSG00000116580	ENST00000437809	Transcript	missense_variant	benign(0.001)
chr1	161277173	161277173	*MPZ*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P90	p.E37Q	ENSG00000158887	ENST00000533357	Transcript	missense_variant	benign(0.409)
chr1	175046848	175046848	*TNN*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.D98E	ENSG00000120332	ENST00000239462	Transcript	missense_variant	benign(0.158)
chr1	175048753	175048753	*TNN*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.R232C	ENSG00000120332	ENST00000239462	Transcript	missense_variant	benign(0.009)
chr1	179035966	179035966	*FAM20B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P90	p.I324F	ENSG00000116199	ENST00000263733	Transcript	missense_variant	probably_damaging(0.997)
chr1	179562594	179562594	*TDRD5*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.X78_splice	ENSG00000162782	ENST00000444136	Transcript	splice_acceptor_variant	NA
chr1	201838826	201838826	*IPO9*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.D705Y	ENSG00000198700	ENST00000361565	Transcript	missense_variant	probably_damaging(0.974)
chr1	22165342	22165342	*HSPG2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A3376S	ENSG00000142798	ENST00000374695	Transcript	missense_variant	possibly_damaging(0.876)
chr1	221912939	221912939	*DUSP10*	Missense_Mutation	.	SNP	C	C	A	rs138574623	shanshan_et_al_P90	p.V50F	ENSG00000143507	ENST00000366899	Transcript	missense_variant	benign(0.004)
chr1	231472123	231472123	*EXOC8*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P90	p.H457D	ENSG00000116903	ENST00000360394	Transcript	missense_variant	benign(0.031)
chr1	232596667	232596667	*SIPA1L2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P90	p.I1021V	ENSG00000116991	ENST00000366630	Transcript	missense_variant	possibly_damaging(0.557)
chr1	232650572	232650572	*SIPA1L2*	Nonsense_Mutation	.	SNP	C	C	A	rs567235653	shanshan_et_al_P90	p.E172*	ENSG00000116991	ENST00000366630	Transcript	stop_gained	NA
chr1	237729945	237729945	*RYR2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A1098D	ENSG00000198626	ENST00000366574	Transcript	missense_variant	benign(0.223)
chr1	240370867	240370867	*FMN2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.G919C	ENSG00000155816	ENST00000319653	Transcript	missense_variant	unknown(0)
chr1	26316019	26316019	*PAFAH2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.R55L	ENSG00000158006	ENST00000374282	Transcript	missense_variant	probably_damaging(0.984)
chr1	29639164	29639164	*PTPRU*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.R1068L	ENSG00000060656	ENST00000345512	Transcript	missense_variant	probably_damaging(0.999)
chr1	32084816	32084816	*HCRTR1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.G8V	ENSG00000121764	ENST00000403528	Transcript	missense_variant	benign(0.04)
chr1	40228862	40228862	*BMP8B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A321S	ENSG00000116985	ENST00000372827	Transcript	missense_variant	probably_damaging(0.965)
chr1	43022042	43022042	*CCDC30*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.S214I	ENSG00000186409	ENST00000428554	Transcript	missense_variant	probably_damaging(0.925)
chr1	897290	897290	*KLHL17*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P90	p.S192A	ENSG00000187961	ENST00000338591	Transcript	missense_variant	benign(0.18)
chr10	11523836	11523836	*USP6NL*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P90	p.F354L	ENSG00000148429	ENST00000277575	Transcript	missense_variant	benign(0.061)
chr10	50339858	50339858	*FAM170B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A218S	ENSG00000172538	ENST00000311787	Transcript	missense_variant	possibly_damaging(0.751)
chr10	61828560	61828560	*ANK3*	Missense_Mutation	.	SNP	C	C	T	rs561525408	shanshan_et_al_P90	p.D4027N	ENSG00000151150	ENST00000280772	Transcript	missense_variant	probably_damaging(0.978)
chr11	10796819	10796819	*CTR9*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.R984L	ENSG00000198730	ENST00000361367	Transcript	missense_variant	benign(0.25)

chr11	118359339	118359339	*KMT2A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.C1448F	ENSG00000118058	ENST00000534358	Transcript	missense_variant	probably_damaging(0.996)
chr11	123477491	123477491	*GRAMD1B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.D357Y	ENSG00000023171	ENST00000529750	Transcript	missense_variant	benign(0.171)
chr11	130275690	130275690	*ADAMTS8*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.D811E	ENSG00000134917	ENST00000257359	Transcript	missense_variant	benign(0.038)
chr11	133792581	133792581	*IGSF9B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.P722T	ENSG00000080854	ENST00000533871	Transcript	missense_variant	probably_damaging(0.999)
chr11	16847695	16847695	*PLEKHA7*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A439S	ENSG00000166689	ENST00000355661	Transcript	missense_variant	benign(0.089)
chr11	17633783	17633783	*OTOG*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.H2078Q	ENSG00000188162	ENST00000399391	Transcript	missense_variant	benign(0.267)
chr11	20658776	20658776	*SLC6A5*	Missense_Mutation	.	SNP	G	G	A	rs138885115	shanshan_et_al_P90	p.R599H	ENSG00000165970	ENST00000525748	Transcript	missense_variant	probably_damaging(0.987)
chr11	34378751	34378751	*ABTB2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.R127L	ENSG00000166016	ENST00000435224	Transcript	missense_variant	possibly_damaging(0.713)
chr11	46910976	46910976	*LRP4*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P90	p.H734R	ENSG00000134569	ENST00000378623	Transcript	missense_variant	benign(0.001)
chr11	551827	551827	*LRRC56*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.G325C	ENSG00000161328	ENST00000270115	Transcript	missense_variant	probably_damaging(1)
chr11	55587215	55587215	*OR5D18*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P90	p.N37S	ENSG00000186119	ENST00000339976	Transcript	missense_variant	benign(0)
chr11	55587398	55587398	*OR5D18*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.C98F	ENSG00000186119	ENST00000339976	Transcript	missense_variant	probably_damaging(1)
chr11	61563713	61563713	*FEN1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.V294M	ENSG00000168496	ENST00000305885	Transcript	missense_variant	benign(0.036)
chr11	63683082	63683082	*RCOR2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P90	p.D43E	ENSG00000167771	ENST00000301459	Transcript	missense_variant	benign(0.191)
chr11	66278161	66278161	*BBS1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.A11S	ENSG00000174483	ENST00000318312	Transcript	missense_variant	benign(0.002)
chr11	7817647	7817647	*OR5P2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.L281F	ENSG00000183303	ENST00000329434	Transcript	missense_variant	possibly_damaging(0.799)
chr11	87908378	87908378	*RAB38*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.V59L	ENSG00000123892	ENST00000246662	Transcript	missense_variant	possibly_damaging(0.641)
chr12	104054121	104054121	*STAB2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.L583F	ENSG00000136011	ENST00000388867	Transcript	missense_variant	probably_damaging(1)
chr12	110819631	110819631	*ANAPC7*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.G387V	ENSG00000196510	ENST00000455511	Transcript	missense_variant	possibly_damaging(0.543)
chr12	52579220	52579220	*KRT80*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.G151E	ENSG00000167767	ENST00000394815	Transcript	missense_variant	benign(0.006)
chr12	52985302	52985302	*KRT72*	Nonsense_Mutation	.	SNP	G	G	T	rs112771714	shanshan_et_al_P90	p.Y303*	ENSG00000170486	ENST00000293745	Transcript	stop_gained	NA
chr12	55820602	55820602	*OR6C76*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P90	p.T189S	ENSG00000185821	ENST00000328314	Transcript	missense_variant	possibly_damaging(0.902)
chr12	66232350	66232350	*HMGA2*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.X83_splice	ENSG00000149948	ENST00000403681	Transcript	splice_donor_variant	NA
chr12	6965218	6965218	*USP5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P90	p.F114L	ENSG00000111667	ENST00000229268	Transcript	missense_variant	benign(0.002)
chr12	70929938	70929938	*PTPRB*	Missense_Mutation	.	SNP	C	C	T	rs144389405	shanshan_et_al_P90	p.G1983D	ENSG00000127329	ENST00000334414	Transcript	missense_variant	probably_damaging(1)
chr12	99949993	99949993	*KLRF1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.T184K	ENSG00000150045	ENST00000279544	Transcript	missense_variant	benign(0.017)
chr13	20233359	20233359	*MPHOSPH8*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P90	p.V574A	ENSG00000196199	ENST00000361479	Transcript	missense_variant	probably_damaging(0.999)
chr13	29600913	29600913	*MTUS2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A703D	ENSG00000132938	ENST00000431530	Transcript	missense_variant	possibly_damaging(0.847)
chr13	36367616	36367616	*DCLK1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.D649Y	ENSG00000133083	ENST00000255448	Transcript	missense_variant	probably_damaging(0.934)
chr13	38320109	38320109	*TRPC4*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P90	p.R288G	ENSG00000133107	ENST00000379681	Transcript	missense_variant	possibly_damaging(0.856)
chr13	52325468	52325468	*WDFY2*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P90	p.Y250D	ENSG00000139668	ENST00000298125	Transcript	missense_variant	possibly_damaging(0.625)
chr13	88329796	88329796	*SLITRK5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.G718D	ENSG00000165300	ENST00000325089	Transcript	missense_variant	benign(0.017)
chr13	88329958	88329958	*SLITRK5*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.S772Y	ENSG00000165300	ENST00000325089	Transcript	missense_variant	possibly_damaging(0.515)
chr14	105405796	105405796	*AHNAK2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.S5331Y	ENSG00000185567	ENST00000333244	Transcript	missense_variant	possibly_damaging(0.86)
chr14	105417611	105417611	*AHNAK2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.D1393N	ENSG00000185567	ENST00000333244	Transcript	missense_variant	possibly_damaging(0.728)
chr14	22102091	22102091	*OR10G2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.A303D	ENSG00000255582	ENST00000542433	Transcript	missense_variant	probably_damaging(0.938)

chr14	24649736	24649736	*IPO4*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P90	p.K1053T	ENSG00000196497	ENST00000354464	Transcript	missense_variant	benign(0.024)
chr15	25616012	25616012	*UBE3A*	Nonsense_Mutation	.	SNP	G	G	A	rs111033594	shanshan_et_al_P90	p.R440*	ENSG00000114062	ENST00000397954	Transcript	stop_gained	NA
chr15	33928648	33928648	*RYR3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.M1151I	ENSG00000198838	ENST00000389232	Transcript	missense_variant	possibly_damaging(0.718)
chr15	48441237	48441237	*MYEF2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P90	p.S544T	ENSG00000104177	ENST00000324324	Transcript	missense_variant	possibly_damaging(0.676)
chr15	48888545	48888545	*FBN1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.G158V	ENSG00000166147	ENST00000316623	Transcript	missense_variant	probably_damaging(0.999)
chr15	60639885	60639885	*ANXA2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.D340Y	ENSG00000182718	ENST00000332680	Transcript	missense_variant	probably_damaging(0.99)
chr15	78836555	78836555	*PSMA4*	Missense_Mutation	.	SNP	G	G	T	rs115517781	shanshan_et_al_P90	p.G78V	ENSG00000041357	ENST00000044462	Transcript	missense_variant	probably_damaging(0.997)
chr15	83332351	83332351	*AP3B2*	Missense_Mutation	.	SNP	G	G	T	rs201703765	shanshan_et_al_P90	p.P801T	ENSG00000103723	ENST00000261722	Transcript	missense_variant	possibly_damaging(0.641)
chr16	1505182	1505182	*CLCN7*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.D351Y	ENSG00000103249	ENST00000382745	Transcript	missense_variant	benign(0.367)
chr16	3490822	3490822	*ZNF597*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.D49Y	ENSG00000167981	ENST00000301744	Transcript	missense_variant	probably_damaging(0.956)
chr16	47533729	47533729	*PHKB*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.G77S	ENSG00000102893	ENST00000323584	Transcript	missense_variant	benign(0.133)
chr16	86601020	86601020	*FOXC2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.A27S	ENSG00000176692	ENST00000320354	Transcript	missense_variant	benign(0.192)
chr17	37783692	37783692	*PPP1R1B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.P16H	ENSG00000131771	ENST00000254079	Transcript	missense_variant	probably_damaging(0.996)
chr17	39458727	39458727	*KRTAP2 9-1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.C126F	ENSG00000212658	ENST00000391353	Transcript	missense_variant	possibly_damaging(0.553)
chr17	39553443	39553443	*KRT31*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P90	NA	ENSG00000094796	ENST00000251645	Transcript	splice_donor_variant	NA
chr17	39646022	39646022	*KRT36*	Missense_Mutation	.	SNP	C	C	A	rs199500732	shanshan_et_al_P90	p.R32L	ENSG00000126337	ENST00000328119	Transcript	missense_variant	benign(0.173)
chr17	43923828	43923828	*SPPL2C*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.R519L	ENSG00000185294	ENST00000329196	Transcript	missense_variant	probably_damaging(0.986)
chr17	46928502	46928502	*CALCOCO2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P90	p.K223E	ENSG00000136436	ENST00000448105	Transcript	missense_variant	benign(0.03)
chr17	48585974	48585974	*MYCBPAP*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A23E	ENSG00000136449	ENST00000323776	Transcript	missense_variant	benign(0.05)
chr17	61498172	61498172	*TANC2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.A1610V	ENSG00000170921	ENST00000424789	Transcript	missense_variant	probably_damaging(0.985)
chr17	61557709	61557709	*ACE*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P90	p.T223A	ENSG00000159640	ENST00000290866	Transcript	missense_variant	benign(0.093)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P90	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr18	72343937	72343937	*ZNF407*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.R321Q	ENSG00000215421	ENST00000299687	Transcript	missense_variant	benign(0.002)
chr19	12937655	12937655	*RTBDN*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.C164*	ENSG00000132026	ENST00000322912	Transcript	stop_gained	NA
chr19	36370299	36370299	*APLP1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.G638C	ENSG00000105290	ENST00000221891	Transcript	missense_variant	probably_damaging(1)
chr19	49657920	49657920	*HRC*	Missense_Mutation	.	SNP	C	C	T	rs200730671	shanshan_et_al_P90	p.G192E	ENSG00000130528	ENST00000252825	Transcript	missense_variant	benign(0.014)
chr19	5131936	5131936	*KDM4B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.K608N	ENSG00000127663	ENST00000159111	Transcript	missense_variant	possibly_damaging(0.788)
chr19	53770380	53770380	*VN1R4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.R180H	ENSG00000228567	ENST00000311170	Transcript	missense_variant	benign(0)
chr19	5587409	5587409	*SAFB2*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P90	NA	ENSG00000130254	ENST00000252542	Transcript	frameshift_variant	NA
chr19	57868600	57868600	*ZNF304*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.A455S	ENSG00000131845	ENST00000391705	Transcript	missense_variant	probably_damaging(0.931)
chr19	7058607	7058607	*MBD3L3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.P4T	ENSG00000182315	ENST00000333843	Transcript	missense_variant	benign(0.113)
chr2	110372870	110372870	*SOWAHC*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.E268D	ENSG00000198142	ENST00000356454	Transcript	missense_variant	benign(0.179)
chr2	128322829	128322829	*MYO7B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.D52N	ENSG00000169994	ENST00000428314	Transcript	missense_variant	benign(0.021)
chr2	160843807	160843807	*PLA2R1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.H633N	ENSG00000153246	ENST00000283243	Transcript	missense_variant	benign(0.001)
chr2	166848676	166848676	*SCN1A*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P90	p.D1703E	ENSG00000144285	ENST00000303395	Transcript	missense_variant	probably_damaging(0.978)
chr2	171092540	171092540	*MYO3B*	Missense_Mutation	.	SNP	G	G	T	rs200288720	shanshan_et_al_P90	p.A215S	ENSG00000071909	ENST00000408978	Transcript	missense_variant	benign(0.318)

chr2	18112837	18112837	*KCNS3*	Missense_Mutation	.	SNP	G	G	T	rs142972265	shansha n_et_al_P90	p.A188S	ENSG00000170745	ENST00000403915	Transcript	missense_variant	probably_damaging(0.93)
chr2	209308253	209308253	*PTH2R*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P90	p.K230N	ENSG00000144407	ENST00000272847	Transcript	missense_variant	benign(0.236)
chr2	220331955	220331955	*SPEG*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.A981S	ENSG00000072195	ENST00000312358	Transcript	missense_variant	probably_damaging(0.994)
chr2	220371069	220371069	*GMPPA*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P90	p.N363Y	ENSG00000144591	ENST00000358215	Transcript	missense_variant	probably_damaging(0.999)
chr2	220494354	220494354	*SLC4A3*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P90	p.A183V	ENSG00000114923	ENST00000376372	Transcript	missense_variant	benign(0.001)
chr2	222298873	222298874	*EPHA4*	Frame_Shift_Del	.	DEL	AC	AC	-	novel	shansha n_et_al_P90	p.M828Ifs*7	ENSG00000116106	ENST00000281821	Transcript	frameshift_variant	NA
chr2	232389978	232389978	*NMUR1*	Missense_Mutation	.	SNP	G	G	T	rs200825519	shansha n_et_al_P90	p.P353T	ENSG00000171596	ENST00000305141	Transcript	missense_variant	probably_damaging(1)
chr2	240036802	240036802	*HDAC4*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P90	p.E575*	ENSG00000068024	ENST00000345617	Transcript	stop_gained	NA
chr2	266775 81	266775 81	*DRC1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P90	p.W662*	ENSG00000157856	ENST00000288710	Transcript	stop_gained	NA
chr2	375166 51	375166 51	*PRKD3*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P90	p.G189R	ENSG00000115825	ENST00000379076	Transcript	missense_variant	possibly_damaging(0.742)
chr2	551557 91	551557 91	*EML6*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.A1303S	ENSG00000214595	ENST00000356458	Transcript	missense_variant	benign(0.002)
chr2	713047 31	713047 31	*NAGK*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.G316V	ENSG00000124357	ENST00000455662	Transcript	missense_variant	probably_damaging(0.999)
chr2	713751 87	713751 87	*MPHOSPH10*	Frame_Shift_Del	.	DEL	C	C	-	novel	shansha n_et_al_P90	p.P540Qfs*2	ENSG00000124383	ENST00000244230	Transcript	frameshift_variant	NA
chr2	747838 94	747838 94	*DOK1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.G367C	ENSG00000115325	ENST00000233668	Transcript	missense_variant	probably_damaging(0.994)
chr2	967956 92	967956 92	*ASTL*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.P249T	ENSG00000188886	ENST00000342380	Transcript	missense_variant	possibly_damaging(0.836)
chr20	305849 86	305849 86	*XKR7*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P90	p.A489E	ENSG00000260903	ENST00000562532	Transcript	missense_variant	benign(0.224)
chr20	337117 38	337117 38	*EDEM2*	Nonsense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P90	p.Q357*	ENSG00000088298	ENST00000374492	Transcript	stop_gained	NA
chr20	338685 47	338685 47	*EIF6*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P90	p.Q93H	ENSG00000242372	ENST00000374450	Transcript	missense_variant	benign(0.008)
chr20	354435 97	354435 97	*SOGA1*	Missense_Mutation	.	SNP	G	G	A	rs529136326	shansha n_et_al_P90	p.P750S	ENSG00000149639	ENST00000237536	Transcript	missense_variant	benign(0.037)
chr20	407271 80	407271 80	*PTPRT*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.P1243T	ENSG00000196090	ENST00000373187	Transcript	missense_variant	probably_damaging(0.999)
chr20	501400 58	501400 58	*NFATC2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P90	p.P241L	ENSG00000101096	ENST00000396009	Transcript	missense_variant	probably_damaging(0.999)
chr20	572689 16	572689 16	*NPEPL1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.A92S	ENSG00000215440	ENST00000356091	Transcript	missense_variant	benign(0.139)
chr20	623669 17	623669 17	*ZGPAT*	Splice_Site	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.X486_splice	ENSG00000197114	ENST00000328969	Transcript	splice_donor_variant	NA
chr21	316617 69	316617 69	*KRTAP25-1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.H14N	ENSG00000232263	ENST00000416044	Transcript	missense_variant	benign(0.014)
chr21	337169 79	337169 79	*URB1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P90	p.C1386Y	ENSG00000142207	ENST00000382751	Transcript	missense_variant	probably_damaging(0.984)
chr22	183790 39	183790 39	*MICAL3*	Missense_Mutation	.	SNP	G	G	C	rs367876917	shansha n_et_al_P90	p.T432R	ENSG00000243156	ENST00000441493	Transcript	missense_variant	benign(0.007)
chr22	322009 02	322009 02	*DEPDC5*	Splice_Site	.	SNP	G	G	A	novel	shansha n_et_al_P90	p.X406_splice	ENSG00000100150	ENST00000382112	Transcript	splice_donor_variant	NA
chr3	113380252	113380252	*KIAA2018*	Missense_Mutation	.	SNP	G	G	A	rs367995838	shansha n_et_al_P90	p.R93W	ENSG00000176542	ENST00000316407	Transcript	missense_variant	probably_damaging(0.999)
chr3	128853696	128853696	*ISY1-RAB43*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P90	p.E174Q	ENSG00000261796	ENST00000418265	Transcript	missense_variant	probably_damaging(0.993)
chr3	131100666	131100666	*NUDT16*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P90	p.R6S	ENSG00000198585	ENST00000502852	Transcript	missense_variant	unknown(0)
chr3	136707 11	136707 11	*FBLN2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P90	p.V921M	ENSG00000163520	ENST00000404922	Transcript	missense_variant	possibly_damaging(0.583)
chr3	138474692	138474692	*PIK3CB*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P90	p.D101Y	ENSG00000051382	ENST00000477593	Transcript	missense_variant	probably_damaging(0.999)
chr3	182615091	182615091	*ATP11B*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P90	p.M1017V	ENSG00000058063	ENST00000323116	Transcript	missense_variant	benign(0.006)
chr3	194081566	194081566	*LRRC15*	Missense_Mutation	.	SNP	A	A	T	rs141103070	shansha n_et_al_P90	p.N75K	ENSG00000172061	ENST00000439944	Transcript	missense_variant	benign(0.003)
chr3	504154 88	504154 88	*CACNA2D2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P90	p.G477V	ENSG00000007402	ENST00000479441	Transcript	missense_variant	probably_damaging(1)
chr4	113435851	113435851	*NEUROG2*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P90	p.Y261N	ENSG00000178403	ENST00000313341	Transcript	missense_variant	possibly_damaging(0.651)

chr4	138452122	138452122	*PCDH18*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.P374L	ENSG00000189184	ENST00000344876	Transcript	missense_variant	probably_damaging(0.936)
chr4	78815299	78815299	*MRPL1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.D189Y	ENSG00000169288	ENST00000315567	Transcript	missense_variant	probably_damaging(0.918)
chr4	858426	858426	*GPR78*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.R227S	ENSG00000155269	ENST00000382487	Transcript	missense_variant	possibly_damaging(0.672)
chr4	89649749	89649749	*FAM13A*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P90	p.K1003Q	ENSG00000138640	ENST00000264344	Transcript	missense_variant	probably_damaging(0.999)
chr5	121758812	121758812	*SNCAIP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.G127D	ENSG00000064692	ENST00000261368	Transcript	missense_variant	benign(0.006)
chr5	140264201	140264201	*PCDHA13*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A783E	ENSG00000239389	ENST00000289272	Transcript	missense_variant	benign(0)
chr5	140720777	140720777	*PCDHGA2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.R747W	ENSG00000081853	ENST00000394576	Transcript	missense_variant	probably_damaging(0.915)
chr5	146798103	146798103	*DPYSL3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P90	p.T188A	ENSG00000113657	ENST00000343218	Transcript	missense_variant	probably_damaging(0.994)
chr5	160071232	160071232	*ATP10B*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P90	p.R261G	ENSG00000118322	ENST00000327245	Transcript	missense_variant	possibly_damaging(0.9)
chr5	40853925	40853925	*CARD6*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.E831*	ENSG00000132357	ENST00000254691	Transcript	stop_gained	NA
chr5	55081594	55081594	*DDX4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.E253D	ENSG00000152670	ENST00000505374	Transcript	missense_variant	benign(0.02)
chr6	144508366	144508366	*STX11*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.R201L	ENSG00000135604	ENST00000367568	Transcript	missense_variant	probably_damaging(0.994)
chr6	149997839	149997839	*LATS1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P90	p.S876R	ENSG00000131023	ENST00000543571	Transcript	missense_variant	probably_damaging(0.968)
chr6	159618553	159618553	*FNDC1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.S67I	ENSG00000164694	ENST00000297267	Transcript	missense_variant	unknown(0)
chr6	168352295	168352295	*MLLT4*	Frame_Shift_Ins	.	INS	-	-	G	novel	shanshan_et_al_P90	p.E1414Gfs*7	ENSG00000130396	ENST00000392108	Transcript	frameshift_variant	NA
chr6	26022174	26022174	*HIST1H4A*	Missense_Mutation	.	SNP	G	G	T	rs559774306	shanshan_et_al_P90	p.A90S	ENSG00000196176	ENST00000359907	Transcript	missense_variant	possibly_damaging(0.731)
chr6	26217347	26217347	*HIST1H2AE*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P90	p.P49A	ENSG00000168274	ENST00000303910	Transcript	missense_variant	benign(0.036)
chr6	28327532	28327532	*ZKSCAN3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.A57S	ENSG00000189298	ENST00000377255	Transcript	missense_variant	probably_damaging(1)
chr6	33635036	33635036	*ITPR3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P90	p.R561P	ENSG00000096433	ENST00000374316	Transcript	missense_variant	benign(0.088)
chr6	50683324	50683324	*TFAP2D*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P90	p.Q179E	ENSG00000008197	ENST00000008391	Transcript	missense_variant	benign(0.005)
chr6	83767661	83767661	*UBE3D*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.T53I	ENSG00000118420	ENST00000369747	Transcript	missense_variant	possibly_damaging(0.87)
chr6	86282031	86282031	*SNX14*	Frame_Shift_Del	.	DEL	TCGTTTACATT	TCGTTTACATT	-	novel	shanshan_et_al_P90	p.K108Tfs*2	ENSG00000135317	ENST00000314673	Transcript	frameshift_variant	NA
chr7	138711555	138711555	*ZC3HAV1L*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P90	p.H262R	ENSG00000146858	ENST00000275766	Transcript	missense_variant	benign(0)
chr7	142658054	142658054	*KEL*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.L121I	ENSG00000197993	ENST00000355265	Transcript	missense_variant	possibly_damaging(0.844)
chr7	150269312	150269312	*GIMAP4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.G52C	ENSG00000133574	ENST00000255945	Transcript	missense_variant	probably_damaging(0.997)
chr7	150648887	150648887	*KCNH2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.L532M	ENSG00000055118	ENST00000262186	Transcript	missense_variant	probably_damaging(0.999)
chr7	27213258	27213258	*HOXA10*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.A223V	ENSG00000253293	ENST00000283921	Transcript	missense_variant	benign(0.007)
chr7	32535362	32535362	*AVL9*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.G14V	ENSG00000105778	ENST00000318709	Transcript	missense_variant	probably_damaging(0.996)
chr7	47920360	47920360	*PKD1L1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.S1162R	ENSG00000158683	ENST00000289672	Transcript	missense_variant	benign(0.016)
chr7	47944053	47944053	*PKD1L1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.T618K	ENSG00000158683	ENST00000289672	Transcript	missense_variant	probably_damaging(0.996)
chr7	82595337	82595337	*PCLO*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.A1256D	ENSG00000186472	ENST00000333891	Transcript	missense_variant	unknown(0)
chr8	10468264	10468264	*RP1L1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.A1115V	ENSG00000183638	ENST00000382483	Transcript	missense_variant	possibly_damaging(0.855)
chr8	144681304	144681304	*TIGD5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.A411T	ENSG00000179886	ENST00000504548	Transcript	missense_variant	benign(0.019)
chr8	144942421	144942421	*EPPK1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.M1667I	ENSG00000227184	ENST00000525985	Transcript	missense_variant	benign(0.311)
chr8	87683304	87683304	*CNGB3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A121S	ENSG00000170289	ENST00000320005	Transcript	missense_variant	benign(0.005)
chr8	93029523	93029523	*RUNX1T1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.P64S	ENSG00000079102	ENST00000436581	Transcript	missense_variant	probably_damaging(0.985)

chr8	97157059	97157059	*GDF6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.G367V	ENSG00000156466	ENST00000287020	Transcript	missense_variant	probably_damaging(1)
chr9	140919585	140919585	*CACNA1B*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P90	p.M1083V	ENSG00000148408	ENST00000371372	Transcript	missense_variant	benign(0)
chr9	71628567	71628567	*PRKACG*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.A148S	ENSG00000165059	ENST00000377276	Transcript	missense_variant	possibly_damaging(0.832)
chr9	88650301	88650301	*GOLM1*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.Q333*	ENSG00000135052	ENST00000388712	Transcript	stop_gained	NA
chr9	92220635	92220635	*GADD45G*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.G70V	ENSG00000130222	ENST00000252506	Transcript	missense_variant	possibly_damaging(0.865)
chrX	106844339	106844339	*FRMPD3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P90	p.H1057N	ENSG00000147234	ENST00000276185	Transcript	missense_variant	benign(0.006)
chrX	108647579	108647580	*GUCY2F*	Frame_Shift_Del	.	DEL	AG	AG	-	novel	shanshan_et_al_P90	p.S701*	ENSG00000101890	ENST00000218006	Transcript	frameshift_variant	NA
chrX	110463640	110463640	*PAK3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P90	p.A570T	ENSG00000077264	ENST00000360648	Transcript	missense_variant	benign(0.193)
chrX	130220331	130220331	*ARHGAP36*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P90	p.A437V	ENSG00000147256	ENST00000276211	Transcript	missense_variant	possibly_damaging(0.579)
chrX	130408836	130408836	*IGSF1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P90	p.P1168H	ENSG00000147255	ENST00000370903	Transcript	missense_variant	probably_damaging(1)
chrX	32418133	32418133	*MXRA5*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P90	p.I638T	ENSG00000101825	ENST00000217939	Transcript	missense_variant	probably_damaging(1)
chrX	601797	601797	*SHOX*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P90	p.G203A	ENSG00000185960	ENST00000381578	Transcript	missense_variant	possibly_damaging(0.556)
chr1	159410218	159410218	*OR10J1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P95	p.V224F	ENSG00000196184	ENST00000423932	Transcript	missense_variant	possibly_damaging(0.756)
chr10	126454066	126454066	*METTL10*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P95	p.K171Q	ENSG00000203791	ENST00000368836	Transcript	missense_variant	benign(0.114)
chr13	21557710	21557710	*LATS2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P95	p.H712L	ENSG00000150457	ENST00000382592	Transcript	missense_variant	probably_damaging(0.999)
chr14	103569003	103569003	*EXOC3L4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P95	p.A315S	ENSG00000205436	ENST00000380069	Transcript	missense_variant	probably_damaging(0.954)
chr14	32561313	32561313	*ARHGAP5*	Nonsense_Mutation	.	SNP	C	C	T	rs201986816	shanshan_et_al_P95	p.R480*	ENSG00000100852	ENST00000345122	Transcript	stop_gained	NA
chr14	32561340	32561340	*ARHGAP5*	Missense_Mutation	.	SNP	G	G	A	rs783375533	shanshan_et_al_P95	p.E489K	ENSG00000100852	ENST00000345122	Transcript	missense_variant	possibly_damaging(0.811)
chr17	18233896	18233896	*SHMT1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P95	p.I382V	ENSG00000176974	ENST00000316694	Transcript	missense_variant	benign(0.251)
chr19	42854300	42854300	*MEGF8*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P95	p.E767K	ENSG00000105429	ENST00000334370	Transcript	missense_variant	possibly_damaging(0.896)
chr2	20990038	20990038	*C2orf43*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P95	p.K92M	ENSG00000118961	ENST00000237822	Transcript	missense_variant	benign(0.02)
chr20	23016479	23016479	*SSTR4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P95	p.R120L	ENSG00000132671	ENST00000255008	Transcript	missense_variant	probably_damaging(0.914)
chr3	71101704	71101704	*FOXP1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P95	p.G167V	ENSG00000114861	ENST00000491238	Transcript	missense_variant	probably_damaging(0.953)
chr4	367169	367169	*ZNF141*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P95	p.E315K	ENSG00000131127	ENST00000240499	Transcript	missense_variant	probably_damaging(0.966)
chr5	90079728	90079728	*GPR98*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P95	p.S4503G	ENSG00000164199	ENST00000405460	Transcript	missense_variant	possibly_damaging(0.827)
chr6	159653744	159653744	*FNDC1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P95	p.P734S	ENSG00000164694	ENST00000297267	Transcript	missense_variant	unknown(0)
chr6	78172786	78172786	*HTR1B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P95	p.T112I	ENSG00000135312	ENST00000369947	Transcript	missense_variant	benign(0.082)
chr7	91503086	91503086	*MTERF*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P95	p.S341N	ENSG00000127989	ENST00000351870	Transcript	missense_variant	benign(0.003)
chr8	144896218	144896218	*SCRIB*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P95	p.E77V	ENSG00000180900	ENST00000356994	Transcript	missense_variant	probably_damaging(0.998)
chr8	67089558	67089559	*CRH*	In_Frame_Ins	.	INS	-	-	GCG	rs562792458	shanshan_et_al_P95	p.P51dup	ENSG00000147571	ENST00000276571	Transcript	inframe_insertion	NA
chr9	19276317	19276317	*DENND4C*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P95	p.I49V	ENSG00000137145	ENST00000606292	Transcript	missense_variant	probably_damaging(0.998)
chrX	102974188	102974188	*GLRA4*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P95	p.C244S	ENSG00000188828	ENST00000372617	Transcript	missense_variant	probably_damaging(0.949)
chrX	123518158	123518158	*TENM1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P95	p.R2208L	ENSG00000009694	ENST00000422452	Transcript	missense_variant	possibly_damaging(0.908)
chr17	7578419	7578419	*TP53*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P95	p.R171H	ENSG00000141510	ENST00000269305	Transcript	stop_gained	probably_damaging(0.831)
chr17	7576927	7576927	*TP53*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P95	NA	ENSG00000141510	ENST00000269305	Transcript	splice_acceptor_variant	probably_damaging(0.831)
chr1	152328013	152328013	*FLG2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P97	p.S750Y	ENSG00000143520	ENST00000388718	Transcript	missense_variant	unknown(0)

chr1	157667036	157667036	*FCRL3*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P97	p.Q246H	ENSG00000160856	ENST00000368184	Transcript	missense_variant	benign(0.366)
chr1	179504037	179504037	*AXDND1*	Missense_Mutation	.	SNP	g	g	C	novel	shanshan_et_al_P97	p.E991Q	ENSG00000162779	ENST00000367618	Transcript	missense_variant	unknown()
chr1	186322845	186322845	*TPR*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P97	p.A770E	ENSG00000047410	ENST00000367478	Transcript	missense_variant	possibly_damaging(0.587)
chr1	235969266	235969266	*LYST*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P97	p.K1057T	ENSG00000143669	ENST00000389794	Transcript	missense_variant	benign(0.001)
chr1	85736510	85736510	*BCL10*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P97	p.I46K	ENSG00000142867	ENST00000370580	Transcript	missense_variant	benign(0.018)
chr10	123954619	123954619	*TACC2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P97	p.A1967P	ENSG00000138162	ENST00000369005	Transcript	missense_variant	possibly_damaging(0.659)
chr10	79795402	79795402	*RPS24*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P97	p.K68R	ENSG00000138326	ENST00000440692	Transcript	missense_variant	possibly_damaging(0.727)
chr12	53448179	53448179	*TENC1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P97	p.R169L	ENSG00000111077	ENST00000314276	Transcript	missense_variant	probably_damaging(0.998)
chr12	85492755	85492755	*LRRIQ1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P97	p.I1064M	ENSG00000133640	ENST00000393217	Transcript	missense_variant	benign(0.1)
chr14	20846651	20846651	*TEP1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P97	p.Y1799F	ENSG00000129566	ENST00000262715	Transcript	missense_variant	benign(0.006)
chr14	59112176	59112176	*DACT1*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P97	p.Q279*	ENSG00000165617	ENST00000335867	Transcript	stop_gained	NA
chr16	89357447	89357447	*ANKRD11*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P97	p.T124K	ENSG00000167522	ENST00000301030	Transcript	missense_variant	probably_damaging(0.972)
chr17	73774761	73774761	*H3F3B*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P97	p.N109S	ENSG00000132475	ENST00000254810	Transcript	missense_variant	benign(0.063)
chr17	73860691	73860691	*SLC35G6*	Missense_Mutation	.	SNP	C	C	A	rs541352076	shanshan_et_al_P97	p.A263D	ENSG00000259224	ENST00000412468	Transcript	missense_variant	possibly_damaging(0.635)
chr17	7577534	7577534	*TP53*	Missense_Mutation	.	SNP	C	C	A	rs28934571	shanshan_et_al_P97	p.R249S	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.994)
chr18	45395671	45395671	*SMAD2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P97	p.L155V	ENSG00000175387	ENST00000402690	Transcript	missense_variant	benign(0.141)
chr19	49142829	49142829	*CA11*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P97	p.T206I	ENSG00000063180	ENST00000084798	Transcript	missense_variant	probably_damaging(0.995)
chr19	51729596	51729578	*CD33*	Frame_Shift_Del	.	DEL	CCCAACAACTGGTATCTTT	CCCAACAACTGGTATCTTT	-	rs201473304	shanshan_et_al_P97	p.P238Qfs*38	ENSG00000105383	ENST00000262262	Transcript	frameshift_variant	NA
chr2	128389317	128389317	*MYO7B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P97	p.H1720Q	ENSG00000169994	ENST00000428314	Transcript	missense_variant	benign(0.027)
chr2	99978047	99978047	*EIF5B*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P97	p.V228G	ENSG00000158417	ENST00000289371	Transcript	missense_variant	unknown()
chr20	44052928	44052928	*PIGT*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P97	p.A436D	ENSG00000124155	ENST00000279036	Transcript	missense_variant	possibly_damaging(0.799)
chr4	114823765	114823765	*ARSJ*	Frame_Shift_Del	.	DEL	T	T	-	rs200957837	shanshan_et_al_P97	p.T489Lfs*28	ENSG00000180801	ENST00000315366	Transcript	frameshift_variant	NA
chr5	112824069	112824069	*MCC*	Missense_Mutation	.	SNP	t	t	C	rs201571604	shanshan_et_al_P97	p.S15G	ENSG00000171444	ENST00000408903	Transcript	missense_variant	unknown()
chr5	34863077	34863077	*TTC23L*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P97	p.S152A	ENSG00000205838	ENST00000505624	Transcript	missense_variant	benign(0.255)
chr5	86670700	86670700	*RASA1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P97	p.N660Y	ENSG00000145715	ENST00000274376	Transcript	missense_variant	possibly_damaging(0.876)
chr6	42571420	42571420	*UBR2*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P97	p.E211Kfs*8	ENSG00000024048	ENST00000372899	Transcript	frameshift_variant	NA
chr6	53381021	53381021	*GCLC*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P97	NA	ENSG00000001084	ENST00000229416	Transcript	splice_acceptor_variant	NA
chr6	99825264	99825264	*COQ3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P97	p.E162K	ENSG00000132423	ENST00000254759	Transcript	missense_variant	probably_damaging(0.928)
chr7	100281480	100281480	*GIGYF1*	Missense_Mutation	.	SNP	G	G	T	rs140244722	shanshan_et_al_P97	p.R644S	ENSG00000146830	ENST00000275732	Transcript	missense_variant	unknown()
chr7	30491985	30491985	*NOD1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P97	p.R350W	ENSG00000106100	ENST00000222823	Transcript	missense_variant	probably_damaging(0.961)
chr9	79841484	79841484	*VPS13A*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P97	p.N443D	ENSG00000197969	ENST00000360280	Transcript	missense_variant	benign(0.001)
chrX	105179189	105179189	*NRK*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P97	p.E1177A	ENSG00000123572	ENST00000428173	Transcript	missense_variant	benign(0.442)
chrX	119005303	119005303	*RNF113A*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P97	p.E92*	ENSG00000125352	ENST00000371442	Transcript	stop_gained	NA
chrX	40495810	40495810	*CXorf38*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P97	p.E259A	ENSG00000185753	ENST00000327877	Transcript	missense_variant	benign(0.011)
chrX	57619097	57619097	*ZXDB*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P97	p.G206R	ENSG00000198455	ENST00000374888	Transcript	missense_variant	benign(0.002)
chr1	117509574	117509574	*PTGFRN*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.F561L	ENSG00000134247	ENST00000393203	Transcript	missense_variant	probably_damaging(0.964)

chr1	147083667	147083667	*BCL9*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.S11C	ENSG00000116128	ENST00000234739	Transcript	missense_variant	probably_damaging(0.99)
chr1	156589 1	156589 1	*MIB2*	Missense_Mutation	.	SNP	G	G	T	rs199909991	shanshan_et_al_P99	p.R1065L	ENSG00000197530	ENST00000505820	Transcript	missense_variant	probably_damaging(0.982)
chr1	172558369	172558369	*SUCO*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P99	p.D710Y	ENSG00000094975	ENST00000263688	Transcript	missense_variant	benign(0.197)
chr1	185062398	185062398	*RNF2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P99	p.A152S	ENSG00000121481	ENST00000367510	Transcript	missense_variant	benign(0.135)
chr1	203466135	203466135	*OPTC*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.S88C	ENSG00000188770	ENST00000367222	Transcript	missense_variant	possibly_damaging(0.497)
chr1	22150826	22150826	*HSPG2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.G4263E	ENSG00000142798	ENST00000374695	Transcript	missense_variant	probably_damaging(1)
chr1	228526070	228526070	*OBSCN*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P99	p.L6651Rfs*4	ENSG00000154358	ENST00000570156	Transcript	frameshift_variant	NA
chr1	22927164	22927164	*EPHA8*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.I800N	ENSG00000070886	ENST00000166244	Transcript	missense_variant	probably_damaging(0.998)
chr1	229568405	229568405	*ACTA1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P99	p.R118S	ENSG00000143632	ENST00000366684	Transcript	missense_variant	probably_damaging(0.997)
chr1	245862253	245862253	*KIF26B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.V2031D	ENSG00000162849	ENST00000407071	Transcript	missense_variant	unknown(0)
chr1	245927411	245927411	*SMYD3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.V373M	ENSG00000185420	ENST00000388985	Transcript	missense_variant	benign(0.013)
chr1	248004936	248004936	*OR11L1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.W88L	ENSG00000197591	ENST00000355784	Transcript	missense_variant	benign(0.008)
chr1	248309355	248309355	*OR2M5*	Missense_Mutation	.	SNP	G	G	T	rs201158893	shanshan_et_al_P99	p.R302S	ENSG00000162727	ENST00000366476	Transcript	missense_variant	benign(0.001)
chr1	40097227	40097227	*HEYL*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.R58C	ENSG00000163909	ENST00000372852	Transcript	missense_variant	probably_damaging(1)
chr1	45101780	45101780	*RNF220*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.W358R	ENSG00000187147	ENST00000355387	Transcript	missense_variant	probably_damaging(0.998)
chr1	52924039	52924039	*ZCCHC11*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.R1135T	ENSG00000134744	ENST00000257177	Transcript	missense_variant	possibly_damaging(0.708)
chr1	74670620	74670620	*FPGT*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P99	p.E297*	ENSG00000254685	ENST00000609362	Transcript	stop_gained	NA
chr10	115973299	115973299	*TDRD1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.E676K	ENSG00000095627	ENST00000251864	Transcript	missense_variant	probably_damaging(0.953)
chr10	115987852	115987852	*TDRD1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.N1169I	ENSG00000095627	ENST00000251864	Transcript	missense_variant	probably_damaging(0.991)
chr10	22676827	22676827	*SPAG6*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P99	p.I252L	ENSG00000077327	ENST00000376624	Transcript	missense_variant	benign(0.016)
chr10	63976895	63976895	*RTKN2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.L334F	ENSG00000182010	ENST00000373789	Transcript	missense_variant	probably_damaging(0.997)
chr10	70723092	70723092	*DDX21*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P99	p.H218R	ENSG00000165732	ENST00000354185	Transcript	missense_variant	benign(0.045)
chr11	130341136	130341136	*ADAMTS15*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.T646S	ENSG00000166106	ENST00000299164	Transcript	missense_variant	benign(0.023)
chr11	20122660	20122660	*NAV2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.G2179E	ENSG00000166833	ENST00000396087	Transcript	missense_variant	probably_damaging(0.999)
chr11	27114793	27114793	*BBOX1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.Y138F	ENSG00000129151	ENST00000263182	Transcript	missense_variant	benign(0.43)
chr11	57102046	57102046	*SSRP1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.Q44R	ENSG00000149136	ENST00000278412	Transcript	missense_variant	benign(0.09)
chr11	61630785	61630785	*FADS2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.T338S	ENSG00000134824	ENST00000278840	Transcript	missense_variant	possibly_damaging(0.474)
chr11	73074427	73074427	*ARHGEF17*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.S1725C	ENSG00000110237	ENST00000263674	Transcript	missense_variant	probably_damaging(0.997)
chr11	93435990	93435990	*KIAA1731*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.V1834A	ENSG00000166004	ENST00000325212	Transcript	missense_variant	benign(0.27)
chr12	100441357	100441357	*UHRF1BP1L*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P99	p.D1345Ifs*5	ENSG00000111647	ENST00000279907	Transcript	frameshift_variant	NA
chr12	109998867	109998867	*MMAB*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.V188L	ENSG00000139428	ENST00000545712	Transcript	missense_variant	possibly_damaging(0.616)
chr12	124298384	124298384	*DNAH10*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.S1117R	ENSG00000197653	ENST00000409039	Transcript	missense_variant	benign(0.006)
chr12	132426326	132426326	*PUS1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.Q345L	ENSG00000177192	ENST00000376649	Transcript	missense_variant	benign(0.065)
chr12	15800073	15800073	*EPS8*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.R519H	ENSG00000151491	ENST00000281172	Transcript	missense_variant	benign(0.004)
chr12	29936472	29936472	*TMTC1*	Nonsense_Mutation	.	SNP	C	C	T	rs112603144	shanshan_et_al_P99	p.W71*	ENSG00000133687	ENST00000539277	Transcript	stop_gained	NA
chr12	29936501	29936501	*TMTC1*	Missense_Mutation	.	SNP	C	C	T	rs764243334	shanshan_et_al_P99	p.D62N	ENSG00000133687	ENST00000539277	Transcript	missense_variant	benign(0.298)

chr12	67106338	67106338	*CHD4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.G206C	ENSG00000111642	ENST00000357008	Transcript	missense_variant	probably_damaging(0.995)
chr12	72343413	72343413	*TPH2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P99	p.D196Y	ENSG00000139287	ENST00000338850	Transcript	missense_variant	probably_damaging(0.981)
chr12	85449971	85449971	*LRRIQ1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P99	p.E467G	ENSG00000133640	ENST00000393217	Transcript	missense_variant	benign(0.114)
chr13	45978538	45978539	*SLC25A30*	Frame_Shift_Del	.	DEL	AG	AG	-	novel	shanshan_et_al_P99	p.L55Pfs*19	ENSG00000174032	ENST00000539591	Transcript	frameshift_variant	NA
chr15	29428579	29428579	*FAM189A1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P99	p.P306R	ENSG00000104059	ENST00000261275	Transcript	missense_variant	benign(0.403)
chr15	30379683	30379683	*GOLGA8J*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.X161_splice	ENSG00000179938	ENST00000567927	Transcript	splice_donor_variant	NA
chr15	50494759	50494759	*SLC27A2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.K255M	ENSG00000140284	ENST00000267842	Transcript	missense_variant	benign(0.102)
chr15	70960775	70960775	*UACA*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P99	p.S750Vfs*4	ENSG00000137831	ENST00000322954	Transcript	frameshift_variant	NA
chr16	11862261	11862261	*ZC3H7A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.T424S	ENSG00000122299	ENST00000396516	Transcript	missense_variant	benign(0.001)
chr16	23116833	23116833	*USP31*	Frame_Shift_Del	.	DEL	C	C	-	novel	shanshan_et_al_P99	p.V340Yfs*27	ENSG00000103404	ENST00000219689	Transcript	frameshift_variant	NA
chr16	23392021	23392021	*SCNN1B*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.Q608*	ENSG00000168447	ENST00000343070	Transcript	stop_gained	NA
chr16	23544080	23544080	*EARS2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.Q322L	ENSG00000103356	ENST00000449606	Transcript	missense_variant	probably_damaging(0.955)
chr16	29874177	29874177	*CDIPT*	Translation_Start_Site	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.M1?	ENSG00000103502	ENST00000219789	Transcript	initiator_codon_variant	possibly_damaging(0.578)
chr16	88779231	88779231	*CTU2*	Missense_Mutation	.	SNP	C	C	T	rs201058922	shanshan_et_al_P99	p.P219S	ENSG00000174177	ENST00000453996	Transcript	missense_variant	benign(0.001)
chr17	35641738	35641738	*ACACA*	Splice_Site	.	DEL	C	C	-	novel	shanshan_et_al_P99	p.X157_splice	ENSG00000132142	ENST00000353139	Transcript	splice_donor_variant	NA
chr17	37234265	37234265	*PLXDC1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.D363H	ENSG00000161381	ENST00000315392	Transcript	missense_variant	benign(0.237)
chr17	42745523	42745523	*C17orf104*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.S748R	ENSG00000180336	ENST00000409122	Transcript	missense_variant	probably_damaging(0.999)
chr17	43906946	43906946	*CRHR1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P99	p.G152R	ENSG00000120088	ENST00000398285	Transcript	missense_variant	benign(0.001)
chr17	44109017	44109017	*KANSL1*	Missense_Mutation	.	SNP	G	G	T	rs200719065	shanshan_et_al_P99	p.A1048E	ENSG00000120071	ENST00000262419	Transcript	missense_variant	benign(0.267)
chr17	45219658	45219658	*CDC27*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.E445Q	ENSG00000004897	ENST00000531206	Transcript	missense_variant	possibly_damaging(0.55)
chr17	45229185	45229185	*CDC27*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.G359R	ENSG00000004897	ENST00000531206	Transcript	missense_variant	benign(0.15)
chr17	56277584	56277584	*EPX*	Splice_Site	.	SNP	A	A	G	novel	shanshan_et_al_P99	p.X513_splice	ENSG00000121053	ENST00000225371	Transcript	splice_acceptor_variant	NA
chr17	76840227	76840227	*DNAH2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.L1977Q	ENSG00000183914	ENST00000572933	Transcript	missense_variant	probably_damaging(1)
chr17	79916821	79916821	*NOTUM*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.A175T	ENSG00000185269	ENST00000409678	Transcript	missense_variant	benign(0.416)
chr18	14791470	14791470	*ANKRD30B*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.T602S	ENSG00000180777	ENST00000358984	Transcript	missense_variant	benign(0.116)
chr18	18690847	18690847	*ROCK1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.T9A	ENSG00000067900	ENST00000399799	Transcript	missense_variant	benign(0)
chr18	22806182	22806182	*ZNF521*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.N567S	ENSG00000198795	ENST00000361524	Transcript	missense_variant	possibly_damaging(0.907)
chr18	23658119	23658119	*SS18*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.Q51L	ENSG00000141380	ENST00000415083	Transcript	missense_variant	possibly_damaging(0.816)
chr18	52912500	52912500	*ZBTB14*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P99	p.H319Q	ENSG00000198081	ENST00000357006	Transcript	missense_variant	probably_damaging(0.99)
chr18	54362409	54362409	*WDR7*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P99	p.G446A	ENSG00000091157	ENST00000254442	Transcript	missense_variant	possibly_damaging(0.705)
chr19	10428248	10428248	*RAVER1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.F718Y	ENSG00000161847	ENST00000293677	Transcript	missense_variant	probably_damaging(0.946)
chr19	12163615	12163615	*ZNF878*	Translation_Start_Site	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.M1?	ENSG00000257446	ENST00000547628	Transcript	initiator_codon_variant	benign(0.188)
chr19	15569464	15569464	*RASAL3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.P222L	ENSG00000105122	ENST00000343625	Transcript	missense_variant	benign(0.021)
chr19	18901419	18901419	*COMP*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.R57W	ENSG00000105664	ENST00000222271	Transcript	missense_variant	possibly_damaging(0.837)
chr19	21991512	21991512	*ZNF43*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.K443*	ENSG00000198521	ENST00000354959	Transcript	stop_gained	NA
chr19	33321530	33321530	*SLC7A9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.E487V	ENSG00000021488	ENST00000230664	Transcript	missense_variant	possibly_damaging(0.588)

chr19	37734526	37734526	*ZNF383*	Missense_Mutation	.	SNP	C	C	T	rs546518869	shanshan_et_al_P99	p.S463L	ENSG00000188283	ENST00000589413	Transcript	missense_variant	possibly_damaging(0.579)
chr19	38385310	38385310	*WDR87*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.S306C	ENSG00000171804	ENST00000303868	Transcript	missense_variant	possibly_damaging(0.894)
chr19	39056410	39056410	*RYR1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.G4479E	ENSG00000196218	ENST00000355596	Transcript	missense_variant	unknown(0)
chr19	41386147	41386147	*CYP2A7*	Missense_Mutation	.	SNP	C	C	T	rs143990356	shanshan_et_al_P99	p.A166T	ENSG00000198077	ENST00000301146	Transcript	missense_variant	benign(0.023)
chr19	49573943	49573943	*KCNA7*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.I250F	ENSG00000104848	ENST00000221444	Transcript	missense_variant	probably_damaging(0.999)
chr19	50949187	50949187	*MYBPC2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.Y395F	ENSG00000086967	ENST00000357701	Transcript	missense_variant	benign(0.053)
chr19	55872239	55872239	*FAM71E2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.T265S	ENSG00000180043	ENST00000424985	Transcript	missense_variant	benign(0.344)
chr19	58453032	58453032	*ZNF256*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.S382C	ENSG00000152454	ENST00000282308	Transcript	missense_variant	probably_damaging(0.956)
chr19	59151218	59151218	*CAPS*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P99	p.N147H	ENSG00000105519	ENST00000222125	Transcript	missense_variant	possibly_damaging(0.873)
chr19	65863639	65863639	*CD70*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.G82S	ENSG00000125726	ENST00000245903	Transcript	missense_variant	probably_damaging(0.982)
chr19	855775	855775	*ELANE*	Frame_Shift_Del	.	DEL	G	G	-	rs199659114	shanshan_et_al_P99	p.Q194Rfs*18	ENSG00000197561	ENST00000590230	Transcript	frameshift_variant	NA
chr2	131261429	131261429	*POTEI*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.G187E	ENSG00000196834	ENST00000451531	Transcript	missense_variant	benign(0.002)
chr2	131374401	131374401	*POTEJ*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.G150E	ENSG00000222038	ENST00000409602	Transcript	missense_variant	benign(0.002)
chr2	162696317	162696317	*SLC4A10*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.V99A	ENSG00000144290	ENST00000446997	Transcript	missense_variant	benign(0.007)
chr2	175337958	175337958	*GPR155*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.A199S	ENSG00000163328	ENST00000392552	Transcript	missense_variant	benign(0.01)
chr2	198367935	198367935	*HSPE1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P99	p.D87E	ENSG00000115541	ENST00000233893	Transcript	missense_variant	benign(0.029)
chr2	210843267	210843267	*UNC80*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P99	p.T2919A	ENSG00000144406	ENST00000439458	Transcript	missense_variant	probably_damaging(0.979)
chr2	39008842	39008842	*GEMIN6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.N104K	ENSG00000152147	ENST00000281950	Transcript	missense_variant	benign(0.006)
chr20	23016847	23016847	*SSTR4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.L243M	ENSG00000132671	ENST00000255008	Transcript	missense_variant	probably_damaging(0.953)
chr20	34241735	34241735	*RBM12*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.P504S	ENSG00000244462	ENST00000374114	Transcript	missense_variant	probably_damaging(0.998)
chr20	43600795	43600795	*STK4*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P99	p.E38*	ENSG00000101109	ENST00000372806	Transcript	stop_gained	NA
chr22	29966476	29966476	*NIPSNAP1*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P99	p.F48Lfs*32	ENSG00000184117	ENST00000216121	Transcript	frameshift_variant	NA
chr22	38039793	38039793	*SH3BP1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P99	p.R206G	ENSG00000100092	ENST00000357436	Transcript	missense_variant	benign(0.388)
chr22	42180353	42180353	*MEI1*	Missense_Mutation	.	SNP	C	C	T	rs190911941	shanshan_et_al_P99	p.T1033I	ENSG00000167077	ENST00000401548	Transcript	missense_variant	possibly_damaging(0.9)
chr3	128205103	128205103	*GATA2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.H113R	ENSG00000179348	ENST00000341105	Transcript	missense_variant	probably_damaging(0.921)
chr3	184003327	184003327	*ECE2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.R522C	ENSG00000145194	ENST00000402825	Transcript	missense_variant	probably_damaging(1)
chr3	48510523	48510523	*SHISA5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.P236S	ENSG00000164054	ENST00000296444	Transcript	missense_variant	possibly_damaging(0.857)
chr4	10567698	10567698	*CLNK*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.M76K	ENSG00000109684	ENST00000226951	Transcript	missense_variant	benign(0.001)
chr4	140441478	140441478	*SETD7*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.N239Y	ENSG00000145391	ENST00000274031	Transcript	missense_variant	benign(0.001)
chr4	190873347	190873347	*FRG1*	Missense_Mutation	.	SNP	A	A	G	rs730249948	shanshan_et_al_P99	p.E55G	ENSG00000109536	ENST00000226798	Transcript	missense_variant	possibly_damaging(0.466)
chr4	190883004	190883004	*FRG1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.H219Q	ENSG00000109536	ENST00000226798	Transcript	missense_variant	benign(0.034)
chr4	77268879	77268879	*SORCS2*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.X871_splice	ENSG00000184985	ENST00000507866	Transcript	splice_acceptor_variant	NA
chr5	111540117	111540117	*EPB41L4A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.P444L	ENSG00000129595	ENST00000261486	Transcript	missense_variant	benign(0.045)
chr5	139947454	139947454	*SLC35A4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.G234S	ENSG00000176087	ENST00000514199	Transcript	missense_variant	possibly_damaging(0.7)
chr5	145969766	145969766	*PPP2R2B*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.N362S	ENSG00000156475	ENST00000336640	Transcript	missense_variant	possibly_damaging(0.522)
chr5	161580363	161580363	*GABRG2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.L513F	ENSG00000113327	ENST00000414552	Transcript	missense_variant	probably_damaging(0.999)

chr5	26881470	26881470	*CDH9*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.F715L	ENSG00000113100	ENST00000231021	Transcript	missense_variant	probably_damaging(0.987)
chr5	26915890	26915890	*CDH9*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.Y124F	ENSG00000113100	ENST00000231021	Transcript	missense_variant	probably_damaging(0.992)
chr5	32010481	32010481	*PDZD2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P99	p.P434T	ENSG00000133401	ENST00000438447	Transcript	missense_variant	probably_damaging(0.92)
chr5	54404055	54404055	*GZMA*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.G154S	ENSG00000145649	ENST00000274306	Transcript	missense_variant	probably_damaging(0.999)
chr6	109802547	109802547	*ZBTB24*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.E228V	ENSG00000112365	ENST00000230122	Transcript	missense_variant	benign(0)
chr6	111587678	111587678	*KIAA1919*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.S305C	ENSG00000173214	ENST00000368847	Transcript	missense_variant	benign(0.156)
chr6	112462042	112462042	*LAMA4*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P99	p.F966V	ENSG00000112769	ENST00000230538	Transcript	missense_variant	benign(0.003)
chr6	127517012	127517012	*RSPO3*	Missense_Mutation	.	SNP	g	g	A	novel	shanshan_et_al_P99	p.E227K	ENSG00000146374	ENST00000356698	Transcript	missense_variant	benign(0.325)
chr6	151672199	151672199	*AKAP12*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P99	p.M891I	ENSG00000131016	ENST00000406676	Transcript	missense_variant	benign(0.003)
chr6	31712030	31712030	*MSH5*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P99	p.D201H	ENSG00000204410	ENST00000375703	Transcript	missense_variant	possibly_damaging(0.773)
chr7	134800350	134800350	*AGBL3*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P99	p.Q777*	ENSG00000146856	ENST00000436302	Transcript	stop_gained	NA
chr7	143748025	143748025	*OR2A5*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.F177L	ENSG00000221836	ENST00000408906	Transcript	missense_variant	probably_damaging(0.927)
chr7	151970859	151970859	*KMT2C*	Missense_Mutation	.	SNP	C	C	A	rs149992209	shanshan_et_al_P99	p.G315C	ENSG00000055609	ENST00000262189	Transcript	missense_variant	probably_damaging(1)
chr7	44747549	44747549	*OGDH*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P99	p.R1008H	ENSG00000105953	ENST00000222673	Transcript	missense_variant	benign(0.007)
chr7	44874131	44874131	*H2AFV*	Missense_Mutation	.	SNP	A	A	G	rs114398265	shanshan_et_al_P99	p.I119T	ENSG00000105968	ENST00000308153	Transcript	missense_variant	benign(0.002)
chr7	48311617	48311617	*ABCA13*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P99	p.P785R	ENSG00000179869	ENST00000435803	Transcript	missense_variant	benign(0.391)
chr9	111741564	111741564	*CTNNAL1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.Q366H	ENSG00000119326	ENST00000325551	Transcript	missense_variant	benign(0.008)
chr9	130482367	130482367	*TTC16*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P99	p.L146P	ENSG00000167094	ENST00000373289	Transcript	missense_variant	probably_damaging(0.992)
chr9	79318286	79318286	*PRUNE2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P99	p.L2748P	ENSG00000106772	ENST00000376718	Transcript	missense_variant	benign(0.263)
chrX	100808778	100808778	*ARMCX1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P99	p.S289C	ENSG00000126947	ENST00000372829	Transcript	missense_variant	benign(0.025)
chrX	129349898	129349898	*ZNF280C*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P99	p.T569S	ENSG00000056277	ENST00000370978	Transcript	missense_variant	benign(0.01)
chrX	37664381	37664381	*CYBB*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P99	p.Y425C	ENSG00000165168	ENST00000378588	Transcript	missense_variant	probably_damaging(0.996)
chr17	7577120	7577120	*TP53*	Missense_Mutation	.	SNP	C	C	T	rs28934576	shanshan_et_al_P99	p.R273H	ENSG00000141510	ENST00000269305	Transcript	missense_variant	probably_damaging(0.831)
chr1	27277241	27277241	*C1orf172*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P01	p.T349Kfs*17	ENSG00000175707	ENST00000320567	Transcript	frameshift_variant	NA
chr1	29606607	29606607	*PTPRU*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P01	p.I608V	ENSG00000060656	ENST00000345512	Transcript	missense_variant	probably_damaging(0.992)
chr10	76789012	76789012	*KAT6B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P01	p.C1477F	ENSG00000156650	ENST00000287239	Transcript	missense_variant	probably_damaging(0.996)
chr12	58113926	58113926	*OS9*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P01	p.R549G	ENSG00000135506	ENST00000315970	Transcript	missense_variant	benign(0.22)
chr13	100207882	100207882	*TM9SF2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P01	p.Y578C	ENSG00000125304	ENST00000376387	Transcript	missense_variant	probably_damaging(0.995)
chr13	31035512	31035512	*HMGB1*	Missense_Mutation	.	SNP	T	T	A	rs200836895	shanshan_et_al_P01	p.E210D	ENSG00000189403	ENST00000405805	Transcript	missense_variant	unknown(0)
chr13	38160960	38160960	*POSTN*	Missense_Mutation	.	SNP	G	G	T	rs144505887	shanshan_et_al_P01	p.Q238K	ENSG00000133110	ENST00000379747	Transcript	missense_variant	benign(0.441)
chr13	77720304	77720304	*MYCBP2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P01	p.P2356T	ENSG00000005810	ENST00000544440	Transcript	missense_variant	possibly_damaging(0.871)
chr14	90767602	90767602	*NRDE2*	Missense_Mutation	.	SNP	T	T	A	rs548710589	shanshan_et_al_P01	p.D509V	ENSG00000119720	ENST00000354366	Transcript	missense_variant	benign(0.251)
chr15	85406805	85406805	*ALPK3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P01	p.S1680N	ENSG00000136383	ENST00000258888	Transcript	missense_variant	probably_damaging(0.995)
chr17	45219672	45219672	*CDC27*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P01	p.S440Y	ENSG00000004897	ENST00000531206	Transcript	missense_variant	possibly_damaging(0.532)
chr19	17085966	17085966	*CPAMD8*	Missense_Mutation	.	SNP	G	G	A	rs374988485	shanshan_et_al_P01	p.R718C	ENSG00000160111	ENST00000443236	Transcript	missense_variant	probably_damaging(1)
chr2	61441650	61441650	*USP34*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P01	p.D2743H	ENSG00000115464	ENST00000398571	Transcript	missense_variant	probably_damaging(0.995)

chr3	143185925	143185925	*SLC9A9*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P01	p.V475I	ENSG00000181804	ENST00000316549	Transcript	missense_variant	benign(0.036)
chr4	37447784	37447784	*KIAA1239*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P01	p.L1392F	ENSG00000174145	ENST00000309447	Transcript	missense_variant	possibly_damaging(0.646)
chr5	41067320	41067320	*MROH2B*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P01	p.E31Q	ENSG00000171495	ENST00000399564	Transcript	missense_variant	probably_damaging(0.952)
chr6	152485458	152485458	*SYNE1*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P01	p.V7877G	ENSG00000131018	ENST00000367255	Transcript	missense_variant	benign(0.425)
chr7	26232191	26232191	*HNRNPA2B1*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P01	p.Y336C	ENSG00000122566	ENST00000354667	Transcript	missense_variant	probably_damaging(0.962)
chr7	38803062	38803062	*VPS41*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P01	p.D472V	ENSG00000006715	ENST00000310301	Transcript	missense_variant	probably_damaging(0.987)
chr8	141262967	141262968	*TRAPPC9*	Frame_Shift_Ins	.	INS	-	-	A	novel	shansha n_et_al_P01	p.L878Ffs*31	ENSG00000167632	ENST00000389328	Transcript	frameshift_variant	NA
chr1	152084657	152084658	*TCHH*	In_Frame_Ins	.	INS	-	-	CTC	rs558731460	shansha n_et_al_P02	p.E345dup	ENSG00000159450	ENST00000368804	Transcript	inframe_insertion	NA
chr10	73048440	73048440	*UNC5B*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P02	p.S339R	ENSG00000107731	ENST00000335350	Transcript	missense_variant	benign(0.271)
chr12	7045271	7045271	*ATN1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P02	p.G281S	ENSG00000111676	ENST00000356654	Transcript	missense_variant	probably_damaging(0.986)
chr19	12865756	12865756	*BEST2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P02	p.V183M	ENSG00000039987	ENST00000549706	Transcript	missense_variant	possibly_damaging(0.728)
chr19	2042446	2042446	*MKNK2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P02	p.T244P	ENSG00000099875	ENST00000250896	Transcript	missense_variant	benign(0.139)
chr19	38964116	38964116	*RYR1*	Missense_Mutation	.	SNP	C	C	T	rs377185497	shansha n_et_al_P02	p.R1289W	ENSG00000196218	ENST00000355596	Transcript	missense_variant	probably_damaging(0.999)
chr2	103003401	103003401	*IL18R1*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P02	p.N297T	ENSG00000115604	ENST00000409599	Transcript	missense_variant	benign(0.134)
chr20	62340201	62340201	*ZGPAT*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P02	p.V90G	ENSG00000197114	ENST00000328969	Transcript	missense_variant	benign(0.001)
chr5	137589838	137589838	*GFRA3*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P02	p.V266G	ENSG00000146013	ENST00000274721	Transcript	missense_variant	benign(0.284)
chr5	140794631	140794631	*PCDHGA10*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P02	p.V630G	ENSG00000253846	ENST00000398610	Transcript	missense_variant	possibly_damaging(0.771)
chr5	177576714	177576714	*NHP2*	Nonstop_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P02	p.*154Wext*51	ENSG00000145912	ENST00000274606	Transcript	stop_lost	NA
chr6	75884931	75884931	*COL12A1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P02	p.L845F	ENSG00000111799	ENST00000322507	Transcript	missense_variant	benign(0.038)
chr1	225521209	225521209	*DNAH14*	Splice_Site	.	SNP	G	G	C	novel	shansha n_et_al_P06	p.X3267_splice	ENSG00000185842	ENST00000430092	Transcript	splice_donor_variant	NA
chr10	12070765	12070765	*UPF2*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P06	p.Q375L	ENSG00000151461	ENST00000356352	Transcript	missense_variant	benign(0.173)
chr12	123481362	123481362	*PITPNM2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P06	p.Q523P	ENSG00000090975	ENST00000320201	Transcript	missense_variant	benign(0.312)
chr12	53647179	53647179	*MFSD5*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P06	p.V294G	ENSG00000182544	ENST00000534842	Transcript	missense_variant	possibly_damaging(0.828)
chr13	28854667	28854667	*PAN3*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P06	p.D770N	ENSG00000152520	ENST00000380958	Transcript	missense_variant	possibly_damaging(0.81)
chr14	105412138	105412138	*AHNAK2*	Missense_Mutation	.	SNP	A	A	G	rs200384326	shansha n_et_al_P06	p.L3217P	ENSG00000185567	ENST00000332344	Transcript	missense_variant	benign(0)
chr14	105412208	105412208	*AHNAK2*	Missense_Mutation	.	SNP	C	C	G	rs560055178	shansha n_et_al_P06	p.E3194Q	ENSG00000185567	ENST00000332344	Transcript	missense_variant	benign(0.001)
chr15	56126316	56126316	*NEDD4*	Missense_Mutation	.	SNP	C	C	A	rs370100375	shansha n_et_al_P06	p.D1131Y	ENSG00000069869	ENST00000338963	Transcript	missense_variant	probably_damaging(1)
chr16	19126645	19126645	*ITPRIPL2*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P06	p.T288P	ENSG00000205730	ENST00000381440	Transcript	missense_variant	benign(0.348)
chr17	45891195	45891195	*OSBPL7*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P06	p.C453G	ENSG00000006025	ENST00000007414	Transcript	missense_variant	benign(0.021)
chr19	17844026	17844026	*MAP1S*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P06	p.V938G	ENSG00000130479	ENST00000324096	Transcript	missense_variant	benign(0)
chr19	21991504	21991504	*ZNF43*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P06	p.N445K	ENSG00000198521	ENST00000354959	Transcript	missense_variant	benign(0.002)
chr4	39450080	39450080	*KLB*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P06	p.E970G	ENSG00000134962	ENST00000257408	Transcript	missense_variant	benign(0.14)
chr1	152186041	152186042	*HRNR*	Frame_Shift_Ins	.	INS	-	-	GG	novel	shansha n_et_al_P10	p.G2689Pfs*165	ENSG00000197915	ENST00000368801	Transcript	frameshift_variant	NA
chr1	179783089	179783089	*FAM163A*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P10	p.V90G	ENSG00000143340	ENST00000341785	Transcript	missense_variant	benign(0)
chr1	197397096	197397096	*CRB1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.V881I	ENSG00000134376	ENST00000367400	Transcript	missense_variant	possibly_damaging(0.695)
chr1	214832268	214832268	*CENPF*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P10	p.P3013R	ENSG00000117724	ENST00000366955	Transcript	missense_variant	probably_damaging(0.999)

chr1	27057766	27057766	*ARID1A*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P10	p.Q492*	ENSG00000117713	ENST00000324856	Transcript	stop_gained	NA
chr1	42776719	42776719	*FOXJ3*	Splice_Site	.	SNP	A	A	C	novel	shansha n_et_al_P10	NA	ENSG00000198815	ENST00000372572	Transcript	splice_donor_variant	NA
chr10	115986937	115986937	*TDRD1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P10	p.N1094K	ENSG00000095627	ENST00000251864	Transcript	missense_variant	possibly_damaging(0.859)
chr11	46341947	46341947	*CREB3L1*	Missense_Mutation	.	SNP	G	G	A	rs199553915	shansha n_et_al_P10	p.R464Q	ENSG00000157613	ENST00000529193	Transcript	missense_variant	benign(0)
chr11	66512322	66512322	*C11orf80*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P10	p.Y37D	ENSG00000173715	ENST00000360962	Transcript	missense_variant	possibly_damaging(0.683)
chr15	54916034	54916034	*UNC13C*	Frame_Shift_Del	.	DEL	T	T	-	novel	shansha n_et_al_P10	NA	ENSG00000137766	ENST00000260323	Transcript	frameshift_variant	NA
chr15	65553304	65553304	*PARP16*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.P251L	ENSG00000138617	ENST00000261888	Transcript	missense_variant	probably_damaging(1)
chr15	90321534	90321534	*MESP2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_P10	p.L388R	ENSG00000188095	ENST00000341735	Transcript	missense_variant	probably_damaging(0.994)
chr15	93595630	93595630	*RGMA*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.R88C	ENSG00000182175	ENST00000557301	Transcript	missense_variant	probably_damaging(0.999)
chr17	18188822	18188822	*TOP3A*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.T537I	ENSG00000177302	ENST00000321105	Transcript	missense_variant	probably_damaging(0.983)
chr17	35548072	35548072	*ACACA*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P10	p.D1521N	ENSG00000132142	ENST00000353139	Transcript	missense_variant	probably_damaging(0.982)
chr17	71394479	71394479	*PHF23*	Missense_Mutation	.	SNP	t	t	C	novel	shansha n_et_al_P10	p.E256G	ENSG00000040633	ENST00000320316	Transcript	missense_variant	benign(0.143)
chr17	73239608	73239608	*GGA3*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P10	p.I115S	ENSG00000125447	ENST00000245541	Transcript	missense_variant	probably_damaging(0.979)
chr17	73887396	73887396	*TRIM65*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P10	p.A340T	ENSG00000141569	ENST00000269383	Transcript	missense_variant	probably_damaging(1)
chr19	19756502	19756502	*ATP13A1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.S1153L	ENSG00000105726	ENST00000357324	Transcript	missense_variant	benign(0.003)
chr19	50138891	50138891	*RRAS*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.P200L	ENSG00000126458	ENST00000246792	Transcript	missense_variant	benign(0.071)
chr19	54313519	54313519	*NLRP12*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.A465V	ENSG00000142405	ENST00000324134	Transcript	missense_variant	probably_damaging(0.998)
chr19	54403899	54403899	*PRKCG*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.E491K	ENSG00000126583	ENST00000263431	Transcript	missense_variant	possibly_damaging(0.676)
chr2	162087595	162087595	*TANK*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P10	p.V212L	ENSG00000136560	ENST00000392749	Transcript	missense_variant	benign(0.391)
chr2	183731159	183731159	*FRZB*	Missense_Mutation	.	SNP	G	G	A	rs148198789	shansha n_et_al_P10	p.P41L	ENSG00000162998	ENST00000295113	Transcript	missense_variant	possibly_damaging(0.804)
chr20	57485829	57485829	*GNAS*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P10	p.N1020S	ENSG00000087460	ENST00000371100	Transcript	missense_variant	possibly_damaging(0.783)
chr21	31973533	31973533	*KRTAP2-1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P10	p.A32S	ENSG00000186924	ENST00000334680	Transcript	missense_variant	unknown(0)
chr3	12586867	12586867	*C3orf83*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P10	p.Q33K	ENSG00000225526	ENST00000564146	Transcript	missense_variant	benign(0.069)
chr4	101907 4	101907 4	*FGFRL1*	Missense_Mutation	.	SNP	a	a	T	novel	shansha n_et_al_P10	p.H485L	ENSG00000127418	ENST00000398484	Transcript	missense_variant	probably_damaging(0.99)
chr4	82392666	82392666	*SH3TC1*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P10	p.G1208R	ENSG00000125089	ENST00000245105	Transcript	missense_variant	probably_damaging(0.951)
chr6	126288034	126288034	*HINT3*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P10	p.N68I	ENSG00000111911	ENST00000229633	Transcript	missense_variant	possibly_damaging(0.905)
chr6	43274199	43274199	*CRIP3*	Nonsense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P10	p.E129*	ENSG00000146215	ENST00000372569	Transcript	stop_gained	NA
chr7	150269953	150269953	*GIMAP4*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P10	p.K265N	ENSG00000133574	ENST00000255945	Transcript	missense_variant	benign(0.006)
chr7	158540897	158540897	*ESYT2*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P10	p.D571E	ENSG00000117868	ENST00000251527	Transcript	missense_variant	benign(0.003)
chr7	96650088	96650088	*DLX5*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P10	p.L277S	ENSG00000105880	ENST00000222598	Transcript	missense_variant	probably_damaging(0.969)
chr8	59059801	59059801	*FAM110B*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P10	p.V338M	ENSG00000169122	ENST00000361488	Transcript	missense_variant	benign(0.254)
chr9	37441440	37441440	*ZBTB5*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P10	p.L370R	ENSG00000168795	ENST00000307750	Transcript	missense_variant	probably_damaging(0.998)
chr10	45487360	45487360	*RASSF4*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P100	p.Q272L	ENSG00000107551	ENST00000340258	Transcript	missense_variant	possibly_damaging(0.717)
chr11	20178750	20178750	*DBX1*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P100	p.S169P	ENSG00000109851	ENST00000227256	Transcript	missense_variant	benign(0.105)
chr13	76055659	76055659	*TBC1D4*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P100	p.V82G	ENSG00000136111	ENST00000377636	Transcript	missense_variant	benign(0.02)
chr16	568941	568941	*RAB11FIP3*	Splice_Site	.	SNP	A	A	G	novel	shansha n_et_al_P100	p.X547_splice	ENSG00000090565	ENST00000262305	Transcript	splice_acceptor_variant	NA

chr2	118735598	118735598	*CCDC93*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P100	p.G210V	ENSG00000125633	ENST00000376300	Transcript	missense_variant	benign(0.013)
chr2	164467311	164467311	*FIGN*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P100	p.T344K	ENSG00000182263	ENST00000333129	Transcript	missense_variant	benign(0.024)
chr2	169791787	169791787	*ABCB11*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P100	p.A988V	ENSG00000073734	ENST00000263817	Transcript	missense_variant	possibly_damaging(0.794)
chr4	145580881	145580881	*HHIP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P100	p.R241H	ENSG00000164161	ENST00000296575	Transcript	missense_variant	probably_damaging(0.989)
chr5	96315225	96315225	*LNPEP*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P100	p.T135S	ENSG00000113441	ENST00000231368	Transcript	missense_variant	possibly_damaging(0.908)
chr6	138583961	138583961	*KIAA1244*	Missense_Mutation	.	SNP	C	C	A	rs116919932	shanshan_et_al_P100	p.S447R	ENSG00000112379	ENST00000251691	Transcript	missense_variant	benign(0.008)
chr6	24528252	24528252	*ALDH5A1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P100	p.S414T	ENSG00000112294	ENST00000348925	Transcript	missense_variant	benign(0.019)
chr9	109734331	109734331	*ZNF462*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P100	p.H2158R	ENSG00000148143	ENST00000277225	Transcript	missense_variant	probably_damaging(0.989)
chr9	139357484	139357484	*SEC16A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P100	p.T1583M	ENSG00000148396	ENST00000313050	Transcript	missense_variant	probably_damaging(0.99)
chrX	123480532	123480532	*SH2D1A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P100	p.E14K	ENSG00000183918	ENST00000371139	Transcript	missense_variant	probably_damaging(0.998)
chr16	84270589	84270589	*KCNG4*	Frame_Shift_Del	.	DEL	T	T	-	rs371012252	shanshan_et_al_P101	p.K168Sfs*17	ENSG00000168418	ENST00000308251	Transcript	frameshift_variant	NA
chr2	202252434	202252434	*TRAK2*	Missense_Mutation	.	SNP	G	G	T	rs148327247	shanshan_et_al_P101	p.P563H	ENSG00000115993	ENST00000332624	Transcript	missense_variant	probably_damaging(0.999)
chr2	55825578	55825578	*SMEK2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P101	p.K299E	ENSG00000138041	ENST00000345102	Transcript	missense_variant	probably_damaging(0.986)
chr5	54647255	54647255	*KIAA0947*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P101	p.S1760P	ENSG00000164151	ENST00000296564	Transcript	missense_variant	probably_damaging(0.99)
chr7	42017246	42017246	*GLI3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P101	p.P575T	ENSG00000106571	ENST00000395925	Transcript	missense_variant	possibly_damaging(0.835)
chr1	153642663	153642663	*ILF2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P110	p.G17R	ENSG00000143621	ENST00000361891	Transcript	missense_variant	unknown(0)
chr1	167906157	167906157	*DCAF6*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P112	p.R3L	ENSG00000143164	ENST00000367840	Transcript	missense_variant	probably_damaging(0.979)
chr19	38746865	38746865	*PPP1R14A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P112	p.V39I	ENSG00000167641	ENST00000301242	Transcript	missense_variant	probably_damaging(0.928)
chr19	40903858	40903858	*PRX*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P112	p.P134H	ENSG00000105227	ENST00000324001	Transcript	missense_variant	probably_damaging(0.95)
chr20	32255308	32255308	*ACTL10*	Missense_Mutation	.	SNP	C	C	G	rs375925742	shanshan_et_al_P112	p.A2G	ENSG00000182584	ENST00000330271	Transcript	missense_variant	probably_damaging(1)
chr11	73022494	73022494	*ARHGEF17*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P115	p.D937E	ENSG00000110237	ENST00000263674	Transcript	missense_variant	benign(0.001)
chr14	77751890	77751890	*POMT2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P115	p.R473Q	ENSG00000009830	ENST00000261534	Transcript	missense_variant	benign(0.023)
chr16	67681793	67681793	*RLTPR*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P115	p.D335Y	ENSG00000159753	ENST00000334583	Transcript	missense_variant	possibly_damaging(0.707)
chr2	152289674	152289674	*RIF1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P115	p.T337A	ENSG00000080345	ENST00000243326	Transcript	missense_variant	possibly_damaging(0.799)
chr2	231775515	231775515	*GPR55*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P115	p.D55N	ENSG00000135898	ENST00000392040	Transcript	missense_variant	benign(0.008)
chr6	152738068	152738068	*SYNE1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P115	p.R1835H	ENSG00000131018	ENST00000367255	Transcript	missense_variant	benign(0.001)
chr8	57026165	57026165	*MOS*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P115	p.R126H	ENSG00000172680	ENST00000311923	Transcript	missense_variant	benign(0.036)
chr9	386353	386353	*DOCK8*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P115	p.R934Q	ENSG00000107099	ENST00000459981	Transcript	missense_variant	possibly_damaging(0.517)
chr1	202727610	202727610	*KDM5B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P116	p.G369D	ENSG00000117139	ENST00000367265	Transcript	missense_variant	probably_damaging(0.983)
chr13	47260045	47260045	*LRCH1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P116	p.V231L	ENSG00000136141	ENST00000389797	Transcript	missense_variant	possibly_damaging(0.477)
chr4	93278894	93278894	*USP17L24*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P116	p.Y335C	ENSG00000232264	ENST00000504481	Transcript	missense_variant	probably_damaging(1)
chr4	93512	93512	*USP17L28*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P116	p.G212R	ENSG00000231051	ENST00000504543	Transcript	missense_variant	probably_damaging(0.999)
chr5	76342219	76342219	*AGGF1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P116	p.S306R	ENSG00000164252	ENST00000312916	Transcript	missense_variant	benign(0.157)
chr7	102952707	102952707	*PMPCB*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P116	p.L487I	ENSG00000105819	ENST00000249269	Transcript	missense_variant	benign(0.049)
chr9	114090281	114090281	*OR2K2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P116	p.A145S	ENSG00000171133	ENST00000302681	Transcript	missense_variant	benign(0.364)
chr10	13164469	13164469	*OPTN*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P118	p.E288D	ENSG00000123240	ENST00000378748	Transcript	missense_variant	benign(0.071)

chr10	46342668	46342688	*AGAP4*	In_Frame_Del	.	DEL	GCTCCTGCCATCCTGTCCCCA	GCTCCTGCCATCCTGTCCCCA	-	novel	shanshan_et_al_P118	p.G37_A43del	ENSG00000188234	ENST00000448048	Transcript	inframe_deletion	NA
chr19	40834359	40834359	*C19orf47*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P118	p.V171M	ENSG00000160392	ENST00000582783	Transcript	missense_variant	probably_damaging(0.97)
chr21	46687568	46687568	*POFUT2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P118	p.E358V	ENSG00000186866	ENST00000349485	Transcript	missense_variant	benign(0.113)
chr5	140167794	140167794	*PCDHA1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P118	p.A640D	ENSG00000204970	ENST00000504120	Transcript	missense_variant	benign(0.144)
chr8	94767159	94767159	*TMEM67*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P118	p.G6A	ENSG00000164953	ENST00000453321	Transcript	missense_variant	benign(0.034)
chrX	50377499	50377499	*SHROOM4*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P118	p.Q525L	ENSG00000158352	ENST00000376020	Transcript	missense_variant	benign(0.374)
chr1	152282017	152282017	*FLG*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P139	p.T1782K	ENSG00000143631	ENST00000368799	Transcript	missense_variant	benign(0.403)
chr1	19528290	19528290	*UBR4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P139	p.H66Y	ENSG00000127481	ENST00000375254	Transcript	missense_variant	probably_damaging(0.977)
chr1	44402399	44402399	*ARTN*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P139	p.D217Y	ENSG00000117407	ENST00000414809	Transcript	missense_variant	probably_damaging(0.957)
chr1	66384479	66384479	*PDE4B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P139	p.T81M	ENSG00000184588	ENST00000329654	Transcript	missense_variant	benign(0.106)
chr13	95114363	95114363	*DCT*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P139	p.N315S	ENSG00000080166	ENST00000446125	Transcript	missense_variant	benign(0.016)
chr15	59064273	59064273	*FAM63B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P139	p.A227S	ENSG00000128923	ENST00000559228	Transcript	missense_variant	benign(0.033)
chr17	61396327	61396327	*TANC2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P139	p.A410V	ENSG00000170921	ENST00000424789	Transcript	missense_variant	benign(0.044)
chr19	40321395	40321395	*DYRK1B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P139	p.R31Q	ENSG00000105204	ENST00000593685	Transcript	missense_variant	benign(0.13)
chr19	42461207	42461207	*RABAC1*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P139	p.W144*	ENSG00000105404	ENST00000222008	Transcript	stop_gained	NA
chr2	202216087	202216087	*ALS2CR12*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P139	p.P14L	ENSG00000155749	ENST00000405148	Transcript	missense_variant	probably_damaging(0.976)
chr5	149669160	149669160	*CAMK2A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P139	p.T10M	ENSG00000070808	ENST00000398376	Transcript	missense_variant	benign(0.415)
chr5	150506042	150506042	*ANXA6*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P139	p.X326_splice	ENSG00000197043	ENST00000354546	Transcript	splice_acceptor_variant	NA
chr6	107391332	107391332	*BEND3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P139	p.A355S	ENSG00000178409	ENST00000429433	Transcript	missense_variant	benign(0)
chr7	129929507	129929507	*CPA2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P139	p.R394C	ENSG00000158516	ENST00000222481	Transcript	missense_variant	benign(0.017)
chr7	81593617	81593617	*CACNA2D1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P139	p.S878*	ENSG00000153956	ENST00000356860	Transcript	stop_gained	NA
chr9	34724008	34724008	*FAM205A*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P139	p.R1077C	ENSG00000205108	ENST00000378788	Transcript	missense_variant	benign(0)
chrX	47466554	47466554	*SYN1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P139	p.I141V	ENSG00000008056	ENST00000295987	Transcript	missense_variant	benign(0.09)
chrX	69282394	69282394	*OTUD6A*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P139	p.E7G	ENSG00000189401	ENST00000338352	Transcript	missense_variant	probably_damaging(0.986)
chr1	152277884	152277884	*FLG*	Missense_Mutation	.	SNP	T	T	G	rs145597576	shanshan_et_al_P142	p.S3160R	ENSG00000143631	ENST00000368799	Transcript	missense_variant	unknown(0)
chr1	226259113	226259113	*H3F3A*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P142	p.A115G	ENSG00000163041	ENST00000366813	Transcript	missense_variant	possibly_damaging(0.626)
chr11	18269516	18269516	*SAA2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P142	p.S15G	ENSG00000134339	ENST00000526900	Transcript	missense_variant	benign(0)
chr11	60718755	60718755	*SLC15A3*	Missense_Mutation	.	SNP	C	C	A	rs200982819	shanshan_et_al_P142	p.G90V	ENSG00000110446	ENST00000227880	Transcript	missense_variant	probably_damaging(0.927)
chr14	105173863	105173874	*INF2*	In_Frame_Del	.	DEL	CCCCACCCCCAC	CCCCACCCCCAC	-	rs573567814,rs3840831	shanshan_et_al_P142	p.P421_P424del	ENSG00000203485	ENST00000392634	Transcript	inframe_deletion	NA
chr16	20554582	20554582	*ACSM2B*	Missense_Mutation	.	SNP	T	T	G	rs142632912	shanshan_et_al_P142	p.E428D	ENSG00000066813	ENST00000329697	Transcript	missense_variant	benign(0)
chr17	40066498	40066498	*ACLY*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P142	p.E108*	ENSG00000131473	ENST00000352035	Transcript	stop_gained	NA
chr3	97888085	97888085	*OR5H15*	Missense_Mutation	.	SNP	C	C	T	rs62266800	shanshan_et_al_P142	p.T181I	ENSG00000233412	ENST00000356526	Transcript	missense_variant	benign(0)
chr4	190947544	190947544	*FRG2*	Missense_Mutation	.	SNP	G	G	C	rs143585119	shanshan_et_al_P142	p.T109R	ENSG00000205097	ENST00000378763	Transcript	missense_variant	benign(0.003)
chr4	89039366	89039366	*ABCG2*	Nonsense_Mutation	.	SNP	G	G	A	rs200190472	shanshan_et_al_P142	p.R246*	ENSG00000118777	ENST00000237612	Transcript	stop_gained	NA
chr7	99757853	99757853	*GAL3ST4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P142	p.G387S	ENSG00000197093	ENST00000360039	Transcript	missense_variant	benign(0.001)
chr16	25218898	25218898	*NTN3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P146	p.A66T	ENSG00000162068	ENST00000293973	Transcript	missense_variant	benign(0.022)

chr9	43915533	43915533	*CNTNAP3B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P146	p.G1206W	ENSG00000154529	ENST00000377564	Transcript	missense_variant	possibly_damaging(0.662)
chr10	33200967	33200967	*ITGB1*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P147	p.E519*	ENSG00000150093	ENST00000396033	Transcript	stop_gained	NA
chr16	49671974	49671974	*ZNF423*	Missense_Mutation	.	SNP	G	G	T	rs149688169	shanshan_et_al_P147	p.S363R	ENSG00000102935	ENST00000561648	Transcript	missense_variant	possibly_damaging(0.612)
chr19	1255559	1255559	*MIDN*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P147	p.C332F	ENSG00000167470	ENST00000300952	Transcript	missense_variant	benign(0.308)
chr3	48699115	48699115	*CELSR3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P147	p.A318D	ENSG00000008300	ENST00000164024	Transcript	missense_variant	possibly_damaging(0.878)
chr4	3444632	3444632	*HGFAC*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P147	p.Q97H	ENSG00000109758	ENST00000382774	Transcript	missense_variant	benign(0.178)
chr5	140768936	140768936	*PCDHGB4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P147	p.E495D	ENSG00000253953	ENST00000519479	Transcript	missense_variant	benign(0.097)
chr6	75832000	75832000	*DSP*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P147	p.L1902R	ENSG00000096696	ENST00000379802	Transcript	missense_variant	probably_damaging(0.998)
chr8	72987610	72987610	*TRPA1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P147	p.G12A	ENSG00000104321	ENST00000262209	Transcript	missense_variant	benign(0.07)
chrX	147919231	147919231	*AFF2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P147	p.Q383K	ENSG00000155966	ENST00000370460	Transcript	missense_variant	benign(0.001)
chr1	158054241	158054241	*KIRREL*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P18	p.G128C	ENSG00000183853	ENST00000359209	Transcript	missense_variant	possibly_damaging(0.813)
chr1	230468694	230468694	*PGBD5*	Missense_Mutation	.	SNP	C	C	T	rs370203975	shanshan_et_al_P18	p.R321Q	ENSG00000177614	ENST00000525115	Transcript	missense_variant	possibly_damaging(0.886)
chr1	35972610	35972610	*KIAA0319L*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P18	p.C90F	ENSG00000142687	ENST00000325722	Transcript	missense_variant	probably_damaging(0.999)
chr10	102763324	102763324	*LZTS2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P18	p.G157R	ENSG00000107816	ENST00000370220	Transcript	missense_variant	possibly_damaging(0.893)
chr10	115529543	115529543	*PLEKHS1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P18	p.E140*	ENSG00000148735	ENST00000369310	Transcript	stop_gained	NA
chr10	27702765	27702765	*PTCHD3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P18	p.W139R	ENSG00000182077	ENST00000438700	Transcript	missense_variant	probably_damaging(0.964)
chr11	29502387	29502387	*PHLDA2*	Frame_Shift_Ins	.	INS	-	-	G	novel	shanshan_et_al_P18	p.A121Rfs*75	ENSG00000181649	ENST00000314222	Transcript	frameshift_variant	NA
chr15	43045016	43045016	*TTBK2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P18	p.V810I	ENSG00000128881	ENST00000267890	Transcript	missense_variant	benign(0.021)
chr15	48533766	48533766	*SLC12A1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P18	p.V424F	ENSG00000074803	ENST00000396577	Transcript	missense_variant	possibly_damaging(0.602)
chr17	38176090	38176090	*MED24*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P18	p.C934F	ENSG00000008838	ENST00000394128	Transcript	missense_variant	possibly_damaging(0.837)
chr18	45556100	45556100	*ZBTB7C*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P18	p.H464P	ENSG00000184828	ENST00000588982	Transcript	missense_variant	benign(0.188)
chr19	58153454	58153454	*ZNF211*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P18	p.K599E	ENSG00000121417	ENST00000299871	Transcript	missense_variant	benign(0.022)
chr2	20405124	20405124	*SDC1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P18	p.N43S	ENSG00000115884	ENST00000381150	Transcript	missense_variant	benign(0.207)
chr2	220379792	220379792	*ASIC4*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P18	p.T243P	ENSG00000072182	ENST00000347842	Transcript	missense_variant	probably_damaging(0.999)
chr3	110912063	110912063	*PVRL3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P18	p.R434K	ENSG00000177707	ENST00000493615	Transcript	missense_variant	benign(0.002)
chr4	151000301	151000301	*DCLK2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P18	p.G41E	ENSG00000170390	ENST00000302176	Transcript	missense_variant	possibly_damaging(0.818)
chr4	26640392	26640392	*TBC1D19*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P18	p.X124_splice	ENSG00000109680	ENST00000264866	Transcript	splice_acceptor_variant	NA
chr4	92136433	92136433	*USP17L10*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P18	p.D421N	ENSG00000231396	ENST00000417945	Transcript	missense_variant	benign(0.084)
chr7	142569546	142569546	*TRPV6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P18	p.L698F	ENSG00000165125	ENST00000359396	Transcript	missense_variant	probably_damaging(0.918)
chr8	133044243	133044243	*OC90*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P18	p.P306S	ENSG00000258417	ENST00000603859	Transcript	missense_variant	benign(0.055)
chr9	98241284	98241284	*PTCH1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P18	p.E405K	ENSG00000185920	ENST00000331920	Transcript	missense_variant	benign(0.042)
chrX	41419081	41419081	*CASK*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P18	p.I563S	ENSG00000147044	ENST00000378166	Transcript	missense_variant	possibly_damaging(0.786)
chr1	141091888	141091888	*PRDM2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P19	p.R1633I	ENSG00000116731	ENST00000235372	Transcript	missense_variant	unknown(0)
chr1	160788066	160788066	*LY9*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P19	p.C467W	ENSG00000122224	ENST00000263285	Transcript	missense_variant	probably_damaging(0.936)
chr1	173186101	173186101	*ATP13A2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P19	p.L677M	ENSG00000159363	ENST00000326735	Transcript	missense_variant	probably_damaging(0.992)
chr1	85666633	85666633	*SYDE2*	Missense_Mutation	.	SNP	C	C	A	rs532518453	shanshan_et_al_P19	p.G16V	ENSG00000097096	ENST00000341460	Transcript	missense_variant	possibly_damaging(0.769)

chr10	49447708	49447708	*FRMPD2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P19	p.S243I	ENSG00000170324	ENST00000374201	Transcript	missense_variant	possibly_damaging(0.556)
chr10	93601080	93601080	*TNKS2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P19	p.Y572H	ENSG00000107854	ENST00000371627	Transcript	missense_variant	probably_damaging(0.963)
chr13	101997759	101997759	*NALCN*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P19	p.W219*	ENSG00000102452	ENST00000251127	Transcript	stop_gained	NA
chr15	51291348	51291348	*AP4E1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P19	p.E995V	ENSG00000081014	ENST00000261842	Transcript	missense_variant	possibly_damaging(0.589)
chr16	31434434	31434434	*ITGAD*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P19	p.X927_splice	ENSG00000156886	ENST00000389202	Transcript	splice_acceptor_variant	NA
chr17	76046626	76046626	*TNRC6C*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P19	p.G495W	ENSG00000078687	ENST00000335749	Transcript	missense_variant	probably_damaging(0.997)
chr19	11303946	11303946	*KANK2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P19	p.W270C	ENSG00000197256	ENST00000432929	Transcript	missense_variant	probably_damaging(0.999)
chr19	40480001	40480001	*ZBTB7A*	Missense_Mutation	.	SNP	g	g	T	novel	shanshan_et_al_P19	p.R502S	ENSG00000178951	ENST00000322357	Transcript	missense_variant	benign(0.256)
chr19	42796550	42796550	*CIC*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P19	p.S1036N	ENSG00000079432	ENST00000575354	Transcript	missense_variant	possibly_damaging(0.827)
chr19	45209076	45209076	*CEACAM16*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P19	p.C293F	ENSG00000213892	ENST00000587331	Transcript	missense_variant	probably_damaging(0.999)
chr2	198363406	198363406	*HSPD1*	Missense_Mutation	.	SNP	C	C	T	rs200514123	shanshan_et_al_P19	p.G56E	ENSG00000144381	ENST00000388968	Transcript	missense_variant	benign(0.327)
chr4	110454797	110454797	*SEC24B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P19	p.D1182N	ENSG00000138802	ENST00000265175	Transcript	missense_variant	benign(0.045)
chr5	33576716	33576716	*ADAMTS12*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P19	p.P1139S	ENSG00000151388	ENST00000504830	Transcript	missense_variant	benign(0.002)
chr5	43280469	43280469	*NIM1K*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P19	p.D317N	ENSG00000177453	ENST00000512796	Transcript	missense_variant	benign(0.013)
chr6	43039106	43039106	*KLC4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P19	p.V435L	ENSG00000137171	ENST00000259708	Transcript	missense_variant	benign(0.12)
chr8	145947892	145947892	*ZNF251*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P19	p.A385T	ENSG00000198169	ENST00000292562	Transcript	missense_variant	possibly_damaging(0.787)
chr9	101900207	101900207	*TGFBR1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P19	p.G214V	ENSG00000106799	ENST00000374994	Transcript	missense_variant	probably_damaging(1)
chr9	130438977	130438977	*STXBP1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P19	p.E435V	ENSG00000136854	ENST00000373302	Transcript	missense_variant	probably_damaging(0.92)
chr9	88650471	88650471	*GOLM1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P19	p.R276Q	ENSG00000135052	ENST00000388712	Transcript	missense_variant	benign(0)
chr1	167343383	167343383	*POU2F1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P24	p.Q147H	ENSG00000143190	ENST00000367866	Transcript	missense_variant	unknown(0)
chr13	35517088	35517088	*NBEA*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P24	p.E44G	ENSG00000172915	ENST00000400445	Transcript	missense_variant	benign(0.403)
chr14	70175653	70175653	*KIAA0247*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P24	p.E240K	ENSG00000100647	ENST00000342745	Transcript	missense_variant	benign(0.437)
chr17	76798561	76798561	*USP36*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P24	p.K956R	ENSG00000055483	ENST00000542802	Transcript	missense_variant	possibly_damaging(0.654)
chr19	1081739	1081739	*HMHA1*	Splice_Site	.	SNP	T	T	G	novel	shanshan_et_al_P24	p.X809_splice	ENSG00000180448	ENST00000539243	Transcript	splice_donor_variant	NA
chr19	8563760	8563760	*PRAM1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P24	p.P311Q	ENSG00000133246	ENST00000423345	Transcript	missense_variant	benign(0.003)
chr3	167000245	167000245	*ZBBX*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P24	p.L679I	ENSG00000169064	ENST00000455345	Transcript	missense_variant	possibly_damaging(0.629)
chr6	46661477	46661477	*TDRD6*	Missense_Mutation	.	SNP	C	C	T	rs147630987	shanshan_et_al_P24	p.P1871L	ENSG00000180113	ENST00000316081	Transcript	missense_variant	benign(0)
chr1	151789714	151789714	*RORC*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P25	p.S38L	ENSG00000143365	ENST00000318247	Transcript	missense_variant	probably_damaging(0.999)
chr1	155207299	155207299	*GBA*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P25	p.G278R	ENSG00000177628	ENST00000327247	Transcript	missense_variant	probably_damaging(1)
chr1	180155280	180155280	*QSOX1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.L327Q	ENSG00000116260	ENST00000367602	Transcript	missense_variant	probably_damaging(1)
chr1	225510522	225510522	*DNAH14*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.D3071E	ENSG00000185842	ENST00000430092	Transcript	missense_variant	benign(0.011)
chr1	24696306	24696306	*STPG1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P25	p.L199I	ENSG00000001460	ENST00000374409	Transcript	missense_variant	possibly_damaging(0.874)
chr1	36642400	36642400	*MAP7D1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P25	p.S446P	ENSG00000116871	ENST00000373151	Transcript	missense_variant	benign(0.033)
chr1	43779622	43779622	*TIE1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P25	p.T798P	ENSG00000066056	ENST00000372476	Transcript	missense_variant	probably_damaging(0.996)
chr10	118355796	118355796	*PNLIPRP1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P25	p.E179V	ENSG00000187021	ENST00000528052	Transcript	missense_variant	benign(0.386)
chr10	125447468	125447468	*GPR26*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P25	p.V269G	ENSG00000154478	ENST00000284674	Transcript	missense_variant	benign(0.012)

chr10	27323935	27323935	*ANKRD26*	Missense_Mutation	.	SNP	T	T	A	rs370833466	shanshan_et_al_P25	p.Q1148H	ENSG00000107890	ENST00000376087	Transcript	missense_variant	probably_damaging(0.992)
chr11	124619754	124619754	*VSIG2*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P25	p.S146R	ENSG00000019102	ENST00000326621	Transcript	missense_variant	possibly_damaging(0.807)
chr12	1702845	1702845	*FBXL14*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P25	p.I130V	ENSG00000171823	ENST00000339235	Transcript	missense_variant	benign(0.058)
chr12	56881811	56881811	*GLS2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P25	p.L31P	ENSG00000135423	ENST00000311966	Transcript	missense_variant	benign(0.039)
chr12	80190697	80190697	*PPP1R12A*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P25	p.S776R	ENSG00000058272	ENST00000450142	Transcript	missense_variant	benign(0.056)
chr13	36413270	36413270	*DCLK1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P25	p.K360R	ENSG00000133083	ENST00000255448	Transcript	missense_variant	possibly_damaging(0.486)
chr13	42875574	42875574	*AKAP11*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P25	p.K898*	ENSG00000023516	ENST00000025301	Transcript	stop_gained	NA
chr14	33292150	33292150	*AKAP6*	Missense_Mutation	.	SNP	A	A	T	rs148686760	shanshan_et_al_P25	p.I1711F	ENSG00000151320	ENST00000280979	Transcript	missense_variant	benign(0.221)
chr14	60039437	60039437	*CCDC175*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P25	p.I113T	ENSG00000151838	ENST00000537690	Transcript	missense_variant	possibly_damaging(0.713)
chr14	64892794	64892794	*MTHFD1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P25	p.E337D	ENSG00000100714	ENST00000216605	Transcript	missense_variant	possibly_damaging(0.569)
chr15	73889572	73889572	*NPTN*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.Q77L	ENSG00000156642	ENST00000345330	Transcript	missense_variant	probably_damaging(0.953)
chr16	20966288	20966288	*DNAH3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P25	p.R3640W	ENSG00000158486	ENST00000261383	Transcript	missense_variant	probably_damaging(0.995)
chr16	23122282	23122282	*RNPS1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P25	p.G225R	ENSG00000205937	ENST00000565678	Transcript	missense_variant	probably_damaging(1)
chr17	71192869	71192869	*COG1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P25	p.V180G	ENSG00000166685	ENST00000299886	Transcript	missense_variant	possibly_damaging(0.493)
chr19	14857770	14857770	*EMR2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P25	p.W677R	ENSG00000127507	ENST00000315576	Transcript	missense_variant	probably_damaging(0.996)
chr19	22155369	22155369	*ZNF208*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P25	p.H823N	ENSG00000160321	ENST00000397126	Transcript	missense_variant	unknown(0)
chr19	22234389	22234389	*DOT1L*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P25	p.T1184P	ENSG00000104885	ENST00000398665	Transcript	missense_variant	probably_damaging(0.994)
chr19	33953923	33953923	*PEPD*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P25	p.M217V	ENSG00000124299	ENST00000244137	Transcript	missense_variant	benign(0.211)
chr19	35940719	35940719	*FFAR2*	Missense_Mutation	.	SNP	C	C	T	rs531566827	shanshan_et_al_P25	p.R35W	ENSG00000126262	ENST00000599180	Transcript	missense_variant	benign(0.411)
chr19	47207853	47207853	*PRKD2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.S189C	ENSG00000105287	ENST00000438867	Transcript	missense_variant	probably_damaging(0.934)
chr2	131220756	131220756	*POTEI*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P25	p.W954L	ENSG00000196834	ENST00000451531	Transcript	missense_variant	benign(0.25)
chr2	222428585	222428585	*EPHA4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P25	p.R230Q	ENSG00000116106	ENST00000281821	Transcript	missense_variant	possibly_damaging(0.885)
chr20	34797475	34797475	*EPB41L1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.S578R	ENSG00000088367	ENST00000338074	Transcript	missense_variant	benign(0.007)
chr22	28497242	28497242	*TTC28*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P25	p.R1112*	ENSG00000100154	ENST00000397906	Transcript	stop_gained	NA
chr3	194175080	194175080	*ATP13A3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P25	p.I224M	ENSG00000133657	ENST00000439040	Transcript	missense_variant	benign(0.201)
chr3	56694964	56694964	*FAM208A*	Missense_Mutation	.	SNP	T	T	A	rs368441103	shanshan_et_al_P25	p.E414D	ENSG00000163946	ENST00000493960	Transcript	missense_variant	benign(0.03)
chr4	38696488	38696488	*KLF3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P25	p.K273E	ENSG00000109787	ENST00000261438	Transcript	missense_variant	probably_damaging(0.999)
chr4	86898839	86898839	*ARHGAP24*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P25	p.M308T	ENSG00000138639	ENST00000395184	Transcript	missense_variant	probably_damaging(0.914)
chr5	129520215	129520215	*CHSY3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P25	p.R460S	ENSG00000198108	ENST00000305031	Transcript	missense_variant	benign(0.201)
chr5	43174777	43174777	*ZNF131*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P25	p.I438V	ENSG00000172262	ENST00000509634	Transcript	missense_variant	benign(0.038)
chr5	54405971	54405971	*GZMA*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P25	p.H250Q	ENSG00000145649	ENST00000274306	Transcript	missense_variant	possibly_damaging(0.521)
chr5	96101005	96101005	*CAST*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P25	p.N630K	ENSG00000153113	ENST00000395812	Transcript	missense_variant	possibly_damaging(0.757)
chr6	102250231	102250231	*GRIK2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P25	p.R374T	ENSG00000164418	ENST00000421544	Transcript	missense_variant	probably_damaging(0.999)
chr6	119669686	119669686	*MAN1A1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P25	p.V182G	ENSG00000111885	ENST00000368468	Transcript	missense_variant	benign(0.02)
chr6	41711073	41711073	*PGC*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.Q128L	ENSG00000096088	ENST00000373025	Transcript	missense_variant	benign(0.053)
chr6	49754093	49754093	*PGK2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.M270L	ENSG00000170950	ENST00000304801	Transcript	missense_variant	benign(0.007)

chr7	114619578	114619578	*MDFIC*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P25	p.P188S	ENSG00000135272	ENST00000257724	Transcript	missense_variant	probably_damaging(0.999)
chr7	120969739	120969739	*WNT16*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P25	p.E72*	ENSG00000002745	ENST00000222462	Transcript	stop_gained	NA
chr7	27140590	27140590	*HOXA2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P25	p.N296Y	ENSG00000105996	ENST00000222718	Transcript	missense_variant	possibly_damaging(0.73)
chr7	37890314	37890314	*NME8*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P25	p.D59Y	ENSG00000086288	ENST00000199447	Transcript	missense_variant	probably_damaging(0.996)
chr7	86823251	86823251	*DMTF1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P25	p.M621V	ENSG00000135164	ENST00000394703	Transcript	missense_variant	benign(0)
chr7	94037519	94037519	*COL1A2*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P25	p.R222*	ENSG00000164692	ENST00000297268	Transcript	stop_gained	NA
chr7	99128817	99128817	*ZKSCAN5*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P25	p.K489Q	ENSG00000196652	ENST00000394170	Transcript	missense_variant	benign(0.075)
chr8	61178570	61178570	*CA8*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P25	p.E111K	ENSG00000178538	ENST00000317995	Transcript	missense_variant	probably_damaging(0.931)
chr9	113168980	113168980	*SVEP1*	Missense_Mutation	.	SNP	T	T	C	rs375511563	shanshan_et_al_P25	p.H2967R	ENSG00000165124	ENST00000401783	Transcript	missense_variant	benign(0.013)
chrX	100746860	100746860	*ARMCX4*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P25	p.Y1095C	ENSG00000196440	ENST00000423738	Transcript	missense_variant	probably_damaging(0.967)
chrX	128692691	128692691	*OCRL*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P25	p.H174R	ENSG00000122126	ENST00000371113	Transcript	missense_variant	benign(0)
chrX	148037544	148037544	*AFF2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P25	p.E657Q	ENSG00000155966	ENST00000370460	Transcript	missense_variant	benign(0.266)
chrX	71802268	71802268	*PHKA1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P25	p.D1160H	ENSG00000067177	ENST00000373542	Transcript	missense_variant	benign(0.064)
chr1	228468251	228468251	*OBSCN*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P35	p.K3080Q	ENSG00000154358	ENST00000570156	Transcript	missense_variant	probably_damaging(0.969)
chr12	58240172	58240172	*CTDSP2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P35	p.L16Q	ENSG00000175215	ENST00000398073	Transcript	missense_variant	benign(0.001)
chr14	61924300	61924300	*PRKCH*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P35	p.D394V	ENSG00000027075	ENST00000332981	Transcript	missense_variant	probably_damaging(0.977)
chr16	17202790	17202790	*XYLT1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P35	p.L881Q	ENSG00000103489	ENST00000261381	Transcript	missense_variant	possibly_damaging(0.726)
chr17	38975150	38975150	*KRT10*	Frame_Shift_Del	.	DEL	GC	GC	-	novel	shanshan_et_al_P35	p.S546Ifs*34	ENSG00000186395	ENST00000269576	Transcript	frameshift_variant	NA
chr17	48773448	48773448	*ANKRD40*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P35	p.I339M	ENSG00000154945	ENST00000285243	Transcript	missense_variant	benign(0.195)
chr17	77518594	77518594	*KDM6B*	In_Frame_Del	.	DEL	CACCAC	CACCAC	-	rs377654044	shanshan_et_al_P35	p.T753_T754del	ENSG00000132510	ENST00000254846	Transcript	inframe_deletion	NA
chr2	241685218	241685218	*KIF1A*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P35	p.R1104P	ENSG00000130294	ENST00000498729	Transcript	missense_variant	probably_damaging(1)
chr3	12616309	12616309	*MKRN2*	Missense_Mutation	.	SNP	G	G	A	rs199957684	shanshan_et_al_P35	p.E221K	ENSG00000075975	ENST00000170447	Transcript	missense_variant	probably_damaging(0.929)
chr3	183953050	183953050	*VWA5B2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P35	p.T352I	ENSG00000145198	ENST00000426955	Transcript	missense_variant	probably_damaging(0.969)
chr3	38674672	38674672	*SCN5A*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P35	p.R43*	ENSG00000183873	ENST00000413689	Transcript	stop_gained	NA
chr4	87696336	87696336	*PTPN13*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P35	p.D1846N	ENSG00000163629	ENST00000436978	Transcript	missense_variant	probably_damaging(1)
chr5	110712615	110712615	*CAMK4*	Missense_Mutation	.	SNP	G	G	A	rs374581815	shanshan_et_al_P35	p.V121I	ENSG00000152495	ENST00000282356	Transcript	missense_variant	possibly_damaging(0.529)
chr5	36036066	36036066	*UGT3A2*	Missense_Mutation	.	SNP	C	C	T	rs61729693	shanshan_et_al_P35	p.A436T	ENSG00000168671	ENST00000282507	Transcript	missense_variant	probably_damaging(0.998)
chr5	77845332	77845332	*ADCY2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P35	p.F813L	ENSG00000078295	ENST00000338316	Transcript	missense_variant	benign(0.061)
chr6	74528152	74528152	*CD109*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P35	p.V1318A	ENSG00000156535	ENST00000287097	Transcript	missense_variant	possibly_damaging(0.633)
chr10	75549538	75549538	*ZSWIM8*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P39	p.L232M	ENSG00000214655	ENST00000398706	Transcript	missense_variant	probably_damaging(0.994)
chr12	49825	49825	*KDM5A*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P39	p.A2G	ENSG00000073614	ENST00000399788	Transcript	missense_variant	benign(0.009)
chr16	2098068	2098068	*TSC2*	Splice_Site	.	SNP	T	T	G	novel	shanshan_et_al_P39	NA	ENSG00000103197	ENST00000219476	Transcript	splice_donor_variant	NA
chr19	22267878	22267878	*DOT1L*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P39	p.G1423V	ENSG00000104885	ENST00000398665	Transcript	missense_variant	probably_damaging(0.999)
chr4	92230533	92230533	*USP17L12*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P39	p.R392S	ENSG00000227551	ENST00000415041	Transcript	missense_variant	benign(0.004)
chr1	150039960	150039960	*VPS45*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P48	p.E16K	ENSG00000136631	ENST00000369130	Transcript	missense_variant	benign(0.017)
chr1	155448157	155448157	*ASH1L*	Missense_Mutation	.	SNP	T	T	C	rs138098710	shanshan_et_al_P48	p.M1502V	ENSG00000116539	ENST00000392403	Transcript	missense_variant	benign(0.013)

chr1	16353256	16353256	*CLCNKA*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_ P48	p.A214G	ENSG00000186510	ENST00000331433	Transcript	missense_variant	benign(0)
chr1	169356403	169356403	*BLZF1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_ P48	p.E396K	ENSG00000117475	ENST00000367808	Transcript	missense_variant	benign(0.371)
chr1	169509601	169509601	*F5*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P48	p.N1576S	ENSG00000198734	ENST00000367797	Transcript	missense_variant	benign(0.03)
chr1	224318274	224318274	*FBXO28*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_ P48	p.Q123P	ENSG00000143756	ENST00000366862	Transcript	missense_variant	possibly_damaging(0.497)
chr1	225195220	225195220	*DNAH14*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_ P48	p.S361A	ENSG00000185842	ENST00000400952	Transcript	missense_variant	benign(0.048)
chr1	231471924	231471924	*EXOC8*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_ P48	p.K523T	ENSG00000116903	ENST00000360394	Transcript	missense_variant	benign(0.07)
chr1	247875463	247875463	*OR6F1*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_ P48	p.A199P	ENSG00000169214	ENST00000302084	Transcript	missense_variant	possibly_damaging(0.555)
chr1	248128836	248128836	*OR2AK2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_ P48	p.T68I	ENSG00000187080	ENST00000366480	Transcript	missense_variant	benign(0.009)
chr10	22045653	22045653	*DNAJC1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_ P48	p.V543D	ENSG00000136770	ENST00000376980	Transcript	missense_variant	unknown(0)
chr10	93619301	93619301	*TNKS2*	Missense_Mutation	.	SNP	T	T	G	novel	shansha n_et_al_ P48	p.I1059M	ENSG00000107854	ENST00000371627	Transcript	missense_variant	possibly_damaging(0.651)
chr11	71238639	71238639	*KRTAP5-7*	Missense_Mutation	.	SNP	A	A	G	rs199903176	shansha n_et_al_ P48	p.Y98C	ENSG00000244411	ENST00000398536	Transcript	missense_variant	unknown(0)
chr12	26784800	26784800	*ITPR2*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P48	p.Q978R	ENSG00000123104	ENST00000381340	Transcript	missense_variant	possibly_damaging(0.806)
chr13	31035512	31035512	*HMGB1*	Missense_Mutation	.	SNP	T	T	A	rs200836895	shansha n_et_al_ P48	p.E210D	ENSG00000189403	ENST00000405805	Transcript	missense_variant	unknown(0)
chr16	30748863	30748863	*SRCAP*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_ P48	p.P2501R	ENSG00000080603	ENST00000262518	Transcript	missense_variant	unknown(0)
chr17	39254149	39254149	*KRTAP4-8*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_ P48	p.T63S	ENSG00000204880	ENST00000333822	Transcript	missense_variant	unknown(0)
chr19	42911506	42911506	*LIPE*	Missense_Mutation	.	SNP	C	C	T	rs368796207	shansha n_et_al_ P48	p.G653S	ENSG00000079435	ENST00000244289	Transcript	missense_variant	probably_damaging(0.999)
chr19	45867689	45867689	*ERCC2*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_ P48	p.H237Q	ENSG00000104884	ENST00000391945	Transcript	missense_variant	probably_damaging(0.992)
chr2	97808515	97808515	*ANKRD36*	Missense_Mutation	.	SNP	G	G	A	rs201265245	shansha n_et_al_ P48	p.E282K	ENSG00000135976	ENST00000420699	Transcript	missense_variant	benign(0.292)
chr20	33222436	33222436	*PIGU*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_ P48	p.I151N	ENSG00000101464	ENST00000374820	Transcript	missense_variant	possibly_damaging(0.714)
chr20	411016	411016	*RBCK1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_ P48	p.G492D	ENSG00000125826	ENST00000356286	Transcript	missense_variant	probably_damaging(1)
chr3	196921348	196921348	*DLG1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_ P48	p.E144V	ENSG00000075711	ENST00000346964	Transcript	missense_variant	benign(0.038)
chr3	97888085	97888085	*OR5H15*	Missense_Mutation	.	SNP	C	C	T	rs62266800	shansha n_et_al_ P48	p.T181I	ENSG00000233412	ENST00000355656	Transcript	missense_variant	benign(0)
chr4	13603468	13603468	*BOD1L1*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_ P48	p.S1686G	ENSG00000038219	ENST00000407378	Transcript	missense_variant	probably_damaging(0.997)
chr4	187084640	187084640	*FAM149A*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_ P48	p.R299K	ENSG00000109794	ENST00000227065	Transcript	missense_variant	possibly_damaging(0.688)
chr6	44221265	44221265	*HSP90AB1*	Missense_Mutation	.	SNP	C	C	A	rs200104342	shansha n_et_al_ P48	p.A702D	ENSG00000096384	ENST00000371554	Transcript	missense_variant	benign(0.039)
chr8	28232938	28232938	*CSMD1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_ P48	p.K3093N	ENSG00000183117	ENST00000537824	Transcript	missense_variant	possibly_damaging(0.562)
chr8	81897558	81897558	*PAG1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_ P48	p.T110I	ENSG00000076641	ENST00000220597	Transcript	missense_variant	probably_damaging(0.923)
chrX	48762221	48762221	*SLC35A2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_ P48	p.P322L	ENSG00000102100	ENST00000247138	Transcript	missense_variant	benign(0.006)
chrX	70443741	70443741	*GJB1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_ P48	p.S62C	ENSG00000169562	ENST00000374022	Transcript	missense_variant	probably_damaging(0.973)
chrY	24315260	24315260	*RBMY1F*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_ P48	p.S400A	ENSG00000169800	ENST00000303766	Transcript	missense_variant	benign(0.001)
chr1	164761941	164761941	*PBX1*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_ P50	p.Q159R	ENSG00000185630	ENST00000420696	Transcript	missense_variant	possibly_damaging(0.593)
chr1	236433273	236433273	*ERO1LB*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_ P50	p.C42R	ENSG00000086619	ENST00000354619	Transcript	missense_variant	probably_damaging(0.999)
chr10	105233196	105233196	*CALHM3*	Missense_Mutation	.	SNP	A	A	G	rs112393722	shansha n_et_al_ P50	p.L270P	ENSG00000183128	ENST00000369783	Transcript	missense_variant	benign(0)
chr11	1605983	1605983	*KRTAP5-1*	Missense_Mutation	.	SNP	G	G	C	rs590071202	shansha n_et_al_ P50	p.A166G	ENSG00000205869	ENST00000382171	Transcript	missense_variant	unknown(0)
chr12	58121327	58121327	*AGAP2*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_ P50	p.C966R	ENSG00000135439	ENST00000547588	Transcript	missense_variant	probably_damaging(0.996)
chr13	99555311	99555311	*DOCK9*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_ P50	p.G364E	ENSG00000088387	ENST00000376460	Transcript	missense_variant	probably_damaging(1)

chr19	39058446	39058446	*RYR1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P50	p.E4516D	ENSG00000196218	ENST00000359596	Transcript	missense_variant	unknown(0)
chr2	10059883	10059883	*TAF1B*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P50	p.E500G	ENSG00000115750	ENST00000263663	Transcript	missense_variant	benign(0.055)
chr22	21133604	21133604	*SERPIND1*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P50	p.K2*	ENSG00000099937	ENST00000215727	Transcript	stop_gained	NA
chr3	98251631	98251631	*GPR15*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P50	p.V252F	ENSG00000154165	ENST00000284311	Transcript	missense_variant	benign(0.003)
chr8	113323360	113323360	*CSMD3*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P50	p.G2578*	ENSG00000164796	ENST00000297405	Transcript	stop_gained	NA
chr8	141745351	141745351	*PTK2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P50	p.S677C	ENSG00000169398	ENST00000340930	Transcript	missense_variant	possibly_damaging(0.483)
chrX	70361781	70361781	*MED12*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P50	p.A2153T	ENSG00000184634	ENST00000374080	Transcript	missense_variant	unknown(0)
chr1	114522991	114522991	*OLFML3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.H51L	ENSG00000116774	ENST00000320334	Transcript	missense_variant	benign(0.003)
chr1	226026499	226026499	*EPHX1*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P52	p.H170R	ENSG00000143819	ENST00000366837	Transcript	missense_variant	benign(0.062)
chr15	41509343	41509343	*EXD1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.L13Q	ENSG00000178997	ENST00000314992	Transcript	missense_variant	probably_damaging(0.955)
chr15	73996270	73996270	*CD276*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.E335V	ENSG00000103855	ENST00000318443	Transcript	missense_variant	probably_damaging(0.988)
chr17	37566514	37566514	*MED1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P52	p.A654S	ENSG00000125686	ENST00000300651	Transcript	missense_variant	benign(0.007)
chr17	78188451	78188451	*SGSH*	Missense_Mutation	.	SNP	G	G	C	rs535751912	shanshan_et_al_P52	p.L157V	ENSG00000181523	ENST00000326317	Transcript	missense_variant	benign(0.03)
chr19	14164812	14164812	*PALM3*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P52	p.G543R	ENSG00000187867	ENST00000340790	Transcript	missense_variant	benign(0.023)
chr19	32959683	32959683	*DPY19L3*	Missense_Mutation	.	SNP	A	A	T	rs200092939	shanshan_et_al_P52	p.Y554F	ENSG00000178904	ENST00000342179	Transcript	missense_variant	possibly_damaging(0.722)
chr19	56423504	56423504	*NLRP13*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P52	p.S560Y	ENSG00000173572	ENST00000342929	Transcript	missense_variant	possibly_damaging(0.459)
chr2	130930883	130930883	*SMPD4*	Missense_Mutation	.	SNP	T	T	C	rs374584781	shanshan_et_al_P52	p.Y144C	ENSG00000136699	ENST00000409031	Transcript	missense_variant	probably_damaging(0.966)
chr2	160732148	160732148	*LY75*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P52	p.P594L	ENSG00000054219	ENST00000554112	Transcript	missense_variant	probably_damaging(0.992)
chr2	168726411	168726411	*B3GALT1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P52	p.W288R	ENSG00000172318	ENST00000392690	Transcript	missense_variant	benign(0.007)
chr2	206884550	206884550	*INO80D*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P52	p.R440W	ENSG00000114933	ENST00000403263	Transcript	missense_variant	benign(0.321)
chr2	212248411	212248411	*ERBB4*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P52	p.S1286P	ENSG00000178568	ENST00000342788	Transcript	missense_variant	possibly_damaging(0.685)
chr20	47261025	47261025	*PREX1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P52	p.S1175R	ENSG00000124126	ENST00000371941	Transcript	missense_variant	probably_damaging(0.939)
chr3	44839427	44839427	*KIF15*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.R359S	ENSG00000163808	ENST00000326047	Transcript	missense_variant	probably_damaging(0.999)
chr5	137212 42	137212 42	*DNAH5*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.L4049Q	ENSG00000039139	ENST00000265104	Transcript	missense_variant	probably_damaging(0.928)
chr5	33984538	33984538	*SLC45A2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P52	p.V51L	ENSG00000164175	ENST00000296589	Transcript	missense_variant	possibly_damaging(0.889)
chr6	34825597	34825597	*UHRF1BP1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.Y557F	ENSG00000065060	ENST00000192788	Transcript	missense_variant	possibly_damaging(0.652)
chr6	38548105	38548105	*BTBD9*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P52	p.G308V	ENSG00000183826	ENST00000481247	Transcript	missense_variant	unknown(0)
chr7	91706293	91706293	*AKAP9*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.E2246V	ENSG00000127914	ENST00000356239	Transcript	missense_variant	probably_damaging(0.999)
chr8	82356823	82356823	*PMP2*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.L87Q	ENSG00000147588	ENST00000256103	Transcript	missense_variant	probably_damaging(0.927)
chrX	135488023	135488023	*GPR112*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P52	p.M2943L	ENSG00000156920	ENST00000394143	Transcript	missense_variant	benign(0)
chrX	138699712	138699712	*MCF2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P52	p.Q380L	ENSG00000101977	ENST00000519895	Transcript	missense_variant	possibly_damaging(0.576)
chrX	44703875	44703875	*DUSP21*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P52	p.V166E	ENSG00000189037	ENST00000339042	Transcript	missense_variant	benign(0.421)
chr1	156498302	156498302	*IQGAP3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P53	p.H1558Y	ENSG00000183856	ENST00000361170	Transcript	missense_variant	benign(0.278)
chr1	164646 59	164646 60	*EPHA2*	Frame_Shift_Ins	.	INS	-	-	A	novel	shanshan_et_al_P53	p.Y334Lfs*47	ENSG00000142627	ENST00000358432	Transcript	frameshift_variant	NA
chr1	197111506	197111506	*ASPM*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P53	p.K626E	ENSG00000066279	ENST00000367409	Transcript	missense_variant	benign(0.298)
chr1	216497627	216497627	*USH2A*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P53	p.E404A	ENSG00000042781	ENST00000307340	Transcript	missense_variant	benign(0.002)

chr1	27105550	27105550	*ARID1A*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P53	p.R1721*	ENSG00000117713	ENST00000324856	Transcript	stop_gained	NA
chr1	63789511	63789511	*FOXD3*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P53	p.L261R	ENSG00000187140	ENST00000371116	Transcript	missense_variant	unknown(0)
chr10	135438998	135438998	*FRG2B*	Missense_Mutation	.	SNP	G	G	T	rs200937977	shanshan_et_al_P53	p.R148S	ENSG00000225899	ENST00000425520	Transcript	missense_variant	benign(0)
chr10	136560040	136560040	*PRPF18*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P53	p.S249L	ENSG00000165630	ENST00000378572	Transcript	missense_variant	possibly_damaging(0.622)
chr10	88676986	88676986	*BMPR1A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P53	p.K257N	ENSG00000107779	ENST00000372037	Transcript	missense_variant	benign(0.078)
chr11	119210481	119210481	*C1QTNF5*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P53	p.C98G	ENSG00000223953	ENST00000445041	Transcript	missense_variant	probably_damaging(0.997)
chr12	112318261	112318261	*MAPKAPK5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P53	p.A197V	ENSG00000089022	ENST00000551404	Transcript	missense_variant	probably_damaging(0.954)
chr12	132393312	132393312	*ULK1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P53	p.S147F	ENSG00000177169	ENST00000321867	Transcript	missense_variant	possibly_damaging(0.887)
chr12	41967566	41967566	*PDZRN4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P53	p.M995I	ENSG00000165966	ENST00000402685	Transcript	missense_variant	probably_damaging(0.958)
chr12	51458232	51458233	*CSRNP2*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P53	p.T310Nfs*10	ENSG00000110925	ENST00000228515	Transcript	frameshift_variant	NA
chr14	21897454	21897454	*CHD8*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P53	p.Q295P	ENSG00000100888	ENST00000399982	Transcript	missense_variant	benign(0.001)
chr16	16291888	16291888	*ABCC6*	Missense_Mutation	.	SNP	T	T	C	rs142007498	shanshan_et_al_P53	p.Y443C	ENSG00000091262	ENST00000205557	Transcript	missense_variant	possibly_damaging(0.895)
chr16	30680920	30680920	*FBRS*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P53	p.P966R	ENSG00000156860	ENST00000356166	Transcript	missense_variant	unknown(0)
chr17	5436190	5436190	*NLRP1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P53	p.T1083M	ENSG00000091592	ENST00000572272	Transcript	missense_variant	benign(0.284)
chr17	54969228	54969228	*TRIM25*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P53	p.R576W	ENSG00000121060	ENST00000316881	Transcript	missense_variant	probably_damaging(0.999)
chr17	57951937	57951937	*TUBD1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P53	p.L299F	ENSG00000108423	ENST00000325752	Transcript	missense_variant	probably_damaging(0.932)
chr19	14066781	14066781	*DCAF15*	Missense_Mutation	.	SNP	G	G	T	rs369880054	shanshan_et_al_P53	p.V142L	ENSG00000132017	ENST00000254337	Transcript	missense_variant	possibly_damaging(0.578)
chr19	16612312	16612312	*C19orf44*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P53	p.G237S	ENSG00000105072	ENST00000221671	Transcript	missense_variant	probably_damaging(0.933)
chr19	36360590	36360590	*APLP1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P53	p.A57S	ENSG00000105290	ENST00000221891	Transcript	missense_variant	probably_damaging(0.998)
chr2	22637824 9	22637824 9	*NYAP2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P53	p.D128E	ENSG00000144460	ENST00000272907	Transcript	missense_variant	benign(0.031)
chr2	75118019	75118019	*HK2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P53	p.A902V	ENSG00000159399	ENST00000290573	Transcript	missense_variant	possibly_damaging(0.524)
chr4	1806099	1806099	*FGFR3*	Missense_Mutation	.	SNP	A	A	G	rs121913485	shanshan_et_al_P53	p.Y375C	ENSG00000068078	ENST00000340107	Transcript	missense_variant	possibly_damaging(0.882)
chr6	78632903	78632903	*MEI4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P53	p.T333I	ENSG00000269964	ENST00000602452	Transcript	missense_variant	benign(0.005)
chr9	22006092	22006092	*CDKN2B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P53	p.A104E	ENSG00000147883	ENST00000276925	Transcript	missense_variant	probably_damaging(0.997)
chrX	53224432	53224432	*KDM5C*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P53	p.S1094Y	ENSG00000126012	ENST00000375401	Transcript	missense_variant	probably_damaging(1)
chr1	27092812	27092812	*ARID1A*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P56	p.G945*	ENSG00000117713	ENST00000324856	Transcript	stop_gained	NA
chr1	64515434	64515434	*ROR1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P56	p.C79R	ENSG00000185483	ENST00000371079	Transcript	missense_variant	probably_damaging(1)
chr10	54031200	54031200	*PRKG1*	Missense_Mutation	.	SNP	C	C	T	rs147351459	shanshan_et_al_P56	p.R422C	ENSG00000185532	ENST00000373980	Transcript	missense_variant	benign(0.008)
chr11	26660711	26660711	*ANO3*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P56	p.L688F	ENSG00000134343	ENST00000256737	Transcript	missense_variant	probably_damaging(1)
chr13	24874584	24874584	*SPATA13*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P56	p.A1210V	ENSG00000182957	ENST00000424834	Transcript	missense_variant	possibly_damaging(0.621)
chr13	75886884	75886884	*TBC1D4*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P56	p.M791I	ENSG00000136111	ENST00000377636	Transcript	missense_variant	probably_damaging(0.989)
chr14	10100535 8	10100535 8	*BEGAIN*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P56	p.R244W	ENSG00000183092	ENST00000443071	Transcript	missense_variant	probably_damaging(0.997)
chr2	16287530 5	16287530 5	*DPP4*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P56	p.E452*	ENSG00000197635	ENST00000360534	Transcript	stop_gained	NA
chr3	48463868	48463868	*PLXNB1*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P56	p.V431F	ENSG00000164050	ENST00000358536	Transcript	missense_variant	probably_damaging(0.994)
chr7	12903706 1	12903706 1	*AHCYL2*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P56	p.X241_splice	ENSG00000158467	ENST00000325006	Transcript	splice_acceptor_variant	NA
chr8	77766065	77766065	*ZFHX4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P56	p.R2303Q	ENSG00000091656	ENST00000521891	Transcript	missense_variant	possibly_damaging(0.608)

chr10	102765470	102765470	*LZTS2*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P60	p.E442*	ENSG00000107816	ENST00000370220	Transcript	stop_gained	NA
chr12	29936562	29936562	*TMTC1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P60	p.Y41*	ENSG00000133687	ENST00000539277	Transcript	stop_gained	NA
chr16	61761054	61761054	*CDH8*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P60	p.P494T	ENSG00000150394	ENST00000577390	Transcript	missense_variant	possibly_damaging(0.879)
chr18	95938401	95938401	*PPP4R1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P60	p.L74V	ENSG00000154845	ENST00000400556	Transcript	missense_variant	probably_damaging(0.997)
chr19	57641113	57641113	*USP29*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P60	p.V357D	ENSG00000131864	ENST00000254181	Transcript	missense_variant	benign(0.265)
chr4	56212724	56212724	*SRD5A3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P60	p.R74I	ENSG00000128039	ENST00000264228	Transcript	missense_variant	probably_damaging(0.962)
chr8	123985481	123985481	*ZHX2*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P60	NA	ENSG00000178764	ENST00000314393	Transcript	splice_acceptor_variant	NA
chr15	75652935	75652935	*MAN2C1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P61	p.H519N	ENSG00000140400	ENST00000565683	Transcript	missense_variant	probably_damaging(0.984)
chr16	22546903	22546903	*NPIPB5*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P61	p.G867R	ENSG00000243716	ENST00000424340	Transcript	missense_variant	benign(0.007)
chr17	73239555	73239555	*SPEM1*	Nonsense_Mutation	.	SNP	C	C	T	rs201288589	shanshan_et_al_P61	p.R52*	ENSG00000181323	ENST00000323675	Transcript	stop_gained	NA
chr17	77525342	77525343	*KDM6B*	In_Frame_Del	.	DEL	CAGAAGGAGCAT	CAGAAGGAGCAT	-	rs547582872	shanshan_et_al_P61	p.Q976_H979del	ENSG00000132510	ENST00000254846	Transcript	inframe_deletion	NA
chr7	92902016	92902016	*CCDC132*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P61	p.Q258*	ENSG00000004766	ENST00000305866	Transcript	stop_gained	NA
chrX	38145763	38145763	*RPGR*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P61	p.E830G	ENSG00000156313	ENST00000378505	Transcript	missense_variant	unknown(0)
chr1	151679994	151679994	*CELF3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P64	p.T254I	ENSG00000159409	ENST00000290583	Transcript	missense_variant	possibly_damaging(0.664)
chr1	156641644	156641644	*NES*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.P779H	ENSG00000132688	ENST00000368223	Transcript	missense_variant	possibly_damaging(0.847)
chr1	209788657	209788657	*LAMB3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P64	p.H1160Y	ENSG00000196878	ENST00000391911	Transcript	missense_variant	benign(0.002)
chr1	48231758	48231758	*TRABD2B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P64	p.P457L	ENSG00000269113	ENST00000606738	Transcript	missense_variant	benign(0.002)
chr1	52498475	52498475	*KTI12*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P64	p.R320H	ENSG00000198841	ENST00000371614	Transcript	missense_variant	probably_damaging(0.978)
chr10	95275289	95275289	*CEP55*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P64	p.Q219L	ENSG00000138180	ENST00000371485	Transcript	missense_variant	benign(0.102)
chr12	29936562	29936562	*TMTC1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.Y41*	ENSG00000133687	ENST00000539277	Transcript	stop_gained	NA
chr12	56725444	56725444	*ANO2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P64	p.R973L	ENSG00000047617	ENST00000327087	Transcript	missense_variant	unknown(0)
chr17	27042493	27042493	*RAB34*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P64	p.A195S	ENSG00000109113	ENST00000447716	Transcript	missense_variant	benign(0.023)
chr17	73753544	73753544	*ITGB4*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P64	p.T1793P	ENSG00000132470	ENST00000200181	Transcript	missense_variant	benign(0.011)
chr18	28970783	28970783	*DSG4*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.E228*	ENSG00000175065	ENST00000359747	Transcript	stop_gained	NA
chr19	18775476	18775476	*ABHD17A*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P64	p.P274R	ENSG00000129968	ENST00000250974	Transcript	missense_variant	possibly_damaging(0.767)
chr2	212576833	212576833	*ERBB4*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P64	p.F356L	ENSG00000178568	ENST00000342788	Transcript	missense_variant	probably_damaging(0.995)
chr2	233899657	233899657	*NEU2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.D345Y	ENSG00000115488	ENST00000233840	Transcript	missense_variant	probably_damaging(0.992)
chr3	75790810	75790811	*ZNF717*	Frame_Shift_Ins	.	INS	-	-	T	novel	shanshan_et_al_P64	p.L46Pfs*24	ENSG00000227124	ENST00000422325	Transcript	frameshift_variant	NA
chr4	119659414	119659414	*SEC24D*	Splice_Site	.	SNP	A	A	T	novel	shanshan_et_al_P64	p.X832_splice	ENSG00000150961	ENST00000280551	Transcript	splice_donor_variant	NA
chr4	130023842	130023842	*C4orf33*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.G26V	ENSG00000151470	ENST00000281146	Transcript	missense_variant	benign(0.045)
chr5	60825973	60825973	*ZSWIM6*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.M644I	ENSG00000130449	ENST00000252744	Transcript	missense_variant	benign(0.037)
chr7	103180757	103180757	*RELN*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P64	p.G2273S	ENSG00000189056	ENST00000428762	Transcript	missense_variant	probably_damaging(0.999)
chr7	116423410	116423410	*MET*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P64	p.M1247L	ENSG00000105976	ENST00000318493	Transcript	missense_variant	benign(0.011)
chr7	64168481	64168481	*ZNF107*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P64	p.I600R	ENSG00000196247	ENST00000395391	Transcript	missense_variant	benign(0.012)
chr7	64168486	64168486	*ZNF107*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P64	p.Y602H	ENSG00000196247	ENST00000395391	Transcript	missense_variant	benign(0.012)
chr8	113246675	113246675	*CSMD3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P64	p.M3553I	ENSG00000164796	ENST00000297405	Transcript	missense_variant	benign(0.002)

chr9	125239745	125239745	*OR1J1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.A154E	ENSG00000136834	ENST00000259357	Transcript	missense_variant	possibly_damaging(0.898)
chr9	43915533	43915533	*CNTNAP3B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P64	p.G1206W	ENSG00000154529	ENST00000377564	Transcript	missense_variant	possibly_damaging(0.662)
chrX	16669136	16669136	*S100G*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P64	p.T3A	ENSG00000169906	ENST00000380200	Transcript	missense_variant	benign(0)
chr19	55086435	55086435	*LILRA2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P67	p.A197G	ENSG00000239998	ENST00000251377	Transcript	missense_variant	benign(0)
chr19	55086447	55086447	*LILRA2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P67	p.N201S	ENSG00000239998	ENST00000251377	Transcript	missense_variant	benign(0)
chr2	33747102	33747102	*RASGRP3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P67	p.H150R	ENSG00000152689	ENST00000403687	Transcript	missense_variant	probably_damaging(0.998)
chr1	228459745	228459745	*OBSCN*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P69	p.Q1937K	ENSG00000154358	ENST00000570156	Transcript	missense_variant	probably_damaging(0.97)
chr1	65309803	65309803	*JAK1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P69	p.L783F	ENSG00000162434	ENST00000342505	Transcript	missense_variant	probably_damaging(0.997)
chr10	120353658	120353658	*PRLHR*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P69	p.S367C	ENSG00000119973	ENST00000239032	Transcript	missense_variant	possibly_damaging(0.705)
chr12	45810530	45810530	*ANO6*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P69	p.A708V	ENSG00000177119	ENST00000423947	Transcript	missense_variant	probably_damaging(1)
chr14	102467512	102467512	*DYNC1H1*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P69	p.E1406*	ENSG00000197102	ENST00000360184	Transcript	stop_gained	NA
chr18	56587556	56587556	*ZNF532*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P69	p.H679Q	ENSG00000074657	ENST00000336078	Transcript	missense_variant	probably_damaging(0.976)
chr2	61713084	61713084	*XPO1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P69	p.F776C	ENSG00000082898	ENST00000401558	Transcript	missense_variant	probably_damaging(0.999)
chr3	172474804	172474804	*ECT2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P69	p.S112L	ENSG00000114346	ENST00000392692	Transcript	missense_variant	benign(0.211)
chr9	84045336	84045336	*PTPRD*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P69	NA	ENSG00000153707	ENST00000381196	Transcript	splice_donor_variant	NA
chrX	107979388	107979388	*IRS4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P69	p.R63W	ENSG00000133124	ENST00000372129	Transcript	missense_variant	probably_damaging(0.998)
chr1	16999828	16999828	*FAM231A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.R111W	ENSG00000237847	ENST00000434336	Transcript	missense_variant	benign(0)
chr1	22657408 3	22657408 3	*PARP1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.D260N	ENSG00000143799	ENST00000366794	Transcript	missense_variant	benign(0.13)
chr11	7642253	7642253	*PPFIBP2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P70	p.T236A	ENSG00000166387	ENST00000299492	Transcript	missense_variant	possibly_damaging(0.759)
chr12	108986087	108986087	*TMEM119*	Missense_Mutation	.	SNP	C	C	T	rs539667542	shanshan_et_al_P70	p.A25T	ENSG00000183160	ENST00000392806	Transcript	missense_variant	possibly_damaging(0.648)
chr12	79689895	79689895	*SYT1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P70	p.M174R	ENSG00000067715	ENST00000261205	Transcript	missense_variant	benign(0.006)
chr13	32914434	32914434	*BRCA2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.A1981V	ENSG00000139618	ENST00000544455	Transcript	missense_variant	probably_damaging(1)
chr14	101349285	101349285	*RTL1*	Missense_Mutation	.	SNP	G	G	A	rs373195780	shanshan_et_al_P70	p.A614V	ENSG00000254656	ENST00000534062	Transcript	missense_variant	benign(0.01)
chr15	59500001	59500001	*LDHAL6B*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P70	p.Y288N	ENSG00000171989	ENST00000307144	Transcript	missense_variant	probably_damaging(0.996)
chr16	16387533	16387533	*NOMO3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P70	p.A1157T	ENSG00000103226	ENST00000399336	Transcript	missense_variant	benign(0.013)
chr16	18512317	18512317	*NOMO2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.A1157T	ENSG00000185164	ENST00000381474	Transcript	missense_variant	benign(0.013)
chr16	23200705	23200705	*SCNN1G*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.R111C	ENSG00000166828	ENST00000300061	Transcript	missense_variant	possibly_damaging(0.788)
chr16	48175175	48175175	*ABCC12*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.R122H	ENSG00000140798	ENST00000311303	Transcript	missense_variant	benign(0.127)
chr16	69170708	69170708	*CIRH1A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.A90V	ENSG00000141076	ENST00000314423	Transcript	missense_variant	benign(0.074)
chr17	263553	263553	*C17orf97*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P70	p.P307T	ENSG00000187624	ENST00000360127	Transcript	missense_variant	benign(0)
chr2	71576596	71576596	*ZNF638*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.P171L	ENSG00000075292	ENST00000409544	Transcript	missense_variant	probably_damaging(0.999)
chr20	47688903	47688903	*CSE1L*	Frame_Shift_Del	.	DEL	AT	AT	-	novel	shanshan_et_al_P70	p.D283Efs*26	ENSG00000124207	ENST00000262982	Transcript	frameshift_variant	NA
chr21	30410695	30410695	*USP16*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P70	p.E226*	ENSG00000156256	ENST00000334352	Transcript	stop_gained	NA
chr22	19344435	19344435	*HIRA*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P70	p.A792S	ENSG00000100084	ENST00000263208	Transcript	missense_variant	benign(0.061)
chr22	38204131	38204131	*GCAT*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P70	p.R53C	ENSG00000100116	ENST00000323205	Transcript	missense_variant	benign(0.009)
chr3	45972616	45972616	*FYCO1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P70	p.S1400T	ENSG00000163820	ENST00000296137	Transcript	missense_variant	probably_damaging(0.997)

chr4	189061115	189061115	*TRIML1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P70	p.H135N	ENSG00000184108	ENST00000332517	Transcript	missense_variant	benign(0.01)
chr5	154396819	154396819	*KIF4B*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P70	p.Q1134K	ENSG00000226650	ENST00000435029	Transcript	missense_variant	benign(0.001)
chr5	169101307	169101307	*DOCK2*	Frame_Shift_Del	.	DEL	A	A	-	novel	shansha n_et_al_P70	p.K111Rfs*10	ENSG00000134516	ENST00000256935	Transcript	frameshift_variant	NA
chr5	176004723	176004723	*CDHR2*	Missense_Mutation	.	SNP	C	C	T	rs200908807	shansha n_et_al_P70	p.T479M	ENSG00000074276	ENST00000510636	Transcript	missense_variant	possibly_damaging(0.879)
chr6	25653642	25653642	*SCGN*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P70	p.A39T	ENSG00000079689	ENST00000377961	Transcript	missense_variant	benign(0.044)
chr6	31324628	31324628	*HLA-B*	Missense_Mutation	.	SNP	G	G	T	rs151341114	shansha n_et_al_P70	p.F60L	ENSG00000234745	ENST00000412585	Transcript	missense_variant	probably_damaging(0.995)
chr6	32009879	32009879	*TNXB*	Missense_Mutation	.	SNP	C	C	T	rs376281266	shansha n_et_al_P70	p.E556K	ENSG00000168477	ENST00000451343	Transcript	missense_variant	probably_damaging(0.974)
chr7	127014776	127014776	*ZNF800*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P70	p.P205R	ENSG00000048405	ENST00000393313	Transcript	missense_variant	benign(0.083)
chr8	113529433	113529433	*CSMD3*	Missense_Mutation	.	SNP	C	C	T	rs138068999	shansha n_et_al_P70	p.R1529H	ENSG00000164796	ENST00000297405	Transcript	missense_variant	probably_damaging(0.993)
chr9	35674185	35674185	*CA9*	Missense_Mutation	.	SNP	C	C	T	rs113670057	shansha n_et_al_P70	p.P77S	ENSG00000107159	ENST00000378357	Transcript	missense_variant	possibly_damaging(0.641)
chrX	105011452	105011452	*IL1RAPL2*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P70	p.G620A	ENSG00000189108	ENST00000372582	Transcript	missense_variant	benign(0.005)
chrX	105970265	105970265	*RNF128*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P70	p.A41G	ENSG00000133135	ENST00000255499	Transcript	missense_variant	benign(0.063)
chrX	53112240	53112240	*TSPYL2*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P70	p.R187T	ENSG00000184205	ENST00000375442	Transcript	missense_variant	benign(0.057)
chrX	70523144	70523144	*ITGB1BP2*	Missense_Mutation	.	SNP	A	A	C	novel	shansha n_et_al_P70	p.N117T	ENSG00000147166	ENST00000373829	Transcript	missense_variant	benign(0.039)
chr1	12921443	12921443	*PRAMEF2*	Missense_Mutation	.	SNP	T	T	C	rs201306561	shansha n_et_al_P74	p.Y412H	ENSG00000120952	ENST00000240189	Transcript	missense_variant	benign(0.005)
chr1	13448489	13448489	*PRAMEF13*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P74	p.Y329F	ENSG00000204495	ENST00000376132	Transcript	missense_variant	benign(0.003)
chr1	19415467	19415467	*UBR4*	Frame_Shift_Del	.	DEL	A	A	-	novel	shansha n_et_al_P74	p.I4740Lfs*38	ENSG00000127481	ENST00000375254	Transcript	frameshift_variant	NA
chr10	102763480	102763480	*LZTS2*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P74	p.A209T	ENSG00000107816	ENST00000370220	Transcript	missense_variant	benign(0.004)
chr10	115336953	115336953	*HABP2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P74	p.L126F	ENSG00000148702	ENST00000351270	Transcript	missense_variant	probably_damaging(0.969)
chr10	135233650	135233650	*RP11-108K14.8*	Missense_Mutation	.	SNP	C	C	T	rs201924847	shansha n_et_al_P74	p.P334L	ENSG00000254536	ENST00000468317	Transcript	missense_variant	benign(0.002)
chr11	113269863	113269863	*ANKK1*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P74	p.Q391L	ENSG00000170209	ENST00000303941	Transcript	missense_variant	benign(0.201)
chr11	5411452	5411452	*OR51M1*	Missense_Mutation	.	SNP	G	G	A	rs372583895	shansha n_et_al_P74	p.R275H	ENSG00000184698	ENST00000328611	Transcript	missense_variant	probably_damaging(0.944)
chr12	74592223	74592223	*ACSM4*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P74	p.R99Q	ENSG00000215009	ENST00000399422	Transcript	missense_variant	benign(0.073)
chr14	65252602	65252602	*SPTB*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P74	p.F1210S	ENSG00000070182	ENST00000389722	Transcript	missense_variant	benign(0.431)
chr15	91832782	91832784	*SV2B*	In_Frame_Del	.	DEL	CTT	CTT	-	novel	shansha n_et_al_P74	p.F582del	ENSG00000185518	ENST00000394232	Transcript	inframe_deletion	NA
chr17	75930002	75930002	*WRAP53*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P74	p.V209L	ENSG00000141499	ENST00000316024	Transcript	missense_variant	benign(0.001)
chr19	13211506	13211506	*LYL1*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P74	p.R131Q	ENSG00000104903	ENST00000264824	Transcript	missense_variant	probably_damaging(0.994)
chr19	53517740	53517740	*ERVV-1*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P74	p.C133S	ENSG00000269526	ENST00000602168	Transcript	missense_variant	probably_damaging(0.952)
chr19	53552901	53552901	*ERVV-2*	Missense_Mutation	.	SNP	T	T	A	novel	shansha n_et_al_P74	p.C133S	ENSG00000268964	ENST00000601417	Transcript	missense_variant	possibly_damaging(0.723)
chr2	177017521	177017521	*HOXD4*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P74	p.M207V	ENSG00000170166	ENST00000306324	Transcript	missense_variant	probably_damaging(0.996)
chr2	32582383	32582383	*BIRC6*	Missense_Mutation	.	SNP	g	g	T	novel	shansha n_et_al_P74	p.V52F	ENSG00000115760	ENST00000421745	Transcript	missense_variant	unknown(0)
chr2	65541233	65541233	*SPRED2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P74	p.R220Q	ENSG00000198369	ENST00000356388	Transcript	missense_variant	benign(0.36)
chr3	97251308	97251308	*EPHA6*	Missense_Mutation	.	SNP	A	A	T	novel	shansha n_et_al_P74	p.R769S	ENSG00000080224	ENST00000389672	Transcript	missense_variant	benign(0.407)
chr4	30724929	30724929	*PCDH7*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P74	p.V629M	ENSG00000169851	ENST00000543491	Transcript	missense_variant	probably_damaging(0.995)
chr5	161520898	161520898	*GABRG2*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P74	p.T58A	ENSG00000113327	ENST00000414552	Transcript	missense_variant	possibly_damaging(0.73)
chr5	37179516	37179516	*C5orf42*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P74	p.R1923G	ENSG00000197603	ENST00000425232	Transcript	missense_variant	benign(0)

chr7	151879655	151879655	*KMT2C*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P74	p.Q1764*	ENSG00000055609	ENST00000262189	Transcript	stop_gained	NA
chr8	10465894	10465894	*RP1L1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P74	p.G1905D	ENSG00000183638	ENST00000382483	Transcript	missense_variant	unknown(0)
chr9	133730260	133730260	*ABL1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P74	p.G109V	ENSG00000097007	ENST00000318560	Transcript	missense_variant	probably_damaging(1)
chr9	135374987	135374987	*C9orf171*	Missense_Mutation	.	SNP	G	G	A	rs561494397	shanshan_et_al_P74	p.R211Q	ENSG00000188523	ENST00000343036	Transcript	missense_variant	possibly_damaging(0.868)
chr9	43627372	43627372	*SPATA31A6*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P74	p.T439A	ENSG00000185775	ENST00000332857	Transcript	missense_variant	benign(0.02)
chr9	97555152	97555152	*C9orf3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P74	p.N357S	ENSG00000148120	ENST00000375315	Transcript	missense_variant	benign(0.004)
chrX	129058934	129058934	*UTP14A*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P74	p.R504S	ENSG00000156697	ENST00000394422	Transcript	missense_variant	benign(0.175)
chr1	230883258	230883258	*CAPN9*	Missense_Mutation	.	SNP	C	C	T	rs199941171	shanshan_et_al_P79	p.R6W	ENSG00000135773	ENST00000271971	Transcript	missense_variant	possibly_damaging(0.582)
chr1	86934709	86934709	*CLCA1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P79	p.A19T	ENSG00000016490	ENST00000234701	Transcript	missense_variant	benign(0.012)
chr12	49361759	49361759	*WNT10B*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P79	p.M227I	ENSG00000169884	ENST00000301061	Transcript	missense_variant	possibly_damaging(0.473)
chr15	55932003	55932003	*PRTG*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P79	p.P721S	ENSG00000166450	ENST00000389286	Transcript	missense_variant	benign(0.083)
chr17	38638626	38638626	*TNS4*	Missense_Mutation	.	SNP	G	G	A	rs142919679	shanshan_et_al_P79	p.S515L	ENSG00000131746	ENST00000254051	Transcript	missense_variant	probably_damaging(1)
chr18	10789289	10789289	*PIEZO2*	Nonsense_Mutation	.	SNP	g	g	A	novel	shanshan_et_al_P79	p.Q653*	ENSG00000154864	ENST00000503781	Transcript	stop_gained	NA
chr3	75788394	75788394	*ZNF717*	Missense_Mutation	.	SNP	C	C	G	rs201974353	shanshan_et_al_P79	p.R127T	ENSG00000227124	ENST00000422325	Transcript	missense_variant	possibly_damaging(0.587)
chr8	7806745	7806745	*ZNF705B*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P79	p.M36T	ENSG00000215356	ENST00000443676	Transcript	missense_variant	benign(0)
chr9	132636945	132636945	*USP20*	Missense_Mutation	.	SNP	G	G	A	rs118142639	shanshan_et_al_P79	p.D611N	ENSG00000136878	ENST00000315480	Transcript	missense_variant	benign(0.341)
chr1	113933701	113933701	*MAGI3*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P80	p.Q16*	ENSG00000081026	ENST00000307546	Transcript	stop_gained	NA
chr1	158263012	158263012	*CD1C*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P80	p.F300L	ENSG00000158481	ENST00000368170	Transcript	missense_variant	benign(0)
chr1	174987615	174987615	*MRPS14*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P80	p.A48G	ENSG00000120333	ENST00000476371	Transcript	missense_variant	possibly_damaging(0.86)
chr1	186106036	186106036	*HMCN1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P80	p.S4517T	ENSG00000143341	ENST00000271588	Transcript	missense_variant	probably_damaging(0.989)
chr1	186281392	186281392	*PRG4*	Nonsense_Mutation	.	SNP	T	T	A	rs138093894	shanshan_et_al_P80	p.Y1293*	ENSG00000116690	ENST00000445192	Transcript	stop_gained	NA
chr1	26161753	26161753	*AUNIP*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P80	p.V269F	ENSG00000127423	ENST00000374298	Transcript	missense_variant	benign(0)
chr10	105233320	105233320	*CALHM3*	Missense_Mutation	.	SNP	C	C	T	rs537251257	shanshan_et_al_P80	p.E229K	ENSG00000183128	ENST00000369783	Transcript	missense_variant	possibly_damaging(0.901)
chr10	16893363	16893363	*CUBN*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P80	p.M3178I	ENSG00000107611	ENST00000377833	Transcript	missense_variant	benign(0.003)
chr10	49986752	49986752	*WDFY4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P80	p.R1091H	ENSG00000128815	ENST00000325239	Transcript	missense_variant	possibly_damaging(0.884)
chr11	85397172	85397172	*CCDC89*	Translation_Start_Site	.	SNP	A	A	G	novel	shanshan_et_al_P80	p.M1?	ENSG00000179071	ENST00000316398	Transcript	initiator_codon_variant	benign(0)
chr12	56142675	56142675	*GDF11*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P80	p.P251T	ENSG00000135414	ENST00000257868	Transcript	missense_variant	possibly_damaging(0.897)
chr12	57389405	57389405	*GPR182*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P80	p.Y138H	ENSG00000166856	ENST00000300098	Transcript	missense_variant	possibly_damaging(0.521)
chr12	75804410	75804410	*GLIPR1L2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P80	p.Y144C	ENSG00000180481	ENST00000550916	Transcript	missense_variant	probably_damaging(0.996)
chr12	80714376	80714376	*OTOGL*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P80	p.Y1317F	ENSG00000165899	ENST00000458043	Transcript	missense_variant	benign(0.341)
chr14	81259455	81259455	*CEP128*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P80	NA	ENSG00000100629	ENST00000555265	Transcript	splice_acceptor_variant	NA
chr14	93723599	93723599	*BTBD7*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P80	p.L517S	ENSG00000011114	ENST00000334746	Transcript	missense_variant	possibly_damaging(0.664)
chr16	30616450	30616450	*ZNF689*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P80	p.R213H	ENSG00000156853	ENST00000287461	Transcript	missense_variant	probably_damaging(0.97)
chr17	55038183	55038183	*COIL*	Missense_Mutation	.	SNP	C	C	G	rs201582973	shanshan_et_al_P80	p.L66F	ENSG00000121058	ENST00000240316	Transcript	missense_variant	probably_damaging(1)
chr19	38673170	38673170	*SIPA1L3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P80	p.S1407L	ENSG00000105738	ENST00000222345	Transcript	missense_variant	benign(0.001)
chr19	44531609	44531609	*ZNF222*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P80	p.M77L	ENSG00000159885	ENST00000391960	Transcript	missense_variant	benign(0.124)

chr19	5611378	5611378	*SAFB2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P80	p.P300A	ENSG00000130254	ENST00000252542	Transcript	missense_variant	benign(0.013)
chr19	5649263	5649263	*SAFB*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P80	p.P301A	ENSG00000160633	ENST00000588852	Transcript	missense_variant	benign(0.007)
chr19	8130840	8130840	*FBN3*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P80	p.Q2798R	ENSG00000142449	ENST00000600128	Transcript	missense_variant	benign(0.001)
chr2	166848129	166848129	*SCN1A*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P80	p.R1886*	ENSG00000144285	ENST00000303395	Transcript	stop_gained	NA
chr2	219320415	219320415	*USP37*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P80	p.I914V	ENSG00000135913	ENST00000258399	Transcript	missense_variant	benign(0.023)
chr2	226447616	226447616	*NYAP2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P80	p.Y495N	ENSG00000144460	ENST00000272907	Transcript	missense_variant	benign(0.209)
chr20	53205321	53205321	*DOK5*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P80	p.T129A	ENSG00000101134	ENST00000262593	Transcript	missense_variant	benign(0)
chr22	46773045	46773045	*CELSR1*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P80	p.N2499K	ENSG00000075275	ENST00000262738	Transcript	missense_variant	probably_damaging(0.909)
chr3	134670397	134670397	*EPHB1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P80	p.P103L	ENSG00000154928	ENST00000398015	Transcript	missense_variant	benign(0.097)
chr3	142443561	142443561	*TRPC1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P80	p.A54T	ENSG00000144935	ENST00000476941	Transcript	missense_variant	possibly_damaging(0.473)
chr3	52443757	52443757	*BAP1*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P80	p.L14Sfs*58	ENSG00000163930	ENST00000460680	Transcript	frameshift_variant	NA
chr3	97983712	97983712	*OR5H6*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P80	p.C195Y	ENSG00000230301	ENST00000383696	Transcript	missense_variant	possibly_damaging(0.739)
chr4	79500256	79500256	*ANXA3*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P80	p.Y60C	ENSG00000138772	ENST00000264908	Transcript	missense_variant	probably_damaging(1)
chr4	83350506	83350506	*HNRNPDL*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P80	p.P113Lfs*11	ENSG00000152795	ENST00000295470	Transcript	frameshift_variant	NA
chr5	155756543	155756543	*SGCD*	Splice_Site	.	SNP	G	G	T	novel	shanshan_et_al_P80	NA	ENSG00000170624	ENST00000337851	Transcript	splice_acceptor_variant	NA
chr6	21594893	21594893	*SOX4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P80	p.G43D	ENSG00000124766	ENST00000244745	Transcript	missense_variant	possibly_damaging(0.529)
chr6	35773583	35773583	*LHFPL5*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P80	p.Q46*	ENSG00000197753	ENST00000360215	Transcript	stop_gained	NA
chr7	135421920	135421920	*FAM180A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P80	p.P35Q	ENSG00000189320	ENST00000338588	Transcript	missense_variant	possibly_damaging(0.751)
chr7	140159588	140159588	*MKRN1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P80	p.N155D	ENSG00000133606	ENST00000255977	Transcript	missense_variant	benign(0.001)
chr9	124532835	124532835	*DAB2IP*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P80	p.S609Y	ENSG00000136848	ENST00000259371	Transcript	missense_variant	possibly_damaging(0.807)
chr9	140136272	140136272	*TUBB4B*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P80	p.E53*	ENSG00000188229	ENST00000340384	Transcript	stop_gained	NA
chrX	117883695	117883695	*IL13RA1*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P80	p.P148A	ENSG00000131724	ENST00000371666	Transcript	missense_variant	possibly_damaging(0.475)
chrX	13753378	13753378	*OFD1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P80	p.F8L	ENSG00000046651	ENST00000340096	Transcript	missense_variant	benign(0)
chrX	41333734	41333734	*NYX*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P80	p.R343H	ENSG00000188937	ENST00000342595	Transcript	missense_variant	benign(0.001)
chr1	155183422	155183422	*MTX1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.R445Q	ENSG00000173171	ENST00000368376	Transcript	missense_variant	benign(0.356)
chr1	28280979	28280979	*SMPDL3B*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.G211D	ENSG00000130768	ENST00000373894	Transcript	missense_variant	probably_damaging(0.939)
chr11	47193243	47193243	*ARFGAP2*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P81	p.D261N	ENSG00000149182	ENST00000524782	Transcript	missense_variant	benign(0.007)
chr12	50190859	50190859	*NCKAP5L*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P81	p.G262W	ENSG00000167566	ENST00000335999	Transcript	missense_variant	probably_damaging(0.992)
chr12	51754557	51754557	*GALNT6*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P81	p.Y372S	ENSG00000139629	ENST00000543196	Transcript	missense_variant	probably_damaging(0.999)
chr12	76424952	76424952	*PHLDA1*	Missense_Mutation	.	SNP	c	c	G	rs200070422	shanshan_et_al_P81	p.Q190H	ENSG00000139289	ENST00000266671	Transcript	missense_variant	benign(0.387)
chr14	92488154	92488154	*TRIP11*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P81	p.A112S	ENSG00000100815	ENST00000267622	Transcript	missense_variant	probably_damaging(0.982)
chr16	25704316	25704316	*HS3ST4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.G193E	ENSG00000182601	ENST00000331351	Transcript	missense_variant	probably_damaging(0.997)
chr16	57508784	57508784	*DOK4*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P81	p.V174M	ENSG00000125170	ENST00000340099	Transcript	missense_variant	benign(0.255)
chr16	84213059	84213059	*TAF1C*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P81	p.L700I	ENSG00000103168	ENST00000567759	Transcript	missense_variant	possibly_damaging(0.625)
chr17	63554672	63554672	*AXIN2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.R23W	ENSG00000168646	ENST00000307078	Transcript	missense_variant	probably_damaging(1)
chr17	74053597	74053597	*SRP68*	Nonsense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.Q289*	ENSG00000167881	ENST00000307877	Transcript	stop_gained	NA

chr19	1863111	1863111	*KLF16*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P81	p.C129F	ENSG00000129911	ENST00000250916	Transcript	missense_variant	probably_damaging(0.962)
chr19	22847579	22847579	*ZNF492*	Missense_Mutation	.	SNP	T	T	A	rs201599839	shanshan_et_al_P81	p.C370S	ENSG00000229676	ENST00000456783	Transcript	missense_variant	possibly_damaging(0.591)
chr19	22847597	22847597	*ZNF492*	Missense_Mutation	.	SNP	C	C	T	rs199953047	shanshan_et_al_P81	p.R376W	ENSG00000229676	ENST00000456783	Transcript	missense_variant	benign(0)
chr19	41633809	41633809	*CYP2F1*	Missense_Mutation	.	SNP	G	G	A	rs139951793	shanshan_et_al_P81	p.R433H	ENSG00000197446	ENST00000331105	Transcript	missense_variant	benign(0.006)
chr2	185803163	185803163	*ZNF804A*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P81	p.G1014C	ENSG00000170396	ENST00000302277	Transcript	missense_variant	probably_damaging(0.999)
chr2	198266713	198266713	*SF3B1*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P81	p.G740E	ENSG00000115524	ENST00000335508	Transcript	missense_variant	possibly_damaging(0.686)
chr3	141595684	141595684	*ATP1B3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P81	p.A14V	ENSG00000069849	ENST00000286371	Transcript	missense_variant	possibly_damaging(0.608)
chr5	10397404	10397404	*Mar/06*	Splice_Site	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.X288_splice	ENSG00000145495	ENST00000274140	Transcript	splice_acceptor_variant	NA
chr5	127493768	127493768	*SLC12A2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.G796D	ENSG00000064651	ENST00000262461	Transcript	missense_variant	probably_damaging(0.979)
chr5	36958268	36958268	*NIPBL*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P81	p.A98V	ENSG00000164190	ENST00000282516	Transcript	missense_variant	benign(0.092)
chr6	137519730	137519730	*IFNGR1*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P81	p.K303T	ENSG00000027697	ENST00000367739	Transcript	missense_variant	probably_damaging(0.992)
chr6	138428333	138428333	*PERP*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P81	p.W49R	ENSG00000112378	ENST00000421351	Transcript	missense_variant	possibly_damaging(0.867)
chr6	42931432	42931432	*GNMT*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P81	p.K292N	ENSG00000124713	ENST00000372808	Transcript	missense_variant	benign(0.065)
chr6	75950914	75950914	*COX7A2*	Missense_Mutation	.	SNP	G	G	A	rs371766385	shanshan_et_al_P81	p.P61L	ENSG00000112695	ENST00000370081	Transcript	missense_variant	possibly_damaging(0.516)
chr7	107580698	107580698	*LAMB1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P81	p.T1166M	ENSG00000091136	ENST00000222399	Transcript	missense_variant	probably_damaging(0.932)
chr7	140453149	140453149	*BRAF*	Missense_Mutation	.	SNP	C	C	G	rs121913361	shanshan_et_al_P81	p.G596R	ENSG00000157764	ENST00000288602	Transcript	missense_variant	possibly_damaging(0.705)
chr9	101891223	101891226	*TGFBR1*	Frame_Shift_Del	.	DEL	ACAG	ACAG	-	novel	shanshan_et_al_P81	p.D63Kfs*9	ENSG00000106799	ENST00000374994	Transcript	frameshift_variant	NA
chr1	13427399	13427399	*PRAMEF9*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P82	p.K326R	ENSG00000204501	ENST00000376152	Transcript	missense_variant	benign(0.329)
chr1	13669054	13669054	*PRAMEF14*	Missense_Mutation	.	SNP	C	C	T	rs201993989	shanshan_et_al_P82	p.D426N	ENSG00000204481	ENST00000334600	Transcript	missense_variant	benign(0.001)
chr1	208219299	208219299	*PLXNA2*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P82	p.Y1140C	ENSG00000076356	ENST00000367033	Transcript	missense_variant	probably_damaging(0.99)
chr12	53069162	53069163	*KRT1*	Frame_Shift_Del	.	DEL	TG	TG	-	novel	shanshan_et_al_P82	p.S583Rfs*70	ENSG00000167768	ENST00000252244	Transcript	frameshift_variant	NA
chr1	12919642	12919642	*PRAMEF2*	Missense_Mutation	.	SNP	G	G	A	rs142476002	shanshan_et_al_P86	p.A128T	ENSG00000120952	ENST00000240189	Transcript	missense_variant	benign(0.024)
chr1	13368564	13368564	*PRAMEF5*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P86	p.D421G	ENSG00000204502	ENST00000376168	Transcript	missense_variant	benign(0.023)
chr1	159912834	159912834	*IGSF9*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P86	p.E56K	ENSG00000085552	ENST00000368094	Transcript	missense_variant	probably_damaging(0.999)
chr1	16475486	16475486	*EPHA2*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P86	p.C70W	ENSG00000142627	ENST00000358432	Transcript	missense_variant	probably_damaging(1)
chr1	175334260	175334260	*TNR*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P86	p.T825S	ENSG00000116147	ENST00000367674	Transcript	missense_variant	benign(0.041)
chr1	27023479	27023479	*ARID1A*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P86	p.Y195*	ENSG00000117713	ENST00000324856	Transcript	stop_gained	NA
chr1	27276585	27276586	*C1orf172*	Frame_Shift_Ins	.	INS	-	-	C	novel	shanshan_et_al_P86	p.P392Tfs*98	ENSG00000175707	ENST00000320567	Transcript	frameshift_variant	NA
chr1	3421997	3421997	*MEGF6*	Missense_Mutation	.	SNP	C	C	T	rs375445762	shanshan_et_al_P86	p.R681H	ENSG00000162591	ENST00000356575	Transcript	missense_variant	benign(0.014)
chr1	94370099	94370099	*GCLM*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P86	p.I58V	ENSG00000023909	ENST00000370238	Transcript	missense_variant	benign(0.001)
chr10	96602680	96602680	*CYP2C19*	Missense_Mutation	.	SNP	G	G	A	rs201509150	shanshan_et_al_P86	p.A350T	ENSG00000165841	ENST00000371321	Transcript	missense_variant	probably_damaging(0.997)
chr11	551197	551197	*LRRC56*	Missense_Mutation	.	SNP	G	G	A	rs373134692	shanshan_et_al_P86	p.E231K	ENSG00000161328	ENST00000270115	Transcript	missense_variant	probably_damaging(0.935)
chr11	6953879	6953879	*ZNF215*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P86	p.V126L	ENSG00000149054	ENST00000278319	Transcript	missense_variant	possibly_damaging(0.611)
chr17	56603076	56603076	*Sep/04*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P86	p.R188Q	ENSG00000108387	ENST00000457347	Transcript	missense_variant	probably_damaging(0.989)
chr17	7194440	7194440	*YBX2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P86	p.V144A	ENSG00000006047	ENST00000007699	Transcript	missense_variant	benign(0.418)
chr17	78897335	78897335	*RPTOR*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P86	p.N890K	ENSG00000141564	ENST00000306801	Transcript	missense_variant	possibly_damaging(0.554)

chr19	18391847	18391847	*JUND*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P86	p.Q150K	ENSG00000130522	ENST00000252818	Transcript	missense_variant	possibly_damaging(0.745)
chr19	22940832	22940832	*ZNF99*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P86	p.G627R	ENSG00000213973	ENST00000596209	Transcript	missense_variant	probably_damaging(0.979)
chr22	24919686	24919686	*UPB1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P86	p.V339A	ENSG00000100024	ENST00000326010	Transcript	missense_variant	possibly_damaging(0.828)
chr3	148559623	148559623	*CPB1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P86	p.G163E	ENSG00000153002	ENST00000491148	Transcript	missense_variant	possibly_damaging(0.686)
chr3	31707911	31707911	*TRNT1*	Missense_Mutation	.	SNP	C	C	G	rs183596892	shanshan_et_al_P86	p.P23A	ENSG00000072756	ENST00000251607	Transcript	missense_variant	benign(0)
chr4	82300933	82300933	*SH3TC1*	Missense_Mutation	.	SNP	G	G	A	rs140634088	shanshan_et_al_P86	p.R891Q	ENSG00000125089	ENST00000245105	Transcript	missense_variant	benign(0.015)
chr5	112177141	112177141	*APC*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P86	p.K1950N	ENSG00000134982	ENST00000457016	Transcript	missense_variant	probably_damaging(0.999)
chr5	167881041	167881041	*WWC1*	Missense_Mutation	.	SNP	a	a	G	rs140933524	shanshan_et_al_P86	p.E865G	ENSG00000113645	ENST00000521089	Transcript	missense_variant	benign(0.001)
chr7	146536869	146536869	*CNTNAP2*	Missense_Mutation	.	SNP	G	G	A	rs138924087	shanshan_et_al_P86	p.R92Q	ENSG00000174469	ENST00000361727	Transcript	missense_variant	probably_damaging(0.998)
chr9	131020815	131020815	*GOLGA2*	Missense_Mutation	.	SNP	c	c	A	rs62587120	shanshan_et_al_P86	p.E709D	ENSG00000167110	ENST00000421699	Transcript	missense_variant	benign(0.043)
chr9	43625244	43625244	*SPATA31A6*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P86	p.P1148Q	ENSG00000185775	ENST00000332857	Transcript	missense_variant	possibly_damaging(0.719)
chrX	12736328	12736328	*FRMPD4*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P86	p.G1128E	ENSG00000169933	ENST00000380682	Transcript	missense_variant	benign(0.001)
chr1	43885836	43885836	*SZT2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P88	p.R368H	ENSG00000198198	ENST00000562955	Transcript	missense_variant	probably_damaging(0.978)
chr11	64701305	64701305	*PPP2R5B*	Missense_Mutation	.	SNP	G	G	A	rs368931364	shanshan_et_al_P88	p.G495S	ENSG00000068971	ENST00000164133	Transcript	missense_variant	possibly_damaging(0.855)
chr11	6953546	6953546	*ZNF215*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P88	p.N15D	ENSG00000149054	ENST00000278319	Transcript	missense_variant	benign(0.214)
chr12	29450110	29450110	*FAR2*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P88	p.I177Sfs*8	ENSG00000064763	ENST00000536681	Transcript	frameshift_variant	NA
chr13	113770009	113770009	*F7*	Missense_Mutation	.	SNP	G	G	A	rs563972504	shanshan_et_al_P88	p.G156S	ENSG00000057593	ENST00000375581	Transcript	missense_variant	probably_damaging(0.992)
chr17	76456275	76456275	*DNAH17*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P88	p.A3121E	ENSG00000187775	ENST00000389840	Transcript	missense_variant	benign(0.119)
chr19	56029559	56029559	*SSC5D*	Missense_Mutation	.	SNP	G	G	C	rs201344068	shanshan_et_al_P88	p.D1306H	ENSG00000179954	ENST00000389623	Transcript	missense_variant	unknown(0)
chr19	57327976	57327976	*PEG3*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P88	p.P612S	ENSG00000198300	ENST00000326441	Transcript	missense_variant	benign(0.008)
chr20	4776504	4776504	*RASSF2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P88	p.S82P	ENSG00000101265	ENST00000379400	Transcript	missense_variant	benign(0.048)
chr3	14206941	14206941	*XPC*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P88	p.N256D	ENSG00000154767	ENST00000285021	Transcript	missense_variant	benign(0.013)
chr5	137756620	137756620	*KDM3B*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P88	p.P1314L	ENSG00000120733	ENST00000314358	Transcript	missense_variant	possibly_damaging(0.668)
chr6	116441262	116441262	*COL10A1*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P88	p.S673A	ENSG00000123500	ENST00000327673	Transcript	missense_variant	probably_damaging(0.993)
chr6	75865411	75865411	*COL12A1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P88	p.P1137L	ENSG00000111799	ENST00000322507	Transcript	missense_variant	probably_damaging(0.998)
chr8	27296873	27296873	*PTK2B*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P88	p.N598H	ENSG00000120899	ENST00000397501	Transcript	missense_variant	possibly_damaging(0.684)
chrX	111020157	111020157	*TRPC5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P88	p.S769N	ENSG00000072315	ENST00000262839	Transcript	missense_variant	benign(0.005)
chrX	151138721	151138721	*GABRE*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P88	p.E70D	ENSG00000102287	ENST00000370328	Transcript	missense_variant	benign(0.042)
chr1	204197210	204197210	*PLEKHA6*	Splice_Site	.	SNP	C	C	A	novel	shanshan_et_al_P89	NA	ENSG00000143850	ENST00000272203	Transcript	splice_donor_variant	NA
chr10	88702983	88702983	*MMRN2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P89	p.V520L	ENSG00000173269	ENST00000372027	Transcript	missense_variant	benign(0.002)
chr12	48143297	48143297	*RAPGEF3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P89	p.E306V	ENSG00000079337	ENST00000449771	Transcript	missense_variant	possibly_damaging(0.769)
chr13	101728275	101728275	*NALCN*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P89	p.M1301I	ENSG00000102452	ENST00000251127	Transcript	missense_variant	benign(0.009)
chr17	44396988	44396988	*SPNS2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P89	p.S528R	ENSG00000183018	ENST00000329078	Transcript	missense_variant	benign(0.255)
chr17	78109813	78109813	*EIF4A3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P89	p.M403I	ENSG00000141543	ENST00000269349	Transcript	missense_variant	possibly_damaging(0.885)
chr21	14982827	14982827	*POTED*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P89	p.M93T	ENSG00000166351	ENST00000299443	Transcript	missense_variant	benign(0)
chr3	184008140	184008140	*ECE2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P89	p.R668L	ENSG00000145194	ENST00000402825	Transcript	missense_variant	benign(0.187)

chr5	121759202	121759202	*SNCAIP*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P89	p.D257G	ENSG00000064692	ENST00000261368	Transcript	missense_variant	benign(0.009)
chr6	79656478	79656478	*PHIP*	Missense_Mutation	.	SNP	C	C	A	rs531409891	shansha n_et_al_P89	p.R1440S	ENSG00000146247	ENST00000275034	Transcript	missense_variant	benign(0.002)
chr1	13476661	13476661	*PRAMEF18*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_1	p.S159F	ENSG00000204491	ENST00000376126	Transcript	missense_variant	benign(0)
chr1	15218643 2	15218643 2	*HRNR*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_1	p.S2558F	ENSG00000197915	ENST00000368801	Transcript	missense_variant	unknown(0)
chr1	15691770 1	15691770 1	*ARHGEF11*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_1	p.P734L	ENSG00000132694	ENST00000368194	Transcript	missense_variant	probably_damaging(0.987)
chr1	17905128 5	17905128 5	*TOR3A*	Nonsense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P8_1	p.Q8*	ENSG00000186283	ENST00000367627	Transcript	stop_gained	NA
chr1	24921937	24921937	*NCMAP*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_1	p.P6T	ENSG00000184454	ENST00000374392	Transcript	missense_variant	benign(0.003)
chr1	94466630	94466630	*ABCA4*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.A2105E	ENSG00000198691	ENST00000370225	Transcript	missense_variant	benign(0.271)
chr10	10001537 4	10001537 4	*LOXL4*	Missense_Mutation	.	SNP	G	G	T	rs564977441	shansha n_et_al_P8_1	p.H517Q	ENSG00000138131	ENST00000260702	Transcript	missense_variant	benign(0.03)
chr10	13421081 2	13421081 2	*PWWP2B*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.G28C	ENSG00000171813	ENST00000305233	Transcript	missense_variant	probably_damaging(1)
chr11	10099904 1	10099904 1	*PGR*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_1	p.A254V	ENSG00000082175	ENST00000325455	Transcript	missense_variant	benign(0.105)
chr11	57100233	57100233	*SSRP1*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_1	p.G212C	ENSG00000149136	ENST00000278412	Transcript	missense_variant	probably_damaging(1)
chr12	20522915	20522915	*PDE3A*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P8_1	p.K233E	ENSG00000172572	ENST00000359062	Transcript	missense_variant	benign(0.08)
chr12	48145302	48145302	*RAPGEF3*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.Q128K	ENSG00000079337	ENST00000449771	Transcript	missense_variant	benign(0.001)
chr12	61385119	61385119	*VWF*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.Q986K	ENSG00000110799	ENST00000261405	Transcript	missense_variant	benign(0.018)
chr13	31037792	31037792	*HMGB1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_1	p.P9L	ENSG00000189403	ENST00000405805	Transcript	missense_variant	benign(0.395)
chr16	70937373	70937373	*WDR90*	Missense_Mutation	.	SNP	G	G	T	rs112960809	shansha n_et_al_P8_1	p.D1061Y	ENSG00000161996	ENST00000293879	Transcript	missense_variant	possibly_damaging(0.817)
chr17	27005119	27005119	*SUPT6H*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.G342V	ENSG00000109111	ENST00000314616	Transcript	missense_variant	possibly_damaging(0.761)
chr17	27492999	27492999	*MYO18A*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_1	p.W320C	ENSG00000196535	ENST00000527372	Transcript	missense_variant	probably_damaging(0.968)
chr17	77521512	77521512	*KDM6B*	Missense_Mutation	.	SNP	C	C	T	rs376654821	shansha n_et_al_P8_1	p.P849L	ENSG00000132510	ENST00000254846	Transcript	missense_variant	benign(0.11)
chr17	79213175	79213175	*C17orf89*	Missense_Mutation	.	SNP	C	C	G	novel	shansha n_et_al_P8_1	p.N4K	ENSG00000224877	ENST00000431388	Transcript	missense_variant	benign(0.005)
chr18	19383976	19383976	*MIB1*	Splice_Site	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.X493_splice	ENSG00000101752	ENST00000261537	Transcript	splice_donor_variant	NA
chr19	10748548	10748548	*SLC44A2*	Missense_Mutation	.	SNP	C	C	T	novel	shansha n_et_al_P8_1	p.T571I	ENSG00000129353	ENST00000335757	Transcript	missense_variant	possibly_damaging(0.808)
chr2	223168992	223168992	*CCDC140*	Missense_Mutation	.	SNP	G	G	C	novel	shansha n_et_al_P8_1	p.R124T	ENSG00000163081	ENST00000295226	Transcript	missense_variant	benign(0.402)
chr20	18365675	18365675	*DZANK1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.T693N	ENSG00000089091	ENST00000262547	Transcript	missense_variant	benign(0.093)
chr21	10942995	10942995	*TPTE*	Nonsense_Mutation	.	SNP	G	G	A	rs147014138	shansha n_et_al_P8_1	p.R198*	ENSG00000166157	ENST00000361285	Transcript	stop_gained	NA
chr3	52541964	52541964	*STAB1*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.E690D	ENSG00000010327	ENST00000321725	Transcript	missense_variant	benign(0.034)
chr3	97356738	97356738	*EPHA6*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.V866F	ENSG00000080224	ENST00000389672	Transcript	missense_variant	probably_damaging(0.999)
chr4	25026464	25026464	*LGI2*	Missense_Mutation	.	SNP	C	C	A	novel	shansha n_et_al_P8_1	p.G131C	ENSG00000153012	ENST00000382114	Transcript	missense_variant	probably_damaging(0.999)
chr4	70453955	70453955	*TADA2B*	Missense_Mutation	.	SNP	A	A	G	novel	shansha n_et_al_P8_1	p.E30G	ENSG00000173011	ENST00000310074	Transcript	missense_variant	possibly_damaging(0.517)
chr4	93378443	93378443	*USP17L26*	Missense_Mutation	.	SNP	T	T	A	rs199755316	shansha n_et_al_P8_1	p.L487Q	ENSG00000229579	ENST00000509660	Transcript	missense_variant	benign(0.15)
chr5	40692182	40692182	*PTGER4*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.S390I	ENSG00000171522	ENST00000302472	Transcript	missense_variant	probably_damaging(0.983)
chr7	148456667	148456667	*CUL1*	Missense_Mutation	.	SNP	G	G	A	novel	shansha n_et_al_P8_1	p.E188K	ENSG00000055130	ENST00000325222	Transcript	missense_variant	probably_damaging(0.964)
chr9	42719198	42719198	*FOXD4L2*	Missense_Mutation	.	SNP	T	T	C	novel	shansha n_et_al_P8_1	p.L378P	ENSG00000204828	ENST00000377590	Transcript	missense_variant	benign(0)
chrX	10786896 1	10786896 1	*COL4A5*	Nonsense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.G1015*	ENSG00000188153	ENST00000328300	Transcript	stop_gained	NA
chrX	29513855	29513855	*ARSH*	Missense_Mutation	.	SNP	G	G	T	novel	shansha n_et_al_P8_1	p.G550W	ENSG00000205667	ENST00000381130	Transcript	missense_variant	benign(0.003)

chr1	204168364	204168364	*GOLT1A*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P91	p.G107S	ENSG00000174567	ENST00000308302	Transcript	missense_variant	benign(0.136)
chr10	13237261	13237261	*MCM10*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P91	p.A657S	ENSG00000065328	ENST00000484800	Transcript	missense_variant	possibly_damaging(0.794)
chr11	128844069	128844069	*ARHGAP32*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P91	p.S994C	ENSG00000134909	ENST00000310343	Transcript	missense_variant	benign(0.002)
chr11	64532008	64532008	*HPX*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P91	p.W292*	ENSG00000110169	ENST00000265983	Transcript	stop_gained	NA
chr16	18169115	18169115	*MAPK8IP3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P91	p.G1010C	ENSG00000138834	ENST00000250894	Transcript	missense_variant	probably_damaging(0.998)
chr16	85132851	85132861	*FAM92B*	Frame_Shift_Del	.	DEL	CTGCCCCTTAA	CTGCCCCTTAA	-	novel	shanshan_et_al_P91	p.K283Sfs*22	ENSG00000153789	ENST00000539556	Transcript	frameshift_variant	NA
chr19	58757694	58757694	*ZNF544*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P91	p.M21V	ENSG00000198131	ENST00000269829	Transcript	missense_variant	benign(0.002)
chr3	133736 3	133736 3	*CNTN6*	Missense_Mutation	.	SNP	C	C	T	rs574681005	shanshan_et_al_P91	p.T178M	ENSG00000134115	ENST00000446702	Transcript	missense_variant	possibly_damaging(0.886)
chr8	145005754	145005754	*PLEC*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P91	p.C888Y	ENSG00000178209	ENST00000322810	Transcript	missense_variant	unknown(0)
chrX	136112369	136112369	*GPR101*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P91	p.G489R	ENSG00000165370	ENST00000298110	Transcript	missense_variant	probably_damaging(0.983)
chr1	152282354	152282354	*FLG*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P94	p.Q1670Rfs*36	ENSG00000143631	ENST00000368799	Transcript	frameshift_variant	NA
chr1	152732155	152732155	*KPRP*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P94	p.A31T	ENSG00000203786	ENST00000368773	Transcript	missense_variant	benign(0.12)
chr1	214811331	214811333	*CENPF*	In_Frame_Del	.	DEL	AGA	AGA	-	novel	shanshan_et_al_P94	p.E525del	ENSG00000117724	ENST00000366955	Transcript	inframe_deletion	NA
chr1	248059481	248059481	*OR2W3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P94	p.T198I	ENSG00000238243	ENST00000537741	Transcript	missense_variant	benign(0.098)
chr1	32936476	32936476	*ZBTB8B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.Y84F	ENSG00000273274	ENST00000609129	Transcript	missense_variant	probably_damaging(0.999)
chr1	39768645	39768645	*MACF1*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P94	p.R900Q	ENSG00000127603	ENST00000545844	Transcript	missense_variant	probably_damaging(0.925)
chr1	72241959	72241959	*NEGR1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.I144N	ENSG00000172260	ENST00000357731	Transcript	missense_variant	probably_damaging(0.934)
chr10	103717439	103717439	*C10orf76*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P94	p.A516S	ENSG00000120029	ENST00000370033	Transcript	missense_variant	benign(0.003)
chr10	135345210	135345210	*CYP2E1*	Frame_Shift_Del	.	DEL	C	C	-	rs372241274	shanshan_et_al_P94	p.L154Cfs*27	ENSG00000130649	ENST00000463117	Transcript	frameshift_variant	NA
chr10	23319572	23319572	*ARMC3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.E698V	ENSG00000165309	ENST00000298032	Transcript	missense_variant	benign(0.288)
chr10	72298947	72298947	*PALD1*	Missense_Mutation	.	SNP	G	G	A	rs368514293	shanshan_et_al_P94	p.G557R	ENSG00000107719	ENST00000263563	Transcript	missense_variant	probably_damaging(0.973)
chr10	75434614	75434614	*AGAP5*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.T602S	ENSG00000172650	ENST00000374094	Transcript	missense_variant	benign(0.18)
chr10	89690843	89690843	*PTEN*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.R84*	ENSG00000171862	ENST00000371953	Transcript	stop_gained	NA
chr11	118959406	118959406	*HMBS*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P94	p.Q50P	ENSG00000256269	ENST00000278715	Transcript	missense_variant	benign(0.317)
chr11	124134780	124134780	*OR8G5*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P94	p.H20Y	ENSG00000255298	ENST00000524943	Transcript	missense_variant	benign(0.002)
chr11	62367715	62367715	*MTA2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P94	p.V38A	ENSG00000149480	ENST00000278823	Transcript	missense_variant	benign(0.386)
chr11	65308644	65308644	*LTBP3*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P94	p.G949D	ENSG00000168056	ENST00000301873	Transcript	missense_variant	probably_damaging(1)
chr11	862706	862706	*TSPAN4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.G74C	ENSG00000214063	ENST00000397404	Transcript	missense_variant	probably_damaging(1)
chr11	94353020	94353020	*PIWIL4*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.V755F	ENSG00000134627	ENST00000299001	Transcript	missense_variant	probably_damaging(0.945)
chr12	122359385	122359385	*WDR66*	Frame_Shift_Del	.	DEL	C	C	-	rs370060195	shanshan_et_al_P94	p.E59Rfs*40	ENSG00000158023	ENST00000288912	Transcript	frameshift_variant	NA
chr12	99640197	99640197	*ANKS1B*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.S734R	ENSG00000185046	ENST00000547776	Transcript	missense_variant	benign(0.342)
chr13	49039389	49039389	*RB1*	Frame_Shift_Del	.	DEL	T	T	-	novel	shanshan_et_al_P94	p.P793Lfs*17	ENSG00000139687	ENST00000267163	Transcript	frameshift_variant	NA
chr15	45814375	45814375	*SLC30A4*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P94	p.R60G	ENSG00000104154	ENST00000261867	Transcript	missense_variant	benign(0.002)
chr15	70961218	70961218	*UACA*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P94	p.R602Q	ENSG00000137831	ENST00000322954	Transcript	missense_variant	benign(0.006)
chr16	2812720	2812720	*SRRM2*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P94	p.N732Tfs*18	ENSG00000167978	ENST00000301740	Transcript	frameshift_variant	NA
chr17	20135522	20135522	*SPECC1*	Missense_Mutation	.	SNP	G	G	A	rs148173661	shanshan_et_al_P94	p.E719K	ENSG00000128487	ENST00000261503	Transcript	missense_variant	probably_damaging(0.998)

chr17	27903575	27903575	*GIT1*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P94	p.S458G	ENSG00000108262	ENST00000394869	Transcript	missense_variant	benign(0.057)
chr17	68171535	68171535	*KCNJ2*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P94	p.G119S	ENSG00000123700	ENST00000243457	Transcript	missense_variant	benign(0.002)
chr17	72340402	72340402	*KIF19*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.L166Q	ENSG00000196169	ENST00000389916	Transcript	missense_variant	benign(0.407)
chr19	10548400	10548400	*ABCA7*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P94	p.G1305R	ENSG00000064687	ENST00000263094	Transcript	missense_variant	probably_damaging(0.992)
chr19	15533953	15533953	*WIZ*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.K773N	ENSG00000011451	ENST00000263381	Transcript	missense_variant	probably_damaging(0.999)
chr19	18273228	18273228	*PIK3R2*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P94	p.N341D	ENSG00000105647	ENST00000222254	Transcript	missense_variant	possibly_damaging(0.839)
chr19	18902021	18902021	*COMP*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P94	p.G20*	ENSG00000105664	ENST00000222721	Transcript	stop_gained	NA
chr19	19136593	19136593	*SUGP2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P94	p.S188R	ENSG00000064607	ENST00000601879	Transcript	missense_variant	possibly_damaging(0.736)
chr19	20044921	20044921	*ZNF93*	Missense_Mutation	.	SNP	G	G	A	rs200332567	shanshan_et_al_P94	p.R386K	ENSG00000184635	ENST00000343769	Transcript	missense_variant	benign(0.006)
chr19	22498378	22498378	*ZNF729*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P94	p.A720G	ENSG00000196350	ENST00000601693	Transcript	missense_variant	probably_damaging(0.96)
chr19	35857833	35857833	*GIPC3*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P94	p.A63D	ENSG00000179855	ENST00000322315	Transcript	missense_variant	possibly_damaging(0.544)
chr19	49841283	49841283	*CD37*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P94	p.F148L	ENSG00000104894	ENST00000323906	Transcript	missense_variant	possibly_damaging(0.543)
chr19	55606107	55606107	*PPP1R12C*	Missense_Mutation	.	SNP	G	G	A	rs369559413	shanshan_et_al_P94	p.P505L	ENSG00000125503	ENST00000263433	Transcript	missense_variant	benign(0.002)
chr2	103335600	103335600	*MFSD9*	Missense_Mutation	.	SNP	C	C	T	rs372925047	shanshan_et_al_P94	p.R235Q	ENSG00000135953	ENST00000258436	Transcript	missense_variant	benign(0.067)
chr2	15307245	15307247	*NBAS*	In_Frame_Del	.	DEL	AGA	AGA	-	novel	shanshan_et_al_P94	NA	ENSG00000151779	ENST00000281513	Transcript	inframe_deletion	NA
chr2	18745093	18745093	*NT5C1B*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.A601D	ENSG00000185013	ENST00000359846	Transcript	missense_variant	probably_damaging(0.987)
chr2	80831222	80831222	*CTNNA2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P94	p.T738K	ENSG00000066032	ENST00000466387	Transcript	missense_variant	benign(0.047)
chr20	15324112	15324112	*SIRPD*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.Y116N	ENSG00000125900	ENST00000381623	Transcript	missense_variant	probably_damaging(0.996)
chr20	30418646	30418646	*MYLK2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P94	p.T417P	ENSG00000101306	ENST00000375994	Transcript	missense_variant	possibly_damaging(0.742)
chr20	49552780	49552780	*DPM1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.L195I	ENSG00000000419	ENST00000371588	Transcript	missense_variant	benign(0.364)
chr20	50701153	50701153	*ZFP64*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.S627R	ENSG00000020256	ENST00000361387	Transcript	missense_variant	benign(0.041)
chr21	30909664	30909664	*GRIK1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.L898M	ENSG00000171189	ENST00000399914	Transcript	missense_variant	probably_damaging(0.991)
chr22	18185059	18185059	*BCL2L13*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.R169S	ENSG00000099968	ENST00000317582	Transcript	missense_variant	possibly_damaging(0.886)
chr22	30682080	30682080	*GATSL3*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.S251C	ENSG00000239282	ENST00000407689	Transcript	missense_variant	possibly_damaging(0.88)
chr3	137483868	137483868	*SOX14*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.R81L	ENSG00000168875	ENST00000306087	Transcript	missense_variant	probably_damaging(1)
chr3	149459450	149459450	*COMMD2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.H153L	ENSG00000114744	ENST00000473414	Transcript	missense_variant	benign(0.008)
chr3	179050845	179050845	*ZNF639*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.R80*	ENSG00000121864	ENST00000326361	Transcript	stop_gained	NA
chr3	27872774	27872774	*CNTN4*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.L84*	ENSG00000144619	ENST00000397461	Transcript	stop_gained	NA
chr3	45869950	45869950	*LZTFL1*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.Q253L	ENSG00000163818	ENST00000296135	Transcript	missense_variant	benign(0.317)
chr3	48728864	48728864	*IP6K2*	Nonsense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P94	p.Y160*	ENSG00000068745	ENST00000328631	Transcript	stop_gained	NA
chr3	96913116	96913116	*MTMR14*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P94	p.A17T	ENSG00000163719	ENST00000296003	Transcript	missense_variant	unknown(0)
chr4	46930264	46930264	*GABRA4*	Missense_Mutation	.	SNP	T	T	G	novel	shanshan_et_al_P94	p.E548A	ENSG00000109158	ENST00000264318	Transcript	missense_variant	benign(0.41)
chr4	55964424	55964424	*KDR*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.L797M	ENSG00000128052	ENST00000263923	Transcript	missense_variant	possibly_damaging(0.601)
chr4	81967509	81967509	*BMP3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.D312Y	ENSG00000152785	ENST00000282701	Transcript	missense_variant	possibly_damaging(0.594)
chr4	890334	890334	*GAK*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.T219S	ENSG00000178950	ENST00000314167	Transcript	missense_variant	possibly_damaging(0.685)
chr5	132038665	132038665	*KIF3A*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.Q493L	ENSG00000131437	ENST00000378746	Transcript	missense_variant	probably_damaging(0.996)

chr5	137496591	137496591	*BRD8*	Nonsense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P94	p.E806*	ENSG00000112983	ENST00000254900	Transcript	stop_gained	NA
chr5	140480240	140480240	*PCDHB3*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.A3S	ENSG00000113205	ENST00000231130	Transcript	missense_variant	benign(0.013)
chr5	143812	14381276	*TRIO*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.L1162H	ENSG00000038382	ENST00000344204	Transcript	missense_variant	probably_damaging(0.995)
chr5	169697839	169697839	*LCP2*	Missense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.E136V	ENSG00000043462	ENST00000046794	Transcript	missense_variant	benign(0.147)
chr5	320898	32089819	*PDZD2*	Nonsense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P94	p.Q2089*	ENSG00000133401	ENST00000438447	Transcript	stop_gained	NA
chr5	708060	70806005	*BDP1*	Missense_Mutation	.	SNP	T	T	G	rs201934669	shanshan_et_al_P94	p.I1029S	ENSG00000145734	ENST00000358731	Transcript	missense_variant	benign(0.067)
chr6	434887	43488766	*POLR1C*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.R301L	ENSG00000171453	ENST00000372389	Transcript	missense_variant	possibly_damaging(0.798)
chr7	126173	126173556	*GRM8*	Missense_Mutation	.	SNP	G	G	T	rs142400397	shanshan_et_al_P94	p.T627K	ENSG00000179603	ENST00000339582	Transcript	missense_variant	probably_damaging(0.988)
chr7	637967	63796736	*ZNF736*	Missense_Mutation	.	SNP	G	G	A	novel	shanshan_et_al_P94	p.E35K	ENSG00000234444	ENST00000423484	Transcript	missense_variant	possibly_damaging(0.896)
chr8	113516	113516187	*CSMD3*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.Y1639N	ENSG00000164796	ENST00000297405	Transcript	missense_variant	probably_damaging(0.995)
chr8	128752	128752857	*MYC*	Missense_Mutation	.	SNP	G	G	C	novel	shanshan_et_al_P94	p.V340L	ENSG00000136997	ENST00000377970	Transcript	missense_variant	benign(0.09)
chr9	101151	101151138	*GABBR2*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P94	p.Q509H	ENSG00000136928	ENST00000259455	Transcript	missense_variant	benign(0.003)
chr9	107595	107595019	*ABCA1*	Frame_Shift_Del	.	DEL	A	A	-	novel	shanshan_et_al_P94	p.W449Gfs*8	ENSG00000165029	ENST00000374736	Transcript	frameshift_variant	NA
chr9	135777	135777083	*TSC1*	Nonsense_Mutation	.	SNP	T	T	A	novel	shanshan_et_al_P94	p.K799*	ENSG00000165699	ENST00000298552	Transcript	stop_gained	NA
chr9	147597	14759790	*FREM1*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.S1772T	ENSG00000164946	ENST00000422223	Transcript	missense_variant	possibly_damaging(0.824)
chr9	164366	16436624	*BNC2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.A523E	ENSG00000173068	ENST00000380672	Transcript	missense_variant	benign(0.171)
chr9	177864	17786417	*SH3GL2*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.K76*	ENSG00000107295	ENST00000380607	Transcript	stop_gained	NA
chr9	407056	40705608	*SPATA31A3*	Nonsense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P94	p.R1089*	ENSG00000147926	ENST00000356699	Transcript	stop_gained	NA
chr9	960549	96054925	*WNK2*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P94	p.L1763F	ENSG00000165238	ENST00000297954	Transcript	missense_variant	unknown(0)
chr1	200055	20005583	*HTR6*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P98	p.A349S	ENSG00000158748	ENST00000289753	Transcript	missense_variant	possibly_damaging(0.661)
chr1	380822	38082234	*RSPO1*	Missense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P98	p.R70S	ENSG00000169218	ENST00000356545	Transcript	missense_variant	probably_damaging(0.926)
chr1	688967	68896781	*RPE65*	Missense_Mutation	.	SNP	C	C	A	rs148859816	shanshan_et_al_P98	p.V473F	ENSG00000116745	ENST00000262340	Transcript	missense_variant	probably_damaging(0.924)
chr10	105889	105889958	*WDR96*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P98	p.I1646T	ENSG00000197748	ENST00000357060	Transcript	missense_variant	benign(0.07)
chr10	128147	128147638	*C10orf90*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P98	p.K623R	ENSG00000154493	ENST00000284694	Transcript	missense_variant	probably_damaging(0.975)
chr11	660313	66031347	*KLC2*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P98	p.A289E	ENSG00000174996	ENST00000417856	Transcript	missense_variant	probably_damaging(0.965)
chr11	795020	7950202	*OR10A6*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P98	p.R3I	ENSG00000175393	ENST00000309838	Transcript	missense_variant	benign(0.008)
chr12	111743	11174371	*TAS2R19*	Missense_Mutation	.	SNP	A	A	G	novel	shanshan_et_al_P98	p.V267A	ENSG00000212124	ENST00000390673	Transcript	missense_variant	benign(0.005)
chr14	218540	21854023	*CHD8*	Missense_Mutation	.	SNP	g	g	T	novel	shanshan_et_al_P98	p.P2499T	ENSG00000100888	ENST00000399982	Transcript	missense_variant	possibly_damaging(0.641)
chr14	737279	73727967	*PAPLN*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P98	p.P710R	ENSG00000100767	ENST00000340738	Transcript	missense_variant	probably_damaging(0.994)
chr16	307452	30745237	*SRCAP*	Nonsense_Mutation	.	SNP	G	G	T	novel	shanshan_et_al_P98	p.E2173*	ENSG00000080603	ENST00000262518	Transcript	stop_gained	NA
chr17	266864	26686410	*TMEM199*	Missense_Mutation	.	SNP	C	C	T	novel	shanshan_et_al_P98	p.R120C	ENSG00000244045	ENST00000292114	Transcript	missense_variant	possibly_damaging(0.908)
chr17	355492	35549227	*ACACA*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P98	p.Y1407C	ENSG00000132142	ENST00000353139	Transcript	missense_variant	probably_damaging(0.999)
chr17	366254	36625495	*ARHGAP23*	Missense_Mutation	.	SNP	C	C	A	novel	shanshan_et_al_P98	p.P587T	ENSG00000225485	ENST00000431231	Transcript	missense_variant	probably_damaging(0.987)
chr17	794789	79478964	*ACTG1*	Frame_Shift_Del	.	DEL	G	G	-	novel	shanshan_et_al_P98	p.N111Tfs*9	ENSG00000184009	ENST00000575842	Transcript	frameshift_variant	NA
chr2	468421	46842196	*PIGF*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P98	p.I36M	ENSG00000151665	ENST00000281382	Transcript	missense_variant	possibly_damaging(0.675)
chr5	134785	134785292	*TIFAB*	Missense_Mutation	.	SNP	A	A	T	novel	shanshan_et_al_P98	p.L113Q	ENSG00000255833	ENST00000537858	Transcript	missense_variant	possibly_damaging(0.459)

chr9	107367427	107367427	*OR13C2*	Missense_Mutation	.	SNP	A	A	C	novel	shanshan_et_al_P98	p.V161G	ENSG00000257019	ENST00000542196	Transcript	missense_variant	benign(0.001)
chrX	117677486	117677486	*DOCK11*	Missense_Mutation	.	SNP	T	T	C	novel	shanshan_et_al_P98	p.Y108H	ENSG00000147251	ENST00000276202	Transcript	missense_variant	probably_damaging(0.999)
chrX	58108898	58108898	*NLGN4X*	Missense_Mutation	.	SNP	C	C	G	novel	shanshan_et_al_P98	p.S804T	ENSG00000146938	ENST00000381095	Transcript	missense_variant	benign(0.001)

Table S5: Predicted synonymous SNVs

Chr	Start	End	Gene	MutationType	SNVType	Ref	Tumor_ref	Tumor_variant	dbSNP142	LibraryName	Annotation	EnsemblGeneID	EnsemblTranscriptID	Transcript
chr1	213068329	213068329	*FLVCR1*	Silent	SNP	A	A	T	novel	chan_et_al_P10	p.A509A	ENSG00000162769	ENST00000366971	Transcript
chr1	3680328	3680328	*CCDC27*	Silent	SNP	C	C	A	rs539234988	chan_et_al_P10	p.I460I	ENSG00000162592	ENST00000294600	Transcript
chr10	22617624	22617624	*BMI1*	Silent	SNP	C	C	T	novel	chan_et_al_P10	p.F189F	ENSG00000168283	ENST00000376663	Transcript
chr11	116767063	116767063	*SIK3*	Silent	SNP	C	C	A	novel	chan_et_al_P10	p.V199V	ENSG00000160584	ENST00000292055	Transcript
chr11	57148164	57148164	*PRG3*	Silent	SNP	G	G	C	novel	chan_et_al_P10	p.L6L	ENSG00000156575	ENST00000287143	Transcript
chr12	112174777	112174777	*ACAD10*	Silent	SNP	C	C	A	rs561759186	chan_et_al_P10	p.I592I	ENSG00000111271	ENST00000455480	Transcript
chr12	9162052	9162052	*KLRG1*	Silent	SNP	C	C	T	rs145154967	chan_et_al_P10	p.C163C	ENSG00000139187	ENST00000356986	Transcript
chr16	75513688	75513688	*CHST6*	Silent	SNP	C	C	A	novel	chan_et_al_P10	p.A13A	ENSG00000183196	ENST00000332272	Transcript
chr17	10267773	10267773	*MYH13*	Silent	SNP	G	G	A	novel	chan_et_al_P10	p.I25I	ENSG00000006788	ENST00000418404	Transcript
chr17	76565535	76565535	*DNAH17*	Silent	SNP	G	G	T	novel	chan_et_al_P10	p.I373I	ENSG00000187775	ENST00000389840	Transcript
chr18	34385407	34385407	*TPGS2*	Silent	SNP	G	G	T	novel	chan_et_al_P10	p.L104L	ENSG00000134779	ENST00000334295	Transcript
chr19	15838925	15838925	*OR10H2*	Silent	SNP	A	A	G	rs61733112	chan_et_al_P10	p.Q24Q	ENSG00000171942	ENST00000305899	Transcript
chr19	43031407	43031407	*CEACAM1*	Silent	SNP	C	C	G	rs79326931	chan_et_al_P10	p.G70G	ENSG00000079385	ENST00000161559	Transcript
chr2	237246885	237246885	*IQCA1*	Silent	SNP	A	A	T	novel	chan_et_al_P10	p.I699I	ENSG00000132321	ENST00000409907	Transcript
chr3	113858473	113858473	*DRD3*	Silent	SNP	C	C	A	novel	chan_et_al_P10	p.L199L	ENSG00000151577	ENST00000383673	Transcript
chr3	121361820	121361820	*HCLS1*	Silent	SNP	G	G	A	novel	chan_et_al_P10	p.V136V	ENSG00000180353	ENST00000314583	Transcript
chr3	58133967	58133967	*FLNB*	Silent	SNP	C	C	A	novel	chan_et_al_P10	p.G1952G	ENSG00000136068	ENST00000490882	Transcript
chr4	185615876	185615876	*PRIMPOL*	Silent	SNP	T	T	C	novel	chan_et_al_P10	p.Y542Y	ENSG00000164306	ENST00000314970	Transcript
chr5	108714675	108714675	*PJA2*	Silent	SNP	A	A	G	novel	chan_et_al_P10	p.D171D	ENSG00000198961	ENST00000361189	Transcript
chr6	155764473	155764473	*NOX3*	Silent	SNP	G	G	A	novel	chan_et_al_P10	p.A140A	ENSG00000074771	ENST00000159060	Transcript
chr6	34824086	34824086	*UHRF1BP1*	Silent	SNP	G	G	T	novel	chan_et_al_P10	p.L397L	ENSG00000065060	ENST00000192788	Transcript
chr7	55912377	55912377	*Sep/14*	Silent	SNP	G	G	A	novel	chan_et_al_P10	p.D70D	ENSG00000154997	ENST00000388975	Transcript
chrX	50350698	50350698	*SHROOM4*	Silent	SNP	c	c	T	novel	chan_et_al_P10	p.E1148E	ENSG00000158352	ENST00000376020	Transcript
chr12	32906968	32906968	*YARS2*	Silent	SNP	T	T	A	novel	chan_et_al_P4	p.T277T	ENSG00000139131	ENST00000324868	Transcript
chr13	114530072	114530072	*GAS6*	Silent	SNP	G	G	T	novel	chan_et_al_P4	p.I458I	ENSG00000183087	ENST00000327773	Transcript
chr15	84907103	84907103	*GOLGA6L4*	Silent	SNP	G	G	A	novel	chan_et_al_P4	p.E76E	ENSG00000184206	ENST00000510439	Transcript
chr16	57832000	57832000	*KIFC3*	Silent	SNP	C	C	T	novel	chan_et_al_P4	p.P52P	ENSG00000140859	ENST00000379655	Transcript
chr5	70785392	70785392	*BDP1*	Silent	SNP	C	C	T	novel	chan_et_al_P4	p.L459L	ENSG00000145734	ENST00000358731	Transcript
chr7	129668850	129668850	*ZC3HC1*	Silent	SNP	G	G	A	rs191694541	chan_et_al_P4	p.P171P	ENSG00000091732	ENST00000358303	Transcript
chr7	72987224	72987224	*TBL2*	Silent	SNP	G	G	A	novel	chan_et_al_P4	p.I225I	ENSG00000106638	ENST00000305632	Transcript
chrX	23353043	23353043	*PTCHD1*	Silent	SNP	C	C	A	novel	chan_et_al_P4	p.L17L	ENSG00000165186	ENST00000379361	Transcript
chrX	57936462	57936462	*ZXDA*	Silent	SNP	G	G	A	rs60293829	chan_et_al_P4	p.N131N	ENSG00000198205	ENST00000358697	Transcript
chr1	12321055	12321055	*VPS13D*	Silent	SNP	A	A	C	novel	chan_et_al_P5	p.P421P	ENSG00000048707	ENST00000358136	Transcript
chr1	186648497	186648497	*PTGS2*	Silent	SNP	G	G	A	rs200215667	chan_et_al_P5	p.C42C	ENSG00000073756	ENST00000367468	Transcript
chr1	19201992	19201992	*ALDH4A1*	Silent	SNP	G	G	T	novel	chan_et_al_P5	p.I448I	ENSG00000159423	ENST00000375341	Transcript
chr1	215768774	215768774	*KCTD3*	Silent	SNP	G	G	T	novel	chan_et_al_P5	p.G298G	ENSG00000136636	ENST00000259154	Transcript
chr1	3395162	3395162	*ARHGEF16*	Silent	SNP	C	C	A	novel	chan_et_al_P5	p.L600L	ENSG00000130762	ENST00000378378	Transcript
chr12	53207603	53207603	*KRT4*	Silent	SNP	A	A	G	novel	chan_et_al_P5	p.F80F	ENSG00000170477	ENST00000551956	Transcript
chr12	53207606	53207606	*KRT4*	Silent	SNP	G	G	A	novel	chan_et_al_P5	p.G79G	ENSG00000170477	ENST00000551956	Transcript

chr13	25671827	25671827	*PABPC3*	Silent	SNP	C	C	T	rs184056840	chan_et_al_P5	p.T497T	ENSG00000151846	ENST00000281589	Transcript
chr14	36155748	36155748	*RALGAPA1*	Silent	SNP	C	C	A	rs116939827	chan_et_al_P5	p.S853S	ENSG00000174373	ENST00000307138	Transcript
chr16	27244460	27244460	*NSMCE1*	Silent	SNP	C	C	T	novel	chan_et_al_P5	p.L115L	ENSG00000169189	ENST00000361439	Transcript
chr16	87451234	87451234	*ZCCHC14*	Silent	SNP	C	C	A	rs374632777	chan_et_al_P5	p.A268A	ENSG00000140948	ENST00000268616	Transcript
chr19	11123765	11123765	*SMARCA4*	Silent	SNP	C	C	T	novel	chan_et_al_P5	p.P805P	ENSG00000127616	ENST00000429416	Transcript
chr19	57133369	57133369	*ZNF71*	Silent	SNP	G	G	C	rs371614088	chan_et_al_P5	p.G238G	ENSG00000197951	ENST00000328070	Transcript
chr2	228128542	228128542	*COL4A3*	Silent	SNP	G	G	T	novel	chan_et_al_P5	p.L399L	ENSG00000169031	ENST00000396578	Transcript
chr22	50279728	50279728	*ZBED4*	Silent	SNP	C	C	A	rs141200268	chan_et_al_P5	p.T806T	ENSG00000100426	ENST00000216268	Transcript
chr3	128780792	128780792	*GP9*	Silent	SNP	C	C	T	novel	chan_et_al_P5	p.A70A	ENSG00000169704	ENST00000307395	Transcript
chr3	38138150	38138150	*DLEC1*	Silent	SNP	C	C	T	novel	chan_et_al_P5	p.F754F	ENSG00000008226	ENST00000308059	Transcript
chr3	75788390	75788390	*ZNF717*	Silent	SNP	A	A	C	novel	chan_et_al_P5	p.V128V	ENSG00000227124	ENST00000422325	Transcript
chr4	48035062	48035062	*NIPAL1*	Silent	SNP	C	C	T	novel	chan_et_al_P5	p.T141T	ENSG00000163293	ENST00000295461	Transcript
chr6	136564000	136564000	*MTFR2*	Silent	SNP	G	G	T	rs201167393	chan_et_al_P5	p.R94R	ENSG00000146410	ENST00000420702	Transcript
chr7	72744286	72744286	*FKBP6*	Silent	SNP	C	C	A	novel	chan_et_al_P5	p.V133V	ENSG00000077800	ENST00000252037	Transcript
chr8	22106684	22106684	*POLR3D*	Silent	SNP	C	C	A	novel	chan_et_al_P5	p.T261T	ENSG00000168495	ENST00000397802	Transcript
chr8	99161081	99161081	*POP1*	Silent	SNP	G	G	T	novel	chan_et_al_P5	p.G583G	ENSG00000104356	ENST00000401707	Transcript
chr10	76788668	76788668	*KAT6B*	Silent	SNP	a	a	G	novel	chan_et_al_P9	p.E1362E	ENSG00000156650	ENST00000287239	Transcript
chr16	72821648	72821648	*ZFHX3*	Silent	SNP	g	g	A	novel	chan_et_al_P9	p.G3509G	ENSG00000140836	ENST00000268489	Transcript
chr17	36338296	36338296	*TBC1D3*	Silent	SNP	C	C	G	novel	chan_et_al_P9	p.T460T	ENSG00000197681	ENST00000537432	Transcript
chr19	4508849	4508849	*PLIN4*	Silent	SNP	C	C	A	novel	chan_et_al_P9	p.V1197V	ENSG00000167676	ENST00000301286	Transcript
chr20	31828045	31828045	*BPIFA1*	Silent	SNP	G	G	T	novel	chan_et_al_P9	p.L145L	ENSG00000198183	ENST00000354297	Transcript
chr21	47851679	47851679	*PCNT*	Silent	SNP	G	G	A	novel	chan_et_al_P9	p.L2767L	ENSG00000160299	ENST00000359568	Transcript
chr3	122634629	122634629	*SEMA5B*	Silent	SNP	G	G	A	rs187567378	chan_et_al_P9	p.T653T	ENSG00000082684	ENST00000451055	Transcript
chr8	18074438	18074438	*NAT1*	Silent	SNP	C	C	G	novel	chan_et_al_P9	p.L12L	ENSG00000171428	ENST00000545197	Transcript
chr9	100919760	100919760	*CORO2A*	Silent	SNP	G	G	T	rs369567914	chan_et_al_P9	p.L61L	ENSG00000106789	ENST00000343933	Transcript
chrX	70328481	70328481	*IL2RG*	Silent	SNP	G	G	T	novel	chan_et_al_P9	p.I274I	ENSG00000147168	ENST00000374202	Transcript
chr1	222903391	222903391	*BROX*	Silent	SNP	G	G	T	novel	chan_et_al_P1	p.L287L	ENSG00000162819	ENST00000340934	Transcript
chr1	43675479	43675479	*WDR65*	Silent	SNP	C	C	T	novel	chan_et_al_P1	p.R607R	ENSG00000243710	ENST00000528956	Transcript
chr1	9833406	9833406	*CLSTN1*	Silent	SNP	G	G	A	novel	chan_et_al_P1	p.V46V	ENSG00000171603	ENST00000377298	Transcript
chr10	11789402	11789402	*ECHDC3*	Silent	SNP	G	G	C	novel	chan_et_al_P1	p.L75L	ENSG00000134463	ENST00000379215	Transcript
chr10	128841381	128841381	*DOCK1*	Silent	SNP	T	T	A	novel	chan_et_al_P1	p.V697V	ENSG00000150760	ENST00000280333	Transcript
chr11	120340076	120340076	*ARHGEF12*	Silent	SNP	C	C	A	novel	chan_et_al_P1	p.V978V	ENSG00000196914	ENST00000397843	Transcript
chr11	56143408	56143408	*OR8U1*	Silent	SNP	C	C	T	novel	chan_et_al_P1	p.C103C	ENSG00000172199	ENST00000302270	Transcript
chr11	74015415	74015415	*P4HA3*	Silent	SNP	G	G	T	novel	chan_et_al_P1	p.T81T	ENSG00000149380	ENST00000331597	Transcript
chr12	54107617	54107617	*CALCOCO1*	Silent	SNP	G	G	A	novel	chan_et_al_P1	p.G553G	ENSG00000012822	ENST00000550804	Transcript
chr12	8990943	8990943	*A2ML1*	Silent	SNP	A	A	T	novel	chan_et_al_P1	p.T289T	ENSG00000166535	ENST00000299698	Transcript
chr13	72440884	72440884	*DACH1*	Silent	SNP	G	G	T	novel	chan_et_al_P1	p.I8I	ENSG00000165659	ENST00000305425	Transcript
chr16	88802631	88802631	*PIEZO1*	Silent	SNP	G	G	A	novel	chan_et_al_P1	p.T494T	ENSG00000103335	ENST00000301015	Transcript
chr17	9683221	9683221	*DHRS7C*	Silent	SNP	C	C	A	rs371028236	chan_et_al_P1	p.G134G	ENSG00000184544	ENST00000330255	Transcript
chr18	64172337	64172337	*CDH19*	Silent	SNP	C	C	T	novel	chan_et_al_P1	p.E677E	ENSG00000071991	ENST00000262150	Transcript
chr19	1008622	1008622	*GRIN3B*	Silent	SNP	G	G	A	novel	chan_et_al_P1	p.L824L	ENSG00000116032	ENST00000234389	Transcript

chr19	43433667	43433667	*PSG7*	Silent	SNP	T	T	A	novel	chan_et_al_P1	p.A212A	ENSG00000221878	ENST00000406070	Transcript
chr19	9324953	9324953	*OR7D4*	Silent	SNP	C	C	A	novel	chan_et_al_P1	p.V187V	ENSG00000174667	ENST00000308682	Transcript
chr2	237395535	237395535	*IQCA1*	Silent	SNP	T	T	C	novel	chan_et_al_P1	p.R219R	ENSG00000132321	ENST00000409907	Transcript
chr20	36870302	36870302	*KIAA1755*	Silent	SNP	G	G	A	rs150134184	chan_et_al_P1	p.H77H	ENSG00000149633	ENST00000279024	Transcript
chr22	41982090	41982090	*PMM1*	Silent	SNP	G	G	A	novel	chan_et_al_P1	p.D65D	ENSG00000100417	ENST00000216259	Transcript
chr22	46931655	46931655	*CELSR1*	Silent	SNP	G	G	A	novel	chan_et_al_P1	p.D471D	ENSG00000075275	ENST00000262738	Transcript
chr3	112736355	112736355	*C3orf17*	Silent	SNP	T	T	A	novel	chan_et_al_P1	p.A67A	ENSG00000163608	ENST00000314400	Transcript
chr3	194320255	194320255	*KCNH8*	Silent	SNP	C	C	A	novel	chan_et_al_P1	p.I288I	ENSG00000183960	ENST00000328405	Transcript
chr3	49843419	49843419	*UBA7*	Silent	SNP	C	C	T	novel	chan_et_al_P1	p.G940G	ENSG00000182179	ENST00000333486	Transcript
chr4	160252591	160252591	*RAPGEF2*	Silent	SNP	G	G	T	novel	chan_et_al_P1	p.R331R	ENSG00000109756	ENST00000264431	Transcript
chr4	190947558	190947558	*FRG2*	Silent	SNP	G	G	A	novel	chan_et_al_P1	p.D104D	ENSG00000205097	ENST00000378763	Transcript
chr5	140590651	140590651	*PCDHB12*	Silent	SNP	C	C	A	novel	chan_et_al_P1	p.R724R	ENSG00000120328	ENST00000239450	Transcript
chr5	149375117	149375117	*TIGD6*	Silent	SNP	C	C	T	novel	chan_et_al_P1	p.L265L	ENSG00000164296	ENST00000296736	Transcript
chr5	156924044	156924044	*ADAM19*	Silent	SNP	C	C	A	novel	chan_et_al_P1	p.P484P	ENSG00000135074	ENST00000257527	Transcript
chr5	176562224	176562224	*NSD1*	Silent	SNP	T	T	A	novel	chan_et_al_P1	p.S40S	ENSG00000165671	ENST00000439151	Transcript
chr5	74675285	74675285	*COL4A3BP*	Silent	SNP	T	T	C	novel	chan_et_al_P1	p.G715G	ENSG00000113163	ENST00000380494	Transcript
chr6	26124007	26124007	*HIST1H2BC*	Silent	SNP	C	C	T	novel	chan_et_al_P1	p.V42V	ENSG00000180596	ENST00000314332	Transcript
chr7	151372554	151372554	*PRKAG2*	Silent	SNP	C	C	T	rs149820808	chan_et_al_P1	p.P212P	ENSG00000106617	ENST00000287878	Transcript
chr7	18669052	18669052	*HDAC9*	Silent	SNP	G	G	T	novel	chan_et_al_P1	p.R248R	ENSG00000048052	ENST00000441542	Transcript
chr8	37720518	37720518	*RAB11FIP1*	Silent	SNP	G	G	A	rs139962167	chan_et_al_P1	p.R1249R	ENSG00000156675	ENST00000330843	Transcript
chr9	131821549	131821549	*FAM73B*	Silent	SNP	C	C	A	rs550208218	chan_et_al_P1	p.L264L	ENSG00000148343	ENST00000358369	Transcript
chrX	34149640	34149640	*FAM47A*	Silent	SNP	G	G	T	novel	chan_et_al_P1	p.P252P	ENSG00000185448	ENST00000346193	Transcript
chr1	114515768	114515768	*HIPK1*	Silent	SNP	G	G	A	novel	chan_et_al_P2	p.P1089P	ENSG00000163349	ENST00000369558	Transcript
chr1	155629592	155629592	*YY1AP1*	Silent	SNP	C	C	T	novel	chan_et_al_P2	p.V841V	ENSG00000163374	ENST00000368339	Transcript
chr11	58391926	58391926	*CNTF*	Silent	SNP	C	C	T	novel	chan_et_al_P2	p.F178F	ENSG00000242689	ENST00000361987	Transcript
chr11	71945329	71945329	*INPPL1*	Silent	SNP	C	C	G	rs370210488	chan_et_al_P2	p.L739L	ENSG00000165458	ENST00000298229	Transcript
chr13	78320977	78320977	*SLAIN1*	Silent	SNP	T	T	C	novel	chan_et_al_P2	p.N251N	ENSG00000139737	ENST00000488699	Transcript
chr16	4829776	4829776	*Sep/12*	Silent	SNP	A	A	G	novel	chan_et_al_P2	p.P246P	ENSG00000140623	ENST00000268231	Transcript
chr19	30500143	30500143	*URI1*	Silent	SNP	t	t	C	rs1127493	chan_et_al_P2	p.D306D	ENSG00000105176	ENST00000542441	Transcript
chr19	40909686	40909686	*PRX*	Silent	SNP	G	G	T	novel	chan_et_al_P2	p.G37G	ENSG00000105227	ENST00000324001	Transcript
chr19	41173904	41173904	*NUMBL*	Silent	SNP	t	t	C	rs79658769	chan_et_al_P2	p.Q433Q	ENSG00000105245	ENST00000252891	Transcript
chr20	30584399	30584399	*XKR7*	Silent	SNP	G	G	A	novel	chan_et_al_P2	p.P293P	ENSG00000260903	ENST00000562532	Transcript
chr20	44841805	44841805	*CDH22*	Silent	SNP	C	C	T	novel	chan_et_al_P2	p.Q287Q	ENSG00000149654	ENST00000372262	Transcript
chr22	29750746	29750746	*AP1B1*	Silent	SNP	G	G	A	rs138572174	chan_et_al_P2	p.Y277Y	ENSG00000100280	ENST00000357586	Transcript
chr3	104209433	104209433	*ATP2B2*	Silent	SNP	G	G	A	novel	chan_et_al_P2	p.D342D	ENSG00000157087	ENST00000360273	Transcript
chr3	38597188	38597188	*SCN5A*	Silent	SNP	G	G	A	rs199473266	chan_et_al_P2	p.L1501L	ENSG00000183873	ENST00000413689	Transcript
chr4	123201092	123201092	*KIAA1109*	Silent	SNP	A	A	G	novel	chan_et_al_P2	p.Q2918Q	ENSG00000138688	ENST00000264501	Transcript
chr7	794296	794296	*HEATR2*	Silent	SNP	C	C	T	novel	chan_et_al_P2	p.C365C	ENSG00000164818	ENST00000297440	Transcript
chr7	95219000	95219000	*PDK4*	Silent	SNP	G	G	T	novel	chan_et_al_P2	p.I241I	ENSG00000004799	ENST00000005178	Transcript
chr1	159166233	159166233	*CADM3*	Silent	SNP	C	C	T	rs373766355	chan_et_al_P3	p.R291R	ENSG00000162706	ENST00000368124	Transcript
chr10	82329971	82329971	*SH2D4B*	Silent	SNP	C	C	T	novel	chan_et_al_P3	p.I82I	ENSG00000178217	ENST00000339284	Transcript

chr11	67432799	67432799	*ALDH3B2*	Silent	SNP	G	G	A	rs80147122	chan_et_al_P3	p.R221R	ENSG00000132746	ENST00000349015	Transcript
chr19	22155760	22155760	*ZNF208*	Silent	SNP	G	G	A	novel	chan_et_al_P3	p.P692P	ENSG00000160321	ENST00000397126	Transcript
chr19	38229801	38229801	*ZNF573*	Silent	SNP	T	T	A	novel	chan_et_al_P3	p.V530V	ENSG00000189144	ENST00000590414	Transcript
chr19	49254508	49254508	*FUT1*	Silent	SNP	G	G	A	novel	chan_et_al_P3	p.L11L	ENSG00000174951	ENST00000310160	Transcript
chr19	49657751	49657751	*HRC*	Silent	SNP	a	a	G	novel	chan_et_al_P3	p.D248D	ENSG00000130528	ENST00000252825	Transcript
chr4	174223204	174223204	*GALNT7*	Silent	SNP	A	A	C	novel	chan_et_al_P3	p.P385P	ENSG00000109586	ENST00000265000	Transcript
chr4	9212865	9212865	*USP17L10*	Silent	SNP	C	C	T	novel	chan_et_al_P3	p.A161A	ENSG00000231396	ENST00000417945	Transcript
chr1	145765381	145765381	*GPR89A*	Silent	SNP	T	T	C	novel	chan_et_al_P6	p.L383L	ENSG00000117262	ENST00000313835	Transcript
chr1	152187271	152187271	*HRNR*	Silent	SNP	C	C	T	novel	chan_et_al_P6	p.Q2278Q	ENSG00000197915	ENST00000368801	Transcript
chr1	152187274	152187274	*HRNR*	Silent	SNP	A	A	G	novel	chan_et_al_P6	p.G2277G	ENSG00000197915	ENST00000368801	Transcript
chr10	105372785	105372785	*SH3PXD2A*	Silent	SNP	A	A	G	novel	chan_et_al_P6	p.T333T	ENSG00000107957	ENST00000355946	Transcript
chr11	121498265	121498265	*SORL1*	Silent	SNP	T	T	G	novel	chan_et_al_P6	p.G2122G	ENSG00000137642	ENST00000260197	Transcript
chr11	55322523	55322523	*OR4C15*	Silent	SNP	C	C	A	novel	chan_et_al_P6	p.I247I	ENSG00000181939	ENST00000314644	Transcript
chr16	81942185	81942185	*PLCG2*	Silent	SNP	C	C	T	novel	chan_et_al_P6	p.T574T	ENSG00000197943	ENST00000359376	Transcript
chr17	3366003	3366003	*SPATA22*	Silent	SNP	G	G	A	novel	chan_et_al_P6	p.T77T	ENSG00000141255	ENST00000573128	Transcript
chr17	45234725	45234725	*CDC27*	Silent	SNP	T	T	C	novel	chan_et_al_P6	p.T167T	ENSG00000004897	ENST00000531206	Transcript
chr18	57136721	57136721	*CCBE1*	Silent	SNP	C	C	T	novel	chan_et_al_P6	p.E128E	ENSG00000183287	ENST00000439986	Transcript
chr19	22155130	22155130	*ZNF208*	Silent	SNP	G	G	T	rs554213637	chan_et_al_P6	p.S902S	ENSG00000160321	ENST00000397126	Transcript
chr19	52660102	52660102	*ZNF836*	Silent	SNP	T	T	C	novel	chan_et_al_P6	p.V278V	ENSG00000196267	ENST00000322146	Transcript
chr19	58850515	58850515	*ZSCAN22*	Silent	SNP	G	G	A	novel	chan_et_al_P6	p.E433E	ENSG00000182318	ENST00000329665	Transcript
chr2	217364737	217364737	*RPL37A*	Silent	SNP	C	C	G	novel	chan_et_al_P6	p.G66G	ENSG00000197756	ENST00000491306	Transcript
chr4	99214581	99214581	*RAP1GDS1*	Silent	SNP	G	G	A	novel	chan_et_al_P6	p.K10K	ENSG00000138698	ENST00000339360	Transcript
chr6	143095087	143095087	*HIVEP2*	Silent	SNP	A	A	C	novel	chan_et_al_P6	p.G263G	ENSG00000010818	ENST00000367603	Transcript
chr8	101727766	101727766	*PABPC1*	Silent	SNP	T	T	C	rs201406152	chan_et_al_P6	p.E189E	ENSG00000070756	ENST00000318607	Transcript
chr8	101727796	101727796	*PABPC1*	Silent	SNP	T	T	C	rs200041005	chan_et_al_P6	p.R179R	ENSG00000070756	ENST00000318607	Transcript
chrX	49034493	49034493	*PRICKLE3*	Silent	SNP	G	G	A	novel	chan_et_al_P6	p.G268G	ENSG00000012211	ENST00000376317	Transcript
chr1	152186149	152186149	*HRNR*	Silent	SNP	G	G	A	novel	chan_et_al_P7	p.S2652S	ENSG00000197915	ENST00000368801	Transcript
chr10	116064562	116064562	*AFAP1L2*	Silent	SNP	G	G	A	novel	chan_et_al_P7	p.G400G	ENSG00000169129	ENST00000304129	Transcript
chr12	88566485	88566485	*TMTC3*	Silent	SNP	T	T	C	novel	chan_et_al_P7	p.L388L	ENSG00000139324	ENST00000266712	Transcript
chr15	83105037	83105037	*GOLGA6L20*	Silent	SNP	A	A	G	novel	chan_et_al_P7	p.E412E	ENSG00000196648	ENST00000561062	Transcript
chr16	2506805	2506805	*CCNF*	Silent	SNP	C	C	T	novel	chan_et_al_P7	p.D715D	ENSG00000162063	ENST00000397066	Transcript
chr16	5134816	5134816	*ALG1*	Silent	SNP	G	G	A	rs1063203	chan_et_al_P7	p.E443E	ENSG00000033011	ENST00000262374	Transcript
chr17	17797047	17797047	*TOM1L2*	Silent	SNP	A	A	G	novel	chan_et_al_P7	p.V98V	ENSG00000175662	ENST00000379504	Transcript
chr22	21346076	21346076	*LZTR1*	Silent	SNP	C	C	T	novel	chan_et_al_P7	p.D317D	ENSG00000099949	ENST00000215739	Transcript
chr6	146708079	146708079	*GRM1*	Silent	SNP	G	G	A	novel	chan_et_al_P7	p.E552E	ENSG00000152822	ENST00000361719	Transcript
chr7	27825018	27825018	*TAX1BP1*	Silent	SNP	T	T	C	novel	chan_et_al_P7	p.S254S	ENSG00000106052	ENST00000396319	Transcript
chr8	74507500	74507500	*STAU2*	Silent	SNP	T	T	C	novel	chan_et_al_P7	p.T354T	ENSG00000040341	ENST00000524300	Transcript
chr17	27085351	27085351	*FAM222B*	Silent	SNP	G	G	A	novel	chan_et_al_P8	p.G542G	ENSG00000173065	ENST00000341217	Transcript
chr19	33493226	33493226	*RHPN2*	Silent	SNP	T	T	C	rs201303400	chan_et_al_P8	p.L344L	ENSG00000131941	ENST00000254260	Transcript
chr19	50169227	50169227	*BCL2L12*	Silent	SNP	G	G	A	rs201895036	chan_et_al_P8	p.V49V	ENSG00000126453	ENST00000246785	Transcript
chr20	44983764	44983764	*SLC35C2*	Silent	SNP	G	G	A	novel	chan_et_al_P8	p.I175I	ENSG00000080189	ENST00000372227	Transcript

chr3	165547928	165547928	*BCHE*	Silent	SNP	T	T	C	rs138271111	chan_et_al_P8	p.Q298Q	ENSG00000114200	ENST00000264381	Transcript
chr3	50380428	50380428	*ZMYND10*	Silent	SNP	G	G	A	novel	chan_et_al_P8	p.S207S	ENSG00000004838	ENST00000231749	Transcript
chr4	5053596	5053596	*STK32B*	Silent	SNP	C	C	T	novel	chan_et_al_P8	p.G2G	ENSG00000152953	ENST00000282908	Transcript
chr6	153292490	153292490	*FBXO5*	Silent	SNP	A	A	T	novel	chan_et_al_P8	p.P384P	ENSG00000112029	ENST00000229758	Transcript
chr7	48391935	48391935	*ABCA13*	Silent	SNP	A	A	T	rs376331882	chan_et_al_P8	p.L3513L	ENSG00000179869	ENST00000435803	Transcript
chr1	229462620	229462620	*CCSAP*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.V167V	ENSG00000154429	ENST00000284617	Transcript
chr1	31842400	31842400	*FABP3*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.V26V	ENSG00000121769	ENST00000373713	Transcript
chr1	41006314	41006314	*ZNF684*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.L24L	ENSG00000117010	ENST00000372699	Transcript
chr1	67470050	67470050	*SLC35D1*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L347L	ENSG00000116704	ENST00000235345	Transcript
chr1	75037452	75037452	*C1orf173*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.S1314S	ENSG00000178965	ENST00000326665	Transcript
chr10	50738886	50738886	*ERCC6*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.T141T	ENSG00000225830	ENST00000355832	Transcript
chr11	104905020	104905020	*CASP1*	Silent	SNP	C	C	T	rs12289229	sia_et_al_P1	p.P63P	ENSG00000137752	ENST00000533400	Transcript
chr11	122944212	122944212	*CLMP*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.P364P	ENSG00000166250	ENST00000448775	Transcript
chr11	31815201	31815201	*PAX6*	Silent	SNP	C	C	T	rs146433004	sia_et_al_P1	p.P319P	ENSG00000007372	ENST00000419022	Transcript
chr11	66239881	66239881	*PELI3*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.L132L	ENSG00000174516	ENST00000320740	Transcript
chr12	49171511	49171511	*ADCY6*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L341L	ENSG00000174233	ENST00000307885	Transcript
chr13	28964183	28964183	*FLT1*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L573L	ENSG00000102755	ENST00000282397	Transcript
chr13	42795488	42795488	*DGKH*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.I1177I	ENSG00000102780	ENST00000337343	Transcript
chr13	47409407	47409407	*HTR2A*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.I327I	ENSG00000102468	ENST00000378688	Transcript
chr14	35231009	35231009	*BAZ1A*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.L1399L	ENSG00000198604	ENST00000360310	Transcript
chr14	55433217	55433217	*WDHD1*	Silent	SNP	C	C	T	novel	sia_et_al_P1	p.Q762Q	ENSG00000198554	ENST00000360586	Transcript
chr14	74443740	74443740	*ENTPD5*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.V180V	ENSG00000187097	ENST00000334696	Transcript
chr14	92471611	92471611	*TRIP11*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.T903T	ENSG00000100815	ENST00000267622	Transcript
chr14	99865112	99865112	*SETD3*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.T563T	ENSG00000183576	ENST00000331768	Transcript
chr15	45444545	45444545	*DUOX1*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.L1085L	ENSG00000137857	ENST00000321429	Transcript
chr15	89843187	89843187	*FANCI*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L931L	ENSG00000140525	ENST00000310775	Transcript
chr16	11362838	11362838	*TNP2*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.R94R	ENSG00000178279	ENST00000312693	Transcript
chr16	66783125	66783125	*DYNC1LI2*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.L91L	ENSG00000135720	ENST00000258198	Transcript
chr16	68100261	68100261	*DUS2*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.T153T	ENSG00000167264	ENST00000565263	Transcript
chr17	10536920	10536920	*MYH3*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.L1545L	ENSG00000109063	ENST00000583535	Transcript
chr17	41165654	41165654	*IFI35*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.V181V	ENSG00000068079	ENST00000438323	Transcript
chr18	10789167	10789167	*PIEZO2*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.G693G	ENSG00000154864	ENST00000503781	Transcript
chr19	41888799	41888799	*TMEM91*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.G111G	ENSG00000142046	ENST00000392002	Transcript
chr2	122106220	122106220	*CLASP1*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.L1427L	ENSG00000074054	ENST00000263710	Transcript
chr2	152522015	152522015	*NEB*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.G1690G	ENSG00000183091	ENST00000397345	Transcript
chr2	190584533	190584533	*ANKAR*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.A820A	ENSG00000151687	ENST00000520309	Transcript
chr2	222310898	222310898	*EPHA4*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.R573R	ENSG00000116106	ENST00000281821	Transcript
chr2	27850274	27850274	*CCDC121*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.V293V	ENSG00000176714	ENST00000394775	Transcript
chr2	39944319	39944319	*TMEM178A*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L274L	ENSG00000152154	ENST00000281961	Transcript
chr2	86400876	86400876	*IMMT*	Silent	SNP	C	C	A	rs527824042	sia_et_al_P1	p.S106S	ENSG00000132305	ENST00000410111	Transcript
chr2	88367494	88367494	*SMYD1*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.R37R	ENSG00000115593	ENST00000419482	Transcript

chr2	8936946	8936946	*KIDINS220*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.V351V	ENSG00000134313	ENST00000256707	Transcript
chr20	23584195	23584195	*CST9*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.V144V	ENSG00000173335	ENST00000376971	Transcript
chr20	48252876	48252876	*B4GALT5*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.P380P	ENSG00000158470	ENST00000371711	Transcript
chr20	50312672	50312672	*ATP9A*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.V169V	ENSG00000054793	ENST00000338821	Transcript
chr21	43256725	43256725	*PRDM15*	Silent	SNP	G	G	A	novel	sia_et_al_P1	p.L711L	ENSG00000141956	ENST00000269844	Transcript
chr22	37966706	37966706	*LGALS2*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L42L	ENSG00000100079	ENST00000215886	Transcript
chr3	168834508	168834508	*MECOM*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.S261S	ENSG00000085276	ENST00000264674	Transcript
chr3	182933805	182933805	*MCF2L2*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.I816I	ENSG00000053524	ENST00000328913	Transcript
chr3	37778451	37778451	*ITGA9*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L737L	ENSG00000144668	ENST00000264741	Transcript
chr3	69168891	69168891	*LMOD3*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.A205A	ENSG00000163380	ENST00000420581	Transcript
chr4	103527673	103527673	*NFKB1*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.V591V	ENSG00000109320	ENST00000226574	Transcript
chr4	166215602	166215602	*KLHL2*	Silent	SNP	C	C	A	rs557525121	sia_et_al_P1	p.T216T	ENSG00000109466	ENST00000514860	Transcript
chr4	166981277	166981277	*TLL1*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.V648V	ENSG00000038295	ENST00000061240	Transcript
chr5	134914177	134914177	*CXCL14*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.V51V	ENSG00000145824	ENST00000337225	Transcript
chr5	140256764	140256764	*PCDHA12*	Silent	SNP	G	G	T	novel	sia_et_al_P1	p.P569P	ENSG00000251664	ENST00000398631	Transcript
chr5	94988904	94988904	*RFESD*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.T48T	ENSG00000175449	ENST00000458310	Transcript
chr6	117252585	117252585	*RFX6*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.S901S	ENSG00000185002	ENST00000332958	Transcript
chr6	119245237	119245237	*MCM9*	Silent	SNP	C	C	A	rs150976419	sia_et_al_P1	p.V120V	ENSG00000111877	ENST00000316316	Transcript
chr6	159687129	159687129	*FNDC1*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.I1766I	ENSG00000164694	ENST00000297267	Transcript
chr6	34826071	34826071	*UHRF1BP1*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.S646S	ENSG00000065060	ENST00000192788	Transcript
chr6	70049357	70049357	*BAI3*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.G1140G	ENSG00000135298	ENST00000370598	Transcript
chr9	136649534	136649534	*VAV2*	Silent	SNP	G	G	A	novel	sia_et_al_P1	p.N513N	ENSG00000160293	ENST00000371850	Transcript
chr9	16437133	16437133	*BNC2*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.R353R	ENSG00000173068	ENST00000380672	Transcript
chr9	35382423	35382423	*UNC13B*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.A826A	ENSG00000198722	ENST00000378495	Transcript
chr9	5772661	5772661	*KIAA1432*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L1238L	ENSG00000107036	ENST00000414202	Transcript
chr9	8341813	8341813	*PTPRD*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.L1609L	ENSG00000153707	ENST00000381196	Transcript
chrX	101660533	101660533	*CLCN4*	Silent	SNP	C	C	A	novel	sia_et_al_P1	p.S169S	ENSG00000073464	ENST00000380833	Transcript
chr16	84125394	84125394	*MBTPS1*	Silent	SNP	G	G	A	rs113848224	sia_et_al_P2	p.D302D	ENSG00000140943	ENST00000343411	Transcript
chr22	22842998	22842998	*ZNF280B*	Silent	SNP	G	G	A	novel	sia_et_al_P2	p.D242D	ENSG00000198477	ENST00000360412	Transcript
chr4	24878169	24878169	*CCDC149*	Silent	SNP	G	G	T	novel	sia_et_al_P2	p.R72R	ENSG00000181982	ENST00000504487	Transcript
chr4	40099071	40099071	*N4BP2*	Silent	SNP	A	A	G	rs142810144	sia_et_al_P2	p.L37L	ENSG00000078177	ENST00000261435	Transcript
chr9	107589436	107589436	*ABCA1*	Silent	SNP	C	C	A	novel	sia_et_al_P2	p.L710L	ENSG00000165029	ENST00000374736	Transcript
chr1	110593019	110593019	*STRIP1*	Silent	SNP	G	G	T	rs371816452	sia_et_al_P7	p.T648T	ENSG00000143093	ENST00000369795	Transcript
chr1	117527447	117527447	*PTGFRN*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V771V	ENSG00000134247	ENST00000393203	Transcript
chr1	119466182	119466182	*TBX15*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.V140V	ENSG00000092607	ENST00000207157	Transcript
chr1	149898653	149898653	*SF3B4*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L107L	ENSG00000143368	ENST00000271628	Transcript
chr1	153736332	153736332	*INTS3*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.V597V	ENSG00000143624	ENST00000318967	Transcript
chr1	158435639	158435639	*OR10K1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.G96G	ENSG00000173285	ENST00000289451	Transcript
chr1	158435678	158435678	*OR10K1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.S109S	ENSG00000173285	ENST00000289451	Transcript
chr1	158576876	158576876	*OR10Z1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I216I	ENSG00000198967	ENST00000361284	Transcript
chr1	169581594	169581594	*SELP*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.T274T	ENSG00000174175	ENST00000263686	Transcript

chr1	182026207	182026207	*ZNF648*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.D313D	ENSG00000179930	ENST00000339948	Transcript
chr1	203683378	203683378	*ATP2B4*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L793L	ENSG00000058668	ENST00000357681	Transcript
chr1	211439 3	211439 3	*EIF4G3*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L1439L	ENSG00000075151	ENST00000602326	Transcript
chr1	226062005	226062005	*TMEM63A*	Silent	SNP	C	C	A	rs151265418	sia_et_al_P7	p.L83L	ENSG00000196187	ENST00000366835	Transcript
chr1	229781656	229781656	*URB2*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L1282L	ENSG00000135763	ENST00000258243	Transcript
chr1	296318 9	296318 9	*PTPRU*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.R927R	ENSG00000060656	ENST00000345512	Transcript
chr1	360689 4	360689 4	*PSMB2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R170R	ENSG00000126067	ENST00000373237	Transcript
chr1	537165 1	537165 1	*LRP8*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L839L	ENSG00000157193	ENST00000306052	Transcript
chr1	537229 4	537229 4	*LRP8*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.P794P	ENSG00000157193	ENST00000306052	Transcript
chr10	119805531	119805531	*RAB11FIP2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.S48S	ENSG00000107560	ENST00000355624	Transcript
chr10	129903138	129903138	*MKI67*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L2322L	ENSG00000148773	ENST00000368654	Transcript
chr10	129910000	129910000	*MKI67*	Silent	SNP	A	A	G	novel	sia_et_al_P7	p.H723H	ENSG00000148773	ENST00000368654	Transcript
chr10	248856 71	248856 71	*ARHGAP21*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R1159R	ENSG00000107863	ENST00000396432	Transcript
chr11	105821 39	105821 39	*LYVE1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V202V	ENSG00000133800	ENST00000256178	Transcript
chr11	113102986	113102986	*NCAM1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.T435T	ENSG00000149294	ENST00000316851	Transcript
chr11	124440273	124440273	*OR8A1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V103V	ENSG00000196119	ENST00000284287	Transcript
chr11	4615418	4615418	*OR52I1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V50V	ENSG00000232268	ENST00000530443	Transcript
chr11	466903 46	466903 46	*ATG13*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V444V	ENSG00000175224	ENST00000528494	Transcript
chr11	5009489	5009489	*MMP26*	Silent	SNP	C	C	T	novel	sia_et_al_P7	p.F16F	ENSG00000167346	ENST00000380390	Transcript
chr11	554328 8	554328 8	*OR4C6*	Silent	SNP	C	C	T	novel	sia_et_al_P7	p.D82D	ENSG00000181903	ENST00000314259	Transcript
chr11	610697 70	610697 70	*DDB1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L1058L	ENSG00000167986	ENST00000301764	Transcript
chr12	105307 36	105307 36	*KLRK1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.P176P	ENSG00000213809	ENST00000240618	Transcript
chr12	116446910	116446910	*MED13L*	Silent	SNP	G	G	T	rs149631695	sia_et_al_P7	p.V436V	ENSG00000123066	ENST00000281928	Transcript
chr12	120599330	120599330	*GCN1L1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.S800S	ENSG00000089154	ENST00000300648	Transcript
chr12	341792 65	341792 65	*ALG10*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R279R	ENSG00000139133	ENST00000266483	Transcript
chr12	419005 06	419005 06	*PDZRN4*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L364L	ENSG00000165966	ENST00000402685	Transcript
chr12	432321	432321	*KDM5A*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V734V	ENSG00000073614	ENST00000399788	Transcript
chr12	492281 57	492281 57	*DDX23*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V502V	ENSG00000174243	ENST00000308025	Transcript
chr12	511023 42	511023 42	*DIP2B*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L882L	ENSG00000066084	ENST00000301180	Transcript
chr12	541069 10	541069 10	*CALCOCO1*	Silent	SNP	C	C	A	rs544723354	sia_et_al_P7	p.L624L	ENSG00000012822	ENST00000550804	Transcript
chr12	668383 80	668383 80	*GRIP1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I505I	ENSG00000155974	ENST00000398016	Transcript
chr12	711397 83	711397 83	*PTPRR*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I274I	ENSG00000153233	ENST00000283228	Transcript
chr12	947616 20	947616 20	*CCDC41*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.R431R	ENSG00000173588	ENST00000397809	Transcript
chr13	111090369	111090369	*COL4A2*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.G282G	ENSG00000134871	ENST00000360467	Transcript
chr13	269675 80	269675 80	*CDK8*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I241I	ENSG00000132964	ENST00000381527	Transcript
chr13	327452 69	327452 69	*FRY*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L671L	ENSG00000073910	ENST00000380250	Transcript
chr14	250768 60	250768 60	*GZMH*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.A99A	ENSG00000100450	ENST00000216338	Transcript
chr14	380618 96	380618 96	*FOXA1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V31V	ENSG00000129514	ENST00000250448	Transcript
chr14	715430 61	715430 61	*PCNX*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L1754L	ENSG00000100731	ENST00000304743	Transcript
chr14	761212 76	761212 76	*C14orf1*	Silent	SNP	G	G	T	rs374591682	sia_et_al_P7	p.L59L	ENSG00000133935	ENST00000256319	Transcript
chr15	284783 83	284783 83	*HERC2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L1528L	ENSG00000128731	ENST00000261609	Transcript

chr15	40093606	40093606	*GPR176*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L425L	ENSG00000166073	ENST00000561100	Transcript
chr15	66786837	66786837	*SNAPC5*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L78L	ENSG00000174446	ENST00000316634	Transcript
chr15	77406921	77406921	*PEAK1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.P1606P	ENSG00000173517	ENST00000560626	Transcript
chr16	20494463	20494463	*ACSM2A*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V531V	ENSG00000183747	ENST00000573854	Transcript
chr16	27504019	27504019	*GTF3C1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.S964S	ENSG00000077235	ENST00000356183	Transcript
chr16	70590917	70590917	*SF3B3*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.L665L	ENSG00000189091	ENST00000302516	Transcript
chr16	70708287	70708287	*MTSS1L*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.S325S	ENSG00000132613	ENST00000338779	Transcript
chr16	88653043	88653043	*ZC3H18*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.P213P	ENSG00000158545	ENST00000301011	Transcript
chr17	15642064	15642064	*TBC1D26*	Silent	SNP	C	C	A	rs377458137	sia_et_al_P7	p.S139S	ENSG00000214946	ENST00000437605	Transcript
chr17	16203286	16203286	*PIGL*	Silent	SNP	C	C	A	rs374713933	sia_et_al_P7	p.I140I	ENSG00000108474	ENST00000225609	Transcript
chr17	37676248	37676248	*CDK12*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L1001L	ENSG00000167258	ENST00000447079	Transcript
chr17	38910715	38910715	*KRT25*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I145I	ENSG00000204897	ENST00000312150	Transcript
chr17	56350905	56350905	*MPO*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.A497A	ENSG00000005381	ENST00000225275	Transcript
chr17	61613182	61613182	*KCNH6*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I418I	ENSG00000173826	ENST00000583023	Transcript
chr18	7034684	7034684	*LAMA1*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.N615N	ENSG00000101680	ENST00000389658	Transcript
chr19	110684	110684	*OR4F17*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V2V	ENSG00000176695	ENST00000585993	Transcript
chr19	16060003	16060003	*OR10H4*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L62L	ENSG00000176231	ENST00000322107	Transcript
chr19	17760369	17760369	*UNC13A*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.D489D	ENSG00000130477	ENST00000519716	Transcript
chr19	18311237	18311237	*RAB3A*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R83R	ENSG00000105649	ENST00000222256	Transcript
chr19	33133033	33133033	*ANKRD27*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.A267A	ENSG00000105186	ENST00000306065	Transcript
chr19	36045956	36045956	*ATP4A*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L783L	ENSG00000105675	ENST00000262623	Transcript
chr19	49693551	49693551	*TRPM4*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L702L	ENSG00000130529	ENST00000252826	Transcript
chr19	53613139	53613139	*ZNF415*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I53I	ENSG00000170954	ENST00000500065	Transcript
chr19	53741683	53741683	*ZNF677*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V99V	ENSG00000197928	ENST00000333952	Transcript
chr19	55452870	55452870	*NLRP7*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.A70A	ENSG00000167634	ENST00000588756	Transcript
chr2	100209774	100209774	*AFF3*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.P808P	ENSG00000144218	ENST00000356421	Transcript
chr2	113378088	113378088	*ROCK2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I1041I	ENSG00000134318	ENST00000315872	Transcript
chr2	113420464	113420464	*SLC20A1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.G634G	ENSG00000144136	ENST00000272542	Transcript
chr2	176804342	176804342	*KIAA1715*	Silent	SNP	G	G	T	rs369301283	sia_et_al_P7	p.P250P	ENSG00000144320	ENST00000272748	Transcript
chr2	198334883	198334883	*COQ10B*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.T179T	ENSG00000115520	ENST00000263960	Transcript
chr2	204785555	204785555	*PUM2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.A582A	ENSG00000055917	ENST00000338086	Transcript
chr2	276045688	276045688	*PPM1G*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L513L	ENSG00000115241	ENST00000344034	Transcript
chr2	32770915	32770915	*BIRC6*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V4266V	ENSG00000115760	ENST00000421745	Transcript
chr2	39515407	39515407	*MAP4K3*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.F443F	ENSG00000011566	ENST00000263881	Transcript
chr2	71012577	71012577	*FIGLA*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.T193T	ENSG00000183733	ENST00000332372	Transcript
chr2	75101000	75101000	*HK2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V207V	ENSG00000159399	ENST00000290573	Transcript
chr2	9650150	9650150	*ADAM17*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V434V	ENSG00000151694	ENST00000310823	Transcript
chr20	36488739	36488739	*CTNNBL1*	Silent	SNP	C	C	A	rs200817413	sia_et_al_P7	p.I532I	ENSG00000132792	ENST00000361383	Transcript
chr20	44669224	44669224	*SLC12A5*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I298I	ENSG00000124140	ENST00000454036	Transcript
chr20	4913179	4913179	*SLC23A2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.S10S	ENSG00000089057	ENST00000379333	Transcript
chr21	18981414	18981414	*BTG3*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R17R	ENSG00000154640	ENST00000339775	Transcript

chr21	45651284	45651284	*ICOSLG*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V247V	ENSG00000160223	ENST00000407780	Transcript
chr22	36205941	36205941	*RBFOX2*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.H116H	ENSG00000100320	ENST00000438146	Transcript
chr3	12861587	12861587	*CAND2*	Silent	SNP	C	C	A	rs544377883	sia_et_al_P7	p.R983R	ENSG00000144712	ENST00000456430	Transcript
chr3	39452253	39452253	*RPSA*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V87V	ENSG00000168028	ENST00000301821	Transcript
chr3	47910778	47910778	*MAP4*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R967R	ENSG00000047849	ENST00000360240	Transcript
chr3	58380820	58380820	*PXK*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L237L	ENSG00000168297	ENST00000356151	Transcript
chr3	71027076	71027076	*FOXP1*	Silent	SNP	G	G	T	rs564136633	sia_et_al_P7	p.V419V	ENSG00000114861	ENST00000491238	Transcript
chr4	110763678	110763678	*RRH*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I258I	ENSG00000180245	ENST00000317735	Transcript
chr4	122780312	122780312	*BBS7*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L121L	ENSG00000138686	ENST00000264499	Transcript
chr4	144618199	144618199	*FREM3*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.V1210V	ENSG00000183090	ENST00000329798	Transcript
chr4	158073928	158073928	*GLRB*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.P321P	ENSG00000109738	ENST00000264428	Transcript
chr4	3219628	3219628	*HTT*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I2397I	ENSG00000197386	ENST00000355072	Transcript
chr4	76811272	76811272	*PPEF2*	Silent	SNP	G	G	T	rs199592989	sia_et_al_P7	p.T85T	ENSG00000156194	ENST00000286719	Transcript
chr4	81121372	81121372	*PRDM8*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L46L	ENSG00000152784	ENST00000339711	Transcript
chr5	101709182	101709182	*SLCO6A1*	Silent	SNP	T	T	A	rs375156373	sia_et_al_P7	p.L678L	ENSG00000205359	ENST00000506729	Transcript
chr5	112870083	112870083	*YTHDC2*	Silent	SNP	G	G	T	rs138017553	sia_et_al_P7	p.S308S	ENSG00000047188	ENST00000161863	Transcript
chr5	132269980	132269980	*AFF4*	Silent	SNP	G	G	T	rs200345107	sia_et_al_P7	p.P259P	ENSG00000072364	ENST00000265343	Transcript
chr5	146778813	146778813	*DPYSL3*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.A485A	ENSG00000113657	ENST00000343218	Transcript
chr5	170319425	170319425	*RANBP17*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.P97P	ENSG00000204764	ENST00000523189	Transcript
chr5	32263326	32263326	*MTMR12*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.T202T	ENSG00000150712	ENST00000382142	Transcript
chr5	35065389	35065389	*PRLR*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I557I	ENSG00000113494	ENST00000382002	Transcript
chr5	83259159	83259159	*EDIL3*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.T386T	ENSG00000164176	ENST00000296591	Transcript
chr6	116559439	116559439	*NT5DC1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L337L	ENSG00000178425	ENST00000319550	Transcript
chr6	131973684	131973684	*ENPP3*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.R94R	ENSG00000154269	ENST00000414305	Transcript
chr6	158537272	158537272	*SERAC1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L482L	ENSG00000122335	ENST00000367104	Transcript
chr6	160453600	160453600	*IGF2R*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L300L	ENSG00000197081	ENST00000356956	Transcript
chr6	24576797	24576797	*KIAA0319*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.A511A	ENSG00000137261	ENST00000378214	Transcript
chr6	44249952	44249952	*TCTE1*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.L397L	ENSG00000146221	ENST00000371505	Transcript
chr7	128481399	128481399	*FLNC*	Silent	SNP	T	T	A	novel	sia_et_al_P7	p.P663P	ENSG00000128591	ENST00000325888	Transcript
chr7	143018576	143018576	*CLCN1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.P184P	ENSG00000188037	ENST00000343257	Transcript
chr7	30485768	30485768	*NOD1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I814I	ENSG00000106100	ENST00000222823	Transcript
chr7	37136311	37136311	*ELMO1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R405R	ENSG00000155849	ENST00000310758	Transcript
chr7	66660288	66660288	*TYW1*	Silent	SNP	C	C	T	novel	sia_et_al_P7	p.H647H	ENSG00000198874	ENST00000359626	Transcript
chr7	77708295	77708295	*MAGI2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L1225L	ENSG00000187391	ENST00000354212	Transcript
chr7	95457402	95457402	*DYNC1I1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L133L	ENSG00000158560	ENST00000324972	Transcript
chr8	142161735	142161735	*DENND3*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L211L	ENSG00000105339	ENST00000262585	Transcript
chr8	42694511	42694511	*THAP1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R29R	ENSG00000131931	ENST00000254250	Transcript
chr8	53071491	53071491	*ST18*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I591I	ENSG00000147488	ENST00000276480	Transcript
chr8	67507977	67507977	*MYBL1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I176I	ENSG00000185697	ENST00000522677	Transcript
chr9	115221775	115221775	*HSDL2*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.G354G	ENSG00000119471	ENST00000398805	Transcript
chr9	125377343	125377343	*OR1Q1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.V109V	ENSG00000165202	ENST00000297913	Transcript

chr9	130210655	130210655	*RPL12*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.R114R	ENSG00000197958	ENST00000361436	Transcript
chr9	134467542	134467542	*RAPGEF1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L738L	ENSG00000107263	ENST00000372190	Transcript
chr9	140952642	140952642	*CACNA1B*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I1416I	ENSG00000148408	ENST00000371372	Transcript
chr9	140972605	140972605	*CACNA1B*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.S1663S	ENSG00000148408	ENST00000371372	Transcript
chr9	186758 8	186758 8	*ADAMTSL1*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.L373L	ENSG00000178031	ENST00000380548	Transcript
chr9	80144144	80144144	*GNA14*	Silent	SNP	G	G	T	rs140939256	sia_et_al_P7	p.T50T	ENSG00000156049	ENST00000341700	Transcript
chrX	120182738	120182738	*GLUD2*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.I400I	ENSG00000182890	ENST00000328078	Transcript
chrX	123164892	123164892	*STAG2*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.R69R	ENSG00000101972	ENST00000218089	Transcript
chrX	128657216	128657216	*SMARCA1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.T44T	ENSG00000102038	ENST00000371122	Transcript
chrX	129208025	129208025	*ELF4*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I113I	ENSG00000102034	ENST00000308167	Transcript
chrX	149944711	149944711	*CD99L2*	Silent	SNP	G	G	A	novel	sia_et_al_P7	p.A197A	ENSG00000102181	ENST00000370377	Transcript
chrX	153053535	153053535	*IDH3G*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.I134I	ENSG00000067829	ENST00000217901	Transcript
chrX	153215033	153215033	*HCFC1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.A2013A	ENSG00000172534	ENST00000310441	Transcript
chrX	153590377	153590377	*FLNA*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.T932T	ENSG00000196924	ENST00000369850	Transcript
chrX	153763436	153763436	*G6PD*	Silent	SNP	C	C	A	novel	sia_et_al_P7	p.P174P	ENSG00000160211	ENST00000393562	Transcript
chrX	48374310	48374310	*PORCN*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L352L	ENSG00000102312	ENST00000326194	Transcript
chrX	54569681	54569681	*GNL3L*	Silent	SNP	C	C	T	novel	sia_et_al_P7	p.A144A	ENSG00000130119	ENST00000336470	Transcript
chrX	57162692	57162692	*SPIN2A*	Silent	SNP	C	C	T	novel	sia_et_al_P7	p.R113R	ENSG00000147059	ENST00000374908	Transcript
chrX	6968346	6968346	*HDHD1*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.S249S	ENSG00000130021	ENST00000424830	Transcript
chrX	74698810	74698810	*ZDHHC15*	Silent	SNP	G	G	T	novel	sia_et_al_P7	p.L58L	ENSG00000102383	ENST00000373367	Transcript
chr11	4608651	4608651	*OR52I2*	Silent	SNP	G	G	T	novel	sia_et_al_P3	p.V203V	ENSG00000226288	ENST00000312614	Transcript
chr11	5862858	5862858	*OR52E6*	Silent	SNP	A	A	G	novel	sia_et_al_P3	p.N90N	ENSG00000205409	ENST00000329322	Transcript
chr11	68549415	68549415	*CPT1A*	Silent	SNP	G	G	T	novel	sia_et_al_P3	p.A392A	ENSG00000110090	ENST00000265641	Transcript
chr13	42404754	42404754	*VWA8*	Silent	SNP	G	G	A	rs145835358	sia_et_al_P3	p.S537S	ENSG00000102763	ENST00000379310	Transcript
chr13	46544045	46544045	*ZC3H13*	Silent	SNP	G	G	T	novel	sia_et_al_P3	p.P878P	ENSG00000123200	ENST00000282007	Transcript
chr15	33261538	33261538	*FMN1*	Silent	SNP	G	G	A	novel	sia_et_al_P3	p.C565C	ENSG00000248905	ENST00000334528	Transcript
chr15	87089355	87089355	*AGBL1*	Silent	SNP	C	C	A	novel	sia_et_al_P3	p.V890V	ENSG00000166748	ENST00000441037	Transcript
chr17	10359150	10359150	*MYH4*	Silent	SNP	G	G	A	novel	sia_et_al_P3	p.P679P	ENSG00000264424	ENST00000255381	Transcript
chr17	72691385	72691385	*CD300LF*	Silent	SNP	G	G	T	novel	sia_et_al_P3	p.S241S	ENSG00000186074	ENST00000326165	Transcript
chr20	47768137	47768137	*STAU1*	Silent	SNP	G	G	T	novel	sia_et_al_P3	p.P164P	ENSG00000124214	ENST00000371856	Transcript
chr21	32598078	32598078	*TIAM1*	Silent	SNP	G	G	T	novel	sia_et_al_P3	p.V591V	ENSG00000156299	ENST00000286827	Transcript
chr3	52773650	52773650	*NEK4*	Silent	SNP	C	C	A	novel	sia_et_al_P3	p.G698G	ENSG00000114904	ENST00000233027	Transcript
chr4	48106966	48106966	*TXK*	Silent	SNP	G	G	A	novel	sia_et_al_P3	p.Y151Y	ENSG00000074966	ENST00000264316	Transcript
chr4	95201910	95201910	*SMARCAD1*	Silent	SNP	C	C	A	novel	sia_et_al_P3	p.I862I	ENSG00000163104	ENST00000354268	Transcript
chr6	133072449	133072449	*VNN2*	Silent	SNP	C	C	A	novel	sia_et_al_P3	p.G345G	ENSG00000112303	ENST00000326499	Transcript
chr6	49409597	49409597	*MUT*	Silent	SNP	G	G	T	novel	sia_et_al_P3	p.R588R	ENSG00000146085	ENST00000274813	Transcript
chr6	62442649	62442649	*KHDRBS2*	Silent	SNP	C	C	A	novel	sia_et_al_P3	p.G277G	ENSG00000112232	ENST00000281156	Transcript
chr8	113842013	113842013	*CSMD3*	Silent	SNP	G	G	A	novel	sia_et_al_P3	p.I587I	ENSG00000164796	ENST00000297405	Transcript
chr8	145066228	145066228	*GRINA*	Silent	SNP	C	C	A	novel	sia_et_al_P3	p.P225P	ENSG00000178719	ENST00000313269	Transcript
chrX	105149316	105149316	*NRK*	Silent	SNP	C	C	A	novel	sia_et_al_P3	p.P275P	ENSG00000123572	ENST00000428173	Transcript
chrX	133372322	133372322	*ATXN3L*	Silent	SNP	A	A	T	novel	sia_et_al_P3	p.P274P	ENSG00000123594	ENST00000380622	Transcript

chr1	222736616	222736616	*TAF1A*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.L328L	ENSG00000143498	ENST00000350027	Transcript
chr1	233137304	233137304	*PCNXL2*	Silent	SNP	C	C	T	novel	sia_et_al_P4	p.R1692R	ENSG00000135749	ENST00000258229	Transcript
chr10	115917421	115917421	*C10orf118*	Silent	SNP	C	C	T	novel	sia_et_al_P4	p.K217K	ENSG00000165813	ENST00000369287	Transcript
chr10	127436455	127436455	*EDRF1*	Silent	SNP	C	C	T	novel	sia_et_al_P4	p.A999A	ENSG00000107938	ENST00000356792	Transcript
chr11	49974418	49974418	*OR4C13*	Silent	SNP	A	A	T	rs147639676	sia_et_al_P4	p.V148V	ENSG00000258817	ENST00000555099	Transcript
chr12	109895851	109895851	*KCTD10*	Silent	SNP	G	G	A	novel	sia_et_al_P4	p.V140V	ENSG00000110906	ENST00000228495	Transcript
chr12	72936094	72936094	*TRHDE*	Silent	SNP	G	G	A	novel	sia_et_al_P4	p.L537L	ENSG00000072657	ENST00000261180	Transcript
chr14	35005424	35005424	*EAPP*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.L44L	ENSG00000129518	ENST00000250454	Transcript
chr15	91298167	91298167	*BLM*	Silent	SNP	C	C	T	rs375632163	sia_et_al_P4	p.D362D	ENSG00000197299	ENST00000355112	Transcript
chr16	15185190	15185190	*RRN3*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.L78L	ENSG00000085721	ENST00000198767	Transcript
chr16	28619696	28619696	*SULT1A1*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.L96L	ENSG00000196502	ENST00000395609	Transcript
chr16	9017143	9017143	*USP7*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.R104R	ENSG00000187555	ENST00000344836	Transcript
chr17	10399807	10399807	*MYH1*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.V1572V	ENSG00000109061	ENST00000226207	Transcript
chr17	64179355	64179355	*CEP112*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.V21V	ENSG00000154240	ENST00000392769	Transcript
chr2	233413012	233413012	*TIGD1*	Silent	SNP	G	G	T	rs184548685	sia_et_al_P4	p.I527I	ENSG00000221944	ENST00000408957	Transcript
chr20	10620428	10620428	*JAG1*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.P1125P	ENSG00000101384	ENST00000254958	Transcript
chr20	44664532	44664532	*SLC12A5*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.S155S	ENSG00000124140	ENST00000454036	Transcript
chr20	60971415	60971415	*CABLES2*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.T161T	ENSG00000149679	ENST00000279101	Transcript
chr22	44127667	44127667	*EFCAB6*	Silent	SNP	G	G	A	novel	sia_et_al_P4	p.H223H	ENSG00000186976	ENST00000262726	Transcript
chr3	119582366	119582366	*GSK3B*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.L345L	ENSG00000082701	ENST00000316626	Transcript
chr3	148928165	148928165	*CP*	Silent	SNP	C	C	A	rs267599642	sia_et_al_P4	p.G132G	ENSG00000047457	ENST00000264613	Transcript
chr3	186961357	186961357	*MASP1*	Silent	SNP	A	A	G	rs141985299	sia_et_al_P4	p.S381S	ENSG00000127241	ENST00000296280	Transcript
chr3	194366673	194366673	*KCNH8*	Silent	SNP	C	C	T	rs145114975	sia_et_al_P4	p.S349S	ENSG00000183960	ENST00000328405	Transcript
chr3	196434674	196434674	*CEP19*	Silent	SNP	G	G	A	novel	sia_et_al_P4	p.Y84Y	ENSG00000174007	ENST00000409690	Transcript
chr3	235741578	235741578	*UBE2E2*	Silent	SNP	C	C	T	novel	sia_et_al_P4	p.L158L	ENSG00000182247	ENST00000396703	Transcript
chr4	155531223	155531223	*FGG*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.G176G	ENSG00000171557	ENST00000336098	Transcript
chr4	173852380	173852380	*GALNTL6*	Silent	SNP	C	C	T	rs183071930	sia_et_al_P4	p.Y370Y	ENSG00000174473	ENST00000506823	Transcript
chr6	111701355	111701355	*REV3L*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.G428G	ENSG00000009413	ENST00000358835	Transcript
chr6	145079081	145079081	*UTRN*	Silent	SNP	G	G	T	rs147309348	sia_et_al_P4	p.P2817P	ENSG00000152818	ENST00000367545	Transcript
chr6	165749671	165749671	*PDE10A*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.P736P	ENSG00000112541	ENST00000539869	Transcript
chr7	233532331	233532331	*IGF2BP3*	Silent	SNP	A	A	G	rs143670921	sia_et_al_P4	p.F479F	ENSG00000136231	ENST00000258729	Transcript
chr8	139144923	139144923	*FAM135B*	Silent	SNP	G	G	T	rs371041013	sia_et_al_P4	p.I1378I	ENSG00000147724	ENST00000395297	Transcript
chr8	223969955	223969955	*PPP3CC*	Silent	SNP	G	G	A	novel	sia_et_al_P4	p.A454A	ENSG00000120910	ENST00000397775	Transcript
chr9	106877053	106877053	*SMC2*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.T538T	ENSG00000136824	ENST00000286398	Transcript
chrX	105144634	105144634	*NRK*	Silent	SNP	T	T	A	novel	sia_et_al_P4	p.I245I	ENSG00000123572	ENST00000428173	Transcript
chrX	114250350	114250350	*IL13RA2*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.P43P	ENSG00000123496	ENST00000371936	Transcript
chrX	135574270	135574270	*BRS3*	Silent	SNP	C	C	A	rs369993360	sia_et_al_P4	p.T312T	ENSG00000102239	ENST00000370648	Transcript
chrX	155904331	155904331	*ACE2*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.T519T	ENSG00000130234	ENST00000427411	Transcript
chrX	156190114	156190114	*ACE2*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.L7L	ENSG00000130234	ENST00000427411	Transcript
chrX	2990175	2990175	*ARSF*	Silent	SNP	G	G	T	novel	sia_et_al_P4	p.L40L	ENSG00000062096	ENST00000381127	Transcript
chrX	30870895	30870895	*TAB3*	Silent	SNP	C	C	A	novel	sia_et_al_P4	p.T570T	ENSG00000157625	ENST00000378933	Transcript

chr1	100623898	100623898	*LRRC39*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.L134L	ENSG00000122477	ENST00000370138	Transcript
chr1	120298052	120298052	*HMGCS2*	Silent	SNP	G	G	T	rs267597953	sia_et_al_P5	p.S395S	ENSG00000134240	ENST00000369406	Transcript
chr1	158262616	158262616	*CD1C*	Silent	SNP	C	C	A	rs375607782	sia_et_al_P5	p.R281R	ENSG00000158481	ENST00000368170	Transcript
chr1	97564048	97564048	*DPYD*	Silent	SNP	G	G	T	novel	sia_et_al_P5	p.I921I	ENSG00000188641	ENST00000370192	Transcript
chr11	121360781	121360781	*SORL1*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.T240T	ENSG00000137642	ENST00000260197	Transcript
chr12	107109318	107109318	*RFX4*	Silent	SNP	C	C	T	novel	sia_et_al_P5	p.T387T	ENSG00000111783	ENST00000357881	Transcript
chr12	26781087	26781087	*ITPR2*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.L981L	ENSG00000123104	ENST00000381340	Transcript
chr15	87899307	87899307	*NTRK3*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.V26V	ENSG00000140538	ENST00000360948	Transcript
chr16	3778538	3778538	*CREBBP*	Silent	SNP	G	G	T	novel	sia_et_al_P5	p.A2170A	ENSG00000005339	ENST00000262367	Transcript
chr19	52327805	52327805	*FPR3*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.L268L	ENSG00000187474	ENST00000339223	Transcript
chr2	171910274	171910274	*TLK1*	Silent	SNP	G	G	T	novel	sia_et_al_P5	p.L243L	ENSG00000198586	ENST00000431350	Transcript
chr20	1615977	1615977	*SIRPG*	Silent	SNP	G	G	T	novel	sia_et_al_P5	p.V339V	ENSG00000089012	ENST00000303415	Transcript
chr21	33975543	33975543	*C21orf59*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.L198L	ENSG00000159079	ENST00000290155	Transcript
chr4	85710962	85710962	*WDFY3*	Silent	SNP	A	A	G	novel	sia_et_al_P5	p.L1196L	ENSG00000163625	ENST00000295888	Transcript
chr5	169186777	169186777	*DOCK2*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.L815L	ENSG00000134516	ENST00000256935	Transcript
chr5	52780041	52780041	*FST*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.T213T	ENSG00000134363	ENST00000256759	Transcript
chr6	129475768	129475768	*LAMA2*	Silent	SNP	C	C	A	novel	sia_et_al_P5	p.T382T	ENSG00000196569	ENST00000421865	Transcript
chr6	165863839	165863839	*PDE10A*	Silent	SNP	C	C	A	rs140543916	sia_et_al_P5	p.T79T	ENSG00000112541	ENST00000539869	Transcript
chr9	20414034	20414034	*MLLT3*	Silent	SNP	G	G	T	novel	sia_et_al_P5	p.L270L	ENSG00000171843	ENST00000380338	Transcript
chr1	167962478	167962478	*DCAF6*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.R235R	ENSG00000143164	ENST00000367840	Transcript
chr1	179604945	179604945	*TDRD5*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.I481I	ENSG00000162782	ENST00000444136	Transcript
chr1	60107002	60107002	*FGGY*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.P424P	ENSG00000172456	ENST00000371218	Transcript
chr10	103559016	103559016	*MGEA5*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.P464P	ENSG00000198408	ENST00000361464	Transcript
chr10	105659880	105659880	*OBFC1*	Silent	SNP	G	G	T	rs149919798	sia_et_al_P6	p.R133R	ENSG00000107960	ENST00000224950	Transcript
chr10	149505204	149505204	*DCLRE1C*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.P654P	ENSG00000152457	ENST00000378278	Transcript
chr11	108760588	108760588	*ZBED5*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.A145A	ENSG00000236287	ENST00000432999	Transcript
chr11	113619039	113619039	*ZW10*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.I343I	ENSG00000086827	ENST00000200135	Transcript
chr11	123894415	123894415	*OR10G9*	Silent	SNP	G	G	T	rs150463109	sia_et_al_P6	p.G232G	ENSG00000236981	ENST00000375024	Transcript
chr11	130775864	130775864	*SNX19*	Silent	SNP	G	G	A	novel	sia_et_al_P6	p.P809P	ENSG00000120451	ENST00000265909	Transcript
chr12	268786822	268786822	*ITPR2*	Silent	SNP	C	C	T	rs538364234	sia_et_al_P6	p.V60V	ENSG00000123104	ENST00000381340	Transcript
chr12	48528042	48528042	*PFKM*	Silent	SNP	A	A	T	novel	sia_et_al_P6	p.V278V	ENSG00000152556	ENST00000340802	Transcript
chr12	96059704	96059704	*NTN4*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V544V	ENSG00000074527	ENST00000343702	Transcript
chr13	103389103	103389103	*CCDC168*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.P19P	ENSG00000175820	ENST00000322527	Transcript
chr13	24380137	24380137	*MIPEP*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.L600L	ENSG00000027001	ENST00000382172	Transcript
chr14	71413709	71413709	*PCNX*	Silent	SNP	C	C	A	rs201771415	sia_et_al_P6	p.V77V	ENSG00000100731	ENST00000304743	Transcript
chr14	92958088	92958088	*SLC24A4*	Silent	SNP	C	C	T	novel	sia_et_al_P6	p.G539G	ENSG00000140090	ENST00000532405	Transcript
chr15	102358560	102358560	*OR4F15*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.S57S	ENSG00000182854	ENST00000332238	Transcript
chr15	43109236	43109236	*TTBK2*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.R199R	ENSG00000128881	ENST00000267890	Transcript
chr17	56536280	56536280	*HSF5*	Silent	SNP	G	G	T	rs115217765	sia_et_al_P6	p.T523T	ENSG00000176160	ENST00000323777	Transcript
chr18	6243366	6243366	*L3MBTL4*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.T129T	ENSG00000154655	ENST00000284898	Transcript
chr19	55329954	55329954	*KIR3DL1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V85V	ENSG00000167633	ENST00000391728	Transcript

chr2	166850762	166850762	*SCN1A*	Silent	SNP	C	C	T	novel	sia_et_al_P6	p.V1582V	ENSG00000144285	ENST00000303395	Transcript
chr2	173362813	173362813	*ITGA6*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V1033V	ENSG00000091409	ENST00000409080	Transcript
chr2	201722749	201722749	*CLK1*	Silent	SNP	G	G	A	novel	sia_et_al_P6	p.R246R	ENSG00000013441	ENST00000434813	Transcript
chr2	206921457	206921457	*INO80D*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.L143L	ENSG00000114933	ENST00000403263	Transcript
chr2	230638870	230638870	*TRIP12*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.L1804L	ENSG00000153827	ENST00000283943	Transcript
chr2	32530569	32530569	*YIPF4*	Silent	SNP	G	G	A	novel	sia_et_al_P6	p.V203V	ENSG00000119820	ENST00000238831	Transcript
chr2	55561698	55561698	*CCDC88A*	Silent	SNP	G	G	A	novel	sia_et_al_P6	p.R753R	ENSG00000115355	ENST00000336838	Transcript
chr20	48456085	48456085	*SLC9A8*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.L99L	ENSG00000197818	ENST00000417961	Transcript
chr3	108156535	108156535	*MYH15*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.A1049A	ENSG00000144821	ENST00000273353	Transcript
chr3	133336166	133336166	*TOPBP1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V1199V	ENSG00000163781	ENST00000260810	Transcript
chr3	142185289	142185289	*ATR*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.I2258I	ENSG00000175054	ENST00000350721	Transcript
chr3	97806493	97806493	*OR5AC2*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.L159L	ENSG00000196578	ENST00000358642	Transcript
chr4	108820740	108820740	*SGMS2*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V155V	ENSG00000164023	ENST00000394684	Transcript
chr4	187530367	187530367	*FAT1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V3392V	ENSG00000083857	ENST00000441802	Transcript
chr5	112214516	112214516	*REEP5*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.V179V	ENSG00000129625	ENST00000379638	Transcript
chr5	139722396	139722396	*HBEGF*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V74V	ENSG00000113070	ENST00000230990	Transcript
chr5	40937684	40937684	*C7*	Silent	SNP	C	C	T	novel	sia_et_al_P6	p.N153N	ENSG00000112936	ENST00000313164	Transcript
chr6	117687255	117687255	*ROS1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.S932S	ENSG00000047936	ENST00000368508	Transcript
chr6	127648216	127648216	*ECHDC1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V104V	ENSG00000093144	ENST00000531967	Transcript
chr6	159187985	159187985	*EZR*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.G574G	ENSG00000092820	ENST00000367075	Transcript
chr6	47776009	47776009	*OPN5*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.T292T	ENSG00000124818	ENST00000371211	Transcript
chr6	76715074	76715074	*IMPG1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.L355L	ENSG00000112706	ENST00000369950	Transcript
chr7	102962501	102962501	*DNAJC2*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.R321R	ENSG00000105821	ENST00000379263	Transcript
chr7	105915482	105915482	*NAMPT*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.T76T	ENSG00000105835	ENST00000222553	Transcript
chr8	2065727	2065727	*MYOM2*	Silent	SNP	C	C	A	rs138045217	sia_et_al_P6	p.R1147R	ENSG00000036448	ENST00000262113	Transcript
chr8	28981637	28981637	*KIF13B*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.R1086R	ENSG00000197892	ENST00000524189	Transcript
chr8	38928833	38928833	*ADAM9*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.P536P	ENSG00000168615	ENST00000487273	Transcript
chr8	67803178	67803178	*MCMDC2*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.S384S	ENSG00000178460	ENST00000422365	Transcript
chr9	108125158	108125158	*SLC44A1*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.A319A	ENSG00000070214	ENST00000374720	Transcript
chr9	113449505	113449505	*MUSK*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V105V	ENSG00000030304	ENST00000374448	Transcript
chr9	132671210	132671210	*FNBP1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.V418V	ENSG00000187239	ENST00000446176	Transcript
chr9	19328112	19328112	*DENND4C*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.G735G	ENSG00000137145	ENST00000602925	Transcript
chr9	79955183	79955183	*VPS13A*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.L2288L	ENSG00000197969	ENST00000360280	Transcript
chrX	131219977	131219977	*FRMD7*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.G156G	ENSG00000165694	ENST00000298542	Transcript
chrX	131516296	131516296	*MBNL3*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.P321P	ENSG00000076770	ENST00000370853	Transcript
chrX	135307016	135307016	*MAP7D3*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.R721R	ENSG00000129680	ENST00000316077	Transcript
chrX	151909154	151909154	*CSAG1*	Silent	SNP	C	C	A	novel	sia_et_al_P6	p.P61P	ENSG00000198930	ENST00000370287	Transcript
chrX	72804369	72804369	*CHIC1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.L156L	ENSG00000204116	ENST00000373502	Transcript
chrY	2712132	2712132	*RPS4Y1*	Silent	SNP	G	G	T	novel	sia_et_al_P6	p.S32S	ENSG00000129824	ENST00000250784	Transcript
chr1	160319995	160319995	*NCSTN*	Silent	SNP	C	C	A	novel	sia_et_al_P8	p.P179P	ENSG00000162736	ENST00000294785	Transcript
chr1	6046302	6046302	*NPHP4*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.P16P	ENSG00000131697	ENST00000378156	Transcript

chr10	129905685	129905685	*MKI67*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.L1473L	ENSG00000148773	ENST00000368654	Transcript
chr11	112084584	112084584	*BCO2*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.T444T	ENSG00000197580	ENST00000357685	Transcript
chr11	33790401	33790401	*FBXO3*	Silent	SNP	C	C	A	novel	sia_et_al_P8	p.L118L	ENSG00000110429	ENST00000265651	Transcript
chr11	3722030	3722030	*NUP98*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.L1184L	ENSG00000110713	ENST00000324932	Transcript
chr11	5969467	5969467	*OR56A3*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.G297G	ENSG00000184478	ENST00000329564	Transcript
chr12	122723269	122723269	*VPS33A*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.V389V	ENSG00000139719	ENST00000267199	Transcript
chr13	23853589	23853589	*SGCG*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.V159V	ENSG00000102683	ENST00000218867	Transcript
chr13	50054394	50054394	*SETDB2*	Silent	SNP	C	C	A	novel	sia_et_al_P8	p.A315A	ENSG00000136169	ENST00000317257	Transcript
chr14	69349590	69349590	*ACTN1*	Silent	SNP	G	G	A	novel	sia_et_al_P8	p.H606H	ENSG00000072110	ENST00000394419	Transcript
chr14	69922577	69922577	*SLC39A9*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.L229L	ENSG00000029364	ENST00000336643	Transcript
chr16	2312358	2312358	*RNPS1*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.P199P	ENSG00000205937	ENST00000565678	Transcript
chr19	53573493	53573493	*ZNF160*	Silent	SNP	G	G	T	rs368897306	sia_et_al_P8	p.I98I	ENSG00000170949	ENST00000429604	Transcript
chr2	198950851	198950851	*PLCL1*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.R870R	ENSG00000115896	ENST00000428675	Transcript
chr2	201485876	201485876	*AOX1*	Silent	SNP	C	C	A	novel	sia_et_al_P8	p.P636P	ENSG00000138356	ENST00000374700	Transcript
chr3	160243735	160243735	*KPNA4*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.T239T	ENSG00000186432	ENST00000334256	Transcript
chr3	164117716	164117716	*RFTN1*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.I279I	ENSG00000131378	ENST00000334133	Transcript
chr3	40523356	40523356	*ZNF619*	Silent	SNP	C	C	A	novel	sia_et_al_P8	p.G9G	ENSG00000177873	ENST00000447116	Transcript
chr4	41016138	41016138	*APBB2*	Silent	SNP	C	C	A	rs533976044	sia_et_al_P8	p.L99L	ENSG00000163697	ENST00000508593	Transcript
chr4	6031503	6031503	*JAKMIP1*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.I795I	ENSG00000152969	ENST00000409021	Transcript
chr6	46849304	46849304	*GPR116*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.V234V	ENSG00000069122	ENST00000283296	Transcript
chr6	74229138	74229138	*EEF1A1*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.T82T	ENSG00000156508	ENST00000316292	Transcript
chr6	87725662	87725662	*HTR1E*	Silent	SNP	C	C	A	rs185147794	sia_et_al_P8	p.R204R	ENSG00000168830	ENST00000305344	Transcript
chr7	131817928	131817928	*PLXNA4*	Silent	SNP	G	G	T	novel	sia_et_al_P8	p.A1823A	ENSG00000221866	ENST00000359827	Transcript
chr9	94518376	94518376	*ROR2*	Silent	SNP	C	C	T	rs78781083	sia_et_al_P8	p.T157T	ENSG00000169071	ENST00000375708	Transcript
chr9	97177454	97177454	*HIATL1*	Silent	SNP	C	C	A	novel	sia_et_al_P8	p.G41G	ENSG00000148110	ENST00000375344	Transcript
chr1	145578184	145578184	*PIAS3*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.C49C	ENSG00000131788	ENST00000393045	Transcript
chr1	147126324	147126324	*ACP6*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.N255N	ENSG00000162836	ENST00000369238	Transcript
chr1	155174905	155174905	*THBS3*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.A163A	ENSG00000169231	ENST00000368378	Transcript
chr1	156703938	156703938	*RRNAD1*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.H258H	ENSG00000143303	ENST00000368216	Transcript
chr1	161011523	161011523	*USF1*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.G130G	ENSG00000158773	ENST00000368021	Transcript
chr1	177250079	177250079	*BRINP2*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.Y589Y	ENSG00000198797	ENST00000361539	Transcript
chr1	227333211	227333211	*CDC42BPA*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.D374D	ENSG00000143776	ENST00000366769	Transcript
chr1	241675288	241675288	*FH*	Silent	SNP	G	G	A	rs375878939	gao_et_al_P7	p.N178N	ENSG00000091483	ENST00000366560	Transcript
chr1	241951229	241951229	*WDR64*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.D918D	ENSG00000162843	ENST00000366552	Transcript
chr1	248039401	248039401	*TRIM58*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.E357E	ENSG00000162722	ENST00000366481	Transcript
chr1	9005966	9005966	*CA6*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.L7L	ENSG00000131686	ENST00000377436	Transcript
chr1	90473078	90473078	*ZNF326*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.G128G	ENSG00000162664	ENST00000340281	Transcript
chr10	103906796	103906796	*PPRC1*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.A1349A	ENSG00000148840	ENST00000278070	Transcript
chr10	117026385	117026385	*ATRNL1*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.G628G	ENSG00000107518	ENST00000355044	Transcript
chr10	120707555	120707555	*UPF2*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.E378E	ENSG00000151461	ENST00000356352	Transcript
chr10	158898887	158898887	*FAM188A*	Silent	SNP	G	G	T	novel	gao_et_al_P7	p.P50P	ENSG00000148481	ENST00000277632	Transcript

chr10	43089021	43089021	*ZNF33B*	Silent	SNP	G	G	A	rs181768233	gao_et_al_P7	p.H459H	ENSG00000196693	ENST00000359467	Transcript
chr10	61022356	61022356	*FAM13C*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.P358P	ENSG00000148541	ENST00000373868	Transcript
chr10	64973431	64973431	*JMJD1C*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.Q832Q	ENSG00000171988	ENST00000399262	Transcript
chr10	71142486	71142486	*HK1*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.T507T	ENSG00000156515	ENST00000404387	Transcript
chr11	114393803	114393803	*NXPE1*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.K160K	ENSG00000095110	ENST00000251921	Transcript
chr11	133790623	133790623	*IGSF9B*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.P999P	ENSG00000080854	ENST00000533871	Transcript
chr11	18735535	18735535	*IGSF22*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.R653R	ENSG00000179057	ENST00000513874	Transcript
chr11	36511967	36511967	*TRAF6*	Silent	SNP	G	G	A	rs539301101	gao_et_al_P7	p.L330L	ENSG00000175104	ENST00000526995	Transcript
chr11	45671982	45671982	*CHST1*	Silent	SNP	A	A	C	novel	gao_et_al_P7	p.P164P	ENSG00000175264	ENST00000308064	Transcript
chr11	65785745	65785745	*DNHD1*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.G2683G	ENSG00000179532	ENST00000254579	Transcript
chr11	66612455	66612455	*RCE1*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.P189P	ENSG00000173653	ENST00000309657	Transcript
chr11	73074813	73074813	*ARHGEF17*	Silent	SNP	C	C	T	rs540041126	gao_et_al_P7	p.S1756S	ENSG00000110237	ENST00000263674	Transcript
chr12	109334671	109334671	*SVOP*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.I154I	ENSG00000166111	ENST00000299134	Transcript
chr12	117964882	117964882	*KSR2*	Silent	SNP	C	C	T	rs374220992	gao_et_al_P7	p.T615T	ENSG00000171435	ENST00000339824	Transcript
chr12	132688068	132688068	*GALNT9*	Silent	SNP	G	G	T	novel	gao_et_al_P7	p.A49A	ENSG00000182870	ENST00000397325	Transcript
chr12	18891760	18891760	*CAPZA3*	Silent	SNP	G	G	A	rs370457183	gao_et_al_P7	p.T186T	ENSG00000177938	ENST00000317658	Transcript
chr12	31254802	31254802	*DDX11*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.C696C	ENSG00000013573	ENST00000407793	Transcript
chr12	40757324	40757324	*LRRK2*	Silent	SNP	C	C	G	novel	gao_et_al_P7	p.L2383L	ENSG00000188906	ENST00000298910	Transcript
chr12	50024381	50024381	*PRPF40B*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.P19P	ENSG00000110844	ENST00000548825	Transcript
chr12	57592362	57592362	*LRP1*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.T3195T	ENSG00000123384	ENST00000243077	Transcript
chr12	91502232	91502232	*LUM*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.A175A	ENSG00000139329	ENST00000266718	Transcript
chr13	103506136	103506136	*ERCC5*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.A98A	ENSG00000134899	ENST00000355739	Transcript
chr13	110861763	110861763	*COL4A1*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.G209G	ENSG00000187498	ENST00000375820	Transcript
chr13	25670945	25670945	*PABPC3*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.D203D	ENSG00000151846	ENST00000281589	Transcript
chr13	84454251	84454251	*SLITRK1*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.P464P	ENSG00000178235	ENST00000377084	Transcript
chr13	95050858	95050858	*GPC6*	Silent	SNP	C	C	T	rs146868653	gao_et_al_P7	p.N476N	ENSG00000183098	ENST00000377047	Transcript
chr14	74706270	74706270	*VSX2*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.T2T	ENSG00000119614	ENST00000261980	Transcript
chr15	72119377	72119377	*MYO9A*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.S2397S	ENSG00000066933	ENST00000356056	Transcript
chr16	48292639	48292639	*LONP2*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.D237D	ENSG00000102910	ENST00000285737	Transcript
chr17	36533580	36533580	*SOCS7*	Silent	SNP	C	C	T	rs140480789	gao_et_al_P7	p.R467R	ENSG00000174111	ENST00000577233	Transcript
chr17	41166235	41166235	*IFI35*	Silent	SNP	C	C	T	rs537370701	gao_et_al_P7	p.R262R	ENSG00000068079	ENST00000438323	Transcript
chr17	4722779	4722779	*PLD2*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.A788A	ENSG00000129219	ENST00000263088	Transcript
chr17	60455357	60455357	*EFCAB3*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.L39L	ENSG00000172421	ENST00000450662	Transcript
chr17	72771784	72771784	*NAT9*	Silent	SNP	G	G	T	novel	gao_et_al_P7	p.P18P	ENSG00000109065	ENST00000357814	Transcript
chr17	79862724	79862724	*PCYT2*	Silent	SNP	G	G	A	rs201803263	gao_et_al_P7	p.R403R	ENSG00000185813	ENST00000538721	Transcript
chr18	10800402	10800402	*PIEZO2*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.N437N	ENSG00000154864	ENST00000503781	Transcript
chr18	12674600	12674600	*CEP76*	Silent	SNP	T	T	A	novel	gao_et_al_P7	p.T592T	ENSG00000101624	ENST00000262127	Transcript
chr19	14521079	14521079	*DDX39A*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.S227S	ENSG00000123136	ENST00000242776	Transcript
chr19	31768185	31768185	*TSHZ3*	Silent	SNP	C	C	T	rs535430454	gao_et_al_P7	p.P838P	ENSG00000121297	ENST00000240587	Transcript
chr19	36940377	36940377	*ZNF566*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.K254K	ENSG00000186017	ENST00000454319	Transcript
chr19	40882567	40882567	*PLD3*	Silent	SNP	C	C	T	rs147721393	gao_et_al_P7	p.G357G	ENSG00000105223	ENST00000409587	Transcript

chr19	42312734	42312734	*EBI3*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.P51P	ENSG00000105246	ENST00000221847	Transcript
chr19	51647844	51647844	*SIGLEC7*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.I205I	ENSG00000168995	ENST00000317643	Transcript
chr19	57328739	57328739	*PEG3*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.R357R	ENSG00000198300	ENST00000326441	Transcript
chr19	58132729	58132729	*ZNF134*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.H414H	ENSG00000213762	ENST00000396161	Transcript
chr19	58926940	58926940	*ZNF584*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.E73E	ENSG00000171574	ENST00000306910	Transcript
chr19	6418725	6418725	*KHSRP*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.I256I	ENSG00000088247	ENST00000398148	Transcript
chr2	101624700	101624700	*TBC1D8*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.S1002S	ENSG00000204634	ENST00000376840	Transcript
chr2	108499208	108499208	*RGPD4*	Silent	SNP	C	C	T	rs200239667	gao_et_al_P7	p.N1715N	ENSG00000196862	ENST00000408999	Transcript
chr2	131976212	131976212	*POTEE*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.N79N	ENSG00000188219	ENST00000356920	Transcript
chr2	166847962	166847962	*SCN1A*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.T1941T	ENSG00000144285	ENST00000303395	Transcript
chr2	190617610	190617610	*OSGEPL1*	Silent	SNP	G	G	A	rs549547329	gao_et_al_P7	p.P353P	ENSG00000128694	ENST00000264151	Transcript
chr2	242122067	242122067	*PPP1R7*	Silent	SNP	C	C	T	rs528914663	gao_et_al_P7	p.N304N	ENSG00000115685	ENST00000234038	Transcript
chr2	250226107	250226107	*CENPO*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.S40S	ENSG00000138092	ENST00000380834	Transcript
chr20	199559833	199559833	*RIN2*	Silent	SNP	C	C	A	novel	gao_et_al_P7	p.S487S	ENSG00000132669	ENST00000255006	Transcript
chr20	254936111	254936111	*NINL*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.V103V	ENSG00000101004	ENST00000278886	Transcript
chr21	45544542	45544542	*PWP2*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.H633H	ENSG00000241945	ENST00000291576	Transcript
chr21	45716295	45716295	*AIRE*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.L511L	ENSG00000160224	ENST00000291582	Transcript
chr21	46117158	46117158	*KRTAP10-12*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.V14V	ENSG00000189169	ENST00000400365	Transcript
chr22	18650797	18650797	*USP18*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.K207K	ENSG00000184979	ENST00000215794	Transcript
chr22	33255211	33255211	*TIMP3*	Silent	SNP	C	C	T	rs201199240	gao_et_al_P7	p.N161N	ENSG00000100234	ENST00000266085	Transcript
chr22	38014526	38014526	*GGA1*	Silent	SNP	C	C	T	rs574222429	gao_et_al_P7	p.N92N	ENSG00000100083	ENST00000343632	Transcript
chr3	111298038	111298038	*CD96*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.G252G	ENSG00000153283	ENST00000283285	Transcript
chr3	121981118	121981118	*CASR*	Silent	SNP	G	G	A	rs200443784	gao_et_al_P7	p.T412T	ENSG00000036828	ENST00000498619	Transcript
chr3	124952457	124952457	*ZNF148*	Silent	SNP	C	C	T	rs150187376	gao_et_al_P7	p.S371S	ENSG00000163848	ENST00000360647	Transcript
chr3	147990004	147990004	*C3orf20*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.A689A	ENSG00000131379	ENST00000253697	Transcript
chr3	49153007	49153007	*USP19*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.E584E	ENSG00000172046	ENST00000434032	Transcript
chr3	49569585	49569585	*DAG1*	Silent	SNP	C	C	T	rs374490206	gao_et_al_P7	p.G547G	ENSG00000173402	ENST00000545947	Transcript
chr3	51968759	51968759	*RRP9*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.R356R	ENSG00000114767	ENST00000232888	Transcript
chr3	57542997	57542997	*PDE12*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.T297T	ENSG00000174840	ENST00000311180	Transcript
chr4	156825218	156825218	*TDO2*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.S28S	ENSG00000151790	ENST00000536354	Transcript
chr4	159820988	159820988	*PROM1*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.A812A	ENSG00000007062	ENST00000510224	Transcript
chr4	160178555	160178555	*PROM1*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.P337P	ENSG00000007062	ENST00000510224	Transcript
chr4	177109111	177109111	*FAM184B*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.T166T	ENSG00000047662	ENST00000265018	Transcript
chr4	187630385	187630385	*FAT1*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.P199P	ENSG00000083857	ENST00000441802	Transcript
chr4	4303986	4303986	*ZBTB49*	Silent	SNP	C	C	A	novel	gao_et_al_P7	p.T141T	ENSG00000168826	ENST00000337872	Transcript
chr5	131312380	131312380	*ACSL6*	Silent	SNP	G	G	A	rs141656216	gao_et_al_P7	p.N317N	ENSG00000164398	ENST00000379264	Transcript
chr5	133644391	133644391	*CDKL3*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.L303L	ENSG00000006837	ENST00000265334	Transcript
chr5	140236983	140236983	*PCDHA10*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.N450N	ENSG00000250120	ENST00000307360	Transcript
chr5	140516354	140516354	*PCDHB5*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.N446N	ENSG00000113209	ENST00000231134	Transcript
chr5	149500571	149500571	*PDGFRB*	Silent	SNP	G	G	A	rs55830572	gao_et_al_P7	p.C822C	ENSG00000113721	ENST00000261799	Transcript
chr5	149927851	149927851	*NDST1*	Silent	SNP	C	C	T	rs374191724	gao_et_al_P7	p.D739D	ENSG00000070614	ENST00000261797	Transcript

chr5	154396818	154396818	*KIF4B*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.E1133E	ENSG00000226650	ENST00000435029	Transcript
chr5	176931362	176931362	*DOK3*	Silent	SNP	C	C	T	rs531951657	gao_et_al_P7	p.P371P	ENSG00000146094	ENST00000357198	Transcript
chr5	197472622	197472622	*CDH18*	Silent	SNP	G	G	A	rs368155280	gao_et_al_P7	p.D104D	ENSG00000145526	ENST00000507958	Transcript
chr5	50128685	50128685	*PARP8*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.S768S	ENSG00000151883	ENST00000281631	Transcript
chr5	76624847	76624847	*PDE8B*	Silent	SNP	C	C	T	rs370696702	gao_et_al_P7	p.S205S	ENSG00000113231	ENST00000264917	Transcript
chr5	88056898	88056898	*MEF2C*	Silent	SNP	G	G	A	rs569860731	gao_et_al_P7	p.P121P	ENSG00000081189	ENST00000340208	Transcript
chr5	89990325	89990325	*GPR98*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.N2584N	ENSG00000164199	ENST00000405460	Transcript
chr6	158066871	158066871	*ZDHHC14*	Silent	SNP	C	C	T	rs61996312	gao_et_al_P7	p.D285D	ENSG00000175048	ENST00000359775	Transcript
chr6	167754357	167754357	*TTLL2*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.T323T	ENSG00000120440	ENST00000239587	Transcript
chr6	26246942	26246942	*HIST1H4G*	Silent	SNP	G	G	T	novel	gao_et_al_P7	p.V88V	ENSG00000124578	ENST00000244537	Transcript
chr6	90494812	90494812	*MDN1*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.P456P	ENSG00000112159	ENST00000369393	Transcript
chr7	140394600	140394600	*ADCK2*	Silent	SNP	G	G	A	rs374278300	gao_et_al_P7	p.P626P	ENSG00000133597	ENST00000072869	Transcript
chr7	142626178	142626178	*TRPV5*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.S175S	ENSG00000127412	ENST00000265310	Transcript
chr7	38505830	38505830	*AMPH*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.V203V	ENSG00000078053	ENST00000356264	Transcript
chr7	40132790	40132790	*CDK13*	Silent	SNP	G	G	A	rs201950690	gao_et_al_P7	p.A1214A	ENSG00000065883	ENST00000181839	Transcript
chr7	82453643	82453643	*PCLO*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.G4835G	ENSG00000186472	ENST00000333891	Transcript
chr8	110986369	110986369	*KCNV1*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.A83A	ENSG00000164794	ENST00000524391	Transcript
chr8	140630852	140630852	*KCNK9*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.A258A	ENSG00000169427	ENST00000520439	Transcript
chr8	25715965	25715965	*EBF2*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.T466T	ENSG00000221818	ENST00000520164	Transcript
chr8	30890269	30890269	*PURG*	Silent	SNP	G	G	T	novel	gao_et_al_P7	p.G10G	ENSG00000172733	ENST00000475541	Transcript
chr9	129870801	129870801	*ANGPTL2*	Silent	SNP	G	G	A	rs376334260	gao_et_al_P7	p.C70C	ENSG00000136859	ENST00000373425	Transcript
chr9	134393861	134393861	*POMT1*	Silent	SNP	C	C	T	rs568246978	gao_et_al_P7	p.D456D	ENSG00000130714	ENST00000372228	Transcript
chr9	190563599	190563599	*HAUS6*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.P950P	ENSG00000147874	ENST00000380502	Transcript
chr9	34125218	34125218	*DCAF12*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.L46L	ENSG00000198876	ENST00000361264	Transcript
chr9	35808822	35808822	*NPR2*	Silent	SNP	T	T	C	novel	gao_et_al_P7	p.T986T	ENSG00000159899	ENST00000342694	Transcript
chrX	129045422	129045422	*TLR7*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.V305V	ENSG00000196664	ENST00000380659	Transcript
chrX	152083321	152083321	*ZNF185*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.T34T	ENSG00000147394	ENST00000535861	Transcript
chrX	153689726	153689726	*PLXNA3*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.S294S	ENSG00000130827	ENST00000369682	Transcript
chrX	168598500	168598500	*TXLNG*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.P516P	ENSG00000086712	ENST00000380122	Transcript
chrX	20043953	20043953	*MAP7D2*	Silent	SNP	C	C	T	rs144221752	gao_et_al_P7	p.A375A	ENSG00000184368	ENST00000379643	Transcript
chrX	2852903	2852903	*ARSE*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.C580C	ENSG00000157399	ENST00000381134	Transcript
chrX	3242226	3242226	*MXRA5*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.S500S	ENSG00000101825	ENST00000217939	Transcript
chrX	54276563	54276563	*WNK3*	Silent	SNP	A	A	G	novel	gao_et_al_P7	p.N859N	ENSG00000196632	ENST00000354646	Transcript
chrX	79973224	79973224	*BRWD3*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.S693S	ENSG00000165288	ENST00000373275	Transcript
chrX	85403687	85403687	*DACH2*	Silent	SNP	C	C	T	novel	gao_et_al_P7	p.G21G	ENSG00000126733	ENST00000373125	Transcript
chrX	85906055	85906055	*DACH2*	Silent	SNP	G	G	A	rs193043717	gao_et_al_P7	p.A219A	ENSG00000126733	ENST00000373125	Transcript
chrX	99663116	99663116	*PCDH19*	Silent	SNP	G	G	A	novel	gao_et_al_P7	p.S160S	ENSG00000165194	ENST00000373034	Transcript
chr1	16356255	16356255	*CLCNKA*	Silent	SNP	C	C	A	novel	gao_et_al_P3	p.I419I	ENSG00000186510	ENST00000331433	Transcript
chr1	167059483	167059483	*GPA33*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.A14A	ENSG00000143167	ENST00000367868	Transcript
chr1	197390743	197390743	*CRB1*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.A595A	ENSG00000134376	ENST00000367400	Transcript
chr1	36774067	36774067	*SH3D21*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.P239P	ENSG00000214193	ENST00000453908	Transcript

chr1	75699746	75699746	*SLC44A5*	Silent	SNP	A	A	G	novel	gao_et_al_P3	p.L260L	ENSG00000137968	ENST00000370855	Transcript
chr10	101439600	101439600	*ENTPD7*	Silent	SNP	C	C	G	novel	gao_et_al_P3	p.L172L	ENSG00000198018	ENST00000370489	Transcript
chr11	5475549	5475549	*OR51I2*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.S277S	ENSG00000187918	ENST00000341449	Transcript
chr11	7818367	7818367	*OR5P2*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.I41I	ENSG00000183303	ENST00000329434	Transcript
chr12	29648372	29648372	*OVCH1*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.I100I	ENSG00000187950	ENST00000318184	Transcript
chr13	19751301	19751301	*TUBA3C*	Silent	SNP	C	C	T	rs140548354	gao_et_al_P3	p.P274P	ENSG00000198033	ENST00000400113	Transcript
chr13	19751346	19751346	*TUBA3C*	Silent	SNP	T	T	G	novel	gao_et_al_P3	p.L259L	ENSG00000198033	ENST00000400113	Transcript
chr13	29041095	29041095	*FLT1*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.A111A	ENSG00000102755	ENST00000282397	Transcript
chr14	105408330	105408330	*AHNAK2*	Silent	SNP	C	C	A	novel	gao_et_al_P3	p.V4486V	ENSG00000185567	ENST00000333244	Transcript
chr14	58796315	58796315	*ARID4A*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.T244T	ENSG00000032219	ENST00000355431	Transcript
chr15	49304869	49304869	*SECISBP2L*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.L569L	ENSG00000138593	ENST00000559471	Transcript
chr17	10312711	10312711	*MYH8*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.T594T	ENSG00000133020	ENST00000403437	Transcript
chr17	4689504	4689504	*VMO1*	Silent	SNP	G	G	A	novel	gao_et_al_P3	p.A48A	ENSG00000182853	ENST00000328739	Transcript
chr17	48699077	48699077	*CACNA1G*	Silent	SNP	G	G	C	novel	gao_et_al_P3	p.P1994P	ENSG00000006283	ENST00000359106	Transcript
chr19	12692256	12692256	*ZNF490*	Silent	SNP	G	G	T	novel	gao_et_al_P3	p.T211T	ENSG00000188033	ENST00000311437	Transcript
chr19	36243720	36243720	*LIN37*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.A59A	ENSG00000267796	ENST00000301159	Transcript
chr19	56370241	56370241	*NLRP4*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.A494A	ENSG00000160505	ENST00000301295	Transcript
chr2	108625087	108625087	*SLC5A7*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.S354S	ENSG00000115665	ENST00000264047	Transcript
chr2	133540571	133540571	*NCKAP5*	Silent	SNP	G	G	T	novel	gao_et_al_P3	p.A1271A	ENSG00000176771	ENST00000409261	Transcript
chr2	157612118	157612118	*DDX1*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.T475T	ENSG00000079785	ENST00000381341	Transcript
chr2	168107559	168107559	*XIRP2*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.A3219A	ENSG00000163092	ENST00000409195	Transcript
chr2	215838691	215838691	*ABCA12*	Silent	SNP	G	G	C	novel	gao_et_al_P3	p.S1848S	ENSG00000144452	ENST00000272895	Transcript
chr2	98275067	98275067	*ACTR1B*	Silent	SNP	T	T	A	rs546130794	gao_et_al_P3	p.S160S	ENSG00000115073	ENST00000289228	Transcript
chr20	54972411	54972411	*CSTF1*	Silent	SNP	A	A	G	novel	gao_et_al_P3	p.S106S	ENSG00000101138	ENST00000217109	Transcript
chr3	130116918	130116918	*COL6A5*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.I1318I	ENSG00000172752	ENST00000265379	Transcript
chr3	184588530	184588530	*VPS8*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.A557A	ENSG00000156931	ENST00000437079	Transcript
chr3	38739842	38739842	*SCN10A*	Silent	SNP	G	G	T	novel	gao_et_al_P3	p.I1623I	ENSG00000185313	ENST00000449082	Transcript
chr3	40574131	40574131	*ZNF621*	Silent	SNP	T	T	C	novel	gao_et_al_P3	p.P290P	ENSG00000172888	ENST00000339296	Transcript
chr3	50103761	50103761	*RBM6*	Silent	SNP	C	C	T	novel	gao_et_al_P3	p.T923T	ENSG00000004534	ENST00000266022	Transcript
chr4	135121437	135121437	*PABPC4L*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.A304A	ENSG00000254535	ENST00000529122	Transcript
chr4	26744204	26744204	*TBC1D19*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.R434R	ENSG00000109680	ENST00000264866	Transcript
chr4	75937804	75937804	*PARM1*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.S71S	ENSG00000169116	ENST00000307428	Transcript
chr5	1278759	1278759	*TERT*	Silent	SNP	G	G	A	rs370808390	gao_et_al_P3	p.S761S	ENSG00000164362	ENST00000310581	Transcript
chr5	130498292	130498292	*HINT1*	Silent	SNP	A	A	G	novel	gao_et_al_P3	p.I63I	ENSG00000169567	ENST00000304043	Transcript
chr5	154396212	154396212	*KIF4B*	Silent	SNP	G	G	T	novel	gao_et_al_P3	p.V931V	ENSG00000226650	ENST00000435029	Transcript
chr5	90002109	90002109	*GPR98*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.V2876V	ENSG00000164199	ENST00000405460	Transcript
chr7	154595639	154595639	*DPP6*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.L491L	ENSG00000130226	ENST00000377770	Transcript
chr7	66236895	66236895	*KCTD7*	Silent	SNP	T	T	G	novel	gao_et_al_P3	p.L3L	ENSG00000243335	ENST00000510829	Transcript
chr7	98501070	98501070	*TRRAP*	Silent	SNP	A	A	T	rs370423667	gao_et_al_P3	p.A322A	ENSG00000196367	ENST00000359863	Transcript
chr8	130763807	130763807	*GSDMC*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.I308I	ENSG00000147697	ENST00000276708	Transcript
chr8	30416418	30416418	*RBPMS*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.P181P	ENSG00000157110	ENST00000320203	Transcript

chr9	115805686	115805686	*ZFP37*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.P404P	ENSG00000136866	ENST00000374227	Transcript
chr9	27524814	27524814	*IFNK*	Silent	SNP	G	G	T	novel	gao_et_al_P3	p.L160L	ENSG00000147896	ENST00000276943	Transcript
chrX	119048799	119048799	*AKAP14*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.A133A	ENSG00000186471	ENST00000371431	Transcript
chrX	123839053	123839053	*TENM1*	Silent	SNP	T	T	A	novel	gao_et_al_P3	p.A275A	ENSG00000009694	ENST00000422452	Transcript
chrX	77270221	77270221	*ATP7A*	Silent	SNP	A	A	T	novel	gao_et_al_P3	p.V823V	ENSG00000165240	ENST00000341514	Transcript
chr1	152283582	152283582	*FLG*	Silent	SNP	G	G	A	novel	gao_et_al_P1	p.S1260S	ENSG00000143631	ENST00000368799	Transcript
chr1	223396739	223396739	*SUSD4*	Silent	SNP	G	G	A	novel	gao_et_al_P1	p.S432S	ENSG00000143502	ENST00000343846	Transcript
chr1	86048659	86048659	*CYR61*	Silent	SNP	G	G	A	rs9658588	gao_et_al_P1	p.P360P	ENSG00000142871	ENST00000451137	Transcript
chr10	48388205	48388205	*RBP3*	Silent	SNP	T	T	C	novel	gao_et_al_P1	p.A891A	ENSG00000107618	ENST00000224600	Transcript
chr11	48238529	48238529	*OR4B1*	Silent	SNP	C	C	T	novel	gao_et_al_P1	p.P56P	ENSG00000175619	ENST00000309562	Transcript
chr12	64536212	64536212	*SRGAP1*	Silent	SNP	G	G	A	rs138568906	gao_et_al_P1	p.T1006T	ENSG00000196935	ENST00000355086	Transcript
chr16	72828004	72828004	*ZFHX3*	Silent	SNP	C	C	T	novel	gao_et_al_P1	p.T2859T	ENSG00000140836	ENST00000268489	Transcript
chr16	89351924	89351924	*ANKRD11*	Silent	SNP	G	G	A	rs200484387	gao_et_al_P1	p.P342P	ENSG00000167522	ENST00000301030	Transcript
chr17	12656384	12656384	*MYOCD*	Silent	SNP	C	C	T	novel	gao_et_al_P1	p.S593S	ENSG00000141052	ENST00000425538	Transcript
chr17	74475014	74475014	*RHBDF2*	Silent	SNP	C	C	T	rs3744044	gao_et_al_P1	p.P211P	ENSG00000129667	ENST00000313080	Transcript
chr17	909353	909353	*ABR*	Silent	SNP	C	C	T	rs80119159	gao_et_al_P1	p.K849K	ENSG00000159842	ENST00000302538	Transcript
chr19	5700902	5700902	*LONP1*	Silent	SNP	G	G	A	rs549948118	gao_et_al_P1	p.I468I	ENSG00000196365	ENST00000360614	Transcript
chr19	5771045	5771045	*CATSPERD*	Silent	SNP	C	C	T	novel	gao_et_al_P1	p.L575L	ENSG00000174898	ENST00000381624	Transcript
chr19	847918	847918	*PRTN3*	Silent	SNP	G	G	C	rs371384666	gao_et_al_P1	p.V240V	ENSG00000196415	ENST00000234347	Transcript
chr2	105984066	105984066	*FHL2*	Silent	SNP	A	A	G	rs397517960	gao_et_al_P1	p.Y154Y	ENSG00000115641	ENST00000358129	Transcript
chr2	231406741	231406741	*SP100*	Silent	SNP	A	A	G	novel	gao_et_al_P1	p.E846E	ENSG00000067066	ENST00000340126	Transcript
chr20	23666534	23666534	*CST4*	Silent	SNP	G	G	C	novel	gao_et_al_P1	p.A141A	ENSG00000101441	ENST00000217423	Transcript
chr21	47831357	47831357	*PCNT*	Silent	SNP	C	C	T	rs192388432	gao_et_al_P1	p.G1790G	ENSG00000160299	ENST00000359568	Transcript
chr4	9213165	9213165	*USP17L10*	Silent	SNP	G	G	A	novel	gao_et_al_P1	p.A261A	ENSG00000231396	ENST00000417945	Transcript
chr5	140590540	140590540	*PCDHB12*	Silent	SNP	T	T	C	novel	gao_et_al_P1	p.T687T	ENSG00000120328	ENST00000239450	Transcript
chr5	484646	484646	*SLC9A3*	Silent	SNP	C	C	T	rs139319603	gao_et_al_P1	p.S307S	ENSG00000066230	ENST00000264938	Transcript
chr6	117638336	117638336	*ROS1*	Silent	SNP	A	A	G	novel	gao_et_al_P1	p.L2035L	ENSG00000047936	ENST00000368508	Transcript
chr6	129588346	129588346	*LAMA2*	Silent	SNP	C	C	T	rs142126511	gao_et_al_P1	p.D768D	ENSG00000196569	ENST00000421865	Transcript
chr7	47341803	47341803	*TNS3*	Silent	SNP	C	C	T	novel	gao_et_al_P1	p.A1175A	ENSG00000136205	ENST00000398879	Transcript
chr7	99720167	99720167	*CNPY4*	Silent	SNP	C	C	T	rs142050123	gao_et_al_P1	p.H103H	ENSG00000166997	ENST00000262932	Transcript
chr9	35606025	35606025	*TESK1*	Silent	SNP	C	C	T	novel	gao_et_al_P1	p.N88N	ENSG00000107140	ENST00000336395	Transcript
chrX	75004770	75004770	*MAGEE2*	Silent	SNP	T	T	C	novel	gao_et_al_P1	p.L39L	ENSG00000186675	ENST00000373359	Transcript
chr1	150998049	150998049	*PRUNE*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.K193K	ENSG00000143363	ENST00000271620	Transcript
chr1	151681543	151681543	*CELF3*	Silent	SNP	G	G	A	rs200147307	gao_et_al_P2	p.F139F	ENSG00000159409	ENST00000290583	Transcript
chr1	152283582	152283582	*FLG*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.S1260S	ENSG00000143631	ENST00000368799	Transcript
chr1	153705789	153705789	*KAZN*	Silent	SNP	G	G	A	rs146334402	gao_et_al_P2	p.T220T	ENSG00000189337	ENST00000376030	Transcript
chr1	167780136	167780136	*ADCY10*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.L1499L	ENSG00000143199	ENST00000367851	Transcript
chr1	195460999	195460999	*EMC1*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.I922I	ENSG00000127463	ENST00000477853	Transcript
chr1	202276473	202276473	*LGR6*	Silent	SNP	C	C	T	rs146190126	gao_et_al_P2	p.N408N	ENSG00000133067	ENST00000367278	Transcript
chr1	223396739	223396739	*SUSD4*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.S432S	ENSG00000143502	ENST00000343846	Transcript
chr1	53675934	53675934	*CPT2*	Silent	SNP	T	T	C	rs140853350	gao_et_al_P2	p.P196P	ENSG00000157184	ENST00000371486	Transcript

chr1	6007194	6007194	*NPHP4*	Silent	SNP	C	C	A	rs201464887	gao_et_al_P2	p.V363V	ENSG00000131697	ENST00000378156	Transcript
chr10	120934043	120934043	*PRDX3*	Silent	SNP	A	A	G	rs145513398	gao_et_al_P2	p.V77V	ENSG00000165672	ENST00000298510	Transcript
chr10	28900746	28900746	*WAC*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.A444A	ENSG00000095787	ENST00000354911	Transcript
chr10	96522576	96522576	*CYP2C19*	Silent	SNP	G	G	T	novel	gao_et_al_P2	p.V38V	ENSG00000165841	ENST00000371321	Transcript
chr11	4945480	4945480	*OR51G1*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.S30S	ENSG00000176879	ENST00000321961	Transcript
chr11	65812848	65812848	*GAL3ST3*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.K13K	ENSG00000175229	ENST00000312006	Transcript
chr11	88300963	88300963	*GRM5*	Silent	SNP	A	A	G	rs145801912	gao_et_al_P2	p.L630L	ENSG00000168959	ENST00000418177	Transcript
chr12	14706267	14706267	*PLBD1*	Silent	SNP	G	G	A	rs78856185	gao_et_al_P2	p.D65D	ENSG00000121316	ENST00000240617	Transcript
chr12	45269126	45269126	*NELL2*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.L72L	ENSG00000184613	ENST00000437801	Transcript
chr12	64536212	64536212	*SRGAP1*	Silent	SNP	G	G	A	rs138568906	gao_et_al_P2	p.T1006T	ENSG00000196935	ENST00000355086	Transcript
chr14	24880375	24880375	*NYNRIN*	Silent	SNP	A	A	G	rs553952299	gao_et_al_P2	p.V836V	ENSG00000205978	ENST00000382554	Transcript
chr15	64495353	64495353	*CSNK1G1*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.G345G	ENSG00000169118	ENST00000303052	Transcript
chr16	23713587	23713587	*ERN2*	Silent	SNP	G	G	A	rs368051154	gao_et_al_P2	p.H411H	ENSG00000134398	ENST00000256797	Transcript
chr16	72828004	72828004	*ZFHX3*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.T2859T	ENSG00000140836	ENST00000268489	Transcript
chr16	89351924	89351924	*ANKRD11*	Silent	SNP	G	G	A	rs200484387	gao_et_al_P2	p.P342P	ENSG00000167522	ENST00000301030	Transcript
chr17	27901855	27901855	*GIT1*	Silent	SNP	C	C	T	rs201810676	gao_et_al_P2	p.R726R	ENSG00000108262	ENST00000394869	Transcript
chr17	4644059	4644059	*ZMYND15*	Silent	SNP	G	G	A	rs138373624	gao_et_al_P2	p.G72G	ENSG00000141497	ENST00000573751	Transcript
chr17	59560871	59560871	*TBX4*	Silent	SNP	C	C	T	rs545088929	gao_et_al_P2	p.D544D	ENSG00000121075	ENST00000240335	Transcript
chr17	61611436	61611436	*KCNH6*	Silent	SNP	C	C	A	novel	gao_et_al_P2	p.R289R	ENSG00000173826	ENST00000583023	Transcript
chr17	62135276	62135276	*ERN1*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.H428H	ENSG00000178607	ENST00000433197	Transcript
chr17	76565320	76565320	*DNAH17*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.V404V	ENSG00000187775	ENST00000389840	Transcript
chr18	47429084	47429084	*MYO5B*	Silent	SNP	G	G	C	novel	gao_et_al_P2	p.L897L	ENSG00000167306	ENST00000285039	Transcript
chr19	12882035	12882035	*HOOK2*	Silent	SNP	G	G	C	rs534976470	gao_et_al_P2	p.L233L	ENSG00000095066	ENST00000397668	Transcript
chr19	14952246	14952246	*OR7A10*	Silent	SNP	G	G	T	rs187236921	gao_et_al_P2	p.S148S	ENSG00000127515	ENST00000248058	Transcript
chr19	18965450	18965450	*UPF1*	Silent	SNP	G	G	T	rs201936003	gao_et_al_P2	p.V399V	ENSG00000005007	ENST00000262803	Transcript
chr19	3728628	3728628	*TJP3*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.A34A	ENSG00000105289	ENST00000589378	Transcript
chr19	44276218	44276218	*KCNN4*	Silent	SNP	G	G	A	rs200350667	gao_et_al_P2	p.I251I	ENSG00000104783	ENST00000262888	Transcript
chr19	49633775	49633775	*PPFIA3*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.L266L	ENSG00000177380	ENST00000334186	Transcript
chr19	49967770	49967770	*ALDH16A1*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.G476G	ENSG00000161618	ENST00000293350	Transcript
chr19	54721302	54721302	*LILRB3*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.P546P	ENSG00000204577	ENST00000245620	Transcript
chr19	5700902	5700902	*LONP1*	Silent	SNP	G	G	A	rs549948118	gao_et_al_P2	p.I468I	ENSG00000196365	ENST00000360614	Transcript
chr19	847918	847918	*PRTN3*	Silent	SNP	G	G	C	rs371384666	gao_et_al_P2	p.V240V	ENSG00000196415	ENST00000234347	Transcript
chr2	105984066	105984066	*FHL2*	Silent	SNP	A	A	G	rs397517960	gao_et_al_P2	p.Y154Y	ENSG00000115641	ENST00000358129	Transcript
chr2	128528436	128528436	*WDR33*	Silent	SNP	C	C	T	rs140087774	gao_et_al_P2	p.Q40Q	ENSG00000136709	ENST00000322313	Transcript
chr2	204941944	204941944	*PUM2*	Silent	SNP	C	C	T	rs187424529	gao_et_al_P2	p.A365A	ENSG00000055917	ENST00000338086	Transcript
chr2	338101077	338101077	*FAM98A*	Silent	SNP	T	T	G	rs573575800	gao_et_al_P2	p.S431S	ENSG00000119812	ENST00000238823	Transcript
chr2	70188512	70188512	*ASPRV1*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.P103P	ENSG00000244617	ENST00000320256	Transcript
chr20	20493897	20493897	*RALGAPA2*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.P1372P	ENSG00000188559	ENST00000202677	Transcript
chr20	23666534	23666534	*CST4*	Silent	SNP	G	G	C	novel	gao_et_al_P2	p.A141A	ENSG00000101441	ENST00000217423	Transcript
chr21	46012150	46012150	*KRTAP10-6*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.C72C	ENSG00000188155	ENST00000400368	Transcript
chr21	47831357	47831357	*PCNT*	Silent	SNP	C	C	T	rs192388432	gao_et_al_P2	p.G1790G	ENSG00000160299	ENST00000359568	Transcript

chr22	23656784	23656784	*BCR*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.L1203L	ENSG00000186716	ENST00000305877	Transcript
chr3	133672574	133672574	*SLCO2A1*	Silent	SNP	C	C	T	rs149443780	gao_et_al_P2	p.P219P	ENSG00000174640	ENST00000310926	Transcript
chr3	158386797	158386797	*LXN*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.T165T	ENSG00000079257	ENST00000264265	Transcript
chr3	46874459	46874459	*PRSS42*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.T203T	ENSG00000178055	ENST00000429665	Transcript
chr3	48623675	48623675	*COL7A1*	Silent	SNP	A	A	C	novel	gao_et_al_P2	p.L1185L	ENSG00000114270	ENST00000328333	Transcript
chr3	48694594	48694594	*CELSR3*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.I1312I	ENSG00000008300	ENST00000164024	Transcript
chr3	9032292	9032292	*SRGAP3*	Silent	SNP	C	C	T	rs527933052	gao_et_al_P2	p.A930A	ENSG00000196220	ENST00000383836	Transcript
chr4	146824081	146824081	*ZNF827*	Silent	SNP	G	G	A	rs147898239	gao_et_al_P2	p.D110D	ENSG00000151612	ENST00000379448	Transcript
chr4	156721152	156721152	*GUCY1B3*	Silent	SNP	A	A	G	novel	gao_et_al_P2	p.Q367Q	ENSG00000061918	ENST00000264424	Transcript
chr4	178854 75	178854 75	*LCORL*	Silent	SNP	T	T	C	rs547682002	gao_et_al_P2	p.E559E	ENSG00000178177	ENST00000382226	Transcript
chr4	72205211	72205211	*SLC4A4*	Silent	SNP	G	G	A	rs549042834	gao_et_al_P2	p.K126K	ENSG00000080493	ENST00000425175	Transcript
chr5	140590540	140590540	*PCDHB12*	Silent	SNP	T	T	C	novel	gao_et_al_P2	p.T687T	ENSG00000120328	ENST00000239450	Transcript
chr5	176013810	176013810	*CDHR2*	Silent	SNP	C	C	T	rs3749626	gao_et_al_P2	p.L941L	ENSG00000074276	ENST00000510636	Transcript
chr6	129588346	129588346	*LAMA2*	Silent	SNP	C	C	T	rs142126511	gao_et_al_P2	p.D768D	ENSG00000196569	ENST00000421865	Transcript
chr6	70878558	70878558	*COL19A1*	Silent	SNP	C	C	T	rs370691639	gao_et_al_P2	p.G851G	ENSG00000082293	ENST00000322773	Transcript
chr7	154760531	154760531	*PAXIP1*	Silent	SNP	C	C	T	rs371796152	gao_et_al_P2	p.P460P	ENSG00000157212	ENST00000404141	Transcript
chr7	47341803	47341803	*TNS3*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.A1175A	ENSG00000136205	ENST00000398879	Transcript
chr7	6731250	6731250	*ZNF12*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.E441E	ENSG00000164631	ENST00000405858	Transcript
chr7	99720167	99720167	*CNPY4*	Silent	SNP	C	C	T	rs142050123	gao_et_al_P2	p.H103H	ENSG00000166997	ENST00000262932	Transcript
chr8	121290801	121290801	*COL14A1*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.R1155R	ENSG00000187955	ENST00000297848	Transcript
chr8	145161777	145161777	*MAF1*	Silent	SNP	G	G	A	rs191280172	gao_et_al_P2	p.L220L	ENSG00000179632	ENST00000322428	Transcript
chr9	116276808	116276808	*RGS3*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.V516V	ENSG00000138835	ENST00000374140	Transcript
chr9	33295121	33295121	*NFX1*	Silent	SNP	G	G	A	novel	gao_et_al_P2	p.Q243Q	ENSG00000086102	ENST00000379540	Transcript
chr9	35606025	35606025	*TESK1*	Silent	SNP	C	C	T	novel	gao_et_al_P2	p.N88N	ENSG00000107140	ENST00000336395	Transcript
chrX	109697316	109697316	*RGAG1*	Silent	SNP	A	A	C	novel	gao_et_al_P2	p.A1157A	ENSG00000243978	ENST00000465301	Transcript
chrX	128890523	128890523	*XPNPEP2*	Silent	SNP	G	G	C	novel	gao_et_al_P2	p.G453G	ENSG00000122121	ENST00000371106	Transcript
chrX	75004770	75004770	*MAGEE2*	Silent	SNP	T	T	C	novel	gao_et_al_P2	p.L39L	ENSG00000186675	ENST00000373359	Transcript
chr1	161928312	161928312	*ATF6*	Silent	SNP	T	T	C	novel	gao_et_al_P4	p.H627H	ENSG00000118217	ENST00000367942	Transcript
chr1	176853557	176853557	*ASTN1*	Silent	SNP	T	T	G	novel	gao_et_al_P4	p.P1048P	ENSG00000152092	ENST00000361833	Transcript
chr10	71969413	71969413	*PPA1*	Silent	SNP	A	A	G	novel	gao_et_al_P4	p.P180P	ENSG00000180817	ENST00000373232	Transcript
chr10	93732	93732	*TUBB8*	Silent	SNP	A	A	G	novel	gao_et_al_P4	p.F200F	ENSG00000173876	ENST00000309812	Transcript
chr11	55418629	55418629	*OR4S2*	Silent	SNP	T	T	C	novel	gao_et_al_P4	p.L84L	ENSG00000174982	ENST00000312422	Transcript
chr15	86251254	86251254	*AKAP13*	Silent	SNP	C	C	T	novel	gao_et_al_P4	p.C1827C	ENSG00000170776	ENST00000361243	Transcript
chr19	22171649	22171649	*ZNF208*	Silent	SNP	G	G	A	rs375118705	gao_et_al_P4	p.D22D	ENSG00000160321	ENST00000397126	Transcript
chr22	31850225	31850225	*EIF4ENIF1*	Silent	SNP	G	G	T	novel	gao_et_al_P4	p.R473R	ENSG00000184708	ENST00000397525	Transcript
chr3	25635089	25635089	*RARB*	Silent	SNP	A	A	T	novel	gao_et_al_P4	p.G294G	ENSG00000077092	ENST00000330688	Transcript
chr3	97868967	97868967	*OR5H14*	Silent	SNP	A	A	G	rs189802566	gao_et_al_P4	p.L246L	ENSG00000236032	ENST00000437310	Transcript
chr6	158317894	158317894	*SNX9*	Silent	SNP	T	T	C	novel	gao_et_al_P4	p.S112S	ENSG00000130340	ENST00000392185	Transcript
chr1	97250698	97250698	*PTBP2*	Silent	SNP	C	C	T	novel	gao_et_al_P5	p.Y264Y	ENSG00000117569	ENST00000426398	Transcript
chr13	102029142	102029142	*NALCN*	Silent	SNP	G	G	A	novel	gao_et_al_P5	p.L185L	ENSG00000102452	ENST00000251127	Transcript
chr13	39264982	39264982	*FREM2*	Silent	SNP	T	T	C	novel	gao_et_al_P5	p.C1167C	ENSG00000150893	ENST00000280481	Transcript

chr20	35441131	35441131	*SOGA1*	Silent	SNP	T	T	C	novel	gao_et_al_P5	p.E811E	ENSG00000149639	ENST00000237536	Transcript
chr22	26181407	26181407	*MYO18B*	Silent	SNP	C	C	T	novel	gao_et_al_P5	p.N775N	ENSG00000133454	ENST00000335473	Transcript
chr3	10088404	10088404	*FANCD2*	Silent	SNP	C	C	T	novel	gao_et_al_P5	p.Y425Y	ENSG00000144554	ENST00000287647	Transcript
chr3	6903168	6903168	*GRM7*	Silent	SNP	G	G	T	novel	gao_et_al_P5	p.A31A	ENSG00000196277	ENST00000357716	Transcript
chr5	141016349	141016349	*HDAC3*	Silent	SNP	C	C	T	novel	gao_et_al_P5	p.K3K	ENSG00000171720	ENST00000305264	Transcript
chr8	145947626	145947626	*ZNF251*	Silent	SNP	G	G	A	novel	gao_et_al_P5	p.S473S	ENSG00000198169	ENST00000292562	Transcript
chrX	101858722	101858722	*ARMCX5*	Silent	SNP	C	C	A	novel	gao_et_al_P5	p.V551V	ENSG00000125962	ENST00000604957	Transcript
chr1	40036920	40036920	*PABPC4*	Silent	SNP	G	G	T	novel	gao_et_al_P6	p.L163L	ENSG00000090621	ENST00000372858	Transcript
chr1	45294904	45294904	*PTCH2*	Silent	SNP	C	C	A	novel	gao_et_al_P6	p.L432L	ENSG00000117425	ENST00000372192	Transcript
chr10	98079036	98079036	*DNTT*	Silent	SNP	A	A	C	rs370448388	gao_et_al_P6	p.S132S	ENSG00000107447	ENST00000371174	Transcript
chr16	20748361	20748361	*THUMPD1*	Silent	SNP	T	T	C	novel	gao_et_al_P6	p.A301A	ENSG00000066654	ENST00000381337	Transcript
chr17	43013680	43013680	*KIF18B*	Silent	SNP	C	C	A	novel	gao_et_al_P6	p.V11V	ENSG00000186185	ENST00000593135	Transcript
chr17	45517900	45517900	*EFCAB13*	Silent	SNP	A	A	C	novel	gao_et_al_P6	p.P914P	ENSG00000178852	ENST00000331493	Transcript
chr17	72773478	72773478	*TMEM104*	Silent	SNP	T	T	G	rs202104975	gao_et_al_P6	p.G3G	ENSG00000109066	ENST00000335464	Transcript
chr18	29122488	29122488	*DSG2*	Silent	SNP	G	G	T	novel	gao_et_al_P6	p.V669V	ENSG00000046604	ENST00000261590	Transcript
chr19	14991802	14991802	*OR7A17*	Silent	SNP	C	C	A	novel	gao_et_al_P6	p.R122R	ENSG00000185385	ENST00000327462	Transcript
chr21	43982190	43982190	*SLC37A1*	Silent	SNP	C	C	T	novel	gao_et_al_P6	p.G328G	ENSG00000160190	ENST00000352133	Transcript
chr4	1389448	1389448	*CRIPAK*	Silent	SNP	T	T	C	rs530576391	gao_et_al_P6	p.P383P	ENSG00000179979	ENST00000324803	Transcript
chr4	57349346	57349346	*SRP72*	Silent	SNP	C	C	G	novel	gao_et_al_P6	p.T289T	ENSG00000174780	ENST00000342756	Transcript
chr4	82013540	82013540	*PRKG2*	Silent	SNP	C	C	T	novel	gao_et_al_P6	p.E731E	ENSG00000138669	ENST00000395578	Transcript
chr6	138615217	138615217	*KIAA1244*	Silent	SNP	T	T	C	novel	gao_et_al_P6	p.L1152L	ENSG00000112379	ENST00000251691	Transcript
chr7	143771618	143771618	*OR2A25*	Silent	SNP	G	G	T	novel	gao_et_al_P6	p.L102L	ENSG00000221933	ENST00000408898	Transcript
chr8	68128825	68128825	*ARFGEF1*	Silent	SNP	C	C	T	novel	gao_et_al_P6	p.L1562L	ENSG00000066777	ENST00000262215	Transcript
chr1	156883242	156883242	*PEAR1*	Silent	SNP	G	G	A	rs55864969	Patient1	p.G857G	ENSG00000187800	ENST00000338302	Transcript
chr1	195664008	195664008	*EMC1*	Silent	SNP	A	A	C	rs143222669	Patient1	p.A286A	ENSG00000127463	ENST00000477853	Transcript
chr1	22973910	22973910	*C1QC*	Silent	SNP	C	C	T	rs151045868	Patient1	p.V124V	ENSG00000159189	ENST00000374639	Transcript
chr1	26608853	26608853	*UBXN11*	Silent	SNP	G	G	A	novel	Patient1	p.G500G	ENSG00000158062	ENST00000374222	Transcript
chr1	44584585	44584585	*KLF17*	Silent	SNP	C	C	T	rs147568330	Patient1	p.Y2Y	ENSG00000171872	ENST00000372299	Transcript
chr10	21074757	21074757	*NEBL*	Silent	SNP	G	G	A	rs144946187	Patient1	p.D988D	ENSG00000078114	ENST00000377122	Transcript
chr11	124767126	124767126	*ROBO4*	Silent	SNP	G	G	T	rs117911608	Patient1	p.I34I	ENSG00000154133	ENST00000306534	Transcript
chr11	64789222	64789222	*ARL2*	Silent	SNP	C	C	T	rs61736632	Patient1	p.H150H	ENSG00000213465	ENST00000246747	Transcript
chr12	122862233	122862233	*CLIP1*	Silent	SNP	T	T	C	rs139445702	Patient1	p.R120R	ENSG00000130779	ENST00000540338	Transcript
chr12	125834800	125834800	*TMEM132B*	Silent	SNP	G	G	A	rs73233395	Patient1	p.S285S	ENSG00000139364	ENST00000299308	Transcript
chr13	28240021	28240021	*POLR1D*	Silent	SNP	C	C	T	novel	Patient1	p.S100S	ENSG00000186184	ENST00000399697	Transcript
chr15	29398920	29398920	*APBA2*	Silent	SNP	G	G	A	rs140055297	Patient1	p.P605P	ENSG00000034053	ENST00000558402	Transcript
chr15	49088220	49088220	*CEP152*	Silent	SNP	T	T	C	novel	Patient1	p.L226L	ENSG00000103995	ENST00000380950	Transcript
chr16	25264321	25264321	*ZKSCAN2*	Silent	SNP	T	T	C	novel	Patient1	p.E208E	ENSG00000155592	ENST00000328086	Transcript
chr16	28606772	28606772	*SULT1A2*	Silent	SNP	C	C	G	rs369200053	Patient1	p.L96L	ENSG00000197165	ENST00000395630	Transcript
chr17	58236599	58236599	*CA4*	Silent	SNP	A	A	T	rs140515828	Patient1	p.A251A	ENSG00000167434	ENST00000300900	Transcript
chr18	60021667	60021667	*TNFRSF11A*	Silent	SNP	C	C	T	rs35003467	Patient1	p.P109P	ENSG00000141655	ENST00000586569	Transcript
chr19	18279665	18279665	*PIK3R2*	Silent	SNP	C	C	T	rs146987351	Patient1	p.I646I	ENSG00000105647	ENST00000222254	Transcript

chr19	375860	375860	*THEG*	Silent	SNP	G	G	A	novel	Patient1	p.Y37Y	ENSG00000105549	ENST00000342640	Transcript
chr19	42729380	42729380	*ZNF526*	Silent	SNP	C	C	T	rs138082392	Patient1	p.C275C	ENSG00000167625	ENST00000301215	Transcript
chr19	42874936	42874936	*MEGF8*	Silent	SNP	C	C	T	rs138235390	Patient1	p.C2296C	ENSG00000105429	ENST00000334370	Transcript
chr19	43585274	43585274	*PSG2*	Silent	SNP	A	A	G	novel	Patient1	p.T63T	ENSG00000242221	ENST00000406487	Transcript
chr19	46289059	46289059	*DMWD*	Silent	SNP	G	G	A	rs61744166	Patient1	p.S565S	ENSG00000185800	ENST00000270223	Transcript
chr19	54627164	54627164	*PRPF31*	Silent	SNP	G	G	A	novel	Patient1	p.E188E	ENSG00000105618	ENST00000321030	Transcript
chr2	114257388	114257388	*FOXD4L1*	Silent	SNP	C	C	T	rs144904377	Patient1	p.P185P	ENSG00000184492	ENST00000306507	Transcript
chr2	220432098	220432098	*OBSL1*	Silent	SNP	C	C	T	rs181182663	Patient1	p.P578P	ENSG00000124006	ENST00000404537	Transcript
chr2	242681922	242681922	*D2HGDH*	Silent	SNP	C	C	T	rs142473303	Patient1	p.P141P	ENSG00000180902	ENST00000321264	Transcript
chr2	97526963	97526963	*SEMA4C*	Silent	SNP	C	C	T	rs71427097	Patient1	p.A634A	ENSG00000168758	ENST00000305476	Transcript
chr20	61916244	61916244	*ARFGAP1*	Silent	SNP	C	C	T	rs143810518	Patient1	p.N258N	ENSG00000101199	ENST00000353546	Transcript
chr20	62221778	62221778	*GMEB2*	Silent	SNP	G	G	A	novel	Patient1	p.P419P	ENSG00000101216	ENST00000266068	Transcript
chr22	50885628	50885628	*SBF1*	Silent	SNP	G	G	A	rs146489206	Patient1	p.D1875D	ENSG00000100241	ENST00000380817	Transcript
chr3	10106539	10106539	*FANCD2*	Silent	SNP	C	C	G	rs55856815	Patient1	p.T716T	ENSG00000144554	ENST00000287647	Transcript
chr3	114058008	114058008	*ZBTB20*	Silent	SNP	G	G	T	rs139619357	Patient1	p.T690T	ENSG00000181722	ENST00000474710	Transcript
chr5	1081855	1081855	*SLC12A7*	Silent	SNP	G	G	A	rs148022833	Patient1	p.N378N	ENSG00000113504	ENST00000264930	Transcript
chr5	150503872	150503872	*ANXA6*	Silent	SNP	C	C	T	rs138779149	Patient1	p.A371A	ENSG00000197043	ENST00000354546	Transcript
chr6	306152844	306152844	*C6orf136*	Silent	SNP	G	G	A	rs116816200	Patient1	p.T92T	ENSG00000204564	ENST00000293604	Transcript
chr6	32035616	32035616	*TNXB*	Silent	SNP	G	G	A	novel	Patient1	p.F2122F	ENSG00000168477	ENST00000375244	Transcript
chr8	140744252	140744252	*TRAPPC9*	Silent	SNP	G	G	A	rs112551069	Patient1	p.F1181F	ENSG00000167632	ENST00000389328	Transcript
chr9	78973463	78973463	*PCSK5*	Silent	SNP	T	T	G	rs17721466	Patient1	p.P1736P	ENSG00000099139	ENST00000545128	Transcript
chr9	93637006	93637006	*SYK*	Silent	SNP	C	C	T	rs41274652	Patient1	p.Y352Y	ENSG00000165025	ENST00000375754	Transcript
chrX	129147159	129147159	*BCORL1*	Silent	SNP	C	C	T	rs375461860	Patient1	p.A137A	ENSG00000085185	ENST00000540052	Transcript
chrX	135431916	135431916	*GPR112*	Silent	SNP	C	C	G	novel	Patient1	p.G2017G	ENSG00000156920	ENST00000394143	Transcript
chrX	142795342	142795342	*SPANXN2*	Silent	SNP	G	G	A	novel	Patient1	p.D112D	ENSG00000203924	ENST00000370498	Transcript
chrX	9862731	9862731	*SHROOM2*	Silent	SNP	G	G	A	rs74461072	Patient1	p.S261S	ENSG00000146950	ENST00000380913	Transcript
chr1	201180243	201180243	*IGFN1*	Silent	SNP	A	A	G	rs367952435	Patient2	p.L2074L	ENSG00000163395	ENST00000335211	Transcript
chr10	75525331	75525331	*SEC24C*	Silent	SNP	C	C	T	novel	Patient2	p.C450C	ENSG00000176986	ENST00000339365	Transcript
chr11	124179778	124179778	*OR8D1*	Silent	SNP	C	C	T	novel	Patient2	p.K295K	ENSG00000196341	ENST00000357821	Transcript
chr16	88804712	88804712	*PIEZO1*	Silent	SNP	G	G	A	novel	Patient2	p.A257A	ENSG00000103335	ENST00000301015	Transcript
chr18	12122369	12122369	*ANKRD62*	Silent	SNP	A	A	G	novel	Patient2	p.K436K	ENSG00000181626	ENST00000587848	Transcript
chr1	200572455	200572455	*KIF14*	Silent	SNP	A	A	G	novel	Patient3	p.I626I	ENSG00000118193	ENST00000367350	Transcript
chr1	203652507	203652507	*ATP2B4*	Silent	SNP	G	G	A	novel	Patient3	p.L58L	ENSG00000058668	ENST00000357681	Transcript
chr10	126682468	126682468	*CTBP2*	Silent	SNP	C	C	T	rs79993000	Patient3	p.R829R	ENSG00000175029	ENST00000309035	Transcript
chr11	64060676	64060676	*KCNK4*	Silent	SNP	C	C	T	novel	Patient3	p.I62I	ENSG00000182450	ENST00000539216	Transcript
chr14	80328040	80328040	*NRXN3*	Silent	SNP	G	G	A	rs143519887	Patient3	p.P973P	ENSG00000021645	ENST00000554719	Transcript
chr17	18874870	18874870	*FAM83G*	Silent	SNP	G	G	A	rs377066158	Patient3	p.P758P	ENSG00000188522	ENST00000388995	Transcript
chr17	21454548	21454548	*C17orf51*	Silent	SNP	A	A	C	novel	Patient3	p.P46P	ENSG00000212719	ENST00000391411	Transcript
chr19	20728217	20728217	*ZNF737*	Silent	SNP	C	C	T	rs538867044	Patient3	p.K264K	ENSG00000237440	ENST00000427401	Transcript
chr19	55377279	55377279	*KIR3DL2*	Silent	SNP	T	T	C	novel	Patient3	p.H340H	ENSG00000240403	ENST00000326321	Transcript
chr2	201133941	201133941	*WDR35*	Silent	SNP	T	T	A	novel	Patient3	p.V1157V	ENSG00000118965	ENST00000345530	Transcript

chr2	95539270	95539270	*TEKT4*	Silent	SNP	C	C	T	novel	Patient3	p.A168A	ENSG00000163060	ENST00000295201	Transcript
chr20	4705281	4705281	*PRND*	Silent	SNP	C	C	A	novel	Patient3	p.G28G	ENSG00000171864	ENST00000305817	Transcript
chr3	49847050	49847050	*UBA7*	Silent	SNP	C	C	T	novel	Patient3	p.A671A	ENSG00000182179	ENST00000333486	Transcript
chr4	190884251	190884251	*FRG1*	Silent	SNP	A	A	G	rs373370001	Patient3	p.R248R	ENSG00000109536	ENST00000226798	Transcript
chr8	139606339	139606339	*COL22A1*	Silent	SNP	G	G	A	novel	Patient3	p.G1512G	ENSG00000169436	ENST00000303045	Transcript
chr9	193319811	193319811	*DENND4C*	Silent	SNP	A	A	T	novel	Patient3	p.I753I	ENSG00000137145	ENST00000602925	Transcript
chr1	85331381	85331381	*LPAR3*	Silent	SNP	G	G	A	novel	Patient4	p.T141T	ENSG00000171517	ENST00000440886	Transcript
chr10	126683062	126683062	*CTBP2*	Silent	SNP	G	G	A	novel	Patient4	p.L792L	ENSG00000175029	ENST00000309035	Transcript
chr11	192565667	192565667	*E2F8*	Silent	SNP	G	G	A	novel	Patient4	p.L164L	ENSG00000129173	ENST00000527884	Transcript
chr13	25052321	25052321	*PARP4*	Silent	SNP	A	A	G	rs149727830	Patient4	p.H514H	ENSG00000102699	ENST00000381989	Transcript
chr17	57759079	57759079	*CLTC*	Silent	SNP	C	C	A	novel	Patient4	p.V1107V	ENSG00000141367	ENST00000269122	Transcript
chr19	55086835	55086835	*LILRA2*	Silent	SNP	T	T	C	novel	Patient4	p.Y256Y	ENSG00000239998	ENST00000251377	Transcript
chr19	55086973	55086973	*LILRA2*	Silent	SNP	C	C	G	novel	Patient4	p.S302S	ENSG00000239998	ENST00000251377	Transcript
chr19	55286867	55286867	*KIR2DL1*	Silent	SNP	C	C	T	novel	Patient4	p.Y207Y	ENSG00000125498	ENST00000336077	Transcript
chr19	55333198	55333198	*KIR3DL1*	Silent	SNP	A	A	T	novel	Patient4	p.A278A	ENSG00000167633	ENST00000391728	Transcript
chr8	65493743	65493743	*BHLHE22*	Silent	SNP	C	C	T	novel	Patient4	p.S132S	ENSG00000180828	ENST00000321870	Transcript
chrX	12905265	12905265	*TLR7*	Silent	SNP	T	T	C	novel	Patient4	p.Y546Y	ENSG00000196664	ENST00000380659	Transcript
chrX	69478800	69478800	*P2RY4*	Silent	SNP	A	A	G	novel	Patient4	p.R225R	ENSG00000186912	ENST00000374519	Transcript
chr1	167096396	167096396	*DUSP27*	Silent	SNP	G	G	A	rs376593703	Patient5	p.T676T	ENSG00000198842	ENST00000361200	Transcript
chr1	237777618	237777618	*RYR2*	Silent	SNP	G	G	A	rs397516541	Patient5	p.T1730T	ENSG00000198626	ENST00000366574	Transcript
chr1	35370532	35370532	*DLGAP3*	Silent	SNP	C	C	G	novel	Patient5	p.G151G	ENSG00000116544	ENST00000373347	Transcript
chr10	126691617	126691617	*CTBP2*	Silent	SNP	C	C	T	novel	Patient5	p.E630E	ENSG00000175029	ENST00000309035	Transcript
chr10	17164817	17164817	*CUBN*	Silent	SNP	A	A	G	novel	Patient5	p.C190C	ENSG00000107611	ENST00000377833	Transcript
chr11	2424013	2424013	*TSSC4*	Silent	SNP	C	C	T	novel	Patient5	p.S50S	ENSG00000184281	ENST00000333256	Transcript
chr11	61537824	61537824	*MYRF*	Silent	SNP	G	G	C	novel	Patient5	p.P189P	ENSG00000124920	ENST00000278836	Transcript
chr11	640152	640152	*DRD4*	Silent	SNP	c	c	T	novel	Patient5	p.L301L	ENSG00000069696	ENST00000176183	Transcript
chr11	64060511	64060511	*KCNK4*	Silent	SNP	G	G	A	novel	Patient5	p.L7L	ENSG00000182450	ENST00000539216	Transcript
chr17	11896084	11896084	*ZNF18*	Silent	SNP	G	G	A	novel	Patient5	p.S21S	ENSG00000154957	ENST00000322748	Transcript
chr17	39274238	39274238	*KRTAP4-11*	Silent	SNP	a	a	G	novel	Patient5	p.C110C	ENSG00000212721	ENST00000391413	Transcript
chr19	15063766	15063766	*SLC1A6*	Silent	SNP	C	C	T	novel	Patient5	p.T491T	ENSG00000105143	ENST00000221742	Transcript
chr19	55341661	55341661	*KIR3DL1*	Silent	SNP	T	T	A	novel	Patient5	p.P422P	ENSG00000167633	ENST00000391728	Transcript
chr19	6222405	6222405	*MLLT1*	Silent	SNP	t	t	G	novel	Patient5	p.P279P	ENSG00000130382	ENST00000252674	Transcript
chr21	45876938	45876938	*LRRC3*	Silent	SNP	C	C	T	rs141489159	Patient5	p.S137S	ENSG00000160233	ENST00000291592	Transcript
chr22	37098604	37098604	*CACNG2*	Silent	SNP	T	T	G	novel	Patient5	p.R6R	ENSG00000166862	ENST00000300105	Transcript
chr3	126208213	126208213	*UROC1*	Silent	SNP	C	C	T	novel	Patient5	p.P598P	ENSG00000159650	ENST00000383579	Transcript
chr6	44221323	44221323	*HSP90AB1*	Silent	SNP	A	A	G	novel	Patient5	p.E721E	ENSG00000096384	ENST00000371554	Transcript
chr7	20824956	20824956	*SP8*	Silent	SNP	c	c	G	rs201180283	Patient5	p.G160G	ENSG00000164651	ENST00000418710	Transcript
chr9	18675858	18675858	*ADAMTSL1*	Silent	SNP	C	C	T	rs142601398	Patient5	p.D363D	ENSG00000178031	ENST00000380548	Transcript
chr9	80646047	80646047	*GNAQ*	Silent	SNP	G	G	A	novel	Patient5	p.D35D	ENSG00000156052	ENST00000286548	Transcript
chrX	189248755	189248755	*PHKA2*	Silent	SNP	G	G	A	novel	Patient5	p.I885I	ENSG00000044446	ENST00000379942	Transcript
chr12	42481627	42481627	*GXYLT1*	Silent	SNP	A	A	G	novel	Patient6	p.S428S	ENSG00000151233	ENST00000398675	Transcript

chr2	209150502	209150502	*PIKFYVE*	Silent	SNP	T	T	C	novel	Patient6	p.H222H	ENSG00000115020	ENST00000264380	Transcript
chr3	46944951	46944951	*PTH1R*	Silent	SNP	C	C	T	rs199557895	Patient6	p.N529N	ENSG00000160801	ENST00000313049	Transcript
chr4	190884251	190884251	*FRG1*	Silent	SNP	A	A	G	rs373370001	Patient6	p.R248R	ENSG00000109536	ENST00000226798	Transcript
chr6	55739442	55739442	*BMP5*	Silent	SNP	C	C	T	novel	Patient6	p.A74A	ENSG00000112175	ENST00000370830	Transcript
chr1	460736 18	460736 18	*NASP*	Silent	SNP	A	A	G	rs200936475	Patient7	p.P345P	ENSG00000132780	ENST00000350030	Transcript
chr1	55505576	55505576	*PCSK9*	Silent	SNP	c	c	G	novel	Patient7	p.L22L	ENSG00000169174	ENST00000302118	Transcript
chr10	93714	93714	*TUBB8*	Silent	SNP	A	A	C	novel	Patient7	p.A206A	ENSG00000173876	ENST00000309812	Transcript
chr12	11183296	11183296	*TAS2R31*	Silent	SNP	A	A	G	rs370468039	Patient7	p.G213G	ENSG00000256436	ENST00000390675	Transcript
chr17	45232068	45232068	*CDC27*	Silent	SNP	A	A	G	rs74710570	Patient7	p.D309D	ENSG00000004897	ENST00000531206	Transcript
chr4	8305914	8305914	*HTRA3*	Silent	SNP	G	G	A	novel	Patient7	p.L368L	ENSG00000170801	ENST00000307358	Transcript
chr4	88537426	88537426	*DSPP*	Silent	SNP	t	t	C	rs371154871	Patient7	p.S1204S	ENSG00000152591	ENST00000399271	Transcript
chr1	1021340	1021340	*C1orf159*	Silent	SNP	G	G	A	rs370347843	Patient8	p.S121S	ENSG00000131591	ENST00000421241	Transcript
chr1	201179961	201179961	*IGFN1*	Silent	SNP	C	C	T	novel	Patient8	p.F1980F	ENSG00000163395	ENST00000335211	Transcript
chr1	201180243	201180243	*IGFN1*	Silent	SNP	A	A	G	rs367952435	Patient8	p.L2074L	ENSG00000163395	ENST00000335211	Transcript
chr1	266088 41	266088 41	*UBXN11*	Silent	SNP	a	a	T	novel	Patient8	p.G504G	ENSG00000158062	ENST00000374222	Transcript
chr11	1651157	1651157	*KRTAP5-5*	Silent	SNP	a	a	G	novel	Patient8	p.G29G	ENSG00000185940	ENST00000399676	Transcript
chr19	22497980	22497980	*ZNF729*	Silent	SNP	C	C	T	rs541205753	Patient8	p.L587L	ENSG00000196350	ENST00000601693	Transcript
chr19	7974743	7974743	*MAP2K7*	Silent	SNP	G	G	A	novel	Patient8	p.G76G	ENSG00000076984	ENST00000397979	Transcript
chr20	607918 99	607918 99	*HRH3*	Silent	SNP	G	G	A	novel	Patient8	p.Y167Y	ENSG00000101180	ENST00000340177	Transcript
chr4	147560493	147560493	*POU4F2*	Silent	SNP	a	a	C	rs532126509	Patient8	p.G67G	ENSG00000151615	ENST00000281321	Transcript
chr7	151945215	151945215	*KMT2C*	Silent	SNP	T	T	C	rs594178	Patient8	p.S768S	ENSG00000055609	ENST00000262189	Transcript
chr8	131922058	131922058	*ADCY8*	Silent	SNP	G	G	A	rs150100724	Patient8	p.S512S	ENSG00000155897	ENST00000286355	Transcript
chr9	211870003	211870003	*IFNA4*	Silent	SNP	C	C	A	novel	Patient8	p.S176S	ENSG00000236637	ENST00000421715	Transcript
chr10	93732	93732	*TUBB8*	Silent	SNP	A	A	G	novel	Patient9	p.F200F	ENSG00000173876	ENST00000309812	Transcript
chr12	147205744	147205744	*PLBD1*	Silent	SNP	c	c	A	novel	Patient9	p.L19L	ENSG00000121316	ENST00000240617	Transcript
chr19	550868 44	550868 44	*LILRA2*	Silent	SNP	A	A	G	novel	Patient9	p.G259G	ENSG00000239998	ENST00000251377	Transcript
chr2	176988303	176988303	*HOXD9*	Silent	SNP	A	A	G	rs200391181	Patient9	p.Q269Q	ENSG00000128709	ENST00000249499	Transcript
chr2	955378 07	955378 07	*TEKT4*	Silent	SNP	A	A	G	novel	Patient9	p.E161E	ENSG00000163060	ENST00000295201	Transcript
chr20	575563 49	575563 49	*NELFCD*	Silent	SNP	C	C	T	novel	Patient9	p.A13A	ENSG00000101158	ENST00000602795	Transcript
chrX	669314 28	669314 28	*AR*	Silent	SNP	C	C	T	novel	Patient9	p.H690H	ENSG00000169083	ENST00000374690	Transcript
chr12	312552 27	312552 27	*DDX11*	Silent	SNP	A	A	G	rs141443776	Patient10	p.A751A	ENSG00000013573	ENST00000407793	Transcript
chr2	114257388	114257388	*FOXD4L1*	Silent	SNP	C	C	T	rs144904377	Patient10	p.P185P	ENSG00000184492	ENST00000306507	Transcript
chr5	175811084	175811084	*NOP16*	Silent	SNP	G	G	A	novel	Patient10	p.S198S	ENSG00000048162	ENST00000510123	Transcript
chr1	156255278	156255278	*TMEM79*	Silent	SNP	G	G	A	rs543664557	Patient11	p.P87P	ENSG00000163472	ENST00000405535	Transcript
chr1	214557074	214557074	*PTPN14*	Silent	SNP	G	G	A	rs201009749	Patient11	p.S708S	ENSG00000152104	ENST00000366956	Transcript
chr10	5247731	5247731	*AKR1C4*	Silent	SNP	G	G	A	novel	Patient11	p.T127T	ENSG00000198610	ENST00000380448	Transcript
chr12	58217738	58217738	*CTDSP2*	Silent	SNP	G	G	A	rs192597051	Patient11	p.T213T	ENSG00000175215	ENST00000398073	Transcript
chr15	72847641	72847641	*ARIH1*	Silent	SNP	G	G	A	novel	Patient11	p.K206K	ENSG00000166233	ENST00000379887	Transcript
chr15	995143400	995143400	*PGPEP1L*	Silent	SNP	C	C	G	novel	Patient11	p.R23R	ENSG00000183571	ENST00000378919	Transcript
chr16	27692775	27692775	*KIAA0556*	Silent	SNP	C	C	T	novel	Patient11	p.F288F	ENSG00000047578	ENST00000261588	Transcript
chr18	44159695	44159695	*LOXHD1*	Silent	SNP	G	G	A	rs371576247	Patient11	p.T569T	ENSG00000167210	ENST00000536736	Transcript

chr19	41787069	41787069	*HNRNPUL1*	Silent	SNP	C	C	G	novel	Patient11	p.G296G	ENSG00000105323	ENST00000392006	Transcript
chr19	55086973	55086973	*LILRA2*	Silent	SNP	C	C	G	novel	Patient11	p.S302S	ENSG00000239998	ENST00000251377	Transcript
chr19	57646463	57646463	*ZIM3*	Silent	SNP	G	G	A	rs372701407	Patient11	p.S414S	ENSG00000141946	ENST00000269834	Transcript
chr2	1670185	1670185	*PXDN*	Silent	SNP	G	G	A	novel	Patient11	p.S364S	ENSG00000130508	ENST00000252804	Transcript
chr2	249837	249837	*SH3YL1*	Silent	SNP	T	T	C	novel	Patient11	p.V40V	ENSG00000035115	ENST00000356150	Transcript
chr2	95537681	95537681	*TEKT4*	Silent	SNP	C	C	G	novel	Patient11	p.L119L	ENSG00000163060	ENST00000295201	Transcript
chr21	45960001	45960001	*KRTAP10-1*	Silent	SNP	G	G	A	novel	Patient11	p.S11S	ENSG00000215455	ENST00000400375	Transcript
chr3	195965760	195965760	*PCYT1A*	Silent	SNP	A	A	G	rs116712058	Patient11	p.H301H	ENSG00000161217	ENST00000292823	Transcript
chr3	61989159	61989159	*PTPRG*	Silent	SNP	G	G	A	novel	Patient11	p.R169R	ENSG00000144724	ENST00000474889	Transcript
chr3	75714010	75714010	*FRG2C*	Silent	SNP	A	A	G	rs373472815	Patient11	p.E73E	ENSG00000172969	ENST00000308062	Transcript
chr4	191003292	191003292	*DUX4L4*	Silent	SNP	C	C	T	novel	Patient11	p.A401A	ENSG00000258834	ENST00000538692	Transcript
chr5	134681689	134681689	*H2AFY*	Silent	SNP	C	C	T	novel	Patient11	p.R249R	ENSG00000113648	ENST00000511689	Transcript
chr6	158454637	158454637	*SYNJ2*	Silent	SNP	G	G	A	novel	Patient11	p.E212E	ENSG00000078269	ENST00000355585	Transcript
chr8	125984476	125984476	*LONRF1*	Silent	SNP	G	G	A	rs376359052	Patient11	p.C290C	ENSG00000154359	ENST00000398246	Transcript
chrX	127185220	127185220	*ACTRT1*	Silent	SNP	A	A	G	novel	Patient11	p.A322A	ENSG00000123165	ENST00000371124	Transcript
chrX	144909378	144909378	*TMEM257*	Silent	SNP	T	T	C	novel	Patient11	p.F61F	ENSG00000221870	ENST00000408967	Transcript
chrX	49084590	49084590	*CACNA1F*	Silent	SNP	G	G	C	novel	Patient11	p.A342A	ENSG00000102001	ENST00000376265	Transcript
chr1	117158748	117158748	*IGSF3*	Silent	SNP	A	A	G	rs199696016	Patient12	p.T125T	ENSG00000143061	ENST00000369483	Transcript
chr1	152275914	152275914	*FLG*	Silent	SNP	C	C	T	novel	Patient12	p.E3816E	ENSG00000143631	ENST00000368799	Transcript
chr1	248458842	248458842	*OR2T12*	Silent	SNP	T	T	C	novel	Patient12	p.L13L	ENSG00000177201	ENST00000317996	Transcript
chr11	100933260	100933260	*PGR*	Silent	SNP	G	G	A	novel	Patient12	p.T710T	ENSG00000082175	ENST00000325455	Transcript
chr12	124887102	124887102	*NCOR2*	Silent	SNP	c	c	T	rs7488825	Patient12	p.Q496Q	ENSG00000196498	ENST00000405201	Transcript
chr15	84908793	84908793	*GOLGA6L4*	Silent	SNP	A	A	G	rs202133768	Patient12	p.L229L	ENSG00000184206	ENST00000510439	Transcript
chr16	1836904	1836904	*NUBP2*	Silent	SNP	C	C	T	novel	Patient12	p.F94F	ENSG00000095906	ENST00000262302	Transcript
chr17	32483456	32483456	*ASIC2*	Silent	SNP	G	G	A	novel	Patient12	p.I32I	ENSG00000108684	ENST00000359872	Transcript
chr19	52888085	52888085	*ZNF880*	Silent	SNP	A	A	C	novel	Patient12	p.R418R	ENSG00000221923	ENST00000422689	Transcript
chr19	9639776	9639776	*ZNF426*	Silent	SNP	T	T	C	novel	Patient12	p.K315K	ENSG00000130818	ENST00000535489	Transcript
chr2	26410403	26410403	*GAREML*	Silent	SNP	C	C	T	rs376916271	Patient12	p.S634S	ENSG00000157833	ENST00000401533	Transcript
chr20	33764122	33764122	*PROCR*	Silent	SNP	C	C	T	novel	Patient12	p.S158S	ENSG00000101000	ENST00000216968	Transcript
chr3	119595335	119595335	*GSK3B*	Silent	SNP	C	C	T	novel	Patient12	p.R278R	ENSG00000082701	ENST00000316626	Transcript
chr4	122735084	122735084	*EXOSC9*	Silent	SNP	C	C	G	novel	Patient12	p.S346S	ENSG00000123737	ENST00000379663	Transcript
chr6	32714075	32714075	*HLA-DQA2*	Silent	SNP	G	G	A	rs199612824	Patient12	p.G224G	ENSG00000237541	ENST00000374940	Transcript
chr7	107594006	107594006	*LAMB1*	Silent	SNP	G	G	A	novel	Patient12	p.Y1016Y	ENSG00000091136	ENST00000222399	Transcript
chrX	100960 93	100960 93	*WWC3*	Silent	SNP	C	C	T	rs370611834	Patient12	p.S724S	ENSG00000047644	ENST00000380861	Transcript
chrX	125299059	125299059	*DCAF12L2*	Silent	SNP	G	G	A	novel	Patient12	p.D283D	ENSG00000198354	ENST00000538699	Transcript
chrX	46949230	46949230	*RGN*	Silent	SNP	G	G	T	novel	Patient12	p.L134L	ENSG00000130988	ENST00000397180	Transcript
chr1	248084859	248084859	*OR2T8*	Silent	SNP	C	C	T	novel	Patient13	p.P180P	ENSG00000177462	ENST00000319968	Transcript
chr1	46073504	46073504	*NASP*	Silent	SNP	G	G	A	novel	Patient13	p.V307V	ENSG00000132780	ENST00000350030	Transcript
chr11	35454045	35454045	*PAMR1*	Silent	SNP	C	C	T	rs368389376	Patient13	p.P691P	ENSG00000149090	ENST00000278360	Transcript
chr14	88946058	88946058	*PTPN21*	Silent	SNP	T	T	G	novel	Patient13	p.R573R	ENSG00000070778	ENST00000556564	Transcript
chr17	39240779	39240779	*KRTAP4-7*	Silent	SNP	c	c	A	novel	Patient13	p.P107P	ENSG00000240871	ENST00000391417	Transcript

chr17	5037241	5037241	*USP6*	Silent	SNP	G	G	A	rs117611547	Patient13	p.V148V	ENSG00000129204	ENST00000574788	Transcript
chr17	61621755	61621755	*KCNH6*	Silent	SNP	C	C	T	novel	Patient13	p.L829L	ENSG00000173826	ENST00000583023	Transcript
chr19	55086844	55086844	*LILRA2*	Silent	SNP	A	A	G	novel	Patient13	p.G259G	ENSG00000239998	ENST00000251377	Transcript
chr2	135741309	135741309	*MAP3K19*	Silent	SNP	T	T	C	novel	Patient13	p.L1053L	ENSG00000176601	ENST00000375845	Transcript
chr4	191003178	191003178	*DUX4L4*	Silent	SNP	C	C	G	novel	Patient13	p.P363P	ENSG00000258834	ENST00000538692	Transcript
chr4	266043	266043	*ZNF732*	Silent	SNP	G	G	T	novel	Patient13	p.G201G	ENSG00000186777	ENST00000419098	Transcript
chr6	31919168	31919168	*CFB*	Silent	SNP	C	C	T	novel	Patient13	p.V1171V	ENSG00000244255	ENST00000456570	Transcript
chr6	33136534	33136534	*COL11A2*	Silent	SNP	G	G	A	novel	Patient13	p.G1199G	ENSG00000204248	ENST00000374708	Transcript
chr7	4089011	4089011	*SDK1*	Silent	SNP	G	G	A	rs139642198	Patient13	p.T878T	ENSG00000146555	ENST00000404826	Transcript
chr9	139690900	139690900	*CCDC183*	Silent	SNP	G	G	A	novel	Patient13	p.K17K	ENSG00000213213	ENST00000338005	Transcript
chr1	241137776	241137776	*PITHD1*	Silent	SNP	C	C	T	rs145680822	Patient14	p.H182H	ENSG00000057757	ENST00000246151	Transcript
chr1	55352613	55352613	*DHCR24*	Silent	SNP	G	G	A	rs79857573	Patient14	p.L60L	ENSG00000116133	ENST00000371269	Transcript
chr10	118443312	118443312	*HSPA12A*	Silent	SNP	C	C	A	novel	Patient14	p.G275G	ENSG00000165868	ENST00000369209	Transcript
chr10	98133462	98133462	*TLL2*	Silent	SNP	G	G	A	rs61740993	Patient14	p.C851C	ENSG00000095587	ENST00000357947	Transcript
chr11	100807050	100807050	*ARHGAP42*	Silent	SNP	T	T	C	rs61734880	Patient14	p.Y273Y	ENSG00000165895	ENST00000298815	Transcript
chr11	111635619	111635619	*PPP2R1B*	Silent	SNP	A	A	G	novel	Patient14	p.Y72Y	ENSG00000137713	ENST00000311129	Transcript
chr11	111746041	111746041	*FDXACB1*	Silent	SNP	A	A	G	novel	Patient14	p.L494L	ENSG00000255561	ENST00000260257	Transcript
chr11	111746231	111746231	*FDXACB1*	Silent	SNP	G	G	A	novel	Patient14	p.S430S	ENSG00000255561	ENST00000260257	Transcript
chr11	111796689	111796689	*C11orf52*	Silent	SNP	T	T	C	novel	Patient14	p.H46H	ENSG00000149300	ENST00000278601	Transcript
chr11	116717136	116717136	*SIK3*	Silent	SNP	G	G	A	rs150767868	Patient14	p.F1256F	ENSG00000160584	ENST00000292055	Transcript
chr11	130067764	130067764	*ST14*	Silent	SNP	G	G	T	rs583863	Patient14	p.T461T	ENSG00000149418	ENST00000278742	Transcript
chr11	58170274	58170274	*OR5B3*	Silent	SNP	G	G	A	rs143648646	Patient14	p.F203F	ENSG00000172769	ENST00000309403	Transcript
chr11	62677790	62677790	*CHRM1*	Silent	SNP	G	G	A	rs141441306	Patient14	p.R261R	ENSG00000168539	ENST00000306960	Transcript
chr11	76371446	76371446	*LRRC32*	Silent	SNP	G	G	A	rs138665218	Patient14	p.A397A	ENSG00000137507	ENST00000407242	Transcript
chr12	46760866	46760866	*SLC38A2*	Silent	SNP	G	G	A	rs36022751	Patient14	p.N158N	ENSG00000134294	ENST00000256689	Transcript
chr12	95927325	95927325	*USP44*	Silent	SNP	C	C	T	rs34987131	Patient14	p.T236T	ENSG00000136014	ENST00000258499	Transcript
chr12	99102458	99102458	*APAF1*	Silent	SNP	A	A	T	novel	Patient14	p.A939A	ENSG00000120868	ENST00000551964	Transcript
chr13	111870226	111870226	*ARHGEF7*	Silent	SNP	C	C	T	rs41275140	Patient14	p.S244S	ENSG00000102606	ENST00000375741	Transcript
chr13	27257047	27257047	*WASF3*	Silent	SNP	G	G	A	rs146991188	Patient14	p.R429R	ENSG00000132970	ENST00000335327	Transcript
chr14	23420782	23420782	*HAUS4*	Silent	SNP	T	T	C	rs45600640	Patient14	p.E149E	ENSG00000092036	ENST00000206474	Transcript
chr14	63856396	63856396	*PPP2R5E*	Silent	SNP	T	T	C	rs61756432	Patient14	p.Q336Q	ENSG00000154001	ENST00000337537	Transcript
chr14	93412737	93412737	*ITPK1*	Silent	SNP	G	G	A	novel	Patient14	p.I280I	ENSG00000100605	ENST00000267615	Transcript
chr15	25602030	25602030	*UBE3A*	Silent	SNP	G	G	A	rs139082033	Patient14	p.Y592Y	ENSG00000114062	ENST00000397954	Transcript
chr15	30011999	30011999	*TJP1*	Silent	SNP	C	C	A	rs368537788	Patient14	p.S995S	ENSG00000104067	ENST00000346128	Transcript
chr15	40565817	40565817	*PAK6*	Silent	SNP	G	G	T	rs35644942	Patient14	p.L561L	ENSG00000137843	ENST00000560346	Transcript
chr15	62214683	62214683	*VPS13C*	Silent	SNP	T	T	C	novel	Patient14	p.V2296V	ENSG00000129003	ENST00000261517	Transcript
chr15	67757539	67757539	*IQCH*	Silent	SNP	C	C	T	rs112419712	Patient14	p.N860N	ENSG00000103599	ENST00000335894	Transcript
chr15	78565495	78565495	*DNAJA4*	Silent	SNP	G	G	A	rs74978019	Patient14	p.T153T	ENSG00000140403	ENST00000394855	Transcript
chr15	90903618	90903618	*ZNF774*	Silent	SNP	G	G	A	rs116910054	Patient14	p.G185G	ENSG00000196391	ENST00000354377	Transcript
chr16	1259406	1259406	*CACNA1H*	Silent	SNP	G	G	A	rs58812334	Patient14	p.S1246S	ENSG00000196557	ENST00000348261	Transcript
chr16	1261258	1261258	*CACNA1H*	Silent	SNP	C	C	T	rs60275734	Patient14	p.C1438C	ENSG00000196557	ENST00000348261	Transcript

chr16	20998720	20998720	*DNAH3*	Silent	SNP	G	G	A	rs111770788	Patient14	p.F2311F	ENSG00000158486	ENST00000261383	Transcript
chr16	2161097	2161097	*PKD1*	Silent	SNP	C	C	A	rs145737766	Patient14	p.L1357L	ENSG00000088710	ENST00000262304	Transcript
chr16	57504000	57504000	*POLR2C*	Silent	SNP	C	C	T	rs149374652	Patient14	p.D189D	ENSG00000102978	ENST00000219252	Transcript
chr16	57938734	57938734	*CNGB1*	Silent	SNP	G	G	A	novel	Patient14	p.I846I	ENSG00000070729	ENST00000251102	Transcript
chr16	81902879	81902879	*PLCG2*	Silent	SNP	C	C	G	rs150276286	Patient14	p.A180A	ENSG00000197943	ENST00000359376	Transcript
chr17	1985191	1985191	*SMG6*	Silent	SNP	G	G	A	rs143629359	Patient14	p.G1198G	ENSG00000070366	ENST00000263073	Transcript
chr17	40765911	40765911	*TUBG1*	Silent	SNP	T	T	C	novel	Patient14	p.P246P	ENSG00000131462	ENST00000251413	Transcript
chr17	4539102	4539102	*ALOX15*	Silent	SNP	A	A	G	novel	Patient14	p.I371I	ENSG00000161905	ENST00000570836	Transcript
chr17	64881123	64881123	*CACNG5*	Silent	SNP	C	C	T	rs139714730	Patient14	p.Y198Y	ENSG00000075429	ENST00000533854	Transcript
chr17	73106432	73106432	*ARMC7*	Silent	SNP	C	C	T	rs74697881	Patient14	p.L17L	ENSG00000125449	ENST00000245543	Transcript
chr18	32374095	32374095	*DTNA*	Silent	SNP	A	A	G	rs146923532	Patient14	p.L81L	ENSG00000134769	ENST00000598334	Transcript
chr18	72997845	72997845	*TSHZ1*	Silent	SNP	C	C	G	rs143523598	Patient14	p.P116P	ENSG00000179981	ENST00000322038	Transcript
chr18	8376139	8376139	*PTPRM*	Silent	SNP	C	C	T	rs377485016	Patient14	p.F1089F	ENSG00000173482	ENST00000580170	Transcript
chr19	19038842	19038842	*DDX49*	Silent	SNP	G	G	C	rs45538835	Patient14	p.G420G	ENSG00000105671	ENST00000247003	Transcript
chr19	40411914	40411914	*FCGBP*	Silent	SNP	G	G	A	rs142872061	Patient14	p.S1238S	ENSG00000090920	ENST00000221347	Transcript
chr19	42703950	42703950	*DEDD2*	Silent	SNP	G	G	A	rs149135613	Patient14	p.C207C	ENSG00000160570	ENST00000595337	Transcript
chr2	121997199	121997199	*TFCP2L1*	Silent	SNP	G	G	A	rs143023699	Patient14	p.Y265Y	ENSG00000115112	ENST00000263707	Transcript
chr2	136564845	136564845	*LCT*	Silent	SNP	C	C	T	rs150640616	Patient14	p.T1342T	ENSG00000115850	ENST00000264162	Transcript
chr2	206480486	206480486	*PARD3B*	Silent	SNP	T	T	C	rs56272619	Patient14	p.P1127P	ENSG00000116117	ENST00000358768	Transcript
chr2	27600814	27600814	*ZNF513*	Silent	SNP	G	G	A	rs61995753	Patient14	p.R408R	ENSG00000163795	ENST00000323703	Transcript
chr2	74589224	74589224	*DCTN1*	Silent	SNP	T	T	C	novel	Patient14	p.T1218T	ENSG00000204843	ENST00000361874	Transcript
chr2	99291511	99291511	*MGAT4A*	Silent	SNP	G	G	A	rs143269181	Patient14	p.N130N	ENSG00000071073	ENST00000264968	Transcript
chr20	44669992	44669992	*SLC12A5*	Silent	SNP	G	G	A	rs138406290	Patient14	p.T316T	ENSG00000124140	ENST00000454036	Transcript
chr21	45168923	45168923	*PDXK*	Silent	SNP	G	G	A	rs61737062	Patient14	p.P142P	ENSG00000160209	ENST00000291565	Transcript
chr22	42610793	42610793	*TCF20*	Silent	SNP	G	G	A	novel	Patient14	p.S173S	ENSG00000100207	ENST00000359486	Transcript
chr22	50615417	50615417	*PANX2*	Silent	SNP	G	G	A	rs150278474	Patient14	p.A92A	ENSG00000073150	ENST00000395842	Transcript
chr3	129546814	129546814	*TMCC1*	Silent	SNP	T	T	C	rs114554412	Patient14	p.Q136Q	ENSG00000172765	ENST00000393238	Transcript
chr3	138188988	138188988	*ESYT3*	Silent	SNP	G	G	A	rs201243595	Patient14	p.K530K	ENSG00000158220	ENST00000389567	Transcript
chr3	33431826	33431826	*UBP1*	Silent	SNP	C	C	T	rs41285089	Patient14	p.K540K	ENSG00000153560	ENST00000283629	Transcript
chr3	3888101	3888101	*LRRN1*	Silent	SNP	T	T	C	rs35191979	Patient14	p.Y592Y	ENSG00000175928	ENST00000319331	Transcript
chr3	51458183	51458183	*VPRBP*	Silent	SNP	G	G	A	novel	Patient14	p.P298P	ENSG00000145041	ENST00000335891	Transcript
chr3	52507794	52507794	*NISCH*	Silent	SNP	G	G	A	rs76608301	Patient14	p.S238S	ENSG00000010322	ENST00000345716	Transcript
chr4	139965977	139965977	*CCRN4L*	Silent	SNP	G	G	A	rs138904656	Patient14	p.T215T	ENSG00000151014	ENST00000280614	Transcript
chr4	175604008	175604008	*GLRA3*	Silent	SNP	C	C	T	rs41279513	Patient14	p.Q219Q	ENSG00000145451	ENST00000274093	Transcript
chr7	43827595	43827595	*BLVRA*	Silent	SNP	G	G	A	rs1802849	Patient14	p.A35A	ENSG00000106605	ENST00000402924	Transcript
chr7	5662719	5662719	*RNF216*	Silent	SNP	G	G	A	rs149012430	Patient14	p.N848N	ENSG00000011275	ENST00000389902	Transcript
chr7	99693747	99693747	*MCM7*	Silent	SNP	C	C	T	rs61749909	Patient14	p.T415T	ENSG00000166508	ENST00000303887	Transcript
chr8	92201794	92201794	*LRRC69*	Silent	SNP	A	A	C	rs182104008	Patient14	p.P232P	ENSG00000214954	ENST00000448384	Transcript
chr9	130289485	130289485	*FAM129B*	Silent	SNP	G	G	A	novel	Patient14	p.Y101Y	ENSG00000136830	ENST00000373312	Transcript
chr9	35091844	35091844	*PIGO*	Silent	SNP	C	C	G	rs41274877	Patient14	p.L680L	ENSG00000165282	ENST00000378617	Transcript
chrX	153047267	153047267	*SRPK3*	Silent	SNP	G	G	A	novel	Patient14	p.E123E	ENSG00000184343	ENST00000370101	Transcript

chrX	153699508	153699508	*PLXNA3*	Silent	SNP	C	C	T	novel	Patient14	p.H1739H	ENSG00000130827	ENST00000369682	Transcript
chrX	47307591	47307591	*ZNF41*	Silent	SNP	A	A	T	rs148848609	Patient14	p.A526A	ENSG00000147124	ENST00000377065	Transcript
chr1	10468170	10468170	*PGD*	Silent	SNP	G	G	A	novel	Patient15	p.V164V	ENSG00000142657	ENST00000270776	Transcript
chr11	64878864	64878864	*VPS51*	Silent	SNP	C	C	T	novel	Patient15	p.R718R	ENSG00000149823	ENST00000279281	Transcript
chr16	1291510	1291510	*TPSAB1*	Silent	SNP	G	G	A	rs375711119	Patient15	p.P103P	ENSG00000172236	ENST00000338844	Transcript
chr16	48122520	48122520	*ABCC12*	Silent	SNP	G	G	A	novel	Patient15	p.L1137L	ENSG00000140798	ENST00000311303	Transcript
chr17	42429559	42429559	*GRN*	Silent	SNP	G	G	A	novel	Patient15	p.V452V	ENSG00000030582	ENST00000053867	Transcript
chr18	76873333	76873333	*ATP9B*	Silent	SNP	C	C	G	novel	Patient15	p.L179L	ENSG00000166377	ENST00000426216	Transcript
chr19	10089594	10089594	*COL5A3*	Silent	SNP	G	G	A	rs535590291	Patient15	p.P979P	ENSG00000080573	ENST00000264828	Transcript
chr19	35843162	35843162	*FFAR1*	Silent	SNP	C	C	T	novel	Patient15	p.C236C	ENSG00000126266	ENST00000246553	Transcript
chr19	9212975	9212975	*OR7G2*	Silent	SNP	G	G	T	novel	Patient15	p.A336A	ENSG00000170923	ENST00000305456	Transcript
chr20	37524285	37524285	*PPP1R16B*	Silent	SNP	G	G	A	novel	Patient15	p.E133E	ENSG00000101445	ENST00000299824	Transcript
chr21	45826563	45826563	*TRPM2*	Silent	SNP	C	C	T	rs201296589	Patient15	p.N959N	ENSG00000142185	ENST00000397928	Transcript
chr3	185375176	185375176	*IGF2BP2*	Silent	SNP	C	C	T	novel	Patient15	p.E428E	ENSG00000073792	ENST00000382199	Transcript
chr3	75832493	75832493	*ZNF717*	Silent	SNP	G	G	C	novel	Patient15	p.G7G	ENSG00000227124	ENST00000422325	Transcript
chr5	176939516	176939516	*DDX41*	Silent	SNP	T	T	A	novel	Patient15	p.P510P	ENSG00000183258	ENST00000507955	Transcript
chr6	109906352	109906352	*AK9*	Silent	SNP	C	C	T	novel	Patient15	p.K696K	ENSG00000155085	ENST00000424296	Transcript
chr6	137245735	137245735	*SLC35D3*	Silent	SNP	G	G	A	rs200380943	Patient15	p.S384S	ENSG00000182747	ENST00000331858	Transcript
chr6	33261280	33261280	*RGL2*	Silent	SNP	G	G	A	novel	Patient15	p.V542V	ENSG00000237441	ENST00000497454	Transcript
chr8	43054556	43054556	*HGSNAT*	Silent	SNP	C	C	T	rs200678234	Patient15	p.V584V	ENSG00000165102	ENST00000379644	Transcript
chr9	69423310	69423310	*ANKRD20A4*	Silent	SNP	T	T	C	novel	Patient15	p.L536L	ENSG00000172014	ENST00000357336	Transcript
chrX	105355133	105355133	*MID1*	Silent	SNP	G	G	A	rs140708189	Patient15	p.C25C	ENSG00000101871	ENST00000317552	Transcript
chr11	9770684	9770684	*SWAP70*	Silent	SNP	G	G	A	novel	shanshan_et_al_P122	p.K535K	ENSG00000133789	ENST00000318950	Transcript
chr12	89819052	89819052	*POC1B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P122	p.T406T	ENSG00000139323	ENST00000313546	Transcript
chr15	91025246	91025246	*IQGAP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P122	p.K1128K	ENSG00000140575	ENST00000268182	Transcript
chr19	55435147	55435147	*NLRP7*	Silent	SNP	G	G	A	novel	shanshan_et_al_P122	p.S1025S	ENSG00000167634	ENST00000588756	Transcript
chr19	55857643	55857643	*SUV420H2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P122	p.D211D	ENSG00000133247	ENST00000255613	Transcript
chr7	128640615	128640615	*TNPO3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P122	p.L293L	ENSG00000064419	ENST00000265388	Transcript
chr8	1719266	1719266	*CLN8*	Silent	SNP	C	C	T	rs386834129	shanshan_et_al_P122	p.L16L	ENSG00000182372	ENST00000331322	Transcript
chr11	3060460	3060460	*CARS*	Silent	SNP	C	C	T	rs573223137	shanshan_et_al_P132	p.A205A	ENSG00000110619	ENST00000380525	Transcript
chr17	45216198	45216198	*CDC27*	Silent	SNP	C	C	T	novel	shanshan_et_al_P132	p.E543E	ENSG00000004897	ENST00000531206	Transcript
chr2	207407998	207407998	*ADAM23*	Silent	SNP	C	C	G	novel	shanshan_et_al_P132	p.T226T	ENSG00000114948	ENST00000264377	Transcript
chr1	9778973	9778973	*PIK3CD*	Silent	SNP	G	G	A	novel	shanshan_et_al_P42	p.A414A	ENSG00000171608	ENST00000377346	Transcript
chr12	57397394	57397394	*ZBTB39*	Silent	SNP	C	C	A	novel	shanshan_et_al_P42	p.L436L	ENSG00000166860	ENST00000300101	Transcript
chr15	72641497	72641497	*HEXA*	Silent	SNP	T	T	G	novel	shanshan_et_al_P46	p.T303T	ENSG00000213614	ENST00000268097	Transcript
chr20	44538169	44538169	*PLTP*	Silent	SNP	G	G	A	rs541113399	shanshan_et_al_P46	p.F157F	ENSG00000100979	ENST00000477313	Transcript
chr4	62849178	62849178	*LPHN3*	Silent	SNP	G	G	T	rs371382597	shanshan_et_al_P46	p.V963V	ENSG00000150471	ENST00000514591	Transcript
chr7	65610481	65610481	*CRCP*	Silent	SNP	C	C	T	novel	shanshan_et_al_P46	p.I97I	ENSG00000241258	ENST00000395326	Transcript
chr1	153516379	153516379	*S100A4*	Silent	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.A54A	ENSG00000196154	ENST00000368716	Transcript
chr1	8926426	8926426	*ENO1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.K193K	ENSG00000074800	ENST00000234590	Transcript
chr11	124761322	124761322	*ROBO4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_6	p.L607L	ENSG00000154133	ENST00000306534	Transcript

chr14	35548176	35548176	*FAM177A1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.I150I	ENSG00000151327	ENST00000280987	Transcript	
chr15	77134192	77134192	*SCAPER*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_6	p.H92H	ENSG00000140386	ENST00000563290	Transcript	
chr15	90190067	90190067	*KIF7*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.R594R	ENSG00000166813	ENST00000394412	Transcript	
chr22	18900874	18900874	*PRODH*	Silent	SNP	G	G	T	rs199660947	shanshan_et_al_P8_6	p.G539G	ENSG00000100033	ENST00000357068	Transcript	
chr22	29885618	29885618	*NEFH*	Silent	SNP	T	T	A	rs367989424	shanshan_et_al_P8_6	p.P663P	ENSG00000100285	ENST00000310624	Transcript	
chr22	45574342	45574342	*NUP50*	Silent	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.K188K	ENSG00000093000	ENST00000347635	Transcript	
chr22	45691543	45691543	*UPK3A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_6	p.V269V	ENSG00000100373	ENST00000216211	Transcript	
chr22	50893148	50893148	*SBF1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.V1612V	ENSG00000100241	ENST00000380817	Transcript	
chr3	100467162	100467162	*TFG*	Silent	SNP	T	T	C	novel	shanshan_et_al_P8_6	p.T330T	ENSG00000114354	ENST00000240851	Transcript	
chr3	124732413	124732413	*HEG1*	Silent	SNP	A	A	G	rs369359384	shanshan_et_al_P8_6	p.S670S	ENSG00000173706	ENST00000311127	Transcript	
chr3	151165231	151165231	*IGSF10*	Silent	SNP	C	C	A	novel	shanshan_et_al_P8_6	p.V846V	ENSG00000152580	ENST00000282466	Transcript	
chr3	47324545	47324545	*KLHL18*	Silent	SNP	G	G	A	rs200266681	shanshan_et_al_P8_6	p.E30E	ENSG00000114648	ENST00000232766	Transcript	
chr5	139906654	139906654	*ANKHD1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.V1694V	ENSG00000131503	ENST00000297183	Transcript	
chr5	158630641	158630641	*RNF145*	Silent	SNP	c	c	T	rs74841177,rs368977591	shanshan_et_al_P8_6	p.K25K	ENSG00000145860	ENST00000518802	Transcript	
chr5	98240676	98240676	*CHD1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.S60S	ENSG00000153922	ENST00000284049	Transcript	
chr6	110550168	110550168	*CDC40*	Silent	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.S517S	ENSG00000168438	ENST00000368932	Transcript	
chr6	162389900	162389900	*GMPR*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_6	p.S22S	ENSG00000137198	ENST00000259727	Transcript	
chr7	152522195	152522195	*ACTR3B*	Silent	SNP	C	C	T	rs200914813	shanshan_et_al_P8_6	p.R313R	ENSG00000133627	ENST00000256001	Transcript	
chr8	52396204	52396204	*PXDNL*	Silent	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.L175L	ENSG00000147485	ENST00000356297	Transcript	
chr9	70883886	70883886	*CBWD3*	Silent	SNP	A	A	G	novel	shanshan_et_al_P8_6	p.Q233Q	ENSG00000196873	ENST00000360171	Transcript	
chr1	10471591	10471591	*PGD*	Silent	SNP	G	G	A	novel	shanshan_et_al_P03	p.A212A	ENSG00000142657	ENST00000270776	Transcript	
chr1	161021414	161021414	*ARHGAP30*	Silent	SNP	A	A	C	novel	shanshan_et_al_P03	p.G370G	ENSG00000186517	ENST00000368013	Transcript	
chr1	29344901	29344901	*EPB41*	Silent	SNP	G	G	A	rs201509659	shanshan_et_al_P03	p.P357P	ENSG00000159023	ENST00000343067	Transcript	
chr10	11527879	11527879	*USP6NL*	Silent	SNP	C	C	T	novel	shanshan_et_al_P03	p.L249L	ENSG00000148429	ENST00000277575	Transcript	
chr10	21805486	21805486	*SKIDA1*	Silent	SNP	c	c	T	novel	shanshan_et_al_P03	p.E422E	ENSG00000180592	ENST00000449193	Transcript	
chr12	52867063	52867063	*KRT6C*	Silent	SNP	G	G	A	rs527527882	shanshan_et_al_P03	p.D153D	ENSG00000170465	ENST00000252250	Transcript	
chr13	10338524	10338524	*CCDC168*	Silent	SNP	G	G	A	rs577146331	shanshan_et_al_P03	p.D1312D	ENSG00000175820	ENST00000322527	Transcript	
chr22	17072073	17072073	*CCT8L2*	Silent	SNP	T	T	G	novel	shanshan_et_al_P03	p.A456A	ENSG00000198445	ENST00000359963	Transcript	
chr4	183714431	183714431	*TENM3*	Silent	SNP	G	G	A	rs140050384	shanshan_et_al_P03	p.T2202T	ENSG00000218336	ENST00000511685	Transcript	
chr4	256780800	256780800	*SLC34A2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P03	p.P594P	ENSG00000157765	ENST00000382051	Transcript	
chr5	137518441	137518441	*KIF20A*	Silent	SNP	G	G	T	novel	shanshan_et_al_P03	p.L227L	ENSG00000112984	ENST00000394894	Transcript	
chrX	26235571	26235571	*MAGEB5*	Silent	SNP	G	G	C	novel	shanshan_et_al_P03	p.L51L	ENSG00000188408	ENST00000602297	Transcript	
chr11	111897008	111897008	*DLAT*	Silent	SNP	T	T	G	novel	shanshan_et_al_P07	p.G122G	ENSG00000150768	ENST00000280346	Transcript	
chr18	72020864	72020864	*C18orf63*	Silent	SNP	C	C	T	novel	shanshan_et_al_P07	p.G454G	ENSG00000206043	ENST00000579455	Transcript	
chr19	18857898	18857898	*CRTC1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P07	p.S155S	ENSG00000105662	ENST00000338797	Transcript	
chr19	36018596	36018596	*SBSN*	Silent	SNP	T	T	C	novel	shanshan_et_al_P07	p.A196A	ENSG00000189001	ENST00000452271	Transcript	
chr19	4159713	4159713	*CREB3L3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P07	p.V170V	ENSG00000060566	ENST00000078445	Transcript	
chr10	71968993	71968993	*PPA1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P107	p.V231V	ENSG00000180817	ENST00000373232	Transcript	
chr10	90497497	90497497	*LIPK*	Silent	SNP	C	C	T	novel	shanshan_et_al_P107	p.L259L	ENSG00000204021	ENST00000404190	Transcript	
chr10	98144423	98144423	*TLL2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P107	p.S705S	ENSG00000095587	ENST00000357947	Transcript	
chr12	113806984	113806984	*PLBD2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P107	p.A118A	ENSG00000151176	ENST00000280800	Transcript	

chr12	129181894	129181894	*TMEM132C*	Silent	SNP	C	C	T	novel	shanshan_et_al_P107	p.N685N	ENSG00000181234	ENST00000435159	Transcript
chr15	24922841	24922841	*NPAP1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P107	p.A609A	ENSG00000185823	ENST00000329468	Transcript
chr1	272694633	272694633	*NUDC*	Silent	SNP	G	G	A	rs147512061	shanshan_et_al_P108	p.A216A	ENSG00000090273	ENST00000321265	Transcript
chr11	117100449	117100449	*PCSK7*	Silent	SNP	G	G	A	novel	shanshan_et_al_P108	p.L38L	ENSG00000160613	ENST00000320934	Transcript
chr12	88589318	88589318	*TMTC3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P108	p.D879D	ENSG00000139324	ENST00000266712	Transcript
chr15	34147045	34147045	*RYR3*	Silent	SNP	T	T	C	rs376267599	shanshan_et_al_P108	p.L4647L	ENSG00000198838	ENST00000389232	Transcript
chr15	40660551	40660551	*DISP2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P108	p.F746F	ENSG00000140323	ENST00000267889	Transcript
chr15	89391214	89391214	*ACAN*	Silent	SNP	C	C	T	novel	shanshan_et_al_P108	p.G559G	ENSG00000157766	ENST00000439576	Transcript
chr19	11598621	11598621	*ZNF653*	Silent	SNP	C	C	A	novel	shanshan_et_al_P108	p.A219A	ENSG00000161914	ENST00000293771	Transcript
chr19	45648183	45648183	*PPP1R37*	Silent	SNP	C	C	G	novel	shanshan_et_al_P108	p.L353L	ENSG00000104866	ENST00000221462	Transcript
chr5	149431584	149431584	*HMGXB3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P108	p.D1236D	ENSG00000113716	ENST00000502717	Transcript
chr8	145692708	145692708	*KIFC2*	Silent	SNP	G	G	C	novel	shanshan_et_al_P108	p.R151R	ENSG00000167702	ENST00000301332	Transcript
chr9	33030547	33030547	*DNAJA1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P108	p.S175S	ENSG00000086061	ENST00000330899	Transcript
chrX	69263794	69263794	*AWAT2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P108	p.S83S	ENSG00000147160	ENST00000276101	Transcript
chr1	236212233	236212233	*NID1*	Silent	SNP	G	G	A	rs368248311	shanshan_et_al_P111	p.P94P	ENSG00000116962	ENST00000264187	Transcript
chr10	59959035	59959035	*IPMK*	Silent	SNP	G	G	A	rs200443361	shanshan_et_al_P111	p.Y198Y	ENSG00000151151	ENST00000373935	Transcript
chr10	71255367	71255367	*TSPAN15*	Silent	SNP	C	C	T	rs140147623	shanshan_et_al_P111	p.N125N	ENSG00000099282	ENST00000373290	Transcript
chr11	73879639	73879639	*C2CD3*	Silent	SNP	T	T	C	novel	shanshan_et_al_P111	p.P25P	ENSG00000168014	ENST00000313663	Transcript
chr12	8375111	8375111	*FAM90A1*	Silent	SNP	C	C	T	rs142985337	shanshan_et_al_P111	p.A234A	ENSG00000171847	ENST00000538603	Transcript
chr15	43903421	43903421	*STRC*	Silent	SNP	C	C	T	novel	shanshan_et_al_P111	p.G1077G	ENSG00000242866	ENST00000450892	Transcript
chr16	20435280	20435280	*ACSM5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P111	p.T270T	ENSG00000183549	ENST00000331849	Transcript
chr2	113539278	113539278	*IL1A*	Silent	SNP	T	T	C	novel	shanshan_et_al_P111	p.V74V	ENSG00000115008	ENST00000263339	Transcript
chr5	147051334	147051334	*JAKMIP2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P111	p.P12P	ENSG00000176049	ENST00000265272	Transcript
chr6	24875951	24875951	*FAM65B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P111	p.A23A	ENSG00000111913	ENST00000259698	Transcript
chr5	177419740	177419740	*PROP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P120	p.L217L	ENSG00000175325	ENST00000308304	Transcript
chr8	2038013	2038013	*MYOM2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P120	p.T609T	ENSG00000036448	ENST00000262113	Transcript
chr1	117107911	117107911	*FBXO2*	Silent	SNP	c	c	G	rs61749273	shanshan_et_al_P129	p.A41A	ENSG00000116661	ENST00000354287	Transcript
chr1	25228934	25228934	*RUNX3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P129	p.P323P	ENSG00000020633	ENST00000399916	Transcript
chr11	120008562	120008562	*TRIM29*	Silent	SNP	G	G	A	novel	shanshan_et_al_P129	p.L60L	ENSG00000137699	ENST00000341846	Transcript
chr13	50285084	50285084	*KPNA3*	Silent	SNP	A	A	G	novel	shanshan_et_al_P129	p.D282D	ENSG00000102753	ENST00000261667	Transcript
chr16	108756	108756	*RHBDF1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P129	p.V717V	ENSG00000007384	ENST00000262316	Transcript
chr16	24135257	24135257	*PRKCB*	Silent	SNP	C	C	T	rs116346810	shanshan_et_al_P129	p.T340T	ENSG00000166501	ENST00000303531	Transcript
chr17	4443106	4443106	*MYBBP1A*	Silent	SNP	A	A	T	novel	shanshan_et_al_P129	p.P1197P	ENSG00000132382	ENST00000381556	Transcript
chr19	56029534	56029534	*SSC5D*	Silent	SNP	A	A	G	novel	shanshan_et_al_P129	p.T1297T	ENSG00000179954	ENST00000389623	Transcript
chr19	7119591	7119591	*INSR*	Silent	SNP	G	G	A	novel	shanshan_et_al_P129	p.S1221S	ENSG00000171105	ENST00000302850	Transcript
chr2	152135364	152135364	*NMI*	Silent	SNP	A	A	G	novel	shanshan_et_al_P129	p.L106L	ENSG00000123609	ENST00000243346	Transcript
chr2	206036979	206036979	*PARD3B*	Silent	SNP	G	G	A	novel	shanshan_et_al_P129	p.G493G	ENSG00000116117	ENST00000358768	Transcript
chr2	233899020	233899020	*NEU2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P129	p.H132H	ENSG00000115488	ENST00000233840	Transcript
chr2	39222277	39222277	*SOS1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P129	p.S1111S	ENSG00000115904	ENST00000426016	Transcript
chr3	75788390	75788390	*ZNF717*	Silent	SNP	A	A	C	novel	shanshan_et_al_P129	p.V128V	ENSG00000227124	ENST00000422325	Transcript
chr4	9247083	9247083	*USP17L17*	Silent	SNP	C	C	A	novel	shanshan_et_al_P129	p.T493T	ENSG00000249104	ENST00000511568	Transcript

chr9	123152034	123152034	*CDK5RAP2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P129	p.A1870A	ENSG00000136861	ENST00000349780	Transcript	
chrX	118771070	118771070	*Sep/06*	Silent	SNP	G	G	A	novel	shanshan_et_al_P129	p.T292T	ENSG00000125354	ENST00000343984	Transcript	
chrX	129173244	129173244	*BCORL1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P129	p.K1535K	ENSG00000085185	ENST00000540052	Transcript	
chr1	42049239	42049239	*HIVEP3*	Silent	SNP	G	G	A	rs199930261	shanshan_et_al_P133	p.N410N	ENSG00000127124	ENST00000372583	Transcript	
chr10	50594558	50594558	*DRGX*	Silent	SNP	G	G	A	rs377612688	shanshan_et_al_P133	p.Y169Y	ENSG00000165606	ENST00000434016	Transcript	
chr10	64136198	64136198	*ZNF365*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.P82P	ENSG00000138311	ENST00000410046	Transcript	
chr10	72513565	72513565	*ADAMTS14*	Silent	SNP	G	G	A	rs370803022	shanshan_et_al_P133	p.T916T	ENSG00000138316	ENST00000373208	Transcript	
chr11	18739542	18739542	*IGSF22*	Silent	SNP	G	G	A	rs376212297	shanshan_et_al_P133	p.N303N	ENSG00000179057	ENST00000513874	Transcript	
chr11	46800054	46800054	*CKAP5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.D843D	ENSG00000175216	ENST00000529230	Transcript	
chr12	52886667	52886667	*KRT6A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.F102F	ENSG00000205420	ENST00000330722	Transcript	
chr13	52523858	52523858	*ATP7B*	Silent	SNP	C	C	T	rs141872590	shanshan_et_al_P133	p.T935T	ENSG00000123191	ENST00000242839	Transcript	
chr14	23828142	23828142	*EFS*	Silent	SNP	C	C	T	novel	shanshan_et_al_P133	p.P398P	ENSG00000100842	ENST00000216733	Transcript	
chr14	65009472	65009472	*HSPA2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P133	p.I635I	ENSG00000126803	ENST00000247207	Transcript	
chr15	86259119	86259119	*AKAP13*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.S1904S	ENSG00000170776	ENST00000361243	Transcript	
chr17	6928050	6928050	*BCL6B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P133	p.S244S	ENSG00000161940	ENST00000293805	Transcript	
chr17	73723903	73723903	*ITGB4*	Silent	SNP	C	C	T	novel	shanshan_et_al_P133	p.L146L	ENSG00000132470	ENST00000200181	Transcript	
chr18	59166595	59166595	*CDH20*	Silent	SNP	G	G	A	rs369126362	shanshan_et_al_P133	p.T141T	ENSG00000101542	ENST00000262717	Transcript	
chr19	31768611	31768611	*TSHZ3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P133	p.K696K	ENSG00000121297	ENST00000240587	Transcript	
chr19	3964908	3964908	*DAPK3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.R48R	ENSG00000167657	ENST00000545797	Transcript	
chr19	47844845	47844845	*C5AR2*	Silent	SNP	C	C	T	rs372248694	shanshan_et_al_P133	p.S263S	ENSG00000134830	ENST00000595464	Transcript	
chr19	52942411	52942411	*ZNF534*	Silent	SNP	G	G	A	rs113700997	shanshan_et_al_P133	p.A579A	ENSG00000198633	ENST00000332323	Transcript	
chr2	189904068	189904068	*COL5A2*	Silent	SNP	G	G	A	rs199904322	shanshan_et_al_P133	p.P1285P	ENSG00000204262	ENST00000374866	Transcript	
chr2	220088899	220088899	*ATG9A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.D398D	ENSG00000198925	ENST00000409618	Transcript	
chr4	57522119	57522119	*HOPX*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.I34I	ENSG00000171476	ENST00000554144	Transcript	
chr5	136448178	136448178	*SPOCK1*	Silent	SNP	G	G	A	rs146810579	shanshan_et_al_P133	p.P140P	ENSG00000152377	ENST00000394945	Transcript	
chr6	146755884	146755884	*GRM1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P133	p.Y1179Y	ENSG00000152822	ENST00000361719	Transcript	
chr7	100285712	100285712	*GIGYF1*	Silent	SNP	G	G	A	rs202246782	shanshan_et_al_P133	p.G19G	ENSG00000146830	ENST00000275732	Transcript	
chr7	156752835	156752835	*NOM1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P133	p.S533S	ENSG00000146909	ENST00000275820	Transcript	
chr7	2020096	2020096	*MAD1L1*	Silent	SNP	G	G	A	rs113127342	shanshan_et_al_P133	p.D499D	ENSG00000002822	ENST00000406869	Transcript	
chr7	69064885	69064885	*AUTS2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.S82S	ENSG00000158321	ENST00000342771	Transcript	
chr7	73752935	73752935	*CLIP2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P133	p.G93G	ENSG00000106665	ENST00000223398	Transcript	
chr7	99802682	99802682	*STAG3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P133	p.Q1002Q	ENSG00000066923	ENST00000426455	Transcript	
chr1	32381586	32381586	*PTP4A2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P134	p.E33E	ENSG00000184007	ENST00000344035	Transcript	
chr1	3784569	3784569	*DFFB*	Silent	SNP	C	C	G	novel	shanshan_et_al_P134	p.G154G	ENSG00000169598	ENST00000378209	Transcript	
chr11	57886041	57886041	*OR9I1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P134	p.L292L	ENSG00000172377	ENST00000302610	Transcript	
chr12	108985455	108985455	*TMEM119*	Silent	SNP	C	C	T	rs370682335	shanshan_et_al_P134	p.P235P	ENSG00000183160	ENST00000392806	Transcript	
chr12	58014749	58014749	*SLC26A10*	Silent	SNP	C	C	T	novel	shanshan_et_al_P134	p.G88G	ENSG00000135502	ENST00000320442	Transcript	
chr12	80770982	80770982	*OTOGL*	Silent	SNP	T	T	A	novel	shanshan_et_al_P134	p.P2278P	ENSG00000165899	ENST00000458043	Transcript	
chr16	28499036	28499036	*CLN3*	Silent	SNP	G	G	C	novel	shanshan_et_al_P134	p.P107P	ENSG00000188603	ENST00000569430	Transcript	
chr16	731334	731334	*STUB1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P134	p.I114I	ENSG00000103266	ENST00000219548	Transcript	
chr17	2604454	2604454	*CLUH*	Silent	SNP	G	G	A	rs375888870	shanshan_et_al_P134	p.F297F	ENSG00000132361	ENST00000570628	Transcript	

chr18	54162526	54162526	*EPB41L3*	Silent	SNP	C	C	T	rs201925314	shanshan_et_al_P134	p.P544P	ENSG00000082397	ENST00000341928	Transcript
chr19	984437	984437	*WDR18*	Silent	SNP	C	C	T	novel	shanshan_et_al_P134	p.G28G	ENSG00000065268	ENST00000251289	Transcript
chrX	100747980	100747980	*ARMCX4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P134	p.Q1468Q	ENSG00000196440	ENST00000423738	Transcript
chr1	42922566	42922566	*PPCS*	Silent	SNP	A	A	T	novel	shanshan_et_al_P137	p.P110P	ENSG00000127125	ENST00000372561	Transcript
chr12	20769211	20769211	*PDE3A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P137	p.S439S	ENSG00000172572	ENST00000359062	Transcript
chr5	5306757	5306757	*ADAMTS16*	Silent	SNP	C	C	T	rs199905954	shanshan_et_al_P137	p.C1109C	ENSG00000145536	ENST00000274181	Transcript
chr5	63991419	63991419	*FAM159B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P137	p.L93L	ENSG00000145642	ENST00000389074	Transcript
chr6	83847259	83847259	*DOPEY1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P137	p.V1166V	ENSG00000083097	ENST00000349129	Transcript
chr8	102705020	102705020	*NCALD*	Silent	SNP	G	G	A	rs375021007	shanshan_et_al_P137	p.D161D	ENSG00000104490	ENST00000395923	Transcript
chr8	131149206	131149206	*ASAP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P137	p.L387L	ENSG00000153317	ENST00000357668	Transcript
chr15	68617541	68617541	*ITGA11*	Silent	SNP	G	G	A	rs111998611	shanshan_et_al_P144	p.V750V	ENSG00000137809	ENST00000315757	Transcript
chr16	9857975	9857975	*GRIN2A*	Silent	SNP	G	G	A	rs150487431	shanshan_et_al_P144	p.P1142P	ENSG00000183454	ENST00000396573	Transcript
chr19	40433036	40433036	*FCGBP*	Silent	SNP	G	G	A	novel	shanshan_et_al_P144	p.T411T	ENSG00000090920	ENST00000221347	Transcript
chr20	1616925	1616925	*SIRPG*	Silent	SNP	G	G	A	novel	shanshan_et_al_P144	p.D219D	ENSG00000089012	ENST00000303415	Transcript
chr20	30746284	30746284	*TM9SF4*	Silent	SNP	C	C	T	rs78926209	shanshan_et_al_P144	p.G512G	ENSG00000101337	ENST00000398022	Transcript
chr21	34950679	34950679	*DONSON*	Silent	SNP	C	C	T	novel	shanshan_et_al_P144	p.P545P	ENSG00000159147	ENST00000303071	Transcript
chr3	142840789	142840789	*CHST2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P144	p.G377G	ENSG00000175040	ENST00000309575	Transcript
chr3	164905979	164905979	*SLITRK3*	Silent	SNP	A	A	G	novel	shanshan_et_al_P144	p.S880S	ENSG00000121871	ENST00000475390	Transcript
chr4	177649010	177649010	*VEGFC*	Silent	SNP	G	G	A	novel	shanshan_et_al_P144	p.S158S	ENSG00000150630	ENST00000280193	Transcript
chr1	160105259	160105259	*ATP1A2*	Silent	SNP	C	C	T	rs140707454	shanshan_et_al_P17	p.N717N	ENSG00000018625	ENST00000361216	Transcript
chr11	6291978	6291978	*CCKBR*	Silent	SNP	C	C	T	novel	shanshan_et_al_P17	p.D252D	ENSG00000110148	ENST00000334619	Transcript
chr11	7083660	7083660	*NLRP14*	Silent	SNP	C	C	T	rs114183300	shanshan_et_al_P17	p.N967N	ENSG00000158077	ENST00000299481	Transcript
chr12	52845665	52845665	*KRT6B*	Silent	SNP	G	G	T	rs141114189	shanshan_et_al_P17	p.G66G	ENSG00000185479	ENST00000252252	Transcript
chr16	2049636	2049636	*ZNF598*	Silent	SNP	C	C	T	rs117748995	shanshan_et_al_P17	p.E638E	ENSG00000167962	ENST00000431526	Transcript
chr16	3254390	3254390	*OR1F1*	Silent	SNP	C	C	T	rs113788191	shanshan_et_al_P17	p.S48S	ENSG00000168124	ENST00000304646	Transcript
chr7	129350276	129350276	*NRF1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P17	p.E276E	ENSG00000106459	ENST00000393232	Transcript
chr19	22940344	22940344	*ZNF99*	Silent	SNP	A	A	G	rs71357944	shanshan_et_al_P29	p.Y789Y	ENSG00000213973	ENST00000596209	Transcript
chr20	62038300	62038300	*KCNQ2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P29	p.P772P	ENSG00000075043	ENST00000359125	Transcript
chr7	64168758	64168758	*ZNF107*	Silent	SNP	T	T	C	rs369397657	shanshan_et_al_P29	p.Y692Y	ENSG00000196247	ENST00000395391	Transcript
chr8	145114792	145114792	*OPLAH*	Silent	SNP	G	G	A	novel	shanshan_et_al_P29	p.T48T	ENSG00000178814	ENST00000426825	Transcript
chr10	21805480	21805480	*SKIDA1*	Silent	SNP	t	t	C	rs201836118	shanshan_et_al_P33	p.E424E	ENSG00000180592	ENST00000449193	Transcript
chr3	69244442	69244442	*FRMD4B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P33	p.L436L	ENSG00000114541	ENST00000398540	Transcript
chr4	92554844	92554844	*USP17L19*	Silent	SNP	G	G	T	novel	shanshan_et_al_P33	p.T127T	ENSG00000248920	ENST00000515566	Transcript
chr5	176522365	176522365	*FGFR4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P33	p.V518V	ENSG00000160867	ENST00000292408	Transcript
chr1	222802659	222802659	*MIA3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P59	p.G699G	ENSG00000154305	ENST00000344922	Transcript
chr1	78900055	78900055	*PER3*	Silent	SNP	T	T	A	rs11121034	shanshan_et_al_P59	p.A1007A	ENSG00000049246	ENST00000361923	Transcript
chr12	30906290	30906290	*CAPRIN2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P59	p.I136I	ENSG00000110888	ENST00000298892	Transcript
chr12	53207801	53207801	*KRT4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P59	p.G14G	ENSG00000170477	ENST00000551956	Transcript
chr13	78335108	78335108	*SLAIN1*	Silent	SNP	G	G	A	rs143426312	shanshan_et_al_P59	p.L356L	ENSG00000139737	ENST00000488699	Transcript
chr17	36508652	36508652	*SOCS7*	Silent	SNP	G	G	A	novel	shanshan_et_al_P59	p.L175L	ENSG00000174111	ENST00000577233	Transcript
chr2	220038876	220038876	*CNPPD1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P59	p.L188L	ENSG00000115649	ENST00000409789	Transcript

chr2	99978267	99978267	*EIF5B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P59	p.T301T	ENSG00000158417	ENST00000289371	Transcript
chr3	193855521	193855521	*HES1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P59	p.F114F	ENSG00000114315	ENST00000232424	Transcript
chr7	42085104	42085104	*GLI3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P59	p.A235A	ENSG00000106571	ENST00000395925	Transcript
chr8	141669637	141669637	*PTK2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P59	p.V1042V	ENSG00000169398	ENST00000340930	Transcript
chr19	1620980	1620980	*TCF3*	Silent	SNP	G	G	C	rs201663318	shanshan_et_al_P66	p.P360P	ENSG00000071564	ENST00000262965	Transcript
chr5	118844906	118844906	*HSD17B4*	Silent	SNP	C	C	T	novel	shanshan_et_al_P66	p.G493G	ENSG00000133835	ENST00000504811	Transcript
chr6	170871013	170871013	*TBP*	Silent	SNP	A	A	G	rs574714675	shanshan_et_al_P66	p.Q63Q	ENSG00000112592	ENST00000392092	Transcript
chr1	162725527	162725527	*DDR2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P01	p.N213N	ENSG00000162733	ENST00000367922	Transcript
chr10	101715326	101715326	*DNMBP*	Silent	SNP	T	T	G	novel	shanshan_et_al_P01	p.P635P	ENSG00000107554	ENST00000324109	Transcript
chr11	621598	621598	*CDHR5*	Silent	SNP	G	G	A	rs144446111	shanshan_et_al_P01	p.D157D	ENSG00000099834	ENST00000358353	Transcript
chr12	12871865	12871865	*CDKN1B*	Silent	SNP	A	A	G	novel	shanshan_et_al_P01	p.R194R	ENSG00000111276	ENST00000228872	Transcript
chr12	56096665	56096665	*ITGA7*	Silent	SNP	G	G	T	novel	shanshan_et_al_P01	p.G135G	ENSG00000135424	ENST00000553804	Transcript
chr4	190946919	190946919	*FRG2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P01	p.R212R	ENSG00000205097	ENST00000378763	Transcript
chr4	30724925	30724925	*PCDH7*	Silent	SNP	G	G	T	novel	shanshan_et_al_P01	p.V627V	ENSG00000169851	ENST00000543491	Transcript
chr1	237778092	237778092	*RYR2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P02	p.R1888R	ENSG00000198626	ENST00000366574	Transcript
chr17	74136156	74136156	*FOXJ1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P02	p.P107P	ENSG00000129654	ENST00000322957	Transcript
chr19	10433378	10433378	*RAVER1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P02	p.N389N	ENSG00000161847	ENST00000293677	Transcript
chr20	10386276	10386276	*MKKS*	Silent	SNP	T	T	C	novel	shanshan_et_al_P02	p.Q444Q	ENSG00000125863	ENST00000347364	Transcript
chr22	44368864	44368864	*SAMM50*	Silent	SNP	C	C	T	rs371328727	shanshan_et_al_P02	p.P181P	ENSG00000100347	ENST00000350028	Transcript
chr1	32650194	32650194	*TXLNA*	Silent	SNP	C	C	T	novel	shanshan_et_al_P05	p.L192L	ENSG00000084652	ENST00000373609	Transcript
chr1	44063705	44063705	*PTPRF*	Silent	SNP	G	G	A	novel	shanshan_et_al_P05	p.L700L	ENSG00000142949	ENST00000359947	Transcript
chr11	58956711	58956711	*DTX4*	Silent	SNP	A	A	C	novel	shanshan_et_al_P05	p.P358P	ENSG00000110042	ENST00000227451	Transcript
chr12	112669484	112669484	*HECTD4*	Silent	SNP	T	T	C	novel	shanshan_et_al_P05	p.A1865A	ENSG00000173064	ENST00000550722	Transcript
chr15	24923954	24923954	*NPAP1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P05	p.S980S	ENSG00000185823	ENST00000329468	Transcript
chr17	39240887	39240887	*KRTAP4-7*	Silent	SNP	C	C	G	novel	shanshan_et_al_P05	p.T143T	ENSG00000240871	ENST00000391417	Transcript
chr2	242651416	242651416	*ING5*	Silent	SNP	A	A	C	novel	shanshan_et_al_P05	p.R138R	ENSG00000168395	ENST00000313552	Transcript
chr7	102281066	102281066	*UPK3BL*	Silent	SNP	G	G	C	novel	shanshan_et_al_P05	p.L89L	ENSG00000267368	ENST00000340457	Transcript
chr7	57188582	57188582	*ZNF479*	Silent	SNP	A	A	T	novel	shanshan_et_al_P05	p.T180T	ENSG00000185177	ENST00000331162	Transcript
chr8	26627987	26627987	*ADRA1A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P05	p.L360L	ENSG00000120907	ENST00000380586	Transcript
chrX	55753756	55753756	*RRAGB*	Silent	SNP	T	T	C	novel	shanshan_et_al_P05	p.H81H	ENSG00000083750	ENST00000262850	Transcript
chrX	91131848	91131848	*PCDH11X*	Silent	SNP	T	T	A	novel	shanshan_et_al_P05	p.V203V	ENSG00000102290	ENST00000373094	Transcript
chr1	53975565	53975565	*GLIS1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P06	p.P498P	ENSG00000174332	ENST00000312233	Transcript
chr1	63789113	63789113	*FOXD3*	Silent	SNP	A	A	G	novel	shanshan_et_al_P06	p.G128G	ENSG00000187140	ENST00000371116	Transcript
chr11	64138808	64138808	*RPS6KA4*	Silent	SNP	A	A	C	novel	shanshan_et_al_P06	p.A725A	ENSG00000162302	ENST00000334205	Transcript
chr17	15406337	15406337	*TVP23C*	Silent	SNP	T	T	G	novel	shanshan_et_al_P06	p.P224P	ENSG00000175106	ENST00000225576	Transcript
chr2	197189845	197189845	*HECW2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P06	p.G200G	ENSG00000138411	ENST00000260983	Transcript
chrX	107436895	107436895	*COL4A6*	Silent	SNP	T	T	G	novel	shanshan_et_al_P06	p.P346P	ENSG00000197565	ENST00000372216	Transcript
chr1	38450443	38450443	*SF3A3*	Silent	SNP	C	C	G	novel	shanshan_et_al_P08	p.V104V	ENSG00000183431	ENST00000373019	Transcript
chr1	45345664	45345664	*EIF2B3*	Silent	SNP	T	T	G	novel	shanshan_et_al_P08	p.I267I	ENSG00000070785	ENST00000360403	Transcript
chr10	50835782	50835782	*CHAT*	Silent	SNP	G	G	A	rs529337162	shanshan_et_al_P08	p.T354T	ENSG00000070748	ENST00000337653	Transcript
chr12	57648757	57648757	*R3HDM2*	Silent	SNP	A	A	C	novel	shanshan_et_al_P08	p.G910G	ENSG00000179912	ENST00000347140	Transcript

chr16	22547298	22547298	*NPIPB5*	Silent	SNP	G	G	T	novel	shanshan_et_al_P08	p.G998G	ENSG00000243716	ENST00000424340	Transcript	
chr19	15376285	15376285	*BRD4*	Silent	SNP	A	A	G	rs113935053	shanshan_et_al_P08	p.P243P	ENSG00000141867	ENST00000263377	Transcript	
chr19	48041622	48041622	*ZNF541*	Silent	SNP	T	T	G	novel	shanshan_et_al_P08	p.P976P	ENSG00000118156	ENST00000314121	Transcript	
chr19	54760159	54760159	*LILRB5*	Silent	SNP	C	C	A	novel	shanshan_et_al_P08	p.V134V	ENSG00000105609	ENST00000449561	Transcript	
chr19	58198693	58198693	*ZNF551*	Silent	SNP	C	C	A	rs573207173	shanshan_et_al_P08	p.L350L	ENSG00000204519	ENST00000282296	Transcript	
chr2	18234709 2	18234709 2	*ITGA4*	Silent	SNP	T	T	C	novel	shanshan_et_al_P08	p.Y282Y	ENSG00000115232	ENST00000397033	Transcript	
chr20	35414921	35414921	*SOGA1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P08	p.G1651G	ENSG00000149639	ENST00000237536	Transcript	
chr3	132350312	132350312	*ACAD11*	Silent	SNP	T	T	A	novel	shanshan_et_al_P08	p.I238I	ENSG00000240303	ENST00000264990	Transcript	
chr3	157131877	157131877	*VEPH1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P08	p.V233V	ENSG00000197415	ENST00000362010	Transcript	
chr3	75788390	75788390	*ZNF717*	Silent	SNP	A	A	C	novel	shanshan_et_al_P08	p.V128V	ENSG00000227124	ENST00000422325	Transcript	
chr4	183714734	183714734	*TENM3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P08	p.L2303L	ENSG00000218336	ENST00000511685	Transcript	
chr5	180657785	180657785	*TRIM41*	Silent	SNP	G	G	T	novel	shanshan_et_al_P08	p.L285L	ENSG00000146063	ENST00000315073	Transcript	
chr7	84628984	84628984	*SEMA3D*	Silent	SNP	G	G	T	novel	shanshan_et_al_P08	p.V702V	ENSG00000153993	ENST00000284136	Transcript	
chrX	27998042	27998042	*DCAF8L1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P08	p.S470S	ENSG00000226372	ENST00000441525	Transcript	
chr1	33330385	33330385	*FNDC5*	Silent	SNP	G	G	C	novel	shanshan_et_al_P09	p.L96L	ENSG00000160097	ENST00000609187	Transcript	
chr11	102465482	102465482	*MMP20*	Silent	SNP	G	G	A	novel	shanshan_et_al_P09	p.F320F	ENSG00000137674	ENST00000260228	Transcript	
chr16	1291564	1291564	*TPSAB1*	Silent	SNP	C	C	T	rs1064777	shanshan_et_al_P09	p.D121D	ENSG00000172236	ENST00000338844	Transcript	
chr19	42909667	42909667	*LIPE*	Silent	SNP	G	G	T	novel	shanshan_et_al_P09	p.G804G	ENSG00000079435	ENST00000244289	Transcript	
chr20	4229146	4229146	*ADRA1D*	Silent	SNP	C	C	A	novel	shanshan_et_al_P09	p.S153S	ENSG00000171873	ENST00000379453	Transcript	
chrX	128722924	128722924	*OCRL*	Silent	SNP	A	A	G	novel	shanshan_et_al_P09	p.P801P	ENSG00000122126	ENST00000371113	Transcript	
chr1	50317156	50317156	*AGBL4*	Silent	SNP	C	C	T	novel	shanshan_et_al_P10	p.G23G	ENSG00000186094	ENST00000371839	Transcript	
chr17	41168536	41168536	*VAT1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P10	p.R296R	ENSG00000108828	ENST00000355653	Transcript	
chr19	22155715	22155715	*ZNF208*	Silent	SNP	G	G	A	rs201994264	shanshan_et_al_P10	p.N707N	ENSG00000160321	ENST00000397126	Transcript	
chr19	36545987	36545987	*WDR62*	Silent	SNP	A	A	C	novel	shanshan_et_al_P10	p.P38P	ENSG00000075702	ENST00000401500	Transcript	
chr2	24202681 0	24202681 0	*SNED1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P10	p.Y1375Y	ENSG00000162804	ENST00000310397	Transcript	
chr3	39230862	39230862	*XIRP1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P10	p.P25P	ENSG00000168334	ENST00000340369	Transcript	
chr12	101577953	101577953	*SLC5A8*	Silent	SNP	A	A	G	novel	shanshan_et_al_P101	p.L337L	ENSG00000256870	ENST00000536262	Transcript	
chr2	179843292	179843292	*CCDC141*	Silent	SNP	T	T	C	novel	shanshan_et_al_P101	p.A112A	ENSG00000163492	ENST00000420890	Transcript	
chr5	170323065	170323065	*RANBP17*	Silent	SNP	A	A	G	novel	shanshan_et_al_P101	p.E145E	ENSG00000204764	ENST00000523189	Transcript	
chr19	47933667	47933667	*SLC8A2*	Silent	SNP	G	G	T	rs147198367	shanshan_et_al_P112	p.I815I	ENSG00000118160	ENST00000236877	Transcript	
chr11	124180558	124180558	*OR8D1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P113	p.Y35Y	ENSG00000196341	ENST00000357821	Transcript	
chr19	33602733	33602733	*GPATCH1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P113	p.S563S	ENSG00000076650	ENST00000170564	Transcript	
chr19	49920500	49920500	*CCDC155*	Silent	SNP	C	C	T	novel	shanshan_et_al_P113	p.L508L	ENSG00000161609	ENST00000447857	Transcript	
chr19	7166394	7166394	*INSR*	Silent	SNP	C	C	T	novel	shanshan_et_al_P113	p.E544E	ENSG00000171105	ENST00000302850	Transcript	
chr3	35835429	35835429	*ARPP21*	Silent	SNP	T	T	C	novel	shanshan_et_al_P113	p.A807A	ENSG00000172995	ENST00000458225	Transcript	
chr3	56651150	56651150	*CCDC66*	Silent	SNP	T	T	C	novel	shanshan_et_al_P113	p.N618N	ENSG00000180376	ENST00000394672	Transcript	
chr5	127866289	127866289	*FBN2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P113	p.S145S	ENSG00000138829	ENST00000508053	Transcript	
chr6	33263862	33263862	*RGL2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P113	p.T237T	ENSG00000237441	ENST00000497454	Transcript	
chr7	102135502	102135502	*RASA4B*	Silent	SNP	G	G	A	novel	shanshan_et_al_P113	p.R401R	ENSG00000170667	ENST00000541662	Transcript	
chr7	82580151	82580151	*PCLO*	Silent	SNP	G	G	A	novel	shanshan_et_al_P113	p.I3251I	ENSG00000186472	ENST00000333891	Transcript	
chr18	34647437	34647437	*KIAA1328*	Silent	SNP	G	G	T	novel	shanshan_et_al_P115	p.L387L	ENSG00000150477	ENST00000280020	Transcript	

chr18	51795970	51795970	*POLI*	Silent	SNP	G	G	A	rs368901560	shanshan_et_al_P115	p.E18E	ENSG00000101751	ENST00000579534	Transcript
chr6	20419982	20419982	*SYNGR3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P116	p.G41G	ENSG00000127561	ENST00000248121	Transcript
chr19	56029591	56029591	*SSC5D*	Silent	SNP	T	T	C	novel	shanshan_et_al_P116	p.T1316T	ENSG00000179954	ENST00000389623	Transcript
chr1	176863905	176863905	*ASTN1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P118	p.P911P	ENSG00000152092	ENST00000361833	Transcript
chr1	152057842	152057842	*TCHHL1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.S772S	ENSG00000182898	ENST00000368806	Transcript
chr1	223178411	223178411	*DISP1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A1224A	ENSG00000154309	ENST00000284476	Transcript
chr1	248903065	248903065	*LYPD8*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.T29T	ENSG00000266949	ENST00000590317	Transcript
chr1	266941402	266941402	*ZNF683*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.P87P	ENSG00000176083	ENST00000374204	Transcript
chr1	46472002	46472002	*MAST2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.T279T	ENSG00000086015	ENST00000361297	Transcript
chr1	55152062	55152062	*MROH7*	Silent	SNP	C	C	T	novel	shanshan_et_al_P119	p.C884C	ENSG00000184313	ENST00000421030	Transcript
chr1	57349294	57349294	*C8A*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.V265V	ENSG00000157131	ENST00000361249	Transcript
chr1	64643545	64643545	*ROR1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.S607S	ENSG00000185483	ENST00000371079	Transcript
chr11	68030220	68030220	*C11orf24*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.T81T	ENSG00000171067	ENST00000304271	Transcript
chr11	93528081	93528081	*MED17*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P289P	ENSG00000042429	ENST00000251871	Transcript
chr12	11218256	11218256	*ACAD10*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.T642T	ENSG00000111271	ENST00000455480	Transcript
chr12	48357474	48357474	*GALNT8*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.T87T	ENSG00000130035	ENST00000252318	Transcript
chr12	53722674	53722674	*SP7*	Silent	SNP	T	T	A	rs369878239	shanshan_et_al_P119	p.T184T	ENSG00000170374	ENST00000536324	Transcript
chr12	57442078	57442078	*MYO1A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P119	p.V10V	ENSG00000166866	ENST00000442789	Transcript
chr13	110817273	110817273	*COL4A1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P1362P	ENSG00000187498	ENST00000375820	Transcript
chr13	28623522	28623522	*FLT3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.V345V	ENSG00000122025	ENST00000241453	Transcript
chr15	33905481	33905481	*RYR3*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.S754S	ENSG00000198838	ENST00000389232	Transcript
chr15	43820880	43820880	*MAP1A*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.P2403P	ENSG00000166963	ENST00000300231	Transcript
chr15	78921777	78921777	*CHRNB4*	Silent	SNP	G	G	T	novel	shanshan_et_al_P119	p.L290L	ENSG00000117971	ENST00000261751	Transcript
chr16	19528491	19528491	*GDE1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.T94T	ENSG00000006007	ENST00000353258	Transcript
chr16	50745688	50745688	*NOD2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P622P	ENSG00000167207	ENST00000300589	Transcript
chr16	71509706	71509706	*ZNF19*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.T248T	ENSG00000157429	ENST00000288177	Transcript
chr17	10544603	10544603	*MYH3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.P682P	ENSG00000109063	ENST00000583535	Transcript
chr17	61558959	61558959	*ACE*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A326A	ENSG00000159640	ENST00000290866	Transcript
chr17	77975497	77975497	*CHD3*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.L406L	ENSG00000170004	ENST00000380358	Transcript
chr18	29510942	29510942	*LPIN2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.V183V	ENSG00000101577	ENST00000261596	Transcript
chr19	55832369	55832369	*TMEM150B*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.L12L	ENSG00000180061	ENST00000326652	Transcript
chr2	112786192	112786192	*MERTK*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A917A	ENSG00000153208	ENST00000295408	Transcript
chr2	186654677	186654677	*FSIP2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.L1027L	ENSG00000188738	ENST00000343098	Transcript
chr2	189867050	189867050	*COL3A1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P806P	ENSG00000168542	ENST00000330436	Transcript
chr2	214878801	214878801	*SPAG16*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.T509T	ENSG00000144451	ENST00000331683	Transcript
chr2	230312255	230312255	*DNER*	Silent	SNP	T	T	C	rs372614670	shanshan_et_al_P119	p.G421G	ENSG00000187957	ENST00000341772	Transcript
chr2	238257010	238257010	*COL6A3*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P2316P	ENSG00000163359	ENST00000295550	Transcript
chr2	32668631	32668631	*BIRC6*	Silent	SNP	A	A	G	rs61754194	shanshan_et_al_P119	p.S1437S	ENSG00000115760	ENST00000421745	Transcript
chr2	32730271	32730271	*BIRC6*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A3233A	ENSG00000115760	ENST00000421745	Transcript
chr2	55791498	55791498	*SMEK2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.P737P	ENSG00000138041	ENST00000345102	Transcript
chr2	66667702	66667702	*MEIS1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A130A	ENSG00000143995	ENST00000272369	Transcript

chr20	34022535	34022535	*GDF5*	Silent	SNP	A	A	G	novel	shanshan_et_al_P119	p.I226I	ENSG00000125965	ENST00000374372	Transcript
chr21	19629064	19629064	*CHODL*	Silent	SNP	T	T	C	rs567256236	shanshan_et_al_P119	p.N106N	ENSG00000154645	ENST00000299295	Transcript
chr21	43319388	43319388	*C2CD2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.P548P	ENSG00000157617	ENST00000380486	Transcript
chr3	111988887	111988887	*SLC9C1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.I217I	ENSG00000172139	ENST00000305815	Transcript
chr3	170529111	170529111	*PLCL2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P119	p.D565D	ENSG00000154822	ENST00000418129	Transcript
chr3	32932313	32932313	*TRIM71*	Silent	SNP	G	G	A	novel	shanshan_et_al_P119	p.E539E	ENSG00000206557	ENST00000383763	Transcript
chr3	38622494	38622494	*SCN5A*	Silent	SNP	G	G	C	novel	shanshan_et_al_P119	p.A1052A	ENSG00000183873	ENST00000413689	Transcript
chr3	51929251	51929251	*IQCF1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.A91A	ENSG00000173389	ENST00000310914	Transcript
chr4	100830266	100830266	*WDR1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.V413V	ENSG00000071127	ENST00000499869	Transcript
chr4	106576777	106576777	*ARHGEF38*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.A377A	ENSG00000236699	ENST00000420470	Transcript
chr4	134084217	134084217	*PCDH10*	Silent	SNP	T	T	C	novel	shanshan_et_al_P119	p.S961S	ENSG00000138650	ENST00000264360	Transcript
chr4	152498952	152498952	*FAM160A1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P119	p.G152G	ENSG00000164142	ENST00000435205	Transcript
chr4	25675937	25675937	*SLC34A2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P119	p.A412A	ENSG00000157765	ENST00000382051	Transcript
chr4	87622437	87622437	*PTPN13*	Silent	SNP	A	A	T	rs375363885	shanshan_et_al_P119	p.P226P	ENSG00000163629	ENST00000436978	Transcript
chr5	154315430	154315430	*GEMIN5*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.S160S	ENSG00000082516	ENST00000285873	Transcript
chr5	158747495	158747495	*IL12B*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A172A	ENSG00000113302	ENST00000231228	Transcript
chr5	178563024	178563024	*ADAMTS2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P119	p.L657L	ENSG00000087116	ENST00000282582	Transcript
chr6	42619808	42619808	*UBR2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.T871T	ENSG00000024048	ENST00000372899	Transcript
chr6	49574885	49574885	*RHAG*	Silent	SNP	T	T	C	novel	shanshan_et_al_P119	p.A372A	ENSG00000112077	ENST00000371175	Transcript
chr6	80203462	80203462	*LCA5*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.L242L	ENSG00000135338	ENST00000393959	Transcript
chr7	105909612	105909612	*NAMPT*	Silent	SNP	G	G	C	novel	shanshan_et_al_P119	p.V198V	ENSG00000105835	ENST00000222553	Transcript
chr7	45701681	45701681	*ADCY1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.S491S	ENSG00000164742	ENST00000029723	Transcript
chr7	48431656	48431656	*ABCA13*	Silent	SNP	C	C	G	rs147058958	shanshan_et_al_P119	p.T3931T	ENSG00000179869	ENST00000435803	Transcript
chr7	50514509	50514509	*FIGNL1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P119	p.E159E	ENSG00000132436	ENST00000419119	Transcript
chr7	82583237	82583237	*PCLO*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P2344P	ENSG00000186472	ENST00000333891	Transcript
chr7	94539923	94539923	*PPP1R9A*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.A166A	ENSG00000158528	ENST00000433360	Transcript
chr8	110302071	110302071	*NUDCD1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.L244L	ENSG00000120526	ENST00000239690	Transcript
chr8	110980551	110980551	*KCNV1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P423P	ENSG00000164794	ENST00000524391	Transcript
chr8	139715588	139715588	*COL22A1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.G840G	ENSG00000169436	ENST00000303045	Transcript
chr8	38008322	38008322	*STAR*	Silent	SNP	T	T	C	novel	shanshan_et_al_P119	p.T5T	ENSG00000147465	ENST00000276449	Transcript
chr9	114486151	114486151	*C9orf84*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P561P	ENSG00000165181	ENST00000374287	Transcript
chr9	116060057	116060057	*RNF183*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.S136S	ENSG00000165188	ENST00000478815	Transcript
chr9	15744747	15744747	*CCDC171*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.G842G	ENSG00000164989	ENST00000380701	Transcript
chr9	97041103	97041103	*ZNF169*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P3P	ENSG00000175787	ENST00000339535	Transcript
chrX	114245343	114245343	*IL13RA2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A190A	ENSG00000123496	ENST00000371936	Transcript
chrX	118219478	118219478	*KIAA1210*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.A1572A	ENSG00000250423	ENST00000402510	Transcript
chrX	129389536	129389536	*TLR8*	Silent	SNP	A	A	G	novel	shanshan_et_al_P119	p.L599L	ENSG00000101916	ENST00000218032	Transcript
chrX	135430026	135430026	*GPR112*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.P1387P	ENSG00000156920	ENST00000394143	Transcript
chrX	140969477	140969477	*MAGEC3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P119	p.Q268Q	ENSG00000165509	ENST00000298296	Transcript
chrX	47060933	47060933	*UBA1*	Silent	SNP	G	G	C	novel	shanshan_et_al_P119	p.G245G	ENSG00000130985	ENST00000335972	Transcript
chrX	78010453	78010453	*LPAR4*	Silent	SNP	T	T	C	novel	shanshan_et_al_P119	p.N29N	ENSG00000147145	ENST00000443539	Transcript

chrX	99848912	99848912	*TNMD*	Silent	SNP	T	T	A	novel	shanshan_et_al_P119	p.T67T	ENSG00000000005	ENST00000373031	Transcript
chrY	14952176	14952176	*USP9Y*	Silent	SNP	A	A	T	novel	shanshan_et_al_P119	p.T1908T	ENSG00000114374	ENST00000338981	Transcript
chr1	99753679	99753679	*LPPR4*	Silent	SNP	C	C	T	rs202236446	shanshan_et_al_P121	p.S127S	ENSG00000117600	ENST00000370185	Transcript
chr11	17582329	17582329	*OTOG*	Silent	SNP	A	A	T	novel	shanshan_et_al_P121	p.P484P	ENSG00000188162	ENST00000399391	Transcript
chr12	63989812	63989812	*DPY19L2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P121	p.P489P	ENSG00000177990	ENST00000324472	Transcript
chr2	188228181	188228181	*CALCRL*	Silent	SNP	T	T	C	novel	shanshan_et_al_P121	p.S183S	ENSG00000064989	ENST00000409998	Transcript
chr3	45988342	45988342	*CXCR6*	Silent	SNP	C	C	T	novel	shanshan_et_al_P121	p.I123I	ENSG00000172215	ENST00000458629	Transcript
chr3	98288890	98288890	*TADA3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P121	p.D233D	ENSG00000171148	ENST00000301964	Transcript
chr6	129621954	129621954	*LAMA2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P121	p.I1037I	ENSG00000196569	ENST00000421865	Transcript
chr7	35912362	35912362	*Sep/07*	Silent	SNP	G	G	T	novel	shanshan_et_al_P121	p.V122V	ENSG00000122545	ENST00000399034	Transcript
chrX	177641562	177641562	*SCML1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P121	p.V44V	ENSG00000047634	ENST00000380041	Transcript
chr10	82331298	82331298	*SH2D4B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P123	p.A153A	ENSG00000178217	ENST00000339284	Transcript
chr10	93581	93581	*TUBB8*	Silent	SNP	G	G	T	novel	shanshan_et_al_P123	p.R251R	ENSG00000173876	ENST00000309812	Transcript
chr11	76873949	76873949	*MYO7A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P123	p.N535N	ENSG00000137474	ENST00000409709	Transcript
chr12	52627311	52627311	*KRT7*	Silent	SNP	G	G	A	novel	shanshan_et_al_P123	p.R77R	ENSG00000135480	ENST00000331817	Transcript
chr15	58855830	58855830	*LIPC*	Silent	SNP	G	G	A	rs115544443	shanshan_et_al_P123	p.T432T	ENSG00000166035	ENST00000356113	Transcript
chr16	72831382	72831382	*ZFHX3*	Silent	SNP	T	T	C	rs112722798	shanshan_et_al_P123	p.Q1733Q	ENSG00000140836	ENST00000268489	Transcript
chr17	79654108	79654108	*HGS*	Silent	SNP	C	C	T	rs11541091	shanshan_et_al_P123	p.L92L	ENSG00000185359	ENST00000329138	Transcript
chr18	76757181	76757181	*SALL3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P123	p.G1254G	ENSG00000256463	ENST00000537592	Transcript
chr19	10624875	10624875	*S1PR5*	Silent	SNP	C	C	T	novel	shanshan_et_al_P123	p.L271L	ENSG00000180739	ENST00000439028	Transcript
chr19	33089162	33089162	*ANKRD27*	Silent	SNP	T	T	C	novel	shanshan_et_al_P123	p.G1014G	ENSG00000105186	ENST00000306065	Transcript
chr19	47126919	47126919	*PTGIR*	Silent	SNP	G	G	A	novel	shanshan_et_al_P123	p.Y188Y	ENSG00000160013	ENST00000291294	Transcript
chr19	52471891	52471891	*ZNF350*	Silent	SNP	A	A	G	rs369158170	shanshan_et_al_P123	p.L60L	ENSG00000256683	ENST00000243644	Transcript
chr3	160137316	160137316	*SMC4*	Silent	SNP	A	A	C	novel	shanshan_et_al_P123	p.G614G	ENSG00000113810	ENST00000357388	Transcript
chr3	183209922	183209922	*KLHL6*	Silent	SNP	G	G	A	novel	shanshan_et_al_P123	p.I553I	ENSG00000172578	ENST00000341319	Transcript
chr5	150663622	150663622	*SLC36A3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P123	p.L360L	ENSG00000186334	ENST00000377713	Transcript
chr7	102280728	102280728	*UPK3BL*	Silent	SNP	G	G	A	novel	shanshan_et_al_P123	p.L136L	ENSG00000267368	ENST00000340457	Transcript
chr7	141795424	141795424	*MGAM*	Silent	SNP	G	G	A	novel	shanshan_et_al_P123	p.Q1610Q	ENSG00000257335	ENST00000549489	Transcript
chr9	105636505	105636505	*DMRT2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P123	p.L260L	ENSG00000173253	ENST00000382251	Transcript
chr9	213344669	213344669	*KLHL9*	Silent	SNP	G	G	A	novel	shanshan_et_al_P123	p.S130S	ENSG00000198642	ENST00000359039	Transcript
chr9	99701255	99701255	*NUTM2G*	Silent	SNP	C	C	A	novel	shanshan_et_al_P123	p.R684R	ENSG00000188152	ENST00000372322	Transcript
chrX	73811695	73811695	*RLIM*	Silent	SNP	A	A	G	rs374955178	shanshan_et_al_P123	p.S485S	ENSG00000131263	ENST00000332687	Transcript
chr1	245530375	245530375	*KIF26B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P125	p.H235H	ENSG00000162849	ENST00000407071	Transcript
chr12	122748705	122748705	*VPS33A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P125	p.L48L	ENSG00000139719	ENST00000267199	Transcript
chr22	50968978	50968978	*ODF3B*	Silent	SNP	G	G	T	novel	shanshan_et_al_P125	p.P231P	ENSG00000177989	ENST00000329363	Transcript
chr7	53523563	53523563	*TNRC18*	Silent	SNP	G	G	A	rs549034306	shanshan_et_al_P125	p.P2722P	ENSG00000182095	ENST00000430969	Transcript
chrX	112150733	112150733	*ARHGAP6*	Silent	SNP	T	T	C	rs78939852	shanshan_et_al_P125	p.S264S	ENSG00000047648	ENST00000337414	Transcript
chr4	155411772	155411772	*DCHS2*	Silent	SNP	G	G	A	rs571321208	shanshan_et_al_P127	p.L246L	ENSG00000197410	ENST00000339452	Transcript
chr6	154735543	154735543	*CNKSR3*	Silent	SNP	G	G	C	rs558624920	shanshan_et_al_P127	p.P320P	ENSG00000153721	ENST00000607772	Transcript
chr1	151867527	151867527	*THEM4*	Silent	SNP	A	A	C	novel	shanshan_et_al_P128	p.R81R	ENSG00000159445	ENST00000368814	Transcript
chr10	43615037	43615037	*RET*	Silent	SNP	C	C	T	novel	shanshan_et_al_P128	p.R817R	ENSG00000165731	ENST00000355710	Transcript

chr11	134387233	134387233	*BTBD10*	Silent	SNP	A	A	G	novel	shanshan_et_al_P128	p.T223T	ENSG00000148925	ENST00000278174	Transcript
chr11	171228288	171228288	*PIK3C2A*	Silent	SNP	T	T	A	novel	shanshan_et_al_P128	p.S1335S	ENSG00000011405	ENST00000265970	Transcript
chr11	34938235	34938235	*PDHX*	Silent	SNP	G	G	A	novel	shanshan_et_al_P128	p.P11P	ENSG00000110435	ENST00000227868	Transcript
chr12	124399435	124399435	*DNAH10*	Silent	SNP	C	C	T	rs375713954	shanshan_et_al_P128	p.S3419S	ENSG00000197653	ENST00000409039	Transcript
chr15	63882902	63882902	*USP3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P128	p.G480G	ENSG00000140455	ENST00000380324	Transcript
chr17	55183902	55183902	*AKAP1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P128	p.A359A	ENSG00000121057	ENST00000337714	Transcript
chr17	57741313	57741313	*CLTC*	Silent	SNP	A	A	G	novel	shanshan_et_al_P128	p.A493A	ENSG00000141367	ENST00000269122	Transcript
chr19	56206342	56206342	*EPN1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P128	p.L591L	ENSG00000063245	ENST00000411543	Transcript
chr3	150931202	150931202	*P2RY14*	Silent	SNP	C	C	T	rs144133888	shanshan_et_al_P128	p.P301P	ENSG00000174944	ENST00000309170	Transcript
chr3	151166575	151166575	*IGSF10*	Silent	SNP	C	C	A	rs146034413	shanshan_et_al_P128	p.P398P	ENSG00000152580	ENST00000282466	Transcript
chr3	175455171	175455171	*NAALADL2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P128	p.V658V	ENSG00000177694	ENST00000454872	Transcript
chr3	196449409	196449409	*PIGX*	Silent	SNP	A	A	T	novel	shanshan_et_al_P128	p.R59R	ENSG00000163964	ENST00000314118	Transcript
chr3	44285300	44285300	*TOPAZ1*	Silent	SNP	G	G	A	rs144334708	shanshan_et_al_P128	p.P434P	ENSG00000173769	ENST00000309765	Transcript
chr4	144618046	144618046	*FREM3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P128	p.Q1261Q	ENSG00000183090	ENST00000329798	Transcript
chr4	57311145	57311145	*EVC*	Silent	SNP	C	C	T	novel	shanshan_et_al_P128	p.F127F	ENSG00000072840	ENST00000382674	Transcript
chr4	89589096	89589096	*HERC3*	Silent	SNP	A	A	G	novel	shanshan_et_al_P128	p.P499P	ENSG00000138641	ENST00000402738	Transcript
chr5	138773156	138773156	*DNAJC18*	Silent	SNP	T	T	G	rs375033291	shanshan_et_al_P128	p.A44A	ENSG00000170464	ENST00000302060	Transcript
chr5	140230276	140230276	*PCDHA9*	Silent	SNP	C	C	T	novel	shanshan_et_al_P128	p.C732C	ENSG00000204961	ENST00000532602	Transcript
chr6	42713053	42713053	*TBCC*	Silent	SNP	C	C	G	novel	shanshan_et_al_P128	p.V253V	ENSG00000124659	ENST00000244625	Transcript
chr7	47408116	47408116	*TNS3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P128	p.L709L	ENSG00000136205	ENST00000398879	Transcript
chr9	134151534	134151534	*FAM78A*	Silent	SNP	G	G	C	novel	shanshan_et_al_P128	p.S11S	ENSG00000126882	ENST00000372271	Transcript
chrX	23410817	23410817	*PTCHD1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P128	p.T394T	ENSG00000165186	ENST00000379361	Transcript
chr1	103352460	103352460	*COL11A1*	Silent	SNP	T	T	C	rs375667862	shanshan_et_al_P13	p.K1587K	ENSG00000060718	ENST00000370096	Transcript
chr1	207720622	207720622	*CR1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P13	p.Q841Q	ENSG00000203710	ENST00000367049	Transcript
chr10	49917882	49917882	*WDFY4*	Silent	SNP	G	G	T	novel	shanshan_et_al_P13	p.G35G	ENSG00000128815	ENST00000325239	Transcript
chr15	75219215	75219215	*COX5A*	Silent	SNP	A	A	T	novel	shanshan_et_al_P13	p.L77L	ENSG00000178741	ENST00000322347	Transcript
chr17	40966589	40966589	*BECN1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P13	p.V311V	ENSG00000126581	ENST00000361523	Transcript
chr17	46627903	46627903	*HOXB3*	Silent	SNP	C	C	G	novel	shanshan_et_al_P13	p.P363P	ENSG00000120093	ENST00000470495	Transcript
chr19	55317435	55317435	*KIR2DL4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P13	p.R131R	ENSG00000189013	ENST00000345540	Transcript
chr2	175337917	175337917	*GPR155*	Silent	SNP	C	C	G	novel	shanshan_et_al_P13	p.L212L	ENSG00000163328	ENST00000392552	Transcript
chr2	97217747	97217747	*ARID5A*	Silent	SNP	T	T	A	novel	shanshan_et_al_P13	p.P494P	ENSG00000196843	ENST00000357485	Transcript
chr21	35468082	35468082	*SLC5A3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P13	p.G195G	ENSG00000272962	ENST00000608209	Transcript
chr21	40665932	40665932	*BRWD1*	Silent	SNP	A	A	T	rs150276787	shanshan_et_al_P13	p.I212I	ENSG00000185658	ENST00000333229	Transcript
chr5	178392020	178392020	*ZNF454*	Silent	SNP	A	A	T	novel	shanshan_et_al_P13	p.A205A	ENSG00000178187	ENST00000320129	Transcript
chr6	26460025	26460025	*BTN2A1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P13	p.Y133Y	ENSG00000112763	ENST00000312541	Transcript
chr7	123092932	123092932	*IQUB*	Silent	SNP	C	C	G	novel	shanshan_et_al_P13	p.L747L	ENSG00000164675	ENST00000466202	Transcript
chr7	31912917	31912917	*PDE1C*	Silent	SNP	G	G	T	novel	shanshan_et_al_P13	p.I259I	ENSG00000154678	ENST00000396193	Transcript
chr9	139368612	139368612	*SEC16A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P13	p.P1152P	ENSG00000148396	ENST00000313050	Transcript
chr9	5919945	5919945	*KIAA2026*	Silent	SNP	T	T	C	novel	shanshan_et_al_P13	p.T2017T	ENSG00000183354	ENST00000399933	Transcript
chr9	77436710	77436710	*TRPM6*	Silent	SNP	G	G	A	novel	shanshan_et_al_P13	p.G295G	ENSG00000119121	ENST00000360774	Transcript
chrX	44037654	44037654	*EFHC2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P13	p.F636F	ENSG00000183690	ENST00000420999	Transcript

chr1	154280511	154280511	*KAZN*	Silent	SNP	T	T	A	novel	shanshan_et_al_P130	p.A520A	ENSG00000189337	ENST00000376030	Transcript
chr1	155927566	155927566	*ARHGEF2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P130	p.V551V	ENSG00000116584	ENST00000361247	Transcript
chr1	247978864	247978864	*OR14A16*	Silent	SNP	G	G	A	novel	shanshan_et_al_P130	p.P56P	ENSG00000196772	ENST00000357627	Transcript
chr10	18266928	18266928	*SLC39A12*	Silent	SNP	C	C	G	novel	shanshan_et_al_P130	p.T283T	ENSG00000148482	ENST00000377369	Transcript
chr10	52834576	52834576	*PRKG1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.R76R	ENSG00000185532	ENST00000373980	Transcript
chr11	123479437	123479437	*GRAMD1B*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.V385V	ENSG00000023171	ENST00000529750	Transcript
chr11	5776918	5776918	*OR52N4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.T316T	ENSG00000181074	ENST00000317254	Transcript
chr11	65618597	65618597	*SNX32*	Silent	SNP	C	C	T	novel	shanshan_et_al_P130	p.C225C	ENSG00000172803	ENST00000308342	Transcript
chr12	122862410	122862410	*CLIP1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.G61G	ENSG00000130779	ENST00000540338	Transcript
chr12	31493293	31493293	*TEAD4*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.P365P	ENSG00000197905	ENST00000359864	Transcript
chr12	57828687	57828687	*INHBC*	Silent	SNP	T	T	A	novel	shanshan_et_al_P130	p.L6L	ENSG00000175189	ENST00000309668	Transcript
chr14	24040569	24040569	*JPH4*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.S457S	ENSG00000092051	ENST00000397118	Transcript
chr14	63174772	63174772	*KCNH5*	Silent	SNP	A	A	G	novel	shanshan_et_al_P130	p.N807N	ENSG00000140015	ENST00000322893	Transcript
chr14	94420793	94420793	*ASB2*	Silent	SNP	G	G	A	rs146382240	shanshan_et_al_P130	p.G116G	ENSG00000100628	ENST00000555019	Transcript
chr16	37818284	37818284	*CREBBP*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.V1613V	ENSG00000005339	ENST00000262367	Transcript
chr17	48266604	48266604	*COL1A1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P130	p.I954I	ENSG00000108821	ENST00000225964	Transcript
chr18	47329219	47329219	*ACAA2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.V7V	ENSG00000167315	ENST00000285093	Transcript
chr19	41596379	41596379	*CYP2A13*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.G188G	ENSG00000197838	ENST00000330436	Transcript
chr19	86611966	86611966	*ADAMTS10*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.G395G	ENSG00000142303	ENST00000270328	Transcript
chr2	220246123	220246123	*DNPEP*	Silent	SNP	A	A	G	novel	shanshan_et_al_P130	p.Y391Y	ENSG00000123992	ENST00000273075	Transcript
chr2	64863208	64863208	*SERTAD2*	Silent	SNP	C	C	T	rs373945219	shanshan_et_al_P130	p.G266G	ENSG00000179833	ENST00000313349	Transcript
chr2	90008569	90008569	*MBOAT2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.S408S	ENSG00000143797	ENST00000330597	Transcript
chr22	19709171	19709171	*Sep/05*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.A242A	ENSG00000184702	ENST00000457784	Transcript
chr22	26688730	26688730	*SEZ6L*	Silent	SNP	C	C	T	novel	shanshan_et_al_P130	p.S151S	ENSG00000100095	ENST00000248933	Transcript
chr3	137717926	137717926	*CLDN18*	Silent	SNP	G	G	A	novel	shanshan_et_al_P130	p.L72L	ENSG00000066405	ENST00000343735	Transcript
chr3	168833418	168833418	*MECOM*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.R625R	ENSG00000085276	ENST00000264674	Transcript
chr3	186331011	186331011	*AHSG*	Silent	SNP	T	T	C	novel	shanshan_et_al_P130	p.Y27Y	ENSG00000145192	ENST00000441641	Transcript
chr3	189688629	189688629	*LEPREL1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P130	p.T623T	ENSG00000090530	ENST00000331932	Transcript
chr4	183836170	183836170	*DCTD*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.G61G	ENSG00000129187	ENST00000357067	Transcript
chr4	30724764	30724764	*PCDH7*	Silent	SNP	C	C	T	novel	shanshan_et_al_P130	p.L574L	ENSG00000169851	ENST00000543491	Transcript
chr4	87968323	87968323	*AFF1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P130	p.P212P	ENSG00000172493	ENST00000395146	Transcript
chr4	93463569	93463569	*USP17L27*	Silent	SNP	C	C	T	novel	shanshan_et_al_P130	p.A161A	ENSG00000235780	ENST00000505574	Transcript
chr6	74072590	74072590	*KHDC3L*	Silent	SNP	C	C	A	novel	shanshan_et_al_P130	p.R46R	ENSG00000203908	ENST00000370367	Transcript
chr6	84765103	84765103	*MRAP2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P130	p.T22T	ENSG00000135324	ENST00000257767	Transcript
chr7	131883300	131883300	*PLXNA4*	Silent	SNP	G	G	T	novel	shanshan_et_al_P130	p.V894V	ENSG00000221866	ENST00000359827	Transcript
chr7	53477795	53477795	*TNRC18*	Silent	SNP	C	C	A	rs553098750	shanshan_et_al_P130	p.T2955T	ENSG00000182095	ENST00000430969	Transcript
chr8	28573681	28573681	*EXTL3*	Silent	SNP	G	G	C	novel	shanshan_et_al_P130	p.T35T	ENSG00000012232	ENST00000522062	Transcript
chr9	74344996	74344996	*TMEM2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P130	p.G649G	ENSG00000135048	ENST00000377044	Transcript
chrX	68382434	68382434	*PJA1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P130	p.K216K	ENSG00000181191	ENST00000361478	Transcript
chr1	156554689	156554689	*TTC24*	Silent	SNP	C	C	G	novel	shanshan_et_al_P131	p.L424L	ENSG00000187862	ENST00000368236	Transcript
chr1	158590176	158590176	*SPTA1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.S2067S	ENSG00000163554	ENST00000368147	Transcript

chr1	20005645	20005645	*HTR6*	Silent	SNP	G	G	T	novel	shanshan_et_al_P131	p.V369V	ENSG00000158748	ENST00000289753	Transcript
chr1	248524891	248524891	*OR2T4*	Silent	SNP	C	C	T	rs200949727	shanshan_et_al_P131	p.N3N	ENSG00000196944	ENST00000366475	Transcript
chr1	26515327	26515327	*CNKSR1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P131	p.L585L	ENSG00000142675	ENST00000361530	Transcript
chr10	1245940	1245940	*ADARB2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P131	p.P610P	ENSG00000185736	ENST00000381312	Transcript
chr11	102487587	102487587	*MMP20*	Silent	SNP	G	G	T	novel	shanshan_et_al_P131	p.L110L	ENSG00000137674	ENST00000260228	Transcript
chr11	6806814	6806814	*OR2AG1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P131	p.P182P	ENSG00000170803	ENST00000307401	Transcript
chr12	21788503	21788503	*LDHB*	Silent	SNP	G	G	A	novel	shanshan_et_al_P131	p.D326D	ENSG00000111716	ENST00000396076	Transcript
chr12	48145291	48145291	*RAPGEF3*	Silent	SNP	A	A	T	novel	shanshan_et_al_P131	p.S131S	ENSG00000079337	ENST00000449771	Transcript
chr12	86377356	86377356	*MGAT4C*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.S80S	ENSG00000182050	ENST00000604798	Transcript
chr15	100801716	100801716	*ADAMTS17*	Silent	SNP	C	C	T	novel	shanshan_et_al_P131	p.P333P	ENSG00000140470	ENST00000268070	Transcript
chr15	25963545	25963545	*ATP10A*	Silent	SNP	C	C	T	rs142993802	shanshan_et_al_P131	p.A455A	ENSG00000206190	ENST00000356865	Transcript
chr15	30385103	30385103	*GOLGA8J*	Silent	SNP	T	T	C	novel	shanshan_et_al_P131	p.H493H	ENSG00000179938	ENST00000567927	Transcript
chr15	42129008	42129008	*JMJD7*	Silent	SNP	G	G	T	rs376080091	shanshan_et_al_P131	p.A244A	ENSG00000243789	ENST00000397299	Transcript
chr16	23208733	23208733	*SCNN1G*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.S354S	ENSG00000166828	ENST00000300061	Transcript
chr17	39882134	39882134	*HAP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P131	p.P461P	ENSG00000173805	ENST00000347901	Transcript
chr17	41886396	41886396	*MPP3*	Silent	SNP	T	T	C	novel	shanshan_et_al_P131	p.V503V	ENSG00000161647	ENST00000398389	Transcript
chr17	42165866	42165866	*HDAC5*	Silent	SNP	A	A	C	novel	shanshan_et_al_P131	p.T497T	ENSG00000108840	ENST00000259283	Transcript
chr17	60743871	60743871	*MRC2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P131	p.Q250Q	ENSG00000001028	ENST00000330375	Transcript
chr18	28934553	28934553	*DSG1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P131	p.P798P	ENSG00000134760	ENST00000257192	Transcript
chr19	964249	964249	*ARID3A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P131	p.G256G	ENSG00000116017	ENST00000263620	Transcript
chr2	210518155	210518155	*MAP2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P131	p.A87A	ENSG00000078018	ENST00000360351	Transcript
chr2	74641666	74641666	*C2orf81*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.T519T	ENSG00000159239	ENST00000290390	Transcript
chr20	36789850	36789850	*TGM2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.V54V	ENSG00000198959	ENST00000361475	Transcript
chr22	19118954	19118954	*TSSK2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P131	p.V14V	ENSG00000206203	ENST00000399635	Transcript
chr3	113442357	113442357	*NAA50*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.V59V	ENSG00000121579	ENST00000240922	Transcript
chr3	182590191	182590191	*ATP11B*	Silent	SNP	A	A	G	novel	shanshan_et_al_P131	p.K638K	ENSG00000058063	ENST00000323116	Transcript
chr4	37447057	37447057	*KIAA1239*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.L1149L	ENSG00000174145	ENST00000309447	Transcript
chr4	90170056	90170056	*GPRIN3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.T402T	ENSG00000185477	ENST00000260938	Transcript
chr5	154396215	154396215	*KIF4B*	Silent	SNP	A	A	G	novel	shanshan_et_al_P131	p.L932L	ENSG00000226650	ENST00000435029	Transcript
chr6	161807841	161807841	*PARK2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.S384S	ENSG00000185345	ENST00000366898	Transcript
chr6	52943682	52943682	*FBXO9*	Silent	SNP	C	C	T	rs570338169	shanshan_et_al_P131	p.G141G	ENSG00000112146	ENST00000244426	Transcript
chr6	74121997	74121997	*DDX43*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.V450V	ENSG00000080007	ENST00000370336	Transcript
chr7	20438506	20438506	*ITGB8*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.V390V	ENSG00000105855	ENST00000022273	Transcript
chr7	26179176	26179176	*IQCE*	Silent	SNP	G	G	T	novel	shanshan_et_al_P131	p.T169T	ENSG00000106012	ENST00000402050	Transcript
chr8	119936895	119936895	*TNFRSF11B*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.G308G	ENSG00000164761	ENST00000329730	Transcript
chr8	28320796	28320796	*CSMD1*	Silent	SNP	G	G	C	novel	shanshan_et_al_P131	p.G2878G	ENSG00000183117	ENST00000537824	Transcript
chr8	57228583	57228583	*SDR16C5*	Silent	SNP	T	T	A	novel	shanshan_et_al_P131	p.V108V	ENSG00000170786	ENST00000303749	Transcript
chr1	155264362	155264362	*PKLR*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.S292S	ENSG00000143627	ENST00000342741	Transcript
chr1	176671803	176671803	*PAPPA2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P135	p.L1099L	ENSG00000116183	ENST00000367662	Transcript
chr1	180904413	180904413	*KIAA1614*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.S456S	ENSG00000135835	ENST00000367588	Transcript
chr1	54607096	54607096	*CDCP2*	Silent	SNP	G	G	A	rs565290091	shanshan_et_al_P135	p.G146G	ENSG00000157211	ENST00000371330	Transcript

chr11	20805362	20805362	*NELL1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P135	p.R107R	ENSG00000165973	ENST00000357134	Transcript
chr11	82989841	82989841	*CCDC90B*	Silent	SNP	T	T	A	novel	shanshan_et_al_P135	p.V84V	ENSG00000137500	ENST00000529689	Transcript
chr14	10541557	10541557	*AHNAK2*	Silent	SNP	G	G	A	rs375265904	shanshan_et_al_P135	p.L2071L	ENSG00000185567	ENST00000333244	Transcript
chr14	10541854	10541854	*AHNAK2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P135	p.L1081L	ENSG00000185567	ENST00000333244	Transcript
chr14	21681156	21681156	*HNRNPC*	Silent	SNP	A	A	C	novel	shanshan_et_al_P135	p.S175S	ENSG00000092199	ENST00000320084	Transcript
chr16	16371277	16371277	*NOMO3*	Silent	SNP	T	T	C	novel	shanshan_et_al_P135	p.S898S	ENSG00000103226	ENST00000399336	Transcript
chr16	22316521	22316521	*POLR3E*	Silent	SNP	A	A	G	novel	shanshan_et_al_P135	p.L27L	ENSG00000058600	ENST00000299853	Transcript
chr16	22547298	22547298	*NPIPB5*	Silent	SNP	G	G	T	novel	shanshan_et_al_P135	p.G998G	ENSG00000243716	ENST00000424340	Transcript
chr16	29997924	29997924	*TAOK2*	Silent	SNP	A	A	C	novel	shanshan_et_al_P135	p.S777S	ENSG00000149930	ENST00000308893	Transcript
chr16	68011904	68011904	*DPEP3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.E256E	ENSG00000141096	ENST00000268793	Transcript
chr17	12917796	12917796	*ELAC2*	Silent	SNP	T	T	G	rs200345003	shanshan_et_al_P135	p.A150A	ENSG00000006744	ENST00000338034	Transcript
chr18	93373179	93373179	*TWSG1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P135	p.L30L	ENSG00000128791	ENST00000262120	Transcript
chr19	38126005	38126005	*ZFP30*	Silent	SNP	T	T	G	novel	shanshan_et_al_P135	p.S479S	ENSG00000120784	ENST00000351218	Transcript
chr19	50399165	50399165	*IL4I1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.L75L	ENSG00000104951	ENST00000595948	Transcript
chr19	50399300	50399300	*IL4I1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.L30L	ENSG00000104951	ENST00000595948	Transcript
chr19	54746179	54746179	*LILRA6*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.F26F	ENSG00000244482	ENST00000396365	Transcript
chr19	58864349	58864349	*A1BG*	Silent	SNP	C	C	T	rs199641094	shanshan_et_al_P135	p.S95S	ENSG00000121410	ENST00000263100	Transcript
chr19	64757566	64757566	*DENND1C*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.P262P	ENSG00000205744	ENST00000381480	Transcript
chr2	107460197	107460197	*ST6GAL2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.A79A	ENSG00000144057	ENST00000409382	Transcript
chr2	37455310	37455310	*CEBPZ*	Silent	SNP	T	T	C	novel	shanshan_et_al_P135	p.L342L	ENSG00000115816	ENST00000234170	Transcript
chr2	47672701	47672701	*MSH2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P135	p.L431L	ENSG00000095002	ENST00000233146	Transcript
chr21	45821606	45821606	*TRPM2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P135	p.A788A	ENSG00000142185	ENST00000397928	Transcript
chr21	46066966	46066966	*KRTAP10-11*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.V197V	ENSG00000243489	ENST00000334670	Transcript
chr22	46658521	46658521	*PKDREJ*	Silent	SNP	C	C	G	rs146407770	shanshan_et_al_P135	p.L233L	ENSG00000130943	ENST00000253255	Transcript
chr3	130743530	130743530	*ASTE1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.F207F	ENSG00000034533	ENST00000264992	Transcript
chr3	46728593	46728593	*ALS2CL*	Silent	SNP	T	T	A	novel	shanshan_et_al_P135	p.S138S	ENSG00000178038	ENST00000318962	Transcript
chr3	58092555	58092555	*FLNB*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.Y632Y	ENSG00000136068	ENST00000490882	Transcript
chr4	11800595	11800595	*TRAM1L1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P135	p.I200I	ENSG00000174599	ENST00000310754	Transcript
chr4	26483689	26483689	*CCKAR*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.S286S	ENSG00000163394	ENST00000295589	Transcript
chr5	140503002	140503002	*PCDHB4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P135	p.A474A	ENSG00000181818	ENST00000194152	Transcript
chr5	159437658	159437658	*TTC1*	Silent	SNP	C	C	T	rs370867147	shanshan_et_al_P135	p.S41S	ENSG00000113312	ENST00000238238	Transcript
chr6	158900821	158900821	*TULP4*	Silent	SNP	G	G	A	rs200699760	shanshan_et_al_P135	p.S355S	ENSG00000130338	ENST00000367097	Transcript
chr6	69348639	69348639	*BAI3*	Silent	SNP	T	T	G	novel	shanshan_et_al_P135	p.A24A	ENSG00000135298	ENST00000370598	Transcript
chr6	99374622	99374622	*FBXL4*	Silent	SNP	T	T	G	novel	shanshan_et_al_P135	p.V81V	ENSG00000112234	ENST00000369244	Transcript
chr7	150878359	150878359	*ASB10*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.D257D	ENSG00000146926	ENST00000420175	Transcript
chr7	27187159	27187159	*HOXA6*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.A70A	ENSG00000106006	ENST00000222728	Transcript
chr7	36895324	36895324	*ELMO1*	Silent	SNP	T	T	C	rs142425368	shanshan_et_al_P135	p.L672L	ENSG00000155849	ENST00000310758	Transcript
chr7	944739	944739	*ADAP1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.L153L	ENSG00000105963	ENST00000265846	Transcript
chr8	114111149	114111149	*CSMD3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P135	p.I251I	ENSG00000164796	ENST00000297405	Transcript
chr8	143602256	143602256	*BAI1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P135	p.I998I	ENSG00000181790	ENST00000517894	Transcript
chr9	164370855	164370855	*BNC2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.S369S	ENSG00000163068	ENST00000380672	Transcript

chr9	93375582	93375582	*DIRAS2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P135	p.L176L	ENSG00000165023	ENST00000375765	Transcript	
chrX	125686088	125686088	*DCAF12L1*	Silent	SNP	G	G	C	novel	shanshan_et_al_P135	p.G168G	ENSG00000198889	ENST00000371126	Transcript	
chr1	211840485	211840485	*NEK2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P139	p.L358L	ENSG00000117650	ENST00000366999	Transcript	
chr12	106708150	106708150	*TCP11L2*	Silent	SNP	A	A	C	novel	shanshan_et_al_P139	p.R58R	ENSG00000166046	ENST00000299045	Transcript	
chr15	99482579	99482579	*IGF1R*	Silent	SNP	C	C	A	novel	shanshan_et_al_P139	p.V1149V	ENSG00000140443	ENST00000268035	Transcript	
chr21	28296534	28296534	*ADAMTS5*	Silent	SNP	C	C	T	novel	shanshan_et_al_P139	p.P877P	ENSG00000154736	ENST00000284987	Transcript	
chr1	184679567	184679567	*EDEM3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P140	p.L602L	ENSG00000116406	ENST00000318130	Transcript	
chr10	51866195	51866195	*FAM21A*	Silent	SNP	A	A	G	novel	shanshan_et_al_P140	p.A613A	ENSG00000099290	ENST00000282633	Transcript	
chr12	29502037	29502037	*ERGIC2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P140	p.D234D	ENSG00000087502	ENST00000360150	Transcript	
chr13	36049595	36049595	*MAB21L1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P140	p.S227S	ENSG00000180660	ENST00000379919	Transcript	
chr14	37641547	37641547	*SLC25A21*	Silent	SNP	G	G	T	novel	shanshan_et_al_P140	p.A3A	ENSG00000183032	ENST00000331299	Transcript	
chr15	59500153	59500153	*LDHAL6B*	Silent	SNP	C	C	A	novel	shanshan_et_al_P140	p.L338L	ENSG00000171989	ENST00000307144	Transcript	
chr16	90025448	90025448	*DEF8*	Silent	SNP	C	C	A	novel	shanshan_et_al_P140	p.I194I	ENSG00000140995	ENST00000268676	Transcript	
chr19	18896845	18896845	*COMP*	Silent	SNP	G	G	A	novel	shanshan_et_al_P140	p.D473D	ENSG00000105664	ENST00000222771	Transcript	
chr19	806448	806448	*PTBP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P140	p.L337L	ENSG00000011304	ENST00000356948	Transcript	
chr2	141762979	141762979	*LRP1B*	Silent	SNP	A	A	G	novel	shanshan_et_al_P140	p.L810L	ENSG00000168702	ENST00000389484	Transcript	
chr2	153533164	153533164	*PRPF40A*	Silent	SNP	T	T	C	novel	shanshan_et_al_P140	p.A262A	ENSG00000196504	ENST00000410080	Transcript	
chr20	31954677	31954677	*CDK5RAP1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P140	p.V510V	ENSG00000101391	ENST00000346416	Transcript	
chr20	43251494	43251494	*ADA*	Silent	SNP	C	C	T	novel	shanshan_et_al_P140	p.L252L	ENSG00000196839	ENST00000372874	Transcript	
chr5	127626569	127626569	*FBN2*	Silent	SNP	G	G	C	rs145583277	shanshan_et_al_P140	p.R2100R	ENSG00000138829	ENST00000508053	Transcript	
chr7	76112348	76112348	*DTX2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P140	p.T264T	ENSG00000091073	ENST00000324432	Transcript	
chr9	101784396	101784396	*COL15A1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P140	p.P575P	ENSG00000204291	ENST00000375001	Transcript	
chr11	58190258	58190258	*OR5B2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P141	p.G159G	ENSG00000172365	ENST00000302581	Transcript	
chr12	56384564	56384564	*RAB5B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P141	p.A138A	ENSG00000111540	ENST00000360299	Transcript	
chr15	32890342	32890342	*GOLGA8N*	Silent	SNP	T	T	G	novel	shanshan_et_al_P141	p.S185S	ENSG00000232653	ENST00000448387	Transcript	
chr15	74032879	74032879	*C15orf59*	Silent	SNP	C	C	A	novel	shanshan_et_al_P141	p.A87A	ENSG00000205363	ENST00000569673	Transcript	
chr16	11076740	11076740	*CLEC16A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P141	p.F321F	ENSG00000038532	ENST00000409790	Transcript	
chr16	50136292	50136292	*HEATR3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P141	p.I622I	ENSG00000155393	ENST00000299192	Transcript	
chr16	50136298	50136298	*HEATR3*	Silent	SNP	T	T	C	novel	shanshan_et_al_P141	p.I624I	ENSG00000155393	ENST00000299192	Transcript	
chr17	37604108	37604108	*MED1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P141	p.A25A	ENSG00000125686	ENST00000300651	Transcript	
chr17	61958860	61958860	*GH2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P141	p.L10L	ENSG00000136487	ENST00000332800	Transcript	
chr18	54068245	54068245	*EPB41L3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P141	p.A767A	ENSG00000082397	ENST00000341928	Transcript	
chr19	54314454	54314454	*NLRP12*	Silent	SNP	G	G	A	novel	shanshan_et_al_P141	p.L153L	ENSG00000142405	ENST00000324134	Transcript	
chr21	17246830	17246830	*USP25*	Silent	SNP	A	A	G	novel	shanshan_et_al_P141	p.R928R	ENSG00000155313	ENST00000285679	Transcript	
chr4	20543217	20543217	*SLIT2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P141	p.A706A	ENSG00000145147	ENST00000505154	Transcript	
chr4	68424635	68424635	*STAP1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P141	p.R36R	ENSG00000035720	ENST00000265404	Transcript	
chr6	100965917	100965917	*ASCC3*	Silent	SNP	A	A	C	novel	shanshan_et_al_P141	p.S1959S	ENSG00000112249	ENST00000369162	Transcript	
chr7	144064388	144064388	*ARHGEF5*	Silent	SNP	C	C	T	novel	shanshan_et_al_P141	p.P1157P	ENSG00000050327	ENST00000005617	Transcript	
chr7	32582833	32582833	*AVL9*	Silent	SNP	C	C	T	novel	shanshan_et_al_P141	p.P58P	ENSG00000105778	ENST00000318709	Transcript	
chr9	86530464	86530464	*KIF27*	Silent	SNP	G	G	A	novel	shanshan_et_al_P141	p.L15L	ENSG00000165115	ENST00000297814	Transcript	
chr10	93581	93581	*TUBB8*	Silent	SNP	G	G	T	novel	shanshan_et_al_P142	p.R251R	ENSG00000173876	ENST00000309812	Transcript	

chr13	73350222	73350222	*DIS3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P142	p.I221I	ENSG00000083520	ENST00000377767	Transcript
chr17	60689860	60689860	*TLK2*	Silent	SNP	A	A	G	rs199800827	shanshan_et_al_P142	p.T729T	ENSG00000146872	ENST00000346027	Transcript
chr8	55538932	55538932	*RP1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P142	p.P830P	ENSG00000104237	ENST00000220676	Transcript
chrX	240246677	240246677	*KLHL15*	Silent	SNP	G	G	C	novel	shanshan_et_al_P142	p.L48L	ENSG00000174010	ENST00000328046	Transcript
chr1	158517848	158517848	*OR6Y1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P143	p.R16R	ENSG00000197532	ENST00000302617	Transcript
chr1	168054847	168054847	*GPR161*	Silent	SNP	G	G	A	rs374744784	shanshan_et_al_P143	p.G524G	ENSG00000143147	ENST00000537209	Transcript
chr11	65810688	65810688	*GAL3ST3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P143	p.R192R	ENSG00000175229	ENST00000312006	Transcript
chr17	72287244	72287244	*DNAI2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P143	p.L232L	ENSG00000171595	ENST00000446837	Transcript
chrX	77224545	77224545	*PGAM4*	Silent	SNP	C	C	T	novel	shanshan_et_al_P143	p.V197V	ENSG00000226784	ENST00000458128	Transcript
chr1	186026508	186026508	*HMCN1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P145	p.L2429L	ENSG00000143341	ENST00000271588	Transcript
chr10	21805393	21805393	*SKIDA1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P145	p.S453S	ENSG00000180592	ENST00000449193	Transcript
chr12	52775154	52775154	*KRT84*	Silent	SNP	G	G	A	novel	shanshan_et_al_P145	p.Y356Y	ENSG00000161849	ENST00000257951	Transcript
chr2	75261997	75261997	*CD163L1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P145	p.T1149T	ENSG00000177675	ENST00000313599	Transcript
chr15	28356918	28356918	*HERC2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P145	p.T4832T	ENSG00000128731	ENST00000261609	Transcript
chr17	61987179	61987179	*CSHL1*	Silent	SNP	C	C	T	rs200319165	shanshan_et_al_P145	p.L187L	ENSG00000204414	ENST00000309894	Transcript
chr19	39915157	39915157	*PLEKHG2*	Silent	SNP	A	A	C	novel	shanshan_et_al_P145	p.P1128P	ENSG00000090924	ENST00000409794	Transcript
chr19	42490076	42490076	*ATP1A3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P145	p.E195E	ENSG00000105409	ENST00000545399	Transcript
chr2	17006314	17006314	*LRP2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P145	p.P2361P	ENSG00000081479	ENST00000263816	Transcript
chr20	46311827	46311827	*SULF2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P145	p.F325F	ENSG00000196562	ENST00000359930	Transcript
chr22	38689302	38689302	*CSNK1E*	Silent	SNP	G	G	A	rs532233715	shanshan_et_al_P145	p.L414L	ENSG00000213923	ENST00000396832	Transcript
chr3	111996684	111996684	*SLC9C1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P145	p.G114G	ENSG00000172139	ENST00000305815	Transcript
chr3	119459504	119459504	*MAATS1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P145	p.L548L	ENSG00000183833	ENST00000273390	Transcript
chr3	189585699	189585699	*TP63*	Silent	SNP	A	A	T	novel	shanshan_et_al_P145	p.P320P	ENSG00000073282	ENST00000264731	Transcript
chr6	26032105	26032105	*HIST1H3B*	Silent	SNP	G	G	A	rs143413138	shanshan_et_al_P145	p.L62L	ENSG00000124693	ENST00000244661	Transcript
chr7	146805246	146805246	*CNTNAP2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P145	p.D186D	ENSG00000174469	ENST00000361727	Transcript
chr7	148513802	148513802	*EZH2*	Silent	SNP	A	A	C	novel	shanshan_et_al_P145	p.P493P	ENSG00000106462	ENST00000320356	Transcript
chr9	104238277	104238277	*TMEM246*	Silent	SNP	C	C	A	novel	shanshan_et_al_P145	p.L366L	ENSG00000165152	ENST00000374851	Transcript
chrX	151303136	151303136	*MAGEA10*	Silent	SNP	A	A	G	novel	shanshan_et_al_P145	p.N319N	ENSG00000124260	ENST00000370323	Transcript
chrX	151869367	151869367	*MAGEA6*	Silent	SNP	A	A	T	novel	shanshan_et_al_P145	p.R19R	ENSG00000197172	ENST00000329342	Transcript
chrX	151936110	151936110	*MAGEA3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P145	p.R19R	ENSG00000221867	ENST00000393902	Transcript
chr19	41354661	41354661	*CYP2A6*	Silent	SNP	T	T	C	rs79584535	shanshan_et_al_P146	p.V117V	ENSG00000255974	ENST00000301141	Transcript
chr11	49204790	49204790	*FOLH1*	Silent	SNP	A	A	G	rs76509850	shanshan_et_al_P147	p.Y277Y	ENSG00000086205	ENST00000256999	Transcript
chr7	150069026	150069026	*REPIN1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P147	p.V289V	ENSG00000214022	ENST00000489432	Transcript
chr1	175489533	175489533	*PADI1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P16	p.L87L	ENSG00000142623	ENST00000375471	Transcript
chr11	64004689	64004689	*VEGFB*	Silent	SNP	A	A	G	rs200085344	shanshan_et_al_P16	p.P135P	ENSG00000173511	ENST00000309422	Transcript
chr13	25044059	25044059	*PARP4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P16	p.F673F	ENSG00000102699	ENST00000381989	Transcript
chr13	31722570	31722570	*HSPH1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P16	p.T395T	ENSG00000120694	ENST00000320027	Transcript
chr17	10408714	10408714	*MYH1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P16	p.G763G	ENSG00000109061	ENST00000226207	Transcript
chr17	2298633	2298633	*MNT*	Silent	SNP	T	T	G	rs199848480	shanshan_et_al_P16	p.P63P	ENSG00000070444	ENST00000174618	Transcript
chr17	62036787	62036787	*SCN4A*	Silent	SNP	G	G	T	rs186182054	shanshan_et_al_P16	p.G619G	ENSG00000007314	ENST00000435607	Transcript
chr21	46900010	46900010	*COL18A1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P16	p.G626G	ENSG00000182871	ENST00000355480	Transcript

chr3	138724379	138724379	*PRR23A*	Silent	SNP	A	A	G	novel	shanshan_et_al_P16	p.G244G	ENSG00000206260	ENST00000383163	Transcript
chr6	143605321	143605321	*AIG1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P16	p.G158G	ENSG00000146416	ENST00000357847	Transcript
chr7	92143195	92143195	*PEX1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P16	p.P442P	ENSG00000127980	ENST00000248633	Transcript
chrX	119590602	119590602	*LAMP2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P18	p.L29L	ENSG00000005893	ENST00000434600	Transcript
chr1	85736473	85736473	*BCL10*	Silent	SNP	T	T	G	novel	shanshan_et_al_P19	p.R58R	ENSG00000142867	ENST00000370580	Transcript
chr15	30654739	30654739	*CHRFAM7A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P19	p.H332H	ENSG00000166664	ENST00000299847	Transcript
chr16	1306632	1306632	*TPSD1*	Silent	SNP	C	C	T	rs377281598	shanshan_et_al_P19	p.C66C	ENSG00000095917	ENST00000211076	Transcript
chr2	74881635	74881635	*SEMA4F*	Silent	SNP	G	G	T	novel	shanshan_et_al_P19	p.S44S	ENSG00000135622	ENST00000357877	Transcript
chr4	367528	367528	*ZNF141*	Silent	SNP	A	A	G	novel	shanshan_et_al_P19	p.Q434Q	ENSG00000131127	ENST00000240499	Transcript
chr1	145748355	145748355	*PDZK1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P20	p.R76R	ENSG00000174827	ENST00000344770	Transcript
chr1	206566048	206566048	*SRGAP2*	Silent	SNP	G	G	C	novel	shanshan_et_al_P20	p.V23V	ENSG00000163486	ENST00000414007	Transcript
chr1	53728185	53728185	*LRP8*	Silent	SNP	C	C	A	novel	shanshan_et_al_P20	p.G569G	ENSG00000157193	ENST00000306052	Transcript
chr10	26377242	26377242	*MYO3A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P20	p.Y490Y	ENSG00000095777	ENST00000265944	Transcript
chr11	61732277	61732277	*FTH1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P20	p.K158K	ENSG00000167996	ENST00000273550	Transcript
chr11	62617326	62617326	*CNGA4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P20	p.P236P	ENSG00000132259	ENST00000379936	Transcript
chr12	66622112	66622112	*IRAK3*	Silent	SNP	C	C	T	rs56274029	shanshan_et_al_P20	p.N283N	ENSG00000090376	ENST00000261233	Transcript
chr13	25671398	25671398	*PABPC3*	Silent	SNP	C	C	T	rs77306665	shanshan_et_al_P20	p.N354N	ENSG00000151846	ENST00000281589	Transcript
chr15	28447283	28447283	*HERC2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P20	p.D2531D	ENSG00000128731	ENST00000261609	Transcript
chr16	30939164	30939164	*FBXL19*	Silent	SNP	A	A	C	rs201873980	shanshan_et_al_P20	p.P189P	ENSG00000099364	ENST00000380310	Transcript
chr20	57269630	57269630	*NPEPL1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P20	p.V163V	ENSG00000215440	ENST00000356091	Transcript
chr7	59595955	59595955	*CCZ1*	Silent	SNP	C	C	T	rs148556585	shanshan_et_al_P20	p.S368S	ENSG00000122674	ENST00000325974	Transcript
chr9	116930696	116930696	*COL27A1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P20	p.G287G	ENSG00000196739	ENST00000356083	Transcript
chr1	156941579	156941579	*ARHGEF11*	Silent	SNP	G	G	A	novel	shanshan_et_al_P24	p.P204P	ENSG00000132694	ENST00000368194	Transcript
chr10	6263669	6263669	*PFKFB3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P24	p.R348R	ENSG00000170525	ENST00000379775	Transcript
chr16	48227877	48227877	*ABCC11*	Silent	SNP	G	G	A	novel	shanshan_et_al_P24	p.C807C	ENSG00000121270	ENST00000394747	Transcript
chr3	73114270	73114270	*PPP4R2*	Silent	SNP	a	a	G	novel	shanshan_et_al_P24	p.E302E	ENSG00000163605	ENST00000356692	Transcript
chr4	9223356	9223356	*USP17L12*	Silent	SNP	C	C	A	novel	shanshan_et_al_P24	p.T493T	ENSG00000227551	ENST00000414150	Transcript
chr7	51287614	51287614	*COBL*	Silent	SNP	T	T	G	rs145775268	shanshan_et_al_P24	p.P23P	ENSG00000106078	ENST00000262651	Transcript
chrX	53440365	53440365	*SMC1A*	Silent	SNP	G	G	T	novel	shanshan_et_al_P24	p.A144A	ENSG00000072501	ENST00000322213	Transcript
chr1	157667027	157667027	*FCRL3*	Silent	SNP	G	G	C	novel	shanshan_et_al_P25	p.A249A	ENSG00000160856	ENST00000368184	Transcript
chr1	200977930	200977930	*KIF21B*	Silent	SNP	T	T	A	novel	shanshan_et_al_P25	p.G138G	ENSG00000116852	ENST00000422435	Transcript
chr1	248790325	248790325	*OR2T11*	Silent	SNP	G	G	A	rs189090137	shanshan_et_al_P25	p.A35A	ENSG00000183130	ENST00000330803	Transcript
chr10	29822291	29822291	*SVIL*	Silent	SNP	C	C	A	novel	shanshan_et_al_P25	p.A335A	ENSG00000197321	ENST00000375398	Transcript
chr12	78582472	78582472	*NAV3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P25	p.I1968I	ENSG00000067798	ENST00000536525	Transcript
chr13	42875594	42875594	*AKAP11*	Silent	SNP	A	A	G	novel	shanshan_et_al_P25	p.T904T	ENSG00000023516	ENST00000002531	Transcript
chr19	49657916	49657916	*HRC*	Silent	SNP	t	t	C	rs7409255	shanshan_et_al_P25	p.E193E	ENSG00000130528	ENST00000252825	Transcript
chr19	58017748	58017748	*ZNF773*	Silent	SNP	T	T	A	rs367636585	shanshan_et_al_P25	p.A95A	ENSG00000152439	ENST00000282292	Transcript
chr2	145157359	145157359	*ZEB2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P25	p.Q465Q	ENSG00000169554	ENST00000555810	Transcript
chr2	28761203	28761203	*PLB1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P25	p.G191G	ENSG00000163803	ENST00000327757	Transcript
chr20	48140610	48140610	*PTGIS*	Silent	SNP	C	C	T	novel	shanshan_et_al_P25	p.Q280Q	ENSG00000124212	ENST00000244043	Transcript
chr4	153809456	153809456	*ARFIP1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P25	p.N321N	ENSG00000164144	ENST00000451320	Transcript

chr4	186425697	186425697	*PDLIM3*	Silent	SNP	C	C	A	rs199895839	shanshan_et_al_P25	p.T279T	ENSG00000154553	ENST00000284770	Transcript
chr4	52743962	52743962	*DCUN1D4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P25	p.K95K	ENSG00000109184	ENST00000334635	Transcript
chr5	37187624	37187624	*C5orf42*	Silent	SNP	T	T	A	novel	shanshan_et_al_P25	p.A1324A	ENSG00000197603	ENST00000425232	Transcript
chr6	147527160	147527160	*STXBP5*	Silent	SNP	A	A	G	novel	shanshan_et_al_P25	p.V68V	ENSG00000164506	ENST00000321680	Transcript
chr6	150240933	150240933	*RAET1G*	Silent	SNP	A	A	G	novel	shanshan_et_al_P25	p.Y35Y	ENSG00000203722	ENST00000367360	Transcript
chr7	45123610	45123610	*NACAD*	Silent	SNP	T	T	G	novel	shanshan_et_al_P25	p.T723T	ENSG00000136274	ENST00000490531	Transcript
chrX	122755252	122755252	*THOC2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P25	p.S1324S	ENSG00000125676	ENST00000245838	Transcript
chrX	49957099	49957099	*AKAP4*	Silent	SNP	A	A	C	novel	shanshan_et_al_P25	p.L755L	ENSG00000147081	ENST00000358526	Transcript
chr1	170606900	170606900	*FAM231C*	Silent	SNP	T	T	C	rs201348804	shanshan_et_al_P26	p.Q89Q	ENSG00000268991	ENST00000600179	Transcript
chr1	46751578	46751578	*LRRC41*	Silent	SNP	T	T	G	novel	shanshan_et_al_P26	p.A317A	ENSG00000132128	ENST00000343304	Transcript
chr14	102510811	102510811	*DYNC1H1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P26	p.Q4295Q	ENSG00000197102	ENST00000360184	Transcript
chr17	65914941	65914941	*BPTF*	Silent	SNP	G	G	A	novel	shanshan_et_al_P26	p.G1805G	ENSG00000171634	ENST00000306378	Transcript
chr19	58049962	58049962	*ZNF549*	Silent	SNP	G	G	A	novel	shanshan_et_al_P26	p.E530E	ENSG00000121406	ENST00000376233	Transcript
chr20	10393521	10393521	*MKKS*	Silent	SNP	T	T	C	novel	shanshan_et_al_P26	p.V214V	ENSG00000125863	ENST00000347364	Transcript
chr4	66270163	66270163	*EPHA5*	Silent	SNP	A	A	T	novel	shanshan_et_al_P26	p.P573P	ENSG00000145242	ENST00000273854	Transcript
chr1	53682484	53682484	*C1orf123*	Silent	SNP	C	C	T	novel	shanshan_et_al_P28	p.R103R	ENSG00000162384	ENST00000294360	Transcript
chr12	12380186	12380186	*SBNO1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P28	p.S947S	ENSG00000139697	ENST00000420886	Transcript
chr13	11446924	11446924	*TMEM255B*	Silent	SNP	G	G	T	novel	shanshan_et_al_P28	p.G61G	ENSG00000184497	ENST00000375353	Transcript
chr14	10234984	10234984	*PPP2R5C*	Silent	SNP	C	C	T	novel	shanshan_et_al_P28	p.F224F	ENSG00000078304	ENST00000422945	Transcript
chr14	23893245	23893245	*MYH7*	Silent	SNP	C	C	T	novel	shanshan_et_al_P28	p.E931E	ENSG00000092054	ENST00000355349	Transcript
chr15	30382058	30382058	*GOLGA8J*	Silent	SNP	C	C	A	novel	shanshan_et_al_P28	p.R344R	ENSG00000179938	ENST00000567927	Transcript
chr16	16235069	16235069	*ABCC1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P28	p.G1509G	ENSG00000103222	ENST00000399410	Transcript
chr16	25807780	25807780	*CEMP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P28	p.A99A	ENSG00000205923	ENST00000382350	Transcript
chr17	12877484	12877484	*ARHGAP44*	Silent	SNP	G	G	C	novel	shanshan_et_al_P28	p.P540P	ENSG00000006740	ENST00000379672	Transcript
chr19	36633825	36633825	*CAPNS1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P28	p.S116S	ENSG00000126247	ENST00000246533	Transcript
chr19	41307092	41307092	*EGLN2*	Silent	SNP	C	C	T	rs199636440	shanshan_et_al_P28	p.R205R	ENSG00000269858	ENST00000595726	Transcript
chr19	51165297	51165297	*SHANK1*	Silent	SNP	G	G	A	rs145388631	shanshan_et_al_P28	p.Y2137Y	ENSG00000161681	ENST00000292941	Transcript
chr2	125405360	125405360	*CNTNAP5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P28	p.Q633Q	ENSG00000155052	ENST00000431078	Transcript
chr2	28761203	28761203	*PLB1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P28	p.G191G	ENSG00000163803	ENST00000327757	Transcript
chr2	60688946	60688946	*BCL11A*	Silent	SNP	A	A	G	novel	shanshan_et_al_P28	p.P367P	ENSG00000119866	ENST00000335712	Transcript
chr21	35154395	35154395	*ITSN1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P28	p.R594R	ENSG00000205726	ENST00000381818	Transcript
chr3	52255599	52255599	*TLR9*	Silent	SNP	G	G	A	rs372118821	shanshan_et_al_P28	p.R911R	ENSG00000239732	ENST00000360658	Transcript
chr4	88536166	88536166	*DSPP*	Silent	SNP	T	T	C	novel	shanshan_et_al_P28	p.D784D	ENSG00000152591	ENST00000399271	Transcript
chr5	139231295	139231295	*NRG2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P28	p.R556R	ENSG00000158458	ENST00000361474	Transcript
chr5	140625308	140625308	*PCDHB15*	Silent	SNP	G	G	T	novel	shanshan_et_al_P28	p.L54L	ENSG00000113248	ENST00000231173	Transcript
chr5	159840963	159840963	*SLU7*	Silent	SNP	G	G	A	novel	shanshan_et_al_P28	p.R116R	ENSG00000164609	ENST00000302951	Transcript
chr6	72491866	72491866	*RREB1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P28	p.L1738L	ENSG00000124782	ENST00000379938	Transcript
chr7	157931188	157931188	*PTPRN2*	Silent	SNP	G	G	T	rs569193564	shanshan_et_al_P28	p.L310L	ENSG00000155093	ENST00000389418	Transcript
chr8	144462013	144462013	*RHPN1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P28	p.Y320Y	ENSG00000158106	ENST00000289013	Transcript
chr8	145583704	145583704	*SLC52A2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P28	p.P184P	ENSG00000185803	ENST00000532887	Transcript
chr13	29001983	29001983	*FLT1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P34	p.D394D	ENSG00000102755	ENST00000282397	Transcript

chr19	57133360	57133360	*ZNF71*	Silent	SNP	C	C	T	novel	shanshan_et_al_P34	p.I235I	ENSG00000197951	ENST00000328070	Transcript
chr3	134920360	134920360	*EPHB1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P34	p.L725L	ENSG00000154928	ENST00000398015	Transcript
chr10	134464009	134464009	*INPP5A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P35	p.T102T	ENSG00000068383	ENST00000368594	Transcript
chr10	48236619	48236619	*AGAP9*	Silent	SNP	T	T	C	novel	shanshan_et_al_P35	p.S462S	ENSG00000198035	ENST00000456984	Transcript
chr12	129822359	129822359	*TMEM132D*	Silent	SNP	C	C	T	rs374844718	shanshan_et_al_P35	p.A373A	ENSG00000151952	ENST00000422113	Transcript
chr14	101347295	101347295	*RTL1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P35	p.P1277P	ENSG00000254656	ENST00000534062	Transcript
chr14	34266729	34266729	*NPAS3*	Silent	SNP	C	C	T	rs140754640	shanshan_et_al_P35	p.S456S	ENSG00000151322	ENST00000356141	Transcript
chr8	100844767	100844767	*VPS13B*	Silent	SNP	A	A	C	novel	shanshan_et_al_P35	p.P3192P	ENSG00000132549	ENST00000358544	Transcript
chr12	6887514	6887514	*LAG3*	Silent	SNP	g	g	C	novel	shanshan_et_al_P39	p.P512P	ENSG00000089692	ENST00000203629	Transcript
chr18	74962519	74962519	*GALR1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P39	p.V5V	ENSG00000166573	ENST00000299727	Transcript
chr2	109088922	109088922	*ATP6V1C2*	Silent	SNP	C	C	T	rs201222169	shanshan_et_al_P39	p.Y142Y	ENSG00000143882	ENST00000272238	Transcript
chr3	65425591	65425591	*MAGI1*	Silent	SNP	t	t	C	rs79701778	shanshan_et_al_P39	p.Q411Q	ENSG00000151276	ENST00000402939	Transcript
chr6	30558337	30558337	*ABCF1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P39	p.A799A	ENSG00000204574	ENST00000326195	Transcript
chr1	157660082	157660082	*FCRL3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P41	p.G551G	ENSG00000160856	ENST00000368184	Transcript
chr12	6729407	6729407	*LPAR5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P41	p.A336A	ENSG00000184574	ENST00000329858	Transcript
chr16	4659862	4659862	*UBALD1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P41	p.A102A	ENSG00000153443	ENST00000283474	Transcript
chr17	45234350	45234350	*CDC27*	Silent	SNP	C	C	T	novel	shanshan_et_al_P41	p.Q257Q	ENSG00000004897	ENST00000531206	Transcript
chr18	5395656	5395656	*EPB41L3*	Silent	SNP	C	C	T	rs547679814	shanshan_et_al_P41	p.T1008T	ENSG00000082397	ENST00000341928	Transcript
chr21	27124418	27124418	*GABPA*	Silent	SNP	A	A	G	novel	shanshan_et_al_P41	p.Q142Q	ENSG00000154727	ENST00000354828	Transcript
chr7	5643166	5643166	*FSCN1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P41	p.R343R	ENSG00000075618	ENST00000382361	Transcript
chr8	22009360	22009360	*LGI3*	Silent	SNP	G	G	A	rs73670358	shanshan_et_al_P41	p.F216F	ENSG00000168481	ENST00000306317	Transcript
chrX	47429396	47429396	*ARAF*	Silent	SNP	T	T	G	novel	shanshan_et_al_P41	p.P508P	ENSG00000078061	ENST00000377045	Transcript
chr1	158669801	158669801	*OR6K2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P44	p.L214L	ENSG00000196171	ENST00000359610	Transcript
chr1	45268672	45268672	*PLK3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P44	p.L265L	ENSG00000173846	ENST00000372201	Transcript
chr17	7578177	7578177	*TP53*	Silent	SNP	C	C	T	rs267605076	shanshan_et_al_P44	p.E224E	ENSG00000141510	ENST00000269305	Transcript
chr19	56703300	56703300	*ZSCAN5B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P44	p.V169V	ENSG00000197213	ENST00000586855	Transcript
chr2	113007828	113007828	*ZC3H8*	Silent	SNP	T	T	C	novel	shanshan_et_al_P44	p.T32T	ENSG00000144161	ENST00000409573	Transcript
chr2	180641366	180641366	*SLC25A18*	Silent	SNP	G	G	A	novel	shanshan_et_al_P44	p.L52L	ENSG00000182902	ENST00000327451	Transcript
chr22	36962434	36962434	*CACNG2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P44	p.I134I	ENSG00000166862	ENST00000300305	Transcript
chr5	167693100	167693100	*MYO10*	Silent	SNP	C	C	T	rs373213907	shanshan_et_al_P44	p.T311T	ENSG00000145555	ENST00000513610	Transcript
chr6	129766876	129766876	*LAMA2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P44	p.L2113L	ENSG00000196569	ENST00000421865	Transcript
chr9	117092830	117092830	*ORM2*	Silent	SNP	G	G	T	rs376538069	shanshan_et_al_P44	p.T77T	ENSG00000228278	ENST00000431067	Transcript
chrX	79698068	79698068	*FAM46D*	Silent	SNP	T	T	G	novel	shanshan_et_al_P44	p.T10T	ENSG00000174016	ENST00000538312	Transcript
chr1	109816200	109816200	*CELSR2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.P2884P	ENSG00000143126	ENST00000271332	Transcript
chr1	113257630	113257630	*PPM1J*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.G98G	ENSG00000155367	ENST00000309276	Transcript
chr1	113257684	113257684	*PPM1J*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.L80L	ENSG00000155367	ENST00000309276	Transcript
chr1	113633952	113633952	*LRIG2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.H84H	ENSG00000198799	ENST00000361127	Transcript
chr1	116931616	116931616	*ATP1A1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.A243A	ENSG00000163399	ENST00000537345	Transcript
chr1	145589314	145589314	*NUDT17*	Silent	SNP	A	A	T	rs149964397	shanshan_et_al_P48	p.I38I	ENSG00000186364	ENST00000334513	Transcript
chr1	152080425	152080425	*TCHH*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.R1756R	ENSG00000159450	ENST00000368804	Transcript
chr1	154931489	154931489	*PYGO2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.P329P	ENSG00000163348	ENST00000368457	Transcript

chr1	156646862	156646862	*NES*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.A65A	ENSG00000132688	ENST00000368223	Transcript
chr1	169454864	169454864	*SLC19A2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.R47R	ENSG00000117479	ENST00000236137	Transcript
chr1	177247850	177247850	*BRINP2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.R388R	ENSG00000198797	ENST00000361539	Transcript
chr1	181058413	181058413	*IER5*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.V125V	ENSG00000162783	ENST00000367577	Transcript
chr1	207083113	207083113	*FAIM3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.I314I	ENSG00000162894	ENST00000367091	Transcript
chr1	216405459	216405459	*USH2A*	Silent	SNP	G	G	T	rs397518007	shanshan_et_al_P48	p.G943G	ENSG00000042781	ENST00000307340	Transcript
chr1	252287333	252287333	*RUNX3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.L390L	ENSG00000020633	ENST00000399916	Transcript
chr1	266659000	266659000	*AIM1L*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.I201I	ENSG00000176092	ENST00000527815	Transcript
chr1	407041900	407041900	*RLF*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.S1272S	ENSG00000117000	ENST00000372771	Transcript
chr1	452790511	452790511	*BTBD19*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.V207V	ENSG00000222009	ENST00000450269	Transcript
chr1	457986055	457986055	*MUTYH*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.A160A	ENSG00000132781	ENST00000372098	Transcript
chr1	65318336	65318336	*PLEKHG5*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.S451S	ENSG00000171680	ENST00000537245	Transcript
chr1	746707422	746707422	*FPGT*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.I337I	ENSG00000224685	ENST00000360693	Transcript
chr1	946544778	946544778	*ARHGAP29*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.S532S	ENSG00000137962	ENST00000260526	Transcript
chr10	134942799	134942799	*GPR123*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.G489G	ENSG00000197177	ENST00000392607	Transcript
chr10	48428971	48428971	*GDF10*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.G305G	ENSG00000107623	ENST00000224605	Transcript
chr10	75523678	75523678	*SEC24C*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.A388A	ENSG00000176986	ENST00000339365	Transcript
chr10	76781926	76781926	*KAT6B*	Silent	SNP	a	a	G	novel	shanshan_et_al_P48	p.E1103E	ENSG00000156650	ENST00000287239	Transcript
chr10	81928941	81928941	*ANXA11*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.S115S	ENSG00000122359	ENST00000438331	Transcript
chr10	93999379	93999379	*CPEB3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.N243N	ENSG00000107864	ENST00000265997	Transcript
chr10	97453630	97453630	*TCTN3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.L9L	ENSG00000119977	ENST00000371217	Transcript
chr11	111747600	111747600	*FDXACB1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.G155G	ENSG00000255561	ENST00000260257	Transcript
chr11	118650344	118650344	*DDX6*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.I122I	ENSG00000110367	ENST00000264018	Transcript
chr11	118772958	118772958	*BCL9L*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.G498G	ENSG00000186174	ENST00000334801	Transcript
chr11	119003915	119003915	*HINFP*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.G375G	ENSG00000172273	ENST00000350777	Transcript
chr11	161918412	161918412	*KRTAP5-2*	Silent	SNP	G	G	A	rs36134435	shanshan_et_al_P48	p.G99G	ENSG00000205867	ENST00000412090	Transcript
chr11	365976833	365976833	*RAG1*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.L943L	ENSG00000166349	ENST00000299440	Transcript
chr11	492047900	492047900	*FOLH1*	Silent	SNP	A	A	G	rs76509850	shanshan_et_al_P48	p.Y277Y	ENSG00000086205	ENST00000256999	Transcript
chr11	615392122	615392122	*MYRF*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.A327A	ENSG00000124920	ENST00000278836	Transcript
chr11	645210899	645210899	*PYGM*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.G435G	ENSG00000068976	ENST00000016413	Transcript
chr11	653872855	653872855	*PCNXL3*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.P630P	ENSG00000197136	ENST00000355703	Transcript
chr11	663584477	663584477	*CCDC87*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L680L	ENSG00000182791	ENST00000333861	Transcript
chr11	666104088	666104088	*C11orf80*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.P612P	ENSG00000173715	ENST00000360962	Transcript
chr11	670528944	670528944	*ADRBK1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.V681V	ENSG00000173020	ENST00000308595	Transcript
chr11	672231133	672231133	*CABP4*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.P73P	ENSG00000175544	ENST00000325656	Transcript
chr11	673519778	673519778	*GSTP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.Q27Q	ENSG00000184207	ENST00000398606	Transcript
chr11	751738366	751738366	*GDPD5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.F72F	ENSG00000158555	ENST00000336898	Transcript
chr11	759076544	759076544	*WNT11*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.E64E	ENSG00000085741	ENST00000323263	Transcript
chr11	769166577	769166577	*MYO7A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.A1877A	ENSG00000137474	ENST00000409709	Transcript
chr11	845712584	845712584	*STK33*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.A354A	ENSG00000130413	ENST00000447869	Transcript
chr11	945329338	945329338	*AMOTL1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.A194A	ENSG00000166025	ENST00000433060	Transcript

chr1	9750904	9750904	*SWAP70*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.K268K	ENSG00000133789	ENST00000318950	Transcript
chr12	124288305	124288305	*DNAH10*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.R786R	ENSG00000197653	ENST00000409039	Transcript
chr12	124829156	124829156	*NCOR2*	Silent	SNP	C	C	T	rs193097789	shanshan_et_al_P48	p.P1567P	ENSG00000196498	ENST00000405201	Transcript
chr12	133067384	133067384	*FBRSL1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.S76S	ENSG00000112787	ENST00000434748	Transcript
chr12	279510633	279510633	*KLHL42*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.V494V	ENSG00000087448	ENST00000381271	Transcript
chr12	324805388	324805388	*BICD1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.S383S	ENSG00000151746	ENST00000281474	Transcript
chr12	463423122	463423122	*SCAF11*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.V102V	ENSG00000139218	ENST00000369367	Transcript
chr12	507493677	507493677	*FAM186A*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.D416D	ENSG00000185958	ENST00000327337	Transcript
chr12	575750500	575750500	*LRP1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.R1880R	ENSG00000123384	ENST00000243077	Transcript
chr12	579206833	579206833	*MBD6*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.P585P	ENSG00000166987	ENST00000355673	Transcript
chr12	764001010	764001010	*CD163*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.T665T	ENSG00000177575	ENST00000359156	Transcript
chr12	990198044	990198044	*IKBIP*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.E346E	ENSG00000166130	ENST00000299157	Transcript
chr13	113731509	113731509	*MCF2L*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.S548S	ENSG00000126217	ENST00000535094	Transcript
chr13	32907274	32907274	*BRCA2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.L553L	ENSG00000139618	ENST00000544455	Transcript
chr14	105683882	105683882	*BRF1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.R591R	ENSG00000185024	ENST00000546474	Transcript
chr14	105716694	105716694	*BTBD6*	Silent	SNP	G	G	A	rs375087285	shanshan_et_al_P48	p.G381G	ENSG00000184887	ENST00000392554	Transcript
chr14	33015449	33015449	*AKAP6*	Silent	SNP	A	A	T	rs141344509	shanshan_et_al_P48	p.P530P	ENSG00000151320	ENST00000280979	Transcript
chr14	45564733	45564733	*PRPF39*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.G97G	ENSG00000185246	ENST00000355765	Transcript
chr14	45639913	45639913	*FANCM*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.V708V	ENSG00000187790	ENST00000267430	Transcript
chr14	53019994	53019994	*GPR137C*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.G43G	ENSG00000180998	ENST00000321662	Transcript
chr14	58036654	58036654	*SLC35F4*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.A362A	ENSG00000151812	ENST00000339762	Transcript
chr14	58831189	58831189	*ARID4A*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.G794G	ENSG00000132219	ENST00000355431	Transcript
chr14	60756627	60756627	*PPM1A*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.A425A	ENSG00000100614	ENST00000325642	Transcript
chr14	61451460	61451460	*SLC38A6*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.L83L	ENSG00000139974	ENST00000354886	Transcript
chr14	73577787	73577787	*RBM25*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.I647I	ENSG00000119707	ENST00000261973	Transcript
chr14	77844289	77844289	*SAMD15*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.V176V	ENSG00000100583	ENST00000216471	Transcript
chr14	89629148	89629148	*FOXN3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.S361S	ENSG00000053254	ENST00000345097	Transcript
chr15	41988429	41988429	*MGA*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.T407T	ENSG00000174197	ENST00000219905	Transcript
chr15	41988480	41988480	*MGA*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.E424E	ENSG00000174197	ENST00000219905	Transcript
chr15	42977397	42977397	*STARD9*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.L1207L	ENSG00000159433	ENST00000290607	Transcript
chr15	43816251	43816251	*MAP1A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.E860E	ENSG00000166963	ENST00000300231	Transcript
chr15	45404807	45404807	*DUOX2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.R90R	ENSG00000140279	ENST00000603300	Transcript
chr15	45555416	45555416	*SLC28A2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.N140N	ENSG00000137860	ENST00000347644	Transcript
chr15	51792001	51792001	*DMXL2*	Silent	SNP	G	G	A	rs368031898	shanshan_et_al_P48	p.S1140S	ENSG00000104093	ENST00000543779	Transcript
chr15	57925900	57925900	*GCOM1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.R298R	ENSG00000137878	ENST00000380569	Transcript
chr15	75653996	75653996	*MAN2C1*	Silent	SNP	G	G	T	rs141487118	shanshan_et_al_P48	p.I389I	ENSG00000140400	ENST00000556683	Transcript
chr15	75654023	75654023	*MAN2C1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.L380L	ENSG00000140400	ENST00000556683	Transcript
chr15	89424922	89424922	*HAPLN3*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.T53T	ENSG00000140511	ENST00000359595	Transcript
chr16	11000927	11000927	*CIITA*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.R526R	ENSG00000179583	ENST00000324288	Transcript
chr16	14202527	14202527	*UNKL*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.S485S	ENSG00000059145	ENST00000389221	Transcript
chr16	21441097	21441097	*PKD1*	Silent	SNP	C	C	T	rs572474052	shanshan_et_al_P48	p.A3534A	ENSG00000008710	ENST00000262304	Transcript

chr16	2166895	2166895	*PKD1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.G515G	ENSG00000088710	ENST00000262304	Transcript
chr16	24579131	24579131	*RBBP6*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.K657K	ENSG00000122257	ENST00000319715	Transcript
chr16	2765787	2765787	*PRSS27*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.G56G	ENSG00000172382	ENST00000302641	Transcript
chr16	29845386	29845386	*MVP*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.T192T	ENSG00000013364	ENST00000357402	Transcript
chr16	29888787	29888787	*SEZ6L2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.L572L	ENSG00000174938	ENST00000308713	Transcript
chr16	29999233	29999233	*TAOK2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L1214L	ENSG00000149930	ENST00000308893	Transcript
chr16	48230144	48230144	*ABCC11*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.G801G	ENSG00000121270	ENST00000394747	Transcript
chr16	55601274	55601274	*CAPNS2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.G202G	ENSG00000256812	ENST00000457326	Transcript
chr16	56226240	56226240	*GNAO1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.A31A	ENSG00000087258	ENST00000262494	Transcript
chr16	58589423	58589423	*CNOT1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.R875R	ENSG00000125107	ENST00000317147	Transcript
chr16	66600704	66600704	*CMTM1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.P96P	ENSG00000089505	ENST00000379500	Transcript
chr16	68014188	68014188	*DPEP3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.P57P	ENSG00000141096	ENST00000268793	Transcript
chr16	745843	745843	*FBXL16*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.S238S	ENSG00000127585	ENST00000397621	Transcript
chr16	85690255	85690255	*GSE1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.L432L	ENSG00000131149	ENST00000253458	Transcript
chr16	85695026	85695026	*GSE1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.R639R	ENSG00000131149	ENST00000253458	Transcript
chr17	1183553	1183553	*TUSC5*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.A86A	ENSG00000184811	ENST00000333813	Transcript
chr17	18061118	18061118	*MYO15A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.L2957L	ENSG00000091536	ENST00000205890	Transcript
chr17	18150992	18150992	*FLII*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.S822S	ENSG00000177731	ENST00000327031	Transcript
chr17	26800748	26800748	*SLC13A2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.Q6Q	ENSG00000007216	ENST00000444914	Transcript
chr17	26906833	26906833	*SPAG5*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.P940P	ENSG00000076382	ENST00000321765	Transcript
chr17	27085546	27085546	*FAM222B*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.G477G	ENSG00000173065	ENST00000341217	Transcript
chr17	33464585	33464585	*NLE1*	Silent	SNP	G	G	C	rs147948223	shanshan_et_al_P48	p.G204G	ENSG00000073536	ENST00000442241	Transcript
chr17	38296888	38296888	*CASC3*	Silent	SNP	g	g	C	novel	shanshan_et_al_P48	p.P29P	ENSG00000108349	ENST00000264645	Transcript
chr17	39550271	39550271	*KRT31*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.R416R	ENSG00000094796	ENST00000225245	Transcript
chr17	49338245	49338245	*UTP18*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.E100E	ENSG00000101260	ENST00000225298	Transcript
chr17	56247931	56247931	*OR4D2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.R305R	ENSG00000255713	ENST00000545221	Transcript
chr17	58469292	58469292	*USP32*	Silent	SNP	G	G	C	rs376214408	shanshan_et_al_P48	p.A3A	ENSG00000170832	ENST00000300896	Transcript
chr17	65909166	65909166	*BPTF*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.V1722V	ENSG00000171634	ENST00000306378	Transcript
chr17	72264394	72264394	*NEURL4*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.G807G	ENSG00000215041	ENST00000399464	Transcript
chr17	73813520	73813520	*UNK*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.G406G	ENSG00000132478	ENST00000589666	Transcript
chr17	74004447	74004447	*EVPL*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.L1613L	ENSG00000167880	ENST00000303607	Transcript
chr17	80132528	80132528	*ALOXE3*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.P590P	ENSG00000179148	ENST00000318227	Transcript
chr17	83476198	83476198	*NDEL1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.S10S	ENSG00000166579	ENST00000334527	Transcript
chr18	28720064	28720064	*DSC1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.G487G	ENSG00000134765	ENST00000257198	Transcript
chr19	10202170	10202170	*C19orf66*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.G169G	ENSG00000130813	ENST00000253110	Transcript
chr19	12807054	12807054	*FBXW9*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.V114V	ENSG00000132004	ENST00000393261	Transcript
chr19	12807108	12807108	*FBXW9*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.A96A	ENSG00000132004	ENST00000393261	Transcript
chr19	13873558	13873558	*CCDC130*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.T289T	ENSG00000104957	ENST00000558660	Transcript
chr19	14001210	14001210	*C19orf57*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.V153V	ENSG00000132016	ENST00000346736	Transcript
chr19	15220525	15220525	*SYDE1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.P147P	ENSG00000105137	ENST00000342784	Transcript
chr19	17650546	17650546	*FAM129C*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.Q348Q	ENSG00000167483	ENST00000333593	Transcript

chr19	18546276	18546276	*ISYNA1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.A424A	ENSG00000105655	ENST00000338128	Transcript
chr19	19625466	19625466	*TSSK6*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.S257S	ENSG00000178093	ENST00000360913	Transcript
chr19	19656778	19656778	*CILP2*	Silent	SNP	C	C	A	rs577556072	shanshan_et_al_P48	p.R1142R	ENSG00000160161	ENST00000291495	Transcript
chr19	22497225	22497225	*ZNF729*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.R336R	ENSG00000196350	ENST00000601693	Transcript
chr19	22908942	22908942	*LINGO3*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.V294V	ENSG00000220008	ENST00000585527	Transcript
chr19	33072204	33072204	*PDCD5*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.R13R	ENSG00000105185	ENST00000590247	Transcript
chr19	36431191	36431191	*LRFN3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.E288E	ENSG00000126243	ENST00000588831	Transcript
chr19	36674631	36674631	*ZNF565*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L79L	ENSG00000196357	ENST00000392173	Transcript
chr19	38713189	38713189	*DPF1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.P90P	ENSG00000101332	ENST00000355526	Transcript
chr19	39591629	39591629	*DAPK3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.V434V	ENSG00000167657	ENST00000545797	Transcript
chr19	39591809	39591809	*DAPK3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.A428A	ENSG00000167657	ENST00000545797	Transcript
chr19	39798369	39798369	*LRFN1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.G740G	ENSG00000128011	ENST00000248668	Transcript
chr19	39798513	39798513	*LRFN1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.G692G	ENSG00000128011	ENST00000248668	Transcript
chr19	39911626	39911626	*PLEKHG2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.R479R	ENSG00000090924	ENST00000409794	Transcript
chr19	46215359	46215359	*FBXO46*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.R465R	ENSG00000177051	ENST00000317683	Transcript
chr19	46215956	46215956	*FBXO46*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.S266S	ENSG00000177051	ENST00000317683	Transcript
chr19	50979418	50979418	*FAM71E1*	Silent	SNP	T	T	A	rs577788365	shanshan_et_al_P48	p.G76G	ENSG00000142530	ENST00000559590	Transcript
chr19	51135932	51135932	*SYT3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.P95P	ENSG00000213023	ENST00000338916	Transcript
chr19	52861161	52861161	*PTPRS*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.V12V	ENSG00000105426	ENST00000357368	Transcript
chr19	55686573	55686573	*SYT5*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.A225A	ENSG00000129990	ENST00000354308	Transcript
chr19	55686588	55686588	*SYT5*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.G220G	ENSG00000129990	ENST00000354308	Transcript
chr19	56090223	56090223	*ZNF579*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.G261G	ENSG00000218891	ENST00000325421	Transcript
chr19	58858921	58858921	*A1BG*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.P426P	ENSG00000121410	ENST00000263100	Transcript
chr19	64546846	64546846	*SLC25A23*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.S176S	ENSG00000125648	ENST00000301454	Transcript
chr19	67071216	67071216	*C3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.Q737Q	ENSG00000125730	ENST00000245907	Transcript
chr19	77949088	77949088	*CLEC4G*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.E208E	ENSG00000182566	ENST00000328853	Transcript
chr2	113955392	113955392	*PSD4*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.V842V	ENSG00000125637	ENST00000245796	Transcript
chr2	183105010	183105010	*PDE1A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.L75L	ENSG00000115252	ENST00000435564	Transcript
chr2	186603438	186603438	*FSIP2*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.R28R	ENSG00000188738	ENST00000343098	Transcript
chr2	186654992	186654992	*FSIP2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.F1132F	ENSG00000188738	ENST00000343098	Transcript
chr2	186673167	186673167	*FSIP2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.L6467L	ENSG00000188738	ENST00000343098	Transcript
chr2	201437373	201437373	*SGOL2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.A768A	ENSG00000163535	ENST00000357799	Transcript
chr2	220435022	220435022	*OBSL1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.A311A	ENSG00000124006	ENST00000404537	Transcript
chr2	233350836	233350836	*ECEL1*	Silent	SNP	g	g	A	novel	shanshan_et_al_P48	p.A176A	ENSG00000171551	ENST00000330546	Transcript
chr2	233350929	233350929	*ECEL1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.L145L	ENSG00000171551	ENST00000330546	Transcript
chr2	241534101	241534101	*CAPN10*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.A324A	ENSG00000142330	ENST00000393184	Transcript
chr2	242743542	242743542	*GAL3ST2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.P386P	ENSG00000154252	ENST00000191923	Transcript
chr2	45808925	45808925	*SRBD1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.S280S	ENSG00000068784	ENST00000263736	Transcript
chr2	50149355	50149355	*NRXN1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.Y1457Y	ENSG00000179915	ENST00000404971	Transcript
chr2	54482617	54482617	*TSPYL6*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.L224L	ENSG00000178021	ENST00000317802	Transcript
chr2	54857104	54857104	*SPTBN1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.L915L	ENSG00000115306	ENST00000356805	Transcript

chr2	97427813	97427813	*CNNM4*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L359L	ENSG00000158158	ENST00000377075	Transcript
chr20	25457575	25457575	*NINL*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.A784A	ENSG00000101004	ENST00000278886	Transcript
chr20	33874908	33874908	*FAM83C*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.L558L	ENSG00000125998	ENST00000374408	Transcript
chr20	34263084	34263084	*NFS1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.R277R	ENSG00000244005	ENST00000374092	Transcript
chr20	34521233	34521233	*ATRN*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.G123G	ENSG00000088812	ENST00000262919	Transcript
chr20	34828450	34828450	*AAR2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.A220A	ENSG00000131043	ENST00000373932	Transcript
chr20	35060255	35060255	*DLGAP4*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.R45R	ENSG00000080845	ENST00000373913	Transcript
chr20	36625715	36625715	*ADAM33*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.G27G	ENSG00000149451	ENST00000356518	Transcript
chr20	60218695	60218695	*LRRN4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.F674F	ENSG00000125872	ENST00000378858	Transcript
chr20	60333595	60333595	*LRRN4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.R29R	ENSG00000125872	ENST00000378858	Transcript
chr21	47821507	47821507	*PCNT*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L1612L	ENSG00000160299	ENST00000359568	Transcript
chr22	17600377	17600377	*CECR6*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.P547P	ENSG00000183307	ENST00000331437	Transcript
chr22	17601004	17601004	*CECR6*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.L338L	ENSG00000183307	ENST00000331437	Transcript
chr22	18301251	18301251	*MICAL3*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.P1392P	ENSG00000243156	ENST00000441493	Transcript
chr22	19968814	19968814	*ARVCF*	Silent	SNP	G	G	A	rs372801506	shanshan_et_al_P48	p.D272D	ENSG00000099889	ENST00000263207	Transcript
chr22	20100738	20100738	*TRMT2A*	Silent	SNP	G	G	A	rs373087127	shanshan_et_al_P48	p.F484F	ENSG00000099899	ENST00000252136	Transcript
chr22	42177730	42177730	*MEI1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L990L	ENSG00000167077	ENST00000401548	Transcript
chr22	51065762	51065762	*ARSA*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.R99R	ENSG00000100299	ENST00000216124	Transcript
chr3	113890819	113890819	*DRD3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L7L	ENSG00000151577	ENST00000383673	Transcript
chr3	124456962	124456962	*UMPS*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.I286I	ENSG00000114491	ENST00000232607	Transcript
chr3	147114201	147114201	*ZIC4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.V92V	ENSG00000174963	ENST00000525172	Transcript
chr3	160156078	160156078	*TRIM59*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.K298K	ENSG00000213186	ENST00000309784	Transcript
chr3	184041339	184041339	*EIF4G1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.D751D	ENSG00000114867	ENST00000424196	Transcript
chr3	194362854	194362854	*LSG1*	Silent	SNP	A	A	G	rs144371439	shanshan_et_al_P48	p.H640H	ENSG00000041802	ENST00000265245	Transcript
chr3	2908611	2908611	*CNTN4*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.T210T	ENSG00000144619	ENST00000397461	Transcript
chr3	32611890	32611890	*DYNC1LI1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.V56V	ENSG00000144635	ENST00000273130	Transcript
chr3	36780133	36780133	*DCLK3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.L6L	ENSG00000163673	ENST00000416516	Transcript
chr3	48460755	48460755	*PLXNB1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.A910A	ENSG00000164050	ENST00000358536	Transcript
chr3	87309236	87309236	*POU1F1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.A254A	ENSG00000064835	ENST00000344265	Transcript
chr4	102942727	102942727	*BANK1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.A421A	ENSG00000153064	ENST00000322953	Transcript
chr4	104119462	104119462	*CENPE*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.G5G	ENSG00000138778	ENST00000265148	Transcript
chr4	106395118	106395118	*PPA2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.R30R	ENSG00000138777	ENST00000341695	Transcript
chr4	128996124	128996124	*LARP1B*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.T6T	ENSG00000138709	ENST00000326639	Transcript
chr4	144621694	144621694	*FREM3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.Y45Y	ENSG00000183090	ENST00000329798	Transcript
chr4	144621763	144621763	*FREM3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.L22L	ENSG00000183090	ENST00000329798	Transcript
chr4	151850140	151850140	*LRBA*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.L98L	ENSG00000198589	ENST00000357115	Transcript
chr4	153864431	153864431	*FHDC1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.P74P	ENSG00000137460	ENST00000511601	Transcript
chr4	248241800	248241800	*CCDC149*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.R327R	ENSG00000181982	ENST00000504487	Transcript
chr4	71508337	71508337	*ENAM*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.P398P	ENSG00000132464	ENST00000396073	Transcript
chr4	77631342	77631342	*SHROOM3*	Silent	SNP	T	T	C	rs377175218	shanshan_et_al_P48	p.T119T	ENSG00000138771	ENST00000296043	Transcript
chr4	77676313	77676313	*SHROOM3*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.L1559L	ENSG00000138771	ENST00000296043	Transcript

chr4	860856	860856	*GAK*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.A920A	ENSG00000178950	ENST00000314167	Transcript
chr5	1038314	1038314	*NKD2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.S394S	ENSG00000145506	ENST00000296849	Transcript
chr5	108382808	108382808	*FER*	Silent	SNP	T	T	C	rs144241765	shanshan_et_al_P48	p.I611I	ENSG00000151422	ENST00000281092	Transcript
chr5	134914499	134914499	*CXCL14*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.S2S	ENSG00000145824	ENST00000337225	Transcript
chr5	139743713	139743713	*SLC4A9*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.T467T	ENSG00000113073	ENST00000230993	Transcript
chr5	140626019	140626019	*PCDHB15*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.P291P	ENSG00000113248	ENST00000231173	Transcript
chr5	140626037	140626037	*PCDHB15*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.L297L	ENSG00000113248	ENST00000231173	Transcript
chr5	145647244	145647244	*RBM27*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.I788I	ENSG00000091009	ENST00000265271	Transcript
chr5	146777328	146777328	*DPYSL3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.L568L	ENSG00000113657	ENST00000343218	Transcript
chr5	150110697	150110697	*DCTN4*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.Q218Q	ENSG00000132912	ENST00000446090	Transcript
chr5	153406044	153406044	*FAM114A2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.L276L	ENSG00000055147	ENST00000351797	Transcript
chr5	172550192	172550192	*CREBRF*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.I597I	ENSG00000164463	ENST00000296953	Transcript
chr5	173416404	173416404	*C5orf47*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.G46G	ENSG00000185056	ENST00000340147	Transcript
chr5	66461613	66461613	*MAST4*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.P2202P	ENSG00000069020	ENST00000403625	Transcript
chr5	76926230	76926230	*OTP*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.A279A	ENSG00000171540	ENST00000306422	Transcript
chr6	110942487	110942487	*CDK19*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.Q399Q	ENSG00000155111	ENST00000368911	Transcript
chr6	123851694	123851694	*TRDN*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.K147K	ENSG00000186439	ENST00000398178	Transcript
chr6	131941016	131941016	*MED23*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.S206S	ENSG00000112282	ENST00000368068	Transcript
chr6	24436900	24436900	*GPLD1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.E754E	ENSG00000112293	ENST00000230036	Transcript
chr6	37250070	37250070	*TBC1D22B*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.P177P	ENSG00000065491	ENST00000373491	Transcript
chr6	53520056	53520056	*KLHL31*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.K5K	ENSG00000124743	ENST00000370905	Transcript
chr7	100086493	100086493	*NYAP1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.P383P	ENSG00000166924	ENST00000300179	Transcript
chr7	100466428	100466428	*TRIP6*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.E225E	ENSG00000087077	ENST00000200457	Transcript
chr7	102416767	102416767	*CYP2W1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.D98D	ENSG00000073067	ENST00000308919	Transcript
chr7	158282434	158282434	*PTPRN2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.C52C	ENSG00000155093	ENST00000389418	Transcript
chr7	32598608	32598608	*AVL9*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.G249G	ENSG00000105778	ENST00000318709	Transcript
chr7	42950161	42950161	*C7orf25*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.G171G	ENSG00000136197	ENST00000431882	Transcript
chr7	48018409	48018409	*HUS1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.I19I	ENSG00000136273	ENST00000258774	Transcript
chr7	75864507	75864507	*SRRM3*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.A41A	ENSG00000177679	ENST00000326382	Transcript
chr7	92732615	92732615	*SAMD9*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.T932T	ENSG00000205413	ENST00000379958	Transcript
chr8	103373424	103373424	*UBR5*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.L40L	ENSG00000104517	ENST00000520539	Transcript
chr8	125868200	125868200	*LONRF1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.I570I	ENSG00000154359	ENST00000398246	Transcript
chr8	126071725	126071725	*KIAA0196*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.T527T	ENSG00000164961	ENST00000318410	Transcript
chr8	144378460	144378460	*ZNF696*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.G205G	ENSG00000185730	ENST00000330143	Transcript
chr8	144801003	144801003	*MAPK15*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.R115R	ENSG00000181085	ENST00000338033	Transcript
chr8	144803831	144803831	*MAPK15*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.L439L	ENSG00000181085	ENST00000338033	Transcript
chr8	146033246	146033246	*ZNF517*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.R315R	ENSG00000197363	ENST00000359971	Transcript
chr8	38250492	38250492	*LETM2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.L113L	ENSG00000165046	ENST00000523983	Transcript
chr8	67577171	67577171	*VCPIP1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P48	p.R675R	ENSG00000175073	ENST00000310421	Transcript
chr8	68075993	68075993	*CSPP1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.S885S	ENSG00000104218	ENST00000262210	Transcript
chr8	87490210	87490210	*MFHAS1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.V516V	ENSG00000147324	ENST00000276282	Transcript

chr9	110249754	110249754	*KLF4*	Silent	SNP	C	C	G	novel	shanshan_et_al_P48	p.L307L	ENSG00000136826	ENST00000374672	Transcript
chr9	131591054	131591054	*C9orf114*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.R56R	ENSG00000198917	ENST00000361256	Transcript
chr9	131760819	131760819	*NUP188*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.L1144L	ENSG00000095319	ENST00000372577	Transcript
chr9	139372026	139372026	*SEC16A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.G14G	ENSG00000148396	ENST00000313050	Transcript
chr9	139840115	139840115	*C8G*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.V56V	ENSG00000176919	ENST00000224181	Transcript
chr9	139887131	139887131	*C9orf142*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.T53T	ENSG00000148362	ENST00000371620	Transcript
chr9	140007249	140007249	*DPP7*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.C293C	ENSG00000176978	ENST00000371579	Transcript
chr9	140115413	140115413	*RNF208*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.A84A	ENSG00000212864	ENST00000392827	Transcript
chr9	33463058	33463058	*NOL6*	Silent	SNP	G	G	T	novel	shanshan_et_al_P48	p.P1036P	ENSG00000165271	ENST00000455041	Transcript
chr9	80881552	80881552	*CEP78*	Silent	SNP	A	A	T	novel	shanshan_et_al_P48	p.G681G	ENSG00000148019	ENST00000376597	Transcript
chr9	91996211	91996211	*SEMA4D*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.P499P	ENSG00000187764	ENST00000450295	Transcript
chr9	96422680	96422680	*PHF2*	Silent	SNP	t	t	C	novel	shanshan_et_al_P48	p.P512P	ENSG00000197724	ENST00000359246	Transcript
chrX	100547866	100547866	*TAF7L*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.Q56Q	ENSG00000102387	ENST00000372907	Transcript
chrX	103432954	103432954	*FAM199X*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.S321S	ENSG00000123575	ENST00000449342	Transcript
chrX	117815734	117815734	*DOCK11*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.V1980V	ENSG00000147251	ENST00000427602	Transcript
chrX	119077488	119077488	*NKAP*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.S27S	ENSG00000101882	ENST00000371410	Transcript
chrX	119676867	119676867	*CUL4B*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.V444V	ENSG00000158290	ENST00000404115	Transcript
chrX	132436952	132436952	*GPC4*	Silent	SNP	G	G	C	novel	shanshan_et_al_P48	p.A538A	ENSG00000076716	ENST00000370828	Transcript
chrX	133379248	133379248	*CCDC160*	Silent	SNP	A	A	C	novel	shanshan_et_al_P48	p.R140R	ENSG00000203952	ENST00000517294	Transcript
chrX	153039093	153039093	*PLXNB3*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.P1091P	ENSG00000198753	ENST00000538966	Transcript
chrX	153174938	153174938	*ARHGAP4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P48	p.G862G	ENSG00000089820	ENST00000370028	Transcript
chrX	153431600	153431600	*PIGA*	Silent	SNP	T	T	A	novel	shanshan_et_al_P48	p.A321A	ENSG00000165195	ENST00000333590	Transcript
chrX	153533767	153533767	*TKTL1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.L82L	ENSG00000007350	ENST00000369915	Transcript
chrX	155742374	155742374	*BMX*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.S664S	ENSG00000102010	ENST00000357607	Transcript
chrX	186748555	186748555	*RS1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.Y34Y	ENSG00000102104	ENST00000379984	Transcript
chrX	41333915	41333915	*NYX*	Silent	SNP	A	A	G	novel	shanshan_et_al_P48	p.P403P	ENSG00000188937	ENST00000342595	Transcript
chrX	45051137	45051137	*CXorf36*	Silent	SNP	T	T	C	novel	shanshan_et_al_P48	p.K119K	ENSG00000147113	ENST00000398000	Transcript
chrX	50438815	50438815	*SHROOM4*	Silent	SNP	G	G	A	novel	shanshan_et_al_P48	p.S80S	ENSG00000158352	ENST00000376020	Transcript
chrX	69255291	69255291	*EDA*	Silent	SNP	C	C	T	novel	shanshan_et_al_P48	p.I336I	ENSG00000158813	ENST00000374552	Transcript
chr1	186276186	186276186	*PRG4*	Silent	SNP	A	A	C	rs529978025	shanshan_et_al_P50	p.P445P	ENSG00000116690	ENST00000445192	Transcript
chr2	183867979	183867979	*NCKAP1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P50	p.V104V	ENSG00000061676	ENST00000360982	Transcript
chr21	40555216	40555216	*PSMG1*	Silent	SNP	G	G	T	rs371137353	shanshan_et_al_P50	p.P32P	ENSG00000183527	ENST00000331573	Transcript
chr5	1294023	1294023	*TERT*	Silent	SNP	G	G	T	novel	shanshan_et_al_P50	p.A326A	ENSG00000164362	ENST00000310581	Transcript
chr1	47075713	47075713	*MOB3C*	Silent	SNP	G	G	A	rs201064368	shanshan_et_al_P51	p.R246R	ENSG00000142961	ENST00000271139	Transcript
chr1	77510056	77510056	*ST6GALNAC5*	Silent	SNP	C	C	A	novel	shanshan_et_al_P51	p.V143V	ENSG00000117069	ENST00000477717	Transcript
chr10	33113486	33113486	*C10ORF68*	Silent	SNP	A	A	G	rs200418217	shanshan_et_al_P51	p.T321T	ENSG00000150076	ENST00000375028	Transcript
chr11	122944224	122944224	*CLMP*	Silent	SNP	G	G	T	novel	shanshan_et_al_P51	p.P360P	ENSG00000166250	ENST00000448775	Transcript
chr17	74474996	74474996	*RHBDF2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P51	p.L217L	ENSG00000129667	ENST00000313080	Transcript
chr4	190947588	190947588	*FRG2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P51	p.N94N	ENSG00000205097	ENST00000378763	Transcript
chr8	101178075	101178075	*SPAG1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P51	p.T58T	ENSG00000104450	ENST00000388798	Transcript
chr8	143624772	143624772	*BAI1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P51	p.K1474K	ENSG00000181790	ENST00000517894	Transcript

chr9	140087030	140087030	*TPRN*	Silent	SNP	C	C	T	rs149705183	shanshan_et_al_P51	p.E613E	ENSG00000176058	ENST00000409012	Transcript	
chr12	7343153	7343153	*PEX5*	Silent	SNP	A	A	G	novel	shanshan_et_al_P52	p.A60A	ENSG00000139197	ENST00000434354	Transcript	
chr14	32561159	32561159	*ARHGAP5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P52	p.V428V	ENSG00000100852	ENST00000345122	Transcript	
chr14	95669526	95669526	*CLMN*	Silent	SNP	G	G	T	rs377316318	shanshan_et_al_P52	p.S720S	ENSG00000165959	ENST00000298912	Transcript	
chr17	61910486	61910486	*SMARCD2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P52	p.A495A	ENSG00000108604	ENST00000448276	Transcript	
chr2	86831392	86831392	*RNF103*	Silent	SNP	T	T	G	novel	shanshan_et_al_P52	p.T544T	ENSG00000239305	ENST00000237455	Transcript	
chr3	65425591	65425591	*MAGI1*	Silent	SNP	t	t	C	rs79701778	shanshan_et_al_P52	p.Q411Q	ENSG00000151276	ENST00000402939	Transcript	
chr5	140574441	140574441	*PCDHB10*	Silent	SNP	T	T	A	novel	shanshan_et_al_P52	p.V772V	ENSG00000120324	ENST00000239446	Transcript	
chr5	51878945	51878945	*ADAMTS16*	Silent	SNP	A	A	T	novel	shanshan_et_al_P52	p.V340V	ENSG00000145536	ENST00000274181	Transcript	
chr6	38862563	38862563	*DNAH8*	Silent	SNP	A	A	T	novel	shanshan_et_al_P52	p.I2673I	ENSG00000124721	ENST00000359357	Transcript	
chr1	12978377	12978377	*PRAMEF7*	Silent	SNP	C	C	T	novel	shanshan_et_al_P53	p.C161C	ENSG00000204510	ENST00000361079	Transcript	
chr1	13388838	13388838	*PRAMEF8*	Silent	SNP	G	G	A	novel	shanshan_et_al_P53	p.C161C	ENSG00000182330	ENST00000357367	Transcript	
chr12	11353132	11353132	*DTX1*	Silent	SNP	C	C	T	rs536396846	shanshan_et_al_P53	p.G517G	ENSG00000135144	ENST00000257600	Transcript	
chr15	70386901	70386901	*TLE3*	Silent	SNP	G	G	T	rs569173982	shanshan_et_al_P53	p.S68S	ENSG00000140332	ENST00000558939	Transcript	
chr16	67696157	67696157	*PARD6A*	Silent	SNP	C	C	A	rs375500965	shanshan_et_al_P53	p.L216L	ENSG00000102981	ENST00000219255	Transcript	
chr16	8952269	8952269	*CARHSP1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P53	p.S73S	ENSG00000153048	ENST00000396593	Transcript	
chr17	17700957	17700957	*RAI1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P53	p.V1565V	ENSG00000108557	ENST00000353383	Transcript	
chr19	57286803	57286803	*ZIM2*	Silent	SNP	C	C	T	rs191866455	shanshan_et_al_P53	p.P279P	ENSG00000269699	ENST00000391708	Transcript	
chr21	46011655	46011655	*KRTAP10-6*	Silent	SNP	C	C	G	novel	shanshan_et_al_P53	p.V237V	ENSG00000188155	ENST00000400368	Transcript	
chr22	37769496	37769496	*ELFN2*	Silent	SNP	G	G	C	novel	shanshan_et_al_P53	p.G693G	ENSG00000166897	ENST00000402918	Transcript	
chr22	38895436	38895436	*DDX17*	Silent	SNP	G	G	A	novel	shanshan_et_al_P53	p.P169P	ENSG00000100201	ENST00000396821	Transcript	
chr5	36679852	36679852	*SLC1A3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P53	p.H328H	ENSG00000079215	ENST00000265113	Transcript	
chr6	10695230	10695230	*PAK1IP1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P53	p.V4V	ENSG00000111845	ENST00000379568	Transcript	
chr7	57522840	57522840	*ZNF716*	Silent	SNP	T	T	C	novel	shanshan_et_al_P53	p.N76N	ENSG00000182111	ENST00000420713	Transcript	
chr8	10469346	10469346	*RP1L1*	Silent	SNP	C	C	T	rs185177994	shanshan_et_al_P53	p.P754P	ENSG00000183638	ENST00000382483	Transcript	
chr8	65527782	65527782	*CYP7B1*	Silent	SNP	A	A	G	novel	shanshan_et_al_P53	p.H286H	ENSG00000172817	ENST00000310193	Transcript	
chr9	140087045	140087045	*TPRN*	Silent	SNP	C	C	T	rs76275509	shanshan_et_al_P53	p.E608E	ENSG00000176058	ENST00000409012	Transcript	
chr9	187777800	187777800	*ADAMTSL1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P53	p.L1185L	ENSG00000178031	ENST00000380548	Transcript	
chr1	130356300	130356300	*PRAMEF22*	Silent	SNP	T	T	C	novel	shanshan_et_al_P56	p.L30L	ENSG00000204508	ENST00000376187	Transcript	
chr12	56109880	56109880	*RP11-644F5.10*	Silent	SNP	G	G	A	novel	shanshan_et_al_P56	p.R15R	ENSG00000258311	ENST00000550412	Transcript	
chr9	43861205	43861205	*CNTNAP3B*	Silent	SNP	A	A	C	rs571362831	shanshan_et_al_P56	p.R693R	ENSG00000154529	ENST00000377564	Transcript	
chrX	69385729	69385729	*IGBP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P56	p.K306K	ENSG00000089289	ENST00000342206	Transcript	
chr1	13450642	13450642	*PRAMEF13*	Silent	SNP	A	A	T	novel	shanshan_et_al_P58	p.P65P	ENSG00000204495	ENST00000376132	Transcript	
chr1	207072737	207072737	*IL24*	Silent	SNP	C	C	A	novel	shanshan_et_al_P58	p.T40T	ENSG00000162892	ENST00000391929	Transcript	
chr1	41094539	41094539	*RIMS3*	Silent	SNP	A	A	G	novel	shanshan_et_al_P58	p.D219D	ENSG00000117016	ENST00000372684	Transcript	
chr1	53544202	53544202	*PODN*	Silent	SNP	G	G	A	novel	shanshan_et_al_P58	p.L388L	ENSG00000174348	ENST00000313253	Transcript	
chr10	81319120	81319120	*SFTPA2*	Silent	SNP	G	G	C	novel	shanshan_et_al_P58	p.G40G	ENSG00000185303	ENST00000372325	Transcript	
chr11	56237071	56237071	*OR5M3*	Silent	SNP	T	T	C	novel	shanshan_et_al_P58	p.K301K	ENSG00000174937	ENST00000312240	Transcript	
chr12	58089821	58089821	*OS9*	Silent	SNP	G	G	A	novel	shanshan_et_al_P58	p.K160K	ENSG00000135506	ENST00000315970	Transcript	
chr12	96707168	96707168	*CDK17*	Silent	SNP	T	T	C	novel	shanshan_et_al_P58	p.S116S	ENSG00000059758	ENST00000261211	Transcript	
chr15	91035806	91035806	*IQGAP1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P58	p.Q1497Q	ENSG00000140575	ENST00000268182	Transcript	

chr2	109383358	109383358	*RANBP2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P58	p.Q2121Q	ENSG00000153201	ENST00000283195	Transcript
chr2	220333672	220333672	*SPEG*	Silent	SNP	G	G	A	novel	shanshan_et_al_P58	p.E1131E	ENSG00000072195	ENST00000312358	Transcript
chr20	9624935	9624935	*PAK7*	Silent	SNP	C	C	T	rs370805526	shanshan_et_al_P58	p.P14P	ENSG00000101349	ENST00000378429	Transcript
chr3	776513711	776513711	*ROBO2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P58	p.P971P	ENSG00000185008	ENST00000487694	Transcript
chr4	108574771	108574771	*PAPSS1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P58	p.E371E	ENSG00000138801	ENST00000265174	Transcript
chr5	127686642	127686642	*FBN2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P58	p.N910N	ENSG00000138829	ENST00000508053	Transcript
chr5	141243670	141243670	*PCDH1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P58	p.E742E	ENSG00000156453	ENST00000287008	Transcript
chr5	149361085	149361085	*SLC26A2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P58	p.P643P	ENSG00000155850	ENST00000286298	Transcript
chr6	159166544	159166544	*SYTL3*	Silent	SNP	A	A	T	novel	shanshan_et_al_P58	p.T296T	ENSG00000164674	ENST00000297239	Transcript
chr7	93519584	93519584	*TFPI2*	Silent	SNP	G	G	T	rs372277275	shanshan_et_al_P58	p.R46R	ENSG00000105825	ENST00000222543	Transcript
chr1	161176249	161176249	*NDUFS2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P60	p.G85G	ENSG00000158864	ENST00000367993	Transcript
chr19	44933054	44933054	*ZNF229*	Silent	SNP	G	G	C	novel	shanshan_et_al_P60	p.G634G	ENSG00000167383	ENST00000588931	Transcript
chr7	44084393	44084393	*DBNL*	Silent	SNP	G	G	T	novel	shanshan_et_al_P60	p.V19V	ENSG00000136279	ENST00000469494	Transcript
chrX	48318131	48318131	*SLC38A5*	Silent	SNP	G	G	T	novel	shanshan_et_al_P60	p.I400I	ENSG00000017483	ENST00000376876	Transcript
chr17	74068486	74068486	*SRP68*	Silent	SNP	A	A	C	novel	shanshan_et_al_P61	p.G29G	ENSG00000167881	ENST00000307877	Transcript
chr19	22574900	22574900	*ZNF98*	Silent	SNP	C	C	T	rs62118622	shanshan_et_al_P61	p.K379K	ENSG00000197360	ENST00000357774	Transcript
chr3	153998553	153998553	*DHX36*	Silent	SNP	T	T	C	novel	shanshan_et_al_P61	p.S825S	ENSG00000174953	ENST00000496811	Transcript
chr1	152279994	152279994	*FLG*	Silent	SNP	T	T	C	novel	shanshan_et_al_P63	p.Q2456Q	ENSG00000143631	ENST00000368799	Transcript
chr2	165986510	165986510	*SCN3A*	Silent	SNP	G	G	A	novel	shanshan_et_al_P63	p.V954V	ENSG00000153253	ENST00000283254	Transcript
chr2	98354472	98354472	*ZAP70*	Silent	SNP	G	G	A	rs115143372	shanshan_et_al_P63	p.P546P	ENSG00000115085	ENST00000264972	Transcript
chr20	53205129	53205129	*DOK5*	Silent	SNP	C	C	T	rs144328268	shanshan_et_al_P63	p.C94C	ENSG00000101134	ENST00000262593	Transcript
chr5	90001230	90001230	*GPR98*	Silent	SNP	C	C	T	novel	shanshan_et_al_P63	p.A2800A	ENSG00000164199	ENST00000405460	Transcript
chr8	126044542	126044542	*KIAA0196*	Silent	SNP	G	G	A	rs554772608	shanshan_et_al_P63	p.T1092T	ENSG00000164961	ENST00000318410	Transcript
chr9	96021359	96021359	*WNK2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P63	p.L843L	ENSG00000165238	ENST00000297954	Transcript
chrX	21875409	21875409	*YY2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P63	p.A269A	ENSG00000230797	ENST00000429584	Transcript
chr13	110847407	110847407	*COL4A1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P64	p.P448P	ENSG00000187498	ENST00000375820	Transcript
chr19	21719956	21719956	*ZNF429*	Silent	SNP	G	G	A	novel	shanshan_et_al_P64	p.K367K	ENSG00000197013	ENST00000358491	Transcript
chr19	23836898	23836898	*ZNF675*	Silent	SNP	T	T	A	novel	shanshan_et_al_P64	p.T279T	ENSG00000197372	ENST00000359788	Transcript
chr20	37126107	37126107	*RALGAPB*	Silent	SNP	G	G	T	novel	shanshan_et_al_P64	p.L167L	ENSG00000170471	ENST00000262879	Transcript
chr3	65425591	65425591	*MAGI1*	Silent	SNP	t	t	C	rs79701778	shanshan_et_al_P64	p.Q411Q	ENSG00000151276	ENST00000402939	Transcript
chr6	159188482	159188482	*EZR*	Silent	SNP	T	T	G	novel	shanshan_et_al_P64	p.A469A	ENSG00000092820	ENST00000367075	Transcript
chr8	143625682	143625682	*BAI1*	Silent	SNP	G	G	T	rs372083025	shanshan_et_al_P64	p.P1553P	ENSG00000181790	ENST00000519494	Transcript
chr8	42045020	42045020	*PLAT*	Silent	SNP	G	G	T	rs141317668	shanshan_et_al_P64	p.G145G	ENSG00000104368	ENST00000220908	Transcript
chr12	20620020	20620020	*DCP1B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P67	p.K368K	ENSG00000151065	ENST00000280665	Transcript
chr1	155733245	155733245	*GON4L*	Silent	SNP	c	c	T	novel	shanshan_et_al_P69	p.E1528E	ENSG00000116580	ENST00000437809	Transcript
chr8	73848937	73848937	*KCNB2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P69	p.I449I	ENSG00000182674	ENST00000523207	Transcript
chr9	190830006	190830006	*HAUS6*	Silent	SNP	G	G	A	novel	shanshan_et_al_P69	p.L245L	ENSG00000147874	ENST00000380502	Transcript
chr12	104048404	104048404	*STAB2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P70	p.A493A	ENSG00000136011	ENST00000388787	Transcript
chr15	48776091	48776091	*FBN1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P70	p.C1254C	ENSG00000166147	ENST00000316623	Transcript
chr15	51799347	51799347	*DMXL2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P70	p.S916S	ENSG00000104093	ENST00000543779	Transcript
chr20	5933137	5933137	*MCM8*	Silent	SNP	C	C	T	novel	shanshan_et_al_P70	p.F72F	ENSG00000125885	ENST00000378896	Transcript

chr22	19511227	19511227	*CLDN5*	Silent	SNP	G	G	C	novel	shanshan_et_al_P70	p.G269G	ENSG00000184113	ENST00000406028	Transcript
chr4	88537195	88537195	*DSPP*	Silent	SNP	T	T	C	novel	shanshan_et_al_P70	p.S1127S	ENSG00000152591	ENST00000399271	Transcript
chr5	140595018	140595018	*PCDHB13*	Silent	SNP	C	C	T	novel	shanshan_et_al_P70	p.I441I	ENSG00000187372	ENST00000341948	Transcript
chr5	140712198	140712198	*PCDHGA1*	Silent	SNP	C	C	T	rs138362456	shanshan_et_al_P70	p.H649H	ENSG00000204956	ENST00000517417	Transcript
chrX	90690678	90690678	*PABPC5*	Silent	SNP	C	C	A	novel	shanshan_et_al_P70	p.L34L	ENSG00000174740	ENST00000312600	Transcript
chr1	196309613	196309613	*KCNT2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P71	p.T547T	ENSG00000162687	ENST00000294725	Transcript
chr1	201195010	201195010	*IGFN1*	Silent	SNP	G	G	A	rs147078170	shanshan_et_al_P71	p.T3515T	ENSG00000163395	ENST00000335211	Transcript
chr1	204126100	204126100	*PLA2G5*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.L25L	ENSG00000127472	ENST00000375108	Transcript
chr1	209974729	209974729	*IRF6*	Silent	SNP	T	T	C	novel	shanshan_et_al_P71	p.L10L	ENSG00000117595	ENST00000367021	Transcript
chr10	105889993	105889993	*WDR96*	Silent	SNP	T	T	C	novel	shanshan_et_al_P71	p.T1634T	ENSG00000197748	ENST00000357060	Transcript
chr11	181087600	181087600	*SAAL1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P71	p.P261P	ENSG00000166788	ENST00000524803	Transcript
chr12	99225879	99225879	*ANKS1B*	Silent	SNP	A	A	T	rs574705271	shanshan_et_al_P71	p.R938R	ENSG00000185046	ENST00000547776	Transcript
chr15	41120653	41120653	*PPP1R14D*	Silent	SNP	G	G	T	rs373800458	shanshan_et_al_P71	p.R63R	ENSG00000166143	ENST00000427255	Transcript
chr15	55783366	55783366	*DYX1C1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P71	p.A120A	ENSG00000256061	ENST00000321149	Transcript
chr16	3283657	3283657	*ZNF200*	Silent	SNP	T	T	A	novel	shanshan_et_al_P71	p.R33R	ENSG00000010539	ENST00000431561	Transcript
chr17	48191581	48191581	*SAMD14*	Silent	SNP	G	G	A	novel	shanshan_et_al_P71	p.P332P	ENSG00000167100	ENST00000503131	Transcript
chr17	65920681	65920681	*BPTF*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.A1909A	ENSG00000171634	ENST00000306378	Transcript
chr19	53058170	53058170	*ZNF808*	Silent	SNP	A	A	T	rs371709428	shanshan_et_al_P71	p.V667V	ENSG00000198482	ENST00000359798	Transcript
chr2	113082677	113082677	*ZC3H6*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.A663A	ENSG00000188177	ENST00000409871	Transcript
chr2	113537149	113537149	*IL1A*	Silent	SNP	G	G	A	rs376957964	shanshan_et_al_P71	p.D138D	ENSG00000115008	ENST00000263339	Transcript
chr2	125555776	125555776	*CNTNAP5*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.T1031T	ENSG00000155052	ENST00000431078	Transcript
chr2	192194682	192194682	*MYO1B*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.A91A	ENSG00000128641	ENST00000392318	Transcript
chr2	197208442	197208442	*HECW2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P71	p.V113V	ENSG00000138411	ENST00000260983	Transcript
chr2	212328208	212328208	*APOB*	Silent	SNP	T	T	A	novel	shanshan_et_al_P71	p.T2304T	ENSG00000084674	ENST00000233242	Transcript
chr2	231941873	231941873	*PSMD1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.T356T	ENSG00000173692	ENST00000308696	Transcript
chr2	74074873	74074873	*STAMBP*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.S245S	ENSG00000124356	ENST00000394070	Transcript
chr22	42908976	42908976	*RRP7A*	Silent	SNP	G	G	A	rs145348367	shanshan_et_al_P71	p.F261F	ENSG00000189306	ENST00000323013	Transcript
chr3	158539398	158539398	*MFSD1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.T341T	ENSG00000118855	ENST00000415822	Transcript
chr3	160395290	160395290	*ARL14*	Silent	SNP	C	C	A	novel	shanshan_et_al_P71	p.I52I	ENSG00000179674	ENST00000320767	Transcript
chr5	77512023	77512023	*AP3B1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P71	p.V214V	ENSG00000132842	ENST00000255194	Transcript
chr8	135612685	135612685	*ZFAT*	Silent	SNP	T	T	A	rs531744957	shanshan_et_al_P71	p.T823T	ENSG00000066827	ENST00000377838	Transcript
chr9	101810231	101810231	*COL15A1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.P914P	ENSG00000204291	ENST00000375001	Transcript
chr9	20982409	20982409	*FOCAD*	Silent	SNP	A	A	T	novel	shanshan_et_al_P71	p.T1564T	ENSG00000188352	ENST00000380249	Transcript
chrX	77913387	77913387	*ZCCHC5*	Silent	SNP	T	T	A	novel	shanshan_et_al_P71	p.A177A	ENSG00000179300	ENST00000321110	Transcript
chr12	57556141	57556141	*LRP1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P74	p.L748L	ENSG00000123384	ENST00000243077	Transcript
chr12	85255570	85255570	*SLC6A15*	Silent	SNP	G	G	A	rs140619291	shanshan_et_al_P74	p.H678H	ENSG00000172041	ENST00000266282	Transcript
chr14	20611945	20611945	*OR4N5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P74	p.L17L	ENSG00000184394	ENST00000333629	Transcript
chr19	19576376	19576376	*GATAD2A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P74	p.G74G	ENSG00000167491	ENST00000360315	Transcript
chr19	50549938	50549938	*ZNF473*	Silent	SNP	C	C	T	novel	shanshan_et_al_P74	p.V746V	ENSG00000142528	ENST00000559561	Transcript
chr2	73717663	73717663	*ALMS1*	Silent	SNP	G	G	A	rs199850691	shanshan_et_al_P74	p.S2858S	ENSG00000116127	ENST00000264448	Transcript
chr6	96971097	96971097	*UFL1*	Silent	SNP	C	C	G	novel	shanshan_et_al_P74	p.L51L	ENSG00000014123	ENST00000369278	Transcript

chr2	45169567	45169567	*SIX3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P79	p.L108L	ENSG00000138083	ENST00000260653	Transcript
chr20	32255633	32255633	*ACTL10*	Silent	SNP	C	C	T	novel	shanshan_et_al_P79	p.N110N	ENSG00000182584	ENST00000330271	Transcript
chr22	40801222	40801222	*SGSM3*	Silent	SNP	G	G	C	novel	shanshan_et_al_P79	p.L184L	ENSG00000100359	ENST00000248929	Transcript
chr3	75788390	75788390	*ZNF717*	Silent	SNP	A	A	C	novel	shanshan_et_al_P79	p.V128V	ENSG00000227124	ENST00000422325	Transcript
chr1	23294085	23294085	*MAP10*	Silent	SNP	G	G	A	novel	shanshan_et_al_P80	p.R29R	ENSG00000212916	ENST00000418460	Transcript
chr1	23455651	23455651	*TARBP1*	Silent	SNP	A	A	C	novel	shanshan_et_al_P80	p.S1163S	ENSG00000059588	ENST00000040877	Transcript
chr11	10668076	10668076	*GUCY1A2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P80	p.L549L	ENSG00000152402	ENST00000282249	Transcript
chr17	8051132	8051132	*PER1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P80	p.A416A	ENSG00000179094	ENST00000317276	Transcript
chr19	10421576	10421576	*FDX1L*	Silent	SNP	C	C	A	novel	shanshan_et_al_P80	p.V116V	ENSG00000267673	ENST00000393708	Transcript
chr19	4902616	4902616	*ARRDC5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P80	p.Y88Y	ENSG00000205784	ENST00000381781	Transcript
chr19	55143558	55143558	*LILRB1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P80	p.S177S	ENSG00000104972	ENST00000324602	Transcript
chr21	39086662	39086662	*KCNJ6*	Silent	SNP	C	C	T	rs376122684	shanshan_et_al_P80	p.T266T	ENSG00000157542	ENST00000609713	Transcript
chr4	83350526	83350526	*HNRNPDL*	Silent	SNP	C	C	A	novel	shanshan_et_al_P80	p.R106R	ENSG00000152795	ENST00000302954	Transcript
chrX	23019839	23019839	*DDX53*	Silent	SNP	A	A	G	novel	shanshan_et_al_P80	p.V555V	ENSG00000184735	ENST00000327968	Transcript
chr1	23380245	23380245	*KCNK1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P81	p.V158V	ENSG00000135750	ENST00000366621	Transcript
chr14	88983510	88983510	*PTPN21*	Silent	SNP	T	T	C	rs377590341	shanshan_et_al_P81	p.A92A	ENSG00000070778	ENST00000556564	Transcript
chr6	29595102	29595102	*SERPINB6*	Silent	SNP	C	C	T	novel	shanshan_et_al_P81	p.L19L	ENSG00000124570	ENST00000380520	Transcript
chrX	12735636	12735636	*FRMPD4*	Silent	SNP	G	G	T	novel	shanshan_et_al_P81	p.R897R	ENSG00000169933	ENST00000380682	Transcript
chr19	51919267	51919267	*SIGLEC10*	Silent	SNP	A	A	G	rs7258638	shanshan_et_al_P82	p.P303P	ENSG00000142512	ENST00000356298	Transcript
chr1	12854370	12854370	*PRAMEF1*	Silent	SNP	A	A	G	rs372514136	shanshan_et_al_P85	p.S198S	ENSG00000116721	ENST00000332296	Transcript
chr1	15102751	15102751	*CDC42SE1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P85	p.A49A	ENSG00000197622	ENST00000439374	Transcript
chr11	12479478	12479478	*HEPACAM*	Silent	SNP	G	G	T	novel	shanshan_et_al_P85	p.T90T	ENSG00000165478	ENST00000298251	Transcript
chr12	49165607	49165607	*ADCY6*	Silent	SNP	A	A	G	novel	shanshan_et_al_P85	p.A979A	ENSG00000174233	ENST00000307885	Transcript
chr14	21992908	21992908	*SALL2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P85	p.H318H	ENSG00000165821	ENST00000327430	Transcript
chr17	29667567	29667567	*NF1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P85	p.V2322V	ENSG00000196712	ENST00000358273	Transcript
chr19	18700265	18700265	*C19orf60*	Silent	SNP	C	C	T	novel	shanshan_et_al_P85	p.G75G	ENSG00000006015	ENST00000358607	Transcript
chr2	20704137	20704137	*GPR1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P85	p.L200L	ENSG00000183671	ENST00000404073	Transcript
chr2	23905657	23905657	*KLHL30*	Silent	SNP	G	G	C	novel	shanshan_et_al_P85	p.S416S	ENSG00000168427	ENST00000409223	Transcript
chr20	44539793	44539793	*PLTP*	Silent	SNP	A	A	C	rs146036087	shanshan_et_al_P85	p.S66S	ENSG00000100979	ENST00000477313	Transcript
chr22	28397455	28397455	*TTC28*	Silent	SNP	G	G	A	novel	shanshan_et_al_P85	p.A1435A	ENSG00000100154	ENST00000397906	Transcript
chr22	42908976	42908976	*RRP7A*	Silent	SNP	G	G	A	rs145348367	shanshan_et_al_P85	p.F261F	ENSG00000189306	ENST00000323013	Transcript
chr3	18832759	18832759	*LPP*	Silent	SNP	T	T	C	novel	shanshan_et_al_P85	p.P359P	ENSG00000145012	ENST00000312675	Transcript
chr4	126239141	126239141	*FAT4*	Silent	SNP	C	C	T	novel	shanshan_et_al_P85	p.I525I	ENSG00000196159	ENST00000339429	Transcript
chr5	80626654	80626654	*ACOT12*	Silent	SNP	A	A	T	novel	shanshan_et_al_P85	p.A499A	ENSG00000172497	ENST00000307624	Transcript
chr6	165752824	165752824	*PDE10A*	Silent	SNP	T	T	C	novel	shanshan_et_al_P85	p.G707G	ENSG00000112541	ENST00000539869	Transcript
chr6	181716177	181716177	*KDM1B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P85	p.C147C	ENSG00000165097	ENST00000292792	Transcript
chr6	24278368	24278368	*DCDC2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P85	p.K277K	ENSG00000146038	ENST00000378454	Transcript
chr13	99515714	99515714	*DOCK9*	Silent	SNP	G	G	C	novel	shanshan_et_al_P86	p.L1125L	ENSG00000088387	ENST00000376460	Transcript
chr16	88501585	88501585	*ZNF469*	Silent	SNP	C	C	T	rs140697844	shanshan_et_al_P86	p.H2541H	ENSG00000225614	ENST00000437464	Transcript
chr18	48345993	48345993	*MRO*	Silent	SNP	C	C	G	novel	shanshan_et_al_P86	p.T33T	ENSG00000134042	ENST00000436348	Transcript
chr6	146480713	146480713	*GRM1*	Silent	SNP	C	C	T	rs143238116	shanshan_et_al_P86	p.G310G	ENSG00000152822	ENST00000361719	Transcript

chr6	44197181	44197181	*SLC29A1*	Silent	SNP	G	G	A	rs8187630	shanshan_et_al_P86	p.P28P	ENSG00000112759	ENST00000393841	Transcript
chr9	116136377	116136377	*HDHD3*	Silent	SNP	C	C	A	rs371445625	shanshan_et_al_P86	p.A86A	ENSG00000119431	ENST00000238379	Transcript
chr11	407887	407887	*SIGIRR*	Silent	SNP	C	C	T	rs537219351	shanshan_et_al_P87	p.L137L	ENSG00000185187	ENST00000431843	Transcript
chr12	52822234	52822234	*KRT75*	Silent	SNP	A	A	T	novel	shanshan_et_al_P87	p.A396A	ENSG00000170454	ENST00000252245	Transcript
chr15	76183325	76183325	*UBE2Q2*	Silent	SNP	C	C	G	novel	shanshan_et_al_P87	p.G333G	ENSG00000140367	ENST00000267938	Transcript
chr16	70883779	70883779	*HYDIN*	Silent	SNP	C	C	T	novel	shanshan_et_al_P87	p.Q4241Q	ENSG00000157423	ENST00000393567	Transcript
chr4	3449285	3449285	*HGFAC*	Silent	SNP	G	G	T	rs147311320	shanshan_et_al_P87	p.T474T	ENSG00000109758	ENST00000382774	Transcript
chrX	152959638	152959638	*SLC6A8*	Silent	SNP	C	C	T	novel	shanshan_et_al_P87	p.S436S	ENSG00000130821	ENST00000253122	Transcript
chr2	175450278	175450278	*WIPF1*	Silent	SNP	T	T	G	novel	shanshan_et_al_P88	p.A8A	ENSG00000115935	ENST00000392547	Transcript
chr6	157099432	157099432	*ARID1B*	Silent	SNP	G	G	A	novel	shanshan_et_al_P88	p.Q123Q	ENSG00000049618	ENST00000346085	Transcript
chr7	140396550	140396550	*NDUFB2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P88	p.S2S	ENSG00000090266	ENST00000476279	Transcript
chr17	69280501	69280501	*BCL6B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P89	p.S244S	ENSG00000161940	ENST00000293805	Transcript
chr17	32560537	32560537	*TMEM39B*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_1	p.V360V	ENSG00000121775	ENST00000336294	Transcript
chr12	132627367	132627367	*DDX51*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_1	p.V192V	ENSG00000185163	ENST00000397333	Transcript
chr14	23456820	23456820	*C14orf93*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_1	p.I407I	ENSG00000100802	ENST00000299088	Transcript
chr15	73615467	73615467	*HCN4*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_1	p.G989G	ENSG00000138622	ENST00000261917	Transcript
chr15	85664165	85664165	*PDE8A*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_1	p.V624V	ENSG00000073417	ENST00000310298	Transcript
chr17	65734445	65734445	*NOL11*	Silent	SNP	T	T	C	novel	shanshan_et_al_P8_1	p.P579P	ENSG00000130935	ENST00000253247	Transcript
chr18	11881047	11881047	*GNAL*	Silent	SNP	C	C	A	rs563746937	shanshan_et_al_P8_1	p.A430A	ENSG00000141404	ENST00000334049	Transcript
chr18	34298327	34298327	*FHOD3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P8_1	p.P847P	ENSG00000134775	ENST00000257209	Transcript
chr19	36001203	36001203	*TBXA2R*	Silent	SNP	C	C	A	rs200600231	shanshan_et_al_P8_1	p.V171V	ENSG00000006638	ENST00000411851	Transcript
chr4	265104	265104	*ZNF732*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_1	p.S514S	ENSG00000186777	ENST00000419098	Transcript
chr6	148861667	148861667	*SASH1*	Silent	SNP	C	C	T	rs569645754	shanshan_et_al_P8_1	p.Y728Y	ENSG00000111961	ENST00000367467	Transcript
chr7	158248267	158248267	*PTPRN2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_1	p.L41L	ENSG00000155093	ENST00000389418	Transcript
chr14	105419298	105419298	*AHNAK2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_2	p.D830D	ENSG00000185567	ENST00000333244	Transcript
chr19	56029174	56029174	*SSC5D*	Silent	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.T1177T	ENSG00000179954	ENST00000389623	Transcript
chr19	6380982	6380982	*GTF2F1*	Silent	SNP	G	G	T	rs371917624	shanshan_et_al_P8_2	p.G388G	ENSG00000125651	ENST00000394456	Transcript
chr2	32093496	32093496	*MEMO1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_2	p.S276S	ENSG00000162959	ENST00000295065	Transcript
chr4	9256582	9256582	*USP17L19*	Silent	SNP	C	C	A	novel	shanshan_et_al_P8_2	p.T493T	ENSG00000248920	ENST00000551566	Transcript
chr7	29874379	29874379	*WIPF3*	Silent	SNP	A	A	C	novel	shanshan_et_al_P8_2	p.P13P	ENSG00000122574	ENST00000409290	Transcript
chr8	141745535	141745535	*PTK2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P8_2	p.I615I	ENSG00000169398	ENST00000340930	Transcript
chr1	186147675	186147675	*HMCN1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.L5357L	ENSG00000143341	ENST00000271588	Transcript
chr1	236730009	236730009	*HEATR1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.L1415L	ENSG00000119285	ENST00000366582	Transcript
chr1	52826715	52826715	*CC2D1B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.E136E	ENSG00000154222	ENST00000371586	Transcript
chr12	46245476	46245476	*ARID2*	Silent	SNP	A	A	T	novel	shanshan_et_al_P8_4	p.G1190G	ENSG00000189079	ENST00000334344	Transcript
chr12	56477668	56477668	*ERBB3*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.A72A	ENSG00000065361	ENST00000267101	Transcript
chr13	99907665	99907665	*GPR18*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.T154T	ENSG00000125245	ENST00000340807	Transcript
chr14	104578866	104578866	*ASPG*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.V569V	ENSG00000166183	ENST00000551177	Transcript
chr14	20502909	20502909	*OR4K13*	Silent	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.R3R	ENSG00000176253	ENST00000315693	Transcript
chr15	28196946	28196946	*OCA2*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.G645G	ENSG00000104044	ENST00000354638	Transcript
chr16	53708938	53708938	*RPGRIP1L*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.Q291Q	ENSG00000103494	ENST00000379925	Transcript

chr16	74750465	74750465	*FA2H*	Silent	SNP	G	G	C	novel	shanshan_et_al_P8_4	p.P273P	ENSG00000103089	ENST00000219368	Transcript
chr17	30536375	30536375	*RHOT1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P8_4	p.D582D	ENSG00000126858	ENST00000358365	Transcript
chr17	6524223	6524223	*KIAA0753*	Silent	SNP	C	C	T	rs189528427	shanshan_et_al_P8_4	p.K400K	ENSG00000198920	ENST00000361413	Transcript
chr17	9808378	9808378	*RCVRN*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.P40P	ENSG00000109047	ENST00000226193	Transcript
chr19	22155715	22155715	*ZNF208*	Silent	SNP	G	G	A	rs201994264	shanshan_et_al_P8_4	p.N707N	ENSG00000160321	ENST00000397126	Transcript
chr19	22941670	22941670	*ZNF99*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.G347G	ENSG00000213973	ENST00000596209	Transcript
chr19	41386496	41386496	*CYP2A7*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.L127L	ENSG00000198077	ENST00000301146	Transcript
chr19	9921611	9921611	*FBXL12*	Silent	SNP	G	G	C	novel	shanshan_et_al_P8_4	p.V314V	ENSG00000127452	ENST00000247977	Transcript
chr2	172585298	172585298	*DYNC1I2*	Silent	SNP	T	T	C	rs62184168	shanshan_et_al_P8_4	p.D443D	ENSG00000077380	ENST00000397119	Transcript
chr2	29274734	29274734	*FAM179A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P8_4	p.P945P	ENSG00000189350	ENST00000379558	Transcript
chr5	140346556	140346556	*PCDHAC2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P8_4	p.L69L	ENSG00000243232	ENST00000289269	Transcript
chr5	151784375	151784375	*NMUR2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.P100P	ENSG00000132911	ENST00000255262	Transcript
chr6	41248704	41248704	*TREM1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.I198I	ENSG00000124731	ENST00000244709	Transcript
chr8	89086879	89086879	*MMP16*	Silent	SNP	G	G	T	novel	shanshan_et_al_P8_4	p.I392I	ENSG00000156103	ENST00000286614	Transcript
chrX	49068742	49068742	*CACNA1F*	Silent	SNP	G	G	A	novel	shanshan_et_al_P8_4	p.I1334I	ENSG00000102001	ENST00000376265	Transcript
chrX	78119791	78119791	*VCX*	Silent	SNP	A	A	G	rs141165637	shanshan_et_al_P8_4	p.E181E	ENSG00000182583	ENST00000381059	Transcript
chr1	182617404	182617404	*RGS8*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.T94T	ENSG00000135824	ENST00000258302	Transcript
chr1	190067439	190067439	*BRINP3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P90	p.G670G	ENSG00000162670	ENST00000367462	Transcript
chr11	109294683	109294683	*C11orf87*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.G108G	ENSG00000185742	ENST00000327419	Transcript
chr11	4976182	4976182	*OR51A2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.L254L	ENSG00000205496	ENST00000380371	Transcript
chr11	71939475	71939475	*INPPL1*	Silent	SNP	G	G	C	novel	shanshan_et_al_P90	p.V110V	ENSG00000165458	ENST00000298229	Transcript
chr12	117768772	117768772	*NOS1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.R35R	ENSG00000089250	ENST00000338101	Transcript
chr12	49167362	49167362	*ADCY6*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.G837G	ENSG00000174233	ENST00000307885	Transcript
chr12	55688438	55688438	*OR6C6*	Silent	SNP	T	T	A	novel	shanshan_et_al_P90	p.L193L	ENSG00000188324	ENST00000358433	Transcript
chr14	24632636	24632636	*IRF9*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.V138V	ENSG00000213928	ENST00000396864	Transcript
chr15	56681518	56681518	*TEX9*	Silent	SNP	A	A	G	novel	shanshan_et_al_P90	p.P105P	ENSG00000151575	ENST00000352903	Transcript
chr16	46501384	46501384	*C16orf96*	Silent	SNP	G	G	T	rs537867141	shanshan_et_al_P90	p.S1082S	ENSG00000205832	ENST00000444310	Transcript
chr17	40257105	40257105	*DHX58*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.G444G	ENSG00000108771	ENST00000251642	Transcript
chr17	71238441	71238441	*C17orf80*	Silent	SNP	T	T	A	novel	shanshan_et_al_P90	p.L524L	ENSG00000141219	ENST00000359042	Transcript
chr18	70023766	70023766	*LAMA1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.G1423G	ENSG00000101680	ENST00000389658	Transcript
chr2	120734565	120734565	*PTPN4*	Silent	SNP	A	A	G	novel	shanshan_et_al_P90	p.Q900Q	ENSG00000088179	ENST00000263708	Transcript
chr2	166211091	166211091	*SCN2A*	Silent	SNP	G	G	C	novel	shanshan_et_al_P90	p.V1103V	ENSG00000136531	ENST00000357398	Transcript
chr2	223160365	223160365	*PAX3*	Silent	SNP	C	C	G	novel	shanshan_et_al_P90	p.T111T	ENSG00000135903	ENST00000392069	Transcript
chr2	86297387	86297387	*POLR1A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.R540R	ENSG00000068654	ENST00000263857	Transcript
chr20	57766452	57766452	*ZNF831*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.P126P	ENSG00000124203	ENST00000371030	Transcript
chr20	62679615	62679615	*SOX18*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.G353G	ENSG00000203883	ENST00000340356	Transcript
chr21	47954002	47954002	*DIP2A*	Silent	SNP	A	A	G	novel	shanshan_et_al_P90	p.T505T	ENSG00000160305	ENST00000417564	Transcript
chr22	44602285	44602285	*PARVG*	Silent	SNP	G	G	T	rs374493877	shanshan_et_al_P90	p.T325T	ENSG00000138964	ENST00000444313	Transcript
chr3	184700404	184700404	*VPS8*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.S1157S	ENSG00000156931	ENST00000437079	Transcript
chr4	8293228	8293228	*HTRA3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P90	p.E280E	ENSG00000170801	ENST00000307358	Transcript
chr4	9336866	9336866	*USP17L26*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.A161A	ENSG00000229579	ENST00000509660	Transcript

chr4	9341611	9341611	*USP17L5*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.A161A	ENSG00000227140	ENST00000507227	Transcript
chr5	140625227	140625227	*PCDHB15*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.G27G	ENSG00000113248	ENST00000231173	Transcript
chr6	106555106	106555106	*PRDM1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.R741R	ENSG00000057657	ENST00000369096	Transcript
chr6	34564043	34564043	*SLC22A23*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.G130G	ENSG00000137266	ENST00000406686	Transcript
chr6	71567899	71567899	*SMAP1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.P412P	ENSG00000112305	ENST00000370455	Transcript
chr7	111368600	111368600	*DOCK4*	Silent	SNP	C	C	A	rs565911216	shanshan_et_al_P90	p.P1877P	ENSG00000128512	ENST00000437633	Transcript
chr7	128454716	128454716	*CCDC136*	Silent	SNP	C	C	A	rs199769669	shanshan_et_al_P90	p.R930R	ENSG00000128596	ENST00000297788	Transcript
chr7	142574544	142574544	*TRPV6*	Silent	SNP	G	G	A	rs138110961	shanshan_et_al_P90	p.I178I	ENSG00000165125	ENST00000359396	Transcript
chr7	215993500	215993500	*DNAH11*	Silent	SNP	T	T	C	novel	shanshan_et_al_P90	p.P274P	ENSG00000105877	ENST00000328843	Transcript
chr7	217894100	217894100	*DNAH11*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.L2937L	ENSG00000105877	ENST00000328843	Transcript
chr7	67316316	67316316	*ZNF12*	Silent	SNP	C	C	G	novel	shanshan_et_al_P90	p.V314V	ENSG00000164631	ENST00000405858	Transcript
chr7	97862809	97862809	*TECPR1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.P532P	ENSG00000205356	ENST00000447648	Transcript
chr8	119936964	119936964	*TNFRSF11B*	Silent	SNP	A	A	G	novel	shanshan_et_al_P90	p.I285I	ENSG00000164761	ENST00000329732	Transcript
chr8	135600604	135600604	*ZFAT*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.G866G	ENSG00000086827	ENST00000377838	Transcript
chr8	56015729	56015729	*XKR4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P90	p.A227A	ENSG00000206579	ENST00000327381	Transcript
chr8	85441565	85441565	*RALYL*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.G16G	ENSG00000184672	ENST00000517638	Transcript
chr9	130272502	130272502	*FAM129B*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.R362R	ENSG00000136830	ENST00000337312	Transcript
chr9	36882080	36882080	*PAX5*	Silent	SNP	G	G	T	novel	shanshan_et_al_P90	p.T311T	ENSG00000196092	ENST00000358127	Transcript
chrX	151886312	151886312	*MAGEA2B*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.F239F	ENSG00000183305	ENST00000331220	Transcript
chrX	151919171	151919171	*MAGEA2*	Silent	SNP	G	G	A	novel	shanshan_et_al_P90	p.F239F	ENSG00000184750	ENST00000543232	Transcript
chrX	51150018	51150018	*CXorf67*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.S50S	ENSG00000187690	ENST00000342995	Transcript
chrX	73961449	73961449	*KIAA2022*	Silent	SNP	C	C	T	novel	shanshan_et_al_P90	p.G981G	ENSG00000050030	ENST00000055682	Transcript
chr1	3753967	3753967	*CEP104*	Silent	SNP	A	A	G	novel	shanshan_et_al_P91	p.F336F	ENSG00000116198	ENST00000378230	Transcript
chr15	76484458	76484458	*C15orf27*	Silent	SNP	G	G	A	rs190417970	shanshan_et_al_P91	p.T306T	ENSG00000169758	ENST00000388942	Transcript
chr3	121353203	121353203	*HCLS1*	Silent	SNP	G	G	T	rs373015540	shanshan_et_al_P91	p.R252R	ENSG00000180353	ENST00000314583	Transcript
chr4	88537141	88537141	*DSPP*	Silent	SNP	T	T	C	novel	shanshan_et_al_P91	p.S1109S	ENSG00000152591	ENST00000399271	Transcript
chr8	124382179	124382179	*ATAD2*	Silent	SNP	a	a	G	novel	shanshan_et_al_P91	p.D271D	ENSG00000156802	ENST00000528794	Transcript
chr1	156909500	156909500	*ARHGEF11*	Silent	SNP	C	C	A	novel	shanshan_et_al_P94	p.G1312G	ENSG00000132694	ENST00000368194	Transcript
chr1	158533025	158533025	*OR6P1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P94	p.L124L	ENSG00000186440	ENST00000334632	Transcript
chr1	200979603	200979603	*TMCO4*	Silent	SNP	T	T	A	novel	shanshan_et_al_P94	p.T64T	ENSG00000162542	ENST00000294543	Transcript
chr1	222825366	222825366	*MIA3*	Silent	SNP	A	A	C	novel	shanshan_et_al_P94	p.S1319S	ENSG00000154305	ENST00000344922	Transcript
chr1	94654872	94654872	*ARHGAP29*	Silent	SNP	T	T	C	novel	shanshan_et_al_P94	p.S492S	ENSG00000137962	ENST00000260526	Transcript
chr11	208881	208881	*RIC8A*	Silent	SNP	C	C	A	novel	shanshan_et_al_P94	p.A9A	ENSG00000177963	ENST00000325207	Transcript
chr12	72956755	72956755	*TRHDE*	Silent	SNP	T	T	A	novel	shanshan_et_al_P94	p.I614I	ENSG00000072657	ENST00000261180	Transcript
chr15	49254658	49254658	*SHC4*	Silent	SNP	C	C	A	novel	shanshan_et_al_P94	p.L185L	ENSG00000185634	ENST00000332408	Transcript
chr15	56132699	56132699	*NEDD4*	Silent	SNP	T	T	C	novel	shanshan_et_al_P94	p.P1006P	ENSG00000069869	ENST00000338963	Transcript
chr16	14494344	14494344	*UNKL*	Silent	SNP	C	C	A	rs375654703	shanshan_et_al_P94	p.A225A	ENSG00000059145	ENST00000389221	Transcript
chr16	89967103	89967103	*TCF25*	Silent	SNP	C	C	T	novel	shanshan_et_al_P94	p.L428L	ENSG00000141002	ENST00000263346	Transcript
chr17	33520403	33520403	*SLC35G3*	Silent	SNP	A	A	T	novel	shanshan_et_al_P94	p.S308S	ENSG00000164729	ENST00000297307	Transcript
chr17	62133123	62133123	*ERN1*	Silent	SNP	C	C	A	novel	shanshan_et_al_P94	p.T528T	ENSG00000178607	ENST00000433197	Transcript
chr18	76754709	76754709	*SALL3*	Silent	SNP	G	G	T	novel	shanshan_et_al_P94	p.S906S	ENSG00000256463	ENST00000537592	Transcript

chr19	30199216	30199216	*C19orf12*	Silent	SNP	T	T	C	novel	shanshan_et_al_P94	p.T46T	ENSG00000131943	ENST00000392278	Transcript
chr19	44237030	44237030	*SMG9*	Silent	SNP	C	C	A	novel	shanshan_et_al_P94	p.T488T	ENSG00000105771	ENST00000270066	Transcript
chr3	54919573	54919573	*CACNA2D3*	Silent	SNP	G	G	T	rs374818350	shanshan_et_al_P94	p.A672A	ENSG00000157445	ENST00000474759	Transcript
chr4	122825507	122825507	*TRPC3*	Silent	SNP	A	A	T	novel	shanshan_et_al_P94	p.A741A	ENSG00000138741	ENST00000379645	Transcript
chr4	74283828	74283828	*ALB*	Silent	SNP	A	A	G	novel	shanshan_et_al_P94	p.L484L	ENSG00000163631	ENST00000295897	Transcript
chr5	74101066	74101066	*FAM169A*	Silent	SNP	G	G	T	novel	shanshan_et_al_P94	p.L238L	ENSG00000198780	ENST00000389156	Transcript
chr7	36336642	36336642	*EEPD1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P94	p.G452G	ENSG00000122547	ENST00000242108	Transcript
chr7	82451998	82451998	*PCLO*	Silent	SNP	C	C	T	novel	shanshan_et_al_P94	p.Q4868Q	ENSG00000186472	ENST00000333891	Transcript
chrX	78618526	78618526	*ITM2A*	Silent	SNP	A	A	T	novel	shanshan_et_al_P94	p.R118R	ENSG00000078596	ENST00000373298	Transcript
chr1	214814366	214814366	*CENPF*	Silent	SNP	C	C	T	novel	shanshan_et_al_P95	p.H895H	ENSG00000117724	ENST00000366955	Transcript
chr15	83481947	83481947	*WHAMM*	Silent	SNP	G	G	A	novel	shanshan_et_al_P95	p.V234V	ENSG00000156232	ENST00000286760	Transcript
chr19	43373002	43373002	*PSG1*	Silent	SNP	G	G	T	rs376541482	shanshan_et_al_P95	p.P298P	ENSG00000231924	ENST00000244296	Transcript
chr19	436191	436191	*SHC2*	Silent	SNP	C	C	A	rs374545079	shanshan_et_al_P95	p.P309P	ENSG00000129946	ENST00000264554	Transcript
chr19	43773563	43773563	*PSG9*	Silent	SNP	A	A	G	novel	shanshan_et_al_P95	p.P7P	ENSG00000183668	ENST00000270077	Transcript
chrX	49033526	49033526	*PRICKLE3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P95	p.Y327Y	ENSG00000012211	ENST00000376317	Transcript
chr1	103343641	103343641	*COL11A1*	Silent	SNP	G	G	A	novel	shanshan_et_al_P97	p.I1785I	ENSG00000060718	ENST00000370096	Transcript
chr12	72969157	72969157	*TRHDE*	Silent	SNP	C	C	A	rs138433001	shanshan_et_al_P97	p.R707R	ENSG00000072657	ENST00000261180	Transcript
chr18	56887632	56887632	*GRP*	Silent	SNP	G	G	A	novel	shanshan_et_al_P97	p.A45A	ENSG00000134443	ENST00000256857	Transcript
chr2	238485933	238485933	*RAB17*	Silent	SNP	C	C	A	rs149848086	shanshan_et_al_P97	p.T134T	ENSG00000124839	ENST00000264601	Transcript
chr3	128631444	128631444	*ACAD9*	Silent	SNP	A	A	G	novel	shanshan_et_al_P97	p.T620T	ENSG00000177646	ENST00000308982	Transcript
chr3	51266100	51266100	*DOCK3*	Silent	SNP	G	G	A	novel	shanshan_et_al_P97	p.E552E	ENSG00000088538	ENST00000266037	Transcript
chr9	130938698	130938698	*CIZ1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P97	p.Q625Q	ENSG00000148337	ENST00000393608	Transcript
chr16	19083402	19083402	*COQ7*	Silent	SNP	C	C	A	rs370724921	shanshan_et_al_P98	p.R76R	ENSG00000167186	ENST00000321998	Transcript
chr17	26902473	26902473	*ALDOC*	Silent	SNP	C	C	T	rs377735389	shanshan_et_al_P98	p.P26P	ENSG00000109107	ENST00000226253	Transcript
chr17	69280501	69280501	*BCL6B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P98	p.S244S	ENSG00000161940	ENST00000293805	Transcript
chr19	35572341	35572341	*MFSD12*	Silent	SNP	G	G	A	novel	shanshan_et_al_P98	p.R56R	ENSG00000161091	ENST00000398558	Transcript
chr19	66784624	66784624	*C3*	Silent	SNP	G	G	A	rs189948635	shanshan_et_al_P98	p.Y1545Y	ENSG00000125730	ENST00000245907	Transcript
chr7	26224323	26224323	*NFE2L3*	Silent	SNP	T	T	C	rs113074870	shanshan_et_al_P98	p.T335T	ENSG00000050344	ENST00000005633	Transcript
chr8	17089978	17089978	*CNOT7*	Silent	SNP	A	A	C	novel	shanshan_et_al_P98	p.S229S	ENSG00000198791	ENST00000361272	Transcript
chr1	104162352	104162352	*AMY2A*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.H230H	ENSG00000243480	ENST00000414303	Transcript
chr1	183109595	183109595	*LAMC1*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.V1510V	ENSG00000135862	ENST00000258341	Transcript
chr1	43649426	43649426	*WDR65*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.V213V	ENSG00000243710	ENST00000528956	Transcript
chr1	91889911	91889911	*GPR157*	Silent	SNP	C	C	T	novel	shanshan_et_al_P99	p.L32L	ENSG00000180758	ENST00000377411	Transcript
chr10	12123583	12123583	*DHTKD1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P99	p.I89I	ENSG00000181192	ENST00000263035	Transcript
chr10	29762890	29762890	*SVIL*	Silent	SNP	C	C	G	novel	shanshan_et_al_P99	p.S1802S	ENSG00000197321	ENST00000375398	Transcript
chr11	105929699	105929699	*KBTBD3*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.L42L	ENSG00000182359	ENST00000525793	Transcript
chr11	148566199	148566199	*PDE3B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.G766G	ENSG00000152270	ENST00000282096	Transcript
chr11	18723250	18723250	*TMEM86A*	Silent	SNP	C	C	T	novel	shanshan_et_al_P99	p.L139L	ENSG00000151117	ENST00000282734	Transcript
chr11	27406880	27406880	*LGR4*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.L179L	ENSG00000205213	ENST00000379214	Transcript
chr11	48327792	48327792	*OR4S1*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.N6N	ENSG00000176555	ENST00000319988	Transcript
chr11	57993975	57993975	*OR52N5*	Silent	SNP	G	G	A	novel	shanshan_et_al_P99	p.A156A	ENSG00000181009	ENST00000317093	Transcript

chr11	62298592	62298592	*AHNAK*	Silent	SNP	T	T	G	novel	shanshan_et_al_P99	p.P1099P	ENSG00000124942	ENST00000378024	Transcript
chr11	63665721	63665721	*MARK2*	Silent	SNP	A	A	G	novel	shanshan_et_al_P99	p.R102R	ENSG00000072518	ENST00000402010	Transcript
chr11	69644364	69644364	*ZNF215*	Silent	SNP	A	A	T	novel	shanshan_et_al_P99	p.S202S	ENSG00000149054	ENST00000278319	Transcript
chr11	86465308	86465308	*TRIM66*	Silent	SNP	C	C	A	novel	shanshan_et_al_P99	p.V705V	ENSG00000166436	ENST00000402157	Transcript
chr12	11288827	11288827	*PTPN11*	Silent	SNP	T	T	G	novel	shanshan_et_al_P99	p.L98L	ENSG00000179295	ENST00000351677	Transcript
chr12	12435213	12435213	*DNAH10*	Silent	SNP	G	G	A	novel	shanshan_et_al_P99	p.Q2311Q	ENSG00000197653	ENST00000409039	Transcript
chr12	56619414	56619414	*NABP2*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.A75A	ENSG00000139579	ENST00000380198	Transcript
chr12	64472797	64472797	*SRGAP1*	Silent	SNP	A	A	T	novel	shanshan_et_al_P99	p.T408T	ENSG00000196935	ENST00000355086	Transcript
chr13	53422047	53422047	*PCDH8*	Silent	SNP	G	G	A	novel	shanshan_et_al_P99	p.A175A	ENSG00000136099	ENST00000377942	Transcript
chr13	66879141	66879141	*PCDH9*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.R1120R	ENSG00000184226	ENST00000544246	Transcript
chr15	92988061	92988061	*ST8SIA2*	Silent	SNP	C	C	A	novel	shanshan_et_al_P99	p.G248G	ENSG00000140557	ENST00000268164	Transcript
chr16	23390074	23390074	*SCNN1B*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.N484N	ENSG00000168447	ENST00000343070	Transcript
chr16	65032724	65032724	*CDH11*	Silent	SNP	A	A	G	novel	shanshan_et_al_P99	p.I88I	ENSG00000140937	ENST00000268603	Transcript
chr17	45219752	45219752	*CDC27*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.R413R	ENSG00000004897	ENST00000531206	Transcript
chr17	58136784	58136784	*HEATR6*	Silent	SNP	T	T	C	rs144009139	shanshan_et_al_P99	p.K574K	ENSG00000068097	ENST00000184956	Transcript
chr18	27057962	27057962	*SMCHD1*	Silent	SNP	A	A	G	rs201805227	shanshan_et_al_P99	p.Q649Q	ENSG00000101596	ENST00000320876	Transcript
chr19	22498424	22498424	*ZNF729*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.T735T	ENSG00000196350	ENST00000601693	Transcript
chr19	39409078	39409078	*SARS2*	Silent	SNP	C	C	T	rs144529043	shanshan_et_al_P99	p.A302A	ENSG00000104835	ENST00000600042	Transcript
chr19	77552987	77552987	*FCER2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P99	p.E205E	ENSG00000104921	ENST00000346664	Transcript
chr2	220343920	220343920	*SPEG*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.S1694S	ENSG00000072195	ENST00000312358	Transcript
chr2	55490860	55490860	*MTIF2*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.T45T	ENSG00000085760	ENST00000394600	Transcript
chr21	28211978	28211978	*ADAMTS1*	Silent	SNP	G	G	T	novel	shanshan_et_al_P99	p.V652V	ENSG00000154734	ENST00000284984	Transcript
chr22	18232904	18232904	*BID*	Silent	SNP	C	C	T	novel	shanshan_et_al_P99	p.R39R	ENSG00000015475	ENST00000317361	Transcript
chr3	132180013	132180013	*DNAJC13*	Silent	SNP	A	A	G	novel	shanshan_et_al_P99	p.V559V	ENSG00000138246	ENST00000260818	Transcript
chr3	31399340	31399340	*IL5RA*	Silent	SNP	T	T	G	novel	shanshan_et_al_P99	p.T136T	ENSG00000091181	ENST00000446632	Transcript
chr3	64607992	64607992	*ADAMTS9*	Silent	SNP	C	C	A	novel	shanshan_et_al_P99	p.V856V	ENSG00000163638	ENST00000498707	Transcript
chr5	134782493	134782493	*C5orf20*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.A102A	ENSG00000251380	ENST00000503143	Transcript
chr5	38412726	38412726	*EGFLAM*	Silent	SNP	C	C	A	novel	shanshan_et_al_P99	p.G490G	ENSG00000164318	ENST00000354891	Transcript
chr5	38506152	38506152	*LIFR*	Silent	SNP	A	A	G	novel	shanshan_et_al_P99	p.L382L	ENSG00000113594	ENST00000263409	Transcript
chr5	488440	488440	*SLC9A3*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.A222A	ENSG00000166230	ENST00000264938	Transcript
chr6	43323428	43323428	*ZNF318*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.A548A	ENSG00000171467	ENST00000361428	Transcript
chr7	27195946	27195946	*HOXA7*	Silent	SNP	G	G	T	novel	shanshan_et_al_P99	p.G73G	ENSG00000122592	ENST00000242159	Transcript
chr8	121021276	121021276	*DEPTOR*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.G335G	ENSG00000155792	ENST00000286234	Transcript
chr8	21560317	21560317	*GFRA2*	Silent	SNP	C	C	T	novel	shanshan_et_al_P99	p.Q406Q	ENSG00000168546	ENST00000052420	Transcript
chr8	72234496	72234496	*EYA1*	Silent	SNP	C	C	T	novel	shanshan_et_al_P99	p.G70G	ENSG00000104313	ENST00000340726	Transcript
chrX	129395744	129395744	*TLR8*	Silent	SNP	T	T	C	novel	shanshan_et_al_P99	p.S805S	ENSG00000101916	ENST00000218032	Transcript
chrX	133379344	133379344	*ATXN3L*	Silent	SNP	T	T	A	novel	shanshan_et_al_P99	p.L40L	ENSG00000123594	ENST00000380622	Transcript

Table S6A

Mutated genes (nonsynonymous) in each group

IDH-gr (n=1306)	KRAS-gr (n=1051)	TP53-gr (n=2630)	Undetermined-gr (n=1991)
A4GNT	*A4GNT*	*A1CF*	*A2M*
ABCA13	*ABCA1*	*AADACL4*	*AADAC*
ABCA7	*ABCA3*	*AAK1*	*AATF*
ABCA9	*ABCD3*	*AARD*	*ABCA1*
ABCB10	*ABCG1*	*ABCA1*	*ABCA10*
ABCC11	*ABHD16B*	*ABCA12*	*ABCA12*
ABCC3	*AC007952.5*	*ABCA13*	*ABCA13*
ABCC4	*ACACB*	*ABCA2*	*ABCA4*
ABCC9	*ACIN1*	*ABCA5*	*ABCA7*
ACACB	*ACSS3*	*ABCA7*	*ABCB11*
ACAD9	*ACTL8*	*ABCB9*	*ABCB7*
ACPL2	*ACTR1B*	*ABCC1*	*ABCC12*
ACSBG2	*ACVR1B*	*ABCC2*	*ABCC5*
ACSF2	*ADAM21*	*ABCD2*	*ABCC6*
ACSL5	*ADAM28*	*ABCD3*	*ABCD2*
ADAM18	*ADAMTS12*	*ABCG2*	*ABCD3*
ADAM22	*ADAMTS18*	*ABL2*	*ABCG2*
ADAMTS6	*ADD3*	*ABRA*	*ABHD17A*
ADAT1	*ADNP2*	*ABTB2*	*ABL1*
ADCY4	*ADPRHL1*	*ACACA*	*ABLIM1*
ADCY5	*ADSS*	*ACAD10*	*ACACA*
ADSL	*AGAP2*	*ACAD11*	*ACAD11*
AFF2	*AGAP4*	*ACAD9*	*ACCSL*
AGXT2	*AHI1*	*ACE*	*ACER3*
AHCTF1	*AHNAK2*	*ACHE*	*ACLY*
AHI1	*AHRR*	*ACIN1*	*ACRV1*
AIFM1	*AIFM1*	*ACKR3*	*ACSL1*
AKAP12	*AIG1*	*ACLY*	*ACSM2A*
AKAP13	*AKAP13*	*ACRV1*	*ACSM2B*
AKAP8	*AKAP8*	*ACSL4*	*ACSM4*
AKAP8L	*AKAP9*	*ACSM5*	*ACSS3*
AKIRIN2	*AKNAD1*	*ACTA1*	*ACTG1*
ALAS1	*ALMS1*	*ACTG2*	*ACTL10*
ALDH1L2	*ALPK2*	*ACTL10*	*ACTRT1*
ALDH3A1	*ALX4*	*ACTR8*	*ADAM30*
ALG8	*AMHR2*	*ACTRT1*	*ADAM9*
ALKBH2	*AMPD1*	*ACTRT2*	*ADAMTS12*
ALKBH8	*ANHX*	*ACVR1B*	*ADAMTS16*

ALOX5AP	*ANK3*	*ACVR2A*	*ADAMTS17*
ALPK3	*ANKFY1*	*ADAM11*	*ADAMTS7*
ALS2CR11	*ANKMY1*	*ADAM17*	*ADAMTS9*
AMBP	*ANKRD17*	*ADAM28*	*ADCY2*
AMD1	*ANKRD20A4*	*ADAM29*	*ADH6*
AMICA1	*ANKRD26*	*ADAM32*	*AEBP2*
AMMECR1L	*ANKRD27*	*ADAM8*	*AFAP1*
AMPD1	*ANKRD30A*	*ADAMTS12*	*AFF1*
ANGPT2	*ANKRD30B*	*ADAMTS14*	*AFF2*
ANGPT4	*ANKRD31*	*ADAMTS15*	*AGAP10*
ANK1	*ANKRD36*	*ADAMTS7*	*AGAP2*
ANKAR	*ANKS1A*	*ADAMTS8*	*AGAP3*
ANKHD1	*ANO3*	*ADAMTS9*	*AGAP4*
ANKIB1	*ANO5*	*ADAMTSL1*	*AGAP5*
ANKK1	*ANO6*	*ADAMTSL3*	*AGGF1*
ANKLE2	*ANPEP*	*ADAMTSL5*	*AGPAT6*
ANKRD26	*ANTXR2*	*ADAP1*	*AHCYL2*
ANKRD30A	*AOC3*	*ADARB2*	*AHNAK*
ANKRD33B	*APBA2*	*ADCK2*	*AHNAK2*
ANKRD36	*APC*	*ADCY5*	*AK9*
ANKS1B	*APC2*	*ADD2*	*AKAP11*
ANO4	*APOE*	*ADGB*	*AKAP6*
ANO6	*AQP1*	*ADH1C*	*AKAP9*
AP1M2	*AR*	*ADPRHL1*	*ALDH5A1*
AP3D1	*ARHGAP31*	*ADRA1D*	*ALG10*
APAF1	*ARHGAP33*	*ADRA2B*	*ALG1L*
APBB2	*ARHGAP35*	*ADSL*	*ALG9*
APOB	*ARHGAP5*	*AFAP1*	*ALKBH8*
AR	*ARHGEF11*	*AFF3*	*ALMS1*
ARAP3	*ARHGEF40*	*AGAP1*	*ALPK1*
ARFGEF1	*ARID1A*	*AGAP10*	*ALPK2*
ARHGAP12	*ARL2BP*	*AGAP2*	*ALPK3*
ARHGAP32	*ARMC3*	*AGAP3*	*ALS2*
ARHGEF11	*ARMCX4*	*AGAP4*	*ALS2CR12*
ARHGEF25	*ARPP21*	*AGBL3*	*AMER3*
ARHGEF3	*ARR3*	*AGPAT6*	*ANAPC5*
ARID1A	*ASAP2*	*AGPAT9*	*ANGPTL4*
ARID1B	*ASCC3*	*AGRN*	*ANK1*
ARID5A	*ASXL3*	*AGTPBP1*	*ANK2*
ARID5B	*ATM*	*AGXT2*	*ANKFN1*
ARMC9	*ATP10A*	*AHCTF1*	*ANKK1*

ARMCX2	*ATP10D*	*AHNAK*	*ANKMY1*
ARSH	*ATP2A3*	*AHNAK2*	*ANKRA2*
ASAP1	*ATPAF2*	*AHRR*	*ANKRD20A4*
ASAP2	*ATPIF1*	*AIFM1*	*ANKRD26*
ASB14	*ATRN*	*AIM1L*	*ANKRD30A*
ASIC3	*ATRNL1*	*AK2*	*ANKRD35*
ASNA1	*AVEN*	*AK9*	*ANKRD36*
ATG2B	*AVPR1A*	*AKAP1*	*ANKRD40*
ATG3	*B4GALNT1*	*AKAP12*	*ANKS1B*
ATG4D	*B4GALNT4*	*AKAP7*	*ANO2*
ATN1	*BARHL2*	*AKNA*	*ANO3*
ATP12A	*BCAT1*	*AKNAD1*	*ANO6*
ATP13A2	*BCORL1*	*AKT3*	*ANXA3*
ATP2A1	*BEND5*	*AKTIP*	*ANXA6*
ATP6AP2	*BHLHE22*	*ALB*	*AP4E1*
ATP8A2	*BMP15*	*ALDH16A1*	*APC*
ATP8B2	*BNC1*	*ALDH2*	*APLP1*
ATXN1L	*BPIFB4*	*ALDH3A1*	*APLP2*
AUTS2	*BPTF*	*ALG13*	*APOB*
AXDND1	*BRAF*	*ALLC*	*APOBEC4*
B3GALTL	*BRCA1*	*ALMS1*	*APP*
BAIAP2L1	*BRSK1*	*ALOXE3*	*AQP7*
BAP1	*BRWD3*	*ALPL*	*ARFGAP2*
BAZ1A	*BSN*	*ALPPL2*	*ARFGEF1*
BAZ2B	*BTG4*	*AMPH*	*ARFGEF2*
BBS7	*BTN3A3*	*ANAPC7*	*ARHGAP11B*
BCAS2	*BZRAP1*	*ANGPTL4*	*ARHGAP15*
BCL11A	*C10orf71*	*ANK3*	*ARHGAP20*
BCL2L11	*C10orf90*	*ANKAR*	*ARHGAP21*
BCLAF1	*C12orf77*	*ANKH*	*ARHGAP23*
BCO2	*C16orf62*	*ANKRA2*	*ARHGAP24*
BEND2	*C1orf141*	*ANKRD11*	*ARHGAP25*
BMPR2	*C2CD4C*	*ANKRD13B*	*ARHGAP32*
BOD1	*C7orf55-LUC7L2*	*ANKRD18A*	*ARHGAP5*
BPTF	*C8A*	*ANKRD18B*	*ARHGEF11*
BRD8	*CA4*	*ANKRD20A1*	*ARHGEF15*
BRDT	*CACNA1A*	*ANKRD26*	*ARHGEF17*
BRIP1	*CACNA1C*	*ANKRD26P1*	*ARHGEF28*
BTF3	*CACNA1D*	*ANKRD30A*	*ARHGEF33*
BTK	*CACNA2D3*	*ANKRD30B*	*ARHGEF39*
BTN3A2	*CACNG3*	*ANKRD34A*	*ARHGEF4*

BUB1B	*CAMSAP3*	*ANKRD35*	*ARID1A*
C10orf113	*CAPN15*	*ANKRD36*	*ARL6IP6*
C10orf76	*CASD1*	*ANKRD46*	*ARMC3*
C11orf71	*CASP8*	*ANKRD62*	*ARMCX4*
C16orf11	*CAST*	*ANKRD7*	*ARSG*
C17orf66	*CBFA2T3*	*ANKS1B*	*ARSH*
C17orf72	*CBLB*	*ANKS3*	*ARTN*
C17orf78	*CBLN4*	*ANKS4B*	*ARVCF*
C17orf97	*CCAR2*	*ANLN*	*ASB11*
C19orf26	*CCDC113*	*ANO6*	*ASB14*
C19orf33	*CCDC116*	*ANPEP*	*ASCC3*
C19orf60	*CCDC122*	*ANXA2*	*ASH1L*
C1orf112	*CCDC148*	*AP3B1*	*ASIC4*
C1orf159	*CCDC158*	*AP3B2*	*ASPH*
C1orf27	*CCDC159*	*AP3D1*	*ASPM*
C1orf87	*CCDC178*	*APEX1*	*ASTN1*
C22orf42	*CCDC30*	*APH1A*	*ATAD3C*
C2CD3	*CCDC62*	*APLP1*	*ATG2B*
C2orf54	*CCDC88B*	*APOB*	*ATG7*
C2orf71	*CCR6*	*APOBEC3A*	*ATL1*
C3orf30	*CCSER2*	*APP*	*ATM*
C6	*CCT6A*	*AQR*	*ATN1*
C7orf26	*CCT6B*	*AR*	*ATP13A1*
C9orf156	*CDC25B*	*ARAF*	*ATP13A2*
C9orf173	*CDC27*	*ARAP3*	*ATP13A3*
CA7	*CDH10*	*ARFGAP2*	*ATP13A5*
CACNA1B	*CDH11*	*ARHGAP21*	*ATP1B3*
CACNA1D	*CDH3*	*ARHGAP23*	*ATP6AP2*
CACNA1H	*CDH6*	*ARHGAP36*	*ATP6V0A1*
CACNA1I	*CDH7*	*ARHGAP5*	*ATP8B1*
CACNA2D1	*CDH9*	*ARHGEF17*	*ATRN*
CACNA2D3	*CDHR4*	*ARHGEF25*	*ATRX*
CALCOCO1	*CDK12*	*ARHGEF38*	*AUNIP*
CALCOCO2	*CDK19*	*ARHGEF40*	*AXIN1*
CALCR	*CDX2*	*ARID1A*	*AXIN2*
CAMK2B	*CDYL*	*ARID1B*	*AZI1*
CAMK2G	*CEACAM18*	*ARID2*	*B3GALT1*
CAMTA1	*CELF3*	*ARID5A*	*BAIAP2L1*
CAPNS1	*CELSR2*	*ARL5C*	*BAP1*
CARD10	*CEP152*	*ARL6IP6*	*BAZ2B*
CARNS1	*CEP192*	*ARMC3*	*BBS2*

CASC1	*CEP290*	*ARMCX1*	*BBS7*
CASKIN1	*CFTR*	*ARPC5*	*BBS9*
CAST	*CHD3*	*ARSA*	*BCL2L13*
CASZ1	*CHD4*	*ARSD*	*BCLAF1*
CATSPERG	*CHD6*	*ARSJ*	*BDP1*
CBFB	*CHD8*	*ASB17*	*BEGAIN*
CBWD6	*CHMP7*	*ASCC2*	*BEND2*
CC2D1B	*CHST6*	*ASIC1*	*BEND3*
CCDC175	*CHST8*	*ASNS*	*BEND5*
CCDC181	*CHSY1*	*ASNSD1*	*BEST2*
CCDC38	*CHUK*	*ASTL*	*BHLHE22*
CCDC39	*CKAP5*	*ATAD2B*	*BICC1*
CCDC42	*CLDN6*	*ATG13*	*BIRC2*
CCDC73	*CLDND2*	*ATG2B*	*BIRC6*
CCDC78	*CLPB*	*ATG4A*	*BLVRA*
CCDC80	*CMTM4*	*ATG5*	*BLZF1*
CCDC88A	*CNPY3*	*ATM*	*BMP3*
CCNI	*CNR1*	*ATP10A*	*BMPR1A*
CCNT1	*CNTNAP2*	*ATP10B*	*BMX*
CCR4	*CNTNAP3B*	*ATP11B*	*BNC2*
CCSER2	*CNTNAP5*	*ATP11C*	*BOD1L1*
CCT8L2	*COA3*	*ATP13A1*	*BPTF*
CD1B	*COBLL1*	*ATP13A2*	*BRAF*
CD1E	*COG6*	*ATP13A3*	*BRCA1*
CD36	*COL11A1*	*ATP13A5*	*BRCA2*
CD44	*COL12A1*	*ATP1A3*	*BRD8*
CD72	*COL22A1*	*ATP1A4*	*BRPF3*
CD86	*COL25A1*	*ATP2C2*	*BRWD3*
CD99L2	*COL7A1*	*ATP5G2*	*BSN*
CDC27	*CP*	*ATP8A1*	*BTAF1*
CDC5L	*CPB1*	*ATP8B3*	*BTBD11*
CDKL3	*CR1*	*ATP8B4*	*BTBD7*
CDRT15	*CRCP*	*ATPAF2*	*BTBD9*
CECR2	*CREB5*	*ATR*	*BTG3*
CELF2	*CREBBP*	*ATRIP*	*BTN3A3*
CENPBD1	*CREBZF*	*ATRN*	*BTRC*
CENPJ	*CRHBP*	*ATRNL1*	*C10orf118*
CEP104	*CROCC*	*ATXN7L2*	*C10orf76*
CEP152	*CRTC3*	*AUTS2*	*C10orf90*
CFHR3	*CSGALNACT2*	*AVL9*	*C11orf1*
CFI	*CSMD1*	*AXDND1*	*C11orf24*

CHAF1A	*CSMD2*	*AXIN1*	*C11orf65*
CHD5	*CSPG4*	*B3GALTL*	*C11orf80*
CHD7	*CST8*	*B3GNT1*	*C12orf43*
CHD8	*CSTF2*	*B4GALNT1*	*C14orf159*
CHIC1	*CT47B1*	*B4GALNT3*	*C14orf37*
CHM	*CTBP2*	*BACH2*	*C14orf80*
CHN1	*CTNNA1*	*BAI1*	*C16orf11*
CHST15	*CTNNA3*	*BAI2*	*C17orf89*
CHST4	*CTNNB1*	*BAI3*	*C17orf97*
CKM	*CTSF*	*BAZ1B*	*C19orf44*
CLDN16	*CTSH*	*BAZ2A*	*C19orf47*
CLEC18A	*CTTNBP2*	*BBOX1*	*C1QB*
CLSPN	*CUBN*	*BBS1*	*C1QTNF5*
CLTA	*CUL9*	*BBS7*	*C1orf172*
CLTC	*CWF19L2*	*BCAM*	*C1orf173*
CLTCL1	*CX3CR1*	*BCAR1*	*C1orf185*
CMTM2	*CXCR4*	*BCAR3*	*C1orf192*
CMTM8	*CYLC1*	*BCHE*	*C1orf194*
CMTR1	*CYLC2*	*BCL10*	*C20orf112*
CNDP1	*CYP11B2*	*BCL9*	*C20orf26*
CNGA2	*CYP21A2*	*BCORL1*	*C2CD3*
CNKSR2	*CYP2A13*	*BDH1*	*C2orf16*
CNN3	*CYSLTR2*	*BDP1*	*C3*
CNOT4	*CYTH3*	*BEND4*	*C3orf83*
CNTN2	*DALRD3*	*BGN*	*C4A*
CNTN4	*DAPK3*	*BHLHE22*	*C4B*
CNTNAP5	*DBF4*	*BIRC6*	*C4orf33*
COASY	*DCAF4L1*	*BMP6*	*C5*
COG5	*DCAF8*	*BMP8B*	*C5orf42*
COG6	*DCAF8L1*	*BPHL*	*C7orf25*
COL15A1	*DCLK1*	*BPI*	*C7orf63*
COL2A1	*DCLK3*	*BRCA2*	*C8orf48*
COL3A1	*DDX41*	*BRCC3*	*C8orf76*
COL5A1	*DDX52*	*BRD1*	*C9orf171*
COL6A1	*DDX59*	*BRINP2*	*C9orf173*
COL6A5	*DENND4B*	*BRWD1*	*C9orf3*
COL9A1	*DEPDC1*	*BSG*	*C9orf43*
COLGALT2	*DET1*	*BSND*	*CA2*
COMMD9	*DGCR14*	*BTBD11*	*CA5A*
COPB1	*DGKG*	*BTN3A3*	*CA8*
COPG1	*DHX36*	*BTNL9*	*CA9*

CPA2	*DIP2A*	*C10orf113*	*CACNA1C*
CPAMD8	*DLAT*	*C10orf12*	*CACNA2D1*
CPO	*DLG2*	*C10orf71*	*CADM1*
CR1	*DLX1*	*C11orf54*	*CADPS*
CRB1	*DLX4*	*C11orf57*	*CALHM3*
CREB1	*DMRTB1*	*C11orf80*	*CAMK2A*
CREBBP	*DMXL1*	*C11orf82*	*CAMK4*
CRNKL1	*DNAH1*	*C12orf10*	*CAMTA1*
CROCC	*DNAH14*	*C12orf60*	*CAMTA2*
CRYBB1	*DNAH3*	*C14orf39*	*CAPN2*
CRYBB2	*DNAH5*	*C16orf3*	*CAPN7*
CSMD1	*DNAH6*	*C17orf104*	*CAPN9*
CSNK1D	*DNAH8*	*C17orf96*	*CAPS2*
CSNK1G1	*DNAJB5*	*C17orf97*	*CASC1*
CSPG4	*DNAJC21*	*C17orf98*	*CASD1*
CSRNP2	*DNM2*	*C18orf56*	*CASK*
CT45A5	*DOCK6*	*C19orf26*	*CASP14*
CT55	*DOCK8*	*C19orf57*	*CASP3*
CTBP2	*DOT1L*	*C1RL*	*CASR*
CTCFL	*DPP9*	*C1orf106*	*CAST*
CTNNA3	*DPRX*	*C1orf127*	*CATSPERB*
CTR9	*DPYSL3*	*C1orf141*	*CBLB*
CUBN	*DSE*	*C1orf167*	*CCAR1*
CUL1	*DTWD1*	*C1orf173*	*CCDC108*
CUL3	*DTX3L*	*C1orf185*	*CCDC112*
CUL5	*DUOX2*	*C1orf35*	*CCDC132*
CUL9	*DUS2*	*C1orf94*	*CCDC140*
CWC27	*DUX4L4*	*C20orf26*	*CCDC144A*
CWH43	*DZANK1*	*C22orf39*	*CCDC158*
CXXC1	*E2F1*	*C22orf43*	*CCDC175*
CXorf30	*E2F5*	*C2CD5*	*CCDC30*
CXorf66	*EBF1*	*C2orf43*	*CCDC47*
CYB5R3	*EBF2*	*C2orf49*	*CCDC6*
CYBRD1	*EBPL*	*C3*	*CCDC64*
CYFIP1	*EFCAB6*	*C4orf29*	*CCDC64B*
CYP17A1	*EIF2AK3*	*C4orf51*	*CCDC70*
CYP26A1	*EIF2B5*	*C5*	*CCDC79*
CYP2A6	*EIF4G2*	*C5orf22*	*CCDC82*
CYP2C19	*ELAC2*	*C5orf42*	*CCDC88A*
DAB1	*ELFN2*	*C5orf51*	*CCDC89*
DACH1	*EMR3*	*C6*	*CCDC92*

DAPK1	*EPB41L4A*	*C6ORF165*	*CCDC93*
DAPK3	*EPHA2*	*C6orf118*	*CCER1*
DAW1	*EPHA6*	*C7orf25*	*CCT2*
DCAF6	*EPHB1*	*C7orf31*	*CCT6B*
DCC	*EPPK1*	*C9orf37*	*CD109*
DDHD1	*ERBB3*	*C9orf84*	*CD160*
DDX19A	*ERC1*	*CA11*	*CD1A*
DDX19B	*ERN1*	*CABS1*	*CD1C*
DDX25	*ESR1*	*CACNA1A*	*CD276*
DDX26B	*ESRRG*	*CACNA1B*	*CD28*
DDX39A	*ETAA1*	*CACNA1C*	*CD37*
DDX5	*ETV6*	*CACNA1D*	*CD46*
DDX56	*EVPL*	*CACNA1E*	*CD8B*
Dec/01	*EYA1*	*CACNA1F*	*CD99L2*
DEFA4	*F2RL1*	*CACNA1H*	*CDAN1*
DENND4A	*F9*	*CACNA1I*	*CDC25C*
DHX15	*FAAH*	*CACNA1S*	*CDC27*
DHX57	*FAM129B*	*CACNA2D1*	*CDC42BPA*
DIP2B	*FAM135B*	*CACNA2D2*	*CDC7*
DKC1	*FAM169B*	*CACNA2D3*	*CDH26*
DKK4	*FAM170A*	*CACNG3*	*CDH8*
DLEC1	*FAM171A1*	*CACNG8*	*CDHR2*
DMKN	*FAM179B*	*CADPS*	*CDKAL1*
DNAH14	*FAM189A1*	*CALCOCO2*	*CDKN2B*
DNAH17	*FAM189B*	*CALCRL*	*CDV3*
DNAH2	*FAM194A*	*CAMK2B*	*CEACAM16*
DNAH5	*FAM209B*	*CAMKK2*	*CELF3*
DNAH9	*FAM47A*	*CAMSAP1*	*CELSR1*
DNAJA2	*FANCB*	*CAMTA1*	*CELSR3*
DNAJC11	*FAT3*	*CAND1*	*CENPF*
DNAJC13	*FAXDC2*	*CAPN14*	*CENPI*
DNAJC5G	*FBXL13*	*CAPN15*	*CENPU*
DND1	*FBXO40*	*CAPN5*	*CEP128*
DOCK10	*FCGBP*	*CAPN6*	*CEP152*
DOCK3	*FCGR3B*	*CAPRIN2*	*CEP350*
DPPA2	*FDFT1*	*CAPS*	*CEP55*
DPYSL3	*FER1L6*	*CAPZA2*	*CHD1L*
DQX1	*FGF11*	*CARD6*	*CHD8*
DRAXIN	*FGFR2*	*CARF*	*CHRD*
DSCAM	*FKBP2*	*CASC5*	*CHSY3*
DSCAML1	*FLRT1*	*CASP5*	*CIC*

DSE	*FLT4*	*CASZ1*	*CIRH1A*
DST	*FNDC3A*	*CAT*	*CIT*
DUOX1	*FOXD4*	*CATSPERG*	*CIZ1*
DUSP27	*FOXI2*	*CBFA2T3*	*CLASP2*
DUX4L4	*FOXP3*	*CBLC*	*CLCA1*
DYSF	*FREM3*	*CBX2*	*CLCA4*
ECE2	*FRG2B*	*CBX4*	*CLCN4*
EFCAB14	*FRRS1L*	*CC2D1A*	*CLCNKA*
EFCAB7	*FRY*	*CC2D2A*	*CLEC4F*
EFNB2	*FSCB*	*CCDC105*	*CLGN*
EFTUD1	*FSCN2*	*CCDC116*	*CLIC5*
EGF	*FSTL4*	*CCDC135*	*CLMN*
EHBP1L1	*FTCD*	*CCDC144A*	*CLSTN1*
EHMT1	*FTMT*	*CCDC168*	*CLTCL1*
EIF2AK3	*FXR2*	*CCDC174*	*CNKSR2*
EIF3A	*G6PC3*	*CCDC176*	*CNOT1*
EIF3K	*GAB4*	*CCDC30*	*CNOT8*
EIF3M	*GALNT9*	*CCDC33*	*CNTN4*
EIF4ENIF1	*GAPDHS*	*CCDC57*	*CNTN6*
ELMO2	*GART*	*CCDC62*	*CNTNAP2*
ELN	*GAS2*	*CCDC66*	*CNTNAP3B*
ELOVL6	*GAS6*	*CCDC82*	*CNTROB*
ELTD1	*GATA1*	*CCDC85B*	*COG1*
ENG	*GATA6*	*CCDC9*	*COG3*
ENHO	*GBP5*	*CCK*	*COIL*
ENO1	*GCC1*	*CCM2*	*COL10A1*
ENOX2	*GCK*	*CCNF*	*COL12A1*
EP400	*GDPD4*	*CCNK*	*COL1A2*
EPB41L3	*GFI1*	*CCNL1*	*COL21A1*
EPB41L4A	*GIGYF1*	*CCPG1*	*COL25A1*
EPB42	*GLTPD2*	*CCSER1*	*COL3A1*
EPHA2	*GLTSCR1*	*CD163L1*	*COL4A3BP*
EPHA7	*GOLGA6A*	*CD19*	*COL4A4*
EPHX2	*GOLGA8J*	*CD1B*	*COL4A5*
EPHX4	*GOLGA8K*	*CD247*	*COL5A1*
EPPK1	*GOT1*	*CD276*	*COL6A2*
ERAP1	*GOT2*	*CD33*	*COL9A1*
ERBB4	*GPBAR1*	*CD38*	*COLEC10*
ERC1	*GPI*	*CD70*	*COMMD2*
ERF	*GPN1*	*CD9*	*COMP*
ERN1	*GPNMB*	*CDC25B*	*COQ9*

ERVMER34-1	*GPR110*	*CDC25C*	*CORIN*
ESCO1	*GPR112*	*CDC27*	*COX5B*
ESPN	*GPR20*	*CDC42BPB*	*COX7A2*
ESRP1	*GPR27*	*CDC7*	*CPA2*
ETAA1	*GPR37*	*CDCA3*	*CPA5*
ETV4	*GPRIN3*	*CDH10*	*CPA6*
ETV6	*GRIA2*	*CDH13*	*CPAMD8*
EVI5	*GRID2*	*CDH19*	*CPB1*
EXOC3L4	*GRIN2B*	*CDH23*	*CPNE3*
EXOC6B	*GRK5*	*CDH4*	*CPNE8*
EXOSC10	*GRK7*	*CDH7*	*CPZ*
EYA1	*GRM8*	*CDH9*	*CRAMP1L*
F13B	*GSE1*	*CDIPT*	*CRAT*
F5	*GTF2H2C*	*CDK5*	*CRB1*
F9	*GUCY1A2*	*CDK6*	*CREB3*
FABP6	*GYPA*	*CDKL3*	*CREB3L1*
FADS2	*HAUS5*	*CDKL5*	*CRIP3*
FAM118B	*HDLBP*	*CEACAM5*	*CRIPAK*
FAM120A	*HEATR2*	*CEACAM6*	*CRKL*
FAM122A	*HECTD2*	*CECR6*	*CRMP1*
FAM149B1	*HELZ2*	*CELSR2*	*CRYGA*
FAM155A	*HERPUD1*	*CELSR3*	*CRYM*
FAM178B	*HIP1*	*CENPB*	*CS*
FAM181B	*HIST1H2AA*	*CENPC*	*CSE1L*
FAM184B	*HIST1H2BC*	*CENPE*	*CSGALNACT2*
FAM186B	*HIST1H4E*	*CEP112*	*CSMD1*
FAM193B	*HLA-DQB1*	*CEP135*	*CSMD3*
FAM19A2	*HLA-G*	*CEP290*	*CSRNP2*
FAM21A	*HMCN1*	*CEP350*	*CSTA*
FAM222B	*HOMER1*	*CERCAM*	*CTAGE8*
FAM3C	*HOOK1*	*CFHR3*	*CTAGE9*
FAM46C	*HOOK2*	*CFI*	*CTBP2*
FAM49B	*HOXA11*	*CFTR*	*CTCFL*
FANCD2	*HOXA13*	*CGNL1*	*CTDSP2*
FAR1	*HOXC9*	*CHD4*	*CTNNA2*
FBF1	*HPN*	*CHD5*	*CTNND2*
FBN1	*HRCT1*	*CHD6*	*CUBN*
FBN2	*HRNR*	*CHD7*	*CUL1*
FBXL4	*HSPB8*	*CHDH*	*CWH43*
FBXL7	*HTR1A*	*CHEK2*	*CXCL13*
FBXO38	*HUWE1*	*CHIC1*	*CXXC11*

FBXO48	*HYDIN*	*CHKB*	*CXorf38*
FBXW4	*IDH1*	*CHL1*	*CYB5R1*
FBXW7	*IGBP1*	*CHMP1A*	*CYB5R3*
FBXW8	*IGDCC3*	*CHMP2B*	*CYB5R4*
FCGBP	*IGF2BP3*	*CHPF2*	*CYP2C18*
FEZF2	*IGF2R*	*CHRNB2*	*CYP2C19*
FGD6	*IGFL1*	*CHST10*	*CYP2E1*
FGG	*IGFN1*	*CHST15*	*CYP2F1*
FHL1	*IL7*	*CHUK*	*CYP4F22*
FKBP3	*IL7R*	*CIITA*	*CYP7B1*
FLG	*IMPA1*	*CINP*	*D2HGDH*
FLII	*IMPG1*	*CITED1*	*DAAM1*
FLT4	*ING2*	*CKAP2*	*DAB2IP*
FN1	*INPP4B*	*CKAP5*	*DAW1*
FNDC3B	*IRS2*	*CKS1B*	*DAZL*
FOCAD	*IRX1*	*CLASRP*	*DBH*
FOXP1	*ITGA11*	*CLCA4*	*DBX1*
FRAS1	*ITLN1*	*CLCN4*	*DCAF15*
FRG1	*ITPK1*	*CLCN6*	*DCAF6*
FRK	*ITPKB*	*CLCN7*	*DCLK1*
FRMPD4	*JAK2*	*CLCNKB*	*DCLK2*
FRRS1L	*KCNA3*	*CLEC17A*	*DCP2*
FRZB	*KCNA5*	*CLEC3B*	*DCT*
FTO	*KCNMA1*	*CLIC5*	*DCTN1*
FTSJ1	*KCNN3*	*CLIP1*	*DCTN6*
FUT10	*KCNQ4*	*CLIP4*	*DCUN1D1*
FXYD4	*KCNQ5*	*CLMN*	*DDX28*
FZD2	*KCTD1*	*CLNK*	*DDX41*
G6PC	*KDM5C*	*CLPTM1*	*DDX50*
GABBR2	*KIAA1009*	*CLPX*	*DDX53*
GABPB2	*KIAA1109*	*CLSPN*	*DDX55*
GABRA5	*KIAA1549L*	*CLUH*	*DDX58*
GABRR1	*KIAA1755*	*CMTR2*	*DDX59*
GAGE2C	*KIAA1919*	*CNBP*	*DDX6*
GALT	*KIF27*	*CNGA3*	*DDX60L*
GARS	*KIF3B*	*CNGA4*	*DENND4C*
GATAD1	*KIF4A*	*CNGB3*	*DFNB31*
GFPT2	*KIR2DL3*	*CNKSR1*	*DGKZ*
GGA3	*KIRREL2*	*CNNM2*	*DIRC2*
GHDC	*KL*	*CNTLN*	*DIS3*
GJB1	*KLC2*	*CNTN1*	*DLAT*

GKAP1	*KLHL12*	*CNTN2*	*DLD*
GLB1L	*KLHL30*	*CNTN3*	*DLG1*
GLIS1	*KLHL5*	*CNTNAP2*	*DLGAP5*
GLP2R	*KLRC2*	*CNTNAP5*	*DLX5*
GNAS	*KLRG1*	*COA3*	*DMD*
GNB5	*KMT2B*	*COBLL1*	*DMGDH*
GNL3L	*KMT2C*	*COG3*	*DMTF1*
GOLGA1	*KMT2D*	*COL11A1*	*DMXL2*
GOLGA6L1	*KPNA2*	*COL12A1*	*DNAH1*
GOLGA8J	*KPRP*	*COL14A1*	*DNAH14*
GON4L	*KRAS*	*COL15A1*	*DNAH17*
GPC3	*KRT10*	*COL19A1*	*DNAH2*
GPC6	*KRT36*	*COL1A2*	*DNAH3*
GPI	*KRT6C*	*COL22A1*	*DNAH5*
GPM6B	*KRT71*	*COL24A1*	*DNAH6*
GPR112	*KRT80*	*COL3A1*	*DNAJB14*
GPR113	*KRTAP9-8*	*COL4A2*	*DNAJC1*
GPR124	*LANCL3*	*COL4A5*	*DNASE1L1*
GPR17	*LARP1*	*COL5A1*	*DNHD1*
GPR21	*LARP1B*	*COL6A2*	*DNMT1*
GPR83	*LCT*	*COL6A5*	*DOCK10*
GPR89A	*LETMD1*	*COL7A1*	*DOCK11*
GPR98	*LGR6*	*COL9A2*	*DOCK2*
GPRASP1	*LILRA2*	*COL9A3*	*DOCK8*
GRB7	*LILRA3*	*COMMD5*	*DOCK9*
GRHL3	*LIMK2*	*COMP*	*DOK4*
GRIA1	*LMF2*	*COQ10A*	*DOK5*
GRIA3	*LMTK2*	*COQ2*	*DOT1L*
GRIK3	*LONP2*	*COQ3*	*DPM1*
GRIN2C	*LPCAT1*	*COX18*	*DPP4*
GRM5	*LPHN3*	*CPA3*	*DPP9*
GSC	*LPIN3*	*CPB1*	*DPY19L3*
GSDMA	*LRCH2*	*CPE*	*DQX1*
GSK3A	*LRP1B*	*CPEB2*	*DSC1*
GSPT1	*LRRC70*	*CPSF3*	*DSC2*
GSTM5	*LRRFIP1*	*CPSF3L*	*DSC3*
GTPBP4	*LRRIQ1*	*CPXM2*	*DSG2*
GUCY1A3	*LRRIQ3*	*CREB3L3*	*DSG4*
GUF1	*LRRK1*	*CREBBP*	*DSP*
GYLTL1B	*LRRN3*	*CRH*	*DST*
HAL	*LRTM1*	*CRHBP*	*DTHD1*

HAS1	*LSP1*	*CRHR1*	*DTL*
HCFC1	*LTBR*	*CRNKL1*	*DTX3*
HDX	*LTN1*	*CRTAC1*	*DUSP21*
HEATR3	*LUC7L3*	*CSDC2*	*DYM*
HEATR5B	*LUZP4*	*CSF2RA*	*DYNC1H1*
HECW2	*LYN*	*CSMD1*	*DYNC1I1*
HERC5	*LYPLA1*	*CSMD3*	*DYNC1LI1*
HIPK2	*M1AP*	*CST1*	*DYRK1B*
HIPK3	*MACF1*	*CSTF3*	*DYTN*
HIST1H1E	*MAGI2*	*CT47A6*	*DZANK1*
HK1	*MAMLD1*	*CTAGE9*	*E2F8*
HLA-DQA2	*MANSC4*	*CTDSP2*	*ECE2*
HLA-DRB5	*MAP1A*	*CTNNA1*	*ECM2*
HMCN1	*MAP2*	*CTNNAL1*	*ECT2*
HMGCS2	*MAP3K1*	*CTNND1*	*EDNRB*
HOMER1	*MAP3K3*	*CTR9*	*EEA1*
HOMEZ	*MAP3K4*	*CTSE*	*EED*
HOXA4	*MAPKAP1*	*CTSH*	*EEF1B2*
HOXB8	*MARS*	*CTU2*	*EEF2K*
HOXC10	*MASP1*	*CUL7*	*EFCAB6*
HOXC11	*MBD2*	*CUX1*	*EFTUD2*
HPS5	*MC4R*	*CWH43*	*EGF*
HRC	*MCF2L2*	*CXCR5*	*EGR1*
HS6ST2	*MCM8*	*CXorf21*	*EHD2*
HSDL2	*MDGA2*	*CXorf27*	*EHF*
HSPG2	*MDH2*	*CXorf38*	*EIF2AK3*
HTATSF1	*MED12*	*CYB561*	*EIF3D*
HTR3B	*MED12L*	*CYBB*	*EIF3E*
HTR5A	*MEF2D*	*CYFIP1*	*EIF4A3*
HTT	*METTL14*	*CYFIP2*	*EMR2*
HUWE1	*METTL22*	*CYLC2*	*ENGASE*
HYDIN	*MICU1*	*CYLD*	*ENKUR*
IBSP	*MID1IP1*	*CYP11A1*	*ENOPH1*
IDE	*MLLT10*	*CYP2A7*	*ENPP2*
IDH1	*MMP16*	*CYP2B6*	*ENPP3*
IDH2	*MMS22L*	*CYP3A43*	*EP300*
IFIH1	*MORC1*	*CYP3A5*	*EPB41*
IFNA7	*MPPED1*	*CYP4A22*	*EPB41L1*
IFT122	*MROH2B*	*CYP7A1*	*EPB41L2*
IFT46	*MRPL23*	*CYP8B1*	*EPB41L5*
IFT81	*MSN*	*CYTH4*	*EPC1*

IGF1R	*MST1*	*CYYR1*	*EPC2*
IGF2R	*MTA3*	*DAB2*	*EPG5*
IGFN1	*MTMR4*	*DAB2IP*	*EPHA2*
IGSF1	*MTNR1B*	*DACT1*	*EPHA4*
IGSF22	*MTO1*	*DAG1*	*EPHA5*
IGSF3	*MYCBPAP*	*DCAF13*	*EPHA6*
IKBKB	*MYF5*	*DCAF15*	*EPHB1*
IL1RAPL1	*MYH13*	*DCAF6*	*EPHX1*
IL22RA1	*MYH3*	*DCC*	*EPHX4*
IL22RA2	*MYH4*	*DCDC1*	*ERBB4*
IL27RA	*MYL3*	*DCHS1*	*ERCC2*
IMMT	*MYO18B*	*DCLK1*	*ERCC6L2*
IMPG2	*MYO5C*	*DCSTAMP*	*ERO1LB*
INADL	*MYOM1*	*DCUN1D2*	*ERVV-1*
INO80	*MYOM3*	*DDHD1*	*ERVV-2*
INPP4B	*N4BP2*	*DDI2*	*ESYT2*
INPP5B	*NAA25*	*DDIT4L*	*ESYT3*
IQCG	*NAALADL2*	*DDX10*	*EVA1C*
IQGAP1	*NACAD*	*DDX17*	*EVI2A*
IQGAP2	*NADSYN1*	*DDX21*	*EVI5*
IRF2BPL	*NALCN*	*DDX28*	*EVPL*
ITGA8	*NANOG*	*DDX4*	*EXD1*
ITGB5	*NARS2*	*DDX46*	*EXOC5*
ITPR1	*NASP*	*DDX49*	*EXOC8*
ITPR2	*NBEA*	*DDX59*	*EXOSC10*
IVNS1ABP	*NBEAL2*	*DDX60*	*EYS*
JARID2	*NCAPG2*	*DDX60L*	*F2R*
KCMF1	*NCF1*	*DEAF1*	*F5*
KCNC1	*NCOA6*	*DEFB110*	*F7*
KCNH1	*NDUFV1*	*DENND4C*	*FADS1*
KCNH7	*NEFH*	*DEPDC1*	*FAM110B*
KCNJ16	*NEMF*	*DEPDC5*	*FAM120B*
KCTD10	*NEUROD1*	*DERA*	*FAM129B*
KDM1A	*NEXN*	*DGKA*	*FAM13A*
KDM5C	*NFKB1*	*DGKG*	*FAM149A*
KDR	*NFKBIB*	*DGKQ*	*FAM153A*
KIAA0100	*NHLRC2*	*DGKZ*	*FAM163A*
KIAA0825	*NHS*	*DGUOK*	*FAM180A*
KIAA1009	*NIPBL*	*DHX30*	*FAM186A*
KIAA1211L	*NKRF*	*DHX37*	*FAM189A1*
KIAA1324	*NLRC3*	*DHX8*	*FAM205A*

KIAA1432	*NLRP11*	*DIAPH2*	*FAM208A*
KIAA1549	*NLRP13*	*DIAPH3*	*FAM231A*
KIAA1671	*NLRP9*	*DIDO1*	*FAM47A*
KIF13A	*NME4*	*DIP2A*	*FAM63B*
KIF19	*NOL8*	*DIP2B*	*FAM72B*
KIF26A	*NOP14*	*DIRAS2*	*FAM92B*
KIF5B	*NOS1*	*DIS3L*	*FAM9A*
KIF7	*NPHS1*	*DISC1*	*FANCB*
KIR2DL1	*NPIPB5*	*DISP2*	*FANCD2*
KIR2DL3	*NR1I3*	*DKK2*	*FAR2*
KIR3DL1	*NRG3*	*DLAT*	*FAT4*
KLC4	*NRIP1*	*DLD*	*FBLN2*
KLHDC8A	*NSUN2*	*DLEC1*	*FBN3*
KLHL2	*NTN5*	*DLGAP1*	*FBRS*
KLHL23	*NTRK3*	*DLGAP2*	*FBXL14*
KLHL24	*NUGGC*	*DLX1*	*FBXL3*
KNCN	*NUP155*	*DMBT1*	*FBXO28*
KNTC1	*NUP50*	*DMD*	*FBXO7*
KRAS	*NUS1*	*DMRT2*	*FBXW7*
KRT10	*NUTM1*	*DNAAF2*	*FCHO2*
KRT18	*NWD1*	*DNAAF3*	*FDXACB1*
KRT28	*NYX*	*DNAH1*	*FERMT3*
KRT40	*OBSL1*	*DNAH10*	*FFAR2*
KRT6C	*OPN1MW*	*DNAH17*	*FFAR3*
KRTAP17-1	*OPN1MW2*	*DNAH2*	*FGFR1*
KRTAP2-4	*OR10AD1*	*DNAH3*	*FGFR3*
KRTAP6-3	*OR10G4*	*DNAH5*	*FGFRL1*
KRTAP9-2	*OR14C36*	*DNAH7*	*FHOD3*
KY	*OR1E2*	*DNAH8*	*FIGN*
LACC1	*OR1L1*	*DNAH9*	*FILIP1L*
LAMA1	*OR2D3*	*DNAJB2*	*FKBP11*
LAMA3	*OR2M7*	*DNAJC13*	*FLG*
LAMB3	*OR4A5*	*DNAJC17*	*FLG2*
LANCL3	*OR4D11*	*DNAJC18*	*FLNA*
LAP3	*OR4D6*	*DNAJC9*	*FLNC*
LAS1L	*OR4F15*	*DNM1L*	*FNBP1*
LATS1	*OR4K13*	*DNMT3B*	*FNDC1*
LDB3	*OR56B1*	*DOCK10*	*FOXD3*
LDHA	*OR5B21*	*DOCK11*	*FOXD4L2*
LEO1	*OR6S1*	*DOCK7*	*FOXE3*
LEPRE1	*OR7C1*	*DOK1*	*FOXJ3*

LIN54	*OSBPL6*	*DOK5*	*FREM1*
LIN9	*OSTN*	*DOK6*	*FRG1*
LIPA	*OVGP1*	*DONSON*	*FRG2*
LLGL2	*PACS1*	*DPH7*	*FRG2B*
LMO7	*PADI2*	*DPP9*	*FRMD4B*
LMOD2	*PADI4*	*DPPA2*	*FRMPD2*
LMOD3	*PANX3*	*DPRX*	*FRMPD4*
LNPEP	*PAPLN*	*DPYSL3*	*FRY*
LONRF1	*PAPOLG*	*DRC1*	*FRYL*
LONRF2	*PAPPA*	*DSP*	*FRZB*
LONRF3	*PARPBP*	*DSTYK*	*FSCN3*
LOR	*PCDH8*	*DTD1*	*FSHR*
LRBA	*PCDHA10*	*DTNB*	*FUK*
LRCH1	*PCDHA12*	*DTX3*	*FYCO1*
LRCH2	*PCDHA13*	*DUOX1*	*FYN*
LRP2	*PCDHA3*	*DUOX2*	*G3BP2*
LRRC2	*PCDHA7*	*DUSP10*	*GABBR2*
LRRC37A3	*PCDHB1*	*DUSP19*	*GABRA1*
LRRC37B	*PCDHB10*	*DUXA*	*GABRA4*
LRRC3B	*PCDHB16*	*DYNC1I1*	*GABRB3*
LRRC70	*PCDHB6*	*DYNC1LI1*	*GABRE*
LRRFIP2	*PCDHGA12*	*DYNC2H1*	*GABRG2*
LRRIQ3	*PCDHGA3*	*DYX1C1*	*GAK*
LSM11	*PCDHGA7*	*E2F4*	*GAL3ST4*
LTBP3	*PCDHGA8*	*E2F8*	*GALNT16*
LTN1	*PCDHGB7*	*EARS2*	*GALNT6*
MAGEB2	*PCDHGC5*	*EBLN1*	*GALNTL5*
MALSU1	*PCK2*	*ECE2*	*GALT*
MALT1	*PCM1*	*ECEL1*	*GAN*
MAML2	*PCSK1*	*ECM2*	*GAPDH*
MAMLD1	*PDCD11*	*EDC4*	*GAPVD1*
MAP2	*PDE3B*	*EDEM2*	*GAS2*
MAP3K5	*PDE4A*	*EEA1*	*GATA5*
MAP7D2	*PDE6H*	*EEF1A2*	*GATA6*
MAPKAP1	*PDE7A*	*EEF2K*	*GATSL3*
MAPKBP1	*PDXDC1*	*EEFSEC*	*GBA*
MAPT	*PDZRN4*	*EFCAB6*	*GBP2*
MAS1	*PEX13*	*EFCC1*	*GCAT*
MBIP	*PHACTR1*	*EFS*	*GCFC2*
MC3R	*PHKA2*	*EGF*	*GCKR*
MCM4	*PHLPP2*	*EGFL6*	*GCLM*

MCM9	*PIEZO1*	*EGFR*	*GCNT2*
MDM1	*PIGC*	*EHBP1*	*GDA*
MDN1	*PIGT*	*EHBP1L1*	*GDF11*
MED12	*PIGV*	*EHHADH*	*GDI2*
MED13L	*PIH1D2*	*EIF2S3*	*GEMIN5*
MED14	*PIK3CA*	*EIF4G2*	*GFRA3*
MED23	*PIK3R4*	*EIF4G3*	*GGA3*
MED9	*PKD2*	*EIF5A2*	*GGNBP2*
MEF2D	*PKHD1L1*	*EIF5B*	*GIMAP4*
MEI1	*PKN2*	*EIF6*	*GIPC3*
MERTK	*PKP4*	*ELANE*	*GIT1*
MESP2	*PLAC8L1*	*ELAVL3*	*GJB1*
METTL22	*PLCG1*	*ELF3*	*GJC1*
METTL25	*PLCG2*	*ELFN2*	*GJD3*
MFAP1	*PLEKHA7*	*ELP2*	*GK*
MFSD2B	*PLIN4*	*EML2*	*GLI3*
MGST2	*PLK2*	*EML5*	*GLIPR1L2*
MICAL3	*PLOD1*	*EML6*	*GLS2*
MINK1	*PLXNA2*	*ENC1*	*GLT8D2*
MIOS	*PMM1*	*ENPP1*	*GNAL*
MKI67	*PNLIP*	*ENPP4*	*GNAQ*
MKRN1	*PNMA5*	*ENPP5*	*GNAS*
MLXIPL	*PNRC2*	*EP400*	*GNB4*
MMAA	*PODN*	*EPAS1*	*GNL3L*
MMP2	*POLA1*	*EPB41L4A*	*GNMT*
MMS19	*POLR3A*	*EPG5*	*GNPTAB*
MOB1A	*POSTN*	*EPHA10*	*GOLGA1*
MOB3B	*POTEF*	*EPHA2*	*GOLGA2*
MON2	*PPARGC1A*	*EPHA3*	*GOLGA4*
MORC1	*PPP1R21*	*EPHA4*	*GOLGA8K*
MORC3	*PPP1R36*	*EPHA6*	*GOLGB1*
MPDZ	*PPP2R2B*	*EPHA8*	*GOLM1*
MRPL2	*PPP4C*	*EPPK1*	*GOLT1A*
MRPS30	*PPT1*	*EPRS*	*GON4L*
MS4A14	*PRAMEF2*	*EPS8*	*GPATCH2L*
MSI2	*PRB1*	*EPS8L1*	*GPD1L*
MTBP	*PRB4*	*EPX*	*GPKOW*
MTERFD2	*PREX2*	*ERBB3*	*GPNMB*
MTHFD1L	*PRKCB*	*ERBB4*	*GPR101*
MTMR12	*PRKCSH*	*ERCC6*	*GPR112*
MTR	*PRMT5*	*ERCC6L2*	*GPR146*

MTSS1	*PROKR1*	*ERICH1*	*GPR149*
MUSK	*PROX2*	*ERO1L*	*GPR15*
MXRA5	*PRPF40B*	*ESCO2*	*GPR174*
MYCBP2	*PRR11*	*ESPL1*	*GPR179*
MYH1	*PRR12*	*ESR1*	*GPR182*
MYH8	*PRRG1*	*ETAA1*	*GPR26*
MYLK2	*PSG4*	*ETV2*	*GPR37*
MYO10	*PSMD3*	*ETV3L*	*GPR55*
MYO15A	*PTCHD3*	*ETV6*	*GPR83*
MYO18A	*PTEN*	*EVC2*	*GPR89A*
MYO1E	*PTP4A2*	*EVI5L*	*GPR98*
MYO5B	*PTPN18*	*EXOC3L4*	*GPS2*
MYO9B	*PTPRB*	*EXOC5*	*GPSM2*
MYOM2	*PTPRU*	*EXOC6B*	*GRIK1*
MYT1	*PTPRZ1*	*EXOC8*	*GRIK2*
NAA20	*PXDN*	*EYA3*	*GRK7*
NACA2	*PYHIN1*	*EYS*	*GRM8*
NADSYN1	*QTRTD1*	*EZH2*	*GSS*
NAP1L1	*RAB3D*	*F11R*	*GTF2E2*
NARF	*RAB43*	*F8*	*GTF2H2C*
NARFL	*RAB4B*	*FAAH*	*GZMA*
NAT2	*RABEP1*	*FABP12*	*H2AFY*
NBEAL1	*RAF1*	*FABP9*	*H3F3A*
NBN	*RASAL1*	*FADS2*	*HABP2*
NCAM2	*RASD2*	*FAH*	*HADHA*
NCAPD2	*RASGRF1*	*FAM105A*	*HAO1*
NCAPD3	*RAVER1*	*FAM111A*	*HAUS6*
NCKAP5	*RBBP6*	*FAM114A2*	*HAVCR2*
NCOA1	*RBM10*	*FAM135B*	*HECTD1*
NCOA4	*RBM26*	*FAM13A*	*HECTD2*
NCOA7	*RBM28*	*FAM13B*	*HECW1*
NCOR2	*RBM42*	*FAM153B*	*HELQ*
NDUFV2	*RBMXL2*	*FAM155A*	*HERC2*
NEB	*RBMXL3*	*FAM160A1*	*HERC6*
NEDD1	*RBP3*	*FAM163A*	*HGFAC*
NEDD9	*RBP5*	*FAM170B*	*HHIP*
NEIL1	*RERE*	*FAM178B*	*HHIPL2*
NEK7	*RERGL*	*FAM179B*	*HIF1A*
NELL1	*RET*	*FAM181A*	*HIF3A*
NEO1	*RFPL4A*	*FAM186A*	*HINT3*
NF1	*RFTN1*	*FAM188B*	*HIPK1*

NFIX	*RFX5*	*FAM189A1*	*HIPK2*
NGDN	*RFX8*	*FAM196B*	*HIPK3*
NIPAL3	*RGPD4*	*FAM200B*	*HIRA*
NISCH	*RIMS2*	*FAM203B*	*HIST1H3I*
NKD1	*RINT1*	*FAM205A*	*HK2*
NKRF	*RIOK3*	*FAM209B*	*HLA-B*
NLGN1	*RLTPR*	*FAM20B*	*HMBS*
NLRP10	*RMDN2*	*FAM211A*	*HMCN1*
NLRP7	*RNF123*	*FAM214A*	*HMGB1*
NME6	*RNF17*	*FAM217A*	*HMGCLL1*
NNAT	*RNF217*	*FAM222A*	*HMGCS1*
NOBOX	*RNF31*	*FAM43A*	*HMGN2*
NOD1	*RNH1*	*FAM47A*	*HMHA1*
NPHP4	*RNMT*	*FAM49A*	*HN1*
NPR3	*ROBO2*	*FAM65B*	*HNRNPA1L2*
NR0B1	*ROBO4*	*FAM71E2*	*HNRNPA2B1*
NR1H3	*ROM1*	*FANCG*	*HNRNPA3*
NR2C1	*RP1*	*FANCI*	*HNRNPDL*
NRCAM	*RP1L1*	*FANK1*	*HNRNPH2*
NRXN3	*RPGRIP1L*	*FARP2*	*HOXA2*
NSUN3	*RPL22*	*FARS2*	*HOXB1*
NSUN4	*RPL3*	*FASTKD2*	*HOXD4*
NTM	*RPRD2*	*FAT1*	*HPSE2*
NUDT12	*RPS6KB2*	*FAT2*	*HPX*
NUMB	*RSRC1*	*FAT3*	*HRNR*
NUP153	*RUNDC3B*	*FBLIM1*	*HS3ST4*
NUP188	*RUNX1T1*	*FBLN2*	*HSP90AB1*
NUP205	*RUVBL1*	*FBN1*	*HSP90B1*
NUP98	*RWDD1*	*FBN2*	*HSPA2*
NUPL1	*RWDD2A*	*FBN3*	*HSPD1*
NXF5	*SACS*	*FBP2*	*HTR3A*
NXPE4	*SAMD11*	*FBXL13*	*HTR6*
OBSCN	*SATB2*	*FBXL14*	*HUWE1*
OLFM3	*SCN1A*	*FBXL15*	*ICOS*
OPLAH	*SCNN1G*	*FBXO36*	*IDE*
OR10H3	*SCUBE1*	*FBXO40*	*IFIH1*
OR10H4	*SCYL2*	*FBXW10*	*IFNGR1*
OR13G1	*SDCCAG3*	*FCF1*	*IFT140*
OR13H1	*SEC11C*	*FCGBP*	*IGBP1*
OR1K1	*SEC24A*	*FCGR1B*	*IGF2R*
OR2AG2	*SEC31B*	*FCGR2A*	*IGFBP6*

OR2L3	*SEC63*	*FCHO1*	*IGFL2*
OR2M5	*SEMA4C*	*FCHO2*	*IGSF10*
OR2M7	*SEMA4G*	*FCRL3*	*IGSF9*
OR2T1	*SENP7*	*FCRL5*	*IL13RA1*
OR4A47	*SENP8*	*FDFT1*	*IL18R1*
OR4F15	*Sep/06*	*FEN1*	*IL1RAPL2*
OR5T2	*SERPINE1*	*FER*	*IL36B*
OR5T3	*SETD1B*	*FER1L6*	*ILF2*
OR5W2	*SFRP1*	*FGB*	*IMPG2*
OR7A10	*SGIP1*	*FGD6*	*INF2*
OSBPL1A	*SGOL2*	*FGF7*	*INO80D*
OSBPL8	*SH2B3*	*FGF9*	*INSC*
OTOGL	*SH2D4B*	*FGFRL1*	*INTS4*
OTOP3	*SH3BP4*	*FGR*	*IP6K2*
OTUD7B	*SHPRH*	*FHAD1*	*IPMK*
PADI3	*SHROOM1*	*FHOD3*	*IPP*
PAGR1	*SIK3*	*FKBP5*	*IPPK*
PAK2	*SIN3A*	*FLG*	*IQCE*
PARD3	*SLC12A2*	*FLG2*	*IQCG*
PARK7	*SLC12A3*	*FLNA*	*IQGAP3*
PARP12	*SLC17A6*	*FLT1*	*IRAK2*
PARP16	*SLC22A25*	*FMN2*	*IRS4*
PARP2	*SLC22A6*	*FMR1*	*ITGA2*
PARP4	*SLC22A9*	*FNDC1*	*ITGA9*
PATE4	*SLC23A2*	*FNDC3B*	*ITGAD*
PAX6	*SLC25A20*	*FNIP2*	*ITGB1*
PBRM1	*SLC2A10*	*FOXC2*	*ITGB1BP2*
PBX4	*SLC30A3*	*FOXD4L3*	*ITGB4*
PCDH1	*SLC36A3*	*FOXD4L4*	*ITGB8*
PCDH10	*SLC38A10*	*FOXI1*	*ITIH3*
PCDH11X	*SLC4A3*	*FOXJ2*	*ITPR1*
PCDH15	*SLC4A8*	*FOXK1*	*ITPR2*
PCDHA1	*SLC6A11*	*FOXN1*	*ITPRIPL2*
PCDHAC2	*SLC6A20*	*FOXP1*	*ITSN1*
PCDHB16	*SLC9A1*	*FPGT*	*JADE1*
PCDHGA12	*SLC9A3*	*FRAS1*	*JADE3*
PCDHGA7	*SLC9A8*	*FREM3*	*JAK1*
PCLO	*SLC9C2*	*FRG1*	*JAKMIP1*
PCMTD1	*SLCO1B1*	*FRMD4B*	*JKAMP*
PCNT	*SLCO1B3*	*FRMD7*	*JUND*
PCNX	*SLCO1C1*	*FRMD8*	*KALRN*

PCOLCE	*SLCO3A1*	*FRMPD2*	*KANK1*
PCYT1A	*SLFN12L*	*FRMPD3*	*KANK2*
PDCD4	*SLITRK1*	*FRMPD4*	*KAT6B*
PDE10A	*SMAD4*	*FSCB*	*KAZN*
PDE11A	*SMARCA1*	*FSD1L*	*KCNA5*
PDE3B	*SMARCA2*	*FSHR*	*KCNC3*
PDE4DIP	*SMARCE1*	*FSTL4*	*KCNG3*
PDE8B	*SMCO2*	*FTSJ1*	*KCNG4*
PDILT	*SNRPN*	*FUBP1*	*KCNJ2*
PELI1	*SNX1*	*FUCA1*	*KCNN4*
PEX26	*SOGA1*	*FUT6*	*KCNQ2*
PEX5L	*SORCS1*	*FYB*	*KCNQ5*
PFKFB2	*SORL1*	*FYCO1*	*KDM3B*
PFKFB4	*SOX2*	*FYN*	*KDM5A*
PGA5	*SP110*	*FZD10*	*KDM5B*
PGD	*SPANXD*	*FZD2*	*KDM5C*
PGM2	*SPATA31A5*	*FZD3*	*KDM6B*
PHC1	*SPATA31A7*	*FZD9*	*KDR*
PHF13	*SPDYE4*	*G2E3*	*KEAP1*
PHF20L1	*SPEG*	*G6PC3*	*KHDC3L*
PHF8	*SPHK2*	*GAB2*	*KHDRBS3*
PHLDA2	*SPICE1*	*GABRA5*	*KIAA0196*
PHYHIP	*SPTBN1*	*GABRG2*	*KIAA0247*
PI4KB	*SQSTM1*	*GABRR2*	*KIAA0319L*
PIF1	*SREBF1*	*GADD45G*	*KIAA0368*
PIGS	*ST18*	*GALC*	*KIAA0430*
PIK3C2B	*STAB1*	*GALNT1*	*KIAA0947*
PIK3CA	*STAB2*	*GALNT10*	*KIAA1109*
PIKFYVE	*STAT4*	*GALNT16*	*KIAA1239*
PITPNM1	*STK11*	*GALNT5*	*KIAA1244*
PJA2	*STK33*	*GALNT8*	*KIAA1377*
PKHD1	*STMN1*	*GALNTL6*	*KIAA1430*
PKP1	*STPG1*	*GAP43*	*KIAA1755*
PKP3	*STRIP1*	*GAS2L2*	*KIF13A*
PLAU	*STRN3*	*GAS7*	*KIF15*
PLCE1	*STRN4*	*GAST*	*KIF18A*
PLCH1	*STX3*	*GATA2*	*KIF19*
PLP2	*SUCLG2*	*GBA*	*KIF1A*
PLS3	*SUGP2*	*GBP1*	*KIF20B*
PLXNA2	*SUSD1*	*GCC2*	*KIF24*
PLXNA3	*SUV39H1*	*GCDH*	*KIF26B*

PLXNA4	*SVIL*	*GCLC*	*KIF3A*
PNPLA3	*SYNE1*	*GCN1L1*	*KIF4B*
PODXL	*SYNE2*	*GCNT3*	*KIRREL*
POGK	*SYNPO*	*GDF3*	*KLB*
POGZ	*SYVN1*	*GDF6*	*KLC2*
POLA2	*SZT2*	*GDI1*	*KLC4*
POLE2	*TACC2*	*GDNF*	*KLF12*
POLR1A	*TACR1*	*GEMIN5*	*KLF16*
POLR2H	*TAF15*	*GEMIN6*	*KLF3*
POR	*TAF1L*	*GFI1B*	*KLHL1*
POTEB2	*TALDO1*	*GFM1*	*KLHL9*
POTEF	*TANC1*	*GGNBP2*	*KLRC1*
POU3F4	*TAOK1*	*GGTLC1*	*KLRK1*
PPAP2B	*TAS1R3*	*GGTLC2*	*KMT2A*
PPAPDC3	*TAS2R31*	*GIGYF1*	*KMT2C*
PPIE	*TAS2R46*	*GIMAP4*	*KPRP*
PPIH	*TBC1D19*	*GJB6*	*KRBA2*
PPL	*TBC1D22B*	*GJC2*	*KRT1*
PPM1G	*TBC1D9B*	*GKAP1*	*KRT10*
PPP1R16B	*TBRG1*	*GLB1L2*	*KRT36*
PPP1R2	*TCP10*	*GLI3*	*KRT38*
PPP1R21	*TDRD3*	*GLRA3*	*KRTAP1-4*
PPP2R3A	*TDRD6*	*GLRA4*	*KRTAP10-1*
PPP2R4	*TECTA*	*GMPPA*	*KRTAP22-1*
PRAMEF1	*TENM3*	*GMPR2*	*KRTAP4-8*
PRAMEF14	*TEX13A*	*GNAI1*	*KRTAP5-1*
PRAMEF9	*TFAP2B*	*GNMT*	*KRTAP5-7*
PRDM9	*TG*	*GNPAT*	*KTI12*
PREX1	*TGFBR2*	*GOLGA8J*	*LAMA1*
PRKAR2A	*THAP3*	*GOLGA8K*	*LAMA4*
PRKCQ	*THSD1*	*GOLGB1*	*LAMB1*
PRM1	*TIAM1*	*GOLM1*	*LAMB3*
PROB1	*TICRR*	*GON4L*	*LAMP2*
PROCA1	*TJP3*	*GPAA1*	*LANCL1*
PRODH2	*TLE3*	*GPAT2*	*LARP1B*
PROSER2	*TLL1*	*GPBP1L1*	*LAS1L*
PRPF38A	*TLR10*	*GPC3*	*LCE2B*
PRPF8	*TLR2*	*GPNMB*	*LCLAT1*
PRPH	*TLX2*	*GPR112*	*LCP2*
PRR14L	*TM7SF2*	*GPR115*	*LDHAL6B*
PRR21	*TM7SF3*	*GPR116*	*LEMD3*

PRRC2C	*TMC5*	*GPR119*	*LEPR*
PRSS16	*TMEM121*	*GPR124*	*LETM1*
PSENEN	*TMEM170B*	*GPR128*	*LGALSL*
PSG1	*TMEM175*	*GPR149*	*LGI2*
PSMC5	*TMEM229B*	*GPR153*	*LGR5*
PSMD1	*TMEM95*	*GPR155*	*LHFPL2*
PSTPIP2	*TMPRSS5*	*GPR158*	*LHFPL5*
PTCHD2	*TOP2B*	*GPR176*	*LILRA2*
PTEN	*TOX4*	*GPR183*	*LILRB2*
PTPN12	*TP53*	*GPR37*	*LIPE*
PTPN13	*TPCN1*	*GPR52*	*LMLN*
PTPN14	*TPK1*	*GPR55*	*LMO7*
PTPN5	*TPR*	*GPR61*	*LNPEP*
PTPRA	*TPSD1*	*GPR64*	*LONRF2*
PUF60	*TRAM1L1*	*GPR78*	*LOXL4*
PXT1	*TRAPPC11*	*GPR89A*	*LPAR4*
QRSL1	*TRIAP1*	*GPR89B*	*LPCAT4*
RAB30	*TRIM16*	*GPR98*	*LPPR1*
RAB35	*TRIM52*	*GPT2*	*LRCH1*
RAB6B	*TRIM6*	*GRAMD1B*	*LRCH2*
RAD21	*TRIM66*	*GRAMD2*	*LRIF1*
RALGAPA1	*TRIM73*	*GREB1*	*LRIG2*
RALGPS2	*TRMT10C*	*GRID2*	*LRIG3*
RANBP3L	*TRMT2A*	*GRIK2*	*LRIT2*
RBBP8	*TRPC4*	*GRIK3*	*LRP12*
RBL2	*TRPC7*	*GRIN2A*	*LRP1B*
RBM19	*TRPM4*	*GRK5*	*LRP5*
RBM42	*TRPM8*	*GRM1*	*LRRC56*
RBM48	*TSKS*	*GRM2*	*LRRC59*
RBPJ	*TSPYL1*	*GRM7*	*LRRFIP1*
RDH10	*TTC34*	*GSDMC*	*LTBP2*
RDH12	*TTK*	*GSTA2*	*LTBP3*
REPS2	*TVP23A*	*GTF2E2*	*LY75*
REV3L	*UBC*	*GTF2IRD1*	*LY9*
RFT1	*UBE2G1*	*GTF2IRD2*	*LYL1*
RFX6	*UBE2S*	*GUCY2C*	*LYNX1*
RFXAP	*UGP2*	*GUCY2F*	*LZTFL1*
RGL1	*UGT3A2*	*GULP1*	*LZTS2*
RGMB	*UHRF1BP1L*	*GXYLT1*	*MACF1*
RGPD3	*UNC13A*	*GYG1*	*MAD2L1BP*
RGS7	*UNC13C*	*GYPA*	*MAGEA12*

RGS8	*UNC79*	*GZMA*	*MAGEC1*
RGSL1	*UNC80*	*H2AFV*	*MAGEC3*
RHD	*USH2A*	*H3F3B*	*MAGI3*
RHOA	*USP22*	*HADHA*	*MAK*
RHPN2	*USP24*	*HAND1*	*MALT1*
RILPL2	*USP26*	*HAPLN2*	*MAN1A1*
RIPK2	*USP36*	*HAPLN3*	*MAN2A1*
RLF	*USP44*	*HCFC2*	*MAN2C1*
RNF113A	*USPL1*	*HCN1*	*MANBA*
RNF31	*VAC14*	*HCN4*	*MAOA*
ROBO1	*VAT1*	*HCRTR1*	*MAP1S*
ROBO3	*VEGFB*	*HCST*	*MAP3K19*
RORC	*VENTX*	*HDAC10*	*MAP3K3*
RP11-1220K2.2	*VN1R2*	*HDAC4*	*MAP3K4*
RPGRIP1L	*VN1R4*	*HDAC5*	*MAP3K5*
RPL3	*VPRBP*	*HDGF*	*MAP4K4*
RPL3L	*VPS13B*	*HDLBP*	*MAP4K5*
RPL7	*VSIG10*	*HEATR3*	*MAP7*
RPS23	*VWA1*	*HEBP2*	*MAP7D1*
RPTN	*VWA3A*	*HECTD2*	*MAP7D3*
RPTOR	*VWC2*	*HECTD3*	*MAP9*
RRN3	*VWF*	*HECTD4*	*MAPK6*
RRP1B	*WBP11*	*HECW1*	*MAPK8IP3*
RSBN1	*WBSCR17*	*HEG1*	*MAPKAP1*
RSRC2	*WDR18*	*HELB*	*MAPKAPK5*
RTEL1	*WDR33*	*HELQ*	*Mar/06*
RTTN	*WDR62*	*HELZ*	*Mar/07*
RUFY1	*WDTC1*	*HENMT1*	*MASP2*
RUNDC1	*WEE2*	*HEPH*	*MBTD1*
RWDD1	*WIPI1*	*HERC1*	*MC2R*
RYR3	*WNK4*	*HERC2*	*MCCC2*
SACS	*WNT5B*	*HEXDC*	*MCF2*
SAGE1	*WNT7B*	*HEY2*	*MCF2L2*
SAMD9	*WNT9B*	*HEYL*	*MCM10*
SAMHD1	*WRAP53*	*HFE*	*MCMDC2*
SBF2	*WSCD1*	*HIRA*	*MCPH1*
SCAF11	*WTAP*	*HIRIP3*	*MDFIC*
SCARB1	*WWC1*	*HIST1H2AA*	*MDN1*
SCGB1D4	*WWOX*	*HIST1H2AE*	*ME1*
SCLY	*XIRP2*	*HIST1H4A*	*MED1*
SCN4A	*XK*	*HIST1H4E*	*MED12*

SCN7A	*XPOT*	*HIVEP1*	*MED12L*
SCN8A	*YARS*	*HK1*	*MED13L*
SCN9A	*ZBED4*	*HLA-DPB1*	*MED18*
SCNN1D	*ZBTB14*	*HMBS*	*MED24*
SEC13	*ZBTB17*	*HMCES*	*MEGF6*
SEC24A	*ZBTB21*	*HMCN1*	*MEGF8*
SEC24B	*ZBTB22*	*HMGA2*	*MEI4*
SEC31A	*ZBTB33*	*HMGCR*	*MERTK*
SEC61A2	*ZC3H11A*	*HMGN5*	*MESP2*
SELPLG	*ZC3H13*	*HNRNPA3*	*MET*
Sep/07	*ZCCHC18*	*HOOK1*	*METTL1*
SERINC3	*ZDHHC21*	*HOXA10*	*METTL24*
SERPINB12	*ZFAND1*	*HOXA3*	*MFSD5*
SETD1B	*ZFC3H1*	*HOXC10*	*MFSD9*
SETD2	*ZFP36L2*	*HOXC9*	*MGST3*
SF3A3	*ZFPM2*	*HPN*	*MIA2*
SFI1	*ZFYVE26*	*HPR*	*MIB1*
SGSM1	*ZHX3*	*HPS5*	*MID2*
SH3D19	*ZIM2*	*HRC*	*MIDN*
SHISA3	*ZKSCAN2*	*HRH1*	*MINPP1*
SHISA5	*ZMYND10*	*HRH3*	*MKI67*
SHPRH	*ZNF107*	*HRNR*	*MKNK2*
SHROOM2	*ZNF131*	*HS3ST2*	*MKRN1*
SIAH3	*ZNF142*	*HSD17B4*	*MKRN2*
SIDT2	*ZNF148*	*HSPA6*	*MLK4*
SIK2	*ZNF189*	*HSPA8*	*MLLT1*
SLC12A5	*ZNF212*	*HSPB3*	*MMAA*
SLC13A1	*ZNF267*	*HSPD1*	*MMP14*
SLC17A3	*ZNF273*	*HSPE1*	*MMRN2*
SLC17A8	*ZNF281*	*HSPG2*	*MMS19*
SLC18A1	*ZNF285*	*HTR1B*	*MON2*
SLC19A3	*ZNF302*	*HTR3E*	*MORC3*
SLC22A1	*ZNF407*	*HUNK*	*MOS*
SLC22A12	*ZNF415*	*HUWE1*	*MPDZ*
SLC22A4	*ZNF418*	*HYDIN*	*MPP1*
SLC24A1	*ZNF43*	*HYOU1*	*MPP7*
SLC24A2	*ZNF430*	*IBTK*	*MRE11A*
SLC25A12	*ZNF445*	*IDH1*	*MRGPRD*
SLC25A23	*ZNF469*	*IFFO2*	*MROH2B*
SLC26A6	*ZNF479*	*IFNGR1*	*MRPL10*
SLC26A8	*ZNF486*	*IGBP1*	*MRPL37*

SLC30A5	*ZNF492*	*IGDCC3*	*MRPS14*
SLC35A2	*ZNF493*	*IGF1R*	*MS4A4A*
SLC35C1	*ZNF502*	*IGF2BP3*	*MST1*
SLC35G6	*ZNF513*	*IGF2R*	*MSTO1*
SLC36A2	*ZNF536*	*IGFN1*	*MTA2*
SLC38A4	*ZNF610*	*IGHMBP2*	*MTHFD1*
SLC4A5	*ZNF618*	*IGSF1*	*MTMR14*
SLC4A7	*ZNF678*	*IGSF10*	*MTMR2*
SLC5A3	*ZNF681*	*IGSF3*	*MTOR*
SLC5A5	*ZNF691*	*IGSF5*	*MTUS1*
SLC5A6	*ZNF695*	*IGSF9*	*MTX1*
SLC6A12	*ZNF71*	*IGSF9B*	*MYBL1*
SLC6A19	*ZNF711*	*IL17RD*	*MYC*
SLC6A2	*ZNF717*	*IL18R1*	*MYCBP2*
SLC6A6	*ZNF720*	*IL2RG*	*MYEF2*
SLC9A6	*ZNF721*	*IL3*	*MYEOV2*
SLC9B2	*ZNF729*	*IL31RA*	*MYH1*
SLCO6A1	*ZNF736*	*IL36A*	*MYH10*
SLFN12	*ZNF775*	*IL36B*	*MYH11*
SLFN13	*ZNF782*	*ILF3*	*MYH2*
SLIT2	*ZNF800*	*INCENP*	*MYH3*
SLK	*ZNF823*	*INHBA*	*MYH4*
SLTM	*ZNF829*	*INO80B*	*MYLK2*
SMAD1	*ZNF90*	*INPP4B*	*MYO10*
SMAD2	*ZNF92*	*INPP5F*	*MYO18A*
SMARCA1	*ZNRF4*	*INPP5K*	*MYO18B*
SMC1A	*ZRSR2*	*INTS4*	*MYO7A*
SMC5	*ZUFSP*	*INVS*	*NAIF1*
SMEK1	*ZZEF1*	*IP6K1*	*NALCN*
SMPDL3A		*IPO13*	*NAMPT*
SNIP1		*IPO4*	*NAP1L3*
SNTN		*IPO5*	*NARG2*
SNX18		*IPO9*	*NARS2*
SOCS4		*IQCA1*	*NAV3*
SOGA1		*IQCE*	*NBAS*
SORCS3		*IQGAP1*	*NBEA*
SOSTDC1		*IQSEC1*	*NCAM2*
SOX30		*IREB2*	*NCAN*
SOX5		*IRF4*	*NCAPD3*
SP1		*IRS2*	*NCKAP1*
SP8		*ISPD*	*NCKAP5L*

SPAG17	*ISX*	*NCMAP*
SPAG9	*ISY1-RAB43*	*NCOA4*
SPATA6	*ITCH*	*NCOR1*
SPEF1	*ITGA11*	*NDRG1*
SPG11	*ITGA7*	*NDUFAF6*
SPICE1	*ITGAD*	*NDUFV2*
SPINK5	*ITGAV*	*NEB*
SPIRE1	*ITGB1*	*NECAB2*
SPOCK1	*ITGB6*	*NECAP2*
SPRY1	*ITGB8*	*NEDD4*
SPTA1	*ITIH2*	*NEGR1*
SPTB	*ITLN1*	*NEIL3*
SPTBN4	*ITM2A*	*NEK9*
SQLE	*ITPK1*	*NELL1*
SRCAP	*ITPR1*	*NES*
SRFBP1	*ITPR3*	*NEU2*
SRP54	*ITSN2*	*NEURL4*
SRPK2	*IVD*	*NFATC2*
SRSF12	*IVL*	*NFRKB*
SSBP4	*JAG1*	*NGEF*
SSH2	*KAL1*	*NHLH2*
ST7L	*KALRN*	*NHP2*
STAB1	*KANSL1*	*NIM1K*
STAMBP	*KARS*	*NIN*
STAP1	*KBTBD7*	*NIPA1*
STAT1	*KCMF1*	*NIPA2*
STAU1	*KCNA3*	*NIPBL*
STIM1	*KCNA4*	*NISCH*
STK11IP	*KCNA7*	*NKAIN3*
STK31	*KCNC2*	*NKRF*
STK36	*KCNG3*	*NLGN4X*
STRN4	*KCNH2*	*NLRP1*
STT3B	*KCNH6*	*NLRP12*
STX12	*KCNJ3*	*NLRP13*
STXBP4	*KCNK10*	*NLRP2*
STXBP6	*KCNQ1*	*NLRP3*
SULF1	*KCNQ2*	*NLRP6*
SUMO2	*KCNQ3*	*NME8*
SYNE1	*KCNQ5*	*NOC3L*
SYNE2	*KCNS3*	*NOL10*
SYNRG	*KCNT1*	*NOMO1*

SYTL3	*KCNT2*	*NOMO2*
SZT2	*KCNU1*	*NOMO3*
TAAR6	*KDM2A*	*NOP2*
TAB3	*KDM4A*	*NOS2*
TAF1B	*KDM4B*	*NOTCH2*
TAF2	*KDM5D*	*NOVA1*
TAP1	*KDM6B*	*NPAT*
TARSL2	*KDR*	*NPFFR2*
TAS2R19	*KDSR*	*NPIPA3*
TAS2R30	*KEL*	*NPIPB5*
TAS2R41	*KIAA0195*	*NPM3*
TBC1D14	*KIAA0753*	*NPTN*
TBC1D16	*KIAA1009*	*NR2C1*
TBC1D8B	*KIAA1033*	*NR2F1*
TBX2	*KIAA1109*	*NRDE2*
TBX22	*KIAA1210*	*NRK*
TCAP	*KIAA1211L*	*NSL1*
TCEAL6	*KIAA1244*	*NT5C1B*
TCF4	*KIAA1279*	*NTM*
TCN1	*KIAA1429*	*NTN3*
TCOF1	*KIAA1549*	*NTRK3*
TDRD5	*KIAA1551*	*NUB1*
TDRD9	*KIAA1731*	*NUCB1*
TDRP	*KIAA1755*	*NUP153*
TECTA	*KIAA1919*	*NUP155*
TEKT1	*KIAA2018*	*NUP210*
TEKT4	*KIF15*	*NUS1*
TENM1	*KIF17*	*NYAP2*
TESPA1	*KIF18A*	*NYX*
TEX14	*KIF1A*	*OAT*
TEX15	*KIF1C*	*OBSCN*
TEX2	*KIF25*	*OC90*
TFDP2	*KIF26B*	*OCA2*
TFPI2	*KIF27*	*OCRL*
TGFBR1	*KIF3B*	*OFD1*
THOC5	*KIF5C*	*OGFOD1*
TIGD4	*KIR2DL1*	*OGFOD2*
TIMM10	*KIR2DL4*	*OLAH*
TIMMDC1	*KIR3DL3*	*OLFML3*
TMC2	*KIRREL3*	*OPHN1*
TMC5	*KLC2*	*OPN1LW*

TMC6	*KLHL11*	*OPTN*
TMED10	*KLHL17*	*OR10A6*
TMED6	*KLHL25*	*OR10G8*
TMEM116	*KLHL3*	*OR10G9*
TMEM128	*KLHL4*	*OR13C2*
TMEM145	*KLHL40*	*OR13C3*
TMEM159	*KLHL5*	*OR1C1*
TMEM175	*KLHL9*	*OR1J1*
TMEM183A	*KLK11*	*OR1L3*
TMEM229A	*KLK15*	*OR2AK2*
TMEM233	*KLLN*	*OR2D3*
TMEM247	*KLRC3*	*OR2G3*
TMEM41A	*KLRD1*	*OR2K2*
TMEM43	*KLRF1*	*OR2M3*
TMEM69	*KMO*	*OR2T4*
TMIE	*KMT2A*	*OR2V2*
TMOD1	*KMT2B*	*OR2W3*
TNC	*KMT2C*	*OR2Y1*
TNFAIP3	*KMT2E*	*OR4C16*
TNFRSF11B	*KNDC1*	*OR4D9*
TNIP3	*KNG1*	*OR4X2*
TOP3B	*KNOP1*	*OR51M1*
TPCN1	*KPNA2*	*OR52B2*
TPM4	*KRAS*	*OR52B4*
TRADD	*KRT1*	*OR56B1*
TRAK1	*KRT14*	*OR5H14*
TRAK2	*KRT17*	*OR5H15*
TREML2	*KRT3*	*OR5H2*
TRIM42	*KRT31*	*OR5H6*
TRIM64B	*KRT32*	*OR5K1*
TRIM72	*KRT36*	*OR5M10*
TRIM73	*KRT37*	*OR5M3*
TRIM77	*KRT6A*	*OR5T1*
TRIP11	*KRT6C*	*OR6A2*
TRMT1	*KRT72*	*OR6C6*
TRMT13	*KRT78*	*OR6C74*
TRPV1	*KRT8*	*OR6F1*
TSC1	*KRT80*	*OR7A17*
TSR1	*KRT85*	*OR8B4*
TSSK4	*KRTAP1-1*	*OR8G5*
TTBK1	*KRTAP1-4*	*ORC1*

TTC17	*KRTAP10-11*	*OS9*
TTC21B	*KRTAP12-2*	*OSBPL1A*
TTC30B	*KRTAP13-4*	*OSBPL7*
TTLL4	*KRTAP2-1*	*OSTM1*
TTLL6	*KRTAP20-2*	*OTOG*
TUBA3E	*KRTAP25-1*	*OTOGL*
TUFT1	*KRTAP29-1*	*OTUD6A*
TULP3	*KRTAP4-11*	*OTX1*
TXNIP	*KRTAP4-3*	*PABPC1*
TYW1	*KRTAP6-2*	*PAG1*
UAP1L1	*KTI12*	*PAICS*
UBAP1	*KTN1*	*PAIP1*
UBAP2	*KY*	*PALB2*
UBC	*KYNU*	*PALD1*
UBE4A	*L3MBTL1*	*PALM*
UBR4	*LAMA1*	*PALM2*
UBR5	*LAMA2*	*PALM3*
UBTF	*LAMA3*	*PAN3*
UCHL5	*LAMA4*	*PAPD4*
UFD1L	*LAMB4*	*PAPD5*
UGP2	*LAMP5*	*PAPLN*
UGT2A1	*LARP1*	*PARD3B*
UGT2B10	*LATS1*	*PARP1*
UGT3A1	*LATS2*	*PARP16*
ULK2	*LAYN*	*PAXBP1*
UNC13A	*LCE1B*	*PBX1*
UNC13B	*LDB2*	*PCDH7*
UNC13D	*LETMD1*	*PCDHA1*
UNC45A	*LGR6*	*PCDHA10*
UROD	*LHFPL3*	*PCDHA2*
USF1	*LHX9*	*PCDHA5*
USHBP1	*LIG4*	*PCDHA9*
USP18	*LILRA3*	*PCDHB3*
USP34	*LILRB2*	*PCDHB7*
USP36	*LILRB5*	*PCDHGA10*
USP43	*LINGO4*	*PCDHGA3*
USP7	*LIPE*	*PCDHGB4*
UTRN	*LIPI*	*PCNX*
UVSSA	*LIPT1*	*PCNXL2*
VASH2	*LMF1*	*PCSK7*
VAV3	*LPA*	*PDE3A*

VCAN	*LPAR5*	*PDE4B*
VCL	*LPIN3*	*PDIA3*
VPS13B	*LRBA*	*PDP2*
VPS13D	*LRCH2*	*PDZD2*
VPS37B	*LRIT1*	*PDZRN4*
VPS53	*LRP1*	*PEAK1*
VWA8	*LRP1B*	*PEAR1*
VWDE	*LRP4*	*PEG3*
WAS	*LRRC15*	*PEPD*
WBP5	*LRRC19*	*PERP*
WDFY3	*LRRC3*	*PEX3*
WDPCP	*LRRC30*	*PGBD5*
WDR52	*LRRC36*	*PGC*
WDR55	*LRRC37A3*	*PGK2*
WDR72	*LRRC37B*	*PGM1*
WDR78	*LRRC38*	*PGM2L1*
WDR87	*LRRC49*	*PGR*
WIPI2	*LRRC4C*	*PHC3*
WLS	*LRRC56*	*PHF12*
WNT5A	*LRRC69*	*PHF14*
WWTR1	*LRRC7*	*PHF20L1*
XPA	*LRRIQ1*	*PHF23*
XYLB	*LRRN2*	*PHF3*
XYLT1	*LRRTM1*	*PHF8*
YME1L1	*LUM*	*PHIP*
YPEL1	*LYG1*	*PHKA1*
YPEL2	*LYPD6*	*PHKB*
YY1	*LYST*	*PHLDA1*
ZBTB10	*LYVE1*	*PHLDA2*
ZBTB39	*LYZL2*	*PHLDB2*
ZBTB44	*LZTS1*	*PHOSPHO1*
ZBTB45	*MACC1*	*PHTF2*
ZC3H13	*MACF1*	*PIAS3*
ZC3H4	*MAD1L1*	*PIEZO2*
ZC3H7A	*MAGEA10*	*PIGF*
ZCCHC14	*MAGEA12*	*PIGM*
ZDHHC11	*MAGEA6*	*PIGU*
ZDHHC2	*MAGEA9*	*PIGX*
ZDHHC4	*MAGEA9B*	*PIH1D2*
ZEB2	*MAGEC1*	*PIK3CG*
ZFAT	*MAGED1*	*PIK3R2*

ZFHX2
ZFHX3
ZFP37
ZFYVE20
ZFYVE26
ZIC1
ZIM2
ZMYM4
ZNF106
ZNF143
ZNF208
ZNF236
ZNF275
ZNF285
ZNF337
ZNF384
ZNF43
ZNF440
ZNF479
ZNF483
ZNF490
ZNF492
ZNF521
ZNF526
ZNF549
ZNF587
ZNF608
ZNF644
ZNF676
ZNF716
ZNF717
ZNF729
ZNF771
ZNF827
ZNF836
ZNF90
ZSCAN2
ZSCAN20

MAGED4
MAGED4B
MAGEE2
MAGI2
MAMLD1
MAOB
MAP1B
MAP1S
MAP2K1
MAP2K7
MAP3K1
MAP3K10
MAP4K1
MAP7
MAP9
MAPK10
MAPK9
MAPKAPK3
MAPKBP1
Mar/02
Mar/06
MATN2
MB
MBD3
MBD3L3
MBOAT2
MCC
MCF2
MCF2L2
MCM5
MCOLN3
MCRS1
MCTP2
MDC1
MDFIC
MDGA2
MDN1
MECOM
MED1
MED12
MED12L

PIKFYVE
PIR
PITPNM2
PIWIL1
PIWIL2
PIWIL4
PKD2
PKN2
PKP3
PLAC8
PLCE1
PLD5
PLEC
PLEK2
PLEKHA6
PLEKHA8
PLEKHS1
PLIN4
PLOD2
PLSCR4
PLXNA2
PLXNA3
PLXNB1
PLXNB3
PLXNC1
PMM2
PMP2
PMPCB
PMS2
PNLIPRP1
PNPLA8
POF1B
POFUT2
POLR1A
POLR1C
POM121L12
POMT2
POSTN
POTED
POTEF
POTEI

MED13	*POTEJ*
MED15	*POTEM*
MED17	*POU2F1*
MEF2A	*PPA1*
MEF2B	*PPA2*
MEGF10	*PPARGC1A*
MEGF6	*PPFIBP2*
MEGF8	*PPIL4*
MEI1	*PPM1E*
MEN1	*PPP1R12A*
MEP1A	*PPP1R12C*
METTL10	*PPP1R14A*
METTL2A	*PPP1R2*
MFGE8	*PPP2R1A*
MFSD1	*PPP2R5B*
MFSD11	*PPP3R1*
MGAM	*PPP4R1*
MGAT5	*PRAM1*
MGAT5B	*PRAMEF13*
MIB2	*PRAMEF14*
MICAL1	*PRAMEF18*
MICAL3	*PRAMEF2*
MICALL2	*PRAMEF5*
MID1	*PRAMEF9*
MINA	*PRDM2*
MIOS	*PREX1*
MIPOL1	*PRG4*
MIS18BP1	*PRKAR2B*
MKRN3	*PRKCG*
MLC1	*PRKCH*
MLKL	*PRKD2*
MLLT4	*PRKD3*
MLXIPL	*PRKG1*
MMAB	*PRKRIP1*
MMP21	*PRLHR*
MMP27	*PRODH2*
MMP9	*PROSER1*
MNS1	*PRPF18*
MNX1	*PRPF38A*
MOB3B	*PRPF40A*
MOCS3	*PRPF8*

MON2	*PRR23C*
MORF4L1	*PRRC2B*
MPDZ	*PRSS16*
MPHOSPH10	*PRSS3*
MPHOSPH8	*PRTG*
MPHOSPH9	*PRX*
MPL	*PSEN1*
MPP1	*PSG4*
MPP4	*PSIP1*
MPZ	*PSMA1*
MRAP	*PSMC2*
MRAS	*PSMC6*
MRC1	*PSMD1*
MRC1L1	*PSMD9*
MRGPRX1	*PTCH1*
MROH2A	*PTCHD3*
MROH2B	*PTEN*
MRPL1	*PTGER4*
MRPL44	*PTK2*
MRPL52	*PTK2B*
MRPS23	*PTPN1*
MS4A4A	*PTPN11*
MSC	*PTPN13*
MSH5	*PTPRB*
MSL1	*PTPRD*
MT1H	*PTPRE*
MTERF	*PTPRF*
MTFR1L	*PTPRQ*
MTMR4	*PTPRU*
MTMR7	*PUM1*
MTUS2	*PURG*
MUSK	*PUS1*
MX2	*PUS7*
MXD4	*PVRL3*
MXRA5	*PWWP2B*
MYBPC2	*PXDNL*
MYCBP	*QPCTL*
MYCBP2	*QSER1*
MYCBPAP	*QSOX1*
MYEF2	*R3HDM1*
MYH1	*RAB11FIP3*

MYH13	*RAB21*
MYH14	*RAB34*
MYH4	*RABAC1*
MYH7	*RABGAP1*
MYH8	*RABGAP1L*
MYLK	*RAC1*
MYLK3	*RAD51B*
MYO10	*RAG2*
MYO15A	*RALGAPB*
MYO16	*RALGPS1*
MYO18B	*RANBP1*
MYO1A	*RANBP2*
MYO3B	*RAPGEF3*
MYO5B	*RASA1*
MYO5C	*RASGEF1B*
MYO7A	*RASGRF2*
MYO7B	*RASGRP3*
MYOC	*RASSF2*
MYRIP	*RASSF4*
NAA11	*RASSF6*
NACAD	*RB1*
NADSYN1	*RBCK1*
NAGK	*RBKS*
NAGLU	*RBM33*
NALCN	*RBM34*
NANP	*RBM43*
NAPEPLD	*RBM6*
NARS2	*RBMX*
NAV2	*RBMXL1*
NAV3	*RBMY1F*
NBEA	*REC8*
NBEAL2	*REL*
NBL1	*RELN*
NBN	*REV3L*
NCAPG2	*REXO4*
NCAPH	*RFX5*
NCF1	*RFX7*
NCL	*RGAG1*
NCOA3	*RGL1*
NCOR2	*RGMA*
NCR2	*RGPD8*

NCSTN	*RGS12*
NDC80	*RGS6*
NDOR1	*RHEBL1*
NDST1	*RHOT1*
NDUFS4	*RICTOR*
NEB	*RIF1*
NEFH	*RIN3*
NEK11	*RLTPR*
NEK9	*RMDN2*
NELL1	*RNF128*
NEMF	*RNF168*
NETO1	*RNF19A*
NEUROD2	*RNF20*
NEUROG2	*RNF220*
NF1	*RNPEP*
NF2	*RNPS1*
NFAT5	*ROCK1*
NFATC2	*ROR1*
NFKBIE	*RORC*
NFKBIZ	*ROS1*
NFX1	*RP1*
NFYA	*RP11-108K14.8*
NGFRAP1	*RP1L1*
NIPBL	*RPAP1*
NIPSNAP1	*RPE65*
NKX2-1	*RPGR*
NLGN1	*RPS27A*
NLRP10	*RPS3A*
NLRP11	*RPS4Y2*
NLRP13	*RPS6KA1*
NLRP8	*RPS6KB2*
NLRP9	*RPS6KC1*
NMD3	*RPTOR*
NME8	*RRAS*
NMUR1	*RRH*
NMUR2	*RRN3*
NNT	*RRP7A*
NOD1	*RSBN1*
NODAL	*RSPO1*
NOL11	*RTCA*
NOL4	*RTL1*

NOL6	*RTN1*
NOMO1	*RUNDC3B*
NOP2	*RWDD1*
NOS1	*RYR1*
NOTCH2NL	*RYR2*
NOTUM	*S100A7*
NOXA1	*S100G*
NPAP1	*S1PR4*
NPBWR2	*SAA2*
NPEPL1	*SAC3D1*
NPHP3	*SACM1L*
NPNT	*SAE1*
NPR2	*SAFB*
NPTX2	*SAFB2*
NPY4R	*SAMD10*
NR2F1	*SAR1A*
NR3C1	*SARS*
NRAP	*SCFD1*
NRAS	*SCGN*
NRD1	*SCLT1*
NRIP1	*SCN1A*
NRK	*SCN2B*
NRP2	*SCN4A*
NRXN2	*SCN5A*
NRXN3	*SCN7A*
NSMAF	*SCNN1G*
NSUN2	*SCP2*
NTN5	*SCRN2*
NTRK3	*SDC1*
NUAK2	*SDF4*
NUB1	*SDHD*
NUCB2	*SDK1*
NUDT16	*SEC16A*
NUDT9	*SEC24A*
NUGGC	*SEC24B*
NUP188	*SEC24D*
NUP54	*SEC63*
NUS1	*SELP*
NWD1	*SEMA3A*
NXF2	*SEMA4F*
NXF2B	*SEMA4G*

NXF5	*SENP7*
NYAP1	*Sep/04*
NYAP2	*SERBP1*
NYX	*SERPINA4*
OBP2A	*SERPIND1*
OBSCN	*SERTAD4*
OBSL1	*SETD1B*
OCRL	*SETD2*
ODF2	*SETX*
ODF2L	*SF3B1*
OGDH	*SF3B3*
OGDHL	*SFSWAP*
OIT3	*SGCD*
OLFM1	*SGCG*
OLIG3	*SGSH*
ONECUT2	*SH2D1A*
OPN1MW	*SH3GL2*
OPN1MW2	*SH3TC1*
OPRD1	*SHCBP1*
OPTC	*SHCBP1L*
OR10AD1	*SHPRH*
OR10AG1	*SHROOM3*
OR10G2	*SHROOM4*
OR10G4	*SI*
OR10G7	*SIGLEC6*
OR10J1	*SIK2*
OR10Q1	*SIK3*
OR10T2	*SIPA1L3*
OR11L1	*SIRPB1*
OR13H1	*SIRPD*
OR1E1	*SKOR1*
OR1L1	*SLC12A1*
OR1M1	*SLC12A2*
OR2A25	*SLC15A3*
OR2A5	*SLC17A8*
OR2AK2	*SLC19A3*
OR2C1	*SLC24A5*
OR2M2	*SLC26A3*
OR2M5	*SLC2A2*
OR2S2	*SLC30A4*
OR2V2	*SLC30A5*

OR2Z1	*SLC30A6*
OR3A1	*SLC30A9*
OR4A5	*SLC35A2*
OR4C13	*SLC38A1*
OR4C15	*SLC3A1*
OR4D10	*SLC44A1*
OR4D11	*SLC44A2*
OR4D6	*SLC45A2*
OR4F29	*SLC4A4*
OR4K13	*SLC4A7*
OR4K2	*SLC5A12*
OR4N4	*SLC7A3*
OR51B2	*SLC7A9*
OR51F1	*SLC8A3*
OR51G2	*SLC9A9*
OR51L1	*SLCO4C1*
OR51V1	*SLFN11*
OR52D1	*SLTM*
OR52I2	*SMARCA1*
OR52N5	*SMARCA2*
OR5AP2	*SMARCA4*
OR5C1	*SMARCAD1*
OR5D18	*SMARCC1*
OR5H15	*SMARCC2*
OR5P2	*SMC2*
OR6B1	*SMC5*
OR6C1	*SMEK2*
OR6C2	*SMNDC1*
OR6C76	*SMPD4*
OR6F1	*SMPDL3B*
OR6N1	*SMS*
OR6N2	*SNCA*
OR7C1	*SNCAIP*
OR7D2	*SNRNP40*
OR8H2	*SNTG2*
OR9A2	*SNX31*
OR9A4	*SNX6*
ORMDL3	*SNX7*
OSBPL6	*SNX9*
OTOG	*SOD2*
OTOGL	*SOX14*

OTOL1	*SOX4*
OTOP1	*SOX7*
OTOP3	*SP3*
OVCH1	*SPAG11B*
OVGP1	*SPAG16*
P2RY8	*SPAG8*
PABPC1	*SPATA13*
PABPC4L	*SPATA19*
PACSIN3	*SPATA20*
PAFAH2	*SPATA31A3*
PAK3	*SPATA31A5*
PALMD	*SPATA31A6*
PAM	*SPATA31D1*
PAN2	*SPATA31E1*
PAN3	*SPATA33*
PANK4	*SPECC1*
PANX3	*SPEM1*
PAPD4	*SPICE1*
PAPPA	*SPIDR*
PARL	*SPINK5*
PARN	*SPNS2*
PARP14	*SPRED2*
PARP4	*SPRY2*
PASK	*SPRYD7*
PAX1	*SPTB*
PAX7	*SPTBN1*
PBDC1	*SPTBN5*
PBOV1	*SRBD1*
PBRM1	*SRCAP*
PCBP2	*SRD5A3*
PCDH1	*SRP68*
PCDH10	*SRPK1*
PCDH11Y	*SRRM2*
PCDH18	*SSC5D*
PCDH8	*SSRP1*
PCDHA13	*ST5*
PCDHA2	*STAB1*
PCDHAC2	*STAB2*
PCDHB3	*STAC*
PCDHB5	*STAG2*
PCDHB6	*STAG3*

PCDHB7	*STAM2*
PCDHGA2	*STAT6*
PCDHGA5	*STIL*
PCDHGC5	*STK24*
PCGF1	*STMN1*
PCLO	*STON1-GTF2A1L*
PCNXL3	*STPG1*
PCSK4	*STX17*
PDCD11	*STXBP1*
PDE6H	*SUGP2*
PDLIM3	*SULF2*
PDLIM7	*SULT1A1*
PDZD2	*SULT2A1*
PDZRN3	*SUPT6H*
PDZRN4	*SUPV3L1*
PEG3	*SV2B*
PES1	*SVEP1*
PEX13	*SYDE2*
PEX6	*SYMPK*
PFAS	*SYN1*
PFDN5	*SYNE1*
PFKFB2	*SYNE2*
PFKFB3	*SYNE3*
PFKM	*SYNJ1*
PGF	*SYNPO*
PGM2	*SYNRG*
PGR	*SYP*
PGS1	*SYT1*
PHACTR2	*SYTL3*
PHC1	*SZT2*
PHF2	*TAB3*
PHF20	*TADA2B*
PHF3	*TAF1*
PHF8	*TAF1B*
PHKB	*TAF1C*
PHLDB1	*TAF1L*
PIAS1	*TAF6*
PIEZO1	*TAF6L*
PIGB	*TAF7L*
PIGT	*TANC2*
PIK3C2A	*TANGO6*

PIK3CA	*TANK*
PIK3CB	*TAS2R19*
PIK3CG	*TAS2R38*
PIK3R4	*TBC1D16*
PIKFYVE	*TBC1D19*
PIM2	*TBC1D23*
PIP5K1B	*TBC1D4*
PITPNM1	*TBCK*
PITX2	*TBL1Y*
PJA2	*TCHH*
PKD1L1	*TCN1*
PKD2L1	*TCOF1*
PKHD1L1	*TDP2*
PKNOX2	*TDRD1*
PKP2	*TDRD6*
PLA1A	*TDRD7*
PLA2R1	*TECTA*
PLAG1	*TEKT2*
PLAU	*TEKT4*
PLB1	*TENM1*
PLCB3	*TENM2*
PLCB4	*TENM4*
PLCD4	*TEX10*
PLCG1	*TEX14*
PLCH1	*TFEC*
PLCH2	*TGFB1I1*
PLCL2	*TGFBR1*
PLEKHA7	*TGFBR2*
PLEKHG3	*TGS1*
PLEKHG4B	*THADA*
PLIN4	*THOC2*
PLP1	*THSD1*
PLS1	*THSD7A*
PLXDC1	*THUMPD3*
PLXNA4	*TIAM1*
PLXNB1	*TIAM2*
PLXNB2	*TIE1*
PLXNB3	*TIFAB*
PMF1	*TIMMDC1*
PNISR	*TJP1*
PNKP	*TLK2*

PNMAL1	*TLL1*
PNPLA7	*TLR10*
PODN	*TLR6*
PODXL2	*TM9SF2*
POGK	*TMBIM6*
POLA1	*TMC3*
POLD1	*TMEM119*
POLG	*TMEM181*
POLR1A	*TMEM194B*
POLR2A	*TMEM199*
POLR3F	*TMEM225*
POM121C	*TMEM241*
POM121L12	*TMEM259*
PORCN	*TMEM38A*
POTEI	*TMEM62*
POTEJ	*TMEM67*
POU3F4	*TMTC2*
POU6F1	*TNFRSF9*
PPA1	*TNIP1*
PPARA	*TNIP2*
PPARGC1A	*TNKS2*
PPIL4	*TNR*
PPM1G	*TNRC6C*
PPM1K	*TNS4*
PPME1	*TNXB*
PPP1CC	*TOP2A*
PPP1R1B	*TOP3A*
PPP1R9A	*TOPBP1*
PPP2R2B	*TOR3A*
PPP2R2C	*TP53BP1*
PPP5C	*TPSB2*
PPP6R1	*TPTE*
PPP6R3	*TRABD2B*
PRAMEF1	*TRAF3*
PRAMEF2	*TRAK2*
PRAMEF3	*TRAM2*
PRB1	*TRAPPC12*
PRB3	*TRAPPC13*
PRDM14	*TRAPPC9*
PRDM9	*TRDMT1*
PRICKLE2	*TRIM24*

PRKACG	*TRIM25*
PRKAR1B	*TRIM48*
PRKAR2B	*TRIM65*
PRKCB	*TRIM77*
PRKCD	*TRIML1*
PRKCQ	*TRIO*
PRKCSH	*TRIOBP*
PRKD3	*TRIP11*
PRKRIR	*TRIP12*
PRM2	*TRIP4*
PRND	*TRMT11*
PROM1	*TRNT1*
PROSER2	*TRPA1*
PROX2	*TRPC1*
PRPF38A	*TRPC5*
PRPF40A	*TRPM7*
PRPF8	*TRPV6*
PRPS1L1	*TSC1*
PRR14L	*TSC2*
PRR20C	*TSHZ3*
PRR23A	*TSPAN4*
PRRC2C	*TSPEAR*
PRRX1	*TSPYL2*
PRRX2	*TSTD2*
PRSS3	*TTBK2*
PRSS46	*TTC21B*
PRTG	*TTC28*
PRUNE2	*TTC37*
PSAP	*TTC39C*
PSD3	*TTK*
PSG4	*TTLL10*
PSMA4	*TTLL5*
PSMA5	*TTLL9*
PSMD14	*TUBB4B*
PSME4	*TUBD1*
PSRC1	*TUBGCP4*
PTCD1	*TUFT1*
PTEN	*TUSC5*
PTGER3	*TXLNB*
PTGFRN	*TXNDC12*
PTH2R	*UACA*

PTK2	*UBA6*
PTPN18	*UBE2A*
PTPN20A	*UBE2F*
PTPN3	*UBE2J1*
PTPN4	*UBE2W*
PTPN6	*UBE3B*
PTPRB	*UBE4A*
PTPRD	*UBR3*
PTPRE	*UBR4*
PTPRN2	*UBXN7*
PTPRO	*UGGT1*
PTPRQ	*UGP2*
PTPRT	*UGT2A2*
PTPRU	*UGT2B4*
PTPRZ1	*UGT3A2*
PTRH1	*UHRF1BP1*
PTX3	*ULBP2*
PUS1	*ULK1*
PVR	*ULK2*
PWWP2B	*ULK4*
PXDN	*UNC13C*
PXK	*UNC45B*
PYGM	*UNC5B*
PYHIN1	*UNC80*
PZP	*UPB1*
RAB38	*UPF2*
RAB3GAP1	*UPP2*
RAB3GAP2	*URB1*
RAB41	*USH2A*
RAB4B	*USP16*
RAB6B	*USP17L10*
RAB7L1	*USP17L12*
RABEPK	*USP17L24*
RAD23A	*USP17L26*
RAD51AP2	*USP17L28*
RADIL	*USP17L5*
RAI14	*USP20*
RANBP2	*USP25*
RANBP6	*USP29*
RASA1	*USP34*
RASA3	*USP36*

RASAL3	*USP37*
RASD2	*USP43*
RASGRF1	*USP54*
RASGRF2	*USP9Y*
RAVER1	*UTP14A*
RB1	*UTP20*
RBBP6	*UTP23*
RBBP8	*UTRN*
RBBP8NL	*UTY*
RBL1	*VAV2*
RBL2	*VCAN*
RBM10	*VCX3A*
RBM12	*VDAC3*
RBM28	*VPS13A*
RBM33	*VPS13C*
RBM44	*VPS13D*
RBMXL2	*VPS16*
RBX1	*VPS36*
RCN1	*VPS39*
RCOR2	*VPS41*
RELN	*VPS45*
REPIN1	*VPS4B*
REPS2	*VRK1*
RERG	*VSIG2*
RET	*VSIG4*
RETSAT	*VSTM5*
REXO4	*VWA5B2*
RFPL2	*VWF*
RFPL4A	*WDFY4*
RFWD2	*WDHD1*
RFX3	*WDR25*
RFX4	*WDR33*
RFX7	*WDR48*
RGAG1	*WDR52*
RGS11	*WDR53*
RGS3	*WDR66*
RGS7	*WDR70*
RGS9	*WDR72*
RHNO1	*WDR90*
RHO	*WDR92*
RHOBTB3	*WDR96*

RHOD	*WHSC1L1*
RHPN2	*WIZ*
RICTOR	*WNK2*
RIMBP2	*WNT10A*
RIOK2	*WNT10B*
RIOK3	*WNT16*
RND2	*WRAP53*
RNF113A	*WWC1*
RNF150	*WWC2*
RNF17	*XAB2*
RNF185	*XIRP1*
RNF2	*XIRP2*
RNF20	*XKR9*
RNF220	*XPC*
RNF26	*XPO1*
RNF40	*XPO4*
RNH1	*XRCC6*
ROBO2	*XYLT1*
ROBO4	*YARS2*
ROCK1	*YBX2*
ROM1	*YEATS2*
RORC	*YME1L1*
ROS1	*YTHDC2*
RP1	*YY1AP1*
RP11-830F9.6	*ZBBX*
RP1L1	*ZBTB5*
RPAP1	*ZBTB7A*
RPE	*ZBTB7C*
RPGRIP1	*ZBTB8B*
RPL10	*ZC3H13*
RPL22L1	*ZCCHC18*
RPL29	*ZFC3H1*
RPL3	*ZFHX2*
RPL6	*ZFHX3*
RPL8	*ZFHX4*
RPP40	*ZFP28*
RPS24	*ZFP64*
RPS4X	*ZFYVE20*
RPS6	*ZGPAT*
RRBP1	*ZHX2*
RREB1	*ZKSCAN5*

RRM1	*ZMYND11*
RRP1B	*ZMYND12*
RSBN1	*ZMYND19*
RSL1D1	*ZNF107*
RSPO3	*ZNF12*
RSRC1	*ZNF131*
RSU1	*ZNF202*
RTBDN	*ZNF208*
RTEL1	*ZNF211*
RTKN2	*ZNF215*
RTL1	*ZNF221*
RTN4	*ZNF222*
RTTN	*ZNF235*
RUFY2	*ZNF251*
RUNX1	*ZNF260*
RUNX1T1	*ZNF280C*
RUNX2	*ZNF285*
RUSC2	*ZNF287*
RYR1	*ZNF292*
RYR2	*ZNF326*
RYR3	*ZNF345*
SACS	*ZNF354B*
SAFB2	*ZNF37A*
SAGE1	*ZNF417*
SALL2	*ZNF423*
SAMD15	*ZNF43*
SAMSN1	*ZNF440*
SAP30BP	*ZNF443*
SATL1	*ZNF445*
SBK1	*ZNF462*
SBK3	*ZNF48*
SBNO2	*ZNF480*
SCAF1	*ZNF492*
SCAF11	*ZNF518B*
SCAF4	*ZNF532*
SCAMP3	*ZNF544*
SCFD1	*ZNF555*
SCG5	*ZNF560*
SCLY	*ZNF570*
SCN11A	*ZNF585A*
SCN1A	*ZNF615*

SCN2A
SCN7A
SCN9A
SCNN1A
SCNN1B
SCRIB
SCYL2
SDE2
SDHA
SDHB
SDK1
SDK2
SEC14L6
SEC62
SEC63
SEL1L
SELENBP1
SELP
SEMA3C
SEMA4G
SEMA5B
SEMA6D
SENP2
SEPSECS
Sep/08
SERPINB4
SERTAD4
SESTD1
SETD2
SETD7
SEZ6L2
SF3B3
SFRP2
SGCB
SGK223
SGK494
SGSM1
SH2D5
SH3BP1
SH3PXD2A
SHCBP1L

ZNF638
ZNF639
ZNF644
ZNF667
ZNF674
ZNF676
ZNF678
ZNF689
ZNF705B
ZNF710
ZNF717
ZNF729
ZNF736
ZNF782
ZNF793
ZNF800
ZNF804A
ZNF850
ZNF93
ZNF99
ZSWIM6
ZSWIM8
ZUFSP
ZXDA
ZXDB
ZYG11B

SHISA2

SHISA5

SHMT1

SHOX

SHOX2

SHROOM1

SHROOM2

SHROOM3

SHROOM4

SI

SIAH1

SIGLEC1

SIGLEC15

SIGLEC6

SIGLEC7

SIGLECL1

SIK1

SIK2

SIK3

SIN3A

SIPA1L2

SIPA1L3

SIRT1

SKIL

SKOR2

SLAMF1

SLC10A1

SLC12A5

SLC12A9

SLC16A7

SLC17A9

SLC18A2

SLC18A3

SLC18B1

SLC22A11

SLC22A12

SLC22A25

SLC22A6

SLC24A2

SLC25A30

SLC25A37

SLC25A44
SLC25A52
SLC26A1
SLC27A2
SLC2A14
SLC2A3
SLC34A2
SLC35A4
SLC35F3
SLC35G5
SLC35G6
SLC36A3
SLC37A3
SLC38A1
SLC38A2
SLC44A3
SLC44A5
SLC4A10
SLC4A2
SLC4A3
SLC5A1
SLC5A3
SLC5A5
SLC6A11
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SLC6A3
SLC6A5
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SLC9A1
SLC9A6
SLC9C1
SLCO1C1
SLCO5A1
SLCO6A1
SLITRK1
SLITRK2
SLITRK5
SMAD1
SMAD2

SMAD4

SMARCA4

SMARCAD1

SMARCC2

SMC1A

SMC6

SMCR8

SMEK2

SMPD4

SMYD3

SNAP91

SNCAIP

SND1

SNRPA

SNRPE

SNRPN

SNX1

SNX14

SNX29

SNX4

SOGA1

SOHLH1

SOHLH2

SORCS2

SOS1

SOWAHC

SP110

SPA17

SPACA1

SPACA5

SPACA5B

SPAG17

SPAG6

SPAM1

SPATA13

SPATA2L

SPATA31A1

SPATA31A2

SPATA31A3

SPATA31A5

SPATA31A6

SPATA31A7

SPATA31D1

SPDYE2B

SPECC1

SPEF1

SPEG

SPESP1

SPHKAP

SPICE1

SPIDR

SPIRE1

SPPL2C

SPRED3

SPRY2

SPRY3

SPTBN1

SPTBN4

SPTBN5

SQRDL

SRCIN1

SREK1

SRF

SRGAP3

SRRM4

SRSF4

SS18

SSB

SSBP1

SSC5D

SSH1

SSRP1

SST

SSTR4

SSX2B

ST3GAL2

ST7

ST8SIA5

STAB1

STAB2

STAG2

STAM

STAP1

STARD6

STAT2

STK10

STK11

STK11IP

STK32B

STK33

STK4

STMN1

STON2

STRA6

STRIP1

STRN3

STS

STX11

STXBP5

SUCO

SULT1C3

SULT6B1

SUMF2

SUPT6H

SVEP1

SYBU

SYCP2

SYNDIG1L

SYNE1

SYNE2

SYNPO

SYNPO2

SYNPR

SYPL2

SYT11

SYT13

SYT16

SYTL5

SZT2

TAAR6

TACC2

TACR1

TACSTD2

TAF15
TAF1B
TAF1C
TAF1L
TAF3
TAGLN2
TANC2
TANGO2
TANK
TAOK3
TAS2R19
TAS2R20
TAS2R8
TAS2R9
TBC1D21
TBC1D7
TBC1D8
TBCC
TBL1XR1
TBL1Y
TBP
TBX10
TBX20
TCEAL6
TCEAL7
TCEB3
TCERG1L
TCF20
TCHH
TCN2
TDRD1
TDRD3
TDRD5
TDRD6
TDRD9
TECPR1
TECPR2
TECTB
TEK
TEKT1
TEKT4

TENC1

TENM1

TENM2

TENM3

TEP1

TEX13A

TEX36

TF

TFAP2D

TFB1M

TFEB

TFEC

TG

TGFBR1

THEMIS

THOC7

THSD7A

TICAM1

TICRR

TIE1

TIGD5

TIMD4

TIMM50

TIMM8A

TIMMDC1

TKTL2

TLE4

TLE6

TLL1

TLL2

TLN1

TLR2

TLR5

TM9SF2

TMC2

TMC8

TMEFF1

TMEM121

TMEM131

TMEM132C

TMEM151A

TMEM177

TMEM2

TMEM207

TMEM208

TMEM221

TMEM239

TMEM56

TMEM57

TMEM62

TMEM68

TMIE

TMPO

TMPRSS11D

TMPRSS12

TMPRSS15

TMTC3

TNFAIP1

TNFAIP6

TNFRSF4

TNN

TNNC1

TNRC6B

TNRC6C

TONSL

TOP2B

TOP3B

TOPAZ1

TOX4

TP53

TP53BP2

TP73

TPBG

TPCN2

TPD52

TPD52L1

TPH2

TPO

TPP2

TPR

TRA2A

TRABD2B

TRAF3IP1

TRAPPC10

TRAPPC8

TRHR

TRIB3

TRIM11

TRIM16

TRIM24

TRIM38

TRIM49D1

TRIM51

TRIM58

TRIM62

TRIO

TRIOBP

TRIP12

TRMT10C

TRMT2A

TRO

TRPA1

TRPC4

TRPC5

TRPM1

TRPM2

TRPM3

TRPS1

TSC1

TSC2

TSC22D1

TSFM

TSGA13

TSKS

TSPAN15

TTBK1

TTC12

TTC16

TTC17

TTC21B

TTC23L

TTC28

TTC34

TTC40

TTC7A

TTC9

TTR

TUBA8

TUBE1

TULP2

TULP4

TUSC3

TVP23A

TXK

TXNDC16

TYK2

TYR

UACA

UBA6

UBE2E3

UBE2NL

UBE3A

UBE3B

UBE3D

UBE4B

UBN1

UBOX5

UBP1

UBQLN4

UBR1

UBR2

UBR4

UBR5

UBXN11

UCHL5

UGGT1

UGT1A6

UHMK1

UHRF1BP1L

ULK1

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UNC5D

UNC79

UNC80

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UROC1
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USP26
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USP48
USP5
USP6NL
USP7
UTP11L
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VASN
VAV2
VEGFB
VENTX
VEZF1
VGF
VGLL3
VN1R4
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VPS13B
VPS13C
VPS13D
VPS53
VRTN
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VSTM2B
VWA3A
VWA5A

VWA5B1
VWA5B2
VWDE
VWF
WAC
WDFY2
WDHD1
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WDR19
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WDR33
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WDR49
WDR62
WDR7
WDR87
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WDTC1
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WNK2
WNK3
WNK4
WNT7B
WNT8A
WWC1
WWOX
WWP1
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XDH
XIRP2
XKR4
XKR7
XPO6
XRN2
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YIPF7
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ZBTB16

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ZBTB22

ZBTB24

ZBTB39

ZBTB46

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ZC3H3

ZC3H4

ZC3H6

ZC3H7A

ZC3HAV1L

ZCCHC11

ZDBF2

ZFC3H1

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ZFHX4

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ZFP42

ZFP62

ZFP92

ZFPM2

ZFR2

ZFYVE20

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ZHX3

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ZKSCAN3

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ZNF781
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ZNF799
ZNF804A
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ZNF831
ZNF85
ZNF853
ZNF878
ZNF91
ZNF93
ZNF98

ZP2

ZRSR2

ZSCAN12

ZSCAN2

ZUFSP

ZW10

ZXDB

ZZEF1

ZZZ3

Table S6B

Mutated genes (nonsynonymous) unique to each group

IDH-gr (n=768)	KRAS-gr (n=496)	TP53-gr (n=1670)	Undetermined-gr (n=1240)
ABCA9	*ABCA3*	*A1CF*	*A2M*
ABCB10	*ABCG1*	*AADACL4*	*AADAC*
ABCC11	*ABHD16B*	*AAK1*	*AATF*
ABCC3	*AC007952.5*	*AARD*	*ABCA10*
ABCC4	*ACTL8*	*ABCA2*	*ABCA4*
ABCC9	*ACTR1B*	*ABCA5*	*ABCB11*
ACPL2	*ADAM21*	*ABCB9*	*ABCB7*
ACSBG2	*ADAMTS18*	*ABCC1*	*ABCC12*
ACSF2	*ADD3*	*ABCC2*	*ABCC5*
ACSL5	*ADNP2*	*ABL2*	*ABCC6*
ADAM18	*ADSS*	*ABRA*	*ABHD17A*
ADAM22	*AIG1*	*ABTB2*	*ABL1*
ADAMTS6	*ALX4*	*ACAD10*	*ABLIM1*
ADAT1	*AMHR2*	*ACE*	*ACCSL*
ADCY4	*ANHX*	*ACHE*	*ACER3*
AKAP8L	*ANKFY1*	*ACKR3*	*ACSL1*
AKIRIN2	*ANKRD17*	*ACSL4*	*ACSM2A*
ALAS1	*ANKRD27*	*ACSM5*	*ACSM2B*
ALDH1L2	*ANKRD31*	*ACTA1*	*ACSM4*
ALG8	*ANKS1A*	*ACTG2*	*ACTG1*
ALKBH2	*ANO5*	*ACTR8*	*ADAM30*
ALOX5AP	*ANTXR2*	*ACTRT2*	*ADAM9*
ALS2CR11	*AOC3*	*ACVR2A*	*ADAMTS16*
AMBP	*APBA2*	*ADAM11*	*ADAMTS17*
AMD1	*APC2*	*ADAM17*	*ADCY2*
AMICA1	*APOE*	*ADAM29*	*ADH6*
AMMECR1L	*AQP1*	*ADAM32*	*AEBP2*
ANGPT2	*ARHGAP31*	*ADAM8*	*AFF1*
ANGPT4	*ARHGAP33*	*ADAMTS14*	*AGAP5*
ANKHD1	*ARHGAP35*	*ADAMTS15*	*AGGF1*
ANKIB1	*ARL2BP*	*ADAMTS8*	*AHCYL2*
ANKLE2	*ARPP21*	*ADAMTSL1*	*AKAP11*
ANKRD33B	*ARR3*	*ADAMTSL3*	*AKAP6*
ANO4	*ASXL3*	*ADAMTSL5*	*ALDH5A1*
AP1M2	*ATP10D*	*ADAP1*	*ALG10*
APAF1	*ATP2A3*	*ADARB2*	*ALG1L*
APBB2	*ATPIF1*	*ADCK2*	*ALG9*
ARHGAP12	*AVEN*	*ADD2*	*ALPK1*

ARHGEF3	*AVPR1A*	*ADGB*	*ALS2*
ARID5B	*B4GALNT4*	*ADH1C*	*ALS2CR12*
ARMC9	*BARHL2*	*ADRA1D*	*AMER3*
ARMCX2	*BCAT1*	*ADRA2B*	*ANAPC5*
ASAP1	*BMP15*	*AFF3*	*ANK2*
ASIC3	*BNC1*	*AGAP1*	*ANKFN1*
ASNA1	*BPIFB4*	*AGBL3*	*ANKRD40*
ATG3	*BRSK1*	*AGPAT9*	*ANO2*
ATG4D	*BTG4*	*AGRN*	*ANXA3*
ATP12A	*BZRAP1*	*AGTPBP1*	*ANXA6*
ATP2A1	*C12orf77*	*AIM1L*	*AP4E1*
ATP8A2	*C16orf62*	*AK2*	*APLP2*
ATP8B2	*C2CD4C*	*AKAP1*	*APOBEC4*
ATXN1L	*C7orf55-LUC7L2*	*AKAP7*	*AQP7*
BAZ1A	*C8A*	*AKNA*	*ARFGEF2*
BCAS2	*CA4*	*AKT3*	*ARHGAP11B*
BCL11A	*CAMSAP3*	*AKTIP*	*ARHGAP15*
BCL2L11	*CASP8*	*ALB*	*ARHGAP20*
BCO2	*CBLN4*	*ALDH16A1*	*ARHGAP24*
BMPR2	*CCAR2*	*ALDH2*	*ARHGAP25*
BOD1	*CCDC113*	*ALG13*	*ARHGEF15*
BRDT	*CCDC122*	*ALLC*	*ARHGEF28*
BRIP1	*CCDC148*	*ALOXE3*	*ARHGEF33*
BTF3	*CCDC159*	*ALPL*	*ARHGEF39*
BTK	*CCDC178*	*ALPPL2*	*ARHGEF4*
BTN3A2	*CCDC88B*	*AMPH*	*ARSG*
BUB1B	*CCR6*	*ANAPC7*	*ARTN*
C11orf71	*CCT6A*	*ANKH*	*ARVCF*
C17orf66	*CDH11*	*ANKRD11*	*ASB11*
C17orf72	*CDH3*	*ANKRD13B*	*ASH1L*
C17orf78	*CDH6*	*ANKRD18A*	*ASIC4*
C19orf33	*CDHR4*	*ANKRD18B*	*ASPH*
C19orf60	*CDK12*	*ANKRD20A1*	*ASPM*
C1orf112	*CDK19*	*ANKRD26P1*	*ASTN1*
C1orf159	*CDX2*	*ANKRD34A*	*ATAD3C*
C1orf27	*CDYL*	*ANKRD46*	*ATG7*
C1orf87	*CEACAM18*	*ANKRD62*	*ATL1*
C22orf42	*CEP192*	*ANKRD7*	*ATP1B3*
C2orf54	*CHD3*	*ANKS3*	*ATP6V0A1*
C2orf71	*CHMP7*	*ANKS4B*	*ATP8B1*
C3orf30	*CHST6*	*ANLN*	*ATRX*

C7orf26	*CHST8*	*ANXA2*	*AUNIP*
C9orf156	*CHSY1*	*AP3B1*	*AXIN2*
CA7	*CLDN6*	*AP3B2*	*AZI1*
CALCOCO1	*CLDND2*	*APEX1*	*B3GALT1*
CALCR	*CLPB*	*APH1A*	*BBS2*
CAMK2G	*CMTM4*	*APOBEC3A*	*BBS9*
CAPNS1	*CNPY3*	*AQR*	*BCL2L13*
CARD10	*CNR1*	*ARAF*	*BEGAIN*
CARNS1	*CP*	*ARHGAP36*	*BEND3*
CASKIN1	*CRCP*	*ARHGEF38*	*BEST2*
CBFB	*CREB5*	*ARID2*	*BICC1*
CBWD6	*CREBZF*	*ARL5C*	*BIRC2*
CC2D1B	*CRTC3*	*ARMCX1*	*BLVRA*
CCDC181	*CSMD2*	*ARPC5*	*BLZF1*
CCDC38	*CST8*	*ARSA*	*BMP3*
CCDC39	*CSTF2*	*ARSD*	*BMPR1A*
CCDC42	*CT47B1*	*ARSJ*	*BMX*
CCDC73	*CTNNB1*	*ASB17*	*BNC2*
CCDC78	*CTSF*	*ASCC2*	*BOD1L1*
CCDC80	*CTTNBP2*	*ASIC1*	*BRPF3*
CCNI	*CWF19L2*	*ASNS*	*BTAF1*
CCNT1	*CX3CR1*	*ASNSD1*	*BTBD7*
CCR4	*CXCR4*	*ASTL*	*BTBD9*
CCT8L2	*CYLC1*	*ATAD2B*	*BTG3*
CD1E	*CYP11B2*	*ATG13*	*BTRC*
CD36	*CYP21A2*	*ATG4A*	*C10orf118*
CD44	*CYP2A13*	*ATG5*	*C11orf1*
CD72	*CYSLTR2*	*ATP10B*	*C11orf24*
CD86	*CYTH3*	*ATP11B*	*C11orf65*
CDC5L	*DALRD3*	*ATP11C*	*C12orf43*
CDRT15	*DBF4*	*ATP1A3*	*C14orf159*
CECR2	*DCAF4L1*	*ATP1A4*	*C14orf37*
CELF2	*DCAF8*	*ATP2C2*	*C14orf80*
CENPBD1	*DCAF8L1*	*ATP5G2*	*C17orf89*
CENPJ	*DCLK3*	*ATP8A1*	*C19orf44*
CEP104	*DDX52*	*ATP8B3*	*C19orf47*
CHAF1A	*DENND4B*	*ATP8B4*	*C1QB*
CHM	*DET1*	*ATR*	*C1QTNF5*
CHN1	*DGCR14*	*ATRIP*	*C1orf172*
CHST4	*DHX36*	*ATXN7L2*	*C1orf192*
CKM	*DLG2*	*AVL9*	*C1orf194*

CLDN16	*DLX4*	*B3GNT1*	*C20orf112*
CLEC18A	*DMRTB1*	*B4GALNT3*	*C2orf16*
CLTA	*DMXL1*	*BACH2*	*C3orf83*
CLTC	*DNAJB5*	*BAI1*	*C4A*
CMTM2	*DNAJC21*	*BAI2*	*C4B*
CMTM8	*DNM2*	*BAI3*	*C4orf33*
CMTR1	*DOCK6*	*BAZ1B*	*C7orf63*
CNDP1	*DTWD1*	*BAZ2A*	*C8orf48*
CNGA2	*DTX3L*	*BBOX1*	*C8orf76*
CNN3	*DUS2*	*BBS1*	*C9orf171*
CNOT4	*E2F1*	*BCAM*	*C9orf3*
COASY	*E2F5*	*BCAR1*	*C9orf43*
COG5	*EBF1*	*BCAR3*	*CA2*
COL2A1	*EBF2*	*BCHE*	*CA5A*
COL6A1	*EBPL*	*BCL10*	*CA8*
COLGALT2	*EIF2B5*	*BCL9*	*CA9*
COMMD9	*ELAC2*	*BDH1*	*CADM1*
COPB1	*EMR3*	*BEND4*	*CALHM3*
COPG1	*ESRRG*	*BGN*	*CAMK2A*
CPO	*F2RL1*	*BMP6*	*CAMK4*
CREB1	*FAM169B*	*BMP8B*	*CAMTA2*
CRYBB1	*FAM170A*	*BPHL*	*CAPN2*
CRYBB2	*FAM171A1*	*BPI*	*CAPN7*
CSNK1D	*FAM189B*	*BRCC3*	*CAPN9*
CSNK1G1	*FAM194A*	*BRD1*	*CAPS2*
CT45A5	*FAXDC2*	*BRINP2*	*CASK*
CT55	*FCGR3B*	*BRWD1*	*CASP14*
CUL3	*FGF11*	*BSG*	*CASP3*
CUL5	*FGFR2*	*BSND*	*CASR*
CWC27	*FKBP2*	*BTNL9*	*CATSPERB*
CXXC1	*FLRT1*	*C10orf12*	*CCAR1*
CXorf30	*FNDC3A*	*C11orf54*	*CCDC108*
CXorf66	*FOXD4*	*C11orf57*	*CCDC112*
CYBRD1	*FOXI2*	*C11orf82*	*CCDC132*
CYP17A1	*FOXP3*	*C12orf10*	*CCDC140*
CYP26A1	*FSCN2*	*C12orf60*	*CCDC47*
CYP2A6	*FTCD*	*C14orf39*	*CCDC6*
DAB1	*FTMT*	*C16orf3*	*CCDC64*
DACH1	*FXR2*	*C17orf104*	*CCDC64B*
DAPK1	*GAB4*	*C17orf96*	*CCDC70*
DDX19A	*GALNT9*	*C17orf98*	*CCDC79*

DDX19B	*GAPDHS*	*C18orf56*	*CCDC89*
DDX25	*GART*	*C19orf57*	*CCDC92*
DDX26B	*GAS6*	*C1RL*	*CCDC93*
DDX39A	*GATA1*	*C1orf106*	*CCER1*
DDX5	*GBP5*	*C1orf127*	*CCT2*
DDX56	*GCC1*	*C1orf167*	*CD109*
Dec/01	*GCK*	*C1orf35*	*CD160*
DEFA4	*GDPD4*	*C1orf94*	*CD1A*
DENND4A	*GFI1*	*C22orf39*	*CD1C*
DHX15	*GLTPD2*	*C22orf43*	*CD28*
DHX57	*GLTSCR1*	*C2CD5*	*CD37*
DKC1	*GOLGA6A*	*C2orf43*	*CD46*
DKK4	*GOT1*	*C2orf49*	*CD8B*
DMKN	*GOT2*	*C4orf29*	*CDAN1*
DNAJA2	*GPBAR1*	*C4orf51*	*CDC42BPA*
DNAJC11	*GPN1*	*C5orf22*	*CDH26*
DNAJC5G	*GPR110*	*C5orf51*	*CDH8*
DND1	*GPR20*	*C6ORF165*	*CDHR2*
DOCK3	*GPR27*	*C6orf118*	*CDKAL1*
DRAXIN	*GPRIN3*	*C7orf31*	*CDKN2B*
DSCAM	*GRIA2*	*C9orf37*	*CDV3*
DSCAML1	*GRIN2B*	*C9orf84*	*CEACAM16*
DUSP27	*GSE1*	*CA11*	*CELSR1*
DYSF	*GUCY1A2*	*CABS1*	*CENPF*
EFCAB14	*HAUS5*	*CACNA1E*	*CENPI*
EFCAB7	*HEATR2*	*CACNA1F*	*CENPU*
EFNB2	*HELZ2*	*CACNA1S*	*CEP128*
EFTUD1	*HERPUD1*	*CACNA2D2*	*CEP55*
EHMT1	*HIP1*	*CACNG8*	*CHD1L*
EIF3A	*HIST1H2BC*	*CALCRL*	*CHRD*
EIF3K	*HLA-DQB1*	*CAMKK2*	*CHSY3*
EIF3M	*HLA-G*	*CAMSAP1*	*CIC*
EIF4ENIF1	*HOOK2*	*CAND1*	*CIRH1A*
ELMO2	*HOXA11*	*CAPN14*	*CIT*
ELN	*HOXA13*	*CAPN5*	*CIZ1*
ELOVL6	*HRCT1*	*CAPN6*	*CLASP2*
ELTD1	*HSPB8*	*CAPRIN2*	*CLCA1*
ENG	*HTR1A*	*CAPS*	*CLCNKA*
ENHO	*IGFL1*	*CAPZA2*	*CLEC4F*
ENO1	*IL7*	*CARD6*	*CLGN*
ENOX2	*IL7R*	*CARF*	*CLSTN1*

EPB41L3	*IMPA1*	*CASC5*	*CNOT1*
EPB42	*IMPG1*	*CASP5*	*CNOT8*
EPHA7	*ING2*	*CAT*	*CNTN6*
EPHX2	*IRX1*	*CBLC*	*CNTROB*
ERAP1	*ITPKB*	*CBX2*	*COG1*
ERF	*JAK2*	*CBX4*	*COIL*
ERVMER34-1	*KCNMA1*	*CC2D1A*	*COL10A1*
ESCO1	*KCNN3*	*CC2D2A*	*COL21A1*
ESPN	*KCNQ4*	*CCDC105*	*COL4A3BP*
ESRP1	*KCTD1*	*CCDC135*	*COL4A4*
ETV4	*KIAA1549L*	*CCDC168*	*COLEC10*
F13B	*KIF4A*	*CCDC174*	*COMMD2*
FABP6	*KIRREL2*	*CCDC176*	*COQ9*
FAM118B	*KL*	*CCDC33*	*CORIN*
FAM120A	*KLHL12*	*CCDC57*	*COX5B*
FAM122A	*KLHL30*	*CCDC66*	*COX7A2*
FAM149B1	*KLRC2*	*CCDC85B*	*CPA5*
FAM181B	*KLRG1*	*CCDC9*	*CPA6*
FAM184B	*KMT2D*	*CCK*	*CPNE3*
FAM186B	*KRT71*	*CCM2*	*CPNE8*
FAM193B	*KRTAP9-8*	*CCNF*	*CPZ*
FAM19A2	*LCT*	*CCNK*	*CRAMP1L*
FAM21A	*LIMK2*	*CCNL1*	*CRAT*
FAM222B	*LMF2*	*CCPG1*	*CREB3*
FAM3C	*LMTK2*	*CCSER1*	*CREB3L1*
FAM46C	*LONP2*	*CD163L1*	*CRIP3*
FAM49B	*LPCAT1*	*CD19*	*CRIPAK*
FAR1	*LPHN3*	*CD247*	*CRKL*
FBF1	*LRRK1*	*CD33*	*CRMP1*
FBXL4	*LRRN3*	*CD38*	*CRYGA*
FBXL7	*LRTM1*	*CD70*	*CRYM*
FBXO38	*LSP1*	*CD9*	*CS*
FBXO48	*LTBR*	*CDC42BPB*	*CSE1L*
FBXW4	*LUC7L3*	*CDCA3*	*CSTA*
FBXW8	*LUZP4*	*CDH13*	*CTAGE8*
FEZF2	*LYN*	*CDH19*	*CTNNA2*
FGG	*LYPLA1*	*CDH23*	*CTNND2*
FHL1	*M1AP*	*CDH4*	*CXCL13*
FKBP3	*MANSC4*	*CDIPT*	*CXXC11*
FLII	*MAP1A*	*CDK5*	*CYB5R1*
FN1	*MARS*	*CDK6*	*CYB5R4*

FOCAD	*MASP1*	*CDKL5*	*CYP2C18*
FRK	*MBD2*	*CEACAM5*	*CYP2E1*
FTO	*MC4R*	*CEACAM6*	*CYP2F1*
FUT10	*MCM8*	*CECR6*	*CYP4F22*
FXYD4	*MDH2*	*CENPB*	*CYP7B1*
G6PC	*METTL14*	*CENPC*	*D2HGDH*
GABPB2	*MICU1*	*CENPE*	*DAAM1*
GABRR1	*MID1IP1*	*CEP112*	*DAZL*
GAGE2C	*MLLT10*	*CEP135*	*DBH*
GARS	*MMP16*	*CERCAM*	*DBX1*
GATAD1	*MMS22L*	*CGNL1*	*DCLK2*
GFPT2	*MPPED1*	*CHDH*	*DCP2*
GHDC	*MRPL23*	*CHEK2*	*DCT*
GLB1L	*MSN*	*CHKB*	*DCTN1*
GLIS1	*MTA3*	*CHL1*	*DCTN6*
GLP2R	*MTNR1B*	*CHMP1A*	*DCUN1D1*
GNB5	*MTO1*	*CHMP2B*	*DDX50*
GOLGA6L1	*MYF5*	*CHPF2*	*DDX53*
GPC6	*MYL3*	*CHRNB2*	*DDX55*
GPM6B	*MYOM1*	*CHST10*	*DDX58*
GPR113	*MYOM3*	*CIITA*	*DDX6*
GPR17	*N4BP2*	*CINP*	*DFNB31*
GPR21	*NAA25*	*CITED1*	*DIRC2*
GPRASP1	*NAALADL2*	*CKAP2*	*DIS3*
GRB7	*NANOG*	*CKS1B*	*DLG1*
GRHL3	*NASP*	*CLASRP*	*DLGAP5*
GRIA1	*NCOA6*	*CLCN6*	*DLX5*
GRIA3	*NDUFV1*	*CLCN7*	*DMGDH*
GRIN2C	*NEUROD1*	*CLCNKB*	*DMTF1*
GRM5	*NEXN*	*CLEC17A*	*DMXL2*
GSC	*NFKB1*	*CLEC3B*	*DNAJB14*
GSDMA	*NFKBIB*	*CLIP1*	*DNAJC1*
GSK3A	*NHLRC2*	*CLIP4*	*DNASE1L1*
GSPT1	*NHS*	*CLNK*	*DNHD1*
GSTM5	*NLRC3*	*CLPTM1*	*DNMT1*
GTPBP4	*NME4*	*CLPX*	*DOCK2*
GUCY1A3	*NOL8*	*CLUH*	*DOCK9*
GUF1	*NOP14*	*CMTR2*	*DOK4*
GYLTL1B	*NPHS1*	*CNBP*	*DPM1*
HAL	*NR1I3*	*CNGA3*	*DPP4*
HAS1	*NRG3*	*CNGA4*	*DPY19L3*

HCFC1	*NUP50*	*CNGB3*	*DSC1*
HDX	*NUTM1*	*CNKSR1*	*DSC2*
HEATR5B	*OR14C36*	*CNNM2*	*DSC3*
HECW2	*OR1E2*	*CNTLN*	*DSG2*
HERC5	*OR5B21*	*CNTN1*	*DSG4*
HIST1H1E	*OR6S1*	*CNTN3*	*DTHD1*
HLA-DQA2	*OSTN*	*COL14A1*	*DTL*
HLA-DRB5	*PACS1*	*COL19A1*	*DUSP21*
HMGCS2	*PADI2*	*COL24A1*	*DYM*
HOMEZ	*PADI4*	*COL4A2*	*DYNC1H1*
HOXA4	*PAPOLG*	*COL9A2*	*DYRK1B*
HOXB8	*PARPBP*	*COL9A3*	*DYTN*
HOXC11	*PCDHA12*	*COMMD5*	*ECT2*
HS6ST2	*PCDHA3*	*COQ10A*	*EDNRB*
HSDL2	*PCDHA7*	*COQ2*	*EED*
HTATSF1	*PCDHB1*	*COQ3*	*EEF1B2*
HTR3B	*PCDHB10*	*COX18*	*EFTUD2*
HTR5A	*PCDHGA8*	*CPA3*	*EGR1*
HTT	*PCDHGB7*	*CPE*	*EHD2*
IBSP	*PCK2*	*CPEB2*	*EHF*
IDH2	*PCM1*	*CPSF3*	*EIF3D*
IFNA7	*PCSK1*	*CPSF3L*	*EIF3E*
IFT122	*PDE4A*	*CPXM2*	*EIF4A3*
IFT46	*PDE7A*	*CREB3L3*	*EMR2*
IFT81	*PDXDC1*	*CRH*	*ENGASE*
IGSF22	*PHACTR1*	*CRHR1*	*ENKUR*
IKBKB	*PHKA2*	*CRTAC1*	*ENOPH1*
IL1RAPL1	*PHLPP2*	*CSDC2*	*ENPP2*
IL22RA1	*PIGC*	*CSF2RA*	*ENPP3*
IL22RA2	*PIGV*	*CST1*	*EP300*
IL27RA	*PKP4*	*CSTF3*	*EPB41*
IMMT	*PLAC8L1*	*CT47A6*	*EPB41L1*
INADL	*PLCG2*	*CTNNAL1*	*EPB41L2*
INO80	*PLK2*	*CTNND1*	*EPB41L5*
INPP5B	*PLOD1*	*CTSE*	*EPC1*
IQGAP2	*PMM1*	*CTU2*	*EPC2*
IRF2BPL	*PNLIP*	*CUL7*	*EPHA5*
ITGA8	*PNMA5*	*CUX1*	*EPHX1*
ITGB5	*PNRC2*	*CXCR5*	*ERCC2*
IVNS1ABP	*POLR3A*	*CXorf21*	*ERO1LB*
JARID2	*PPP1R36*	*CXorf27*	*ERVV-1*

KCNC1	*PPP4C*	*CYB561*	*ERVV-2*
KCNH1	*PPT1*	*CYBB*	*ESYT2*
KCNH7	*PRB4*	*CYFIP2*	*ESYT3*
KCNJ16	*PREX2*	*CYLD*	*EVA1C*
KCTD10	*PRMT5*	*CYP11A1*	*EVI2A*
KDM1A	*PROKR1*	*CYP2A7*	*EXD1*
KIAA0100	*PRPF40B*	*CYP2B6*	*F2R*
KIAA0825	*PRR11*	*CYP3A43*	*F7*
KIAA1324	*PRR12*	*CYP3A5*	*FADS1*
KIAA1432	*PRRG1*	*CYP4A22*	*FAM110B*
KIAA1671	*PSMD3*	*CYP7A1*	*FAM120B*
KIF26A	*PTP4A2*	*CYP8B1*	*FAM149A*
KIF5B	*QTRTD1*	*CYTH4*	*FAM153A*
KIF7	*RAB3D*	*CYYR1*	*FAM180A*
KIR3DL1	*RAB43*	*DAB2*	*FAM208A*
KLHDC8A	*RABEP1*	*DACT1*	*FAM231A*
KLHL2	*RAF1*	*DAG1*	*FAM63B*
KLHL23	*RASAL1*	*DCAF13*	*FAM72B*
KLHL24	*RBM26*	*DCDC1*	*FAM92B*
KNCN	*RBMXL3*	*DCHS1*	*FAM9A*
KNTC1	*RBP3*	*DCSTAMP*	*FAR2*
KRT18	*RBP5*	*DCUN1D2*	*FAT4*
KRT28	*RERE*	*DDI2*	*FBRS*
KRT40	*RERGL*	*DDIT4L*	*FBXL3*
KRTAP17-1	*RFTN1*	*DDX10*	*FBXO28*
KRTAP2-4	*RFX8*	*DDX17*	*FBXO7*
KRTAP6-3	*RGPD4*	*DDX21*	*FDXACB1*
KRTAP9-2	*RIMS2*	*DDX4*	*FERMT3*
LACC1	*RINT1*	*DDX46*	*FFAR2*
LAP3	*RNF123*	*DDX49*	*FFAR3*
LDB3	*RNF217*	*DDX60*	*FGFR1*
LDHA	*RNMT*	*DEAF1*	*FGFR3*
LEO1	*RPL22*	*DEFB110*	*FIGN*
LEPRE1	*RPRD2*	*DEPDC5*	*FILIP1L*
LIN54	*RUVBL1*	*DERA*	*FKBP11*
LIN9	*RWDD2A*	*DGKA*	*FLNC*
LIPA	*SAMD11*	*DGKQ*	*FNBP1*
LLGL2	*SATB2*	*DGUOK*	*FOXD3*
LMOD2	*SCUBE1*	*DHX30*	*FOXD4L2*
LMOD3	*SDCCAG3*	*DHX37*	*FOXE3*
LONRF1	*SEC11C*	*DHX8*	*FOXJ3*

LONRF3	*SEC31B*	*DIAPH2*	*FREM1*
LOR	*SEMA4C*	*DIAPH3*	*FRG2*
LRP2	*SENP8*	*DIDO1*	*FRYL*
LRRC2	*Sep/06*	*DIRAS2*	*FSCN3*
LRRC3B	*SERPINE1*	*DIS3L*	*FUK*
LRRFIP2	*SFRP1*	*DISC1*	*G3BP2*
LSM11	*SGIP1*	*DISP2*	*GABRA1*
MAGEB2	*SGOL2*	*DKK2*	*GABRA4*
MALSU1	*SH2B3*	*DLGAP1*	*GABRB3*
MAML2	*SH2D4B*	*DLGAP2*	*GABRE*
MAP7D2	*SH3BP4*	*DMBT1*	*GAK*
MAPT	*SLC12A3*	*DMRT2*	*GAL3ST4*
MAS1	*SLC17A6*	*DNAAF2*	*GALNT6*
MBIP	*SLC22A9*	*DNAAF3*	*GALNTL5*
MC3R	*SLC23A2*	*DNAH10*	*GAN*
MCM4	*SLC25A20*	*DNAH7*	*GAPDH*
MCM9	*SLC2A10*	*DNAJB2*	*GAPVD1*
MDM1	*SLC30A3*	*DNAJC17*	*GATA5*
MED14	*SLC38A10*	*DNAJC18*	*GATSL3*
MED23	*SLC4A8*	*DNAJC9*	*GBP2*
MED9	*SLC6A20*	*DNM1L*	*GCAT*
METTL25	*SLC9A3*	*DNMT3B*	*GCFC2*
MFAP1	*SLC9A8*	*DOCK7*	*GCKR*
MFSD2B	*SLC9C2*	*DOK1*	*GCLM*
MGST2	*SLCO1B1*	*DOK6*	*GCNT2*
MINK1	*SLCO1B3*	*DONSON*	*GDA*
MMP2	*SLCO3A1*	*DPH7*	*GDF11*
MOB1A	*SLFN12L*	*DRC1*	*GDI2*
MRPL2	*SMARCE1*	*DSTYK*	*GFRA3*
MRPS30	*SMCO2*	*DTD1*	*GIPC3*
MS4A14	*SORCS1*	*DTNB*	*GIT1*
MSI2	*SORL1*	*DUSP10*	*GJC1*
MTBP	*SOX2*	*DUSP19*	*GJD3*
MTERFD2	*SPANXD*	*DUXA*	*GK*
MTHFD1L	*SPDYE4*	*DYNC2H1*	*GLIPR1L2*
MTMR12	*SPHK2*	*DYX1C1*	*GLS2*
MTR	*SQSTM1*	*E2F4*	*GLT8D2*
MTSS1	*SREBF1*	*EARS2*	*GNAL*
MYO1E	*ST18*	*EBLN1*	*GNAQ*
MYO9B	*STAT4*	*ECEL1*	*GNB4*
MYOM2	*STX3*	*EDC4*	*GNPTAB*

MYT1	*SUCLG2*	*EDEM2*	*GOLGA2*
NAA20	*SUSD1*	*EEF1A2*	*GOLGA4*
NACA2	*SUV39H1*	*EEFSEC*	*GOLT1A*
NAP1L1	*SVIL*	*EFCC1*	*GPATCH2L*
NARF	*SYVN1*	*EFS*	*GPD1L*
NARFL	*TALDO1*	*EGFL6*	*GPKOW*
NAT2	*TANC1*	*EGFR*	*GPR101*
NBEAL1	*TAOK1*	*EHBP1*	*GPR146*
NCAPD2	*TAS1R3*	*EHHADH*	*GPR15*
NCKAP5	*TAS2R31*	*EIF2S3*	*GPR174*
NCOA1	*TAS2R46*	*EIF4G3*	*GPR179*
NCOA7	*TBC1D22B*	*EIF5A2*	*GPR182*
NEDD1	*TBC1D9B*	*EIF5B*	*GPR26*
NEDD9	*TBRG1*	*EIF6*	*GPS2*
NEIL1	*TCP10*	*ELANE*	*GPSM2*
NEK7	*TFAP2B*	*ELAVL3*	*GRIK1*
NEO1	*THAP3*	*ELF3*	*GSS*
NFIX	*TJP3*	*ELP2*	*H2AFY*
NGDN	*TLE3*	*EML2*	*H3F3A*
NIPAL3	*TLX2*	*EML5*	*HABP2*
NKD1	*TM7SF2*	*EML6*	*HAO1*
NLRP7	*TM7SF3*	*ENC1*	*HAUS6*
NME6	*TMEM170B*	*ENPP1*	*HAVCR2*
NNAT	*TMEM229B*	*ENPP4*	*HECTD1*
NOBOX	*TMEM95*	*ENPP5*	*HERC6*
NPHP4	*TMPRSS5*	*EPAS1*	*HGFAC*
NPR3	*TPK1*	*EPHA10*	*HHIP*
NR0B1	*TPSD1*	*EPHA3*	*HHIPL2*
NR1H3	*TRAM1L1*	*EPHA8*	*HIF1A*
NRCAM	*TRAPPC11*	*EPRS*	*HIF3A*
NSUN3	*TRIAP1*	*EPS8*	*HINT3*
NSUN4	*TRIM52*	*EPS8L1*	*HIPK1*
NUDT12	*TRIM6*	*EPX*	*HIST1H3I*
NUMB	*TRIM66*	*ERCC6*	*HK2*
NUP205	*TRPC7*	*ERICH1*	*HLA-B*
NUP98	*TRPM4*	*ERO1L*	*HMGB1*
NUPL1	*TRPM8*	*ESCO2*	*HMGCLL1*
NXPE4	*TSPYL1*	*ESPL1*	*HMGCS1*
OLFM3	*UBE2G1*	*ETV2*	*HMGN2*
OPLAH	*UBE2S*	*ETV3L*	*HMHA1*
OR10H3	*USP22*	*EVC2*	*HN1*

OR10H4	*USP44*	*EVI5L*	*HNRNPA1L2*
OR13G1	*USPL1*	*EYA3*	*HNRNPA2B1*
OR1K1	*VAC14*	*EZH2*	*HNRNPDL*
OR2AG2	*VAT1*	*F11R*	*HNRNPH2*
OR2L3	*VN1R2*	*F8*	*HOXA2*
OR2T1	*VPRBP*	*FABP12*	*HOXB1*
OR4A47	*VSIG10*	*FABP9*	*HOXD4*
OR5T2	*VWA1*	*FAH*	*HPSE2*
OR5T3	*VWC2*	*FAM105A*	*HPX*
OR5W2	*WBP11*	*FAM111A*	*HS3ST4*
OR7A10	*WBSCR17*	*FAM114A2*	*HSP90AB1*
OSBPL8	*WEE2*	*FAM13B*	*HSP90B1*
OTUD7B	*WIPI1*	*FAM153B*	*HSPA2*
PADI3	*WNT5B*	*FAM160A1*	*HTR3A*
PAGR1	*WNT9B*	*FAM170B*	*HTR6*
PAK2	*WSCD1*	*FAM181A*	*ICOS*
PARD3	*WTAP*	*FAM188B*	*IFT140*
PARK7	*XK*	*FAM196B*	*IGFBP6*
PARP12	*XPOT*	*FAM200B*	*IGFL2*
PARP2	*YARS*	*FAM203B*	*IL13RA1*
PATE4	*ZBED4*	*FAM20B*	*IL1RAPL2*
PAX6	*ZBTB17*	*FAM211A*	*ILF2*
PBX4	*ZBTB33*	*FAM214A*	*INF2*
PCDH11X	*ZC3H11A*	*FAM217A*	*INO80D*
PCDH15	*ZDHHC21*	*FAM222A*	*INSC*
PCMTD1	*ZFAND1*	*FAM43A*	*IP6K2*
PCNT	*ZFP36L2*	*FAM49A*	*IPMK*
PCOLCE	*ZKSCAN2*	*FAM65B*	*IPP*
PCYT1A	*ZMYND10*	*FAM71E2*	*IPPK*
PDCD4	*ZNF142*	*FANCG*	*IQGAP3*
PDE10A	*ZNF148*	*FANCI*	*IRAK2*
PDE11A	*ZNF212*	*FANK1*	*IRS4*
PDE4DIP	*ZNF267*	*FARP2*	*ITGA2*
PDE8B	*ZNF273*	*FARS2*	*ITGA9*
PDILT	*ZNF281*	*FASTKD2*	*ITGB1BP2*
PELI1	*ZNF302*	*FAT1*	*ITGB4*
PEX26	*ZNF418*	*FAT2*	*ITIH3*
PEX5L	*ZNF486*	*FBLIM1*	*ITPRIPL2*
PFKFB4	*ZNF513*	*FBP2*	*ITSN1*
PGA5	*ZNF681*	*FBXL15*	*JADE1*
PGD	*ZNF691*	*FBXO36*	*JADE3*

PHF13	*ZNF695*	*FBXW10*	*JAK1*
PHYHIP	*ZNF711*	*FCF1*	*JAKMIP1*
PI4KB	*ZNF720*	*FCGR1B*	*JKAMP*
PIF1	*ZNF775*	*FCGR2A*	*JUND*
PIGS	*ZNF829*	*FCHO1*	*KANK1*
PIK3C2B	*ZNF92*	*FCRL3*	*KANK2*
PKHD1	*ZNRF4*	*FCRL5*	*KAT6B*
PKP1		*FEN1*	*KAZN*
PLP2		*FER*	*KCNC3*
PLS3		*FGB*	*KCNG4*
PNPLA3		*FGF7*	*KCNJ2*
PODXL		*FGF9*	*KCNN4*
POGZ		*FGR*	*KDM3B*
POLA2		*FHAD1*	*KDM5A*
POLE2		*FKBP5*	*KDM5B*
POLR2H		*FLT1*	*KEAP1*
POR		*FMN2*	*KHDC3L*
POTEB2		*FMR1*	*KHDRBS3*
PPAP2B		*FNIP2*	*KIAA0196*
PPAPDC3		*FOXC2*	*KIAA0247*
PPIE		*FOXD4L3*	*KIAA0319L*
PPIH		*FOXD4L4*	*KIAA0368*
PPL		*FOXI1*	*KIAA0430*
PPP1R16B		*FOXJ2*	*KIAA0947*
PPP2R3A		*FOXK1*	*KIAA1239*
PPP2R4		*FOXN1*	*KIAA1377*
PRKAR2A		*FPGT*	*KIAA1430*
PRM1		*FRMD7*	*KIF20B*
PROB1		*FRMD8*	*KIF24*
PROCA1		*FRMPD3*	*KIF3A*
PRPH		*FSD1L*	*KIF4B*
PRR21		*FUBP1*	*KIRREL*
PSENEN		*FUCA1*	*KLB*
PSG1		*FUT6*	*KLF12*
PSMC5		*FYB*	*KLF16*
PSTPIP2		*FZD10*	*KLF3*
PTCHD2		*FZD3*	*KLHL1*
PTPN12		*FZD9*	*KLRC1*
PTPN14		*G2E3*	*KLRK1*
PTPN5		*GAB2*	*KRBA2*
PTPRA		*GABRR2*	*KRT38*

PUF60	*GADD45G*	*KRTAP10-1*
PXT1	*GALC*	*KRTAP22-1*
QRSL1	*GALNT1*	*KRTAP4-8*
RAB30	*GALNT10*	*KRTAP5-1*
RAB35	*GALNT5*	*KRTAP5-7*
RAD21	*GALNT8*	*LAMB1*
RALGAPA1	*GALNTL6*	*LAMP2*
RALGPS2	*GAP43*	*LANCL1*
RANBP3L	*GAS2L2*	*LCE2B*
RBM19	*GAS7*	*LCLAT1*
RBM48	*GAST*	*LCP2*
RBPJ	*GATA2*	*LDHAL6B*
RDH10	*GBP1*	*LEMD3*
RDH12	*GCC2*	*LEPR*
RFT1	*GCDH*	*LETM1*
RFX6	*GCLC*	*LGALSL*
RFXAP	*GCN1L1*	*LGI2*
RGMB	*GCNT3*	*LGR5*
RGPD3	*GDF3*	*LHFPL2*
RGS8	*GDF6*	*LHFPL5*
RGSL1	*GDI1*	*LMLN*
RHD	*GDNF*	*LOXL4*
RHOA	*GEMIN6*	*LPAR4*
RILPL2	*GFI1B*	*LPCAT4*
RIPK2	*GFM1*	*LPPR1*
RLF	*GGTLC1*	*LRIF1*
ROBO1	*GGTLC2*	*LRIG2*
ROBO3	*GJB6*	*LRIG3*
RP11-1220K2.2	*GJC2*	*LRIT2*
RPL3L	*GLB1L2*	*LRP12*
RPL7	*GLRA3*	*LRP5*
RPS23	*GLRA4*	*LRRC59*
RPTN	*GMPPA*	*LTBP2*
RSRC2	*GMPR2*	*LY75*
RUFY1	*GNAI1*	*LY9*
RUNDC1	*GNPAT*	*LYL1*
SAMD9	*GPAA1*	*LYNX1*
SAMHD1	*GPAT2*	*LZTFL1*
SBF2	*GPBP1L1*	*LZTS2*
SCARB1	*GPR115*	*MAD2L1BP*
SCGB1D4	*GPR116*	*MAGEC3*

SCN8A	*GPR119*	*MAGI3*
SCNN1D	*GPR128*	*MAK*
SEC13	*GPR153*	*MAN1A1*
SEC31A	*GPR155*	*MAN2A1*
SEC61A2	*GPR158*	*MAN2C1*
SELPLG	*GPR176*	*MANBA*
Sep/07	*GPR183*	*MAOA*
SERINC3	*GPR52*	*MAP3K19*
SERPINB12	*GPR61*	*MAP4K4*
SF3A3	*GPR64*	*MAP4K5*
SFI1	*GPR78*	*MAP7D1*
SH3D19	*GPR89B*	*MAP7D3*
SHISA3	*GPT2*	*MAPK6*
SIAH3	*GRAMD1B*	*MAPK8IP3*
SIDT2	*GRAMD2*	*MAPKAPK5*
SLC13A1	*GREB1*	*Mar/07*
SLC17A3	*GRIN2A*	*MASP2*
SLC18A1	*GRM1*	*MBTD1*
SLC22A1	*GRM2*	*MC2R*
SLC22A4	*GRM7*	*MCCC2*
SLC24A1	*GSDMC*	*MCM10*
SLC25A12	*GSTA2*	*MCMDC2*
SLC25A23	*GTF2IRD1*	*MCPH1*
SLC26A6	*GTF2IRD2*	*ME1*
SLC26A8	*GUCY2C*	*MED18*
SLC35C1	*GUCY2F*	*MED24*
SLC36A2	*GULP1*	*MEI4*
SLC38A4	*GXYLT1*	*MET*
SLC4A5	*GYG1*	*METTL1*
SLC5A6	*H2AFV*	*METTL24*
SLC6A12	*H3F3B*	*MFSD5*
SLC6A19	*HAND1*	*MFSD9*
SLC6A2	*HAPLN2*	*MGST3*
SLC6A6	*HAPLN3*	*MIA2*
SLC9B2	*HCFC2*	*MIB1*
SLFN12	*HCN1*	*MID2*
SLFN13	*HCN4*	*MIDN*
SLIT2	*HCRTR1*	*MINPP1*
SLK	*HCST*	*MKNK2*
SMEK1	*HDAC10*	*MKRN2*
SMPDL3A	*HDAC4*	*MLK4*

SNIP1	*HDAC5*	*MLLT1*
SNTN	*HDGF*	*MMP14*
SNX18	*HEBP2*	*MMRN2*
SOCS4	*HECTD3*	*MOS*
SORCS3	*HECTD4*	*MPP7*
SOSTDC1	*HEG1*	*MRE11A*
SOX30	*HELB*	*MRGPRD*
SOX5	*HELZ*	*MRPL10*
SP1	*HENMT1*	*MRPL37*
SP8	*HEPH*	*MRPS14*
SPAG9	*HERC1*	*MSTO1*
SPATA6	*HEXDC*	*MTA2*
SPG11	*HEY2*	*MTHFD1*
SPOCK1	*HEYL*	*MTMR14*
SPRY1	*HFE*	*MTMR2*
SPTA1	*HIRIP3*	*MTOR*
SQLE	*HIST1H2AE*	*MTUS1*
SRFBP1	*HIST1H4A*	*MTX1*
SRP54	*HIVEP1*	*MYBL1*
SRPK2	*HLA-DPB1*	*MYC*
SRSF12	*HMCES*	*MYEOV2*
SSBP4	*HMGA2*	*MYH10*
SSH2	*HMGCR*	*MYH11*
ST7L	*HMGN5*	*MYH2*
STAMBP	*HOXA10*	*NAIF1*
STAT1	*HOXA3*	*NAMPT*
STAU1	*HPR*	*NAP1L3*
STIM1	*HRH1*	*NARG2*
STK31	*HRH3*	*NBAS*
STK36	*HS3ST2*	*NCAN*
STT3B	*HSD17B4*	*NCKAP1*
STX12	*HSPA6*	*NCKAP5L*
STXBP4	*HSPA8*	*NCMAP*
STXBP6	*HSPB3*	*NCOR1*
SULF1	*HSPE1*	*NDRG1*
SUMO2	*HTR1B*	*NDUFAF6*
TAF2	*HTR3E*	*NECAB2*
TAP1	*HUNK*	*NECAP2*
TARSL2	*HYOU1*	*NEDD4*
TAS2R30	*IBTK*	*NEGR1*
TAS2R41	*IFFO2*	*NEIL3*

TBC1D14	*IGHMBP2*	*NES*
TBC1D8B	*IGSF5*	*NEU2*
TBX2	*IGSF9B*	*NEURL4*
TBX22	*IL17RD*	*NFRKB*
TCAP	*IL2RG*	*NGEF*
TCF4	*IL3*	*NHLH2*
TDRP	*IL31RA*	*NHP2*
TESPA1	*IL36A*	*NIM1K*
TEX15	*ILF3*	*NIN*
TEX2	*INCENP*	*NIPA1*
TFDP2	*INHBA*	*NIPA2*
TFPI2	*INO80B*	*NKAIN3*
THOC5	*INPP5F*	*NLGN4X*
TIGD4	*INPP5K*	*NLRP1*
TIMM10	*INVS*	*NLRP12*
TMC6	*IP6K1*	*NLRP2*
TMED10	*IPO13*	*NLRP3*
TMED6	*IPO4*	*NLRP6*
TMEM116	*IPO5*	*NOC3L*
TMEM128	*IPO9*	*NOL10*
TMEM145	*IQCA1*	*NOMO2*
TMEM159	*IQSEC1*	*NOMO3*
TMEM183A	*IREB2*	*NOS2*
TMEM229A	*IRF4*	*NOTCH2*
TMEM233	*ISPD*	*NOVA1*
TMEM247	*ISX*	*NPAT*
TMEM41A	*ISY1-RAB43*	*NPFFR2*
TMEM43	*ITCH*	*NPIPA3*
TMEM69	*ITGA7*	*NPM3*
TMOD1	*ITGAV*	*NPTN*
TNC	*ITGB6*	*NRDE2*
TNFAIP3	*ITIH2*	*NSL1*
TNFRSF11B	*ITM2A*	*NT5C1B*
TNIP3	*ITPR3*	*NTN3*
TPM4	*ITSN2*	*NUCB1*
TRADD	*IVD*	*NUP210*
TRAK1	*IVL*	*OAT*
TREML2	*JAG1*	*OC90*
TRIM42	*KAL1*	*OCA2*
TRIM64B	*KANSL1*	*OFD1*
TRIM72	*KARS*	*OGFOD1*

TRMT1	*KBTBD7*	*OGFOD2*
TRMT13	*KCNA4*	*OLAH*
TRPV1	*KCNA7*	*OLFML3*
TSR1	*KCNC2*	*OPHN1*
TSSK4	*KCNH2*	*OPN1LW*
TTC30B	*KCNH6*	*OPTN*
TTLL4	*KCNJ3*	*OR10A6*
TTLL6	*KCNK10*	*OR10G8*
TUBA3E	*KCNQ1*	*OR10G9*
TULP3	*KCNQ3*	*OR13C2*
TXNIP	*KCNS3*	*OR13C3*
TYW1	*KCNT1*	*OR1C1*
UAP1L1	*KCNT2*	*OR1J1*
UBAP1	*KCNU1*	*OR1L3*
UBAP2	*KDM2A*	*OR2G3*
UBTF	*KDM4A*	*OR2K2*
UFD1L	*KDM4B*	*OR2M3*
UGT2A1	*KDM5D*	*OR2T4*
UGT2B10	*KDSR*	*OR2W3*
UGT3A1	*KEL*	*OR2Y1*
UNC13B	*KIAA0195*	*OR4C16*
UNC13D	*KIAA0753*	*OR4D9*
UNC45A	*KIAA1033*	*OR4X2*
UROD	*KIAA1210*	*OR51M1*
USF1	*KIAA1279*	*OR52B2*
USHBP1	*KIAA1429*	*OR52B4*
USP18	*KIAA1551*	*OR5H14*
UVSSA	*KIAA1731*	*OR5H2*
VASH2	*KIAA2018*	*OR5H6*
VAV3	*KIF17*	*OR5K1*
VCL	*KIF1C*	*OR5M10*
VPS37B	*KIF25*	*OR5M3*
VWA8	*KIF5C*	*OR5T1*
WAS	*KIR2DL4*	*OR6A2*
WBP5	*KIR3DL3*	*OR6C6*
WDFY3	*KIRREL3*	*OR6C74*
WDPCP	*KLHL11*	*OR7A17*
WDR55	*KLHL17*	*OR8B4*
WDR78	*KLHL25*	*OR8G5*
WIPI2	*KLHL3*	*ORC1*
WLS	*KLHL4*	*OS9*

WNT5A
WWTR1
XPA
XYLB
YPEL1
YPEL2
YY1
ZBTB10
ZBTB44
ZBTB45
ZCCHC14
ZDHHC11
ZDHHC2
ZDHHC4
ZEB2
ZFAT
ZFP37
ZIC1
ZMYM4
ZNF106
ZNF143
ZNF236
ZNF275
ZNF483
ZNF526
ZNF549
ZNF587
ZNF608
ZNF716
ZNF771
ZNF827
ZNF836
ZSCAN20

KLHL40
KLK11
KLK15
KLLN
KLRC3
KLRD1
KLRF1
KMO
KMT2E
KNDC1
KNG1
KNOP1
KRT14
KRT17
KRT3
KRT31
KRT32
KRT37
KRT6A
KRT72
KRT78
KRT8
KRT85
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KRTAP12-2
KRTAP13-4
KRTAP2-1
KRTAP20-2
KRTAP25-1
KRTAP29-1
KRTAP4-11
KRTAP4-3
KRTAP6-2
KTN1
KYNU
L3MBTL1
LAMA2
LAMB4
LAMP5
LATS2

OSBPL7
OSTM1
OTUD6A
OTX1
PAG1
PAICS
PAIP1
PALB2
PALD1
PALM
PALM2
PALM3
PAPD5
PARD3B
PARP1
PAXBP1
PBX1
PCDH7
PCDHA5
PCDHA9
PCDHGA10
PCDHGB4
PCNXL2
PCSK7
PDE3A
PDE4B
PDIA3
PDP2
PEAK1
PEAR1
PEPD
PERP
PEX3
PGBD5
PGC
PGK2
PGM1
PGM2L1
PHC3
PHF12
PHF14

LAYN
LCE1B
LDB2
LHFPL3
LHX9
LIG4
LILRB5
LINGO4
LIPI
LIPT1
LMF1
LPA
LPAR5
LRIT1
LRP1
LRP4
LRRC15
LRRC19
LRRC3
LRRC30
LRRC36
LRRC38
LRRC49
LRRC4C
LRRC69
LRRC7
LRRN2
LRRTM1
LUM
LYG1
LYPD6
LYST
LYVE1
LYZL2
LZTS1
MACC1
MAD1L1
MAGEA10
MAGEA6
MAGEA9
MAGEA9B
PHF23
PHIP
PHKA1
PHLDA1
PHLDB2
PHOSPHO1
PHTF2
PIAS3
PIEZO2
PIGF
PIGM
PIGU
PIGX
PIK3R2
PIR
PITPNM2
PIWIL1
PIWIL2
PIWIL4
PLAC8
PLD5
PLEC
PLEK2
PLEKHA6
PLEKHA8
PLEKHS1
PLOD2
PLSCR4
PLXNC1
PMM2
PMP2
PMPCB
PMS2
PNLIPRP1
PNPLA8
POF1B
POFUT2
POLR1C
POMT2
POTED
POTEM

MAGED1	*POU2F1*
MAGED4	*PPA2*
MAGED4B	*PPFIBP2*
MAGEE2	*PPM1E*
MAOB	*PPP1R12A*
MAP1B	*PPP1R12C*
MAP2K1	*PPP1R14A*
MAP2K7	*PPP2R1A*
MAP3K10	*PPP2R5B*
MAP4K1	*PPP3R1*
MAPK10	*PPP4R1*
MAPK9	*PRAM1*
MAPKAPK3	*PRAMEF13*
Mar/02	*PRAMEF18*
MATN2	*PRAMEF5*
MB	*PRDM2*
MBD3	*PRG4*
MBD3L3	*PRKCG*
MBOAT2	*PRKCH*
MCC	*PRKD2*
MCM5	*PRKG1*
MCOLN3	*PRKRIP1*
MCRS1	*PRLHR*
MCTP2	*PROSER1*
MDC1	*PRPF18*
MECOM	*PRR23C*
MED13	*PRRC2B*
MED15	*PRX*
MED17	*PSEN1*
MEF2A	*PSIP1*
MEF2B	*PSMA1*
MEGF10	*PSMC2*
MEN1	*PSMC6*
MEP1A	*PSMD9*
METTL10	*PTCH1*
METTL2A	*PTGER4*
MFGE8	*PTK2B*
MFSD1	*PTPN1*
MFSD11	*PTPN11*
MGAM	*PTPRF*
MGAT5	*PUM1*

MGAT5B
MIB2
MICAL1
MICALL2
MID1
MINA
MIPOL1
MIS18BP1
MKRN3
MLC1
MLKL
MLLT4
MMAB
MMP21
MMP27
MMP9
MNS1
MNX1
MOCS3
MORF4L1
MPHOSPH10
MPHOSPH8
MPHOSPH9
MPL
MPP4
MPZ
MRAP
MRAS
MRC1
MRC1L1
MRGPRX1
MROH2A
MRPL1
MRPL44
MRPL52
MRPS23
MSC
MSH5
MSL1
MT1H
MTERF
PURG
PUS7
PVRL3
PXDNL
QPCTL
QSER1
QSOX1
R3HDM1
RAB11FIP3
RAB21
RAB34
RABAC1
RABGAP1
RABGAP1L
RAC1
RAD51B
RAG2
RALGAPB
RALGPS1
RANBP1
RAPGEF3
RASGEF1B
RASGRP3
RASSF2
RASSF4
RASSF6
RBCK1
RBKS
RBM34
RBM43
RBM6
RBMX
RBMXL1
RBMY1F
REC8
REL
RGMA
RGPD8
RGS12
RGS6
RHEBL1

MTFR1L	*RHOT1*
MTMR7	*RIF1*
MTUS2	*RIN3*
MX2	*RNF128*
MXD4	*RNF168*
MYBPC2	*RNF19A*
MYCBP	*RNPEP*
MYH14	*RNPS1*
MYH7	*ROR1*
MYLK	*RP11-108K14.8*
MYLK3	*RPE65*
MYO16	*RPGR*
MYO1A	*RPS27A*
MYO3B	*RPS3A*
MYO7B	*RPS4Y2*
MYOC	*RPS6KA1*
MYRIP	*RPS6KC1*
NAA11	*RRAS*
NAGK	*RRH*
NAGLU	*RRP7A*
NANP	*RSPO1*
NAPEPLD	*RTCA*
NAV2	*RTN1*
NBL1	*S100A7*
NCAPH	*S100G*
NCL	*S1PR4*
NCOA3	*SAA2*
NCR2	*SAC3D1*
NCSTN	*SACM1L*
NDC80	*SAE1*
NDOR1	*SAFB*
NDST1	*SAMD10*
NDUFS4	*SAR1A*
NEK11	*SARS*
NETO1	*SCGN*
NEUROD2	*SCLT1*
NEUROG2	*SCN2B*
NF2	*SCN5A*
NFAT5	*SCP2*
NFKBIE	*SCRN2*
NFKBIZ	*SDC1*

NFX1	*SDF4*
NFYA	*SDHD*
NGFRAP1	*SEC16A*
NIPSNAP1	*SEC24D*
NKX2-1	*SEMA3A*
NLRP8	*SEMA4F*
NMD3	*Sep/04*
NMUR1	*SERBP1*
NMUR2	*SERPINA4*
NNT	*SERPIND1*
NODAL	*SETX*
NOL11	*SF3B1*
NOL4	*SFSWAP*
NOL6	*SGCD*
NOTCH2NL	*SGCG*
NOTUM	*SGSH*
NOXA1	*SH2D1A*
NPAP1	*SH3GL2*
NPBWR2	*SH3TC1*
NPEPL1	*SHCBP1*
NPHP3	*SIRPB1*
NPNT	*SIRPD*
NPR2	*SKOR1*
NPTX2	*SLC12A1*
NPY4R	*SLC15A3*
NR3C1	*SLC24A5*
NRAP	*SLC26A3*
NRAS	*SLC2A2*
NRD1	*SLC30A4*
NRP2	*SLC30A6*
NRXN2	*SLC30A9*
NSMAF	*SLC3A1*
NUAK2	*SLC44A1*
NUCB2	*SLC44A2*
NUDT16	*SLC45A2*
NUDT9	*SLC4A4*
NUP54	*SLC5A12*
NXF2	*SLC7A3*
NXF2B	*SLC8A3*
NYAP1	*SLC9A9*
OBP2A	*SLCO4C1*

ODF2	*SLFN11*
ODF2L	*SMARCC1*
OGDH	*SMC2*
OGDHL	*SMNDC1*
OIT3	*SMPDL3B*
OLFM1	*SMS*
OLIG3	*SNCA*
ONECUT2	*SNRNP40*
OPRD1	*SNTG2*
OPTC	*SNX31*
OR10AG1	*SNX6*
OR10G2	*SNX7*
OR10G7	*SNX9*
OR10J1	*SOD2*
OR10Q1	*SOX14*
OR10T2	*SOX4*
OR11L1	*SOX7*
OR1E1	*SP3*
OR1M1	*SPAG11B*
OR2A25	*SPAG16*
OR2A5	*SPAG8*
OR2C1	*SPATA19*
OR2M2	*SPATA20*
OR2S2	*SPATA31E1*
OR2Z1	*SPATA33*
OR3A1	*SPEM1*
OR4C13	*SPNS2*
OR4C15	*SPRED2*
OR4D10	*SPRYD7*
OR4F29	*SRBD1*
OR4K2	*SRD5A3*
OR4N4	*SRP68*
OR51B2	*SRPK1*
OR51F1	*SRRM2*
OR51G2	*ST5*
OR51L1	*STAC*
OR51V1	*STAG3*
OR52D1	*STAM2*
OR52I2	*STAT6*
OR52N5	*STIL*
OR5AP2	*STK24*

OR5C1	*STON1-GTF2A1L*
OR5D18	*STX17*
OR5P2	*STXBP1*
OR6B1	*SULF2*
OR6C1	*SULT1A1*
OR6C2	*SULT2A1*
OR6C76	*SUPV3L1*
OR6N1	*SV2B*
OR6N2	*SYDE2*
OR7D2	*SYMPK*
OR8H2	*SYN1*
OR9A2	*SYNE3*
OR9A4	*SYNJ1*
ORMDL3	*SYP*
OTOL1	*SYT1*
OTOP1	*TADA2B*
OVCH1	*TAF1*
P2RY8	*TAF6*
PABPC4L	*TAF6L*
PACSIN3	*TAF7L*
PAFAH2	*TANGO6*
PAK3	*TAS2R38*
PALMD	*TBC1D23*
PAM	*TBC1D4*
PAN2	*TBCK*
PANK4	*TDP2*
PARL	*TDRD7*
PARN	*TEKT2*
PARP14	*TENM4*
PASK	*TEX10*
PAX1	*TGFB1I1*
PAX7	*TGS1*
PBDC1	*THADA*
PBOV1	*THOC2*
PCBP2	*THUMPD3*
PCDH11Y	*TIAM2*
PCDH18	*TIFAB*
PCDHB5	*TJP1*
PCDHGA2	*TLK2*
PCDHGA5	*TLR6*
PCGF1	*TMBIM6*

PCNXL3	*TMC3*
PCSK4	*TMEM119*
PDLIM3	*TMEM181*
PDLIM7	*TMEM194B*
PDZRN3	*TMEM199*
PES1	*TMEM225*
PEX6	*TMEM241*
PFAS	*TMEM259*
PFDN5	*TMEM38A*
PFKFB3	*TMEM67*
PFKM	*TMTC2*
PGF	*TNFRSF9*
PGS1	*TNIP1*
PHACTR2	*TNIP2*
PHF2	*TNKS2*
PHF20	*TNR*
PHLDB1	*TNS4*
PIAS1	*TNXB*
PIGB	*TOP2A*
PIK3C2A	*TOP3A*
PIK3CB	*TOPBP1*
PIM2	*TOR3A*
PIP5K1B	*TP53BP1*
PITX2	*TPSB2*
PKD1L1	*TPTE*
PKD2L1	*TRAF3*
PKNOX2	*TRAM2*
PKP2	*TRAPPC12*
PLA1A	*TRAPPC13*
PLA2R1	*TRAPPC9*
PLAG1	*TRDMT1*
PLB1	*TRIM25*
PLCB3	*TRIM48*
PLCB4	*TRIM65*
PLCD4	*TRIML1*
PLCH2	*TRIP4*
PLCL2	*TRMT11*
PLEKHG3	*TRNT1*
PLEKHG4B	*TRPC1*
PLP1	*TRPM7*
PLS1	*TRPV6*

PLXDC1	*TSHZ3*
PLXNB2	*TSPAN4*
PMF1	*TSPEAR*
PNISR	*TSPYL2*
PNKP	*TSTD2*
PNMAL1	*TTBK2*
PNPLA7	*TTC37*
PODXL2	*TTC39C*
POLD1	*TTLL10*
POLG	*TTLL5*
POLR2A	*TTLL9*
POLR3F	*TUBB4B*
POM121C	*TUBD1*
PORCN	*TUBGCP4*
POU6F1	*TUSC5*
PPARA	*TXLNB*
PPM1K	*TXNDC12*
PPME1	*UBE2A*
PPP1CC	*UBE2F*
PPP1R1B	*UBE2J1*
PPP1R9A	*UBE2W*
PPP2R2C	*UBR3*
PPP5C	*UBXN7*
PPP6R1	*UGT2A2*
PPP6R3	*UGT2B4*
PRAMEF3	*UHRF1BP1*
PRB3	*ULBP2*
PRDM14	*ULK4*
PRICKLE2	*UNC45B*
PRKACG	*UNC5B*
PRKAR1B	*UPB1*
PRKCD	*UPF2*
PRKRIR	*UPP2*
PRM2	*USP16*
PRND	*USP17L12*
PROM1	*USP17L24*
PRPS1L1	*USP17L26*
PRR20C	*USP17L28*
PRR23A	*USP17L5*
PRRX1	*USP20*
PRRX2	*USP25*

PRSS46	*USP37*
PRUNE2	*USP54*
PSAP	*USP9Y*
PSD3	*UTP14A*
PSMA4	*UTP20*
PSMA5	*UTP23*
PSMD14	*UTY*
PSME4	*VCX3A*
PSRC1	*VDAC3*
PTCD1	*VPS16*
PTGER3	*VPS36*
PTGFRN	*VPS39*
PTH2R	*VPS41*
PTPN20A	*VPS45*
PTPN3	*VPS4B*
PTPN4	*VRK1*
PTPN6	*VSIG2*
PTPRN2	*VSIG4*
PTPRO	*VSTM5*
PTPRT	*WDFY4*
PTRH1	*WDR25*
PTX3	*WDR53*
PVR	*WDR66*
PXK	*WDR70*
PYGM	*WDR90*
PZP	*WDR92*
RAB38	*WDR96*
RAB3GAP1	*WHSC1L1*
RAB3GAP2	*WIZ*
RAB41	*WNT10A*
RAB7L1	*WNT10B*
RABEPK	*WNT16*
RAD23A	*WWC2*
RAD51AP2	*XAB2*
RADIL	*XIRP1*
RAI14	*XKR9*
RANBP6	*XPC*
RASA3	*XPO1*
RASAL3	*XPO4*
RBBP8NL	*XRCC6*
RBL1	*YARS2*

RBM12	*YBX2*
RBM44	*YEATS2*
RBX1	*YTHDC2*
RCN1	*YY1AP1*
RCOR2	*ZBBX*
REPIN1	*ZBTB5*
RERG	*ZBTB7A*
RETSAT	*ZBTB7C*
RFPL2	*ZBTB8B*
RFWD2	*ZFP28*
RFX3	*ZFP64*
RFX4	*ZHX2*
RGS11	*ZKSCAN5*
RGS3	*ZMYND12*
RGS9	*ZMYND19*
RHNO1	*ZNF12*
RHO	*ZNF202*
RHOBTB3	*ZNF211*
RHOD	*ZNF221*
RIMBP2	*ZNF222*
RIOK2	*ZNF235*
RND2	*ZNF251*
RNF150	*ZNF260*
RNF185	*ZNF292*
RNF2	*ZNF345*
RNF26	*ZNF37A*
RNF40	*ZNF417*
RP11-830F9.6	*ZNF423*
RPE	*ZNF443*
RPGRIP1	*ZNF462*
RPL10	*ZNF48*
RPL22L1	*ZNF480*
RPL29	*ZNF518B*
RPL6	*ZNF532*
RPL8	*ZNF544*
RPP40	*ZNF555*
RPS24	*ZNF560*
RPS4X	*ZNF570*
RPS6	*ZNF585A*
RRBP1	*ZNF615*
RREB1	*ZNF638*

RRM1
RSL1D1
RSPO3
RSU1
RTBDN
RTKN2
RTN4
RUFY2
RUNX1
RUNX2
RUSC2
SALL2
SAMD15
SAMSN1
SAP30BP
SATL1
SBK1
SBK3
SBNO2
SCAF1
SCAF4
SCAMP3
SCG5
SCN11A
SCN2A
SCNN1A
SCNN1B
SCRIB
SDE2
SDHA
SDHB
SDK2
SEC14L6
SEC62
SEL1L
SELENBP1
SEMA3C
SEMA5B
SEMA6D
SENP2
SEPSECS
ZNF639
ZNF667
ZNF674
ZNF689
ZNF705B
ZNF710
ZNF793
ZNF850
ZNF99
ZSWIM6
ZSWIM8
ZXDA
ZYG11B

Sep/08
SERPINB4
SESTD1
SETD7
SEZ6L2
SFRP2
SGCB
SGK223
SGK494
SH2D5
SH3BP1
SH3PXD2A
SHISA2
SHMT1
SHOX
SHOX2
SIAH1
SIGLEC1
SIGLEC15
SIGLEC7
SIGLECL1
SIK1
SIPA1L2
SIRT1
SKIL
SKOR2
SLAMF1
SLC10A1
SLC12A9
SLC16A7
SLC17A9
SLC18A2
SLC18A3
SLC18B1
SLC22A11
SLC25A30
SLC25A37
SLC25A44
SLC25A52
SLC26A1
SLC27A2

SLC2A14
SLC2A3
SLC34A2
SLC35A4
SLC35F3
SLC35G5
SLC37A3
SLC38A2
SLC44A3
SLC44A5
SLC4A10
SLC4A2
SLC5A1
SLC6A14
SLC6A15
SLC6A3
SLC6A5
SLC8A2
SLC9C1
SLCO5A1
SLITRK2
SLITRK5
SMC6
SMCR8
SMYD3
SNAP91
SND1
SNRPA
SNRPE
SNX14
SNX29
SNX4
SOHLH1
SOHLH2
SORCS2
SOS1
SOWAHC
SPA17
SPACA1
SPACA5
SPACA5B

SPAG6
SPAM1
SPATA2L
SPATA31A1
SPATA31A2
SPDYE2B
SPESP1
SPHKAP
SPPL2C
SPRED3
SPRY3
SQRDL
SRCIN1
SREK1
SRF
SRGAP3
SRRM4
SRSF4
SS18
SSB
SSBP1
SSH1
SST
SSTR4
SSX2B
ST3GAL2
ST7
ST8SIA5
STAM
STARD6
STAT2
STK10
STK32B
STK4
STON2
STRA6
STS
STX11
STXBP5
SUCO
SULT1C3

SULT6B1
SUMF2
SYBU
SYCP2
SYNDIG1L
SYNPO2
SYNPR
SYPL2
SYT11
SYT13
SYT16
SYTL5
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TAF3
TAGLN2
TANGO2
TAOK3
TAS2R20
TAS2R8
TAS2R9
TBC1D21
TBC1D7
TBC1D8
TBCC
TBL1XR1
TBP
TBX10
TBX20
TCEAL7
TCEB3
TCERG1L
TCF20
TCN2
TECPR1
TECPR2
TECTB
TEK
TENC1
TEP1
TEX36
TF

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TFB1M
TFEB
THEMIS
THOC7
TICAM1
TIGD5
TIMD4
TIMM50
TIMM8A
TKTL2
TLE4
TLE6
TLL2
TLN1
TLR5
TMC8
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TMEM151A
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TMEM2
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TMPRSS15
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TNFAIP6
TNFRSF4
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TNNC1
TNRC6B

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TOPAZ1
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TPBG
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TPH2
TPO
TPP2
TRA2A
TRAF3IP1
TRAPPC10
TRAPPC8
TRHR
TRIB3
TRIM11
TRIM38
TRIM49D1
TRIM51
TRIM58
TRIM62
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TRPM2
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TSPAN15
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TTC16
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TTC40
TTC7A
TTC9
TTR
TUBA8
TUBE1

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UBE4B
UBN1
UBOX5
UBP1
UBQLN4
UBR1
UBR2
UBXN11
UGT1A6
UHMK1
UNC5D
UPF1
UPK2
URB2
UROC1
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USP17L21
USP17L22
USP17L25
USP31
USP48
USP5
USP6NL
UTP11L
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VEZF1
VGF
VGLL3

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VSTM2B
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VWA5B1
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WDR19
WDR26
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WDR49
WDR7
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WNK3
WNT8A
WWP1
XAF1
XDH
XKR4
XKR7
XPO6
XRN2
YIPF6
YIPF7
YLPM1
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ZBTB16
ZBTB24
ZBTB46
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ZC3H3
ZC3H6
ZC3HAV1L
ZCCHC11
ZDBF2
ZFP30
ZFP36
ZFP42

ZFP62
ZFP92
ZFR2
ZIM3
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ZKSCAN3
ZMIZ2
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ZNF701
ZNF707
ZNF730
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ZNF781
ZNF787
ZNF799
ZNF831
ZNF85
ZNF853
ZNF878
ZNF91
ZNF98
ZP2
ZSCAN12
ZW10
ZZZ3

Table S6C

Mutated genes (nonsynonymous) that are recurrent in each group

IDH-gr (n=103)	KRAS-gr (n=72)	TP53-gr (n=401)	Undetermined-gr (n=260)
AKAP13	*ADAMTS12*	*ABCA13*	*AATF*
AKAP8	*AHNAK2*	*ABCA2*	*ABCA1*
ANKRD30A	*ARHGAP33*	*ACAD10*	*ABLIM1*
ARHGEF11	*ARID1A*	*ACLY*	*ACACA*
ARID1A	*ATP10A*	*ADAM28*	*AFF1*
ARMC9	*CACNA1D*	*ADAM8*	*AFF2*
ARSH	*CASD1*	*ADAMTS7*	*AHNAK2*
AUTS2	*CCDC62*	*ADPRHL1*	*AKAP11*
BAP1	*CDH9*	*AFF3*	*ANK1*
BCLAF1	*CEP290*	*AHNAK*	*ANKMY1*
BPTF	*CP*	*AHNAK2*	*ANKRA2*
C1orf87	*CSMD2*	*AK9*	*ANKRD26*
CACNA1B	*CUBN*	*AKAP12*	*ANKS1B*
CALCOCO1	*CUL9*	*AMPH*	*ANO3*
CDC27	*DNAH1*	*ANKRD11*	*ANXA3*
CHD8	*DTX3L*	*ANKRD30A*	*ARFGEF2*
CHIC1	*EFCAB6*	*ANKRD30B*	*ARHGAP11B*
CLSPN	*ERN1*	*APLP1*	*ARHGAP20*
CNOT4	*ETAA1*	*APP*	*ARHGAP32*
CYFIP1	*FCGBP*	*ARHGAP5*	*ARHGAP5*
CYP17A1	*HMCN1*	*ARMCX1*	*ARID1A*
CYP2A6	*HOXA11*	*ARSD*	*ASH1L*
DDX25	*HRNR*	*ASNS*	*ASPM*
DKC1	*KCNN3*	*ATM*	*ASTN1*
DNAH5	*KIAA1009*	*ATP10A*	*ATM*
DNAJC13	*KRAS*	*ATP1A3*	*ATP13A3*
DOCK3	*LRP1B*	*AUTS2*	*ATRN*
DUX4L4	*LRRN3*	*AXDND1*	*BAP1*
EIF2AK3	*MORC1*	*B3GNT1*	*BAZ2B*
EIF3A	*MTO1*	*BAI3*	*BEND5*
EIF3M	*MYH3*	*BCAR3*	*BIRC6*
ENOX2	*NALCN*	*BDP1*	*BNC2*
EPB41L3	*NHS*	*BHLHE22*	*BOD1L1*
F5	*OBSL1*	*C10orf12*	*BRAF*
FBN2	*OR4A5*	*C10orf71*	*BSN*
FBXW7	*PAPPA*	*C17orf104*	*C10orf90*
FEZF2	*PCDHGA3*	*C6ORF165*	*C1orf172*
FGD6	*PDXDC1*	*CACNA1B*	*C5orf42*

FOCAD	*PIK3CA*	*CACNA1E*	*C9orf173*
FXYD4	*PTPRB*	*CACNA1F*	*CALHM3*
FZD2	*RBM10*	*CACNA1I*	*CCDC108*
GABBR2	*RBMXL3*	*CACNA2D2*	*CCDC144A*
GNB5	*RIMS2*	*CAMK2B*	*CCDC88A*
GRB7	*ROBO2*	*CAMSAP1*	*CD46*
GRIA1	*RP1L1*	*CARD6*	*CDAN1*
HEATR5B	*SATB2*	*CBFA2T3*	*CDC27*
HECW2	*SCN1A*	*CCDC144A*	*CDC42BPA*
HTT	*SDCCAG3*	*CCNK*	*CENPF*
HUWE1	*SEC24A*	*CD276*	*CHD1L*
IDH1	*SEC63*	*CDC27*	*CHD8*
IFNA7	*SMAD4*	*CDH23*	*CIT*
INPP5B	*STAB1*	*CDH4*	*CIZ1*
ITGB5	*SYNE1*	*CDH7*	*CNTNAP3B*
KIAA0100	*TFAP2B*	*CDH9*	*CNTROB*
KIR2DL1	*TG*	*CELSR2*	*COL12A1*
KRTAP6-3	*TGFBR2*	*CFTR*	*COL25A1*
LRP2	*TIAM1*	*CHD4*	*COL3A1*
LTN1	*TMTC1*	*CLCA4*	*COL4A4*
MAML2	*TP53*	*CLEC17A*	*COL4A5*
MAP7D2	*UNC80*	*CLIP1*	*COX7A2*
MED12	*VSIG10*	*CLSPN*	*CSMD1*
MFSD2B	*VWF*	*CNGB3*	*CSMD3*
MORC1	*ZFC3H1*	*CNTN3*	*CTBP2*
MXRA5	*ZNF107*	*CNTNAP2*	*CUBN*
MYCBP2	*ZNF141*	*COBLL1*	*DAB2IP*
NEB	*ZNF212*	*COL12A1*	*DCAF6*
NEDD9	*ZNF493*	*COL14A1*	*DIS3*
OR2L3	*ZNF610*	*COL15A1*	*DLD*
OR5T2	*ZNF717*	*COL1A2*	*DLG1*
PDILT	*ZNF721*	*COL24A1*	*DMD*
PI4KB	*ZNF729*	*COL4A2*	*DNAH14*
PIK3CA	*ZNF90*	*COL6A5*	*DNAH2*
PKHD1		*COL9A2*	*DNAH3*
PLXNA4		*COQ2*	*DNAH5*
PSMD1		*CPSF3*	*DNAJB14*
PTPN13		*CPXM2*	*DOCK8*
RALGAPA1		*CSMD1*	*DOT1L*
RETSAT		*DCSTAMP*	*DSC1*
RLF		*DDX17*	*DSP*

RPTN
RYR3
SHISA5
SLC17A3
SLC26A8
SLK
SMAD2
SPTBN4
STAB1
STK36
SULF1
SYNE2
SZT2
TCF4
TENM1
TMEM145
TMEM43
TPCN1
TRMT13
TRPV1
UBR5
ZFYVE26
ZNF236
ZNF717

DEPDC5
DISC1
DMBT1
DNAH17
DNAH2
DNAH5
DNAH7
DOK1
DRC1
DSP
DUOX2
ECE2
ECM2
EML6
ENPP5
EP400
EPHA4
EPPK1
ERCC6L2
ESPL1
EYS
FAM181A
FAM186A
FAM189A1
FAM214A
FAM47A
FAM71E2
FAT3
FBLN2
FBN1
FBXW10
FCGBP
FGB
FHOD3
FLG
FMN2
FNDC1
FOXC2
FRAS1
FREM3
FRG1

DST
EPB41L2
EPHA2
EPHA5
EPHA6
ERBB4
EXOC5
EYS
F5
FAM129B
FAT4
FLG
FREM1
FRMD4B
G3BP2
GABRG2
GOLGA2
GPR112
GPR98
GTF2E2
HAUS6
HERC2
HHIP
HMCN1
HMGB1
HRNR
HUWE1
HYDIN
IFIH1
IMPG2
INSC
INTS4
IRS4
ITGA2
ITGB1
KCNC3
KDM6B
KIAA0319L
KIAA0368
KIAA0947
KIF13A

FSCB	*KRT1*
FSTL4	*KRTAP10-1*
FYB	*KRTAP5-5*
GCDH	*LAMA4*
GKAP1	*LAMB1*
GLI3	*LILRA2*
GOLGA8J	*LPCAT4*
GPR112	*LRP12*
GPR115	*LZTS2*
GPR116	*MACF1*
GPR155	*MAOA*
GPR183	*MAP3K5*
GRAMD1B	*MAP9*
GRID2	*MCM10*
GRIN2A	*MED18*
GRM2	*MESP2*
GTF2IRD1	*MKI67*
HDAC10	*MKNK2*
HECTD3	*MKRN2*
HELZ	*MPDZ*
HEPH	*MRPL10*
HERC2	*MYH1*
HMCN1	*MYH4*
HMGCR	*MYO18B*
HNRNPCL1	*NALCN*
HSPD1	*NAP1L3*
HSPG2	*NBAS*
HTR1B	*NBEA*
HTR3E	*NEB*
HUWE1	*NIM1K*
IGBP1	*NIPBL*
IGFN1	*NOMO1*
IGSF9	*NUP210*
IGSF9B	*NYAP2*
IRS2	*OBSCN*
ITGB8	*OLAH*
ITPK1	*OR2Y1*
ITPR1	*OR52B2*
KALRN	*OR5H15*
KCNH2	*OR8G5*
KCNQ5	*OTOP1*

KCNS3
KCNT2
KIAA1109
KIAA1210
KIAA1244
KIAA1731
KIF1A
KIF27
KIR2DL4
KLC2
KMT2A
KMT2C
KMT2E
KRAS
KRT32
KRT36
KRT6A
KRT72
KRT80
KRT85
LATS2
LHFPL3
LILRA3
LRCH2
LRP1B
LRRC4C
LRRC7
LRRIQ1
LYST
MACC1
MAP1B
MAP9
MCTP2
MDC1
MDN1
MED1
MED12
MGAM
MICAL3
MIS18BP1
MKRN3
PAIP1
PCDHA1
PCNX
PDZD2
PEAK1
PEG3
PHF12
PHIP
PHKA1
PHLDA1
PIEZO2
PIGM
PIWIL4
PLOD2
POF1B
POLR1A
POSTN
PRAMEF2
PRG4
PTEN
R3HDM1
RAC1
RALGAPB
RAPGEF3
RASGEF1B
RBMX
RBMXL1
ROS1
RPS6KB2
RTL1
RYR1
SAFB
SEMA4G
SETD2
SF3B3
SH3TC1
SIGLEC6
SKOR1
SMARCC1
SMS
SPATA31A6

MLLT4	*SPICE1*
MMP9	*SPTB*
MNS1	*SPTBN5*
MORF4L1	*SRCAP*
MPHOSPH10	*SRPK1*
MPP1	*STAB1*
MPZ	*STK24*
MRC1	*STON1-GTF2A1L*
MROH2B	*STX17*
MX2	*STXBP1*
MXRA5	*SYNE1*
MYBPC2	*SYNE2*
MYH13	*SYNE3*
MYO7B	*SYTL3*
NALCN	*SZT2*
NAV3	*TAF1B*
NBEA	*TAF6*
NDC80	*TANC2*
NEB	*TBC1D4*
NELL1	*TGFBR1*
NF1	*TIE1*
NF2	*TMTC1*
NFAT5	*TNIP1*
NLRP9	*TNKS2*
NME8	*TRPM7*
NOL11	*TSHZ3*
NPAP1	*TTC21B*
NPIPB5	*TTLL10*
NRK	*TXLNB*
NTN5	*UBA6*
NUP188	*UBR4*
NUP54	*ULBP2*
OBSCN	*UPP2*
OBSL1	*USP36*
OGDHL	*UTRN*
OR2A5	*VPS13A*
OR51F1	*VPS13C*
OR5D18	*VPS13D*
OR6F1	*VPS45*
OR6N1	*WDR96*
OTOG	*WHSC1L1*

OTOP3
OVGP1
PAK3
PAX7
PCDH1
PCDH18
PCDHA13
PCDHGA2
PCLO
PEG3
PHF2
PIK3CA
PIKFYVE
PKD1L1
PKD2L1
PKHD1L1
PLCD4
POLR1A
POLR2A
PPP1R1B
PPP5C
PRKAR2B
PRKCQ
PRM2
PRRC2C
PRSS3
PRUNE2
PTEN
PTPRB
PTPRT
PTPRU
PVR
RANBP2
RASA1
RASAL3
RASGRF1
RB1
RBM10
RCN1
RGS7
RHO
XPO1
YY1AP1
ZC3H13
ZCCHC18
ZFC3H1
ZFHX3
ZFHX4
ZNF107
ZNF208
ZNF215
ZNF221
ZNF292
ZNF423
ZNF480
ZNF492
ZNF544
ZNF717

RHOD
RHPN2
ROBO2
ROBO4
RP11-830F9.6
RP1L1
RUNX1
RUNX1T1
RYR2
RYR3
SCAF11
SCN1A
SCN2A
SCNN1B
SCRIB
SDK1
SEMA5B
SEMA6D
SETD2
SF3B3
SH3BP1
SIK3
SIPA1L2
SIPA1L3
SLC18A3
SLC2A14
SLC35G5
SLC36A3
SLC44A5
SLC4A10
SLC4A3
SLC7A9
SLC9C1
SLCO6A1
SLITRK5
SNCAIP
SOGA1
SPATA2L
SPATA31A5
SPATA31A6
SPATA31A7

SPEG
SPHKAP
SPIRE1
SRCIN1
SSC5D
SSTR4
STAB1
STAP1
STK11
STRA6
SYNE1
SYNE2
SZT2
TAF3
TANC2
TAOK3
TBC1D8
TBP
TDRD1
TDRD5
TECPR1
TENM1
TF
TMTC1
TNN
TNRC6B
TOPAZ1
TP53
TP73
TPD52L1
TPP2
TPR
TRAPPC10
TRIOBP
TRPC4
TRPS1
TSC1
TTC16
TTC28
TYR
UBE3D

UBR1
UBR2
UBR4
UHRF1BP1L
UNC79
USH2A
USP17L10
USP6NL
VPS13B
VPS13D
VWF
WDR87
WNK1
WNK2
WNK4
XAF1
XIRP2
XKR7
ZC3HAV1L
ZCCHC11
ZDBF2
ZFHX3
ZFP30
ZNF141
ZNF157
ZNF208
ZNF280C
ZNF415
ZNF502
ZNF521
ZNF554
ZNF592
ZNF594
ZNF717
ZNF831

Table S6D

Mutated genes (nonsynonymous) that are unique and recurrent in each group

IDH-gr (n=32)	Count	KRAS-gr (n=11)	Count	TP53-gr (n=171)	Count	Undetermined-gr (n=103)	Count
CYP17A1	2	*CP*	2	*ABCA2*	2	*ABLIM1*	2
CYP2A6	2	*DTX3L*	2	*ACAD10*	2	*AFF1*	2
DKC1	2	*HOXA11*	2	*ADAM8*	2	*AKAP11*	2
EIF3M	2	*KCNN3*	2	*AFF3*	2	*ANXA3*	2
ENOX2	2	*PDXDC1*	2	*AMPH*	2	*ARHGAP11B*	2
FEZF2	2	*RBMXL3*	2	*ANKRD11*	2	*ARHGAP20*	2
FOCAD	2	*RIMS2*	2	*ARMCX1*	2	*ASH1L*	2
GNB5	2	*SATB2*	2	*ASNS*	2	*ASPM*	2
GRB7	2	*TFAP2B*	2	*ATP1A3*	2	*ASTN1*	2
HEATR5B	2	*VSIG10*	2	*B3GNT1*	2	*BNC2*	2
HECW2	2	*ZNF212*	2	*BAI3*	2	*BOD1L1*	2
HTT	2			*C10orf12*	2	*C1orf172*	2
ITGB5	2			*C17orf104*	2	*CALHM3*	2
MAML2	2			*C6ORF165*	2	*CCDC108*	2
MAP7D2	2			*CACNA1E*	2	*CD46*	2
MFSD2B	2			*CACNA1F*	2	*CDAN1*	2
NEDD9	2			*CACNA2D2*	2	*CHD1L*	2
OR5T2	2			*CAMSAP1*	2	*CIT*	2
PDILT	2			*CARD6*	2	*COL4A4*	2
PKHD1	2			*CCNK*	2	*COX7A2*	2
RLF	2			*CDH23*	2	*DIS3*	2
SLC26A8	2			*CDH4*	2	*DLG1*	2
SLK	2			*CLEC17A*	2	*DNAJB14*	2
SULF1	2			*CNGB3*	2	*DSC1*	2
TCF4	2			*COL14A1*	2	*EPB41L2*	2
TMEM145	2			*COL24A1*	2	*EPHA5*	2
TMEM43	2			*COL4A2*	2	*FAT4*	2
TRMT13	2			*COL9A2*	2	*FREM1*	2
TRPV1	2			*COQ2*	2	*G3BP2*	2
ZNF236	2			*CPXM2*	2	*GOLGA2*	2
KIAA0100	3			*DCSTAMP*	2	*HAUS6*	2
LRP2	3			*DDX17*	2	*HHIP*	2
				DEPDC5	2	*INSC*	2
				DISC1	2	*ITGA2*	2
				DMBT1	2	*KCNC3*	2
				DNAH7	2	*KIAA0319L*	2
				DOK1	2	*KIAA0368*	2
				DRC1	2	*KIAA0947*	2

EML6	2	*KRTAP5-5*	2
ENPP5	2	*LAMB1*	2
ESPL1	2	*LRP12*	2
FAM181A	2	*MCM10*	2
FAM71E2	2	*MED18*	2
FBXW10	2	*MESP2*	2
FGB	2	*MKNK2*	2
FOXC2	2	*MKRN2*	2
FYB	2	*MRPL10*	2
GCDH	2	*NAP1L3*	2
GPR115	2	*NBAS*	2
GPR183	2	*NIM1K*	2
GRAMD1B	2	*OR2Y1*	2
GRIN2A	2	*OR52B2*	2
GTF2IRD1	2	*OR8G5*	2
HDAC10	2	*PAIP1*	2
HECTD3	2	*PEAK1*	2
HELZ	2	*PHF12*	2
HMGCR	2	*PHIP*	2
HTR1B	2	*PHKA1*	2
HTR3E	2	*PIEZO2*	2
KCNH2	2	*PIGM*	2
KCNS3	2	*PIWIL4*	2
KCNT2	2	*PLOD2*	2
KIAA1210	2	*POF1B*	2
KIAA1731	2	*PRG4*	2
KIR2DL4	2	*R3HDM1*	2
KMT2E	2	*RAC1*	2
KRT32	2	*RALGAPB*	2
KRT6A	2	*RAPGEF3*	2
KRT72	2	*RASGEF1B*	2
KRT85	2	*RBMX*	2
LHFPL3	2	*SAFB*	2
LRRC4C	2	*SH3TC1*	2
LRRC7	2	*SKOR1*	2
LYST	2	*SMARCC1*	2
MACC1	2	*SMS*	2
MAP1B	2	*SPTB*	2
MCTP2	2	*SRPK1*	2
MDC1	2	*STX17*	2
MGAM	2	*STXBP1*	2

MIS18BP1	2	*SYNE3*	2
MKRN3	2	*TAF6*	2
MLLT4	2	*TBC1D4*	2
MMP9	2	*TNIP1*	2
MNS1	2	*TNKS2*	2
MORF4L1	2	*TRPM7*	2
MPHOSPH10	2	*TTLL10*	2
MPZ	2	*ULBP2*	2
MRC1	2	*UPP2*	2
MX2	2	*VPS45*	2
MYBPC2	2	*WDR96*	2
MYO7B	2	*ZNF221*	2
NDC80	2	*ZNF292*	2
NF2	2	*ZNF423*	2
NFAT5	2	*ZNF480*	2
NOL11	2	*CENPF*	3
NPAP1	2	*IRS4*	3
NUP54	2	*LZTS2*	3
OGDHL	2	*PHLDA1*	3
OR2A5	2	*TXLNB*	3
OR51F1	2	*XPO1*	3
OR6N1	2	*ZNF544*	3
PAK3	2	*HMGB1*	4
PAX7	2	*NUP210*	4
PCDH18	2		
PCDHGA2	2		
PHF2	2		
PKD2L1	2		
PLCD4	2		
PPP1R1B	2		
PPP5C	2		
PRM2	2		
PRUNE2	2		
PTPRT	2		
PVR	2		
RASAL3	2		
RCN1	2		
RHO	2		
RHOD	2		
RP11-830F9.6	2		
RUNX1	2		

SCNN1B	*2*
SCRIB	*2*
SEMA5B	*2*
SEMA6D	*2*
SH3BP1	*2*
SLC18A3	*2*
SLC2A14	*2*
SLC35G5	*2*
SLC44A5	*2*
SLC4A10	*2*
SLC9C1	*2*
SPHKAP	*2*
SRCIN1	*2*
SSTR4	*2*
TAF3	*2*
TBC1D8	*2*
TBP	*2*
TECPR1	*2*
TF	*2*
TOPAZ1	*2*
TP73	*2*
TPD52L1	*2*
TPP2	*2*
TRAPPC10	*2*
TRPS1	*2*
TYR	*2*
UBE3D	*2*
UBR2	*2*
USP6NL	*2*
WNK1	*2*
XKR7	*2*
ZC3HAV1L	*2*
ZCCHC11	*2*
ZDBF2	*2*
ZNF157	*2*
ZNF554	*2*
ZNF592	*2*
ZNF594	*2*
CNTN3	*3*
FMN2	*3*
GPR116	*3*

GPR155	*3*
IGSF9B	*3*
POLR2A	*3*
SCN2A	*3*
STRA6	*3*
TNRC6B	*3*
TTC16	*3*
ZNF831	*3*
LATS2	*4*
UBR1	*5*

Table S8E

Genes mutated (synonymous) in each group

IDH-gr (n=411)	KRAS-gr (n=326)	TP53-gr (n=839)	Undetermined-gr (n=946)
ABCA1	*AC018470.1*	*A1BG*	*A1BG*
ACAD10	*ACAN*	*A2ML1*	*AAR2*
ACSM2A	*ACP6*	*ABCA12*	*ABCA13*
ACTR3B	*ACSL6*	*ABCA13*	*ABCC11*
ADAM17	*ACSM5*	*ABCC1*	*ABCC12*
ADAM23	*ADAMTS14*	*AC018470.1*	*ABCF1*
ADAMTSL1	*ADAMTS16*	*ACAA2*	*ABR*
ADCY6	*ADCK2*	*ACAD10*	*AC010327.2*
AFF3	*ADCY8*	*ACAD11*	*ACE2*
AFF4	*AIRE*	*ACAD9*	*ACTL10*
ALDH4A1	*AKAP13*	*ACAN*	*ACTN1*
ALG10	*AMPH*	*ACE*	*ADAM33*
ANKAR	*ANGPTL2*	*ACOT12*	*ADAM9*
ANKHD1	*AR*	*ACTR1B*	*ADAMTS16*
ANKRD27	*ARHGAP30*	*ACTRT1*	*ADAMTS5*
ANKRD62	*ARHGEF17*	*ADA*	*ADAMTSL1*
ANXA6	*ARMCX4*	*ADAM19*	*ADCY10*
APBA2	*ARSE*	*ADAMTS1*	*ADRBK1*
ARFGAP1	*ASAP1*	*ADAMTS10*	*AFAP1L2*
ARHGAP21	*ATG9A*	*ADAMTS17*	*AGAP9*
ARHGEF16	*ATP1A2*	*ADAMTS2*	*AGBL1*
ARL2	*ATP7B*	*ADAMTS9*	*AGBL4*
ATG13	*ATRNL1*	*ADAP1*	*AIM1L*
ATP2B4	*AUTS2*	*ADARB2*	*AK9*
ATP4A	*AWAT2*	*ADCY1*	*AKAP11*
ATP9A	*BCL6B*	*ADCY6*	*AKAP13*
B4GALT5	*BCORL1*	*ADRA1A*	*AKAP4*
BAI3	*BMP5*	*ADRA1D*	*AKAP6*
BAZ1A	*BRINP2*	*AFF1*	*ALB*
BBS7	*BRWD3*	*AHNAK*	*ALDH16A1*
BCORL1	*C18orf63*	*AHNAK2*	*ALDH3B2*
BDP1	*C1orf159*	*AHSG*	*ALDOC*
BHLHE22	*C2CD3*	*AIG1*	*ALG1*
BIRC6	*C3orf20*	*AKAP1*	*ALMS1*
BMI1	*C5AR2*	*AKAP14*	*ALOX15*
BNC2	*CA6*	*AKR1C4*	*ALOXE3*
BPIFA1	*CAPRIN2*	*ALS2CL*	*AMOTL1*
BTG3	*CAPZA3*	*AMY2A*	*ANKRD11*

C14orf1	*CASR*	*ANKRD27*	*ANKRD20A4*
C17orf51	*CCDC168*	*ANKS1B*	*ANXA11*
C1QC	*CCKBR*	*AP3B1*	*AOX1*
C1orf173	*CCT8L2*	*APOB*	*AP1B1*
C6orf136	*CD96*	*ARAF*	*APAF1*
CA4	*CDC27*	*ARHGAP44*	*APBB2*
CACNA1B	*CDC42BPA*	*ARHGAP6*	*ARFGEF1*
CACNG2	*CDH18*	*ARHGEF12*	*ARFIP1*
CALCOCO1	*CDH20*	*ARHGEF2*	*ARHGAP29*
CAND2	*CDK13*	*ARHGEF38*	*ARHGAP4*
CARS	*CDK5RAP2*	*ARHGEF5*	*ARHGAP42*
CASP1	*CDKL3*	*ARID2*	*ARHGAP5*
CBWD3	*CENPO*	*ARID3A*	*ARHGEF11*
CCDC121	*CEP76*	*ARID4A*	*ARHGEF7*
CCDC149	*CHST1*	*ARID5A*	*ARID1B*
CCDC27	*CHST2*	*ARIH1*	*ARID4A*
CCDC41	*CKAP5*	*ARL14*	*ARMC7*
CCSAP	*CLIP2*	*ARMCX4*	*ARMCX5*
CD99L2	*CLN3*	*ARPP21*	*ARRDC5*
CDC27	*CLUH*	*ASB10*	*ARSA*
CDC40	*CNPPD1*	*ASB2*	*ARSF*
CDK12	*COL4A1*	*ASCC3*	*ARVCF*
CDK8	*COL5A2*	*ASPG*	*ASIC2*
CEACAM1	*CRCP*	*ASTE1*	*ASPRV1*
CEP152	*CREB3L3*	*ATP10A*	*ASTN1*
CHD1	*CRTC1*	*ATP11B*	*ATAD2*
CHST6	*DACH2*	*ATP1A2*	*ATF6*
CLASP1	*DAG1*	*ATP1A3*	*ATP1A1*
CLCN1	*DAPK3*	*ATP7A*	*ATP2B2*
CLCN4	*DCAF12*	*ATXN3L*	*ATP6V1C2*
CLIP1	*DDX11*	*AVL9*	*ATP9B*
CLMP	*DDX39A*	*AWAT2*	*ATR*
CLN8	*DFFB*	*BAI1*	*ATRN*
CLTC	*DISP2*	*BAI3*	*ATXN3L*
COL22A1	*DLAT*	*BCL11A*	*AVL9*
COL4A2	*DNAJA1*	*BCORL1*	*BAI1*
COL4A3	*DNHD1*	*BECN1*	*BANK1*
COQ10B	*DOK3*	*BID*	*BCHE*
CORO2A	*DONSON*	*BIRC6*	*BCL10*
CRCP	*DOPEY1*	*BNC2*	*BCL2L12*
CST9	*DRGX*	*BPTF*	*BCL6B*

CTBP2	*DSPP*	*BRD4*	*BCL9L*
CTNNBL1	*EBF2*	*BRINP3*	*BCO2*
CUBN	*EBI3*	*BROX*	*BCR*
CXCL14	*EFCAB3*	*BRWD1*	*BICD1*
D2HGDH	*EFS*	*BTBD10*	*BLM*
DDB1	*EIF5B*	*BTN2A1*	*BLVRA*
DDX23	*EPB41*	*C10ORF68*	*BMX*
DENND3	*EPB41L3*	*C11orf24*	*BPTF*
DENND4C	*ERCC5*	*C11orf87*	*BRCA2*
DGKH	*FAM13C*	*C15orf59*	*BRF1*
DIP2B	*FAM159B*	*C16orf96*	*BRINP2*
DLEC1	*FAM184B*	*C17orf80*	*BRS3*
DLGAP3	*FAM188A*	*C19orf60*	*BTBD19*
DMWD	*FAM65B*	*C1orf123*	*BTBD6*
DNAH17	*FAM90A1*	*C2CD2*	*C10orf118*
DPYSL3	*FAT1*	*C2orf81*	*C11orf52*
DRD3	*FBXO2*	*C3orf17*	*C11orf80*
DRD4	*FCGBP*	*C5orf20*	*C14orf93*
DUOX1	*FGFR4*	*C8A*	*C15orf27*
DUS2	*FH*	*C9orf84*	*C19orf12*
DUSP27	*FOXD4L1*	*CACNA1F*	*C19orf57*
DYNC1I1	*FRG1*	*CACNA1G*	*C19orf66*
DYNC1LI2	*FRMD4B*	*CACNG2*	*C21orf59*
E2F8	*GALNT9*	*CALCOCO1*	*C3*
EDIL3	*GGA1*	*CALCRL*	*C5orf42*
EIF4G3	*GIGYF1*	*CAPNS1*	*C5orf47*
ELF4	*GLI3*	*CAPRIN2*	*C7*
ELMO1	*GPC6*	*CC2D1B*	*C7orf25*
EMC1	*GPR98*	*CCDC136*	*C8G*
ENO1	*GRIN2A*	*CCDC155*	*C9orf114*
ENPP3	*GRM1*	*CCDC171*	*C9orf142*
ENTPD5	*GXYLT1*	*CCDC66*	*CABLES2*
EPHA4	*HAUS6*	*CCDC90B*	*CABP4*
ERCC6	*HES1*	*CCKAR*	*CACNA1H*
FABP3	*HEXA*	*CCKBR*	*CACNA2D3*
FAM177A1	*HIST1H4G*	*CCZ1*	*CACNG5*
FAM83G	*HIVEP3*	*CD163L1*	*CADM3*
FANCD2	*HK1*	*CDC27*	*CAPN10*
FANCI	*HMGXB3*	*CDC42SE1*	*CAPNS2*
FIGLA	*HOPX*	*CDCP2*	*CARHSP1*
FKBP6	*HOXD9*	*CDH11*	*CASC3*

FLNA	*HRH3*	*CDH19*	*CATSPERD*
FLNB	*HSD17B4*	*CDK17*	*CCBE1*
FLNC	*HSPA2*	*CDK5RAP1*	*CCDC130*
FLT1	*HTRA3*	*CDK5RAP2*	*CCDC141*
FLVCR1	*IFI35*	*CEBPZ*	*CCDC149*
FNDC1	*IFNA4*	*CELSR1*	*CCDC160*
FOXA1	*IGFN1*	*CEMP1*	*CCDC168*
FOXD4L1	*IGSF22*	*CENPF*	*CCDC183*
FOXP1	*IGSF9B*	*CHAT*	*CCDC87*
FREM3	*IL1A*	*CHD3*	*CCDC88A*
FRG1	*INSR*	*CHODL*	*CCNF*
FRY	*IPMK*	*CHRNB4*	*CCRN4L*
G6PD	*ITGA11*	*CIZ1*	*CD163*
GAS6	*ITGB4*	*CLCNKA*	*CD1C*
GCN1L1	*JAKMIP2*	*CLDN18*	*CD300LF*
GLRB	*JMJD1C*	*CLEC16A*	*CDC27*
GLUD2	*KCNK9*	*CLIP1*	*CDH22*
GMEB2	*KCNQ2*	*CLMP*	*CDHR2*
GMPR	*KCNV1*	*CLN3*	*CDHR5*
GNA14	*KHSRP*	*CLSTN1*	*CDK19*
GNAQ	*KIF20A*	*CLTC*	*CDKN1B*
GNL3L	*KIF4B*	*CLUH*	*CECR6*
GOLGA6L4	*KIFC2*	*CNGA4*	*CELF3*
GP9	*KMT2C*	*CNKSR1*	*CELSR2*
GPR112	*KPNA3*	*CNKSR3*	*CELSR3*
GPR176	*KRT4*	*CNPPD1*	*CENPE*
GRIP1	*KRT6A*	*CNTNAP2*	*CEP104*
GTF3C1	*KRT6B*	*CNTNAP5*	*CEP112*
GZMH	*KRT6C*	*COL11A1*	*CEP19*
HCFC1	*KRTAP10-12*	*COL15A1*	*CEP78*
HCLS1	*KRTAP5-5*	*COL18A1*	*CFB*
HDHD1	*KSR2*	*COL1A1*	*CHIC1*
HEG1	*LILRA2*	*COL22A1*	*CHRFAM7A*
HERC2	*LIPK*	*COL27A1*	*CHRM1*
HEXA	*LONP2*	*COL3A1*	*CIITA*
HK2	*LPHN3*	*COL4A1*	*CILP2*
HSDL2	*LRP1*	*COL4A3BP*	*CLDN5*
HSP90AB1	*LRRK2*	*COL6A3*	*CLEC4G*
HTR2A	*LUM*	*COL6A5*	*CLK1*
HTT	*MAD1L1*	*COMP*	*CLMN*
ICOSLG	*MAGEB5*	*COX5A*	*CMTM1*

IDH3G	*MAP2K7*	*CR1*	*CNGB1*
IFI35	*MAP7D2*	*CRB1*	*CNNM4*
IGF2R	*MDN1*	*CREBBP*	*CNOT1*
IGFN1	*MEF2C*	*CSHL1*	*CNOT7*
IGSF10	*MIA3*	*CSMD1*	*CNPY4*
IL2RG	*MUC12*	*CSMD3*	*CNTF*
IMMT	*MUC16*	*CSNK1E*	*CNTN4*
INTS3	*MUC4*	*CSTF1*	*CNTNAP3B*
IQCA1	*MUC5B*	*CTDSP2*	*COBL*
IQGAP1	*MUC6*	*CXCR6*	*COL11A2*
ITGA9	*MXRA5*	*CXorf67*	*COL14A1*
KAT6B	*MYBBP1A*	*CYP2A13*	*COL19A1*
KCNH6	*MYO9A*	*CYP2A7*	*COL4A1*
KCNK4	*MYOM2*	*DACH1*	*COL4A6*
KCTD3	*NASP*	*DCAF12L1*	*COL5A3*
KDM5A	*NAT9*	*DCAF8L1*	*COL7A1*
KIAA0319	*NBPF10*	*DCDC2*	*COQ7*
KIAA1432	*NBPF12*	*DCHS2*	*CP*
KIAA1715	*NBPF14*	*DCTD*	*CPEB3*
KIDINS220	*NBPF20*	*DDX1*	*CPT1A*
KIF14	*NCALD*	*DDX43*	*CPT2*
KIF7	*NDST1*	*DEF8*	*CREBBP*
KIFC3	*NELFCD*	*DENND1C*	*CREBRF*
KIR2DL1	*NEU2*	*DEPTOR*	*CRIPAK*
KIR3DL1	*NID1*	*DFFB*	*CSAG1*
KIR3DL2	*NINL*	*DHRS7C*	*CSMD3*
KLF17	*NLRP14*	*DHTKD1*	*CSNK1G1*
KLHL18	*NMI*	*DHX58*	*CSPP1*
KLHL2	*NOM1*	*DIP2A*	*CST4*
KLRG1	*NOP16*	*DIRAS2*	*CUL4B*
KLRK1	*NPAP1*	*DISP1*	*CXCL14*
KRT25	*NPR2*	*DISP2*	*CXorf36*
KRT4	*NRF1*	*DMRT2*	*CYP2A6*
KRTAP4-11	*NUDC*	*DNAH10*	*CYP2C19*
LAMA1	*NXPE1*	*DNAH11*	*CYP2W1*
LGALS2	*OPLAH*	*DNAI2*	*CYP7B1*
LILRA2	*OR1F1*	*DNAJA1*	*CYR61*
LMOD3	*OR9I1*	*DNAJC13*	*DAPK3*
LPAR3	*OSGEPL1*	*DNAJC18*	*DBNL*
LPHN3	*OTOGL*	*DNER*	*DCAF12L2*
LRP8	*PABPC3*	*DNPEP*	*DCAF6*

LRRC3	*PARD3B*	*DOCK1*	*DCLK3*
LYVE1	*PARP8*	*DOCK3*	*DCLRE1C*
MAGI2	*PCDH19*	*DOCK4*	*DCP1B*
MAP4	*PCDHA10*	*DOK5*	*DCTN1*
MAP4K3	*PCDHB5*	*DPEP3*	*DCTN4*
MBTPS1	*PCLO*	*DPP6*	*DCUN1D4*
MCF2L2	*PCSK7*	*DPY19L2*	*DDR2*
MCM9	*PCSK9*	*DSG1*	*DDX17*
MECOM	*PCYT2*	*DSPP*	*DDX41*
MED13L	*PDE12*	*DTX2*	*DDX49*
MEGF8	*PDE3A*	*DTX4*	*DDX51*
MKI67	*PDE8B*	*DUX4L4*	*DDX53*
MLLT1	*PDGFRB*	*DYNC1H1*	*DDX6*
MMP26	*PEG3*	*DYNC1I2*	*DEDD2*
MPO	*PER3*	*DYX1C1*	*DENND4C*
MTFR2	*PGD*	*ECHDC3*	*DHCR24*
MTMR12	*PIAS3*	*EDEM3*	*DHX36*
MTSS1L	*PIEZO2*	*EFHC2*	*DIS3*
MUC16	*PIKFYVE*	*EGFLAM*	*DLGAP4*
MUC6	*PLBD1*	*EGLN2*	*DMXL2*
MYBL1	*PLBD2*	*EIF2B3*	*DNAH10*
MYH13	*PLD2*	*EIF5B*	*DNAH17*
MYH3	*PLD3*	*ELAC2*	*DNAH3*
MYRF	*PLTP*	*ELMO1*	*DNAH8*
N4BP2	*PLXNA3*	*ENTPD7*	*DNAJA4*
NAT1	*POMT1*	*EPB41L3*	*DNAJC2*
NBPF20	*POTEE*	*EPHA5*	*DNMBP*
NCAM1	*POU4F2*	*EPHB1*	*DNTT*
NEB	*PPA1*	*EPN1*	*DOCK11*
NEBL	*PPCS*	*ERBB3*	*DOCK2*
NEFH	*PPP1R37*	*ERGIC2*	*DOCK9*
NFKB1	*PPP1R7*	*EVC*	*DPEP3*
NIPAL1	*PPRC1*	*EXTL3*	*DPF1*
NLRP7	*PRKCB*	*EYA1*	*DPP7*
NOD1	*PROM1*	*EZH2*	*DPYD*
NOX3	*PROP1*	*FA2H*	*DPYSL3*
NRXN3	*PRPF40B*	*FAM129B*	*DRD3*
NSMCE1	*PTH1R*	*FAM160A1*	*DSC1*
NT5DC1	*PTK2*	*FAM179A*	*DSG2*
NUP50	*PTP4A2*	*FAM21A*	*DSPP*
OBSL1	*PURG*	*FAM231C*	*DTNA*

OR10H2	*PWP2*	*FAM46D*	*DTX1*
OR10H4	*RCE1*	*FAM47A*	*DUOX2*
OR10K1	*RGPD4*	*FAM73B*	*DUX4L4*
OR10Z1	*RHBDF1*	*FAM78A*	*DYNC1LI1*
OR1Q1	*RIN2*	*FAT4*	*EAPP*
OR4C6	*RRNAD1*	*FBN2*	*ECEL1*
OR4F17	*RRP9*	*FBXL12*	*ECHDC1*
OR52I1	*RUNX3*	*FBXL19*	*EDA*
OR8A1	*RYR3*	*FBXL4*	*EDRF1*
OR8D1	*SBSN*	*FBXO2*	*EEF1A1*
P2RY4	*SCN1A*	*FBXO9*	*EEPD1*
PABPC3	*Sep/06*	*FCER2*	*EFCAB13*
PARP4	*SIGLEC7*	*FCRL3*	*EFCAB6*
PAX6	*SIRPG*	*FIGNL1*	*EIF4ENIF1*
PCDHA12	*SKIDA1*	*FLG*	*EIF4G1*
PCNT	*SLAIN1*	*FLNB*	*ELFN2*
PCNX	*SLC26A10*	*FLT1*	*EMC1*
PCSK5	*SLC34A2*	*FLT3*	*ENAM*
PDZRN4	*SLITRK1*	*FNDC5*	*ERN1*
PEAK1	*SLITRK3*	*FOCAD*	*ERN2*
PEAR1	*SOCS7*	*FREM3*	*ESYT3*
PELI3	*SOS1*	*FRG2*	*EVPL*
PHKA2	*SPOCK1*	*FRG2C*	*EXOSC9*
PIEZO1	*SSC5D*	*FSCN1*	*EZR*
PIEZO2	*STAG3*	*FSIP2*	*FAIM3*
PIGL	*STRC*	*FTH1*	*FAM114A2*
PIK3CD	*STUB1*	*GABPA*	*FAM129B*
PIK3R2	*SVOP*	*GAL3ST3*	*FAM129C*
PJA2	*TAS2R31*	*GALNT8*	*FAM135B*
PLIN4	*TBC1D8*	*GDE1*	*FAM169A*
PLTP	*TBP*	*GDF5*	*FAM186A*
POC1B	*TCF3*	*GEMIN5*	*FAM199X*
POLR1D	*TDO2*	*GFRA2*	*FAM222B*
POLR3D	*TEKT4*	*GH2*	*FAM71E1*
POP1	*TENM3*	*GLI3*	*FAM83C*
PORCN	*THBS3*	*GOLGA8J*	*FAM98A*
PPEF2	*TIMP3*	*GOLGA8N*	*FANCD2*
PPM1G	*TLL2*	*GPA33*	*FANCM*
PRDM15	*TLR7*	*GPATCH1*	*FAT1*
PRDM8	*TM9SF4*	*GPR1*	*FBN1*
PRG3	*TMEM119*	*GPR112*	*FBRSL1*

PRIMPOL	*TMEM132C*	*GPR155*	*FBXL16*
PRLR	*TMTC3*	*GPR157*	*FBXO3*
PRND	*TRAF6*	*GPR161*	*FBXO46*
PRODH	*TRIM29*	*GPR18*	*FBXO5*
PRPF31	*TRIM58*	*GPR98*	*FBXW9*
PSG2	*TRPV5*	*GPRIN3*	*FCGBP*
PSMB2	*TSHZ3*	*GRAMD1B*	*FCRL3*
PTCHD1	*TSPAN15*	*GRIN3B*	*FDX1L*
PTGFRN	*TTLL2*	*GRP*	*FDXACB1*
PTGS2	*TTN*	*GSDMC*	*FER*
PTPRD	*TUBB8*	*GTF2F1*	*FFAR1*
PTPRR	*TXLNG*	*H2AFY*	*FGG*
PTPRU	*UBXN11*	*HAP1*	*FGGY*
PUM2	*UPF2*	*HDAC5*	*FHDC1*
PXDNL	*USF1*	*HDAC9*	*FHL2*
PXK	*USP17L17*	*HEATR1*	*FHOD3*
RAB11FIP2	*USP17L19*	*HEATR3*	*FLG*
RAB3A	*USP18*	*HEATR6*	*FLII*
RALGAPA1	*USP19*	*HECTD4*	*FMN1*
RANBP17	*USP6NL*	*HECW2*	*FNBP1*
RAPGEF1	*VEGFC*	*HEPACAM*	*FOLH1*
RBFOX2	*VSX2*	*HERC2*	*FOXD3*
RFESD	*WDR18*	*HERC3*	*FOXJ1*
RFX6	*WDR64*	*HES1*	*FOXN3*
RNF145	*WNK3*	*HGFAC*	*FPGT*
ROBO4	*ZBTB49*	*HGS*	*FPR3*
ROCK2	*ZDHHC14*	*HINT1*	*FREM2*
RPL12	*ZNF107*	*HIST1H2BC*	*FREM3*
RPSA	*ZNF134*	*HIST1H3B*	*FRG2*
RRH	*ZNF148*	*HMCN1*	*FRMD7*
RYR2	*ZNF185*	*HMGXB3*	*FRMPD4*
S100A4	*ZNF326*	*HNRNPC*	*FSIP2*
SBF1	*ZNF33B*	*HNRNPUL1*	*FST*
SCAPER	*ZNF365*	*HOXA6*	*FUT1*
SEC24C	*ZNF534*	*HOXA7*	*GAK*
SELP	*ZNF566*	*HOXB3*	*GAL3ST2*
SEMA4C	*ZNF584*	*HSPH1*	*GAL3ST3*
SEMA5B	*ZNF598*	*HTR6*	*GALNT7*
Sep/14	*ZNF653*	*HTRA3*	*GALNTL6*
SERAC1	*ZNF717*	*HYDIN*	*GALR1*
SETD3	*ZNF729*	*IFNK*	*GAREML*

SF3B3	*ZNF99*	*IGFN1*	*GATAD2A*
SF3B4		*IGSF10*	*GCOM1*
SHROOM2		*IL12B*	*GDF10*
SHROOM4		*IL13RA2*	*GDPD5*
SIK3		*IL1A*	*GIT1*
SLC12A5		*IL24*	*GLIS1*
SLC12A7		*IL4I1*	*GLRA3*
SLC1A6		*IL5RA*	*GNAL*
SLC20A1		*ING5*	*GNAO1*
SLC23A2		*INHBC*	*GOLGA6L20*
SLC35D1		*INPPL1*	*GOLGA6L4*
SLCO6A1		*INSR*	*GON4L*
SMARCA1		*IQCA1*	*GPC4*
SMARCA4		*IQCE*	*GPLD1*
SMYD1		*IQCF1*	*GPR116*
SNAPC5		*IQGAP1*	*GPR123*
SP8		*IQUB*	*GPR137C*
SPANXN2		*IRAK3*	*GPR89A*
SPIN2A		*IRF6*	*GRINA*
ST18		*IRF9*	*GRM1*
STAG2		*ITGA4*	*GRM5*
STRIP1		*ITGB8*	*GRM7*
SULT1A2		*ITSN1*	*GRN*
SUV420H2		*JMJD7*	*GSE1*
SWAP70		*JPH4*	*GSK3B*
SYK		*KAZN*	*GSTP1*
TBC1D26		*KBTBD3*	*GUCY1A2*
TBC1D3		*KCNH5*	*GUCY1B3*
TBL2		*KCNH8*	*HAPLN3*
TBX15		*KCNT2*	*HAUS4*
TCTE1		*KCNV1*	*HAUS6*
TEKT4		*KCTD7*	*HBEGF*
TFG		*KDM1B*	*HCLS1*
THAP1		*KHDC3L*	*HCN4*
THEG		*KIAA0196*	*HDAC3*
TLL1		*KIAA0556*	*HDHD3*
TLR7		*KIAA0753*	*HEATR2*
TMEM132B		*KIAA1210*	*HECW2*
TMEM178A		*KIAA1239*	*HGSNAT*
TMEM63A		*KIAA1614*	*HIATL1*
TMEM91		*KIAA1755*	*HINFP*

TNFRSF11A	*KIAA2022*	*HIPK1*
TNP2	*KIAA2026*	*HIVEP2*
TNPO3	*KIF26B*	*HLA-DQA2*
TNXB	*KIF27*	*HMGCS2*
TPGS2	*KIF4B*	*HNRNPDL*
TRAPPC9	*KIFC2*	*HOOK2*
TRIP11	*KIR2DL4*	*HRC*
TRPM4	*KLHL30*	*HRNR*
TSSC4	*KLHL6*	*HSF5*
TTN	*KLHL9*	*HSPA12A*
TYW1	*KPNA3*	*HTR1E*
UBA7	*KRT4*	*HUS1*
UBXN11	*KRT6B*	*IER5*
UHRF1BP1	*KRT7*	*IGBP1*
UNC13A	*KRT75*	*IGF1R*
UNC13B	*KRT84*	*IGF2BP2*
UPK3A	*KRTAP10-1*	*IGF2BP3*
URB2	*KRTAP10-11*	*IGSF3*
UROC1	*KRTAP4-7*	*IKBIP*
VAV2	*LAMA1*	*IL13RA2*
VPS13D	*LAMA2*	*IMPG1*
WDHD1	*LAMC1*	*INO80D*
WDR35	*LCA5*	*INPP5A*
YARS2	*LDHAL6B*	*INPPL1*
YTHDC2	*LDHB*	*IQCH*
ZBED4	*LEPREL1*	*ISYNA1*
ZBTB20	*LGI3*	*ITGA6*
ZBTB39	*LGR4*	*ITGA7*
ZC3H18	*LIFR*	*ITM2A*
ZC3HC1	*LILRA2*	*ITPK1*
ZCCHC14	*LILRA6*	*ITPR2*
ZDHHC15	*LILRB5*	*JAG1*
ZFHX3	*LIN37*	*JAKMIP1*
ZKSCAN2	*LIPC*	*KAT6B*
ZNF18	*LIPE*	*KAZN*
ZNF280B	*LONRF1*	*KCNB2*
ZNF415	*LOXHD1*	*KCNH6*
ZNF526	*LPAR4*	*KCNH8*
ZNF648	*LPAR5*	*KCNJ6*
ZNF677	*LPIN2*	*KCNK1*
ZNF684	*LPP*	*KCNN4*

ZNF71
ZNF717
ZNF737
ZXDA

LPPR4
LRP1B
LRP2
LRP8
LRRC41
LYPD8
MAATS1
MAB21L1
MAGEA10
MAGEA2
MAGEA2B
MAGEA3
MAGEA6
MAGEC3
MAP1A
MAP2
MARK2
MAST2
MBOAT2
MECOM
MED1
MED17
MEIS1
MEMO1
MERTK
MFSD1
MGAM
MGAT4C
MIA3
MKKS
MMP16
MMP20
MNT
MOB3C
MPP3
MRAP2
MRC2
MROH7
MSH2
MTIF2
MUC12

KCTD10
KHDRBS2
KIAA0196
KIAA1109
KIAA1244
KIAA1328
KIF13B
KIF18B
KIF21B
KIR3DL1
KLF4
KLHL15
KLHL31
KLHL42
KPNA4
KRT31
KRTAP10-6
KRTAP4-7
KRTAP5-2
L3MBTL4
LAG3
LAMA2
LAMB1
LAMP2
LARP1B
LCORL
LCT
LETM2
LGR6
LILRA2
LILRB1
LILRB3
LINGO3
LONP1
LONRF1
LRBA
LRFN1
LRFN3
LRIG2
LRP1
LRRC32

MUC16
MUC17
MUC4
MUC5B
MUC6
MYBBP1A
MYH1
MYH3
MYH7
MYH8
MYO10
MYO1A
MYO1B
MYO3A
MYO7A
NAA50
NAALADL2
NABP2
NAMPT
NBPF10
NBPF12
NBPF15
NBPF20
NBPF24
NBPF6
NCKAP5
NELL1
NEU2
NF1
NLRP12
NLRP14
NLRP4
NMI
NMUR2
NOD2
NOMO3
NOS1
NPAP1
NPEPL1
NPIPB5
NRF1
LRRC39
LRRC69
LRRN1
LRRN4
LSG1
LXN
LZTR1
MAF1
MAGEE2
MAGI1
MAN2C1
MAP10
MAP1A
MAP3K19
MAP7D3
MAPK15
MASP1
MAST4
MBD6
MBNL3
MCF2L
MCM7
MCM8
MCMDC2
MED23
MEI1
MFHAS1
MFSD12
MGA
MGAT4A
MGEA5
MIA3
MICAL3
MID1
MIPEP
MKI67
MKKS
MLLT3
MRO
MUC12
MUC16

NRG2	*MUC2*
NSD1	*MUC4*
NUDC	*MUC6*
NUDCD1	*MUSK*
NUTM2G	*MUT*
OCA2	*MUTYH*
OCRL	*MVP*
ODF3B	*MYH1*
OR14A16	*MYH15*
OR1F1	*MYH4*
OR2AG1	*MYO15A*
OR2T4	*MYO18B*
OR4K13	*MYO5B*
OR4S1	*MYO7A*
OR51A2	*MYOCD*
OR51I2	*MYOM2*
OR52N4	*MYRF*
OR52N5	*NACAD*
OR5B2	*NALCN*
OR5M3	*NAMPT*
OR5P2	*NASP*
OR6C6	*NAV3*
OR6K2	*NBPF10*
OR6Y1	*NBPF12*
OR7D4	*NBPF20*
OR8D1	*NCKAP1*
OR8U1	*NCOR2*
OR9I1	*NCSTN*
ORM2	*NDEL1*
OS9	*NDUFB2*
OTOG	*NDUFS2*
OTOGL	*NEDD4*
OVCH1	*NEK2*
P2RY14	*NEK4*
P4HA3	*NELL2*
PABPC3	*NES*
PABPC4L	*NEURL4*
PADI1	*NFE2L3*
PAK7	*NFS1*
PAPPA2	*NFX1*
PAPSS1	*NINL*

PARD3B
PARK2
PARM1
PARP4
PARVG
PAX3
PAX5
PCDH1
PCDH10
PCDH11X
PCDH7
PCDH8
PCDH9
PCDHA9
PCDHAC2
PCDHB12
PCDHB15
PCDHB4
PCLO
PCSK7
PCYT1A
PDE10A
PDE1C
PDE3B
PDHX
PDZK1
PER3
PEX1
PGAM4
PGPEP1L
PIEZO1
PIGX
PIK3C2A
PJA1
PKDREJ
PKLR
PLA2G5
PLB1
PLCL2
PLEKHG2
PLK3
NISCH
NKAP
NKD2
NLE1
NOL11
NOL6
NPAS3
NPHP4
NRK
NRXN1
NTN4
NTRK3
NUBP2
NUDT17
NUMBL
NUP188
NUP98
NYAP1
NYNRIN
NYX
OBFC1
OBSL1
OPN5
OR10G9
OR2A25
OR2T11
OR2T12
OR2T8
OR4B1
OR4C13
OR4C15
OR4D2
OR4F15
OR4N5
OR4S2
OR51G1
OR52E6
OR52I2
OR56A3
OR5AC2
OR5B3

PLTP	*OR5H14*
PLXNA4	*OR6P1*
PMM1	*OR7A10*
PODN	*OR7A17*
POLR1A	*OR7G2*
POLR3E	*OTP*
PPP1R14D	*PABPC1*
PPP1R37	*PABPC4*
PPP1R9A	*PABPC5*
PPP2R5C	*PAK1IP1*
PRAMEF1	*PAK6*
PRAMEF13	*PAMR1*
PRDM1	*PANX2*
PRICKLE3	*PARD3B*
PRKAG2	*PARD6A*
PRKCB	*PAXIP1*
PRKG1	*PCDH7*
PRPF40A	*PCDHB10*
PRR23A	*PCDHB12*
PSG1	*PCDHB13*
PSG7	*PCDHB15*
PSG9	*PCDHGA1*
PSMD1	*PCLO*
PTBP1	*PCNT*
PTCHD1	*PCNX*
PTGIR	*PCNXL2*
PTK2	*PCNXL3*
PTP4A2	*PDCD5*
PTPN11	*PDE10A*
PTPN13	*PDE1A*
PTPN14	*PDE8A*
PTPN4	*PDK4*
PTPRF	*PDLIM3*
PTPRG	*PDXK*
PTPRN2	*PER1*
PXDN	*PEX5*
R3HDM2	*PFKFB3*
RAB11FIP1	*PFKM*
RAB17	*PGD*
RAB5B	*PGR*
RALYL	*PHF2*

RANBP2
RAPGEF2
RAPGEF3
RASA4B
RBM6
RBPMS
RCVRN
RET
RGL2
RGS8
RHAG
RHBDF1
RHBDF2
RHOT1
RHPN1
RIMS3
RLIM
RNF183
ROBO2
ROR1
RPGRIP1L
RRAGB
RREB1
RRP7A
RUNX3
RYR3
S1PR5
SAAL1
SALL2
SALL3
SAMD14
SARS2
SBNO1
SCML1
SCN10A
SCN2A
SCN3A
SCN4A
SCN5A
SCNN1B
SCNN1G
PIGA
PIGO
PITHD1
PKD1
PLAT
PLB1
PLBD1
PLCG2
PLCL1
PLEKHG2
PLEKHG5
PLXNA3
PLXNA4
PLXNB1
PLXNB3
POLI
POLR2C
POU1F1
PPA1
PPA2
PPFIA3
PPM1A
PPM1J
PPP1R16B
PPP2R1B
PPP2R5E
PPP3CC
PPP4R2
PRAMEF22
PRAMEF7
PRAMEF8
PRDX3
PRG4
PRICKLE3
PRKG2
PROCR
PRPF39
PRSS27
PRSS42
PRTN3
PRUNE

SDR16C5	*PRX*
SEC16A	*PSD4*
SECISBP2L	*PSMG1*
SEMA3D	*PTBP2*
Sep/05	*PTCH2*
Sep/06	*PTGIS*
Sep/07	*PTPN21*
SERTAD2	*PTPRM*
SEZ6L	*PTPRN2*
SF3A3	*PTPRS*
SFTPA2	*PUM2*
SH2D4B	*PYGM*
SH3D21	*PYGO2*
SH3YL1	*RAET1G*
SHANK1	*RAG1*
SHC2	*RAI1*
SIGIRR	*RALGAPA2*
SKIDA1	*RALGAPB*
SLAIN1	*RANBP17*
SLC22A23	*RAP1GDS1*
SLC25A18	*RARB*
SLC25A21	*RAVER1*
SLC26A10	*RBBP6*
SLC26A2	*RBM25*
SLC34A2	*RBM27*
SLC36A3	*RBP3*
SLC39A12	*REEP5*
SLC44A5	*REPIN1*
SLC52A2	*REV3L*
SLC5A3	*RFTN1*
SLC5A7	*RFX4*
SLC6A8	*RGAG1*
SLC9A3	*RGL2*
SLC9C1	*RGN*
SLIT2	*RGS3*
SLU7	*RHBDF2*
SMAP1	*RHPN2*
SMC4	*RIC8A*
SMCHD1	*RLF*
SMEK2	*RNF103*
SNX32	*RNF208*

SOCS7	*RNF216*
SOGA1	*RNPS1*
SOS1	*ROR2*
SOX18	*ROS1*
SP7	*RP1*
SPAG1	*RP11-644F5.10*
SPAG16	*RP1L1*
SPEG	*RPL37A*
SPTA1	*RPS4Y1*
SRGAP1	*RPS6KA4*
SRGAP2	*RRN3*
SSC5D	*RS1*
ST6GAL2	*RTL1*
ST6GALNAC5	*RUNX3*
ST8SIA2	*RYR2*
STAMBP	*SALL3*
STAP1	*SAMD15*
STAR	*SAMD9*
STUB1	*SAMM50*
SULF2	*SASH1*
SVIL	*SCAF11*
SYNJ2	*SCN1A*
SYTL3	*SCN5A*
TADA3	*SDK1*
TAOK2	*SEC16A*
TBC1D19	*SEC24C*
TBCC	*SEMA4D*
TCHHL1	*SEMA4F*
TEAD4	*Sep/12*
TECPR1	*SERPINB6*
TEKT4	*SETDB2*
TENM1	*SEZ6L2*
TENM3	*SGCG*
TERT	*SGMS2*
TEX9	*SGOL2*
TFPI2	*SGSM3*
TGM2	*SH2D4B*
THEM4	*SH3PXD2A*
TIGD6	*SHC4*
TLR8	*SHROOM3*
TLR9	*SHROOM4*

TMEM119	*SIGLEC10*
TMEM150B	*SIK3*
TMEM2	*SIRPG*
TMEM246	*SIX3*
TMEM255B	*SLAIN1*
TMEM257	*SLC12A5*
TMEM79	*SLC13A2*
TMEM86A	*SLC19A2*
TMTC3	*SLC1A3*
TNFRSF11B	*SLC24A4*
TNMD	*SLC25A23*
TNRC18	*SLC28A2*
TNS3	*SLC29A1*
TOPAZ1	*SLC35C2*
TP53	*SLC35D3*
TP63	*SLC35F4*
TPRN	*SLC35G3*
TPSAB1	*SLC37A1*
TRAM1L1	*SLC38A2*
TREM1	*SLC38A5*
TRHDE	*SLC38A6*
TRIM29	*SLC39A9*
TRIM41	*SLC44A1*
TRIM66	*SLC4A4*
TRIM71	*SLC4A9*
TRPM2	*SLC5A8*
TRPM6	*SLC6A15*
TRPV6	*SLC8A2*
TRRAP	*SLC9A3*
TSSK2	*SLC9A8*
TTC1	*SLCO2A1*
TTC24	*SMARCAD1*
TTC28	*SMARCD2*
TTN	*SMC1A*
TUBA3C	*SMC2*
TUBB8	*SMG6*
TULP4	*SMG9*
TWSG1	*SNED1*
TXLNA	*SNX19*
UBA1	*SNX9*
UBA7	*SOGA1*

UBALD1	*SORL1*
UBE2Q2	*SP100*
UBR2	*SPAG5*
UPK3BL	*SPATA22*
USP17L17	*SPTBN1*
USP17L19	*SRBD1*
USP17L26	*SRGAP1*
USP17L27	*SRGAP3*
USP17L5	*SRP68*
USP25	*SRP72*
USP3	*SRPK3*
USP9Y	*SRRM3*
VCX	*SSC5D*
VEGFB	*ST14*
VEPH1	*STAB2*
VMO1	*STARD9*
VPS33A	*STAU1*
VPS8	*STAU2*
WDFY4	*STK32B*
WDR1	*STK33*
WDR18	*STXBP5*
WDR65	*SULT1A1*
WDR96	*SUSD4*
WHAMM	*SVIL*
WIPF3	*SWAP70*
WNK2	*SYDE1*
XIRP2	*SYNGR3*
XKR4	*SYT3*
YY2	*SYT5*
ZAP70	*TAB3*
ZC3H6	*TAF1A*
ZC3H8	*TAF7L*
ZCCHC5	*TAOK2*
ZFAT	*TARBP1*
ZFHX3	*TAX1BP1*
ZFP30	*TBC1D22B*
ZFP37	*TBX4*
ZIM3	*TBXA2R*
ZNF12	*TCF20*
ZNF169	*TCF25*
ZNF19	*TCHH*

ZNF200
ZNF208
ZNF215
ZNF318
ZNF350
ZNF454
ZNF479
ZNF490
ZNF541
ZNF549
ZNF551
ZNF598
ZNF621
ZNF653
ZNF683
ZNF71
ZNF717
ZNF729
ZNF808
ZNF831
ZNF99
ZSCAN5B
TCP11L2
TCTN3
TDRD5
TERT
TESK1
TFCP2L1
THOC2
THUMPD1
TIAM1
TIGD1
TJP1
TJP3
TKTL1
TLE3
TLK1
TLK2
TLL2
TMCC1
TMCO4
TMEM104
TMEM132D
TMEM39B
TMTC3
TNS3
TOM1L2
TOPBP1
TPRN
TPSAB1
TPSD1
TRDN
TRHDE
TRIM59
TRIP12
TRIP6
TRMT2A
TRPC3
TRPM2
TSHZ1
TSPYL6
TSSK6
TTBK2

TTN
TUBB8
TUBG1
TUSC5
TVP23C
TXK
UBE2E2
UBE3A
UBP1
UBR5
UFL1
UMPS
UNK
UNKL
UPF1
URI1
USH2A
USP17L10
USP17L12
USP32
USP44
USP6
USP7
UTP18
UTRN
VAT1
VCPIP1
VNN2
VPRBP
VPS13A
VPS13B
VPS13C
VPS33A
VPS51
VWA8
WAC
WASF3
WDFY3
WDR33
WDR62
WIPF1

WNT11
WWC3
XIRP1
XKR7
XPNPEP2
XXyac-YRM2039.2
YIPF4
YY1AP1
ZBED5
ZC3H13
ZEB2
ZFHX3
ZIC4
ZIM2
ZMYND10
ZMYND15
ZNF12
ZNF141
ZNF160
ZNF208
ZNF229
ZNF251
ZNF41
ZNF426
ZNF429
ZNF469
ZNF473
ZNF513
ZNF517
ZNF565
ZNF573
ZNF579
ZNF619
ZNF675
ZNF696
ZNF716
ZNF717
ZNF729
ZNF732
ZNF773
ZNF774

ZNF827

ZNF836

ZNF880

ZNF98

ZSCAN22

ZW10

Table S7: Significantly mutated genes across four groups

IDH-gr

#Gene	Indels	SNV	Tot Muts	Covd Bps	Muts pMbp	*P*-value FCPT	*P*-value LRT	*P*-value CT	FDR FCPT	FDR LRT	FDR CT
IDH1	0	17	17	20372	834.48	0	0	0	0	0	0
BAP1	3	3	6	32323	185.63	2.88E-06	1.00E-10	3.55E-10	0.030926874	1.08E-06	3.81E-06
CDC27	0	4	4	40136	99.66	0.000138357	1.08E-07	4.85E-08	0.989480681	0.000581535	0.000346934
DUX4L4	0	2	2	814	2457	0.003468192	4.68E-08	5.44E-07	1	0.000334854	0.002918879
BCLAF1	0	3	3	44542	67.35	0.005965552	1.89E-06	5.58E-06	1	0.008120709	0.020252215
GNB5	0	2	2	19829	100.86	0.057033116	5.38E-06	5.76E-05	1	0.019221521	0.137337848
SLC26A8	1	2	3	50880	58.96	0.064920998	0.000746362	0.000135602	1	0.244026352	0.22379521
RETSAT	0	2	2	30985	64.55	0.069108394	7.55E-06	0.000104676	1	0.023137962	0.190375412
ITGB5	0	2	2	34949	57.23	0.081326143	0.000119566	0.000155375	1	0.160330748	0.238112075
ARSH	2	0	2	26118	76.58	0.109257069	1.95E-05	0.00037194	1	0.044731116	0.398998685
KIR2DL1	0	2	2	13046	153.3	0.119346906	0.000274018	0.000177903	1	0.244026352	0.254460636
NEDD9	0	2	2	40302	49.63	0.141878707	0.000360794	0.000583899	1	0.244026352	0.555392504
ARID1A	2	1	3	97545	30.76	0.162207976	0.000603296	0.001048591	1	0.244026352	0.594716583
ANKRD30A	0	2	2	54577	36.65	0.168445794	0.0005164	0.000764957	1	0.244026352	0.590106938
AUTS2	0	2	2	54863	36.45	0.170529941	4.70E-05	0.000852636	1	0.077554856	0.590106938
OR2L3	1	1	2	14847	134.71	0.190340646	0.000739789	0.000298029	1	0.244026352	0.336537545
CHIC1	0	2	2	9790	204.29	0.190363958	7.07E-05	0.000251428	1	0.101068761	0.299688544
SHISA5	1	1	2	13466	148.52	0.191497119	0.000745803	0.000586882	1	0.244026352	0.555392504

KRAS-gr

#Gene	Indels	SNV	Tot Muts	Covd Bps	Muts pMbp	*P*-value FCPT	*P*-value LRT	*P*-value CT	FDR FCPT	FDR LRT	FDR CT
KRAS	0	23	23	16110	1427.68	1.35E-21	1.35E-21	0	0	0	0
TMTC1	0	3	3	66254	45.28	0.011245734	3.74E-05	1.03E-05	1	0.133863637	0.044218463
ZNF90	1	1	2	41557	48.13	0.034691265	2.66E-05	3.17E-05	1	0.118665266	0.113434473
SMAD4	1	2	3	68274	43.94	0.037542034	0.000295724	9.97E-05	1	0.317237907	0.286354771
ADAMTS12	0	3	3	112894	26.57	0.063767204	9.99E-05	0.000208004	1	0.238182429	0.318821893
HOXA11	0	2	2	21796	91.76	0.068408109	9.08E-05	0.000106774	1	0.238182429	0.286354771
OR4A5	0	2	2	21488	93.08	0.077863405	0.000118641	0.000135361	1	0.245757123	0.304691343
CDH9	0	2	2	55371	36.12	0.091260446	0.0001541	0.000159608	1	0.245757123	0.304691343
ZNF141	0	2	2	35062	57.04	0.101356486	1.73E-05	0.000182702	1	0.118665266	0.304691343
ARID1A	1	2	3	140685	21.32	0.110408507	0.000276831	0.000625945	1	0.317237907	0.6054195
KCNN3	1	1	2	51440	38.88	0.110465465	0.000222819	0.000184618	1	0.298786119	0.304691343

ZNF610	0	2	2	32200	62.11	0.123342441	0.00029015	0.000337726	1	0.317237907	0.455026486
TFAP2B	0	2	2	30530	65.51	0.185841512	0.00068728	0.000682975	1	0.327124331	0.610550842
PDXDC1	0	2	2	54627	36.61	0.189706876	0.00070208	0.000649016	1	0.327124331	0.6054195

TP53-gr

#Gene	Indels	SNV	Tot Muts	Covd Bps	Muts pMbp	*P*-value FCPT	*P*-value LRT	*P*-value CT	FDR FCPT	FDR LRT	FDR CT
TP53	0	37	37	57445	644.09	9.88E-23	9.88E-23	0	0	0	0
PTEN	0	6	6	55595	107.92	9.36E-07	2.81E-09	8.60E-11	0.009983112	2.00E-05	9.17E-07
LATS2	0	4	4	136193	29.37	0.021003896	1.50E-05	7.84E-05	1	0.053379583	0.18581053
CDC27	0	3	3	118312	25.36	0.104935736	1.92E-05	0.000502087	1	0.058579208	0.465565584
SLC35G5	0	2	2	44781	44.66	0.117372104	2.22E-05	0.000296352	1	0.059227773	0.332647035
HNRNPCL1	0	2	2	39244	50.96	0.133899727	3.00E-05	0.000287845	1	0.071092368	0.332647035
PRM2	0	2	2	19066	104.9	0.15909494	4.58E-05	0.000623224	1	0.09766828	0.474696289
BHLHE22	0	2	2	17290	115.67	0.071965626	0.00010002	7.78E-05	1	0.193920999	0.18581053
EPPK1	0	4	4	291146	13.74	0.087940929	0.000145229	0.001146138	1	0.202005401	0.679281003
GPR183	1	1	2	48824	40.96	0.094098084	0.000159091	0.00022798	1	0.202005401	0.324142621
LHFPL3	1	1	2	32362	61.8	0.097177838	0.000173851	0.000173838	1	0.202005401	0.308953251
DCSTAMP	0	2	2	62503	32	0.104630533	0.000190891	0.000368474	1	0.202005401	0.374211861
GKAP1	0	2	2	51172	39.08	0.110792271	0.000220174	0.000259459	1	0.202005401	0.325499456
USP17L10	0	2	2	37601	53.19	0.113309006	0.000235089	0.000224279	1	0.202005401	0.324142621
RB1	0	5	5	122479	40.82	0.002402729	0.000236437	3.53E-06	1	0.202005401	0.015072228
STRA6	1	2	3	112080	26.77	0.035824805	0.000237122	0.000125466	1	0.202005401	0.243255137
LRCH2	0	3	3	98880	30.34	0.107556725	0.000265211	0.000610801	1	0.202005401	0.474696289
TTC16	0	3	3	121402	24.71	0.125035428	0.000340537	0.000854693	1	0.234278698	0.588001518
TMTC1	0	3	3	129612	23.15	0.053498322	0.000408333	0.000255578	1	0.26389426	0.325499456
RHOD	0	2	2	26348	75.91	0.155135064	0.000458967	0.000486596	1	0.281269871	0.465565584
PEG3	0	3	3	215413	13.93	0.154982895	0.000461595	0.001769001	1	0.281269871	0.679281003
EYS	0	6	6	424849	14.12	0.036137001	0.00047892	0.000361638	1	0.283720181	0.374211861
GPR155	0	3	3	120004	25	0.057646413	0.000547124	0.000214193	1	0.289088291	0.324142621
FGB	1	1	2	68491	29.2	0.193016372	0.000689241	0.00069137	1	0.289088291	0.491494734
CNTNAP2	1	2	3	182622	16.43	0.071797488	0.000693639	0.000532401	1	0.289088291	0.469754045
ZC3HAV1L	0	2	2	24241	82.5	0.188206351	0.000711333	0.000677785	1	0.289088291	0.491494734
IGBP1	0	2	2	45486	43.97	0.19457742	0.000729611	0.000884196	1	0.289088291	0.589289143
FMN2	1	2	3	190688	15.73	0.189242705	0.000730987	0.002370259	1	0.289088291	0.695285729
ARHGAP5	1	2	3	206776	14.51	0.0820038	0.0007713	0.0005726	1	0.2890882	0.4697540

						63	33	83		91	45	
UBR1	1	4	5	244291	20.47	0.02000757	0.000859751	9.84E-05	1	0.306475835	0.209774507	

Udt-gr

#Gene	Indels	SNV	Tot Muts	Covd Bps	Muts pMbp	*P*-value FCPT	*P*-value LRT	*P*-value CT	FDR FCPT	FDR LRT	FDR CT	
ARID1A	2	7	9	354164	25.41	8.86E-07	3.00E-08	3.32E-10	0.01901867	0.000644476	7.13E-06	
HMGB1	0	4	4	39890	100.28	0.000167452	1.47E-07	4.02E-08	1	0.001580171	0.00031202	
BAP1	3	0	3	134775	22.26	0.010821785	3.05E-07	1.79E-05	1	0.001698496	0.04811621	
SPATA31A6	0	4	4	209280	19.11	0.005879296	2.09E-06	1.14E-05	1	0.008966013	0.040783369	
KRTAP5-5	0	2	2	38431	52.04	0.039491468	2.71E-06	3.38E-05	1	0.009708246	0.065835337	
AFF2	0	4	4	244298	16.37	0.044678868	4.18E-06	0.000195011	1	0.010806851	0.199236147	
C9orf173	0	2	2	46690	42.84	0.053481168	4.73E-06	4.85E-05	1	0.010806851	0.075815946	
OR52B2	0	2	2	54916	36.42	0.055242116	5.04E-06	4.95E-05	1	0.010806851	0.075815946	
MED18	0	2	2	39090	51.16	0.057889988	5.60E-06	4.82E-05	1	0.010921337	0.075815946	
CDC27	0	5	5	162738	30.72	0.000819696	1.10E-05	7.60E-07	1	0.019541523	0.004075069	
INSC	0	2	2	110380	18.12	0.092252523	1.28E-05	0.000315662	1	0.019541523	0.260482023	
PHLDA1	1	2	3	45539	65.88	0.019462405	1.34E-05	2.36E-05	1	0.019541523	0.05619379	
OR5H15	0	2	2	57920	34.53	0.091172872	1.37E-05	0.000112621	1	0.019541523	0.145127354	
C1orf172	2	0	2	66621	30.02	0.099874848	1.59E-05	0.000162703	1	0.020858616	0.174540059	
TMTC1	0	2	2	173713	11.51	0.107388894	1.65E-05	0.000501816	1	0.020858616	0.347305116	
MRPL10	0	2	2	51226	39.04	0.116499586	2.26E-05	0.000344149	1	0.026946926	0.27347131	
ZCCHC18	0	2	2	72184	27.71	0.144872099	3.57E-05	0.000402096	1	0.040340695	0.29748172	
TAF6	0	2	2	136653	14.64	0.170760854	4.67E-05	0.000943022	1	0.047752609	0.457097001	
FAM129B	2	0	2	120757	16.56	0.176814462	5.14E-05	0.000844541	1	0.050115588	0.457097001	
MESP2	0	2	2	36352	55.02	0.059050229	6.85E-05	5.97E-05	1	0.063940371	0.08536716	
NAP1L3	0	2	2	91550	21.85	0.198947479	7.29E-05	0.000954533	1	0.065161268	0.457097001	
ZNF544	0	3	3	136799	21.93	0.017471278	8.01E-05	2.94E-05	1	0.066110927	0.062982075	
COX7A2	0	2	2	29463	67.88	0.074798356	0.000108938	0.000152267	1	0.080595532	0.171941917	
ZNF717	1	3	4	117912	33.92	0.005433461	0.00011528	5.11E-06	1	0.082444571	0.021941194	
KDM6B	2	1	3	242729	12.36	0.084786591	0.000146741	0.000544498	1	0.092597688	0.360139854	
NUP210	0	4	4	331661	12.06	0.025443972	0.000158785	0.000149699	1	0.097335179	0.171941917	
LZTS2	0	3	3	104060	28.83	0.109333495	0.000291207	0.000368227	1	0.142282046	0.282153758	
OR2Y1	1	1	2	56804	35.21	0.125153097	0.000291793	0.000289164	1	0.142282046	0.258500169	
TXLNB	1	2	3	138703	21.63	0.040192088	0.000309897	0.000114993	1	0.145180895	0.145127354	
HHIP	0	2	2	139676	14.32	0.1435267	0.0003564	0.0005727	1	0.1593437	0.3601398	

						45	9	13		92	54	
ZNF480	0	2	2	100303	19.94	0.15938869	0.000473965	0.000498081	1	0.191866383	0.347305116	
MKNK2	0	2	2	89774	22.28	0.16501526	0.000493182	0.000566082	1	0.1923859	0.360139854	
CALHM3	0	2	2	53979	37.05	0.16516269	0.000519355	0.000587504	1	0.197848758	0.360139854	
SMS	1	1	2	67189	29.77	0.17094157	0.000560005	0.000903492	1	0.202475318	0.457097001	
HAUS6	1	1	2	180325	11.09	0.18268953 7	0.000582 78	0.001105031	1	0.202475318	0.483845692	
POLR1A	0	3	3	324153	9.25	0.17540352 4	0.000639 27	0.002186022	1	0.217706925	0.663541834	
MKRN2	1	1	2	76422	26.17	0.18549042 5	0.000659 396	0.001047919	1	0.221052058	0.468397978	
RBMX	0	2	2	79075	25.29	0.19897360 3	0.000771 11	0.001141 61	1	0.227081216	0.489864724	
XPO1	0	3	3	207384	14.47	0.18878937 7	0.000883 329	0.001496618	1	0.231119864	0.527282305	

Table S8: Enriched KEGG pathways among SNV-affected genes

IDH-gr

Pathway	Name	Class	Samples Affected	Total Variations	*P*-value	Q-value
hsa00480	Glutathione metabolism	Metabolism; Metabolism of Other Amino Acids	17	22	5.3807E-21	6.34E-21
hsa04146	Peroxisome	Cellular Processes; Transport and Catabolism	17	22	1.3612E-14	2.62E-14
hsa00020	Citrate cycle (TCA cycle)	Metabolism; Carbohydrate Metabolism	17	17	2.3608E-14	2.37E-14
hsa05032	Morphine addiction	Human Diseases; Substance Dependence	4	14	2.4208E-09	1.17E-08
hsa05200	Pathways in cancer	Human Diseases; Cancers	9	27	2.48E-08	2.31E-07
hsa04728	Dopaminergic synapse	Organismal Systems; Nervous System	8	17	4.5668E-08	1.32E-07
hsa04020	Calcium signaling pathway	Environmental Information Processing; Signal Transduction	8	20	5.9603E-07	1.02E-06
hsa04727	GABAergic synapse	Organismal Systems; Nervous System	4	12	6.3368E-07	1.81E-06
hsa04144	Endocytosis	Cellular Processes; Transport and Catabolism	8	19	6.7517E-07	1.28E-06
hsa00230	Purine metabolism	Metabolism; Nucleotide Metabolism	5	15	6.9241E-07	7.39E-07
hsa04062	Chemokine signaling pathway	Organismal Systems; Immune System	8	16	9.7835E-07	1.70E-06
hsa04810	Regulation of actin cytoskeleton	Cellular Processes; Cell Motility	8	19	1.6732E-06	5.14E-06
hsa05166	HTLV-I infection	Human Diseases; Infectious Diseases	9	20	2.0539E-06	1.73E-05
hsa04724	Glutamatergic synapse	Organismal Systems; Nervous System	6	15	2.6556E-06	7.35E-06
hsa04310	Wnt signaling pathway	Environmental Information Processing; Signal Transduction	5	14	3.2571E-06	6.51E-06
hsa04510	Focal adhesion	Cellular Processes; Cell Communication	10	24	4.0703E-06	8.69E-06
hsa04110	Cell cycle	Cellular Processes; Cell Growth and Death	5	13	6.0091E-06	1.07E-05
hsa04725	Cholinergic synapse	Organismal Systems; Nervous System	8	14	8.4115E-06	2.36E-05
hsa00520	Amino sugar and nucleotide sugar metabolism	Metabolism; Carbohydrate Metabolism	3	8	9.0561E-06	1.10E-05
hsa00830	Retinol metabolism	Metabolism; Metabolism of Cofactors and Vitamins	5	10	0.000014502	2.06E-05
hsa04916	Melanogenesis	Organismal Systems; Endocrine System	5	11	0.000015627	5.05E-05
hsa04350	TGF-beta signaling pathway	Environmental Information Processing; Signal Transduction	4	10	0.000016518	4.90E-05
hsa04740	Olfactory transduction	Organismal Systems; Sensory System	9	18	0.000016518	4.90E-05
hsa04520	Adherens junction	Cellular Processes; Cell Communication	6	12	0.000017736	3.89E-05
hsa03040	Spliceosome	Genetic Information Processing; Transcription	4	11	0.000022022	3.49E-05
hsa03320	PPAR signaling pathway	Organismal Systems; Endocrine System	3	8	0.000030298	4.89E-05
hsa04726	Serotonergic synapse	Organismal Systems; Nervous System	8	13	0.000032924	9.32E-05
hsa04512	ECM-receptor interaction	Environmental Information Processing; Signaling Molecules and Interaction	7	16	0.000039346	8.47E-05
hsa04270	Vascular smooth muscle contraction	Organismal Systems; Circulatory System	4	12	0.000050019	9.96E-05
hsa04530	Tight junction	Cellular Processes; Cell Communication	5	12	0.000111423	2.53E-04
hsa05100	Bacterial invasion of epithelial cells	Human Diseases; Infectious Diseases	7	10	0.000170414	0.000895577
hsa04	Cell adhesion molecules	Environmental Information Processing; Signaling	6	12	0.00018	4.02E-

514	(CAMs)	Molecules and Interaction			517	04
hsa04010	MAPK signaling pathway	Environmental Information Processing; Signal Transduction	7	15	0.00020755	0.00035 1024
hsa04610	Complement and coagulation cascades	Organismal Systems; Immune System	4	9	0.00025147	0.00056 5808
hsa04976	Bile secretion	Organismal Systems; Digestive System	3	8	0.00029286	1.19E-03
hsa04340	Hedgehog signaling pathway	Environmental Information Processing; Signal Transduction	3	7	0.00031658	0.00064 8603
hsa00982	Drug metabolism - cytochrome P450	Metabolism; Xenobiotics Biodegradation and Metabolism	4	8	0.00041665	6.14E-04
hsa00980	Metabolism of xenobiotics by cytochrome P450	Metabolism; Xenobiotics Biodegradation and Metabolism	4	8	0.0004262	0.00062 4433
hsa04070	Phosphatidylinositol signaling system	Environmental Information Processing; Signal Transduction	4	10	0.00049446	8.65E-04
hsa04660	T cell receptor signaling pathway	Organismal Systems; Immune System	4	9	0.00049455	1.22E-03
hsa04971	Gastric acid secretion	Organismal Systems; Digestive System	5	9	0.00059864	0.00225 1601
hsa04721	Synaptic vesicle cycle	Organismal Systems; Nervous System	6	8	0.00066557	0.00178 4294
hsa04360	Axon guidance	Organismal Systems; Development	6	12	0.00074497	1.55E-03
hsa04662	B cell receptor signaling pathway	Organismal Systems; Immune System	5	8	0.00096869	0.00241 693
hsa03008	Ribosome biogenesis in eukaryotes	Genetic Information Processing; Translation	4	8	0.0010829	1.63E-03
hsa04912	GnRH signaling pathway	Organismal Systems; Endocrine System	6	10	0.0011405	3.59E-03
hsa00562	Inositol phosphate metabolism	Metabolism; Carbohydrate Metabolism	4	8	0.001357	0.00170 1313
hsa04920	Adipocytokine signaling pathway	Organismal Systems; Endocrine System	3	7	0.0016385	5.36E-03
hsa04330	Notch signaling pathway	Environmental Information Processing; Signal Transduction	4	7	0.0016833	0.00342 09
hsa04630	Jak-STAT signaling pathway	Environmental Information Processing; Signal Transduction	4	9	0.0019318	0.00463 632
hsa04650	Natural killer cell mediated cytotoxicity	Organismal Systems; Immune System	6	9	0.0028256	0.00691 3118
hsa04012	ErbB signaling pathway	Environmental Information Processing; Signal Transduction	5	8	0.0037969	0.00646 4992
hsa04145	Phagosome	Cellular Processes; Transport and Catabolism	6	10	0.0038232	0.00729 8836
hsa04210	Apoptosis	Cellular Processes; Cell Growth and Death	5	7	0.0042706	0.00834 2567
hsa00010	Glycolysis / Gluconeogenesis	Metabolism; Carbohydrate Metabolism	5	6	0.0049873	0.00498 73

KRAS-gr

Pathway	Name	Class	Samples_Affected	Total_Variations	p-value	FDR
hsa04722	Neurotrophin signaling pathway	Organismal Systems; Nervous System	23	41	8.7372E-21	2.37E-20
hsa05166	HTLV-I infection	Human Diseases; Infectious Diseases	23	54	1.7995E-20	1.51E-19
hsa04062	Chemokine signaling pathway	Organismal Systems; Immune System	23	41	5.0701E-18	8.81E-18
hsa04662	B cell receptor signaling pathway	Organismal Systems; Immune System	23	32	1.4462E-17	3.61E-17
hsa04012	ErbB signaling pathway	Environmental Information Processing; Signal Transduction	23	34	2.5812E-17	4.40E-17
hsa04664	Fc epsilon RI signaling pathway	Organismal Systems; Immune System	23	30	8.2756E-17	2.09E-16
hsa04370	VEGF signaling pathway	Environmental Information Processing; Signal Transduction	23	30	1.1868E-16	2.49E-16

hsa04010	MAPK signaling pathway	Environmental Information Processing; Signal Transduction	23	50	2.6158E-16	4.42E-16
hsa04650	Natural killer cell mediated cytotoxicity	Organismal Systems; Immune System	23	34	6.8636E-15	1.68E-14
hsa04910	Insulin signaling pathway	Organismal Systems; Endocrine System	23	37	1.5732E-14	4.89E-14
hsa04660	T cell receptor signaling pathway	Organismal Systems; Immune System	23	31	3E-14	7.41E-14
hsa04725	Cholinergic synapse	Organismal Systems; Nervous System	23	34	4.0698E-14	1.14E-13
hsa04916	Melanogenesis	Organismal Systems; Endocrine System	23	30	5.5643E-14	1.80E-13
hsa04912	GnRH signaling pathway	Organismal Systems; Endocrine System	23	31	7.5014E-13	2.36E-12
hsa04530	Tight junction	Cellular Processes; Cell Communication	23	35	1.5242E-12	3.37E-12
hsa04726	Serotonergic synapse	Organismal Systems; Nervous System	23	31	3.1757E-12	8.99E-12
hsa04360	Axon guidance	Organismal Systems; Development	23	33	2.9361E-11	6.11E-11
hsa04810	Regulation of actin cytoskeleton	Cellular Processes; Cell Motility	23	38	4.6998E-10	1.44E-09
hsa04310	Wnt signaling pathway	Environmental Information Processing; Signal Transduction	10	20	3.6726E-07	7.35E-07
hsa04110	Cell cycle	Cellular Processes; Cell Growth and Death	10	18	2.4611E-06	4.37E-06
hsa05202	Transcriptional misregulation in cancer	Human Diseases; Cancers	11	18	0.00009 1626	8.88E-04
hsa04210	Apoptosis	Cellular Processes; Cell Growth and Death	8	12	0.00013 905	2.72E-04
hsa04666	Fc gamma R-mediated phagocytosis	Organismal Systems; Immune System	8	13	0.00028 74	7.32E-04
hsa04520	Adherens junction	Cellular Processes; Cell Communication	6	11	0.00083 409	0.00182 7745
hsa04350	TGF-beta signaling pathway	Environmental Information Processing; Signal Transduction	4	9	0.00108 87	2.25E-03
hsa04740	Olfactory transduction	Organismal Systems; Sensory System	7	17	0.00120 27	3.57E-03
hsa04115	p53 signaling pathway	Cellular Processes; Cell Growth and Death	7	9	0.00151 77	2.73E-03
hsa04060	Cytokine-cytokine receptor interaction	Environmental Information Processing; Signaling Molecules and Interaction	6	12	0.00375 41	0.00647 9679
hsa04020	Calcium signaling pathway	Environmental Information Processing; Signal Transduction	8	16	0.00426 14	7.31E-03
hsa00230	Purine metabolism	Metabolism; Nucleotide Metabolism	5	11	0.00821 29	8.77E-03

TP53-gr

Pathway	Name	Class	Samples_Affected	Total_Variations	p-value	FDR
hsa04010	MAPK signaling pathway	Environmental Information Processing; Signal Transduction	41	103	8.5758E-34	1.45E-33
hsa04115	p53 signaling pathway	Cellular Processes; Cell Growth and Death	40	55	1.915E-32	3.45E-32
hsa04722	Neurotrophin signaling pathway	Organismal Systems; Nervous System	39	66	5.1098E-28	1.38E-27
hsa04310	Wnt signaling pathway	Environmental Information Processing; Signal Transduction	40	68	1.0961E-26	2.19E-26
hsa04110	Cell cycle	Cellular Processes; Cell Growth and Death	40	67	1.9667E-26	3.49E-26
hsa05166	HTLV-I infection	Human Diseases; Infectious Diseases	41	88	5.9478E-26	5.00E-25
hsa04210	Apoptosis	Cellular Processes; Cell Growth and Death	38	50	4.7631E-24	9.30E-24
hsa05202	Transcriptional misregulation in cancer	Human Diseases; Cancers	39	66	2.5674E-22	2.49E-21

hsa04740	Olfactory transduction	Organismal Systems; Sensory System	30	67	3.2826E-20	9.73E-20
hsa04725	Cholinergic synapse	Organismal Systems; Nervous System	29	47	1.3672E-15	3.83E-15
hsa04510	Focal adhesion	Cellular Processes; Cell Communication	33	68	9.1206E-13	1.95E-12
hsa04020	Calcium signaling pathway	Environmental Information Processing; Signal Transduction	23	52	2.2852E-11	3.92E-11
hsa04728	Dopaminergic synapse	Organismal Systems; Nervous System	19	36	4.2853E-10	1.24E-09
hsa04360	Axon guidance	Organismal Systems; Development	29	45	5.4744E-10	1.14E-09
hsa04070	Phosphatidylinositol signaling system	Environmental Information Processing; Signal Transduction	21	34	1.5611E-09	2.73E-09
hsa04726	Serotonergic synapse	Organismal Systems; Nervous System	29	37	1.5901E-09	4.50E-09
hsa04012	ErbB signaling pathway	Environmental Information Processing; Signal Transduction	21	30	6.1321E-09	1.04E-08
hsa04660	T cell receptor signaling pathway	Organismal Systems; Immune System	24	31	9.0957E-09	2.25E-08
hsa04650	Natural killer cell mediated cytotoxicity	Organismal Systems; Immune System	21	30	3.4243E-08	8.38E-08
hsa04260	Cardiac muscle contraction	Organismal Systems; Circulatory System	11	22	7.583E-08	1.49E-07
hsa04810	Regulation of actin cytoskeleton	Cellular Processes; Cell Motility	30	48	1.3445E-07	4.13E-07
hsa04971	Gastric acid secretion	Organismal Systems; Digestive System	17	25	2.461E-07	9.26E-07
hsa00562	Inositol phosphate metabolism	Metabolism; Carbohydrate Metabolism	18	25	4.032E-07	5.06E-07
hsa04664	Fc epsilon RI signaling pathway	Organismal Systems; Immune System	19	23	5.0967E-07	1.28E-06
hsa04910	Insulin signaling pathway	Organismal Systems; Endocrine System	28	36	5.3981E-07	1.68E-06
hsa04912	GnRH signaling pathway	Organismal Systems; Endocrine System	22	30	5.7779E-07	1.82E-06
hsa04270	Vascular smooth muscle contraction	Organismal Systems; Circulatory System	17	29	1.0009E-06	1.99E-06
hsa04916	Melanogenesis	Organismal Systems; Endocrine System	17	25	1.1676E-06	3.77E-06
hsa04662	B cell receptor signaling pathway	Organismal Systems; Immune System	19	23	3.3343E-06	8.32E-06
hsa04530	Tight junction	Cellular Processes; Cell Communication	27	35	3.5919E-06	7.94E-06
hsa04972	Pancreatic secretion	Organismal Systems; Digestive System	18	28	8.4633E-06	3.23E-05
hsa04512	ECM-receptor interaction	Environmental Information Processing; Signaling Molecules and Interaction	18	33	0.00001438	2.46E-05
hsa04370	VEGF signaling pathway	Environmental Information Processing; Signal Transduction	16	20	0.00001648	3.46E-05
hsa04514	Cell adhesion molecules (CAMs)	Environmental Information Processing; Signaling Molecules and Interaction	15	25	0.00003968	8.62E-05
hsa04062	Chemokine signaling pathway	Organismal Systems; Immune System	22	30	0.00005194	9.03E-05
hsa00380	Tryptophan metabolism	Metabolism; Amino Acid Metabolism	10	13	0.00005644	6.41E-05
hsa05030	Cocaine addiction	Human Diseases; Substance Dependence	9	14	0.00012	5.71E-04
hsa04727	GABAergic synapse	Organismal Systems; Nervous System	16	20	0.00027743	0.00079 4459
hsa04350	TGF-beta signaling pathway	Environmental Information Processing; Signal Transduction	14	18	0.00034819	7.19E-04
hsa04150	mTOR signaling pathway	Environmental Information Processing; Signal Transduction	15	15	0.00063771	0.00123 6176
hsa00020	Citrate cycle (TCA cycle)	Metabolism; Carbohydrate Metabolism	10	10	0.00107 78	1.08E-03
hsa04144	Endocytosis	Cellular Processes; Transport and Catabolism	18	30	0.00119 03	2.26E-03

hsa00564	Glycerophospholipid metabolism	Metabolism; Lipid Metabolism	13	16	0.0016889	2.14E-03
hsa04724	Glutamatergic synapse	Organismal Systems; Nervous System	17	24	0.0021025	5.82E-03
hsa04920	Adipocytokine signaling pathway	Organismal Systems; Endocrine System	13	15	0.0023328	0.007634618
hsa04630	Jak-STAT signaling pathway	Environmental Information Processing; Signal Transduction	16	21	0.0024342	5.84E-03
hsa03008	Ribosome biogenesis in eukaryotes	Genetic Information Processing; Translation	12	16	0.0027793	4.19E-03
hsa04666	Fc gamma R-mediated phagocytosis	Organismal Systems; Immune System	16	19	0.002835	7.22E-03
hsa03010	Ribosome	Genetic Information Processing; Translation	9	9	0.0037087	0.005630075
hsa00230	Purine metabolism	Metabolism; Nucleotide Metabolism	21	25	0.0051803	5.53E-03
hsa00030	Pentose phosphate pathway	Metabolism; Carbohydrate Metabolism	7	7	0.0095791	9.66E-03

Udt-gr

Pathway	Name	Class	Samples_Affected	Total_Variations	p-value	FDR
hsa04740	Olfactory transduction	Organismal Systems; Sensory System	27	46	0.000068194	0.000202175
hsa04360	Axon guidance	Organismal Systems; Development	22	35	0.00012281	0.00025577
hsa04510	Focal adhesion	Cellular Processes; Cell Communication	25	51	0.00086242	0.001841778
hsa04910	Insulin signaling pathway	Organismal Systems; Endocrine System	24	30	0.0034874	0.010849689
hsa04310	Wnt signaling pathway	Environmental Information Processing; Signal Transduction	19	27	0.0041948	0.0083896
hsa04530	Tight junction	Cellular Processes; Cell Communication	18	29	0.0044476	0.009831537
hsa04150	mTOR signaling pathway	Environmental Information Processing; Signal Transduction	13	15	0.0047563	0.009219905

KRAS/TP53 mutated cases

Pathway	Name	Class	Samples_Affected	Total_Variations	p-value	FDR
hsa04722	Neurotrophin signaling pathway	Organismal Systems; Nervous System	5	13	8.3084E-10	2.25E-09
hsa04960	Aldosterone-regulated sodium reabsorption	Organismal Systems; Excretory System	5	7	6.8556E-07	2.37E-06
hsa04010	MAPK signaling pathway	Environmental Information Processing; Signal Transduction	5	14	1.2978E-06	2.19E-06
hsa04210	Apoptosis	Cellular Processes; Cell Growth and Death	5	8	1.8915E-06	3.70E-06
hsa05166	HTLV-I infection	Human Diseases; Infectious Diseases	5	13	3.1852E-06	2.68E-05
hsa04660	T cell receptor signaling pathway	Organismal Systems; Immune System	5	8	0.00001258	3.11E-05
hsa04664	Fc epsilon RI signaling pathway	Organismal Systems; Immune System	5	7	0.00001 3252	3.34E-05
hsa04370	VEGF signaling pathway	Environmental Information Processing; Signal Transduction	5	7	0.00001 5276	3.21E-05
hsa05014	Amyotrophic lateral sclerosis (ALS)	Human Diseases; Neurodegenerative Diseases	5	6	0.00001 6838	7.44E-05
hsa04662	B cell receptor signaling pathway	Organismal Systems; Immune System	5	7	0.00002 9344	7.32E-05
hsa04115	p53 signaling pathway	Cellular Processes; Cell Growth and Death	5	6	0.00004 9968	8.99E-05

hsa04012	ErbB signaling pathway	Environmental Information Processing; Signal Transduction	5	7	0.000078778	0.000134136
hsa04725	Cholinergic synapse	Organismal Systems; Nervous System	5	8	0.000087534	0.000245095
hsa05211	Renal cell carcinoma	Human Diseases; Cancers	5	6	0.00012388	0.00130074
hsa04650	Natural killer cell mediated cytotoxicity	Organismal Systems; Immune System	5	7	0.00014413	0.00035 2629
hsa05202	Transcriptional misregulation in cancer	Human Diseases; Cancers	5	8	0.00026278	0.00254 6945
hsa04530	Tight junction	Cellular Processes; Cell Communication	5	8	0.00034311	0.00075 8454
hsa04360	Axon guidance	Organismal Systems; Development	5	8	0.00045989	0.00095 7787
hsa04916	Melanogenesis	Organismal Systems; Endocrine System	5	6	0.00060392	0.00195 1126
hsa04910	Insulin signaling pathway	Organismal Systems; Endocrine System	5	7	0.00087335	0.00271 7089
hsa04062	Chemokine signaling pathway	Organismal Systems; Immune System	5	7	0.00127 59	0.00221 7426

Table S9: Drug repositioning

Cell Line	Mutation Subgroup	Mutation	Source
SNU-1079	IDH-gr	*IDH1* ^{R132C}	KCLB
EGI-1	KRAS-gr	*KRAS* ^{G12D}	DSMZ
HuCCT-1	KRAS-gr	*KRAS* ^{G12D}	Riken
SNU-1196	TP53-gr	*TP53* ^{R273C}	KCLB
KMCH	TP53-gr	*TP53* $^{Y88C, Y220C}$	Mayo Clinic
WITT	Udt-gr	-	Mayo Clinic
SNU-478	Udt-gr	-	KCLB
RBE	Double mutant	*KRAS* ^{G12V} & *IDH1* ^{R132S}	Riken

IDH-gr Pharmacoresponse Profiles

Drug	Class explained	Mechanism/Targets	IDH-gr DSS	KRAS-gr DSS	TP53-gr DSS	Udt-gr DSS	Patient Group with Max. DSS	Overall Performance (DSS)	DSS(IDH-gr) - DSS(non-IDH-gr)	Differential Inter-group Sensitivity (rank)	Mixed Mutant DSS
Disulfiram	Metabolic modifier	alcohol dehydrogenase inhibitor	**36.7**	24.3	13.2	30.5	IDH-gr	Top 1%	14.1	1	27.09
8-chloro-adenosine	Conventional chemotherapy	Nucleoside analog, RNA synthesis inhibitor	**25.7**	14.5	12.9	15.7	IDH-gr	Top 2%	11.3	3	8.86
Doxorubicin	Conventional chemotherapy	Topoisomerase II inhibitor	**16.6**	6.4	6.7	7.6	IDH-gr	Top 10%	9.7	8	5.32
Bortezomib	Conventional chemotherapy	Proteasome inhibitor (26S subunit)	**35.6**	27.9	27.2	23.8	IDH-gr	Top 1%	9.3	9	20.36
Fludarabine	Conventional chemotherapy	Antimetabolite; Purine analog	**28.5**	16.6	20.4	21.1	IDH-gr	Top 2%	9.2	10	24.62
YM155	Apoptotic modulator	Survivin inhibitor	**41.7**	33.3	36.1	29.0	IDH-gr	Top 1%	9.0	11	39.25
SH-4-54	Other	STAT3 inhibitor	**17.8**	10.8	6.9	10.2	IDH-gr	Top 10%	8.5	12	11.89
	Metabolic modifier	Dihydrofolate reductase inhibitor	**20.1**	9.8	12.4	12.8	IDH-gr	Top 10%	8.4	13	11.08
8-amino-adenosine	Conventional chemotherapy	Nucleoside analog, RNA synthesis inhibitor	**23.7**	18.7	12.4	16.4	IDH-gr	Top 5%	7.8	15	9.83
LY3009120	Kinase inhibitor	pan-RAF inhibitor	**17.7**	10.0	12.4	8.7	IDH-gr	Top 10%	7.4	16	11.67
Dactinomycin	Conventional chemotherapy	RNA and DNA synthesis inhibitor	**36.0**	31.7	24.5	30.1	IDH-gr	Top 1%	7.2	17	31.02
Pevonedistat	Metabolic modifier	NAE inhibitor	**18.2**	16.9	8.5	10.7	IDH-gr	Top 10%	6.2	22	13.16
Radicicol	HSP inhibitor	HSP90 inhibitor	**19.2**	15.1	11.4	13.5	IDH-gr	Top 10%	5.8	23	9.67
SCH772984	Kinase inhibitor	ERK1 & 2 inhibitor	**17.4**	11.0	11.1	12.6	IDH-gr	Top 10%	5.8	24	12.11

AZD-8330	Kinase inhibitor	MEK1/2 inhibitor	**23.3**	16.6	16.9	19.0	IDH-gr	Top 5%	5.8	25	18.34
Plicamycin	Conventional chemotherapy	RNA synthesis inhibitor	**25.3**	23.6	17.7	17.2	IDH-gr	Top 5%	5.8	26	22.86
Carfilzomib	Conventional chemotherapy	Proteasome inhibitor (20S subunit)	**32.1**	30.0	23.1	26.2	IDH-gr	Top 1%	5.7	27	29.3
Ganetespib	HSP inhibitor	HSP90 inhibitor	**20.7**	16.3	14.4	14.6	IDH-gr	Top 5%	5.6	28	12.54
BCI	Other	Dusp6 inhibitor	**23.2**	19.4	16.2	17.6	IDH-gr	Top 5%	5.4	29	18.34
ONX-0914	Other	LMP7 (immunoproteasome)	**22.9**	19.5	15.8	17.2	IDH-gr	Top 5%	5.4	30	17.88
Raltitrexed	Conventional chemotherapy	DHFR/GARFT/thymidylate synthase inhibitor	**19.3**	14.0	16.5	12.0	IDH-gr	Top 10%	5.2	31	12.08
Selinexor	Apoptotic modulator	CRM1 inhibitor	**28.0**	25.8	25.5	17.8	IDH-gr	Top 2%	4.9	33	24.36
OTX015	Differentiating/epigenetic modifier	BRD2, 3, 4	**17.5**	15.8	11.7	10.2	IDH-gr	Top 10%	4.9	34	15.51
Mepacrine	Other	Unclear. PLA2 inhibitor. NF-kB inhibitor, p53 activator	**20.1**	13.3	14.6	17.9	IDH-gr	Top 10%	4.9	35	14.98
CUDC-907	Differentiating/epigenetic modifier	HDAC1/2/3/10, PI3Kalpha inhibitor	**35.7**	34.4	27.6	31.0	IDH-gr	Top 1%	4.7	36	31.83
SNS-032	Kinase inhibitor	CDK inhibitor	**28.5**	25.5	21.4	24.9	IDH-gr	Top 2%	4.6	39	23.27
Prexasertib	Kinase inhibitor	Chk1 inhibitor	**34.4**	32.3	26.9	32.2	IDH-gr	Top 1%	3.9	42	32.54
Refametinib	Kinase inhibitor	MEK1/2 inhibitor	**17.6**	12.4	15.6	13.8	IDH-gr	Top 10%	3.6	45	14.87
Stattic	Other	STAT3 SH2 domain inhibitor	**20.4**	17.9	14.9	19.2	IDH-gr	Top 5%	3.1	49	17.82
UCN-01	Kinase inhibitor	PKCbeta, PDK1, Chk, Cdk2 inhibitor	**27.7**	25.8	24.4	24.0	IDH-gr	Top 2%	3.0	51	26.61
Oprozomib	Conventional chemotherapy	proteasome (20 S) inhibitor	**22.1**	20.7	19.7	17.0	IDH-gr	Top 5%	3.0	52	22.32
JQ1	Differentiating/epigenetic modifier	BET family inhibitor	**16.8**	15.7	15.4	11.0	IDH-gr	Top 10%	2.8	53	14.23
OTSSP167	Kinase inhibitor	MELK inhibitor	**16.9**	16.4	14.2	12.7	IDH-gr	Top 10%	2.5	55	15.62

KRAS-gr Pharmacoresponse Profiles

Drug	Class explained	Mechanism/Targets	IDH-gr DSS	KRAS-gr DSS	TP53-gr DSS	Udt-gr DSS	Patient Group with Max. DSS	Overall Performance (DSS)	DSS(KRAS-gr) - DSS(non-KRAS-gr)	Differential Inter-group Sensitivity (rank)	Mixed Mutant DSS
Vinorelbine	Conventional chemotherapy	Mitotic inhibitor. Vinca alkaloid microtubule depolymerizer	0.0	**31.3**	27.5	28.6	KRAS-gr	Top 1%	12.8	1	17.99
Patupilone	Conventional chemotherapy	Mitotic inhibitor, epothilone microtubule stabilizer	14.7	**28.3**	25.4	21.0	KRAS-gr	Top 2%	10.0	2	12.19
Docet	Conventiona	Mitotic inhibitor,	13.	**29.9**	25.6	24.	KRAS-gr	Top 2%	10.0	3	16.4

axel	l chemotherapy	taxane microtubule stabilizer	5			1					
Paclitaxel	Conventional chemotherapy	Mitotic inhibitor, taxane microtubule stabilizer	21.1	**24.8**	18.9	18.1	KRAS-gr	Top 5%	8.4	4	7.61
Vincristine	Conventional chemotherapy	Mitotic inhibitor. Vinca alkaloid microtubule depolymerizer	14.2	**21.7**	19.0	17.7	KRAS-gr	Top 5%	6.3	5	10.55
Vinblastine	Conventional chemotherapy	Mitotic inhibitor. Vinca alkaloid microtubule depolymerizer	11.0	**21.2**	19.1	18.8	KRAS-gr	Top 5%	6.2	6	10.95
BI 2536	Kinase inhibitor	PLK1 inhibitor	13.0	**20.2**	17.9	17.8	KRAS-gr	Top 10%	6.2	7	7.28
GSK923295	Kinesin inhibitor	CENP-E inhibitor	10.6	**18.8**	17.0	15.1	KRAS-gr	Top 10%	5.6	9	9.84
Dinaciclib	Kinase inhibitor	CDK inhibitor	21.3	**25.0**	17.0	19.2	KRAS-gr	Top 5%	5.4	10	20.96
CUDC-101	Kinase inhibitor	HDAC & EGFR, Her2 inhibitor	16.5	**17.4**	11.7	12.4	KRAS-gr	Top 10%	3.6	12	14.32
PF-00477736	Kinase inhibitor	Chk1 inhibitor	13.7	**16.6**	12.3	12.6	KRAS-gr	Top 10%	3.3	14	14.61
Panobinostat	Differentiating/ epigenetic modifier	HDAC inhibitor	17.0	**18.7**	14.2	17.8	KRAS-gr	Top 10%	2.6	19	15.32
Abexinostat	Differentiating/ epigenetic modifier	HDAC1-selective inhibitor	15.0	**17.1**	13.9	16.3	KRAS-gr	Top 10%	2.6	20	12.74
Luminespib	HSP inhibitor	HSP90 inhibitor	17.0	**17.6**	14.0	15.3	KRAS-gr	Top 10%	2.5	21	14.1
Romidepsin	Differentiating/ epigenetic modifier	HDAC inhibitor	30.9	**32.2**	26.6	32.0	KRAS-gr	Top 1%	2.5	22	29.05
BIIB021	HSP inhibitor	HSP90 inhibitor	16.4	**18.7**	17.2	14.9	KRAS-gr	Top 10%	2.4	23	16.82
Alvocidib	Kinase inhibitor	CDK inhibitor	20.1	**20.3**	17.9	19.1	KRAS-gr	Top 10%	1.6	29	17.87

TP53-gr Pharmacoresponse Profiles

Drug	Class explained	Mechanism/Targets	IDH-gr DSS	KRAS-gr DSS	TP53-gr DSS	Udt-gr DSS	Patient Group with Max. DSS	Overall Performance (%)	DSS(TP53-gr) - DSS(non-TP53-gr)	Differential Inter-group Sensitivity (rank)	Mixed Mutant DSS
Cabazitaxel	Conventional chemotherapy	Taxane microtubule stabilizer, antimitotic	18.6	28.5	**28.6**	24.9	TP53-gr	Top 2%	4.6	12	15.35
SN-38	Conventional chemotherapy	Active metabolite of irinotecan. Topoisomerase I inhibitor	25.7	25.9	**28.4**	21.1	TP53-gr	Top 2%	4.2	17	23.47
GSK-461364	Kinase inhibitor	PLK1 inhibitor	6.3	27.4	**28.1**	22.2	TP53-gr	Top 2%	9.5	1	7.45
Filanesib	Kinesin inhibitor	KSP/Eg5 inhibitor	18.6	20.7	**26.5**	17.5	TP53-gr	Top 2%	7.6	3	0.08
KX2-391	Kinase inhibitor	non-ATP competitive Src inhibitor	13.7	22.3	**24.0**	17.9	TP53-gr	Top 5%	6.0	8	10.42
Rigosertib	Kinase inhibitor	PLK1 inhibitor, non-ATP-comp; Ras-Raf	10.3	20.5	**23.3**	17.1	TP53-gr	Top 5%	7.3	4	9.63

		interaction inhibitor									
MK1775	Kinase inhibitor	Wee1 inhibitor	19.0	19.4	**22.4**	16.0	TP53-gr	Top 5%	4.3	16	16.48
Camptothecin	Conventional chemotherapy	Topoisomerase I inhibitor	19.7	18.8	**22.3**	15.4	TP53-gr	Top 5%	4.3	14	15.15
Topotecan	Conventional chemotherapy	Topoisomerase I inhibitor. Camptothecin analog	13.3	16.1	**20.8**	14.3	TP53-gr	Top 5%	6.2	6	14.43
Teniposide	Conventional chemotherapy	Topoisomerase II inhibitor	15.2	12.6	**18.7**	12.6	TP53-gr	Top 10%	5.2	10	6.75
Methotrexate	Metabolic modifier	Antimetabolite; Anti-folate agent	8.7	8.2	**18.6**	16.0	TP53-gr	Top 10%	7.6	2	6.75

Udt-gr Pharmacoresponse Profiles

Drug	Class explained	Mechanism/Targets	IDH-gr DSS	KRAS-gr DSS	TP53-gr DSS	Udt-gr DSS	Patient Group with Max. DSS	Overall Performance (%)	DSS(Udt-gr) - DSS(non-Udt-gr)	Differential Inter-group Sensitivity (rank)	Mixed Mutant DSS
Omacetaxine	Conventional chemotherapy	Protein synthesis inhib (80 S ribosome)	19.3	23.4	20.6	**24.8**	Udt-gr	Top 5%	3.7	22	20.44
PF-03758309	Kinase inhibitor	PAK inhibitor	19.6	23.7	14.2	**24.2**	Udt-gr	Top 5%	5.0	15	17.07
AZD8055	Kinase inhibitor	mTOR inhibitor	20.0	18.8	17.4	**22.7**	Udt-gr	Top 5%	4.0	20	17.44
Pozioti nib	Kinase inhibitor	pan-HER inhibitor	4.5	2.1	12.4	**22.2**	Udt-gr	Top 5%	15.9	1	0
NVP-BGT226	Kinase inhibitor	PI3K/mTOR inhibitor	20.3	19.7	15.4	**21.7**	Udt-gr	Top 5%	3.2	24	16.55
PF-04691502	Kinase inhibitor	PI3K/mTOR inhibitor	18.0	16.9	19.6	**21.3**	Udt-gr	Top 5%	3.1	25	16.7
Canertinib	Kinase inhibitor	pan-HER inhibitor	7.4	9.0	9.9	**20.2**	Udt-gr	Top 10%	11.4	2	8.44
Omipalisib	Kinase inhibitor	PI3K/mTOR inhibitor	19.1	18.2	18.4	**19.9**	Udt-gr	Top 10%	1.3	37	15.88
Dactolisib	Kinase inhibitor	mTOR/(PI3K) inhibitor	16.5	17.0	13.1	**19.1**	Udt-gr	Top 10%	3.6	23	13.36
Triciribine	Kinase inhibitor	AKT inhibitor	12.3	11.5	10.1	**18.4**	Udt-gr	Top 10%	7.1	8	8.87
Gedatolisib	Kinase inhibitor	PI3K/mTOR inhibitor	13.9	15.9	9.1	**17.4**	Udt-gr	Top 10%	4.4	17	12.79
Pracinostat	Differentiating/ epigenetic modifier	HDAC inhibitor	16.4	17.2	13.2	**17.4**	Udt-gr	Top 10%	1.8	34	14.5
MLN-0128	Kinase inhibitor	mTOR inhibitor	12.6	13.3	13.0	**17.1**	Udt-gr	Top 10%	4.1	18	9.78
Sabutoclax	Apoptotic modulator	pan-Bcl-2 family inhibitor	14.5	12.6	10.5	**16.4**	Udt-gr	Top 10%	3.9	21	12.01
KX2-391	Kinase inhibitor	non-ATP competitive Src inhibitor	13.7	22.3	**24.0**	17.9	TP53-gr	Top 5%	6.0	8	10.42
Rigosertib	Kinase inhibitor	PLK1 inhibitor, non-ATP-comp; Ras-Raf interaction inhibitor	10.3	20.5	**23.3**	17.1	TP53-gr	Top 5%	7.3	4	9.63
MK1775	Kinase inhibitor	Wee1 inhibitor	19.0	19.4	**22.4**	16.0	TP53-gr	Top 5%	4.3	16	16.48

Selected subgroup-targeted drugs depicted in Fig. 4E											
Drug	**Class explained**	**Mechanism/Targets**	**IDH-gr DSS**	**KRAS-gr DSS**	**TP53-gr DSS**	**Udt-gr DSS**	**Patient Group with Max. DSS**	**Overall Performance (DSS)**	**DSS(IDH-gr) - DSS(non-IDH-gr)**	**Differential Inter-group Sensitivity (rank)**	**Mixed Mutant DSS**
Disulfiram	Metabolic modifier	alcohol dehydrogenase inhibitor	**36.7**	24.3	13.2	30.5	IDH-gr	Top 1%	14.1	1	27.09
Pemetrexed	Metabolic modifier	Dihydrofolate reductase inhibitor	**20.1**	9.8	12.4	12.8	IDH-gr	Top 10%	8.4	13	11.08
Pevonedistat	Metabolic modifier	NAE inhibitor	**18.2**	16.9	8.5	10.7	IDH-gr	Top 10%	6.2	22	13.16
Vinorelbine	Conventional chemotherapy	Mitotic inhibitor. Vinca alkaloid microtubule depolymerizer	0.0	**31.3**	27.5	28.6	KRAS-gr	Top 1%	12.8	1	17.99
Patupilone	Conventional chemotherapy	Mitotic inhibitor, epothilone microtubule stabilizer	14.7	**28.3**	25.4	21.0	KRAS-gr	Top 2%	10.0	2	12.19
Docetaxel	Conventional chemotherapy	Mitotic inhibitor, taxane microtubule stabilizer	13.5	**29.9**	25.6	24.1	KRAS-gr	Top 2%	10.0	3	16.4
Paclitaxel	Conventional chemotherapy	Mitotic inhibitor, taxane microtubule stabilizer	21.1	**24.8**	18.9	18.1	KRAS-gr	Top 5%	8.4	4	7.61
Vincristine	Conventional chemotherapy	Mitotic inhibitor. Vinca alkaloid microtubule depolymerizer	14.2	**21.7**	19.0	17.7	KRAS-gr	Top 5%	6.3	5	10.55
Vinblastine	Conventional chemotherapy	Mitotic inhibitor. Vinca alkaloid microtubule depolymerizer	11.0	**21.2**	19.1	18.8	KRAS-gr	Top 5%	6.2	6	10.95
GSK-461364	Kinase inhibitor	PLK1 inhibitor	6.3	27.4	**28.1**	22.2	TP53-gr	Top 2%	9.5	1	7.45
KX2-391	Kinase inhibitor	non-ATP competitive Src inhibitor	13.7	22.3	**24.0**	17.9	TP53-gr	Top 5%	6.0	8	10.42
Rigosertib	Kinase inhibitor	PLK1 inhibitor, non-ATP-comp; Ras-Raf interaction inhibitor	10.3	20.5	**23.3**	17.1	TP53-gr	Top 5%	7.3	4	9.63
MK1775	Kinase inhibitor	Wee1 inhibitor	19.0	19.4	**22.4**	16.0	TP53-gr	Top 5%	4.3	16	16.48
AZD8055	Kinase inhibitor	mTOR inhibitor	20.0	18.8	17.4	**22.7**	Udt-gr	Top 5%	4.0	20	17.44
NVP-BGT226	Kinase inhibitor	PI3K/mTOR inhibitor	20.3	19.7	15.4	**21.7**	Udt-gr	Top 5%	3.2	24	16.55
PF-04691502	Kinase inhibitor	PI3K/mTOR inhibitor	18.0	16.9	19.6	**21.3**	Udt-gr	Top 5%	3.1	25	16.7
Omipalisib	Kinase inhibitor	PI3K/mTOR inhibitor	19.1	18.2	18.4	**19.9**	Udt-gr	Top 10%	1.3	37	15.88
Dactolisib	Kinase inhibitor	mTOR/(PI3K) inhibitor	16.5	17.0	13.1	**19.1**	Udt-gr	Top 10%	3.6	23	13.36
Gedatolisib	Kinase inhibitor	PI3K/mTOR inhibitor	13.9	15.9	9.1	**17.4**	Udt-gr	Top 10%	4.4	17	12.79
MLN-0128	Kinase inhibitor	mTOR inhibitor	12.6	13.3	13.0	**17.1**	Udt-gr	Top 10%	4.1	18	9.78

Table S10: Recurrent CNA cytobands across each group

Average number of enriched CNV segments in each group

Driver groups	Amplification	Deletions
IDH-gr	508	818
KRAS-gr	1127	2018
TP53-gr	2039	3207
Udt-gr	1665	2746

Number of cytobands with recurrent CNV segments reported by GISTIC2 and overlapping genes within the enriched peak of the cytobands

Driver groups	Cytobands	Genes
IDH-gr	22	353
KRAS-gr	14	209
TP53-gr	87	851
Udt-gr	94	631

	IDH-gr	KRAS-gr	TP53-gr	Udt-gr
1p11.2	0	0	1	0
1p12	0	0	0	1
1p36.11	5	0	4	0
1p36.12	0	0	0	2
1p36.21	0	8	0	0
1p36.32	0	0	1	0
1q21.3	0	0	1	1
1q24.3	0	0	0	3
1q42.13	0	0	2	0
2p13.1	0	0	1	0
2p13.3	0	0	0	3
2p21	0	0	0	3
2p24.1	0	0	1	0
2q12.1	0	0	0	2
2q13	0	0	0	3
2q14.3	0	0	0	1
2q21.2	0	0	2	0
2q31.2	0	0	0	2
2q32.2	0	0	3	0
3p14.2	0	9	0	0
3p14.3	26	0	0	0
3p21.31	139	0	3	4
3p22.2	0	0	2	0
3q22.3	0	0	0	3

3q26.2	0	0	1	0
3q27.2	12	0	0	0
3q29	0	0	3	1
4p11	0	0	0	2
4p14	0	0	0	3
4p15.31	0	0	0	1
4p16.3	3	3	3	0
4q28.2	0	0	5	4
4q28.3	0	0	0	1
4q31.1	0	0	1	0
4q34.1	0	0	0	2
4q35.2	3	0	0	0
5p13.3	0	0	0	3
5p15.33	0	0	5	2
5q13.2	0	0	2	0
5q14.1	0	0	4	5
5q15	0	0	0	3
5q21.3	0	3	0	0
5q31.3	0	0	0	1
5q32	2	0	0	0
5q35.1	0	0	0	2
6p12.3	0	0	4	0
6p21.1	0	0	1	1
6p21.2	0	0	0	1
6p21.33	0	0	9	7
6p22.1	0	0	28	0
6p22.3	0	6	0	0
6q12	0	0	1	0
6q21	0	2	42	3
6q26	2	0	0	0
6q27	0	0	0	2
7p11.2	0	0	22	22
7p13	6	0	37	37
7p21.3	0	0	13	13
7p22.1	0	0	36	0
7q11.21	0	0	29	0
7q11.23	0	0	0	76
7q21.3	0	0	0	36
7q22.1	0	0	120	120
7q31.2	0	0	14	14
7q36.1	0	0	58	0

8p11.1	0	0	0	1
8p11.23	19	0	0	0
8p12	0	0	6	4
8p21.2	0	24	0	0
8p21.3	0	40	0	0
8p23.1	0	0	1	0
8q11.23	0	0	0	5
8q21.2	0	0	0	1
8q22.3	0	0	0	2
8q24.12	0	0	0	1
8q24.21	0	0	1	0
9p21.3	5	11	8	2
9p22.1	0	0	0	5
9p24.1	0	0	3	0
9q22.1	0	0	0	2
9q22.33	0	0	1	0
9q33.3	0	0	3	0
9q34.3	4	0	1	0
10p11.22	0	0	2	5
10p13	0	0	0	4
10p14	0	0	0	1
10p15.1	0	0	3	0
10q11.21	0	0	0	2
10q22.3	0	0	2	0
10q24.33	0	0	0	1
10q26.11	0	0	0	1
10q26.13	0	0	3	4
11p11.12	0	0	1	1
11p11.2	19	0	3	0
11p14.1	0	0	0	1
11p15.2	0	0	2	0
11p15.5	0	0	0	7
11q13.2	0	0	3	0
11q13.3	0	0	4	3
11q24.1	0	0	0	2
12p11.1	0	0	1	1
12p12.3	0	0	0	3
12p13.31	0	0	3	0
12q13.13	0	0	2	0
12q13.2	49	0	0	0
12q21.32	0	2	0	0

12q22	0	0	2	0
12q23.1	0	0	3	0
12q24.11	0	0	0	4
13q12.11	0	0	2	4
13q12.2	3	0	0	0
13q31.1	0	0	3	3
13q32.3	0	0	0	2
13q34	0	0	1	0
14q11.2	0	0	1	1
14q24.3	0	0	0	2
14q32.2	0	0	3	0
14q32.33	2	0	2	0
15q11.2	0	0	3	0
15q14	4	0	0	1
15q22.2	0	23	0	0
15q24.3	0	0	2	0
15q26.1	0	0	0	3
16p11.2	0	0	1	9
16p13.3	0	0	5	0
16q22.1	0	0	6	0
16q23.1	0	0	0	1
16q24.2	0	0	0	3
17p11.2	0	0	0	6
17p13.2	0	0	0	2
17p13.3	0	0	8	0
17q11.2	0	0	3	0
17q21.31	0	0	0	2
17q21.32	0	0	0	2
17q23.3	0	0	2	0
17q24.3	0	0	0	2
17q25.3	0	0	1	0
18p11.32	0	0	3	3
18q11.2	0	0	0	5
18q12.2	0	0	2	0
18q21.1	4	0	0	0
18q23	0	4	3	4
19p12	0	3	0	0
19p13.11	0	0	2	0
19p13.3	37	0	2	2
19q13.12	0	0	0	2
19q13.2	0	0	1	0

19q13.33	2	0	0	0
19q13.41	0	0	0	2
19q13.42	0	0	3	3
19q13.43	0	0	0	3
20p11.21	0	0	29	2
20p11.22	0	0	0	2
20p13	0	0	86	0
20q11.21	0	0	49	0
20q13.12	0	0	0	79
20q13.31	0	0	15	0
20q13.33	0	0	84	5
21p11.1	0	0	0	1
21p11.2	0	0	2	0
21q11.2	0	0	0	2
21q21.1	0	0	0	4
21q22.11	0	71	3	0
21q22.2	3	0	0	0
21q22.3	0	0	1	4
22q11.21	4	0	0	0
22q12.1	0	0	4	0
22q13.1	0	0	2	0
22q13.2	0	0	0	4
22q13.31	0	0	0	8

Table S11: Genes that are signifiacntly amplified or deleted within recurrent CNA

Group	GeneName	EntrezID	cytoband	Neurtral (%)	Amplification (%)	Deletion (%)
IDH-gr	*C1orf63*	57035	1p36.11	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*RHCE*	6006	1p36.11	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*RHD*	6007	1p36.11	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TMEM50A*	23585	1p36.11	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TMEM57*	55219	1p36.11	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ABHD6*	57406	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ACOX2*	8309	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ALS2CL*	259173	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*AMIGO3*	386724	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*AMT*	275	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*APEH*	327	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*APPL1*	26060	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ARF4*	378	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ARHGEF3*	50650	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ARIH2*	10425	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ASB14*	142686	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ATRIP*	84126	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*BSN*	8927	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*BSN-AS2*	100132677	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*C3orf18*	51161	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*C3orf62*	375341	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*C3orf65*	646600	3q27.2	Neutral:46.1538461538462	Amp:30.7692307692308	Del:23.0769230769231
IDH-gr	*C3orf70*	285382	3q27.2	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*CACNA2D2*	9254	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CAMKV*	79012	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CAMP*	820	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CCDC12*	151903	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CCDC36*	339834	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CCDC51*	79714	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CCDC66*	285331	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CCDC71*	64925	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CCR1*	1230	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CCR2*	729230	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CCR3*	1232	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CCR5*	1234	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CCR9*	10803	3p21.31	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*CCRL2*	9034	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CDC25A*	993	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CDCP1*	64866	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923

IDH-gr	*CDHR4*	389118	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CELSR3*	1951	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CLEC3B*	7123	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*COL7A1*	1294	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*CSPG5*	10675	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*CXCR6*	10663	3p21.31	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*CYB561D2*	11068	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*DAG1*	1605	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*DALRD3*	55152	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*DGKG*	1608	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*DHX30*	22907	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*DNAH12*	201625	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*DNASE1L3*	1776	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*EHHADH*	1962	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*ERC2*	26059	3p14.3	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*ESRG*	790952	3p14.3	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*ETV5*	2119	3q27.2	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*EXOSC7*	23016	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*FAM107A*	11170	3p14.3	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*FAM208A*	23272	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*FAM212A*	389119	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*FBXW12*	285231	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*FLNB*	2317	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*FYCO1*	79443	3p21.31	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*GMPPB*	29925	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*GNAI2*	2771	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*GNAT1*	2779	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*GPX1*	2876	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*HESX1*	8820	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*HYAL1*	3373	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*HYAL2*	8692	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*HYAL3*	8372	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*IFRD2*	7866	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*IGF2BP2*	10644	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*IL17RD*	54756	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*IMPDH2*	3615	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*IP6K1*	9807	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*IP6K2*	51447	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*KCTD6*	200845	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*KIAA1143*	57456	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*KIF15*	56992	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923

IDH-gr	*KIF9*	64147	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*KLHDC8B*	200942	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*KLHL18*	23276	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*LAMB2*	3913	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*LARS2*	23395	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*LIMD1*	8994	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*LIPH*	200879	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*LRRC2*	79442	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*LRTM1*	57408	3p14.3	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*LTF*	4057	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*LZTFL1*	54585	3p21.31	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*MAP3K13*	9175	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*MAP4*	4134	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MIR1226*	100302232	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MIR191*	406966	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MIR3938*	100500875	3p14.3	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*MIR425*	494337	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MIR4271*	100422952	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MIR4443*	100616407	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MIR4793*	100616112	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*MIR564*	693149	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MIR711*	100313843	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*MON1A*	84315	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MST1*	4485	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*MST1R*	4486	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*MYL3*	4634	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*NAT6*	24142	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*NBEAL2*	23218	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*NCKIPSD*	51517	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*NDUFAF3*	25915	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*NICN1*	84276	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*NME6*	10201	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*NPRL2*	10641	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*NRADDP*	100129354	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*P4HTM*	54681	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PDE12*	201626	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PDHB*	5162	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PFKFB4*	5210	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PLXNB1*	5364	3p21.31	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*PRKAR2A*	5576	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PRSS42*	339906	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923

IDH-gr	*PRSS45*	377047	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PRSS46*	100287362	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PRSS50*	29122	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*PTH1R*	5745	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*PTPN23*	25930	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*PXK*	54899	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*QARS*	5859	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*QRICH1*	54870	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*RASSF1*	11186	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*RBM5*	10181	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*RBM6*	10180	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*RHOA*	387	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*RNF123*	63891	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*RPP14*	11102	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*RTP3*	83597	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SACM1L*	22908	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*SCAP*	22937	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SEMA3B*	7869	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*SEMA3F*	6405	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SENP2*	59343	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*SETD2*	29072	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SHISA5*	51246	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*SLC25A20*	788	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SLC26A6*	65010	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*SLC38A3*	10991	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SLC6A20*	54716	3p21.31	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*SLMAP*	7871	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SMARCC1*	6599	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SPATA12*	353324	3p14.3	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*SPINK8*	646424	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TCTA*	6988	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TDGF1*	6997	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TGM4*	7047	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TMEM115*	11070	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*TMEM158*	25907	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TMEM41A*	90407	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*TMEM42*	131616	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TMEM89*	440955	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*TMIE*	259236	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*TRA2B*	6434	3q27.2	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*TRAIP*	10293	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923

IDH-gr	*TREX1*	11277	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*TUSC2*	11334	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*UBA7*	7318	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*UCN2*	90226	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*UQCRC1*	7384	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*USP19*	10869	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*USP4*	7375	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*VPS8*	23355	3q27.2	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*WDR6*	11180	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*WNT5A*	7474	3p14.3	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*XCR1*	2829	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*ZDHHC3*	51304	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ZMYND10*	51364	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*ZNF197*	10168	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*ZNF35*	7584	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*ZNF445*	353274	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ZNF501*	115560	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*ZNF502*	91392	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*ZNF589*	51385	3p21.31	Neutral:7.69230769230769	Amp:0	Del:92.3076923076923
IDH-gr	*ZNF660*	285349	3p21.31	Neutral:15.3846153846154	Amp:0	Del:84.6153846153846
IDH-gr	*TRIML1*	339976	4q35.2	Neutral:38.4615384615385	Amp:0	Del:61.5384615384615
IDH-gr	*TRIML2*	205860	4q35.2	Neutral:38.4615384615385	Amp:0	Del:61.5384615384615
IDH-gr	*ZFP42*	132625	4q35.2	Neutral:38.4615384615385	Amp:0	Del:61.5384615384615
IDH-gr	*ZNF595*	152687	4p16.3	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*ZNF718*	255403	4p16.3	Neutral:84.6153846153846	Amp:0	Del:15.3846153846154
IDH-gr	*ZNF876P*	642280	4p16.3	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*GRXCR2*	643226	5q32	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*SH3RF2*	153769	5q32	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*CAHM*	100526820	6q26	Neutral:30.7692307692308	Amp:0	Del:69.2307692307692
IDH-gr	*QKI*	9444	6q26	Neutral:23.0769230769231	Amp:0	Del:76.9230769230769
IDH-gr	*DBNL*	28988	7p13	Neutral:46.1538461538462	Amp:38.4615384615385	Del:15.3846153846154
IDH-gr	*PGAM2*	5224	7p13	Neutral:46.1538461538462	Amp:38.4615384615385	Del:15.3846153846154
IDH-gr	*POLR2J4*	84820	7p13	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*SPDYE1*	285955	7p13	Neutral:53.8461538461538	Amp:23.0769230769231	Del:23.0769230769231
IDH-gr	*UBE2D4*	51619	7p13	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*URGCP*	55665	7p13	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*ADRB3*	155	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*ASH2L*	9070	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*BAG4*	9530	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*BRF2*	55290	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*DDHD2*	23259	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308

IDH-gr	*EIF4EBP1*	1978	8p11.23	Neutral:53.8461538461538	Amp:7.69230769230769	Del:38.4615384615385
IDH-gr	*ERLIN2*	11160	8p11.23	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*FGFR1*	2260	8p11.23	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*GOT1L1*	137362	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*GPR124*	25960	8p11.23	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*KCNU1*	157855	8p11.23	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*LETM2*	137994	8p11.23	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*LSM1*	27257	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*PPAPDC1B*	84513	8p11.23	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*PROSC*	11212	8p11.23	Neutral:69.2307692307692	Amp:23.0769230769231	Del:7.69230769230769
IDH-gr	*RAB11FIP1*	80223	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*STAR*	6770	8p11.23	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*WHSC1L1*	54904	8p11.23	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*ZNF703*	80139	8p11.23	Neutral:69.2307692307692	Amp:23.0769230769231	Del:7.69230769230769
IDH-gr	*C9orf53*	51198	9p21.3	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*CDKN2A*	1029	9p21.3	Neutral:61.5384615384615	Amp:0	Del:38.4615384615385
IDH-gr	*CDKN2B-AS1*	100048912	9p21.3	Neutral:61.5384615384615	Amp:0	Del:38.4615384615385
IDH-gr	*MIR31HG*	554202	9p21.3	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*MRPL41*	64975	9q34.3	Neutral:38.4615384615385	Amp:0	Del:61.5384615384615
IDH-gr	*MTAP*	4507	9p21.3	Neutral:61.5384615384615	Amp:0	Del:38.4615384615385
IDH-gr	*SNORA17*	677804	9q34.3	Neutral:46.1538461538462	Amp:0	Del:53.8461538461538
IDH-gr	*SNORA43*	677824	9q34.3	Neutral:46.1538461538462	Amp:0	Del:53.8461538461538
IDH-gr	*ZMYND19*	116225	9q34.3	Neutral:30.7692307692308	Amp:7.69230769230769	Del:61.5384615384615
IDH-gr	*ACP2*	53	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*ARFGAP2*	84364	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*C11orf49*	79096	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*CELF1*	10658	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*CKAP5*	9793	11p11.2	Neutral:76.9230769230769	Amp:0	Del:23.0769230769231
IDH-gr	*DDB2*	1643	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*F2*	2147	11p11.2	Neutral:76.9230769230769	Amp:0	Del:23.0769230769231
IDH-gr	*LRP4*	4038	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*MADD*	8567	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*MYBPC3*	4607	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*NDUFS3*	4722	11p11.2	Neutral:76.9230769230769	Amp:0	Del:23.0769230769231
IDH-gr	*NR1H3*	10062	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*PACSIN3*	29763	11p11.2	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*PSMC3*	5702	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*PTPMT1*	114971	11p11.2	Neutral:76.9230769230769	Amp:0	Del:23.0769230769231
IDH-gr	*RAPSN*	5913	11p11.2	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*SLC39A13*	91252	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*SNORD67*	692108	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308

IDH-gr	*SPI1*	6688	11p11.2	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*BLOC1S1*	2647	12q13.2	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*CD63*	967	12q13.2	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*CDK2*	1017	12q13.2	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*DCD*	117159	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*DGKA*	1606	12q13.2	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*DNAJC14*	85406	12q13.2	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*ERBB3*	2065	12q13.2	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*ESYT1*	23344	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*GDF11*	10220	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*GLYCAM1*	644076	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*IKZF4*	64375	12q13.2	Neutral:84.6153846153846	Amp:0	Del:15.3846153846154
IDH-gr	*ITGA7*	3679	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*LACRT*	90070	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*METTL7B*	196410	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*MMP19*	4327	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*MUCL1*	118430	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*MYL6*	4637	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*MYL6B*	140465	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*NEUROD4*	58158	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR10A7*	121364	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*OR10P1*	121130	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*OR6C1*	390321	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*OR6C2*	341416	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR6C3*	254786	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*OR6C4*	341418	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*OR6C6*	283365	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR6C65*	403282	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR6C68*	403284	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR6C70*	390327	12q13.2	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*OR6C74*	254783	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR6C75*	390323	12q13.2	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*OR6C76*	390326	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR9K2*	441639	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*ORMDL2*	29095	12q13.2	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*PA2G4*	5036	12q13.2	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*PDE1B*	5153	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*PMEL*	6490	12q13.2	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*PPP1R1A*	5502	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*RAB5B*	5869	12q13.2	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*RDH5*	5959	12q13.2	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769

IDH-gr	*RNF41*	10193	12q13.2	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*RPL41*	6171	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*RPS26*	6231	12q13.2	Neutral:84.6153846153846	Amp:0	Del:15.3846153846154
IDH-gr	*SARNP*	84324	12q13.2	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*SMARCC2*	6601	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*SUOX*	6821	12q13.2	Neutral:92.3076923076923	Amp:0	Del:7.69230769230769
IDH-gr	*TMEM198B*	440104	12q13.2	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*WIBG*	84305	12q13.2	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*ZC3H10*	84872	12q13.2	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*GTF3A*	2971	13q12.2	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*RASL11A*	387496	13q12.2	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*RPL21*	6144	13q12.2	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*C14orf80*	283643	14q32.33	Neutral:38.4615384615385	Amp:7.69230769230769	Del:53.8461538461538
IDH-gr	*CRIP1*	1396	14q32.33	Neutral:38.4615384615385	Amp:7.69230769230769	Del:53.8461538461538
IDH-gr	*GOLGA8A*	23015	15q14	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*GOLGA8B*	440270	15q14	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*LPCAT4*	254531	15q14	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*MIR1233-1*	100302160	15q14	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*HDHD2*	84064	18q21.1	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*KATNAL2*	83473	18q21.1	Neutral:53.8461538461538	Amp:30.7692307692308	Del:15.3846153846154
IDH-gr	*TCEB3B*	51224	18q21.1	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*TCEB3C*	162699	18q21.1	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*ABCA7*	10347	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*ARID3A*	1820	19p13.3	Neutral:53.8461538461538	Amp:15.3846153846154	Del:30.7692307692308
IDH-gr	*AZU1*	566	19p13.3	Neutral:69.2307692307692	Amp:0	Del:30.7692307692308
IDH-gr	*BSG*	682	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*C2CD4C*	126567	19p13.3	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*CDC34*	997	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*CFD*	1675	19p13.3	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*CNN2*	1265	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*ELANE*	1991	19p13.3	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*FGF22*	27006	19p13.3	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*FSTL3*	10272	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*FUZ*	80199	19q13.33	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*GRIN3B*	116444	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*GZMM*	3004	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*HCN2*	610	19p13.3	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*HMHA1*	23526	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*KISS1R*	84634	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*LPPR3*	79948	19p13.3	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*MADCAM1*	8174	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154

IDH-gr	*MED16*	10025	19p13.3	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*MED25*	81857	19q13.33	Neutral:53.8461538461538	Amp:15.3846153846154	Del:30.7692307692308
IDH-gr	*MIER2*	54531	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*MIR3187*	100422854	19p13.3	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*MIR4745*	100616459	19p13.3	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*ODF3L2*	284451	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*OR4F17*	81099	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*PALM*	5064	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*POLRMT*	5442	19p13.3	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*PPAP2C*	8612	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*PRSS57*	400668	19p13.3	Neutral:53.8461538461538	Amp:15.3846153846154	Del:30.7692307692308
IDH-gr	*PRTN3*	5657	19p13.3	Neutral:61.5384615384615	Amp:7.69230769230769	Del:30.7692307692308
IDH-gr	*PTBP1*	5725	19p13.3	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*R3HDM4*	91300	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*RNF126*	55658	19p13.3	Neutral:61.5384615384615	Amp:23.0769230769231	Del:15.3846153846154
IDH-gr	*SHC2*	25759	19p13.3	Neutral:84.6153846153846	Amp:7.69230769230769	Del:7.69230769230769
IDH-gr	*THEG*	51298	19p13.3	Neutral:76.9230769230769	Amp:15.3846153846154	Del:7.69230769230769
IDH-gr	*TPGS1*	91978	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*WASH5P*	375690	19p13.3	Neutral:69.2307692307692	Amp:15.3846153846154	Del:15.3846153846154
IDH-gr	*WDR18*	57418	19p13.3	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*B3GALT5*	10317	21q22.2	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*IGSF5*	150084	21q22.2	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*PCP4*	5121	21q22.2	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*C22orf39*	128977	22q11.21	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
IDH-gr	*HIRA*	7290	22q11.21	Neutral:76.9230769230769	Amp:7.69230769230769	Del:15.3846153846154
IDH-gr	*MRPL40*	64976	22q11.21	Neutral:61.5384615384615	Amp:15.3846153846154	Del:23.0769230769231
IDH-gr	*UFD1L*	7353	22q11.21	Neutral:69.2307692307692	Amp:7.69230769230769	Del:23.0769230769231
KRAS-gr	*HNRNPCL1*	343069	1p36.21	Neutral:60	Amp:0	Del:40
KRAS-gr	*PRAMEF10*	343071	1p36.21	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*PRAMEF11*	440560	1p36.21	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*PRAMEF2*	65122	1p36.21	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*PRAMEF22*	653606	1p36.21	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*PRAMEF4*	400735	1p36.21	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*PRAMEF6*	440561	1p36.21	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*PRAMEF7*	441871	1p36.21	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*C3orf14*	57415	3p14.2	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*C3orf67*	200844	3p14.2	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*CADPS*	8618	3p14.2	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*FAM3D*	131177	3p14.2	Neutral:60	Amp:0	Del:40
KRAS-gr	*FEZF2*	55079	3p14.2	Neutral:46.6666666666667	Amp:13.3333333333333	Del:40
KRAS-gr	*FHIT*	2272	3p14.2	Neutral:60	Amp:0	Del:40

KRAS-gr	*PTPRG*	5793	3p14.2	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*SNTN*	132203	3p14.2	Neutral:46.6666666666667	Amp:0	Del:53.3333333333333
KRAS-gr	*SYNPR*	132204	3p14.2	Neutral:46.6666666666667	Amp:0	Del:53.3333333333333
KRAS-gr	*FAM193A*	8603	4p16.3	Neutral:80	Amp:6.66666666666667	Del:13.3333333333333
KRAS-gr	*SH3BP2*	6452	4p16.3	Neutral:66.6666666666667	Amp:13.3333333333333	Del:20
KRAS-gr	*TNIP2*	79155	4p16.3	Neutral:66.6666666666667	Amp:13.3333333333333	Del:20
KRAS-gr	*FBXL17*	64839	5q21.3	Neutral:86.6666666666667	Amp:6.66666666666667	Del:6.66666666666667
KRAS-gr	*FER*	2241	5q21.3	Neutral:73.3333333333333	Amp:6.66666666666667	Del:20
KRAS-gr	*PJA2*	9867	5q21.3	Neutral:73.3333333333333	Amp:13.3333333333333	Del:13.3333333333333
KRAS-gr	*FAM8A1*	51439	6p22.3	Neutral:60	Amp:6.66666666666667	Del:33.3333333333333
KRAS-gr	*KDM1B*	221656	6p22.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*KIF13A*	63971	6p22.3	Neutral:60	Amp:6.66666666666667	Del:33.3333333333333
KRAS-gr	*NHLRC1*	378884	6p22.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*NUP153*	9972	6p22.3	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*OSTM1*	28962	6q21	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*SEC63*	11231	6q21	Neutral:46.6666666666667	Amp:0	Del:53.3333333333333
KRAS-gr	*TPMT*	7172	6p22.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*ADAM28*	10863	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*ADAM7*	8756	8p21.2	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*ADAMDEC1*	27299	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*ADRA1A*	148	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*ATP6V1B2*	526	8p21.3	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*BIN3*	55909	8p21.3	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*BMP1*	649	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*BNIP3L*	665	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*C8orf58*	541565	8p21.3	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*CDCA2*	157313	8p21.2	Neutral:26.6666666666667	Amp:13.3333333333333	Del:60
KRAS-gr	*CHMP7*	91782	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*CHRNA2*	1135	8p21.2	Neutral:26.6666666666667	Amp:13.3333333333333	Del:60
KRAS-gr	*CSGALNACT1*	55790	8p21.3	Neutral:33.3333333333333	Amp:6.66666666666667	Del:60
KRAS-gr	*DOCK5*	80005	8p21.2	Neutral:26.6666666666667	Amp:13.3333333333333	Del:60
KRAS-gr	*DOK2*	9046	8p21.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*DPYSL2*	1808	8p21.2	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*EBF2*	64641	8p21.2	Neutral:33.3333333333333	Amp:6.66666666666667	Del:60
KRAS-gr	*EGR3*	1960	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*ENTPD4*	9583	8p21.3	Neutral:20	Amp:13.3333333333333	Del:66.6666666666667
KRAS-gr	*EPHX2*	2053	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*FAM160B2*	64760	8p21.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*FGF17*	8822	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*GFRA2*	2675	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*GNRH1*	2796	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333

KRAS-gr	*HR*	55806	8p21.3	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*INTS10*	55174	8p21.3	Neutral:33.3333333333333	Amp:6.66666666666667	Del:60
KRAS-gr	*KCTD9*	54793	8p21.2	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*LGI3*	203190	8p21.3	Neutral:53.3333333333333	Amp:0	Del:46.6666666666667
KRAS-gr	*LOXL2*	4017	8p21.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*LPL*	4023	8p21.3	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*LZTS1*	11178	8p21.3	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*MIR320A*	407037	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*NEFL*	4747	8p21.2	Neutral:26.6666666666667	Amp:13.3333333333333	Del:60
KRAS-gr	*NEFM*	4741	8p21.2	Neutral:33.3333333333333	Amp:6.66666666666667	Del:60
KRAS-gr	*NKX2-6*	137814	8p21.2	Neutral:13.3333333333333	Amp:26.6666666666667	Del:60
KRAS-gr	*NKX3-1*	4824	8p21.2	Neutral:13.3333333333333	Amp:13.3333333333333	Del:73.3333333333333
KRAS-gr	*NPM2*	10361	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*NUDT18*	79873	8p21.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*PDLIM2*	64236	8p21.3	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*PEBP4*	157310	8p21.3	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*PHYHIP*	9796	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*PIWIL2*	55124	8p21.3	Neutral:33.3333333333333	Amp:6.66666666666667	Del:60
KRAS-gr	*PNMA2*	10687	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*POLR3D*	661	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*PPP2R2A*	5520	8p21.2	Neutral:26.6666666666667	Amp:6.66666666666667	Del:66.6666666666667
KRAS-gr	*PPP3CC*	5533	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*PTK2B*	2185	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*R3HCC1*	203069	8p21.3	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*REEP4*	80346	8p21.3	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*RHOBTB2*	23221	8p21.3	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*SFTPC*	6440	8p21.3	Neutral:46.6666666666667	Amp:0	Del:53.3333333333333
KRAS-gr	*SH2D4A*	63898	8p21.3	Neutral:33.3333333333333	Amp:6.66666666666667	Del:60
KRAS-gr	*SLC18A1*	6570	8p21.3	Neutral:33.3333333333333	Amp:6.66666666666667	Del:60
KRAS-gr	*SLC25A37*	51312	8p21.2	Neutral:20	Amp:13.3333333333333	Del:66.6666666666667
KRAS-gr	*SLC39A14*	23516	8p21.3	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*SORBS3*	10174	8p21.3	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*STC1*	6781	8p21.2	Neutral:33.3333333333333	Amp:13.3333333333333	Del:53.3333333333333
KRAS-gr	*STMN4*	81551	8p21.2	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*TNFRSF10A*	8797	8p21.3	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*TNFRSF10B*	8795	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*TNFRSF10C*	8794	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*TNFRSF10D*	8793	8p21.3	Neutral:46.6666666666667	Amp:6.66666666666667	Del:46.6666666666667
KRAS-gr	*TRIM35*	23087	8p21.2	Neutral:40	Amp:13.3333333333333	Del:46.6666666666667
KRAS-gr	*XPO7*	23039	8p21.3	Neutral:40	Amp:6.66666666666667	Del:53.3333333333333
KRAS-gr	*C9orf53*	51198	9p21.3	Neutral:33.3333333333333	Amp:0	Del:66.6666666666667

KRAS-gr	*CDKN2A*	1029	9p21.3	Neutral:33.3333333333333	Amp:0	Del:66.6666666666667
KRAS-gr	*CDKN2B*	1030	9p21.3	Neutral:33.3333333333333	Amp:0	Del:66.6666666666667
KRAS-gr	*CDKN2B-AS1*	100048912	9p21.3	Neutral:33.3333333333333	Amp:0	Del:66.6666666666667
KRAS-gr	*DMRTA1*	63951	9p21.3	Neutral:40	Amp:0	Del:60
KRAS-gr	*IFNA1*	3439	9p21.3	Neutral:33.3333333333333	Amp:0	Del:66.6666666666667
KRAS-gr	*IFNA8*	3445	9p21.3	Neutral:40	Amp:0	Del:60
KRAS-gr	*IFNE*	338376	9p21.3	Neutral:40	Amp:0	Del:60
KRAS-gr	*MIR31*	407035	9p21.3	Neutral:40	Amp:0	Del:60
KRAS-gr	*MIR31HG*	554202	9p21.3	Neutral:40	Amp:0	Del:60
KRAS-gr	*MTAP*	4507	9p21.3	Neutral:40	Amp:0	Del:60
KRAS-gr	*C12orf50*	160419	12q21.32	Neutral:66.6666666666667	Amp:20	Del:13.3333333333333
KRAS-gr	*MKRN9P*	400058	12q21.32	Neutral:66.6666666666667	Amp:20	Del:13.3333333333333
KRAS-gr	*ANXA2*	302	15q22.2	Neutral:73.3333333333333	Amp:13.3333333333333	Del:13.3333333333333
KRAS-gr	*APH1B*	83464	15q22.2	Neutral:100	Amp:0	Del:0
KRAS-gr	*BNIP2*	663	15q22.2	Neutral:73.3333333333333	Amp:6.66666666666667	Del:20
KRAS-gr	*C2CD4A*	145741	15q22.2	Neutral:80	Amp:6.66666666666667	Del:13.3333333333333
KRAS-gr	*C2CD4B*	388125	15q22.2	Neutral:60	Amp:6.66666666666667	Del:33.3333333333333
KRAS-gr	*CA12*	771	15q22.2	Neutral:100	Amp:0	Del:0
KRAS-gr	*CCNB2*	9133	15q22.2	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*FAM81A*	145773	15q22.2	Neutral:66.6666666666667	Amp:6.66666666666667	Del:26.6666666666667
KRAS-gr	*FOXB1*	27023	15q22.2	Neutral:80	Amp:6.66666666666667	Del:13.3333333333333
KRAS-gr	*GCNT3*	9245	15q22.2	Neutral:66.6666666666667	Amp:6.66666666666667	Del:26.6666666666667
KRAS-gr	*GTF2A2*	2958	15q22.2	Neutral:66.6666666666667	Amp:6.66666666666667	Del:26.6666666666667
KRAS-gr	*LACTB*	114294	15q22.2	Neutral:86.6666666666667	Amp:6.66666666666667	Del:6.66666666666667
KRAS-gr	*LDHAL6B*	92483	15q22.2	Neutral:80	Amp:6.66666666666667	Del:13.3333333333333
KRAS-gr	*MIR190A*	406965	15q22.2	Neutral:93.3333333333333	Amp:6.66666666666667	Del:0
KRAS-gr	*MIR2116*	100313886	15q22.2	Neutral:80	Amp:6.66666666666667	Del:13.3333333333333
KRAS-gr	*MYO1E*	4643	15q22.2	Neutral:86.6666666666667	Amp:0	Del:13.3333333333333
KRAS-gr	*NARG2*	79664	15q22.2	Neutral:66.6666666666667	Amp:6.66666666666667	Del:26.6666666666667
KRAS-gr	*RAB8B*	51762	15q22.2	Neutral:93.3333333333333	Amp:6.66666666666667	Del:0
KRAS-gr	*RORA*	6095	15q22.2	Neutral:66.6666666666667	Amp:13.3333333333333	Del:20
KRAS-gr	*RPS27L*	51065	15q22.2	Neutral:93.3333333333333	Amp:6.66666666666667	Del:0
KRAS-gr	*TLN2*	83660	15q22.2	Neutral:93.3333333333333	Amp:6.66666666666667	Del:0
KRAS-gr	*TPM1*	7168	15q22.2	Neutral:100	Amp:0	Del:0
KRAS-gr	*VPS13C*	54832	15q22.2	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*CTDP1*	9150	18q23	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*KCNG2*	26251	18q23	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*NFATC1*	4772	18q23	Neutral:46.6666666666667	Amp:13.3333333333333	Del:40
KRAS-gr	*PQLC1*	80148	18q23	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*ZNF675*	171392	19p12	Neutral:66.6666666666667	Amp:0	Del:33.3333333333333
KRAS-gr	*ZNF724P*	440519	19p12	Neutral:66.6666666666667	Amp:0	Del:33.3333333333333

KRAS-gr	*ZNF91*	7644	19p12	Neutral:80	Amp:0	Del:20
KRAS-gr	*ATP5O*	539	21q22.11	Neutral:66.6666666666667	Amp:13.3333333333333	Del:20
KRAS-gr	*C21orf119*	84996	21q22.11	Neutral:86.6666666666667	Amp:0	Del:13.3333333333333
KRAS-gr	*C21orf49*	54067	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*C21orf54*	728409	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*C21orf59*	56683	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*C21orf62*	56245	21q22.11	Neutral:73.3333333333333	Amp:6.66666666666667	Del:20
KRAS-gr	*CLDN17*	26285	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*CLDN8*	9073	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*CRYZL1*	9946	21q22.11	Neutral:66.6666666666667	Amp:0	Del:33.3333333333333
KRAS-gr	*DNAJC28*	54943	21q22.11	Neutral:53.3333333333333	Amp:6.66666666666667	Del:40
KRAS-gr	*DONSON*	29980	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*GART*	2618	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*HUNK*	30811	21q22.11	Neutral:73.3333333333333	Amp:6.66666666666667	Del:20
KRAS-gr	*IFNAR1*	3454	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*IFNAR2*	3455	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*IFNGR2*	3460	21q22.11	Neutral:66.6666666666667	Amp:0	Del:33.3333333333333
KRAS-gr	*IL10RB*	3588	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*ITSN1*	6453	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*KCNE2*	9992	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*KRTAP11-1*	337880	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*KRTAP13-1*	140258	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP13-2*	337959	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP13-3*	337960	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP13-4*	284827	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP15-1*	254950	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP19-1*	337882	21q22.11	Neutral:46.6666666666667	Amp:20	Del:33.3333333333333
KRAS-gr	*KRTAP19-2*	337969	21q22.11	Neutral:46.6666666666667	Amp:20	Del:33.3333333333333
KRAS-gr	*KRTAP19-3*	337970	21q22.11	Neutral:46.6666666666667	Amp:20	Del:33.3333333333333
KRAS-gr	*KRTAP19-4*	337971	21q22.11	Neutral:46.6666666666667	Amp:20	Del:33.3333333333333
KRAS-gr	*KRTAP19-5*	337972	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP19-6*	337973	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP19-7*	337974	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP19-8*	728299	21q22.11	Neutral:66.6666666666667	Amp:13.3333333333333	Del:20
KRAS-gr	*KRTAP20-1*	337975	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP20-2*	337976	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*KRTAP20-3*	337985	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*KRTAP20-4*	100151643	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*KRTAP21-1*	337977	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*KRTAP21-2*	337978	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*KRTAP21-3*	100288323	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667

KRAS-gr	*KRTAP22-1*	337979	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP22-2*	100288287	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP23-1*	337963	21q22.11	Neutral:46.6666666666667	Amp:20	Del:33.3333333333333
KRAS-gr	*KRTAP24-1*	643803	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP25-1*	100131902	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP26-1*	388818	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP27-1*	643812	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*KRTAP6-1*	337966	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP6-2*	337967	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP6-3*	337968	21q22.11	Neutral:53.3333333333333	Amp:20	Del:26.6666666666667
KRAS-gr	*KRTAP7-1*	337878	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*KRTAP8-1*	337879	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*LINC00159*	100551499	21q22.11	Neutral:73.3333333333333	Amp:6.66666666666667	Del:20
KRAS-gr	*LINC00307*	266919	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*LINC00310*	114036	21q22.11	Neutral:66.6666666666667	Amp:6.66666666666667	Del:26.6666666666667
KRAS-gr	*MIR4327*	100422891	21q22.11	Neutral:53.3333333333333	Amp:13.3333333333333	Del:33.3333333333333
KRAS-gr	*MIS18A*	54069	21q22.11	Neutral:73.3333333333333	Amp:6.66666666666667	Del:20
KRAS-gr	*MRAP*	56246	21q22.11	Neutral:73.3333333333333	Amp:6.66666666666667	Del:20
KRAS-gr	*MRPS6*	64968	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*OLIG1*	116448	21q22.11	Neutral:66.6666666666667	Amp:6.66666666666667	Del:26.6666666666667
KRAS-gr	*OLIG2*	10215	21q22.11	Neutral:60	Amp:13.3333333333333	Del:26.6666666666667
KRAS-gr	*SCAF4*	57466	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*SLC5A3*	6526	21q22.11	Neutral:66.6666666666667	Amp:6.66666666666667	Del:26.6666666666667
KRAS-gr	*SNORA80*	677846	21q22.11	Neutral:86.6666666666667	Amp:0	Del:13.3333333333333
KRAS-gr	*SOD1*	6647	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*SON*	6651	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*SYNJ1*	8867	21q22.11	Neutral:73.3333333333333	Amp:0	Del:26.6666666666667
KRAS-gr	*TCP10L*	140290	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*TIAM1*	7074	21q22.11	Neutral:80	Amp:0	Del:20
KRAS-gr	*TMEM50B*	757	21q22.11	Neutral:60	Amp:6.66666666666667	Del:33.3333333333333
KRAS-gr	*URB1*	9875	21q22.11	Neutral:73.3333333333333	Amp:13.3333333333333	Del:13.3333333333333
TP53-gr	*ACTA1*	58	1q42.13	Neutral:37.2093023255814	Amp:48.8372093023256	Del:13.953488372093
TP53-gr	*AJAP1*	55966	1p36.32	Neutral:46.5116279069767	Amp:32.5581395348837	Del:20.9302325581395
TP53-gr	*EMBP1*	647121	1p11.2	Neutral:34.8837209302326	Amp:25.5813953488372	Del:39.5348837209302
TP53-gr	*FAM110D*	79927	1p36.11	Neutral:44.1860465116279	Amp:18.6046511627907	Del:37.2093023255814
TP53-gr	*NUP133*	55746	1q42.13	Neutral:53.4883720930233	Amp:37.2093023255814	Del:9.30232558139535
TP53-gr	*PDIK1L*	149420	1p36.11	Neutral:48.8372093023256	Amp:9.30232558139535	Del:41.8604651162791
TP53-gr	*TCHH*	7062	1q21.3	Neutral:16.2790697674419	Amp:76.7441860465116	Del:6.97674418604651
TP53-gr	*TRIM63*	84676	1p36.11	Neutral:55.8139534883721	Amp:13.953488372093	Del:30.2325581395349
TP53-gr	*ZNF593*	51042	1p36.11	Neutral:44.1860465116279	Amp:18.6046511627907	Del:37.2093023255814
TP53-gr	*ANKRD30BL*	554226	2q21.2	Neutral:67.4418604651163	Amp:16.2790697674419	Del:16.2790697674419

TP53-gr	*C2orf27B*	408029	2q21.2	Neutral:53.4883720930233	Amp:27.906976744186	Del:18.6046511627907
TP53-gr	*COL3A1*	1281	2q32.2	Neutral:34.8837209302326	Amp:48.8372093023256	Del:16.2790697674419
TP53-gr	*DIRC1*	116093	2q32.2	Neutral:39.5348837209302	Amp:44.1860465116279	Del:16.2790697674419
TP53-gr	*KLHL29*	114818	2p24.1	Neutral:55.8139534883721	Amp:32.5581395348837	Del:11.6279069767442
TP53-gr	*MIR1245A*	100302219	2q32.2	Neutral:37.2093023255814	Amp:46.5116279069767	Del:16.2790697674419
TP53-gr	*PCGF1*	84759	2p13.1	Neutral:44.1860465116279	Amp:44.1860465116279	Del:11.6279069767442
TP53-gr	*ARIH2*	10425	3p21.31	Neutral:51.1627906976744	Amp:9.30232558139535	Del:39.5348837209302
TP53-gr	*EPM2AIP1*	9852	3p22.2	Neutral:60.4651162790698	Amp:9.30232558139535	Del:30.2325581395349
TP53-gr	*MECOM*	2122	3q26.2	Neutral:34.8837209302326	Amp:55.8139534883721	Del:9.30232558139535
TP53-gr	*MLH1*	4292	3p22.2	Neutral:69.7674418604651	Amp:2.32558139534884	Del:27.906976744186
TP53-gr	*PAK2*	5062	3q29	Neutral:20.9302325581395	Amp:39.5348837209302	Del:39.5348837209302
TP53-gr	*PIGX*	54965	3q29	Neutral:41.8604651162791	Amp:32.5581395348837	Del:25.5813953488372
TP53-gr	*PRKAR2A*	5576	3p21.31	Neutral:37.2093023255814	Amp:9.30232558139535	Del:53.4883720930233
TP53-gr	*SENP5*	205564	3q29	Neutral:55.8139534883721	Amp:25.5813953488372	Del:18.6046511627907
TP53-gr	*SLC25A20*	788	3p21.31	Neutral:39.5348837209302	Amp:11.6279069767442	Del:48.8372093023256
TP53-gr	*C4orf29*	80167	4q28.2	Neutral:20.9302325581395	Amp:4.65116279069767	Del:74.4186046511628
TP53-gr	*FAM53A*	152877	4p16.3	Neutral:39.5348837209302	Amp:23.2558139534884	Del:37.2093023255814
TP53-gr	*LARP1B*	55132	4q28.2	Neutral:27.906976744186	Amp:2.32558139534884	Del:69.7674418604651
TP53-gr	*MFSD8*	256471	4q28.2	Neutral:30.2325581395349	Amp:4.65116279069767	Del:65.1162790697674
TP53-gr	*PGRMC2*	10424	4q28.2	Neutral:37.2093023255814	Amp:9.30232558139535	Del:53.4883720930233
TP53-gr	*PLK4*	10733	4q28.2	Neutral:25.5813953488372	Amp:6.97674418604651	Del:67.4418604651163
TP53-gr	*SCOC*	60592	4q31.1	Neutral:39.5348837209302	Amp:18.6046511627907	Del:41.8604651162791
TP53-gr	*SLBP*	7884	4p16.3	Neutral:39.5348837209302	Amp:11.6279069767442	Del:48.8372093023256
TP53-gr	*TMEM129*	92305	4p16.3	Neutral:46.5116279069767	Amp:23.2558139534884	Del:30.2325581395349
TP53-gr	*BHMT*	635	5q14.1	Neutral:62.7906976744186	Amp:6.97674418604651	Del:30.2325581395349
TP53-gr	*C5orf38*	153571	5p15.33	Neutral:34.8837209302326	Amp:51.1627906976744	Del:13.953488372093
TP53-gr	*DMGDH*	29958	5q14.1	Neutral:51.1627906976744	Amp:13.953488372093	Del:34.8837209302326
TP53-gr	*HOMER1*	9456	5q14.1	Neutral:44.1860465116279	Amp:11.6279069767442	Del:44.1860465116279
TP53-gr	*IRX1*	79192	5p15.33	Neutral:41.8604651162791	Amp:46.5116279069767	Del:11.6279069767442
TP53-gr	*IRX2*	153572	5p15.33	Neutral:37.2093023255814	Amp:51.1627906976744	Del:11.6279069767442
TP53-gr	*IRX4*	50805	5p15.33	Neutral:32.5581395348837	Amp:51.1627906976744	Del:16.2790697674419
TP53-gr	*JMY*	133746	5q14.1	Neutral:48.8372093023256	Amp:9.30232558139535	Del:41.8604651162791
TP53-gr	*NDUFS6*	4726	5p15.33	Neutral:46.5116279069767	Amp:44.1860465116279	Del:9.30232558139535
TP53-gr	*SERF1B*	728492	5q13.2	Neutral:41.8604651162791	Amp:9.30232558139535	Del:48.8372093023256
TP53-gr	*SMN2*	6607	5q13.2	Neutral:37.2093023255814	Amp:4.65116279069767	Del:58.1395348837209
TP53-gr	*AIM1*	202	6q21	Neutral:53.4883720930233	Amp:20.9302325581395	Del:25.5813953488372
TP53-gr	*AMD1*	262	6q21	Neutral:58.1395348837209	Amp:6.97674418604651	Del:34.8837209302326
TP53-gr	*ARMC2*	84071	6q21	Neutral:48.8372093023256	Amp:20.9302325581395	Del:30.2325581395349
TP53-gr	*ATG5*	9474	6q21	Neutral:37.2093023255814	Amp:32.5581395348837	Del:30.2325581395349
TP53-gr	*BEND3*	57673	6q21	Neutral:46.5116279069767	Amp:16.2790697674419	Del:37.2093023255814
TP53-gr	*BVES*	11149	6q21	Neutral:39.5348837209302	Amp:25.5813953488372	Del:34.8837209302326

TP53-gr	*BVES-AS1*	154442	6q21	Neutral:41.8604651162791	Amp:25.5813953488372	Del:32.5581395348837
TP53-gr	*C6orf203*	51250	6q21	Neutral:44.1860465116279	Amp:13.953488372093	Del:41.8604651162791
TP53-gr	*CCDC162P*	221262	6q21	Neutral:46.5116279069767	Amp:30.2325581395349	Del:23.2558139534884
TP53-gr	*CD164*	8763	6q21	Neutral:41.8604651162791	Amp:25.5813953488372	Del:32.5581395348837
TP53-gr	*CDC40*	51362	6q21	Neutral:44.1860465116279	Amp:25.5813953488372	Del:30.2325581395349
TP53-gr	*CDK19*	23097	6q21	Neutral:46.5116279069767	Amp:25.5813953488372	Del:27.906976744186
TP53-gr	*CEP57L1*	285753	6q21	Neutral:39.5348837209302	Amp:20.9302325581395	Del:39.5348837209302
TP53-gr	*CLIC1*	1192	6p21.33	Neutral:37.2093023255814	Amp:13.953488372093	Del:48.8372093023256
TP53-gr	*DDO*	8528	6q21	Neutral:55.8139534883721	Amp:23.2558139534884	Del:20.9302325581395
TP53-gr	*DEFB110*	245913	6p12.3	Neutral:41.8604651162791	Amp:30.2325581395349	Del:27.906976744186
TP53-gr	*DEFB113*	245927	6p12.3	Neutral:34.8837209302326	Amp:30.2325581395349	Del:34.8837209302326
TP53-gr	*DEFB114*	245928	6p12.3	Neutral:34.8837209302326	Amp:27.906976744186	Del:37.2093023255814
TP53-gr	*DEFB133*	403339	6p12.3	Neutral:41.8604651162791	Amp:30.2325581395349	Del:27.906976744186
TP53-gr	*FIG4*	9896	6q21	Neutral:44.1860465116279	Amp:23.2558139534884	Del:32.5581395348837
TP53-gr	*FOXO3*	2309	6q21	Neutral:51.1627906976744	Amp:34.8837209302326	Del:13.953488372093
TP53-gr	*GABBR1*	2550	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*GPR6*	2830	6q21	Neutral:51.1627906976744	Amp:25.5813953488372	Del:23.2558139534884
TP53-gr	*GSTM2P1*	442245	6q21	Neutral:51.1627906976744	Amp:13.953488372093	Del:34.8837209302326
TP53-gr	*GTF3C6*	112495	6q21	Neutral:39.5348837209302	Amp:9.30232558139535	Del:51.1627906976744
TP53-gr	*HCG4*	54435	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*HCG4B*	80868	6p22.1	Neutral:39.5348837209302	Amp:23.2558139534884	Del:37.2093023255814
TP53-gr	*HCG9*	10255	6p22.1	Neutral:44.1860465116279	Amp:16.2790697674419	Del:39.5348837209302
TP53-gr	*HLA-A*	3105	6p22.1	Neutral:39.5348837209302	Amp:20.9302325581395	Del:39.5348837209302
TP53-gr	*HLA-F*	3134	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*HLA-F-AS1*	285830	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*HLA-G*	3135	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*HLA-H*	3136	6p22.1	Neutral:44.1860465116279	Amp:23.2558139534884	Del:32.5581395348837
TP53-gr	*HLA-J*	3137	6p22.1	Neutral:51.1627906976744	Amp:11.6279069767442	Del:37.2093023255814
TP53-gr	*HSPA1A*	3303	6p21.33	Neutral:37.2093023255814	Amp:16.2790697674419	Del:46.5116279069767
TP53-gr	*HSPA1L*	3305	6p21.33	Neutral:34.8837209302326	Amp:16.2790697674419	Del:48.8372093023256
TP53-gr	*IFITM4P*	340198	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*LACE1*	246269	6q21	Neutral:58.1395348837209	Amp:13.953488372093	Del:27.906976744186
TP53-gr	*LINC00222*	387111	6q21	Neutral:53.4883720930233	Amp:27.906976744186	Del:18.6046511627907
TP53-gr	*LSM2*	57819	6p21.33	Neutral:34.8837209302326	Amp:13.953488372093	Del:51.1627906976744
TP53-gr	*MAS1L*	116511	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*MICAL1*	64780	6q21	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*MOG*	4340	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*MSH5*	4439	6p21.33	Neutral:39.5348837209302	Amp:11.6279069767442	Del:48.8372093023256
TP53-gr	*MSH5-SAPCD1*	100532732	6p21.33	Neutral:39.5348837209302	Amp:11.6279069767442	Del:48.8372093023256
TP53-gr	*NFYA*	4800	6p21.1	Neutral:53.4883720930233	Amp:37.2093023255814	Del:9.30232558139535
TP53-gr	*NR2E1*	7101	6q21	Neutral:58.1395348837209	Amp:16.2790697674419	Del:25.5813953488372

TP53-gr	*OR10C1*	442194	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OR11A1*	26531	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OR12D2*	26529	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OR12D3*	81797	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OR14J1*	442191	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OR2H1*	26716	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OR2H2*	7932	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OR2J2*	26707	6p22.1	Neutral:48.8372093023256	Amp:20.9302325581395	Del:30.2325581395349
TP53-gr	*OR2J3*	442186	6p22.1	Neutral:53.4883720930233	Amp:20.9302325581395	Del:25.5813953488372
TP53-gr	*OR5V1*	81696	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*OSTM1*	28962	6q21	Neutral:53.4883720930233	Amp:11.6279069767442	Del:34.8837209302326
TP53-gr	*PDSS2*	57107	6q21	Neutral:44.1860465116279	Amp:13.953488372093	Del:41.8604651162791
TP53-gr	*PHF3*	23469	6q12	Neutral:34.8837209302326	Amp:37.2093023255814	Del:27.906976744186
TP53-gr	*POPDC3*	64208	6q21	Neutral:39.5348837209302	Amp:27.906976744186	Del:32.5581395348837
TP53-gr	*PPIL6*	285755	6q21	Neutral:51.1627906976744	Amp:18.6046511627907	Del:30.2325581395349
TP53-gr	*PRDM1*	639	6q21	Neutral:34.8837209302326	Amp:37.2093023255814	Del:27.906976744186
TP53-gr	*PREP*	5550	6q21	Neutral:44.1860465116279	Amp:30.2325581395349	Del:25.5813953488372
TP53-gr	*QRSL1*	55278	6q21	Neutral:58.1395348837209	Amp:11.6279069767442	Del:30.2325581395349
TP53-gr	*RPF2*	84154	6q21	Neutral:44.1860465116279	Amp:9.30232558139535	Del:46.5116279069767
TP53-gr	*RTN4IP1*	84816	6q21	Neutral:58.1395348837209	Amp:13.953488372093	Del:27.906976744186
TP53-gr	*SAPCD1*	401251	6p21.33	Neutral:34.8837209302326	Amp:13.953488372093	Del:51.1627906976744
TP53-gr	*SCML4*	256380	6q21	Neutral:60.4651162790698	Amp:20.9302325581395	Del:18.6046511627907
TP53-gr	*SEC63*	11231	6q21	Neutral:44.1860465116279	Amp:18.6046511627907	Del:37.2093023255814
TP53-gr	*SESN1*	27244	6q21	Neutral:44.1860465116279	Amp:20.9302325581395	Del:34.8837209302326
TP53-gr	*SLC16A10*	117247	6q21	Neutral:62.7906976744186	Amp:9.30232558139535	Del:27.906976744186
TP53-gr	*SLC22A16*	85413	6q21	Neutral:48.8372093023256	Amp:25.5813953488372	Del:25.5813953488372
TP53-gr	*SMPD2*	6610	6q21	Neutral:44.1860465116279	Amp:30.2325581395349	Del:25.5813953488372
TP53-gr	*SNORD32B*	692092	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*SNX3*	8724	6q21	Neutral:60.4651162790698	Amp:9.30232558139535	Del:30.2325581395349
TP53-gr	*SOBP*	55084	6q21	Neutral:46.5116279069767	Amp:37.2093023255814	Del:16.2790697674419
TP53-gr	*UBD*	10537	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*VARS*	7407	6p21.33	Neutral:34.8837209302326	Amp:13.953488372093	Del:51.1627906976744
TP53-gr	*VWA7*	80737	6p21.33	Neutral:34.8837209302326	Amp:13.953488372093	Del:51.1627906976744
TP53-gr	*WASF1*	8936	6q21	Neutral:46.5116279069767	Amp:25.5813953488372	Del:27.906976744186
TP53-gr	*ZBTB24*	9841	6q21	Neutral:53.4883720930233	Amp:20.9302325581395	Del:25.5813953488372
TP53-gr	*ZFP57*	346171	6p22.1	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*ZNRD1*	30834	6p22.1	Neutral:51.1627906976744	Amp:9.30232558139535	Del:39.5348837209302
TP53-gr	*ZNRD1-AS1*	80862	6p22.1	Neutral:53.4883720930233	Amp:9.30232558139535	Del:37.2093023255814
TP53-gr	*ABCB8*	11194	7q36.1	Neutral:37.2093023255814	Amp:44.1860465116279	Del:18.6046511627907
TP53-gr	*ABCF2*	10061	7q36.1	Neutral:53.4883720930233	Amp:34.8837209302326	Del:11.6279069767442
TP53-gr	*ACHE*	43	7q22.1	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419

TP53-gr	*ACTB*	60	7p22.1	Neutral:37.2093023255814	Amp:46.5116279069767	Del:16.2790697674419
TP53-gr	*ACTL6B*	51412	7q22.1	Neutral:37.2093023255814	Amp:37.2093023255814	Del:25.5813953488372
TP53-gr	*ACTR3B*	57180	7q36.1	Neutral:58.1395348837209	Amp:27.906976744186	Del:13.953488372093
TP53-gr	*ACTR3C*	653857	7q36.1	Neutral:55.8139534883721	Amp:32.5581395348837	Del:11.6279069767442
TP53-gr	*AEBP1*	165	7p13	Neutral:34.8837209302326	Amp:51.1627906976744	Del:13.953488372093
TP53-gr	*AGAP3*	116988	7q36.1	Neutral:34.8837209302326	Amp:46.5116279069767	Del:18.6046511627907
TP53-gr	*AGFG2*	3268	7q22.1	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*AIMP2*	7965	7p22.1	Neutral:53.4883720930233	Amp:25.5813953488372	Del:20.9302325581395
TP53-gr	*ALKBH4*	54784	7q22.1	Neutral:37.2093023255814	Amp:34.8837209302326	Del:27.906976744186
TP53-gr	*AP1S1*	1174	7q22.1	Neutral:37.2093023255814	Amp:34.8837209302326	Del:27.906976744186
TP53-gr	*AP4M1*	9179	7q22.1	Neutral:34.8837209302326	Amp:39.5348837209302	Del:25.5813953488372
TP53-gr	*ARL4A*	10124	7p21.3	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*ARMC10*	83787	7q22.1	Neutral:53.4883720930233	Amp:27.906976744186	Del:18.6046511627907
TP53-gr	*ARPC1A*	10552	7q22.1	Neutral:41.8604651162791	Amp:30.2325581395349	Del:27.906976744186
TP53-gr	*ARPC1B*	10095	7q22.1	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*ASB10*	136371	7q36.1	Neutral:41.8604651162791	Amp:39.5348837209302	Del:18.6046511627907
TP53-gr	*ASL*	435	7q11.21	Neutral:34.8837209302326	Amp:34.8837209302326	Del:30.2325581395349
TP53-gr	*ASZ1*	136991	7q31.2	Neutral:41.8604651162791	Amp:39.5348837209302	Del:18.6046511627907
TP53-gr	*ATG9B*	285973	7q36.1	Neutral:34.8837209302326	Amp:44.1860465116279	Del:20.9302325581395
TP53-gr	*ATP5J2*	9551	7q22.1	Neutral:41.8604651162791	Amp:37.2093023255814	Del:20.9302325581395
TP53-gr	*ATP5J2-PTCD1*	100526740	7q22.1	Neutral:39.5348837209302	Amp:34.8837209302326	Del:25.5813953488372
TP53-gr	*ATP6V0E2*	155066	7q36.1	Neutral:51.1627906976744	Amp:39.5348837209302	Del:9.30232558139535
TP53-gr	*AZGP1*	563	7q22.1	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*AZGP1P1*	646282	7q22.1	Neutral:39.5348837209302	Amp:39.5348837209302	Del:20.9302325581395
TP53-gr	*BLVRA*	644	7p13	Neutral:67.4418604651163	Amp:30.2325581395349	Del:2.32558139534884
TP53-gr	*BUD31*	8896	7q22.1	Neutral:41.8604651162791	Amp:32.5581395348837	Del:25.5813953488372
TP53-gr	*C1GALT1*	56913	7p22.1	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*C7orf26*	79034	7p22.1	Neutral:46.5116279069767	Amp:34.8837209302326	Del:18.6046511627907
TP53-gr	*C7orf33*	202865	7q36.1	Neutral:67.4418604651163	Amp:16.2790697674419	Del:16.2790697674419
TP53-gr	*C7orf43*	55262	7q22.1	Neutral:37.2093023255814	Amp:37.2093023255814	Del:25.5813953488372
TP53-gr	*C7orf61*	402573	7q22.1	Neutral:37.2093023255814	Amp:32.5581395348837	Del:30.2325581395349
TP53-gr	*CAMK2B*	816	7p13	Neutral:39.5348837209302	Amp:48.8372093023256	Del:11.6279069767442
TP53-gr	*CAPZA2*	830	7q31.2	Neutral:55.8139534883721	Amp:30.2325581395349	Del:13.953488372093
TP53-gr	*CAV1*	857	7q31.2	Neutral:41.8604651162791	Amp:55.8139534883721	Del:2.32558139534884
TP53-gr	*CAV2*	858	7q31.2	Neutral:46.5116279069767	Amp:46.5116279069767	Del:6.97674418604651
TP53-gr	*CCM2*	83605	7p13	Neutral:41.8604651162791	Amp:41.8604651162791	Del:16.2790697674419
TP53-gr	*CCT6A*	908	7p11.2	Neutral:55.8139534883721	Amp:16.2790697674419	Del:27.906976744186
TP53-gr	*CCT6P1*	643253	7q11.21	Neutral:58.1395348837209	Amp:13.953488372093	Del:27.906976744186
TP53-gr	*CCT6P3*	643180	7q11.21	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*CCZ1*	51622	7p22.1	Neutral:55.8139534883721	Amp:20.9302325581395	Del:23.2558139534884
TP53-gr	*CCZ1B*	221960	7p22.1	Neutral:48.8372093023256	Amp:23.2558139534884	Del:27.906976744186

TP53-gr	*CDK5*	1020	7q36.1	Neutral:32.5581395348837	Amp:46.5116279069767	Del:20.9302325581395
TP53-gr	*CFTR*	1080	7q31.2	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*CHCHD2*	51142	7p11.2	Neutral:51.1627906976744	Amp:25.5813953488372	Del:23.2558139534884
TP53-gr	*CHPF2*	54480	7q36.1	Neutral:41.8604651162791	Amp:41.8604651162791	Del:16.2790697674419
TP53-gr	*CLDN15*	24146	7q22.1	Neutral:39.5348837209302	Amp:32.5581395348837	Del:27.906976744186
TP53-gr	*CNPY4*	245812	7q22.1	Neutral:34.8837209302326	Amp:37.2093023255814	Del:27.906976744186
TP53-gr	*COL28A1*	340267	7p21.3	Neutral:46.5116279069767	Amp:44.1860465116279	Del:9.30232558139535
TP53-gr	*COPS6*	10980	7q22.1	Neutral:46.5116279069767	Amp:30.2325581395349	Del:23.2558139534884
TP53-gr	*CPSF4*	10898	7q22.1	Neutral:37.2093023255814	Amp:37.2093023255814	Del:25.5813953488372
TP53-gr	*CRCP*	27297	7q11.21	Neutral:48.8372093023256	Amp:20.9302325581395	Del:30.2325581395349
TP53-gr	*CRYGN*	155051	7q36.1	Neutral:34.8837209302326	Amp:44.1860465116279	Del:20.9302325581395
TP53-gr	*CTTNBP2*	83992	7q31.2	Neutral:46.5116279069767	Amp:44.1860465116279	Del:9.30232558139535
TP53-gr	*CUL1*	8454	7q36.1	Neutral:58.1395348837209	Amp:23.2558139534884	Del:18.6046511627907
TP53-gr	*CUX1*	1523	7q22.1	Neutral:27.906976744186	Amp:41.8604651162791	Del:30.2325581395349
TP53-gr	*CYP3A4*	1576	7q22.1	Neutral:53.4883720930233	Amp:30.2325581395349	Del:16.2790697674419
TP53-gr	*CYP3A43*	64816	7q22.1	Neutral:60.4651162790698	Amp:32.5581395348837	Del:6.97674418604651
TP53-gr	*CYP3A5*	1577	7q22.1	Neutral:55.8139534883721	Amp:34.8837209302326	Del:9.30232558139535
TP53-gr	*CYP3A7*	1551	7q22.1	Neutral:53.4883720930233	Amp:32.5581395348837	Del:13.953488372093
TP53-gr	*CYTH3*	9265	7p22.1	Neutral:55.8139534883721	Amp:32.5581395348837	Del:11.6279069767442
TP53-gr	*DAGLB*	221955	7p22.1	Neutral:55.8139534883721	Amp:27.906976744186	Del:16.2790697674419
TP53-gr	*DBNL*	28988	7p13	Neutral:37.2093023255814	Amp:46.5116279069767	Del:16.2790697674419
TP53-gr	*DDX56*	54606	7p13	Neutral:46.5116279069767	Amp:34.8837209302326	Del:18.6046511627907
TP53-gr	*DNAJC2*	27000	7q22.1	Neutral:53.4883720930233	Amp:23.2558139534884	Del:23.2558139534884
TP53-gr	*DPY19L2P2*	349152	7q22.1	Neutral:51.1627906976744	Amp:27.906976744186	Del:20.9302325581395
TP53-gr	*EGFR*	1956	7p11.2	Neutral:46.5116279069767	Amp:46.5116279069767	Del:6.97674418604651
TP53-gr	*EIF2AK1*	27102	7p22.1	Neutral:53.4883720930233	Amp:20.9302325581395	Del:25.5813953488372
TP53-gr	*EPHB4*	2050	7q22.1	Neutral:37.2093023255814	Amp:37.2093023255814	Del:25.5813953488372
TP53-gr	*EPO*	2056	7q22.1	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*ERV3-1*	2086	7q11.21	Neutral:55.8139534883721	Amp:23.2558139534884	Del:20.9302325581395
TP53-gr	*EZH2*	2146	7q36.1	Neutral:53.4883720930233	Amp:25.5813953488372	Del:20.9302325581395
TP53-gr	*FABP5P3*	220832	7q36.1	Neutral:39.5348837209302	Amp:23.2558139534884	Del:37.2093023255814
TP53-gr	*FAM185A*	222234	7q22.1	Neutral:53.4883720930233	Amp:32.5581395348837	Del:13.953488372093
TP53-gr	*FAM200A*	221786	7q22.1	Neutral:46.5116279069767	Amp:25.5813953488372	Del:27.906976744186
TP53-gr	*FASTK*	10922	7q36.1	Neutral:30.2325581395349	Amp:46.5116279069767	Del:23.2558139534884
TP53-gr	*FBXL13*	222235	7q22.1	Neutral:51.1627906976744	Amp:25.5813953488372	Del:23.2558139534884
TP53-gr	*FBXL18*	80028	7p22.1	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*FBXO24*	26261	7q22.1	Neutral:32.5581395348837	Amp:41.8604651162791	Del:25.5813953488372
TP53-gr	*FIS1*	51024	7q22.1	Neutral:37.2093023255814	Amp:32.5581395348837	Del:30.2325581395349
TP53-gr	*FKBP9L*	360132	7p11.2	Neutral:60.4651162790698	Amp:30.2325581395349	Del:9.30232558139535
TP53-gr	*FOXK1*	221937	7p22.1	Neutral:32.5581395348837	Amp:51.1627906976744	Del:16.2790697674419
TP53-gr	*FSCN1*	6624	7p22.1	Neutral:39.5348837209302	Amp:44.1860465116279	Del:16.2790697674419

TP53-gr	*GAL3ST4*	79690	7q22.1	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*GALNT11*	63917	7q36.1	Neutral:58.1395348837209	Amp:27.906976744186	Del:13.953488372093
TP53-gr	*GALNTL5*	168391	7q36.1	Neutral:53.4883720930233	Amp:25.5813953488372	Del:20.9302325581395
TP53-gr	*GATS*	352954	7q22.1	Neutral:41.8604651162791	Amp:39.5348837209302	Del:18.6046511627907
TP53-gr	*GBAS*	2631	7p11.2	Neutral:51.1627906976744	Amp:13.953488372093	Del:34.8837209302326
TP53-gr	*GBX1*	2636	7q36.1	Neutral:46.5116279069767	Amp:37.2093023255814	Del:16.2790697674419
TP53-gr	*GCK*	2645	7p13	Neutral:32.5581395348837	Amp:53.4883720930233	Del:13.953488372093
TP53-gr	*GIGYF1*	64599	7q22.1	Neutral:37.2093023255814	Amp:39.5348837209302	Del:23.2558139534884
TP53-gr	*GIMAP1*	170575	7q36.1	Neutral:48.8372093023256	Amp:30.2325581395349	Del:20.9302325581395
TP53-gr	*GIMAP2*	26157	7q36.1	Neutral:53.4883720930233	Amp:27.906976744186	Del:18.6046511627907
TP53-gr	*GIMAP4*	55303	7q36.1	Neutral:53.4883720930233	Amp:27.906976744186	Del:18.6046511627907
TP53-gr	*GIMAP5*	55340	7q36.1	Neutral:58.1395348837209	Amp:25.5813953488372	Del:16.2790697674419
TP53-gr	*GIMAP6*	474344	7q36.1	Neutral:51.1627906976744	Amp:30.2325581395349	Del:18.6046511627907
TP53-gr	*GIMAP7*	168537	7q36.1	Neutral:46.5116279069767	Amp:34.8837209302326	Del:18.6046511627907
TP53-gr	*GIMAP8*	155038	7q36.1	Neutral:48.8372093023256	Amp:37.2093023255814	Del:13.953488372093
TP53-gr	*GJC3*	349149	7q22.1	Neutral:60.4651162790698	Amp:30.2325581395349	Del:9.30232558139535
TP53-gr	*GLCCI1*	113263	7p21.3	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*GNB2*	2783	7q22.1	Neutral:32.5581395348837	Amp:41.8604651162791	Del:25.5813953488372
TP53-gr	*GPC2*	221914	7q22.1	Neutral:41.8604651162791	Amp:37.2093023255814	Del:20.9302325581395
TP53-gr	*GRID2IP*	392862	7p22.1	Neutral:46.5116279069767	Amp:34.8837209302326	Del:18.6046511627907
TP53-gr	*GUSB*	2990	7q11.21	Neutral:32.5581395348837	Amp:30.2325581395349	Del:37.2093023255814
TP53-gr	*GUSBP10*	642006	7p11.2	Neutral:58.1395348837209	Amp:27.906976744186	Del:13.953488372093
TP53-gr	*H2AFV*	94239	7p13	Neutral:41.8604651162791	Amp:20.9302325581395	Del:37.2093023255814
TP53-gr	*ICA1*	3382	7p21.3	Neutral:51.1627906976744	Amp:44.1860465116279	Del:4.65116279069767
TP53-gr	*INTS4L1*	285905	7q11.21	Neutral:58.1395348837209	Amp:18.6046511627907	Del:23.2558139534884
TP53-gr	*INTS4L2*	644619	7q11.21	Neutral:58.1395348837209	Amp:18.6046511627907	Del:23.2558139534884
TP53-gr	*KCNH2*	3757	7q36.1	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*KCTD7*	154881	7q11.21	Neutral:46.5116279069767	Amp:23.2558139534884	Del:30.2325581395349
TP53-gr	*KDELR2*	11014	7p22.1	Neutral:48.8372093023256	Amp:27.906976744186	Del:23.2558139534884
TP53-gr	*KPNA7*	402569	7q22.1	Neutral:46.5116279069767	Amp:23.2558139534884	Del:30.2325581395349
TP53-gr	*KRBA1*	84626	7q36.1	Neutral:39.5348837209302	Amp:39.5348837209302	Del:20.9302325581395
TP53-gr	*LANCL2*	55915	7p11.2	Neutral:46.5116279069767	Amp:44.1860465116279	Del:9.30232558139535
TP53-gr	*LINC00174*	285908	7q11.21	Neutral:55.8139534883721	Amp:16.2790697674419	Del:27.906976744186
TP53-gr	*LRCH4*	4034	7q22.1	Neutral:30.2325581395349	Amp:46.5116279069767	Del:23.2558139534884
TP53-gr	*LRRC17*	10234	7q22.1	Neutral:53.4883720930233	Amp:23.2558139534884	Del:23.2558139534884
TP53-gr	*LRRC61*	65999	7q36.1	Neutral:39.5348837209302	Amp:41.8604651162791	Del:18.6046511627907
TP53-gr	*LRWD1*	222229	7q22.1	Neutral:30.2325581395349	Amp:41.8604651162791	Del:27.906976744186
TP53-gr	*MBLAC1*	255374	7q22.1	Neutral:34.8837209302326	Amp:37.2093023255814	Del:27.906976744186
TP53-gr	*MCM7*	4176	7q22.1	Neutral:37.2093023255814	Amp:39.5348837209302	Del:23.2558139534884
TP53-gr	*MEPCE*	56257	7q22.1	Neutral:39.5348837209302	Amp:34.8837209302326	Del:25.5813953488372
TP53-gr	*MET*	4233	7q31.2	Neutral:53.4883720930233	Amp:37.2093023255814	Del:9.30232558139535

TP53-gr	*MIOS*	54468	7p21.3	Neutral:39.5348837209302	Amp:44.1860465116279	Del:16.2790697674419
TP53-gr	*MIR106B*	406900	7q22.1	Neutral:37.2093023255814	Amp:39.5348837209302	Del:23.2558139534884
TP53-gr	*MIR25*	407014	7q22.1	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*MIR3147*	100422939	7p11.2	Neutral:60.4651162790698	Amp:23.2558139534884	Del:16.2790697674419
TP53-gr	*MIR3609*	100500819	7q22.1	Neutral:53.4883720930233	Amp:25.5813953488372	Del:20.9302325581395
TP53-gr	*MIR3907*	100500835	7q36.1	Neutral:34.8837209302326	Amp:44.1860465116279	Del:20.9302325581395
TP53-gr	*MIR4283-1*	100422917	7p11.2	Neutral:32.5581395348837	Amp:30.2325581395349	Del:37.2093023255814
TP53-gr	*MIR4283-2*	100422848	7p11.2	Neutral:32.5581395348837	Amp:30.2325581395349	Del:37.2093023255814
TP53-gr	*MIR4285*	100422858	7q22.1	Neutral:30.2325581395349	Amp:41.8604651162791	Del:27.906976744186
TP53-gr	*MIR4467*	100616367	7q22.1	Neutral:30.2325581395349	Amp:41.8604651162791	Del:27.906976744186
TP53-gr	*MIR4649*	100616346	7p13	Neutral:34.8837209302326	Amp:51.1627906976744	Del:13.953488372093
TP53-gr	*MIR4650-1*	100616310	7q11.21	Neutral:51.1627906976744	Amp:20.9302325581395	Del:27.906976744186
TP53-gr	*MIR4650-2*	100616331	7q11.21	Neutral:51.1627906976744	Amp:20.9302325581395	Del:27.906976744186
TP53-gr	*MIR4653*	100616117	7q22.1	Neutral:39.5348837209302	Amp:34.8837209302326	Del:25.5813953488372
TP53-gr	*MIR4656*	100616465	7p22.1	Neutral:34.8837209302326	Amp:48.8372093023256	Del:16.2790697674419
TP53-gr	*MIR4657*	100616393	7p13	Neutral:39.5348837209302	Amp:23.2558139534884	Del:37.2093023255814
TP53-gr	*MIR4658*	100616439	7q22.1	Neutral:37.2093023255814	Amp:37.2093023255814	Del:25.5813953488372
TP53-gr	*MIR589*	693174	7p22.1	Neutral:41.8604651162791	Amp:39.5348837209302	Del:18.6046511627907
TP53-gr	*MIR671*	768213	7q36.1	Neutral:34.8837209302326	Amp:46.5116279069767	Del:18.6046511627907
TP53-gr	*MIR93*	407050	7q22.1	Neutral:37.2093023255814	Amp:39.5348837209302	Del:23.2558139534884
TP53-gr	*MMD2*	221938	7p22.1	Neutral:46.5116279069767	Amp:30.2325581395349	Del:23.2558139534884
TP53-gr	*MOGAT3*	346606	7q22.1	Neutral:37.2093023255814	Amp:34.8837209302326	Del:27.906976744186
TP53-gr	*MOSPD3*	64598	7q22.1	Neutral:37.2093023255814	Amp:34.8837209302326	Del:27.906976744186
TP53-gr	*MRPS17*	51373	7p11.2	Neutral:53.4883720930233	Amp:11.6279069767442	Del:34.8837209302326
TP53-gr	*MRPS24*	64951	7p13	Neutral:55.8139534883721	Amp:34.8837209302326	Del:9.30232558139535
TP53-gr	*MUC12*	10071	7q22.1	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*MUC17*	140453	7q22.1	Neutral:60.4651162790698	Amp:25.5813953488372	Del:13.953488372093
TP53-gr	*MYH16*	84176	7q22.1	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*MYL10*	93408	7q22.1	Neutral:30.2325581395349	Amp:39.5348837209302	Del:30.2325581395349
TP53-gr	*MYL7*	58498	7p13	Neutral:32.5581395348837	Amp:53.4883720930233	Del:13.953488372093
TP53-gr	*MYO1G*	64005	7p13	Neutral:39.5348837209302	Amp:44.1860465116279	Del:16.2790697674419
TP53-gr	*NACAD*	23148	7p13	Neutral:30.2325581395349	Amp:53.4883720930233	Del:16.2790697674419
TP53-gr	*NAPEPLD*	222236	7q22.1	Neutral:51.1627906976744	Amp:27.906976744186	Del:20.9302325581395
TP53-gr	*NAT16*	375607	7q22.1	Neutral:39.5348837209302	Amp:34.8837209302326	Del:25.5813953488372
TP53-gr	*NDUFA4*	4697	7p21.3	Neutral:46.5116279069767	Amp:37.2093023255814	Del:16.2790697674419
TP53-gr	*NOS3*	4846	7q36.1	Neutral:30.2325581395349	Amp:44.1860465116279	Del:25.5813953488372
TP53-gr	*NPC1L1*	29881	7p13	Neutral:44.1860465116279	Amp:37.2093023255814	Del:18.6046511627907
TP53-gr	*NPTX2*	4885	7q22.1	Neutral:48.8372093023256	Amp:32.5581395348837	Del:18.6046511627907
TP53-gr	*NUB1*	51667	7q36.1	Neutral:48.8372093023256	Amp:32.5581395348837	Del:18.6046511627907
TP53-gr	*NUDCD3*	23386	7p13	Neutral:48.8372093023256	Amp:48.8372093023256	Del:2.32558139534884
TP53-gr	*NXPH1*	30010	7p21.3	Neutral:44.1860465116279	Amp:44.1860465116279	Del:11.6279069767442

TP53-gr	*NYAP1*	222950	7q22.1	Neutral:39.5348837209302	Amp:32.5581395348837	Del:27.906976744186
TP53-gr	*OCM*	654231	7p22.1	Neutral:60.4651162790698	Amp:18.6046511627907	Del:20.9302325581395
TP53-gr	*OGDH*	4967	7p13	Neutral:46.5116279069767	Amp:34.8837209302326	Del:18.6046511627907
TP53-gr	*OR2AE1*	81392	7q22.1	Neutral:65.1162790697674	Amp:30.2325581395349	Del:4.65116279069767
TP53-gr	*ORAI2*	80228	7q22.1	Neutral:37.2093023255814	Amp:34.8837209302326	Del:27.906976744186
TP53-gr	*ORC5*	5001	7q22.1	Neutral:51.1627906976744	Amp:32.5581395348837	Del:16.2790697674419
TP53-gr	*PAPOLB*	56903	7p22.1	Neutral:58.1395348837209	Amp:30.2325581395349	Del:11.6279069767442
TP53-gr	*PCOLCE*	5118	7q22.1	Neutral:34.8837209302326	Amp:37.2093023255814	Del:27.906976744186
TP53-gr	*PDAP1*	11333	7q22.1	Neutral:41.8604651162791	Amp:34.8837209302326	Del:23.2558139534884
TP53-gr	*PDIA4*	9601	7q36.1	Neutral:53.4883720930233	Amp:23.2558139534884	Del:23.2558139534884
TP53-gr	*PGAM2*	5224	7p13	Neutral:37.2093023255814	Amp:48.8372093023256	Del:13.953488372093
TP53-gr	*PHF14*	9678	7p21.3	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*PHKG1*	5260	7p11.2	Neutral:41.8604651162791	Amp:32.5581395348837	Del:25.5813953488372
TP53-gr	*PILRA*	29992	7q22.1	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*PILRB*	29990	7q22.1	Neutral:39.5348837209302	Amp:34.8837209302326	Del:25.5813953488372
TP53-gr	*PLOD3*	8985	7q22.1	Neutral:37.2093023255814	Amp:34.8837209302326	Del:27.906976744186
TP53-gr	*PMPCB*	9512	7q22.1	Neutral:55.8139534883721	Amp:23.2558139534884	Del:20.9302325581395
TP53-gr	*PMS2*	5395	7p22.1	Neutral:55.8139534883721	Amp:23.2558139534884	Del:20.9302325581395
TP53-gr	*PMS2CL*	441194	7p22.1	Neutral:48.8372093023256	Amp:23.2558139534884	Del:27.906976744186
TP53-gr	*PMS2P1*	5379	7q22.1	Neutral:51.1627906976744	Amp:25.5813953488372	Del:23.2558139534884
TP53-gr	*PMS2P4*	5382	7q11.21	Neutral:51.1627906976744	Amp:20.9302325581395	Del:27.906976744186
TP53-gr	*POLD2*	5425	7p13	Neutral:32.5581395348837	Amp:53.4883720930233	Del:13.953488372093
TP53-gr	*POLM*	27434	7p13	Neutral:39.5348837209302	Amp:46.5116279069767	Del:13.953488372093
TP53-gr	*POLR2J*	5439	7q22.1	Neutral:32.5581395348837	Amp:39.5348837209302	Del:27.906976744186
TP53-gr	*POLR2J2*	246721	7q22.1	Neutral:32.5581395348837	Amp:37.2093023255814	Del:30.2325581395349
TP53-gr	*POLR2J3*	548644	7q22.1	Neutral:37.2093023255814	Amp:34.8837209302326	Del:27.906976744186
TP53-gr	*POLR2J4*	84820	7p13	Neutral:44.1860465116279	Amp:34.8837209302326	Del:20.9302325581395
TP53-gr	*POP7*	10248	7q22.1	Neutral:44.1860465116279	Amp:32.5581395348837	Del:23.2558139534884
TP53-gr	*PPIA*	5478	7p13	Neutral:46.5116279069767	Amp:25.5813953488372	Del:27.906976744186
TP53-gr	*PPP1R35*	221908	7q22.1	Neutral:41.8604651162791	Amp:32.5581395348837	Del:25.5813953488372
TP53-gr	*PRKAG2*	51422	7q36.1	Neutral:60.4651162790698	Amp:27.906976744186	Del:11.6279069767442
TP53-gr	*PRKRIP1*	79706	7q22.1	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*PSMC2*	5701	7q22.1	Neutral:60.4651162790698	Amp:23.2558139534884	Del:16.2790697674419
TP53-gr	*PSPH*	5723	7p11.2	Neutral:51.1627906976744	Amp:13.953488372093	Del:34.8837209302326
TP53-gr	*PTCD1*	26024	7q22.1	Neutral:41.8604651162791	Amp:34.8837209302326	Del:23.2558139534884
TP53-gr	*PURB*	5814	7p13	Neutral:48.8372093023256	Amp:25.5813953488372	Del:25.5813953488372
TP53-gr	*PVRIG*	79037	7q22.1	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*RABGEF1*	27342	7q11.21	Neutral:51.1627906976744	Amp:23.2558139534884	Del:25.5813953488372
TP53-gr	*RABL5*	64792	7q22.1	Neutral:37.2093023255814	Amp:27.906976744186	Del:34.8837209302326
TP53-gr	*RAC1*	5879	7p22.1	Neutral:53.4883720930233	Amp:25.5813953488372	Del:20.9302325581395
TP53-gr	*RADIL*	55698	7p22.1	Neutral:46.5116279069767	Amp:37.2093023255814	Del:16.2790697674419

TP53-gr	*RAMP3*	10268	7p13	Neutral:41.8604651162791	Amp:51.1627906976744	Del:6.97674418604651
TP53-gr	*RARRES2*	5919	7q36.1	Neutral:37.2093023255814	Amp:44.1860465116279	Del:18.6046511627907
TP53-gr	*RASA4*	10156	7q22.1	Neutral:30.2325581395349	Amp:41.8604651162791	Del:27.906976744186
TP53-gr	*RBAK*	57786	7p22.1	Neutral:53.4883720930233	Amp:27.906976744186	Del:18.6046511627907
TP53-gr	*RELN*	5649	7q22.1	Neutral:55.8139534883721	Amp:30.2325581395349	Del:13.953488372093
TP53-gr	*REPIN1*	29803	7q36.1	Neutral:39.5348837209302	Amp:41.8604651162791	Del:18.6046511627907
TP53-gr	*RHEB*	6009	7q36.1	Neutral:48.8372093023256	Amp:30.2325581395349	Del:20.9302325581395
TP53-gr	*RNF216*	54476	7p22.1	Neutral:67.4418604651163	Amp:30.2325581395349	Del:2.32558139534884
TP53-gr	*RNF216P1*	441191	7p22.1	Neutral:62.7906976744186	Amp:25.5813953488372	Del:11.6279069767442
TP53-gr	*RPA3*	6119	7p21.3	Neutral:48.8372093023256	Amp:41.8604651162791	Del:9.30232558139535
TP53-gr	*RPL19P12*	100129424	7q22.1	Neutral:53.4883720930233	Amp:32.5581395348837	Del:13.953488372093
TP53-gr	*RSPH10B*	222967	7p22.1	Neutral:41.8604651162791	Amp:23.2558139534884	Del:34.8837209302326
TP53-gr	*RSPH10B2*	728194	7p22.1	Neutral:41.8604651162791	Amp:23.2558139534884	Del:34.8837209302326
TP53-gr	*SAP25*	100316904	7q22.1	Neutral:30.2325581395349	Amp:46.5116279069767	Del:23.2558139534884
TP53-gr	*SBDS*	51119	7q11.21	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*SCIN*	85477	7p21.3	Neutral:48.8372093023256	Amp:44.1860465116279	Del:6.97674418604651
TP53-gr	*SEC61G*	23480	7p11.2	Neutral:41.8604651162791	Amp:48.8372093023256	Del:9.30232558139535
TP53-gr	*Sep/14*	346288	7p11.2	Neutral:53.4883720930233	Amp:13.953488372093	Del:32.5581395348837
TP53-gr	*SERPINE1*	5054	7q22.1	Neutral:39.5348837209302	Amp:30.2325581395349	Del:30.2325581395349
TP53-gr	*SH2B2*	10603	7q22.1	Neutral:27.906976744186	Amp:39.5348837209302	Del:32.5581395348837
TP53-gr	*SLC12A9*	56996	7q22.1	Neutral:37.2093023255814	Amp:39.5348837209302	Del:23.2558139534884
TP53-gr	*SLC26A5*	375611	7q22.1	Neutral:55.8139534883721	Amp:23.2558139534884	Del:20.9302325581395
TP53-gr	*SLC29A4*	222962	7p22.1	Neutral:46.5116279069767	Amp:37.2093023255814	Del:16.2790697674419
TP53-gr	*SLC4A2*	6522	7q36.1	Neutral:30.2325581395349	Amp:48.8372093023256	Del:20.9302325581395
TP53-gr	*SMARCD3*	6604	7q36.1	Neutral:37.2093023255814	Amp:51.1627906976744	Del:11.6279069767442
TP53-gr	*SMURF1*	57154	7q22.1	Neutral:62.7906976744186	Amp:23.2558139534884	Del:13.953488372093
TP53-gr	*SNHG15*	285958	7p13	Neutral:39.5348837209302	Amp:44.1860465116279	Del:16.2790697674419
TP53-gr	*SNORA15*	677803	7p11.2	Neutral:58.1395348837209	Amp:13.953488372093	Del:27.906976744186
TP53-gr	*SNORA22*	677807	7q11.21	Neutral:55.8139534883721	Amp:13.953488372093	Del:30.2325581395349
TP53-gr	*SNORA5A*	654319	7p13	Neutral:37.2093023255814	Amp:48.8372093023256	Del:13.953488372093
TP53-gr	*SNORA5B*	677795	7p13	Neutral:46.5116279069767	Amp:44.1860465116279	Del:9.30232558139535
TP53-gr	*SNORA5C*	677796	7p13	Neutral:37.2093023255814	Amp:48.8372093023256	Del:13.953488372093
TP53-gr	*SPDYE1*	285955	7p13	Neutral:44.1860465116279	Amp:34.8837209302326	Del:20.9302325581395
TP53-gr	*SPDYE2*	441273	7q22.1	Neutral:34.8837209302326	Amp:34.8837209302326	Del:30.2325581395349
TP53-gr	*SPDYE3*	441272	7q22.1	Neutral:39.5348837209302	Amp:32.5581395348837	Del:27.906976744186
TP53-gr	*SPDYE6*	729597	7q22.1	Neutral:46.5116279069767	Amp:27.906976744186	Del:25.5813953488372
TP53-gr	*SRRT*	51593	7q22.1	Neutral:37.2093023255814	Amp:41.8604651162791	Del:20.9302325581395
TP53-gr	*SSPO*	23145	7q36.1	Neutral:39.5348837209302	Amp:44.1860465116279	Del:16.2790697674419
TP53-gr	*ST7*	7982	7q31.2	Neutral:55.8139534883721	Amp:39.5348837209302	Del:4.65116279069767
TP53-gr	*ST7-AS1*	93653	7q31.2	Neutral:58.1395348837209	Amp:30.2325581395349	Del:11.6279069767442
TP53-gr	*ST7-AS2*	93654	7q31.2	Neutral:51.1627906976744	Amp:41.8604651162791	Del:6.97674418604651

TP53-gr	*ST7-OT4*	338069	7q31.2	Neutral:65.1162790697674	Amp:30.2325581395349	Del:4.65116279069767
TP53-gr	*STAG3*	10734	7q22.1	Neutral:62.7906976744186	Amp:25.5813953488372	Del:11.6279069767442
TP53-gr	*STAG3L4*	64940	7q11.21	Neutral:65.1162790697674	Amp:16.2790697674419	Del:18.6046511627907
TP53-gr	*STK17A*	9263	7p13	Neutral:51.1627906976744	Amp:37.2093023255814	Del:11.6279069767442
TP53-gr	*SUMF2*	25870	7p11.2	Neutral:44.1860465116279	Amp:30.2325581395349	Del:25.5813953488372
TP53-gr	*TAF6*	6878	7q22.1	Neutral:34.8837209302326	Amp:37.2093023255814	Del:27.906976744186
TP53-gr	*TBRG4*	9238	7p13	Neutral:34.8837209302326	Amp:51.1627906976744	Del:13.953488372093
TP53-gr	*TES*	26136	7q31.2	Neutral:53.4883720930233	Amp:41.8604651162791	Del:4.65116279069767
TP53-gr	*TFEC*	22797	7q31.2	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*TFR2*	7036	7q22.1	Neutral:34.8837209302326	Amp:37.2093023255814	Del:27.906976744186
TP53-gr	*THSD7A*	221981	7p21.3	Neutral:46.5116279069767	Amp:46.5116279069767	Del:6.97674418604651
TP53-gr	*TMED4*	222068	7p13	Neutral:51.1627906976744	Amp:37.2093023255814	Del:11.6279069767442
TP53-gr	*TMEM106B*	54664	7p21.3	Neutral:46.5116279069767	Amp:41.8604651162791	Del:11.6279069767442
TP53-gr	*TMEM130*	222865	7q22.1	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*TMEM176A*	55365	7q36.1	Neutral:41.8604651162791	Amp:39.5348837209302	Del:18.6046511627907
TP53-gr	*TMEM176B*	28959	7q36.1	Neutral:48.8372093023256	Amp:37.2093023255814	Del:13.953488372093
TP53-gr	*TMUB1*	83590	7q36.1	Neutral:30.2325581395349	Amp:46.5116279069767	Del:23.2558139534884
TP53-gr	*TNRC18*	84629	7p22.1	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*TPST1*	8460	7q11.21	Neutral:58.1395348837209	Amp:18.6046511627907	Del:23.2558139534884
TP53-gr	*TRIM4*	89122	7q22.1	Neutral:67.4418604651163	Amp:27.906976744186	Del:4.65116279069767
TP53-gr	*TRIM56*	81844	7q22.1	Neutral:39.5348837209302	Amp:32.5581395348837	Del:27.906976744186
TP53-gr	*TRIP6*	7205	7q22.1	Neutral:34.8837209302326	Amp:41.8604651162791	Del:23.2558139534884
TP53-gr	*TRRAP*	8295	7q22.1	Neutral:60.4651162790698	Amp:32.5581395348837	Del:6.97674418604651
TP53-gr	*TSC22D4*	81628	7q22.1	Neutral:39.5348837209302	Amp:32.5581395348837	Del:27.906976744186
TP53-gr	*TYW1*	55253	7q11.21	Neutral:60.4651162790698	Amp:16.2790697674419	Del:23.2558139534884
TP53-gr	*UBE2D4*	51619	7p13	Neutral:53.4883720930233	Amp:32.5581395348837	Del:13.953488372093
TP53-gr	*UFSP1*	402682	7q22.1	Neutral:39.5348837209302	Amp:44.1860465116279	Del:16.2790697674419
TP53-gr	*UPK3BL*	100134938	7q22.1	Neutral:32.5581395348837	Amp:39.5348837209302	Del:27.906976744186
TP53-gr	*URGCP*	55665	7p13	Neutral:53.4883720930233	Amp:37.2093023255814	Del:9.30232558139535
TP53-gr	*URGCP-MRPS24*	100534592	7p13	Neutral:55.8139534883721	Amp:37.2093023255814	Del:6.97674418604651
TP53-gr	*USP42*	84132	7p22.1	Neutral:55.8139534883721	Amp:34.8837209302326	Del:9.30232558139535
TP53-gr	*VGF*	7425	7q22.1	Neutral:39.5348837209302	Amp:34.8837209302326	Del:25.5813953488372
TP53-gr	*VKORC1L1*	154807	7q11.21	Neutral:48.8372093023256	Amp:23.2558139534884	Del:27.906976744186
TP53-gr	*VOPP1*	81552	7p11.2	Neutral:48.8372093023256	Amp:44.1860465116279	Del:6.97674418604651
TP53-gr	*VSTM2A*	222008	7p11.2	Neutral:39.5348837209302	Amp:51.1627906976744	Del:9.30232558139535
TP53-gr	*VWDE*	221806	7p21.3	Neutral:48.8372093023256	Amp:41.8604651162791	Del:9.30232558139535
TP53-gr	*WDR86*	349136	7q36.1	Neutral:34.8837209302326	Amp:39.5348837209302	Del:25.5813953488372
TP53-gr	*WIPI2*	26100	7p22.1	Neutral:55.8139534883721	Amp:30.2325581395349	Del:13.953488372093
TP53-gr	*WNT2*	7472	7q31.2	Neutral:51.1627906976744	Amp:46.5116279069767	Del:2.32558139534884
TP53-gr	*XRCC2*	7516	7q36.1	Neutral:48.8372093023256	Amp:25.5813953488372	Del:25.5813953488372
TP53-gr	*YKT6*	10652	7p13	Neutral:46.5116279069767	Amp:46.5116279069767	Del:6.97674418604651

TP53-gr	*ZAN*	7455	7q22.1	Neutral:34.8837209302326	Amp:32.5581395348837	Del:32.5581395348837
TP53-gr	*ZCWPW1*	55063	7q22.1	Neutral:53.4883720930233	Amp:20.9302325581395	Del:25.5813953488372
TP53-gr	*ZDHHC4*	55146	7p22.1	Neutral:51.1627906976744	Amp:27.906976744186	Del:20.9302325581395
TP53-gr	*ZKSCAN1*	7586	7q22.1	Neutral:48.8372093023256	Amp:25.5813953488372	Del:25.5813953488372
TP53-gr	*ZKSCAN5*	23660	7q22.1	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*ZMIZ2*	83637	7p13	Neutral:37.2093023255814	Amp:41.8604651162791	Del:20.9302325581395
TP53-gr	*ZNF107*	51427	7q11.21	Neutral:53.4883720930233	Amp:16.2790697674419	Del:30.2325581395349
TP53-gr	*ZNF117*	51351	7q11.21	Neutral:46.5116279069767	Amp:27.906976744186	Del:25.5813953488372
TP53-gr	*ZNF12*	7559	7p22.1	Neutral:58.1395348837209	Amp:25.5813953488372	Del:16.2790697674419
TP53-gr	*ZNF138*	7697	7q11.21	Neutral:55.8139534883721	Amp:18.6046511627907	Del:25.5813953488372
TP53-gr	*ZNF212*	7988	7q36.1	Neutral:39.5348837209302	Amp:30.2325581395349	Del:30.2325581395349
TP53-gr	*ZNF273*	10793	7q11.21	Neutral:51.1627906976744	Amp:23.2558139534884	Del:25.5813953488372
TP53-gr	*ZNF282*	8427	7q36.1	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*ZNF3*	7551	7q22.1	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*ZNF394*	84124	7q22.1	Neutral:41.8604651162791	Amp:34.8837209302326	Del:23.2558139534884
TP53-gr	*ZNF398*	57541	7q36.1	Neutral:44.1860465116279	Amp:18.6046511627907	Del:37.2093023255814
TP53-gr	*ZNF425*	155054	7q36.1	Neutral:44.1860465116279	Amp:18.6046511627907	Del:37.2093023255814
TP53-gr	*ZNF467*	168544	7q36.1	Neutral:37.2093023255814	Amp:41.8604651162791	Del:20.9302325581395
TP53-gr	*ZNF479*	90827	7p11.2	Neutral:65.1162790697674	Amp:23.2558139534884	Del:11.6279069767442
TP53-gr	*ZNF655*	79027	7q22.1	Neutral:51.1627906976744	Amp:32.5581395348837	Del:16.2790697674419
TP53-gr	*ZNF679*	168417	7q11.21	Neutral:53.4883720930233	Amp:23.2558139534884	Del:23.2558139534884
TP53-gr	*ZNF680*	340252	7q11.21	Neutral:55.8139534883721	Amp:13.953488372093	Del:30.2325581395349
TP53-gr	*ZNF713*	349075	7p11.2	Neutral:51.1627906976744	Amp:11.6279069767442	Del:37.2093023255814
TP53-gr	*ZNF716*	441234	7p11.2	Neutral:62.7906976744186	Amp:13.953488372093	Del:23.2558139534884
TP53-gr	*ZNF727*	442319	7q11.21	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*ZNF736*	728927	7q11.21	Neutral:55.8139534883721	Amp:23.2558139534884	Del:20.9302325581395
TP53-gr	*ZNF746*	155061	7q36.1	Neutral:51.1627906976744	Amp:41.8604651162791	Del:6.97674418604651
TP53-gr	*ZNF767*	79970	7q36.1	Neutral:51.1627906976744	Amp:39.5348837209302	Del:9.30232558139535
TP53-gr	*ZNF775*	285971	7q36.1	Neutral:48.8372093023256	Amp:32.5581395348837	Del:18.6046511627907
TP53-gr	*ZNF777*	27153	7q36.1	Neutral:53.4883720930233	Amp:34.8837209302326	Del:11.6279069767442
TP53-gr	*ZNF783*	100289678	7q36.1	Neutral:39.5348837209302	Amp:32.5581395348837	Del:27.906976744186
TP53-gr	*ZNF786*	136051	7q36.1	Neutral:48.8372093023256	Amp:18.6046511627907	Del:32.5581395348837
TP53-gr	*ZNF789*	285989	7q22.1	Neutral:44.1860465116279	Amp:30.2325581395349	Del:25.5813953488372
TP53-gr	*ZNF853*	54753	7p22.1	Neutral:46.5116279069767	Amp:34.8837209302326	Del:18.6046511627907
TP53-gr	*ZNF862*	643641	7q36.1	Neutral:51.1627906976744	Amp:41.8604651162791	Del:6.97674418604651
TP53-gr	*ZNF890P*	645700	7p22.1	Neutral:48.8372093023256	Amp:27.906976744186	Del:23.2558139534884
TP53-gr	*ZNF92*	168374	7q11.21	Neutral:51.1627906976744	Amp:23.2558139534884	Del:25.5813953488372
TP53-gr	*ZNHIT1*	10467	7q22.1	Neutral:34.8837209302326	Amp:34.8837209302326	Del:30.2325581395349
TP53-gr	*ZSCAN21*	7589	7q22.1	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*DCTN6*	10671	8p12	Neutral:25.5813953488372	Amp:6.97674418604651	Del:67.4418604651163
TP53-gr	*DEFA5*	1670	8p23.1	Neutral:37.2093023255814	Amp:4.65116279069767	Del:58.1395348837209

TP53-gr	*LEPROTL1*	23484	8p12	Neutral:32.5581395348837	Amp:4.65116279069767	Del:62.7906976744186
TP53-gr	*MBOAT4*	619373	8p12	Neutral:30.2325581395349	Amp:4.65116279069767	Del:65.1162790697674
TP53-gr	*MIR548O2*	100616190	8p12	Neutral:27.906976744186	Amp:4.65116279069767	Del:67.4418604651163
TP53-gr	*POU5F1B*	5462	8q24.21	Neutral:20.9302325581395	Amp:79.0697674418605	Del:0
TP53-gr	*RBPMS*	11030	8p12	Neutral:37.2093023255814	Amp:9.30232558139535	Del:53.4883720930233
TP53-gr	*TMEM66*	51669	8p12	Neutral:30.2325581395349	Amp:4.65116279069767	Del:65.1162790697674
TP53-gr	*C9orf156*	51531	9q22.33	Neutral:65.1162790697674	Amp:16.2790697674419	Del:18.6046511627907
TP53-gr	*C9orf53*	51198	9p21.3	Neutral:41.8604651162791	Amp:11.6279069767442	Del:46.5116279069767
TP53-gr	*CDKN2A*	1029	9p21.3	Neutral:44.1860465116279	Amp:13.953488372093	Del:41.8604651162791
TP53-gr	*CDKN2B*	1030	9p21.3	Neutral:39.5348837209302	Amp:16.2790697674419	Del:44.1860465116279
TP53-gr	*CDKN2B-AS1*	100048912	9p21.3	Neutral:46.5116279069767	Amp:11.6279069767442	Del:41.8604651162791
TP53-gr	*DMRTA1*	63951	9p21.3	Neutral:41.8604651162791	Amp:16.2790697674419	Del:41.8604651162791
TP53-gr	*EXD3*	54932	9q34.3	Neutral:37.2093023255814	Amp:30.2325581395349	Del:32.5581395348837
TP53-gr	*INSL4*	3641	9p24.1	Neutral:46.5116279069767	Amp:13.953488372093	Del:39.5348837209302
TP53-gr	*INSL6*	11172	9p24.1	Neutral:48.8372093023256	Amp:11.6279069767442	Del:39.5348837209302
TP53-gr	*JAK2*	3717	9p24.1	Neutral:41.8604651162791	Amp:18.6046511627907	Del:39.5348837209302
TP53-gr	*LMX1B*	4010	9q33.3	Neutral:53.4883720930233	Amp:13.953488372093	Del:32.5581395348837
TP53-gr	*MIR31*	407035	9p21.3	Neutral:37.2093023255814	Amp:23.2558139534884	Del:39.5348837209302
TP53-gr	*MIR31HG*	554202	9p21.3	Neutral:37.2093023255814	Amp:16.2790697674419	Del:46.5116279069767
TP53-gr	*MTAP*	4507	9p21.3	Neutral:37.2093023255814	Amp:11.6279069767442	Del:51.1627906976744
TP53-gr	*ZBTB34*	403341	9q33.3	Neutral:46.5116279069767	Amp:16.2790697674419	Del:37.2093023255814
TP53-gr	*ZBTB43*	23099	9q33.3	Neutral:69.7674418604651	Amp:4.65116279069767	Del:25.5813953488372
TP53-gr	*DLG5*	9231	10q22.3	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*DMBT1*	1755	10q26.13	Neutral:48.8372093023256	Amp:23.2558139534884	Del:27.906976744186
TP53-gr	*FAM53B*	9679	10q26.13	Neutral:46.5116279069767	Amp:18.6046511627907	Del:34.8837209302326
TP53-gr	*METTL10*	399818	10q26.13	Neutral:30.2325581395349	Amp:11.6279069767442	Del:58.1395348837209
TP53-gr	*MIR3155A*	100422989	10p15.1	Neutral:39.5348837209302	Amp:32.5581395348837	Del:27.906976744186
TP53-gr	*PFKFB3*	5209	10p15.1	Neutral:46.5116279069767	Amp:30.2325581395349	Del:23.2558139534884
TP53-gr	*POLR3A*	11128	10q22.3	Neutral:41.8604651162791	Amp:16.2790697674419	Del:41.8604651162791
TP53-gr	*RBM17*	84991	10p15.1	Neutral:46.5116279069767	Amp:30.2325581395349	Del:23.2558139534884
TP53-gr	*ZEB1*	6935	10p11.22	Neutral:34.8837209302326	Amp:48.8372093023256	Del:16.2790697674419
TP53-gr	*ZEB1-AS1*	220930	10p11.22	Neutral:32.5581395348837	Amp:55.8139534883721	Del:11.6279069767442
TP53-gr	*C1QTNF4*	114900	11p11.2	Neutral:34.8837209302326	Amp:18.6046511627907	Del:46.5116279069767
TP53-gr	*CCND1*	595	11q13.3	Neutral:51.1627906976744	Amp:41.8604651162791	Del:6.97674418604651
TP53-gr	*FAM180B*	399888	11p11.2	Neutral:44.1860465116279	Amp:23.2558139534884	Del:32.5581395348837
TP53-gr	*INSC*	387755	11p15.2	Neutral:53.4883720930233	Amp:32.5581395348837	Del:13.953488372093
TP53-gr	*KDM2A*	22992	11q13.2	Neutral:58.1395348837209	Amp:16.2790697674419	Del:25.5813953488372
TP53-gr	*MTCH2*	23788	11p11.2	Neutral:44.1860465116279	Amp:11.6279069767442	Del:44.1860465116279
TP53-gr	*MYEOV*	26579	11q13.3	Neutral:46.5116279069767	Amp:46.5116279069767	Del:6.97674418604651
TP53-gr	*OR4A5*	81318	11p11.12	Neutral:58.1395348837209	Amp:18.6046511627907	Del:23.2558139534884
TP53-gr	*ORAOV1*	220064	11q13.3	Neutral:55.8139534883721	Amp:34.8837209302326	Del:9.30232558139535

TP53-gr	*RHOD*	29984	11q13.2	Neutral:39.5348837209302	Amp:25.5813953488372	Del:34.8837209302326
TP53-gr	*SOX6*	55553	11p15.2	Neutral:37.2093023255814	Amp:44.1860465116279	Del:18.6046511627907
TP53-gr	*SYT12*	91683	11q13.2	Neutral:48.8372093023256	Amp:25.5813953488372	Del:25.5813953488372
TP53-gr	*TPCN2*	219931	11q13.3	Neutral:51.1627906976744	Amp:39.5348837209302	Del:9.30232558139535
TP53-gr	*A2ML1*	144568	12p13.31	Neutral:55.8139534883721	Amp:16.2790697674419	Del:27.906976744186
TP53-gr	*ALG10*	84920	12p11.1	Neutral:53.4883720930233	Amp:37.2093023255814	Del:9.30232558139535
TP53-gr	*ANKS1B*	56899	12q23.1	Neutral:74.4186046511628	Amp:18.6046511627907	Del:6.97674418604651
TP53-gr	*CBX5*	23468	12q13.13	Neutral:53.4883720930233	Amp:32.5581395348837	Del:13.953488372093
TP53-gr	*GOLGA2P5*	55592	12q23.1	Neutral:62.7906976744186	Amp:23.2558139534884	Del:13.953488372093
TP53-gr	*HNRNPA1*	3178	12q13.13	Neutral:58.1395348837209	Amp:32.5581395348837	Del:9.30232558139535
TP53-gr	*MFAP5*	8076	12p13.31	Neutral:51.1627906976744	Amp:20.9302325581395	Del:27.906976744186
TP53-gr	*NUDT4*	11163	12q22	Neutral:65.1162790697674	Amp:25.5813953488372	Del:9.30232558139535
TP53-gr	*RIMKLB*	57494	12p13.31	Neutral:48.8372093023256	Amp:27.906976744186	Del:23.2558139534884
TP53-gr	*UBE2N*	7334	12q22	Neutral:72.0930232558139	Amp:18.6046511627907	Del:9.30232558139535
TP53-gr	*UHRF1BP1L*	23074	12q23.1	Neutral:67.4418604651163	Amp:9.30232558139535	Del:23.2558139534884
TP53-gr	*ING1*	3621	13q34	Neutral:34.8837209302326	Amp:48.8372093023256	Del:16.2790697674419
TP53-gr	*MRP63*	78988	13q12.11	Neutral:23.2558139534884	Amp:6.97674418604651	Del:69.7674418604651
TP53-gr	*NDFIP2*	54602	13q31.1	Neutral:41.8604651162791	Amp:25.5813953488372	Del:32.5581395348837
TP53-gr	*SLITRK1*	114798	13q31.1	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*SPRY2*	10253	13q31.1	Neutral:46.5116279069767	Amp:18.6046511627907	Del:34.8837209302326
TP53-gr	*ZDHHC20*	253832	13q12.11	Neutral:34.8837209302326	Amp:2.32558139534884	Del:62.7906976744186
TP53-gr	*AK7*	122481	14q32.2	Neutral:41.8604651162791	Amp:0	Del:58.1395348837209
TP53-gr	*C14orf80*	283643	14q32.33	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*CRIP1*	1396	14q32.33	Neutral:39.5348837209302	Amp:30.2325581395349	Del:30.2325581395349
TP53-gr	*PAPOLA*	10914	14q32.2	Neutral:30.2325581395349	Amp:16.2790697674419	Del:53.4883720930233
TP53-gr	*POTEM*	641455	14q11.2	Neutral:51.1627906976744	Amp:27.906976744186	Del:20.9302325581395
TP53-gr	*VRK1*	7443	14q32.2	Neutral:34.8837209302326	Amp:20.9302325581395	Del:44.1860465116279
TP53-gr	*CYFIP1*	23191	15q11.2	Neutral:55.8139534883721	Amp:11.6279069767442	Del:32.5581395348837
TP53-gr	*NIPA1*	123606	15q11.2	Neutral:58.1395348837209	Amp:6.97674418604651	Del:34.8837209302326
TP53-gr	*NIPA2*	81614	15q11.2	Neutral:53.4883720930233	Amp:11.6279069767442	Del:34.8837209302326
TP53-gr	*PSTPIP1*	9051	15q24.3	Neutral:41.8604651162791	Amp:32.5581395348837	Del:25.5813953488372
TP53-gr	*TSPAN3*	10099	15q24.3	Neutral:72.0930232558139	Amp:16.2790697674419	Del:11.6279069767442
TP53-gr	*AMDHD2*	51005	16p13.3	Neutral:30.2325581395349	Amp:37.2093023255814	Del:32.5581395348837
TP53-gr	*ATP6V0C*	527	16p13.3	Neutral:27.906976744186	Amp:37.2093023255814	Del:34.8837209302326
TP53-gr	*B3GNT9*	84752	16q22.1	Neutral:41.8604651162791	Amp:20.9302325581395	Del:37.2093023255814
TP53-gr	*C16orf70*	80262	16q22.1	Neutral:39.5348837209302	Amp:16.2790697674419	Del:44.1860465116279
TP53-gr	*CBFB*	865	16q22.1	Neutral:41.8604651162791	Amp:9.30232558139535	Del:48.8372093023256
TP53-gr	*CES4A*	283848	16q22.1	Neutral:30.2325581395349	Amp:20.9302325581395	Del:48.8372093023256
TP53-gr	*CLEC18C*	283971	16q22.1	Neutral:41.8604651162791	Amp:18.6046511627907	Del:39.5348837209302
TP53-gr	*FAHD1*	81889	16p13.3	Neutral:51.1627906976744	Amp:11.6279069767442	Del:37.2093023255814
TP53-gr	*HAGH*	3029	16p13.3	Neutral:39.5348837209302	Amp:23.2558139534884	Del:37.2093023255814

TP53-gr	*PDPR*	55066	16q22.1	Neutral:39.5348837209302	Amp:11.6279069767442	Del:48.8372093023256
TP53-gr	*SNORA64*	26784	16p13.3	Neutral:37.2093023255814	Amp:32.5581395348837	Del:30.2325581395349
TP53-gr	*ZNF720*	124411	16p11.2	Neutral:62.7906976744186	Amp:13.953488372093	Del:23.2558139534884
TP53-gr	*CEP95*	90799	17q23.3	Neutral:53.4883720930233	Amp:44.1860465116279	Del:2.32558139534884
TP53-gr	*CRK*	1398	17p13.3	Neutral:20.9302325581395	Amp:6.97674418604651	Del:72.0930232558139
TP53-gr	*DDX5*	1655	17q23.3	Neutral:51.1627906976744	Amp:48.8372093023256	Del:0
TP53-gr	*DNAH17*	8632	17q25.3	Neutral:30.2325581395349	Amp:41.8604651162791	Del:27.906976744186
TP53-gr	*LRRC37B*	114659	17q11.2	Neutral:67.4418604651163	Amp:13.953488372093	Del:18.6046511627907
TP53-gr	*MYO1C*	4641	17p13.3	Neutral:30.2325581395349	Amp:16.2790697674419	Del:53.4883720930233
TP53-gr	*SERPINF1*	5176	17p13.3	Neutral:34.8837209302326	Amp:11.6279069767442	Del:53.4883720930233
TP53-gr	*SERPINF2*	5345	17p13.3	Neutral:30.2325581395349	Amp:16.2790697674419	Del:53.4883720930233
TP53-gr	*SMYD4*	114826	17p13.3	Neutral:27.906976744186	Amp:9.30232558139535	Del:62.7906976744186
TP53-gr	*SUZ12*	23512	17q11.2	Neutral:65.1162790697674	Amp:11.6279069767442	Del:23.2558139534884
TP53-gr	*TUSC5*	286753	17p13.3	Neutral:27.906976744186	Amp:9.30232558139535	Del:62.7906976744186
TP53-gr	*UTP6*	55813	17q11.2	Neutral:37.2093023255814	Amp:16.2790697674419	Del:46.5116279069767
TP53-gr	*WDR81*	124997	17p13.3	Neutral:27.906976744186	Amp:20.9302325581395	Del:51.1627906976744
TP53-gr	*YWHAE*	7531	17p13.3	Neutral:23.2558139534884	Amp:4.65116279069767	Del:72.0930232558139
TP53-gr	*GALNT1*	2589	18q12.2	Neutral:39.5348837209302	Amp:20.9302325581395	Del:39.5348837209302
TP53-gr	*GALR1*	2587	18q23	Neutral:46.5116279069767	Amp:11.6279069767442	Del:41.8604651162791
TP53-gr	*INO80C*	125476	18q12.2	Neutral:39.5348837209302	Amp:34.8837209302326	Del:25.5813953488372
TP53-gr	*MBP*	4155	18q23	Neutral:51.1627906976744	Amp:13.953488372093	Del:34.8837209302326
TP53-gr	*ROCK1P1*	727758	18p11.32	Neutral:53.4883720930233	Amp:25.5813953488372	Del:20.9302325581395
TP53-gr	*SALL3*	27164	18q23	Neutral:53.4883720930233	Amp:23.2558139534884	Del:23.2558139534884
TP53-gr	*THOC1*	9984	18p11.32	Neutral:55.8139534883721	Amp:18.6046511627907	Del:25.5813953488372
TP53-gr	*USP14*	9097	18p11.32	Neutral:62.7906976744186	Amp:18.6046511627907	Del:18.6046511627907
TP53-gr	*EID2B*	126272	19q13.2	Neutral:32.5581395348837	Amp:44.1860465116279	Del:23.2558139534884
TP53-gr	*EPN1*	29924	19q13.42	Neutral:41.8604651162791	Amp:32.5581395348837	Del:25.5813953488372
TP53-gr	*GMIP*	51291	19p13.11	Neutral:34.8837209302326	Amp:27.906976744186	Del:37.2093023255814
TP53-gr	*LONP1*	9361	19p13.3	Neutral:23.2558139534884	Amp:30.2325581395349	Del:46.5116279069767
TP53-gr	*LPAR2*	9170	19p13.11	Neutral:39.5348837209302	Amp:23.2558139534884	Del:37.2093023255814
TP53-gr	*NLRP9*	338321	19q13.42	Neutral:44.1860465116279	Amp:18.6046511627907	Del:37.2093023255814
TP53-gr	*PRR22*	163154	19p13.3	Neutral:30.2325581395349	Amp:20.9302325581395	Del:48.8372093023256
TP53-gr	*RFPL4A*	342931	19q13.42	Neutral:46.5116279069767	Amp:25.5813953488372	Del:27.906976744186
TP53-gr	*ABHD12*	26090	20p11.21	Neutral:51.1627906976744	Amp:30.2325581395349	Del:18.6046511627907
TP53-gr	*ABHD16B*	140701	20q13.33	Neutral:20.9302325581395	Amp:58.1395348837209	Del:20.9302325581395
TP53-gr	*ACSS1*	84532	20p11.21	Neutral:53.4883720930233	Amp:39.5348837209302	Del:6.97674418604651
TP53-gr	*ADAM33*	80332	20p13	Neutral:46.5116279069767	Amp:30.2325581395349	Del:23.2558139534884
TP53-gr	*ADRA1D*	146	20p13	Neutral:53.4883720930233	Amp:18.6046511627907	Del:27.906976744186
TP53-gr	*ADRM1*	11047	20q13.33	Neutral:27.906976744186	Amp:51.1627906976744	Del:20.9302325581395
TP53-gr	*ANGPT4*	51378	20p13	Neutral:51.1627906976744	Amp:27.906976744186	Del:20.9302325581395
TP53-gr	*ARFGAP1*	55738	20q13.33	Neutral:30.2325581395349	Amp:55.8139534883721	Del:13.953488372093

TP53-gr	*ARFRP1*	10139	20q13.33	Neutral:16.2790697674419	Amp:60.4651162790698	Del:23.2558139534884
TP53-gr	*ASXL1*	171023	20q11.21	Neutral:53.4883720930233	Amp:44.1860465116279	Del:2.32558139534884
TP53-gr	*ATRN*	8455	20p13	Neutral:65.1162790697674	Amp:16.2790697674419	Del:18.6046511627907
TP53-gr	*AVP*	551	20p13	Neutral:39.5348837209302	Amp:30.2325581395349	Del:30.2325581395349
TP53-gr	*BCL2L1*	598	20q11.21	Neutral:39.5348837209302	Amp:39.5348837209302	Del:20.9302325581395
TP53-gr	*BHLHE23*	128408	20q13.33	Neutral:30.2325581395349	Amp:58.1395348837209	Del:11.6279069767442
TP53-gr	*BIRC7*	79444	20q13.33	Neutral:32.5581395348837	Amp:55.8139534883721	Del:11.6279069767442
TP53-gr	*BMP7*	655	20q13.31	Neutral:53.4883720930233	Amp:39.5348837209302	Del:6.97674418604651
TP53-gr	*BPIFA1*	51297	20q11.21	Neutral:55.8139534883721	Amp:41.8604651162791	Del:2.32558139534884
TP53-gr	*BPIFA2*	140683	20q11.21	Neutral:60.4651162790698	Amp:37.2093023255814	Del:2.32558139534884
TP53-gr	*BPIFA3*	128861	20q11.21	Neutral:53.4883720930233	Amp:41.8604651162791	Del:4.65116279069767
TP53-gr	*BPIFA4P*	317716	20q11.21	Neutral:58.1395348837209	Amp:39.5348837209302	Del:2.32558139534884
TP53-gr	*BPIFB1*	92747	20q11.21	Neutral:41.8604651162791	Amp:41.8604651162791	Del:16.2790697674419
TP53-gr	*BPIFB2*	80341	20q11.21	Neutral:41.8604651162791	Amp:53.4883720930233	Del:4.65116279069767
TP53-gr	*BPIFB3*	359710	20q11.21	Neutral:46.5116279069767	Amp:51.1627906976744	Del:2.32558139534884
TP53-gr	*BPIFB4*	149954	20q11.21	Neutral:48.8372093023256	Amp:48.8372093023256	Del:2.32558139534884
TP53-gr	*BPIFB6*	128859	20q11.21	Neutral:44.1860465116279	Amp:51.1627906976744	Del:4.65116279069767
TP53-gr	*C20orf112*	140688	20q11.21	Neutral:27.906976744186	Amp:58.1395348837209	Del:13.953488372093
TP53-gr	*C20orf141*	128653	20p13	Neutral:51.1627906976744	Amp:23.2558139534884	Del:25.5813953488372
TP53-gr	*C20orf166*	128826	20q13.33	Neutral:27.906976744186	Amp:60.4651162790698	Del:11.6279069767442
TP53-gr	*C20orf166-AS1*	253868	20q13.33	Neutral:25.5813953488372	Amp:60.4651162790698	Del:13.953488372093
TP53-gr	*C20orf194*	25943	20p13	Neutral:48.8372093023256	Amp:11.6279069767442	Del:39.5348837209302
TP53-gr	*C20orf195*	79025	20q13.33	Neutral:18.6046511627907	Amp:60.4651162790698	Del:20.9302325581395
TP53-gr	*C20orf197*	284756	20q13.33	Neutral:44.1860465116279	Amp:51.1627906976744	Del:4.65116279069767
TP53-gr	*C20orf201*	198437	20q13.33	Neutral:20.9302325581395	Amp:60.4651162790698	Del:18.6046511627907
TP53-gr	*C20orf202*	400831	20p13	Neutral:62.7906976744186	Amp:20.9302325581395	Del:16.2790697674419
TP53-gr	*C20orf203*	284805	20q11.21	Neutral:32.5581395348837	Amp:44.1860465116279	Del:23.2558139534884
TP53-gr	*C20orf27*	54976	20p13	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*C20orf96*	140680	20p13	Neutral:53.4883720930233	Amp:25.5813953488372	Del:20.9302325581395
TP53-gr	*CABLES2*	81928	20q13.33	Neutral:25.5813953488372	Amp:60.4651162790698	Del:13.953488372093
TP53-gr	*CBFA2T2*	9139	20q11.21	Neutral:58.1395348837209	Amp:34.8837209302326	Del:6.97674418604651
TP53-gr	*CD93*	22918	20p11.21	Neutral:34.8837209302326	Amp:48.8372093023256	Del:16.2790697674419
TP53-gr	*CDC25B*	994	20p13	Neutral:41.8604651162791	Amp:30.2325581395349	Del:27.906976744186
TP53-gr	*CDH26*	60437	20q13.33	Neutral:53.4883720930233	Amp:44.1860465116279	Del:2.32558139534884
TP53-gr	*CDH4*	1002	20q13.33	Neutral:51.1627906976744	Amp:39.5348837209302	Del:9.30232558139535
TP53-gr	*CDK5RAP1*	51654	20q11.21	Neutral:41.8604651162791	Amp:32.5581395348837	Del:25.5813953488372
TP53-gr	*CENPB*	1059	20p13	Neutral:39.5348837209302	Amp:30.2325581395349	Del:30.2325581395349
TP53-gr	*CHRNA4*	1137	20q13.33	Neutral:30.2325581395349	Amp:58.1395348837209	Del:11.6279069767442
TP53-gr	*COL20A1*	57642	20q13.33	Neutral:30.2325581395349	Amp:55.8139534883721	Del:13.953488372093
TP53-gr	*COL9A3*	1299	20q13.33	Neutral:23.2558139534884	Amp:58.1395348837209	Del:18.6046511627907
TP53-gr	*COMMD7*	149951	20q11.21	Neutral:27.906976744186	Amp:37.2093023255814	Del:34.8837209302326

TP53-gr	*COX4I2*	84701	20q11.21	Neutral:34.8837209302326	Amp:39.5348837209302	Del:25.5813953488372
TP53-gr	*CPXM1*	56265	20p13	Neutral:46.5116279069767	Amp:27.906976744186	Del:25.5813953488372
TP53-gr	*CSNK2A1*	1457	20p13	Neutral:72.0930232558139	Amp:13.953488372093	Del:13.953488372093
TP53-gr	*CST1*	1469	20p11.21	Neutral:48.8372093023256	Amp:39.5348837209302	Del:11.6279069767442
TP53-gr	*CST11*	140880	20p11.21	Neutral:62.7906976744186	Amp:25.5813953488372	Del:11.6279069767442
TP53-gr	*CST2*	1470	20p11.21	Neutral:48.8372093023256	Amp:39.5348837209302	Del:11.6279069767442
TP53-gr	*CST3*	1471	20p11.21	Neutral:46.5116279069767	Amp:41.8604651162791	Del:11.6279069767442
TP53-gr	*CST4*	1472	20p11.21	Neutral:48.8372093023256	Amp:39.5348837209302	Del:11.6279069767442
TP53-gr	*CST5*	1473	20p11.21	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*CST7*	8530	20p11.21	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*CST8*	10047	20p11.21	Neutral:60.4651162790698	Amp:27.906976744186	Del:11.6279069767442
TP53-gr	*CST9*	128822	20p11.21	Neutral:58.1395348837209	Amp:32.5581395348837	Del:9.30232558139535
TP53-gr	*CST9L*	128821	20p11.21	Neutral:62.7906976744186	Amp:23.2558139534884	Del:13.953488372093
TP53-gr	*CSTL1*	128817	20p11.21	Neutral:65.1162790697674	Amp:20.9302325581395	Del:13.953488372093
TP53-gr	*CTCFL*	140690	20q13.31	Neutral:51.1627906976744	Amp:44.1860465116279	Del:4.65116279069767
TP53-gr	*DDRGK1*	65992	20p13	Neutral:39.5348837209302	Amp:30.2325581395349	Del:30.2325581395349
TP53-gr	*DEFB115*	245929	20q11.21	Neutral:53.4883720930233	Amp:23.2558139534884	Del:23.2558139534884
TP53-gr	*DEFB116*	245930	20q11.21	Neutral:60.4651162790698	Amp:27.906976744186	Del:11.6279069767442
TP53-gr	*DEFB118*	117285	20q11.21	Neutral:60.4651162790698	Amp:25.5813953488372	Del:13.953488372093
TP53-gr	*DEFB119*	245932	20q11.21	Neutral:60.4651162790698	Amp:27.906976744186	Del:11.6279069767442
TP53-gr	*DEFB121*	245934	20q11.21	Neutral:65.1162790697674	Amp:23.2558139534884	Del:11.6279069767442
TP53-gr	*DEFB122*	245935	20q11.21	Neutral:55.8139534883721	Amp:27.906976744186	Del:16.2790697674419
TP53-gr	*DEFB123*	245936	20q11.21	Neutral:46.5116279069767	Amp:34.8837209302326	Del:18.6046511627907
TP53-gr	*DEFB124*	245937	20q11.21	Neutral:44.1860465116279	Amp:37.2093023255814	Del:18.6046511627907
TP53-gr	*DEFB125*	245938	20p13	Neutral:60.4651162790698	Amp:16.2790697674419	Del:23.2558139534884
TP53-gr	*DEFB126*	81623	20p13	Neutral:55.8139534883721	Amp:13.953488372093	Del:30.2325581395349
TP53-gr	*DEFB127*	140850	20p13	Neutral:51.1627906976744	Amp:16.2790697674419	Del:32.5581395348837
TP53-gr	*DEFB128*	245939	20p13	Neutral:55.8139534883721	Amp:13.953488372093	Del:30.2325581395349
TP53-gr	*DEFB129*	140881	20p13	Neutral:65.1162790697674	Amp:13.953488372093	Del:20.9302325581395
TP53-gr	*DEFB132*	400830	20p13	Neutral:58.1395348837209	Amp:20.9302325581395	Del:20.9302325581395
TP53-gr	*DIDO1*	11083	20q13.33	Neutral:39.5348837209302	Amp:55.8139534883721	Del:4.65116279069767
TP53-gr	*DNAJC5*	80331	20q13.33	Neutral:23.2558139534884	Amp:53.4883720930233	Del:23.2558139534884
TP53-gr	*DNMT3B*	1789	20q11.21	Neutral:48.8372093023256	Amp:39.5348837209302	Del:11.6279069767442
TP53-gr	*DPH3P1*	100132911	20q13.33	Neutral:34.8837209302326	Amp:46.5116279069767	Del:18.6046511627907
TP53-gr	*DUSP15*	128853	20q11.21	Neutral:39.5348837209302	Amp:46.5116279069767	Del:13.953488372093
TP53-gr	*EBF4*	57593	20p13	Neutral:46.5116279069767	Amp:27.906976744186	Del:25.5813953488372
TP53-gr	*EEF1A2*	1917	20q13.33	Neutral:23.2558139534884	Amp:58.1395348837209	Del:18.6046511627907
TP53-gr	*ENTPD6*	955	20p11.21	Neutral:44.1860465116279	Amp:39.5348837209302	Del:16.2790697674419
TP53-gr	*FAM110A*	83541	20p13	Neutral:55.8139534883721	Amp:25.5813953488372	Del:18.6046511627907
TP53-gr	*FAM209A*	200232	20q13.31	Neutral:55.8139534883721	Amp:27.906976744186	Del:16.2790697674419
TP53-gr	*FAM209B*	388799	20q13.31	Neutral:58.1395348837209	Amp:25.5813953488372	Del:16.2790697674419

TP53-gr	*FAM217B*	63939	20q13.33	Neutral:53.4883720930233	Amp:44.1860465116279	Del:2.32558139534884
TP53-gr	*FASTKD5*	60493	20p13	Neutral:41.8604651162791	Amp:18.6046511627907	Del:39.5348837209302
TP53-gr	*FKBP1A*	2280	20p13	Neutral:55.8139534883721	Amp:30.2325581395349	Del:13.953488372093
TP53-gr	*FOXA2*	3170	20p11.21	Neutral:34.8837209302326	Amp:46.5116279069767	Del:18.6046511627907
TP53-gr	*FOXS1*	2307	20q11.21	Neutral:37.2093023255814	Amp:48.8372093023256	Del:13.953488372093
TP53-gr	*FRG1B*	284802	20q11.21	Neutral:48.8372093023256	Amp:27.906976744186	Del:23.2558139534884
TP53-gr	*GATA5*	140628	20q13.33	Neutral:30.2325581395349	Amp:58.1395348837209	Del:11.6279069767442
TP53-gr	*GCNT7*	140687	20q13.31	Neutral:67.4418604651163	Amp:23.2558139534884	Del:9.30232558139535
TP53-gr	*GFRA4*	64096	20p13	Neutral:48.8372093023256	Amp:30.2325581395349	Del:20.9302325581395
TP53-gr	*GGTLC1*	92086	20p11.21	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*GINS1*	9837	20p11.21	Neutral:58.1395348837209	Amp:9.30232558139535	Del:32.5581395348837
TP53-gr	*GMEB2*	26205	20q13.33	Neutral:18.6046511627907	Amp:60.4651162790698	Del:20.9302325581395
TP53-gr	*GNRH2*	2797	20p13	Neutral:48.8372093023256	Amp:23.2558139534884	Del:27.906976744186
TP53-gr	*GZF1*	64412	20p11.21	Neutral:53.4883720930233	Amp:37.2093023255814	Del:9.30232558139535
TP53-gr	*HAR1A*	768096	20q13.33	Neutral:34.8837209302326	Amp:53.4883720930233	Del:11.6279069767442
TP53-gr	*HAR1B*	768097	20q13.33	Neutral:34.8837209302326	Amp:53.4883720930233	Del:11.6279069767442
TP53-gr	*HCK*	3055	20q11.21	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*HM13*	81502	20q11.21	Neutral:39.5348837209302	Amp:37.2093023255814	Del:23.2558139534884
TP53-gr	*HRH3*	11255	20q13.33	Neutral:25.5813953488372	Amp:51.1627906976744	Del:23.2558139534884
TP53-gr	*HSPA12B*	116835	20p13	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*ID1*	3397	20q11.21	Neutral:32.5581395348837	Amp:41.8604651162791	Del:25.5813953488372
TP53-gr	*IDH3B*	3420	20p13	Neutral:53.4883720930233	Amp:27.906976744186	Del:18.6046511627907
TP53-gr	*ITPA*	3704	20p13	Neutral:37.2093023255814	Amp:30.2325581395349	Del:32.5581395348837
TP53-gr	*KCNQ2*	3785	20q13.33	Neutral:30.2325581395349	Amp:55.8139534883721	Del:13.953488372093
TP53-gr	*KIF3B*	9371	20q11.21	Neutral:51.1627906976744	Amp:32.5581395348837	Del:16.2790697674419
TP53-gr	*LAMA5*	3911	20q13.33	Neutral:25.5813953488372	Amp:51.1627906976744	Del:23.2558139534884
TP53-gr	*LIME1*	54923	20q13.33	Neutral:23.2558139534884	Amp:58.1395348837209	Del:18.6046511627907
TP53-gr	*LINC00028*	140875	20q11.21	Neutral:37.2093023255814	Amp:41.8604651162791	Del:20.9302325581395
TP53-gr	*LINC00029*	100144596	20q13.33	Neutral:32.5581395348837	Amp:55.8139534883721	Del:11.6279069767442
TP53-gr	*LINC00176*	284739	20q13.33	Neutral:25.5813953488372	Amp:55.8139534883721	Del:18.6046511627907
TP53-gr	*LINC00261*	140828	20p11.21	Neutral:39.5348837209302	Amp:41.8604651162791	Del:18.6046511627907
TP53-gr	*LINC00266-1*	140849	20q13.33	Neutral:58.1395348837209	Amp:34.8837209302326	Del:6.97674418604651
TP53-gr	*LSM14B*	149986	20q13.33	Neutral:32.5581395348837	Amp:55.8139534883721	Del:11.6279069767442
TP53-gr	*MAPRE1*	22919	20q11.21	Neutral:53.4883720930233	Amp:30.2325581395349	Del:16.2790697674419
TP53-gr	*MAVS*	57506	20p13	Neutral:39.5348837209302	Amp:25.5813953488372	Del:34.8837209302326
TP53-gr	*MIR1-1*	406904	20q13.33	Neutral:27.906976744186	Amp:60.4651162790698	Del:11.6279069767442
TP53-gr	*MIR103A2*	406896	20p13	Neutral:67.4418604651163	Amp:9.30232558139535	Del:23.2558139534884
TP53-gr	*MIR124-3*	406909	20q13.33	Neutral:34.8837209302326	Amp:53.4883720930233	Del:11.6279069767442
TP53-gr	*MIR1257*	100302168	20q13.33	Neutral:46.5116279069767	Amp:44.1860465116279	Del:9.30232558139535
TP53-gr	*MIR1292*	100302138	20p13	Neutral:65.1162790697674	Amp:18.6046511627907	Del:16.2790697674419
TP53-gr	*MIR133A2*	406923	20q13.33	Neutral:30.2325581395349	Amp:58.1395348837209	Del:11.6279069767442

TP53-gr	*MIR1914*	100302137	20q13.33	Neutral:25.5813953488372	Amp:55.8139534883721	Del:18.6046511627907
TP53-gr	*MIR3193*	100422904	20q11.21	Neutral:32.5581395348837	Amp:41.8604651162791	Del:25.5813953488372
TP53-gr	*MIR3196*	100423014	20q13.33	Neutral:34.8837209302326	Amp:53.4883720930233	Del:11.6279069767442
TP53-gr	*MIR4325*	100422883	20q13.31	Neutral:55.8139534883721	Amp:30.2325581395349	Del:13.953488372093
TP53-gr	*MIR4326*	100422945	20q13.33	Neutral:30.2325581395349	Amp:55.8139534883721	Del:13.953488372093
TP53-gr	*MIR4532*	100616353	20q13.31	Neutral:46.5116279069767	Amp:48.8372093023256	Del:4.65116279069767
TP53-gr	*MIR4533*	100616362	20q13.33	Neutral:46.5116279069767	Amp:48.8372093023256	Del:4.65116279069767
TP53-gr	*MIR4758*	100616340	20q13.33	Neutral:27.906976744186	Amp:48.8372093023256	Del:23.2558139534884
TP53-gr	*MIR647*	693232	20q13.33	Neutral:25.5813953488372	Amp:55.8139534883721	Del:18.6046511627907
TP53-gr	*MIR941-1*	100126329	20q13.33	Neutral:23.2558139534884	Amp:53.4883720930233	Del:23.2558139534884
TP53-gr	*MIR941-2*	100126339	20q13.33	Neutral:23.2558139534884	Amp:53.4883720930233	Del:23.2558139534884
TP53-gr	*MIR941-3*	100126352	20q13.33	Neutral:23.2558139534884	Amp:53.4883720930233	Del:23.2558139534884
TP53-gr	*MLLT10P1*	140678	20q11.21	Neutral:58.1395348837209	Amp:18.6046511627907	Del:23.2558139534884
TP53-gr	*MRPS26*	64949	20p13	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*MTRNR2L3*	100462983	20q13.31	Neutral:44.1860465116279	Amp:48.8372093023256	Del:6.97674418604651
TP53-gr	*MYLK2*	85366	20q11.21	Neutral:39.5348837209302	Amp:51.1627906976744	Del:9.30232558139535
TP53-gr	*MYT1*	4661	20q13.33	Neutral:34.8837209302326	Amp:55.8139534883721	Del:9.30232558139535
TP53-gr	*NANP*	140838	20p11.21	Neutral:65.1162790697674	Amp:18.6046511627907	Del:16.2790697674419
TP53-gr	*NAPB*	63908	20p11.21	Neutral:58.1395348837209	Amp:27.906976744186	Del:13.953488372093
TP53-gr	*NINL*	22981	20p11.21	Neutral:55.8139534883721	Amp:25.5813953488372	Del:18.6046511627907
TP53-gr	*NKAIN4*	128414	20q13.33	Neutral:27.906976744186	Amp:58.1395348837209	Del:13.953488372093
TP53-gr	*NOP56*	10528	20p13	Neutral:60.4651162790698	Amp:23.2558139534884	Del:16.2790697674419
TP53-gr	*NPBWR2*	2832	20q13.33	Neutral:23.2558139534884	Amp:60.4651162790698	Del:16.2790697674419
TP53-gr	*NRSN2*	80023	20p13	Neutral:44.1860465116279	Amp:25.5813953488372	Del:30.2325581395349
TP53-gr	*NSFL1C*	55968	20p13	Neutral:62.7906976744186	Amp:27.906976744186	Del:9.30232558139535
TP53-gr	*NTSR1*	4923	20q13.33	Neutral:23.2558139534884	Amp:60.4651162790698	Del:16.2790697674419
TP53-gr	*NXT1*	29107	20p11.21	Neutral:41.8604651162791	Amp:44.1860465116279	Del:13.953488372093
TP53-gr	*OGFR*	11054	20q13.33	Neutral:25.5813953488372	Amp:58.1395348837209	Del:16.2790697674419
TP53-gr	*OPRL1*	4987	20q13.33	Neutral:20.9302325581395	Amp:60.4651162790698	Del:18.6046511627907
TP53-gr	*OSBPL2*	9885	20q13.33	Neutral:30.2325581395349	Amp:51.1627906976744	Del:18.6046511627907
TP53-gr	*OXT*	5020	20p13	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*PANK2*	80025	20p13	Neutral:72.0930232558139	Amp:6.97674418604651	Del:20.9302325581395
TP53-gr	*PCK1*	5105	20q13.31	Neutral:51.1627906976744	Amp:44.1860465116279	Del:4.65116279069767
TP53-gr	*PCMTD2*	55251	20q13.33	Neutral:55.8139534883721	Amp:41.8604651162791	Del:2.32558139534884
TP53-gr	*PCNA*	5111	20p13	Neutral:67.4418604651163	Amp:6.97674418604651	Del:25.5813953488372
TP53-gr	*PDRG1*	81572	20q11.21	Neutral:39.5348837209302	Amp:46.5116279069767	Del:13.953488372093
TP53-gr	*PDYN*	5173	20p13	Neutral:65.1162790697674	Amp:25.5813953488372	Del:9.30232558139535
TP53-gr	*PLAGL2*	5326	20q11.21	Neutral:53.4883720930233	Amp:37.2093023255814	Del:9.30232558139535
TP53-gr	*PMEPA1*	56937	20q13.31	Neutral:48.8372093023256	Amp:46.5116279069767	Del:4.65116279069767
TP53-gr	*POFUT1*	23509	20q11.21	Neutral:55.8139534883721	Amp:34.8837209302326	Del:9.30232558139535
TP53-gr	*PPDPF*	79144	20q13.33	Neutral:23.2558139534884	Amp:58.1395348837209	Del:18.6046511627907

TP53-gr	*PPP1R3D*	5509	20q13.33	Neutral:41.8604651162791	Amp:53.4883720930233	Del:4.65116279069767
TP53-gr	*PRND*	23627	20p13	Neutral:69.7674418604651	Amp:16.2790697674419	Del:13.953488372093
TP53-gr	*PRNP*	5621	20p13	Neutral:69.7674418604651	Amp:16.2790697674419	Del:13.953488372093
TP53-gr	*PRNT*	149830	20p13	Neutral:67.4418604651163	Amp:13.953488372093	Del:18.6046511627907
TP53-gr	*PRPF6*	24148	20q13.33	Neutral:25.5813953488372	Amp:51.1627906976744	Del:23.2558139534884
TP53-gr	*PSMA7*	5688	20q13.33	Neutral:27.906976744186	Amp:60.4651162790698	Del:11.6279069767442
TP53-gr	*PSMF1*	9491	20p13	Neutral:72.0930232558139	Amp:18.6046511627907	Del:9.30232558139535
TP53-gr	*PTK6*	5753	20q13.33	Neutral:20.9302325581395	Amp:58.1395348837209	Del:20.9302325581395
TP53-gr	*PTPRA*	5786	20p13	Neutral:69.7674418604651	Amp:13.953488372093	Del:16.2790697674419
TP53-gr	*PYGB*	5834	20p11.21	Neutral:44.1860465116279	Amp:37.2093023255814	Del:18.6046511627907
TP53-gr	*RAD21L1*	642636	20p13	Neutral:44.1860465116279	Amp:25.5813953488372	Del:30.2325581395349
TP53-gr	*RAE1*	8480	20q13.31	Neutral:41.8604651162791	Amp:53.4883720930233	Del:4.65116279069767
TP53-gr	*RASSF2*	9770	20p13	Neutral:69.7674418604651	Amp:11.6279069767442	Del:18.6046511627907
TP53-gr	*RBCK1*	10616	20p13	Neutral:46.5116279069767	Amp:25.5813953488372	Del:27.906976744186
TP53-gr	*RBM38*	55544	20q13.31	Neutral:34.8837209302326	Amp:48.8372093023256	Del:16.2790697674419
TP53-gr	*REM1*	28954	20q11.21	Neutral:37.2093023255814	Amp:41.8604651162791	Del:20.9302325581395
TP53-gr	*RGS19*	10287	20q13.33	Neutral:20.9302325581395	Amp:60.4651162790698	Del:18.6046511627907
TP53-gr	*RNF24*	11237	20p13	Neutral:65.1162790697674	Amp:6.97674418604651	Del:27.906976744186
TP53-gr	*RPS21*	6227	20q13.33	Neutral:27.906976744186	Amp:58.1395348837209	Del:13.953488372093
TP53-gr	*RSPO4*	343637	20p13	Neutral:58.1395348837209	Amp:23.2558139534884	Del:18.6046511627907
TP53-gr	*RTEL1*	51750	20q13.33	Neutral:18.6046511627907	Amp:60.4651162790698	Del:20.9302325581395
TP53-gr	*RTEL1-TNFRSF6B*	100533107	20q13.33	Neutral:18.6046511627907	Amp:60.4651162790698	Del:20.9302325581395
TP53-gr	*SAMD10*	140700	20q13.33	Neutral:30.2325581395349	Amp:51.1627906976744	Del:18.6046511627907
TP53-gr	*SCRT2*	85508	20p13	Neutral:55.8139534883721	Amp:25.5813953488372	Del:18.6046511627907
TP53-gr	*SDCBP2*	27111	20p13	Neutral:48.8372093023256	Amp:27.906976744186	Del:23.2558139534884
TP53-gr	*SIGLEC1*	6614	20p13	Neutral:39.5348837209302	Amp:30.2325581395349	Del:30.2325581395349
TP53-gr	*SIRPA*	140885	20p13	Neutral:62.7906976744186	Amp:25.5813953488372	Del:11.6279069767442
TP53-gr	*SIRPB1*	10326	20p13	Neutral:55.8139534883721	Amp:32.5581395348837	Del:11.6279069767442
TP53-gr	*SIRPB2*	284759	20p13	Neutral:67.4418604651163	Amp:20.9302325581395	Del:11.6279069767442
TP53-gr	*SIRPD*	128646	20p13	Neutral:62.7906976744186	Amp:27.906976744186	Del:9.30232558139535
TP53-gr	*SIRPG*	55423	20p13	Neutral:65.1162790697674	Amp:27.906976744186	Del:6.97674418604651
TP53-gr	*SLC17A9*	63910	20q13.33	Neutral:30.2325581395349	Amp:58.1395348837209	Del:11.6279069767442
TP53-gr	*SLC23A2*	9962	20p13	Neutral:76.7441860465116	Amp:6.97674418604651	Del:16.2790697674419
TP53-gr	*SLC2A4RG*	56731	20q13.33	Neutral:23.2558139534884	Amp:55.8139534883721	Del:20.9302325581395
TP53-gr	*SLC4A11*	83959	20p13	Neutral:34.8837209302326	Amp:34.8837209302326	Del:30.2325581395349
TP53-gr	*SLCO4A1*	28231	20q13.33	Neutral:27.906976744186	Amp:58.1395348837209	Del:13.953488372093
TP53-gr	*SMOX*	54498	20p13	Neutral:62.7906976744186	Amp:18.6046511627907	Del:18.6046511627907
TP53-gr	*SNORA51*	677831	20p13	Neutral:60.4651162790698	Amp:23.2558139534884	Del:16.2790697674419
TP53-gr	*SNORD110*	692213	20p13	Neutral:62.7906976744186	Amp:20.9302325581395	Del:16.2790697674419
TP53-gr	*SNORD119*	100113378	20p13	Neutral:62.7906976744186	Amp:23.2558139534884	Del:13.953488372093
TP53-gr	*SNORD56*	26793	20p13	Neutral:60.4651162790698	Amp:23.2558139534884	Del:16.2790697674419

TP53-gr	*SNORD57*	26792	20p13	Neutral:60.4651162790698	Amp:23.2558139534884	Del:16.2790697674419
TP53-gr	*SNORD86*	692201	20p13	Neutral:60.4651162790698	Amp:23.2558139534884	Del:16.2790697674419
TP53-gr	*SNPH*	9751	20p13	Neutral:53.4883720930233	Amp:23.2558139534884	Del:23.2558139534884
TP53-gr	*SNRPB*	6628	20p13	Neutral:65.1162790697674	Amp:23.2558139534884	Del:11.6279069767442
TP53-gr	*SNTA1*	6640	20q11.21	Neutral:34.8837209302326	Amp:39.5348837209302	Del:25.5813953488372
TP53-gr	*SOX12*	6666	20p13	Neutral:44.1860465116279	Amp:27.906976744186	Del:27.906976744186
TP53-gr	*SOX18*	54345	20q13.33	Neutral:25.5813953488372	Amp:55.8139534883721	Del:18.6046511627907
TP53-gr	*SPEF1*	25876	20p13	Neutral:41.8604651162791	Amp:27.906976744186	Del:30.2325581395349
TP53-gr	*SPO11*	23626	20q13.31	Neutral:41.8604651162791	Amp:41.8604651162791	Del:16.2790697674419
TP53-gr	*SRMS*	6725	20q13.33	Neutral:20.9302325581395	Amp:58.1395348837209	Del:20.9302325581395
TP53-gr	*SRXN1*	140809	20p13	Neutral:65.1162790697674	Amp:18.6046511627907	Del:16.2790697674419
TP53-gr	*SS18L1*	26039	20q13.33	Neutral:32.5581395348837	Amp:51.1627906976744	Del:16.2790697674419
TP53-gr	*SSTR4*	6754	20p11.21	Neutral:41.8604651162791	Amp:41.8604651162791	Del:16.2790697674419
TP53-gr	*STK35*	140901	20p13	Neutral:65.1162790697674	Amp:23.2558139534884	Del:11.6279069767442
TP53-gr	*STMN3*	50861	20q13.33	Neutral:18.6046511627907	Amp:58.1395348837209	Del:23.2558139534884
TP53-gr	*SUN5*	140732	20q11.21	Neutral:44.1860465116279	Amp:51.1627906976744	Del:4.65116279069767
TP53-gr	*SYCP2*	10388	20q13.33	Neutral:30.2325581395349	Amp:41.8604651162791	Del:27.906976744186
TP53-gr	*SYNDIG1*	79953	20p11.21	Neutral:48.8372093023256	Amp:41.8604651162791	Del:9.30232558139535
TP53-gr	*TAF4*	6874	20q13.33	Neutral:41.8604651162791	Amp:51.1627906976744	Del:6.97674418604651
TP53-gr	*TBC1D20*	128637	20p13	Neutral:60.4651162790698	Amp:16.2790697674419	Del:23.2558139534884
TP53-gr	*TCEA2*	6919	20q13.33	Neutral:20.9302325581395	Amp:60.4651162790698	Del:18.6046511627907
TP53-gr	*TCF15*	6939	20p13	Neutral:62.7906976744186	Amp:20.9302325581395	Del:16.2790697674419
TP53-gr	*TCFL5*	10732	20q13.33	Neutral:34.8837209302326	Amp:44.1860465116279	Del:20.9302325581395
TP53-gr	*TFAP2C*	7022	20q13.31	Neutral:55.8139534883721	Amp:23.2558139534884	Del:20.9302325581395
TP53-gr	*TGM3*	7053	20p13	Neutral:60.4651162790698	Amp:27.906976744186	Del:11.6279069767442
TP53-gr	*TGM6*	343641	20p13	Neutral:58.1395348837209	Amp:20.9302325581395	Del:20.9302325581395
TP53-gr	*THBD*	7056	20p11.21	Neutral:39.5348837209302	Amp:41.8604651162791	Del:18.6046511627907
TP53-gr	*TM9SF4*	9777	20q11.21	Neutral:44.1860465116279	Amp:41.8604651162791	Del:13.953488372093
TP53-gr	*TMC2*	117532	20p13	Neutral:72.0930232558139	Amp:16.2790697674419	Del:11.6279069767442
TP53-gr	*TMEM239*	100288797	20p13	Neutral:51.1627906976744	Amp:23.2558139534884	Del:25.5813953488372
TP53-gr	*TMEM74B*	55321	20p13	Neutral:58.1395348837209	Amp:25.5813953488372	Del:16.2790697674419
TP53-gr	*TNFRSF6B*	8771	20q13.33	Neutral:18.6046511627907	Amp:60.4651162790698	Del:20.9302325581395
TP53-gr	*TPD52L2*	7165	20q13.33	Neutral:30.2325581395349	Amp:53.4883720930233	Del:16.2790697674419
TP53-gr	*TPX2*	22974	20q11.21	Neutral:58.1395348837209	Amp:20.9302325581395	Del:20.9302325581395
TP53-gr	*TRIB3*	57761	20p13	Neutral:46.5116279069767	Amp:25.5813953488372	Del:27.906976744186
TP53-gr	*TSPY26P*	128854	20q11.21	Neutral:51.1627906976744	Amp:39.5348837209302	Del:9.30232558139535
TP53-gr	*TTLL9*	164395	20q11.21	Neutral:46.5116279069767	Amp:41.8604651162791	Del:11.6279069767442
TP53-gr	*UBOX5*	22888	20p13	Neutral:39.5348837209302	Amp:20.9302325581395	Del:39.5348837209302
TP53-gr	*UCKL1*	54963	20q13.33	Neutral:25.5813953488372	Amp:55.8139534883721	Del:18.6046511627907
TP53-gr	*VPS16*	64601	20p13	Neutral:51.1627906976744	Amp:27.906976744186	Del:20.9302325581395
TP53-gr	*VSX1*	30813	20p11.21	Neutral:53.4883720930233	Amp:39.5348837209302	Del:6.97674418604651

TP53-gr	*XKR7*	343702	20q11.21	Neutral:37.2093023255814	Amp:44.1860465116279	Del:18.6046511627907
TP53-gr	*YTHDF1*	54915	20q13.33	Neutral:37.2093023255814	Amp:51.1627906976744	Del:11.6279069767442
TP53-gr	*ZBP1*	81030	20q13.31	Neutral:48.8372093023256	Amp:39.5348837209302	Del:11.6279069767442
TP53-gr	*ZBTB46*	140685	20q13.33	Neutral:20.9302325581395	Amp:55.8139534883721	Del:23.2558139534884
TP53-gr	*ZCCHC3*	85364	20p13	Neutral:48.8372093023256	Amp:27.906976744186	Del:23.2558139534884
TP53-gr	*ZGPAT*	84619	20q13.33	Neutral:20.9302325581395	Amp:58.1395348837209	Del:20.9302325581395
TP53-gr	*ZNF343*	79175	20p13	Neutral:60.4651162790698	Amp:25.5813953488372	Del:13.953488372093
TP53-gr	*ZNF512B*	57473	20q13.33	Neutral:23.2558139534884	Amp:58.1395348837209	Del:18.6046511627907
TP53-gr	*hsa-mir-3195*	-1047	20q13.33	Neutral:30.2325581395349	Amp:53.4883720930233	Del:16.2790697674419
TP53-gr	*IFNAR1*	3454	21q22.11	Neutral:53.4883720930233	Amp:11.6279069767442	Del:34.8837209302326
TP53-gr	*IFNGR2*	3460	21q22.11	Neutral:46.5116279069767	Amp:6.97674418604651	Del:46.5116279069767
TP53-gr	*MIR3687*	100500815	21p11.2	Neutral:34.8837209302326	Amp:23.2558139534884	Del:41.8604651162791
TP53-gr	*TEKT4P2*	100132288	21p11.2	Neutral:51.1627906976744	Amp:4.65116279069767	Del:44.1860465116279
TP53-gr	*TMEM50B*	757	21q22.11	Neutral:39.5348837209302	Amp:6.97674418604651	Del:53.4883720930233
TP53-gr	*TRPM2*	7226	21q22.3	Neutral:41.8604651162791	Amp:20.9302325581395	Del:37.2093023255814
TP53-gr	*CCDC117*	150275	22q12.1	Neutral:48.8372093023256	Amp:9.30232558139535	Del:41.8604651162791
TP53-gr	*CHEK2*	11200	22q12.1	Neutral:39.5348837209302	Amp:11.6279069767442	Del:48.8372093023256
TP53-gr	*CSNK1E*	1454	22q13.1	Neutral:39.5348837209302	Amp:25.5813953488372	Del:34.8837209302326
TP53-gr	*HSCB*	150274	22q12.1	Neutral:39.5348837209302	Amp:16.2790697674419	Del:44.1860465116279
TP53-gr	*KCNJ4*	3761	22q13.1	Neutral:37.2093023255814	Amp:27.906976744186	Del:34.8837209302326
TP53-gr	*XBP1*	7494	22q12.1	Neutral:53.4883720930233	Amp:9.30232558139535	Del:37.2093023255814
Udt-gr	*CDC42*	998	1p36.12	Neutral:41.9354838709677	Amp:8.06451612903226	Del:50
Udt-gr	*LINC00339*	29092	1p36.12	Neutral:30.6451612903226	Amp:3.2258064516129	Del:66.1290322580645
Udt-gr	*METTL13*	51603	1q24.3	Neutral:30.6451612903226	Amp:67.741935483871	Del:1.61290322580645
Udt-gr	*MYOC*	4653	1q24.3	Neutral:50	Amp:43.5483870967742	Del:6.45161290322581
Udt-gr	*NOTCH2*	4853	1p12	Neutral:48.3870967741936	Amp:51.6129032258064	Del:0
Udt-gr	*TCHH*	7062	1q21.3	Neutral:30.6451612903226	Amp:66.1290322580645	Del:3.2258064516129
Udt-gr	*VAMP4*	8674	1q24.3	Neutral:41.9354838709677	Amp:41.9354838709677	Del:16.1290322580645
Udt-gr	*C2orf42*	54980	2p13.3	Neutral:38.7096774193548	Amp:9.67741935483871	Del:51.6129032258064
Udt-gr	*CBWD2*	150472	2q13	Neutral:66.1290322580645	Amp:19.3548387096774	Del:14.5161290322581
Udt-gr	*FAM138B*	654412	2q13	Neutral:58.0645161290323	Amp:35.4838709677419	Del:6.45161290322581
Udt-gr	*FOXD4L1*	200350	2q13	Neutral:51.6129032258064	Amp:33.8709677419355	Del:14.5161290322581
Udt-gr	*MIR548N*	100302152	2q31.2	Neutral:38.7096774193548	Amp:58.0645161290323	Del:3.2258064516129
Udt-gr	*MRPS9*	64965	2q12.1	Neutral:48.3870967741936	Amp:40.3225806451613	Del:11.2903225806452
Udt-gr	*PCBP1*	5093	2p13.3	Neutral:51.6129032258064	Amp:14.5161290322581	Del:33.8709677419355
Udt-gr	*PLEKHH2*	130271	2p21	Neutral:70.9677419354839	Amp:14.5161290322581	Del:14.5161290322581
Udt-gr	*POU3F3*	5455	2q12.1	Neutral:45.1612903225806	Amp:45.1612903225806	Del:9.67741935483871
Udt-gr	*THADA*	63892	2p21	Neutral:64.5161290322581	Amp:17.741935483871	Del:17.741935483871
Udt-gr	*TIA1*	7072	2p13.3	Neutral:51.6129032258064	Amp:8.06451612903226	Del:40.3225806451613
Udt-gr	*TSN*	7247	2q14.3	Neutral:62.9032258064516	Amp:8.06451612903226	Del:29.0322580645161
Udt-gr	*TTN*	7273	2q31.2	Neutral:37.0967741935484	Amp:59.6774193548387	Del:3.2258064516129

Udt-gr	*ZFP36L2*	678	2p21	Neutral:56.4516129032258	Amp:17.741935483871	Del:25.8064516129032
Udt-gr	*ARIH2*	10425	3p21.31	Neutral:30.6451612903226	Amp:4.83870967741935	Del:64.5161290322581
Udt-gr	*C3orf72*	401089	3q22.3	Neutral:53.2258064516129	Amp:22.5806451612903	Del:24.1935483870968
Udt-gr	*FOXL2*	668	3q22.3	Neutral:54.8387096774194	Amp:19.3548387096774	Del:25.8064516129032
Udt-gr	*IP6K2*	51447	3p21.31	Neutral:35.4838709677419	Amp:6.45161290322581	Del:58.0645161290323
Udt-gr	*MUC4*	4585	3q29	Neutral:48.3870967741936	Amp:17.741935483871	Del:33.8709677419355
Udt-gr	*PIK3CB*	5291	3q22.3	Neutral:66.1290322580645	Amp:3.2258064516129	Del:30.6451612903226
Udt-gr	*PRKAR2A*	5576	3p21.31	Neutral:16.1290322580645	Amp:6.45161290322581	Del:77.4193548387097
Udt-gr	*SLC25A20*	788	3p21.31	Neutral:17.741935483871	Amp:9.67741935483871	Del:72.5806451612903
Udt-gr	*C4orf29*	80167	4q28.2	Neutral:41.9354838709677	Amp:1.61290322580645	Del:56.4516129032258
Udt-gr	*CEP44*	80817	4q34.1	Neutral:53.2258064516129	Amp:14.5161290322581	Del:32.258064516129
Udt-gr	*CWH43*	80157	4p11	Neutral:70.9677419354839	Amp:16.1290322580645	Del:12.9032258064516
Udt-gr	*FBXO8*	26269	4q34.1	Neutral:59.6774193548387	Amp:8.06451612903226	Del:32.258064516129
Udt-gr	*LARP1B*	55132	4q28.2	Neutral:48.3870967741936	Amp:1.61290322580645	Del:50
Udt-gr	*MFSD8*	256471	4q28.2	Neutral:50	Amp:1.61290322580645	Del:48.3870967741936
Udt-gr	*N4BP2*	55728	4p14	Neutral:69.3548387096774	Amp:9.67741935483871	Del:20.9677419354839
Udt-gr	*OCIAD2*	132299	4p11	Neutral:61.2903225806452	Amp:12.9032258064516	Del:25.8064516129032
Udt-gr	*PCDH10*	57575	4q28.3	Neutral:58.0645161290323	Amp:29.0322580645161	Del:12.9032258064516
Udt-gr	*PDS5A*	23244	4p14	Neutral:50	Amp:8.06451612903226	Del:41.9354838709677
Udt-gr	*PGRMC2*	10424	4q28.2	Neutral:58.0645161290323	Amp:17.741935483871	Del:24.1935483870968
Udt-gr	*SLIT2*	9353	4p15.31	Neutral:50	Amp:40.3225806451613	Del:9.67741935483871
Udt-gr	*UBE2K*	3093	4p14	Neutral:50	Amp:8.06451612903226	Del:41.9354838709677
Udt-gr	*ANKRD34B*	340120	5q14.1	Neutral:61.2903225806452	Amp:6.45161290322581	Del:32.258064516129
Udt-gr	*C5orf38*	153571	5p15.33	Neutral:51.6129032258064	Amp:41.9354838709677	Del:6.45161290322581
Udt-gr	*CHD1*	1105	5q15	Neutral:56.4516129032258	Amp:24.1935483870968	Del:19.3548387096774
Udt-gr	*DHFR*	1719	5q14.1	Neutral:58.0645161290323	Amp:6.45161290322581	Del:35.4838709677419
Udt-gr	*IRX2*	153572	5p15.33	Neutral:50	Amp:41.9354838709677	Del:8.06451612903226
Udt-gr	*MIR3912*	100500831	5q35.1	Neutral:56.4516129032258	Amp:14.5161290322581	Del:29.0322580645161
Udt-gr	*MSH3*	4437	5q14.1	Neutral:59.6774193548387	Amp:11.2903225806452	Del:29.0322580645161
Udt-gr	*MTRNR2L2*	100462981	5q14.1	Neutral:58.0645161290323	Amp:8.06451612903226	Del:33.8709677419355
Udt-gr	*NPM1*	4869	5q35.1	Neutral:69.3548387096774	Amp:8.06451612903226	Del:22.5806451612903
Udt-gr	*NPR3*	4883	5p13.3	Neutral:66.1290322580645	Amp:27.4193548387097	Del:6.45161290322581
Udt-gr	*PCDHB8*	56128	5q31.3	Neutral:46.7741935483871	Amp:46.7741935483871	Del:6.45161290322581
Udt-gr	*RASGRF2*	5924	5q14.1	Neutral:62.9032258064516	Amp:19.3548387096774	Del:17.741935483871
Udt-gr	*RGMB*	285704	5q15	Neutral:61.2903225806452	Amp:27.4193548387097	Del:11.2903225806452
Udt-gr	*RIOK2*	55781	5q15	Neutral:59.6774193548387	Amp:19.3548387096774	Del:20.9677419354839
Udt-gr	*SUB1*	10923	5p13.3	Neutral:53.2258064516129	Amp:29.0322580645161	Del:17.741935483871
Udt-gr	*ZFR*	51663	5p13.3	Neutral:64.5161290322581	Amp:19.3548387096774	Del:16.1290322580645
Udt-gr	*ABCF1*	23	6p21.33	Neutral:29.0322580645161	Amp:11.2903225806452	Del:59.6774193548387
Udt-gr	*BEND3*	57673	6q21	Neutral:24.1935483870968	Amp:12.9032258064516	Del:62.9032258064516
Udt-gr	*C6orf203*	51250	6q21	Neutral:24.1935483870968	Amp:4.83870967741935	Del:70.9677419354839

Udt-gr	*CDKN1A*	1026	6p21.2	Neutral:62.9032258064516	Amp:22.5806451612903	Del:14.5161290322581
Udt-gr	*GNL1*	2794	6p21.33	Neutral:30.6451612903226	Amp:14.5161290322581	Del:54.8387096774194
Udt-gr	*HLA-E*	3133	6p21.33	Neutral:35.4838709677419	Amp:14.5161290322581	Del:50
Udt-gr	*MIR877*	100126314	6p21.33	Neutral:30.6451612903226	Amp:11.2903225806452	Del:58.0645161290323
Udt-gr	*MLLT4*	4301	6q27	Neutral:45.1612903225806	Amp:20.9677419354839	Del:33.8709677419355
Udt-gr	*MLLT4-AS1*	653483	6q27	Neutral:37.0967741935484	Amp:19.3548387096774	Del:43.5483870967742
Udt-gr	*MRPS18B*	28973	6p21.33	Neutral:32.258064516129	Amp:11.2903225806452	Del:56.4516129032258
Udt-gr	*NFYA*	4800	6p21.1	Neutral:51.6129032258064	Amp:43.5483870967742	Del:4.83870967741935
Udt-gr	*PDSS2*	57107	6q21	Neutral:32.258064516129	Amp:1.61290322580645	Del:66.1290322580645
Udt-gr	*PPP1R10*	5514	6p21.33	Neutral:30.6451612903226	Amp:11.2903225806452	Del:58.0645161290323
Udt-gr	*PRR3*	80742	6p21.33	Neutral:30.6451612903226	Amp:14.5161290322581	Del:54.8387096774194
Udt-gr	*ABHD11*	83451	7q11.23	Neutral:35.4838709677419	Amp:19.3548387096774	Del:45.1612903225806
Udt-gr	*ACHE*	43	7q22.1	Neutral:43.5483870967742	Amp:27.4193548387097	Del:29.0322580645161
Udt-gr	*ACN9*	57001	7q21.3	Neutral:62.9032258064516	Amp:33.8709677419355	Del:3.2258064516129
Udt-gr	*ACTL6B*	51412	7q22.1	Neutral:37.0967741935484	Amp:25.8064516129032	Del:37.0967741935484
Udt-gr	*AEBP1*	165	7p13	Neutral:59.6774193548387	Amp:33.8709677419355	Del:6.45161290322581
Udt-gr	*AGFG2*	3268	7q22.1	Neutral:53.2258064516129	Amp:30.6451612903226	Del:16.1290322580645
Udt-gr	*ALKBH4*	54784	7q22.1	Neutral:43.5483870967742	Amp:20.9677419354839	Del:35.4838709677419
Udt-gr	*AP1S1*	1174	7q22.1	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*AP4M1*	9179	7q22.1	Neutral:48.3870967741936	Amp:32.258064516129	Del:19.3548387096774
Udt-gr	*ARL4A*	10124	7p21.3	Neutral:41.9354838709677	Amp:50	Del:8.06451612903226
Udt-gr	*ARMC10*	83787	7q22.1	Neutral:61.2903225806452	Amp:25.8064516129032	Del:12.9032258064516
Udt-gr	*ARPC1A*	10552	7q22.1	Neutral:50	Amp:16.1290322580645	Del:33.8709677419355
Udt-gr	*ARPC1B*	10095	7q22.1	Neutral:56.4516129032258	Amp:19.3548387096774	Del:24.1935483870968
Udt-gr	*ASB4*	51666	7q21.3	Neutral:45.1612903225806	Amp:51.6129032258064	Del:3.2258064516129
Udt-gr	*ASNS*	440	7q21.3	Neutral:51.6129032258064	Amp:33.8709677419355	Del:14.5161290322581
Udt-gr	*ASZ1*	136991	7q31.2	Neutral:41.9354838709677	Amp:43.5483870967742	Del:14.5161290322581
Udt-gr	*ATP5J2*	9551	7q22.1	Neutral:53.2258064516129	Amp:20.9677419354839	Del:25.8064516129032
Udt-gr	*ATP5J2-PTCD1*	100526740	7q22.1	Neutral:50	Amp:20.9677419354839	Del:29.0322580645161
Udt-gr	*AZGP1*	563	7q22.1	Neutral:62.9032258064516	Amp:27.4193548387097	Del:9.67741935483871
Udt-gr	*AZGP1P1*	646282	7q22.1	Neutral:58.0645161290323	Amp:24.1935483870968	Del:17.741935483871
Udt-gr	*BAIAP2L1*	55971	7q21.3	Neutral:61.2903225806452	Amp:17.741935483871	Del:20.9677419354839
Udt-gr	*BAZ1B*	9031	7q11.23	Neutral:50	Amp:16.1290322580645	Del:33.8709677419355
Udt-gr	*BCL7B*	9275	7q11.23	Neutral:38.7096774193548	Amp:20.9677419354839	Del:40.3225806451613
Udt-gr	*BET1*	10282	7q21.3	Neutral:30.6451612903226	Amp:56.4516129032258	Del:12.9032258064516
Udt-gr	*BHLHA15*	168620	7q21.3	Neutral:62.9032258064516	Amp:19.3548387096774	Del:17.741935483871
Udt-gr	*BLVRA*	644	7p13	Neutral:70.9677419354839	Amp:19.3548387096774	Del:9.67741935483871
Udt-gr	*BRI3*	25798	7q21.3	Neutral:54.8387096774194	Amp:22.5806451612903	Del:22.5806451612903
Udt-gr	*BUD31*	8896	7q22.1	Neutral:51.6129032258064	Amp:19.3548387096774	Del:29.0322580645161
Udt-gr	*C7orf43*	55262	7q22.1	Neutral:43.5483870967742	Amp:29.0322580645161	Del:27.4193548387097
Udt-gr	*C7orf61*	402573	7q22.1	Neutral:48.3870967741936	Amp:19.3548387096774	Del:32.258064516129

Udt-gr	*CALCR*	799	7q21.3	Neutral:40.3225806451613	Amp:50	Del:9.67741935483871
Udt-gr	*CAMK2B*	816	7p13	Neutral:53.2258064516129	Amp:41.9354838709677	Del:4.83870967741935
Udt-gr	*CAPZA2*	830	7q31.2	Neutral:59.6774193548387	Amp:27.4193548387097	Del:12.9032258064516
Udt-gr	*CASD1*	64921	7q21.3	Neutral:45.1612903225806	Amp:43.5483870967742	Del:11.2903225806452
Udt-gr	*CAV1*	857	7q31.2	Neutral:35.4838709677419	Amp:56.4516129032258	Del:8.06451612903226
Udt-gr	*CAV2*	858	7q31.2	Neutral:33.8709677419355	Amp:56.4516129032258	Del:9.67741935483871
Udt-gr	*CCDC132*	55610	7q21.3	Neutral:40.3225806451613	Amp:46.7741935483871	Del:12.9032258064516
Udt-gr	*CCDC146*	57639	7q11.23	Neutral:58.0645161290323	Amp:32.258064516129	Del:9.67741935483871
Udt-gr	*CCL24*	6369	7q11.23	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*CCL26*	10344	7q11.23	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*CCM2*	83605	7p13	Neutral:69.3548387096774	Amp:22.5806451612903	Del:8.06451612903226
Udt-gr	*CCT6A*	908	7p11.2	Neutral:38.7096774193548	Amp:14.5161290322581	Del:46.7741935483871
Udt-gr	*CFTR*	1080	7q31.2	Neutral:40.3225806451613	Amp:48.3870967741936	Del:11.2903225806452
Udt-gr	*CHCHD2*	51142	7p11.2	Neutral:53.2258064516129	Amp:16.1290322580645	Del:30.6451612903226
Udt-gr	*CLDN15*	24146	7q22.1	Neutral:40.3225806451613	Amp:20.9677419354839	Del:38.7096774193548
Udt-gr	*CLDN3*	1365	7q11.23	Neutral:37.0967741935484	Amp:20.9677419354839	Del:41.9354838709677
Udt-gr	*CLDN4*	1364	7q11.23	Neutral:35.4838709677419	Amp:22.5806451612903	Del:41.9354838709677
Udt-gr	*CLIP2*	7461	7q11.23	Neutral:33.8709677419355	Amp:17.741935483871	Del:48.3870967741936
Udt-gr	*CNPY4*	245812	7q22.1	Neutral:43.5483870967742	Amp:27.4193548387097	Del:29.0322580645161
Udt-gr	*COL1A2*	1278	7q21.3	Neutral:37.0967741935484	Amp:59.6774193548387	Del:3.2258064516129
Udt-gr	*COL28A1*	340267	7p21.3	Neutral:40.3225806451613	Amp:54.8387096774194	Del:4.83870967741935
Udt-gr	*COPS6*	10980	7q22.1	Neutral:51.6129032258064	Amp:30.6451612903226	Del:17.741935483871
Udt-gr	*CPSF4*	10898	7q22.1	Neutral:50	Amp:20.9677419354839	Del:29.0322580645161
Udt-gr	*CTTNBP2*	83992	7q31.2	Neutral:48.3870967741936	Amp:48.3870967741936	Del:3.2258064516129
Udt-gr	*CUX1*	1523	7q22.1	Neutral:48.3870967741936	Amp:20.9677419354839	Del:30.6451612903226
Udt-gr	*CYP3A4*	1576	7q22.1	Neutral:56.4516129032258	Amp:37.0967741935484	Del:6.45161290322581
Udt-gr	*CYP3A43*	64816	7q22.1	Neutral:61.2903225806452	Amp:30.6451612903226	Del:8.06451612903226
Udt-gr	*CYP3A5*	1577	7q22.1	Neutral:56.4516129032258	Amp:37.0967741935484	Del:6.45161290322581
Udt-gr	*CYP3A7*	1551	7q22.1	Neutral:48.3870967741936	Amp:45.1612903225806	Del:6.45161290322581
Udt-gr	*DBNL*	28988	7p13	Neutral:58.0645161290323	Amp:30.6451612903226	Del:11.2903225806452
Udt-gr	*DDX56*	54606	7p13	Neutral:51.6129032258064	Amp:24.1935483870968	Del:24.1935483870968
Udt-gr	*DLX5*	1749	7q21.3	Neutral:51.6129032258064	Amp:45.1612903225806	Del:3.2258064516129
Udt-gr	*DLX6*	1750	7q21.3	Neutral:46.7741935483871	Amp:51.6129032258064	Del:1.61290322580645
Udt-gr	*DLX6-AS1*	285987	7q21.3	Neutral:48.3870967741936	Amp:50	Del:1.61290322580645
Udt-gr	*DNAJC2*	27000	7q22.1	Neutral:62.9032258064516	Amp:24.1935483870968	Del:12.9032258064516
Udt-gr	*DNAJC30*	84277	7q11.23	Neutral:38.7096774193548	Amp:22.5806451612903	Del:38.7096774193548
Udt-gr	*DPY19L2P2*	349152	7q22.1	Neutral:53.2258064516129	Amp:30.6451612903226	Del:16.1290322580645
Udt-gr	*DTX2*	113878	7q11.23	Neutral:43.5483870967742	Amp:19.3548387096774	Del:37.0967741935484
Udt-gr	*DTX2P1-UPK3BP1-PMS2P11*	441263	7q11.23	Neutral:41.9354838709677	Amp:19.3548387096774	Del:38.7096774193548
Udt-gr	*DYNC1I1*	1780	7q21.3	Neutral:45.1612903225806	Amp:51.6129032258064	Del:3.2258064516129
Udt-gr	*EGFR*	1956	7p11.2	Neutral:51.6129032258064	Amp:48.3870967741936	Del:0

Udt-gr	*EIF4H*	7458	7q11.23	Neutral:48.3870967741936	Amp:16.1290322580645	Del:35.4838709677419
Udt-gr	*ELN*	2006	7q11.23	Neutral:40.3225806451613	Amp:17.741935483871	Del:41.9354838709677
Udt-gr	*EPHB4*	2050	7q22.1	Neutral:35.4838709677419	Amp:24.1935483870968	Del:40.3225806451613
Udt-gr	*EPO*	2056	7q22.1	Neutral:32.258064516129	Amp:25.8064516129032	Del:41.9354838709677
Udt-gr	*FAM185A*	222234	7q22.1	Neutral:56.4516129032258	Amp:32.258064516129	Del:11.2903225806452
Udt-gr	*FAM200A*	221786	7q22.1	Neutral:62.9032258064516	Amp:17.741935483871	Del:19.3548387096774
Udt-gr	*FBXL13*	222235	7q22.1	Neutral:61.2903225806452	Amp:25.8064516129032	Del:12.9032258064516
Udt-gr	*FBXO24*	26261	7q22.1	Neutral:54.8387096774194	Amp:24.1935483870968	Del:20.9677419354839
Udt-gr	*FGL2*	10875	7q11.23	Neutral:53.2258064516129	Amp:37.0967741935484	Del:9.67741935483871
Udt-gr	*FIS1*	51024	7q22.1	Neutral:40.3225806451613	Amp:20.9677419354839	Del:38.7096774193548
Udt-gr	*FKBP6*	8468	7q11.23	Neutral:48.3870967741936	Amp:17.741935483871	Del:33.8709677419355
Udt-gr	*FKBP9L*	360132	7p11.2	Neutral:62.9032258064516	Amp:27.4193548387097	Del:9.67741935483871
Udt-gr	*FZD9*	8326	7q11.23	Neutral:48.3870967741936	Amp:17.741935483871	Del:33.8709677419355
Udt-gr	*GAL3ST4*	79690	7q22.1	Neutral:41.9354838709677	Amp:30.6451612903226	Del:27.4193548387097
Udt-gr	*GATS*	352954	7q22.1	Neutral:56.4516129032258	Amp:22.5806451612903	Del:20.9677419354839
Udt-gr	*GATSL1*	389523	7q11.23	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*GATSL2*	729438	7q11.23	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*GBAS*	2631	7p11.2	Neutral:40.3225806451613	Amp:12.9032258064516	Del:46.7741935483871
Udt-gr	*GCK*	2645	7p13	Neutral:59.6774193548387	Amp:33.8709677419355	Del:6.45161290322581
Udt-gr	*GIGYF1*	64599	7q22.1	Neutral:38.7096774193548	Amp:29.0322580645161	Del:32.258064516129
Udt-gr	*GJC3*	349149	7q22.1	Neutral:66.1290322580645	Amp:29.0322580645161	Del:4.83870967741935
Udt-gr	*GLCCI1*	113263	7p21.3	Neutral:43.5483870967742	Amp:50	Del:6.45161290322581
Udt-gr	*GNB2*	2783	7q22.1	Neutral:40.3225806451613	Amp:27.4193548387097	Del:32.258064516129
Udt-gr	*GNG11*	2791	7q21.3	Neutral:33.8709677419355	Amp:53.2258064516129	Del:12.9032258064516
Udt-gr	*GNGT1*	2792	7q21.3	Neutral:33.8709677419355	Amp:53.2258064516129	Del:12.9032258064516
Udt-gr	*GPC2*	221914	7q22.1	Neutral:51.6129032258064	Amp:30.6451612903226	Del:17.741935483871
Udt-gr	*GTF2I*	2969	7q11.23	Neutral:48.3870967741936	Amp:14.5161290322581	Del:37.0967741935484
Udt-gr	*GTF2IP1*	2970	7q11.23	Neutral:45.1612903225806	Amp:12.9032258064516	Del:41.9354838709677
Udt-gr	*GTF2IRD1*	9569	7q11.23	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*GTF2IRD2*	84163	7q11.23	Neutral:43.5483870967742	Amp:11.2903225806452	Del:45.1612903225806
Udt-gr	*GTF2IRD2B*	389524	7q11.23	Neutral:40.3225806451613	Amp:14.5161290322581	Del:45.1612903225806
Udt-gr	*GTF2IRD2P1*	401375	7q11.23	Neutral:40.3225806451613	Amp:14.5161290322581	Del:45.1612903225806
Udt-gr	*GUSBP10*	642006	7p11.2	Neutral:64.5161290322581	Amp:25.8064516129032	Del:9.67741935483871
Udt-gr	*H2AFV*	94239	7p13	Neutral:50	Amp:16.1290322580645	Del:33.8709677419355
Udt-gr	*HEPACAM2*	253012	7q21.3	Neutral:38.7096774193548	Amp:58.0645161290323	Del:3.2258064516129
Udt-gr	*HIP1*	3092	7q11.23	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*HSPB1*	3315	7q11.23	Neutral:38.7096774193548	Amp:20.9677419354839	Del:40.3225806451613
Udt-gr	*ICA1*	3382	7p21.3	Neutral:38.7096774193548	Amp:58.0645161290323	Del:3.2258064516129
Udt-gr	*KPNA7*	402569	7q22.1	Neutral:46.7741935483871	Amp:19.3548387096774	Del:33.8709677419355
Udt-gr	*LANCL2*	55915	7p11.2	Neutral:70.9677419354839	Amp:29.0322580645161	Del:0
Udt-gr	*LAT2*	7462	7q11.23	Neutral:43.5483870967742	Amp:17.741935483871	Del:38.7096774193548

Udt-gr	*LIMK1*	3984	7q11.23	Neutral:35.4838709677419	Amp:19.3548387096774	Del:45.1612903225806
Udt-gr	*LMTK2*	22853	7q21.3	Neutral:69.3548387096774	Amp:27.4193548387097	Del:3.2258064516129
Udt-gr	*LRCH4*	4034	7q22.1	Neutral:53.2258064516129	Amp:30.6451612903226	Del:16.1290322580645
Udt-gr	*LRRC17*	10234	7q22.1	Neutral:59.6774193548387	Amp:27.4193548387097	Del:12.9032258064516
Udt-gr	*LRWD1*	222229	7q22.1	Neutral:43.5483870967742	Amp:22.5806451612903	Del:33.8709677419355
Udt-gr	*MBLAC1*	255374	7q22.1	Neutral:43.5483870967742	Amp:27.4193548387097	Del:29.0322580645161
Udt-gr	*MCM7*	4176	7q22.1	Neutral:46.7741935483871	Amp:33.8709677419355	Del:19.3548387096774
Udt-gr	*MDH2*	4191	7q11.23	Neutral:46.7741935483871	Amp:16.1290322580645	Del:37.0967741935484
Udt-gr	*MEPCE*	56257	7q22.1	Neutral:53.2258064516129	Amp:25.8064516129032	Del:20.9677419354839
Udt-gr	*MET*	4233	7q31.2	Neutral:45.1612903225806	Amp:46.7741935483871	Del:8.06451612903226
Udt-gr	*MIOS*	54468	7p21.3	Neutral:48.3870967741936	Amp:45.1612903225806	Del:6.45161290322581
Udt-gr	*MIR106B*	406900	7q22.1	Neutral:48.3870967741936	Amp:32.258064516129	Del:19.3548387096774
Udt-gr	*MIR25*	407014	7q22.1	Neutral:48.3870967741936	Amp:33.8709677419355	Del:17.741935483871
Udt-gr	*MIR3147*	100422939	7p11.2	Neutral:66.1290322580645	Amp:24.1935483870968	Del:9.67741935483871
Udt-gr	*MIR3609*	100500819	7q22.1	Neutral:53.2258064516129	Amp:17.741935483871	Del:29.0322580645161
Udt-gr	*MIR4283-1*	100422917	7p11.2	Neutral:46.7741935483871	Amp:19.3548387096774	Del:33.8709677419355
Udt-gr	*MIR4283-2*	100422848	7p11.2	Neutral:46.7741935483871	Amp:19.3548387096774	Del:33.8709677419355
Udt-gr	*MIR4284*	100422948	7q11.23	Neutral:45.1612903225806	Amp:20.9677419354839	Del:33.8709677419355
Udt-gr	*MIR4285*	100422858	7q22.1	Neutral:51.6129032258064	Amp:19.3548387096774	Del:29.0322580645161
Udt-gr	*MIR4467*	100616367	7q22.1	Neutral:43.5483870967742	Amp:22.5806451612903	Del:33.8709677419355
Udt-gr	*MIR4649*	100616346	7p13	Neutral:56.4516129032258	Amp:33.8709677419355	Del:9.67741935483871
Udt-gr	*MIR4651*	100616270	7q11.23	Neutral:38.7096774193548	Amp:16.1290322580645	Del:45.1612903225806
Udt-gr	*MIR4652*	100616206	7q21.3	Neutral:35.4838709677419	Amp:48.3870967741936	Del:16.1290322580645
Udt-gr	*MIR4653*	100616117	7q22.1	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*MIR4657*	100616393	7p13	Neutral:48.3870967741936	Amp:17.741935483871	Del:33.8709677419355
Udt-gr	*MIR4658*	100616439	7q22.1	Neutral:43.5483870967742	Amp:29.0322580645161	Del:27.4193548387097
Udt-gr	*MIR489*	574442	7q21.3	Neutral:37.0967741935484	Amp:50	Del:12.9032258064516
Udt-gr	*MIR590*	693175	7q11.23	Neutral:45.1612903225806	Amp:19.3548387096774	Del:35.4838709677419
Udt-gr	*MIR591*	693176	7q21.3	Neutral:53.2258064516129	Amp:38.7096774193548	Del:8.06451612903226
Udt-gr	*MIR653*	724023	7q21.3	Neutral:37.0967741935484	Amp:50	Del:12.9032258064516
Udt-gr	*MIR93*	407050	7q22.1	Neutral:48.3870967741936	Amp:33.8709677419355	Del:17.741935483871
Udt-gr	*MLXIPL*	51085	7q11.23	Neutral:41.9354838709677	Amp:17.741935483871	Del:40.3225806451613
Udt-gr	*MOGAT3*	346606	7q22.1	Neutral:40.3225806451613	Amp:20.9677419354839	Del:38.7096774193548
Udt-gr	*MOSPD3*	64598	7q22.1	Neutral:43.5483870967742	Amp:24.1935483870968	Del:32.258064516129
Udt-gr	*MRPS17*	51373	7p11.2	Neutral:43.5483870967742	Amp:9.67741935483871	Del:46.7741935483871
Udt-gr	*MRPS24*	64951	7p13	Neutral:64.5161290322581	Amp:24.1935483870968	Del:11.2903225806452
Udt-gr	*MUC12*	10071	7q22.1	Neutral:54.8387096774194	Amp:24.1935483870968	Del:20.9677419354839
Udt-gr	*MUC17*	140453	7q22.1	Neutral:53.2258064516129	Amp:19.3548387096774	Del:27.4193548387097
Udt-gr	*MYH16*	84176	7q22.1	Neutral:46.7741935483871	Amp:20.9677419354839	Del:32.258064516129
Udt-gr	*MYL10*	93408	7q22.1	Neutral:50	Amp:22.5806451612903	Del:27.4193548387097
Udt-gr	*MYL7*	58498	7p13	Neutral:53.2258064516129	Amp:38.7096774193548	Del:8.06451612903226

Udt-gr	*MYO1G*	64005	7p13	Neutral:61.2903225806452	Amp:25.8064516129032	Del:12.9032258064516
Udt-gr	*NACAD*	23148	7p13	Neutral:59.6774193548387	Amp:29.0322580645161	Del:11.2903225806452
Udt-gr	*NAPEPLD*	222236	7q22.1	Neutral:66.1290322580645	Amp:25.8064516129032	Del:8.06451612903226
Udt-gr	*NAT16*	375607	7q22.1	Neutral:41.9354838709677	Amp:22.5806451612903	Del:35.4838709677419
Udt-gr	*NCF1*	653361	7q11.23	Neutral:37.0967741935484	Amp:19.3548387096774	Del:43.5483870967742
Udt-gr	*NCF1B*	654816	7q11.23	Neutral:38.7096774193548	Amp:19.3548387096774	Del:41.9354838709677
Udt-gr	*NCF1C*	654817	7q11.23	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*NDUFA4*	4697	7p21.3	Neutral:45.1612903225806	Amp:48.3870967741936	Del:6.45161290322581
Udt-gr	*NPC1L1*	29881	7p13	Neutral:54.8387096774194	Amp:22.5806451612903	Del:22.5806451612903
Udt-gr	*NPTX2*	4885	7q22.1	Neutral:56.4516129032258	Amp:25.8064516129032	Del:17.741935483871
Udt-gr	*NSUN5*	55695	7q11.23	Neutral:48.3870967741936	Amp:17.741935483871	Del:33.8709677419355
Udt-gr	*NSUN5P1*	155400	7q11.23	Neutral:45.1612903225806	Amp:17.741935483871	Del:37.0967741935484
Udt-gr	*NSUN5P2*	260294	7q11.23	Neutral:56.4516129032258	Amp:19.3548387096774	Del:24.1935483870968
Udt-gr	*NUDCD3*	23386	7p13	Neutral:59.6774193548387	Amp:35.4838709677419	Del:4.83870967741935
Udt-gr	*NXPH1*	30010	7p21.3	Neutral:41.9354838709677	Amp:56.4516129032258	Del:1.61290322580645
Udt-gr	*NYAP1*	222950	7q22.1	Neutral:38.7096774193548	Amp:25.8064516129032	Del:35.4838709677419
Udt-gr	*OCM2*	4951	7q21.3	Neutral:58.0645161290323	Amp:14.5161290322581	Del:27.4193548387097
Udt-gr	*OGDH*	4967	7p13	Neutral:48.3870967741936	Amp:24.1935483870968	Del:27.4193548387097
Udt-gr	*OR2AE1*	81392	7q22.1	Neutral:70.9677419354839	Amp:24.1935483870968	Del:4.83870967741935
Udt-gr	*ORAI2*	80228	7q22.1	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*ORC5*	5001	7q22.1	Neutral:45.1612903225806	Amp:40.3225806451613	Del:14.5161290322581
Udt-gr	*PCOLCE*	5118	7q22.1	Neutral:45.1612903225806	Amp:25.8064516129032	Del:29.0322580645161
Udt-gr	*PDAP1*	11333	7q22.1	Neutral:54.8387096774194	Amp:19.3548387096774	Del:25.8064516129032
Udt-gr	*PDK4*	5166	7q21.3	Neutral:46.7741935483871	Amp:46.7741935483871	Del:6.45161290322581
Udt-gr	*PEG10*	23089	7q21.3	Neutral:41.9354838709677	Amp:54.8387096774194	Del:3.2258064516129
Udt-gr	*PGAM2*	5224	7p13	Neutral:59.6774193548387	Amp:30.6451612903226	Del:9.67741935483871
Udt-gr	*PHF14*	9678	7p21.3	Neutral:43.5483870967742	Amp:46.7741935483871	Del:9.67741935483871
Udt-gr	*PHKG1*	5260	7p11.2	Neutral:48.3870967741936	Amp:17.741935483871	Del:33.8709677419355
Udt-gr	*PHTF2*	57157	7q11.23	Neutral:54.8387096774194	Amp:27.4193548387097	Del:17.741935483871
Udt-gr	*PILRA*	29992	7q22.1	Neutral:64.5161290322581	Amp:17.741935483871	Del:17.741935483871
Udt-gr	*PILRB*	29990	7q22.1	Neutral:58.0645161290323	Amp:19.3548387096774	Del:22.5806451612903
Udt-gr	*PLOD3*	8985	7q22.1	Neutral:40.3225806451613	Amp:20.9677419354839	Del:38.7096774193548
Udt-gr	*PMPCB*	9512	7q22.1	Neutral:59.6774193548387	Amp:29.0322580645161	Del:11.2903225806452
Udt-gr	*PMS2P1*	5379	7q22.1	Neutral:59.6774193548387	Amp:9.67741935483871	Del:30.6451612903226
Udt-gr	*PMS2P3*	5387	7q11.23	Neutral:51.6129032258064	Amp:11.2903225806452	Del:37.0967741935484
Udt-gr	*PMS2P5*	5383	7q11.23	Neutral:38.7096774193548	Amp:16.1290322580645	Del:45.1612903225806
Udt-gr	*POLD2*	5425	7p13	Neutral:56.4516129032258	Amp:33.8709677419355	Del:9.67741935483871
Udt-gr	*POLM*	27434	7p13	Neutral:62.9032258064516	Amp:30.6451612903226	Del:6.45161290322581
Udt-gr	*POLR2J*	5439	7q22.1	Neutral:45.1612903225806	Amp:20.9677419354839	Del:33.8709677419355
Udt-gr	*POLR2J2*	246721	7q22.1	Neutral:41.9354838709677	Amp:17.741935483871	Del:40.3225806451613
Udt-gr	*POLR2J3*	548644	7q22.1	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484

Udt-gr	*POLR2J4*	84820	7p13	Neutral:50	Amp:19.3548387096774	Del:30.6451612903226
Udt-gr	*POM121*	9883	7q11.23	Neutral:53.2258064516129	Amp:19.3548387096774	Del:27.4193548387097
Udt-gr	*POM121C*	100101267	7q11.23	Neutral:51.6129032258064	Amp:17.741935483871	Del:30.6451612903226
Udt-gr	*POMZP3*	22932	7q11.23	Neutral:51.6129032258064	Amp:17.741935483871	Del:30.6451612903226
Udt-gr	*PON1*	5444	7q21.3	Neutral:41.9354838709677	Amp:51.6129032258064	Del:6.45161290322581
Udt-gr	*PON2*	5445	7q21.3	Neutral:41.9354838709677	Amp:50	Del:8.06451612903226
Udt-gr	*PON3*	5446	7q21.3	Neutral:45.1612903225806	Amp:48.3870967741936	Del:6.45161290322581
Udt-gr	*POP7*	10248	7q22.1	Neutral:37.0967741935484	Amp:25.8064516129032	Del:37.0967741935484
Udt-gr	*POR*	5447	7q11.23	Neutral:45.1612903225806	Amp:17.741935483871	Del:37.0967741935484
Udt-gr	*PPIA*	5478	7p13	Neutral:50	Amp:12.9032258064516	Del:37.0967741935484
Udt-gr	*PPP1R35*	221908	7q22.1	Neutral:51.6129032258064	Amp:20.9677419354839	Del:27.4193548387097
Udt-gr	*PPP1R9A*	55607	7q21.3	Neutral:46.7741935483871	Amp:50	Del:3.2258064516129
Udt-gr	*PRKRIP1*	79706	7q22.1	Neutral:40.3225806451613	Amp:19.3548387096774	Del:40.3225806451613
Udt-gr	*PSMC2*	5701	7q22.1	Neutral:66.1290322580645	Amp:22.5806451612903	Del:11.2903225806452
Udt-gr	*PSPH*	5723	7p11.2	Neutral:37.0967741935484	Amp:11.2903225806452	Del:51.6129032258064
Udt-gr	*PTCD1*	26024	7q22.1	Neutral:50	Amp:20.9677419354839	Del:29.0322580645161
Udt-gr	*PTPN12*	5782	7q11.23	Neutral:62.9032258064516	Amp:19.3548387096774	Del:17.741935483871
Udt-gr	*PURB*	5814	7p13	Neutral:46.7741935483871	Amp:17.741935483871	Del:35.4838709677419
Udt-gr	*PVRIG*	79037	7q22.1	Neutral:50	Amp:22.5806451612903	Del:27.4193548387097
Udt-gr	*RABL5*	64792	7q22.1	Neutral:40.3225806451613	Amp:19.3548387096774	Del:40.3225806451613
Udt-gr	*RAMP3*	10268	7p13	Neutral:58.0645161290323	Amp:37.0967741935484	Del:4.83870967741935
Udt-gr	*RASA4*	10156	7q22.1	Neutral:38.7096774193548	Amp:24.1935483870968	Del:37.0967741935484
Udt-gr	*RELN*	5649	7q22.1	Neutral:48.3870967741936	Amp:46.7741935483871	Del:4.83870967741935
Udt-gr	*RFC2*	5982	7q11.23	Neutral:38.7096774193548	Amp:16.1290322580645	Del:45.1612903225806
Udt-gr	*RHBDD2*	57414	7q11.23	Neutral:37.0967741935484	Amp:19.3548387096774	Del:43.5483870967742
Udt-gr	*RPA3*	6119	7p21.3	Neutral:41.9354838709677	Amp:48.3870967741936	Del:9.67741935483871
Udt-gr	*RPL19P12*	100129424	7q22.1	Neutral:61.2903225806452	Amp:30.6451612903226	Del:8.06451612903226
Udt-gr	*RSBN1L*	222194	7q11.23	Neutral:61.2903225806452	Amp:17.741935483871	Del:20.9677419354839
Udt-gr	*SAP25*	100316904	7q22.1	Neutral:50	Amp:33.8709677419355	Del:16.1290322580645
Udt-gr	*SBDSP1*	155370	7q11.23	Neutral:48.3870967741936	Amp:11.2903225806452	Del:40.3225806451613
Udt-gr	*SCIN*	85477	7p21.3	Neutral:41.9354838709677	Amp:54.8387096774194	Del:3.2258064516129
Udt-gr	*SEC61G*	23480	7p11.2	Neutral:41.9354838709677	Amp:48.3870967741936	Del:9.67741935483871
Udt-gr	*Sep/14*	346288	7p11.2	Neutral:53.2258064516129	Amp:9.67741935483871	Del:37.0967741935484
Udt-gr	*SERPINE1*	5054	7q22.1	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*SGCE*	8910	7q21.3	Neutral:41.9354838709677	Amp:46.7741935483871	Del:11.2903225806452
Udt-gr	*SH2B2*	10603	7q22.1	Neutral:51.6129032258064	Amp:19.3548387096774	Del:29.0322580645161
Udt-gr	*SHFM1*	7979	7q21.3	Neutral:53.2258064516129	Amp:41.9354838709677	Del:4.83870967741935
Udt-gr	*SLC12A9*	56996	7q22.1	Neutral:38.7096774193548	Amp:24.1935483870968	Del:37.0967741935484
Udt-gr	*SLC25A13*	10165	7q21.3	Neutral:45.1612903225806	Amp:50	Del:4.83870967741935
Udt-gr	*SLC26A5*	375611	7q22.1	Neutral:67.741935483871	Amp:17.741935483871	Del:14.5161290322581
Udt-gr	*SMURF1*	57154	7q22.1	Neutral:64.5161290322581	Amp:19.3548387096774	Del:16.1290322580645

Udt-gr	*SNHG15*	285958	7p13	Neutral:61.2903225806452	Amp:25.8064516129032	Del:12.9032258064516
Udt-gr	*SNORA14A*	677801	7q11.23	Neutral:41.9354838709677	Amp:12.9032258064516	Del:45.1612903225806
Udt-gr	*SNORA15*	677803	7p11.2	Neutral:41.9354838709677	Amp:14.5161290322581	Del:43.5483870967742
Udt-gr	*SNORA5A*	654319	7p13	Neutral:56.4516129032258	Amp:32.258064516129	Del:11.2903225806452
Udt-gr	*SNORA5B*	677795	7p13	Neutral:58.0645161290323	Amp:33.8709677419355	Del:8.06451612903226
Udt-gr	*SNORA5C*	677796	7p13	Neutral:56.4516129032258	Amp:32.258064516129	Del:11.2903225806452
Udt-gr	*SPDYE1*	285955	7p13	Neutral:48.3870967741936	Amp:20.9677419354839	Del:30.6451612903226
Udt-gr	*SPDYE2*	441273	7q22.1	Neutral:41.9354838709677	Amp:19.3548387096774	Del:38.7096774193548
Udt-gr	*SPDYE3*	441272	7q22.1	Neutral:45.1612903225806	Amp:19.3548387096774	Del:35.4838709677419
Udt-gr	*SPDYE6*	729597	7q22.1	Neutral:40.3225806451613	Amp:17.741935483871	Del:41.9354838709677
Udt-gr	*SPDYE7P*	441251	7q11.23	Neutral:43.5483870967742	Amp:16.1290322580645	Del:40.3225806451613
Udt-gr	*SPDYE8P*	389517	7q11.23	Neutral:38.7096774193548	Amp:17.741935483871	Del:43.5483870967742
Udt-gr	*SRCRB4D*	136853	7q11.23	Neutral:41.9354838709677	Amp:19.3548387096774	Del:38.7096774193548
Udt-gr	*SRRM3*	222183	7q11.23	Neutral:38.7096774193548	Amp:19.3548387096774	Del:41.9354838709677
Udt-gr	*SRRT*	51593	7q22.1	Neutral:50	Amp:25.8064516129032	Del:24.1935483870968
Udt-gr	*ST7*	7982	7q31.2	Neutral:46.7741935483871	Amp:46.7741935483871	Del:6.45161290322581
Udt-gr	*ST7-AS1*	93653	7q31.2	Neutral:58.0645161290323	Amp:27.4193548387097	Del:14.5161290322581
Udt-gr	*ST7-AS2*	93654	7q31.2	Neutral:46.7741935483871	Amp:45.1612903225806	Del:8.06451612903226
Udt-gr	*ST7-OT4*	338069	7q31.2	Neutral:61.2903225806452	Amp:29.0322580645161	Del:9.67741935483871
Udt-gr	*STAG3*	10734	7q22.1	Neutral:67.741935483871	Amp:20.9677419354839	Del:11.2903225806452
Udt-gr	*STAG3L1*	54441	7q11.23	Neutral:41.9354838709677	Amp:16.1290322580645	Del:41.9354838709677
Udt-gr	*STAG3L2*	442582	7q11.23	Neutral:40.3225806451613	Amp:16.1290322580645	Del:43.5483870967742
Udt-gr	*STAG3L3*	442578	7q11.23	Neutral:38.7096774193548	Amp:19.3548387096774	Del:41.9354838709677
Udt-gr	*STK17A*	9263	7p13	Neutral:56.4516129032258	Amp:35.4838709677419	Del:8.06451612903226
Udt-gr	*STX1A*	6804	7q11.23	Neutral:43.5483870967742	Amp:22.5806451612903	Del:33.8709677419355
Udt-gr	*STYXL1*	51657	7q11.23	Neutral:45.1612903225806	Amp:14.5161290322581	Del:40.3225806451613
Udt-gr	*SUMF2*	25870	7p11.2	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*TAC1*	6863	7q21.3	Neutral:58.0645161290323	Amp:30.6451612903226	Del:11.2903225806452
Udt-gr	*TAF6*	6878	7q22.1	Neutral:46.7741935483871	Amp:29.0322580645161	Del:24.1935483870968
Udt-gr	*TBL2*	26608	7q11.23	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*TBRG4*	9238	7p13	Neutral:58.0645161290323	Amp:33.8709677419355	Del:8.06451612903226
Udt-gr	*TECPR1*	25851	7q21.3	Neutral:54.8387096774194	Amp:20.9677419354839	Del:24.1935483870968
Udt-gr	*TES*	26136	7q31.2	Neutral:38.7096774193548	Amp:51.6129032258064	Del:9.67741935483871
Udt-gr	*TFEC*	22797	7q31.2	Neutral:43.5483870967742	Amp:45.1612903225806	Del:11.2903225806452
Udt-gr	*TFPI2*	7980	7q21.3	Neutral:38.7096774193548	Amp:50	Del:11.2903225806452
Udt-gr	*TFR2*	7036	7q22.1	Neutral:40.3225806451613	Amp:24.1935483870968	Del:35.4838709677419
Udt-gr	*THSD7A*	221981	7p21.3	Neutral:40.3225806451613	Amp:58.0645161290323	Del:1.61290322580645
Udt-gr	*TMED4*	222068	7p13	Neutral:54.8387096774194	Amp:22.5806451612903	Del:22.5806451612903
Udt-gr	*TMEM106B*	54664	7p21.3	Neutral:37.0967741935484	Amp:53.2258064516129	Del:9.67741935483871
Udt-gr	*TMEM120A*	83862	7q11.23	Neutral:40.3225806451613	Amp:20.9677419354839	Del:38.7096774193548
Udt-gr	*TMEM130*	222865	7q22.1	Neutral:48.3870967741936	Amp:22.5806451612903	Del:29.0322580645161

Udt-gr	*TMEM60*	85025	7q11.23	Neutral:61.2903225806452	Amp:19.3548387096774	Del:19.3548387096774
Udt-gr	*TRIM4*	89122	7q22.1	Neutral:70.9677419354839	Amp:25.8064516129032	Del:3.2258064516129
Udt-gr	*TRIM50*	135892	7q11.23	Neutral:50	Amp:16.1290322580645	Del:33.8709677419355
Udt-gr	*TRIM56*	81844	7q22.1	Neutral:41.9354838709677	Amp:22.5806451612903	Del:35.4838709677419
Udt-gr	*TRIM73*	375593	7q11.23	Neutral:38.7096774193548	Amp:20.9677419354839	Del:40.3225806451613
Udt-gr	*TRIM74*	378108	7q11.23	Neutral:38.7096774193548	Amp:20.9677419354839	Del:40.3225806451613
Udt-gr	*TRIP6*	7205	7q22.1	Neutral:46.7741935483871	Amp:24.1935483870968	Del:29.0322580645161
Udt-gr	*TRRAP*	8295	7q22.1	Neutral:79.0322580645161	Amp:19.3548387096774	Del:1.61290322580645
Udt-gr	*TSC22D4*	81628	7q22.1	Neutral:43.5483870967742	Amp:24.1935483870968	Del:32.258064516129
Udt-gr	*UBE2D4*	51619	7p13	Neutral:58.0645161290323	Amp:22.5806451612903	Del:19.3548387096774
Udt-gr	*UFSP1*	402682	7q22.1	Neutral:50	Amp:25.8064516129032	Del:24.1935483870968
Udt-gr	*UPK3B*	80761	7q11.23	Neutral:43.5483870967742	Amp:20.9677419354839	Del:35.4838709677419
Udt-gr	*UPK3BL*	100134938	7q22.1	Neutral:43.5483870967742	Amp:17.741935483871	Del:38.7096774193548
Udt-gr	*URGCP*	55665	7p13	Neutral:62.9032258064516	Amp:24.1935483870968	Del:12.9032258064516
Udt-gr	*URGCP-MRPS24*	100534592	7p13	Neutral:62.9032258064516	Amp:27.4193548387097	Del:9.67741935483871
Udt-gr	*VGF*	7425	7q22.1	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*VOPP1*	81552	7p11.2	Neutral:66.1290322580645	Amp:32.258064516129	Del:1.61290322580645
Udt-gr	*VPS37D*	155382	7q11.23	Neutral:38.7096774193548	Amp:22.5806451612903	Del:38.7096774193548
Udt-gr	*VSTM2A*	222008	7p11.2	Neutral:38.7096774193548	Amp:56.4516129032258	Del:4.83870967741935
Udt-gr	*VWDE*	221806	7p21.3	Neutral:38.7096774193548	Amp:56.4516129032258	Del:4.83870967741935
Udt-gr	*WBSCR16*	81554	7q11.23	Neutral:40.3225806451613	Amp:14.5161290322581	Del:45.1612903225806
Udt-gr	*WBSCR22*	114049	7q11.23	Neutral:43.5483870967742	Amp:20.9677419354839	Del:35.4838709677419
Udt-gr	*WBSCR27*	155368	7q11.23	Neutral:37.0967741935484	Amp:22.5806451612903	Del:40.3225806451613
Udt-gr	*WBSCR28*	135886	7q11.23	Neutral:37.0967741935484	Amp:20.9677419354839	Del:41.9354838709677
Udt-gr	*WNT2*	7472	7q31.2	Neutral:45.1612903225806	Amp:45.1612903225806	Del:9.67741935483871
Udt-gr	*YKT6*	10652	7p13	Neutral:61.2903225806452	Amp:33.8709677419355	Del:4.83870967741935
Udt-gr	*YWHAG*	7532	7q11.23	Neutral:45.1612903225806	Amp:19.3548387096774	Del:35.4838709677419
Udt-gr	*ZAN*	7455	7q22.1	Neutral:32.258064516129	Amp:20.9677419354839	Del:46.7741935483871
Udt-gr	*ZCWPW1*	55063	7q22.1	Neutral:69.3548387096774	Amp:16.1290322580645	Del:14.5161290322581
Udt-gr	*ZKSCAN1*	7586	7q22.1	Neutral:59.6774193548387	Amp:19.3548387096774	Del:20.9677419354839
Udt-gr	*ZKSCAN5*	23660	7q22.1	Neutral:46.7741935483871	Amp:19.3548387096774	Del:33.8709677419355
Udt-gr	*ZMIZ2*	83637	7p13	Neutral:50	Amp:22.5806451612903	Del:27.4193548387097
Udt-gr	*ZNF3*	7551	7q22.1	Neutral:54.8387096774194	Amp:22.5806451612903	Del:22.5806451612903
Udt-gr	*ZNF394*	84124	7q22.1	Neutral:46.7741935483871	Amp:19.3548387096774	Del:33.8709677419355
Udt-gr	*ZNF479*	90827	7p11.2	Neutral:69.3548387096774	Amp:17.741935483871	Del:12.9032258064516
Udt-gr	*ZNF655*	79027	7q22.1	Neutral:64.5161290322581	Amp:20.9677419354839	Del:14.5161290322581
Udt-gr	*ZNF713*	349075	7p11.2	Neutral:46.7741935483871	Amp:8.06451612903226	Del:45.1612903225806
Udt-gr	*ZNF716*	441234	7p11.2	Neutral:66.1290322580645	Amp:16.1290322580645	Del:17.741935483871
Udt-gr	*ZNF789*	285989	7q22.1	Neutral:46.7741935483871	Amp:19.3548387096774	Del:33.8709677419355
Udt-gr	*ZNHIT1*	10467	7q22.1	Neutral:41.9354838709677	Amp:20.9677419354839	Del:37.0967741935484
Udt-gr	*ZP3*	7784	7q11.23	Neutral:41.9354838709677	Amp:17.741935483871	Del:40.3225806451613

Udt-gr	*ZSCAN21*	7589	7q22.1	Neutral:46.7741935483871	Amp:22.5806451612903	Del:30.6451612903226
Udt-gr	*DCAF13*	25879	8q22.3	Neutral:40.3225806451613	Amp:54.8387096774194	Del:4.83870967741935
Udt-gr	*DUSP26*	78986	8p12	Neutral:38.7096774193548	Amp:11.2903225806452	Del:50
Udt-gr	*LYPLA1*	10434	8q11.23	Neutral:51.6129032258064	Amp:16.1290322580645	Del:32.258064516129
Udt-gr	*MIR548O2*	100616190	8p12	Neutral:48.3870967741936	Amp:9.67741935483871	Del:41.9354838709677
Udt-gr	*MRPL15*	29088	8q11.23	Neutral:53.2258064516129	Amp:16.1290322580645	Del:30.6451612903226
Udt-gr	*POTEA*	340441	8p11.1	Neutral:50	Amp:17.741935483871	Del:32.258064516129
Udt-gr	*REXO1L2P*	100288527	8q21.2	Neutral:45.1612903225806	Amp:32.258064516129	Del:22.5806451612903
Udt-gr	*RGS20*	8601	8q11.23	Neutral:53.2258064516129	Amp:16.1290322580645	Del:30.6451612903226
Udt-gr	*RNF122*	79845	8p12	Neutral:35.4838709677419	Amp:11.2903225806452	Del:53.2258064516129
Udt-gr	*SLC25A32*	81034	8q22.3	Neutral:48.3870967741936	Amp:46.7741935483871	Del:4.83870967741935
Udt-gr	*SOX17*	64321	8q11.23	Neutral:54.8387096774194	Amp:30.6451612903226	Del:14.5161290322581
Udt-gr	*TCEA1*	6917	8q11.23	Neutral:48.3870967741936	Amp:16.1290322580645	Del:35.4838709677419
Udt-gr	*TNFRSF11B*	4982	8q24.12	Neutral:35.4838709677419	Amp:59.6774193548387	Del:4.83870967741935
Udt-gr	*UNC5D*	137970	8p12	Neutral:64.5161290322581	Amp:19.3548387096774	Del:16.1290322580645
Udt-gr	*CDKN2B-AS1*	100048912	9p21.3	Neutral:43.5483870967742	Amp:16.1290322580645	Del:40.3225806451613
Udt-gr	*DMRTA1*	63951	9p21.3	Neutral:43.5483870967742	Amp:19.3548387096774	Del:37.0967741935484
Udt-gr	*FAM154A*	158297	9p22.1	Neutral:58.0645161290323	Amp:11.2903225806452	Del:30.6451612903226
Udt-gr	*HAUS6*	54801	9p22.1	Neutral:32.258064516129	Amp:3.2258064516129	Del:64.5161290322581
Udt-gr	*MIR3152*	100422869	9p22.1	Neutral:56.4516129032258	Amp:14.5161290322581	Del:29.0322580645161
Udt-gr	*NXNL2*	158046	9q22.1	Neutral:41.9354838709677	Amp:9.67741935483871	Del:48.3870967741936
Udt-gr	*RRAGA*	10670	9p22.1	Neutral:46.7741935483871	Amp:6.45161290322581	Del:46.7741935483871
Udt-gr	*SCARNA8*	677776	9p22.1	Neutral:35.4838709677419	Amp:1.61290322580645	Del:62.9032258064516
Udt-gr	*SPIN1*	10927	9q22.1	Neutral:43.5483870967742	Amp:3.2258064516129	Del:53.2258064516129
Udt-gr	*ACBD7*	414149	10p13	Neutral:46.7741935483871	Amp:11.2903225806452	Del:41.9354838709677
Udt-gr	*C10orf111*	221060	10p13	Neutral:48.3870967741936	Amp:12.9032258064516	Del:38.7096774193548
Udt-gr	*CCDC7*	221016	10p11.22	Neutral:51.6129032258064	Amp:19.3548387096774	Del:29.0322580645161
Udt-gr	*CELF2*	10659	10p14	Neutral:50	Amp:45.1612903225806	Del:4.83870967741935
Udt-gr	*EPC1*	80314	10p11.22	Neutral:61.2903225806452	Amp:19.3548387096774	Del:19.3548387096774
Udt-gr	*FAM53B*	9679	10q26.13	Neutral:51.6129032258064	Amp:29.0322580645161	Del:19.3548387096774
Udt-gr	*INA*	9118	10q24.33	Neutral:33.8709677419355	Amp:6.45161290322581	Del:59.6774193548387
Udt-gr	*ITGB1*	3688	10p11.22	Neutral:58.0645161290323	Amp:27.4193548387097	Del:14.5161290322581
Udt-gr	*KIF5B*	3799	10p11.22	Neutral:61.2903225806452	Amp:17.741935483871	Del:20.9677419354839
Udt-gr	*LHPP*	64077	10q26.13	Neutral:50	Amp:12.9032258064516	Del:37.0967741935484
Udt-gr	*NKX1-2*	390010	10q26.13	Neutral:54.8387096774194	Amp:11.2903225806452	Del:33.8709677419355
Udt-gr	*NMT2*	9397	10p13	Neutral:54.8387096774194	Amp:9.67741935483871	Del:35.4838709677419
Udt-gr	*NRP1*	8829	10p11.22	Neutral:58.0645161290323	Amp:37.0967741935484	Del:4.83870967741935
Udt-gr	*OAT*	4942	10q26.13	Neutral:59.6774193548387	Amp:9.67741935483871	Del:30.6451612903226
Udt-gr	*RAB11FIP2*	22841	10q26.11	Neutral:50	Amp:33.8709677419355	Del:16.1290322580645
Udt-gr	*RPP38*	10557	10p13	Neutral:51.6129032258064	Amp:12.9032258064516	Del:35.4838709677419
Udt-gr	*ZNF33B*	7582	10q11.21	Neutral:59.6774193548387	Amp:14.5161290322581	Del:25.8064516129032

Udt-gr	*ZNF37BP*	100129482	10q11.21	Neutral:62.9032258064516	Amp:11.2903225806452	Del:25.8064516129032
Udt-gr	*BRSK2*	9024	11p15.5	Neutral:46.7741935483871	Amp:27.4193548387097	Del:25.8064516129032
Udt-gr	*BSX*	390259	11q24.1	Neutral:56.4516129032258	Amp:9.67741935483871	Del:33.8709677419355
Udt-gr	*C11orf63*	79864	11q24.1	Neutral:66.1290322580645	Amp:4.83870967741935	Del:29.0322580645161
Udt-gr	*CCND1*	595	11q13.3	Neutral:61.2903225806452	Amp:24.1935483870968	Del:14.5161290322581
Udt-gr	*DUSP8*	1850	11p15.5	Neutral:43.5483870967742	Amp:24.1935483870968	Del:32.258064516129
Udt-gr	*METTL15*	196074	11p14.1	Neutral:45.1612903225806	Amp:35.4838709677419	Del:19.3548387096774
Udt-gr	*MOB2*	81532	11p15.5	Neutral:48.3870967741936	Amp:24.1935483870968	Del:27.4193548387097
Udt-gr	*MUC2*	4583	11p15.5	Neutral:46.7741935483871	Amp:25.8064516129032	Del:27.4193548387097
Udt-gr	*MUC5B*	727897	11p15.5	Neutral:45.1612903225806	Amp:29.0322580645161	Del:25.8064516129032
Udt-gr	*MUC6*	4588	11p15.5	Neutral:48.3870967741936	Amp:24.1935483870968	Del:27.4193548387097
Udt-gr	*MYEOV*	26579	11q13.3	Neutral:59.6774193548387	Amp:24.1935483870968	Del:16.1290322580645
Udt-gr	*OR4A5*	81318	11p11.12	Neutral:56.4516129032258	Amp:22.5806451612903	Del:20.9677419354839
Udt-gr	*ORAOV1*	220064	11q13.3	Neutral:64.5161290322581	Amp:20.9677419354839	Del:14.5161290322581
Udt-gr	*TOLLIP*	54472	11p15.5	Neutral:51.6129032258064	Amp:24.1935483870968	Del:24.1935483870968
Udt-gr	*AEBP2*	121536	12p12.3	Neutral:64.5161290322581	Amp:9.67741935483871	Del:25.8064516129032
Udt-gr	*ALG10*	84920	12p11.1	Neutral:51.6129032258064	Amp:37.0967741935484	Del:11.2903225806452
Udt-gr	*ANAPC7*	51434	12q24.11	Neutral:46.7741935483871	Amp:4.83870967741935	Del:48.3870967741936
Udt-gr	*ARPC3*	10094	12q24.11	Neutral:33.8709677419355	Amp:8.06451612903226	Del:58.0645161290323
Udt-gr	*CAPZA3*	93661	12p12.3	Neutral:58.0645161290323	Amp:29.0322580645161	Del:12.9032258064516
Udt-gr	*FAM216A*	29902	12q24.11	Neutral:46.7741935483871	Amp:6.45161290322581	Del:46.7741935483871
Udt-gr	*GPN3*	51184	12q24.11	Neutral:38.7096774193548	Amp:8.06451612903226	Del:53.2258064516129
Udt-gr	*PLEKHA5*	54477	12p12.3	Neutral:61.2903225806452	Amp:9.67741935483871	Del:29.0322580645161
Udt-gr	*MPHOSPH8*	54737	13q12.11	Neutral:59.6774193548387	Amp:4.83870967741935	Del:35.4838709677419
Udt-gr	*NDFIP2*	54602	13q31.1	Neutral:46.7741935483871	Amp:24.1935483870968	Del:29.0322580645161
Udt-gr	*PSPC1*	55269	13q12.11	Neutral:53.2258064516129	Amp:4.83870967741935	Del:41.9354838709677
Udt-gr	*SLITRK1*	114798	13q31.1	Neutral:48.3870967741936	Amp:32.258064516129	Del:19.3548387096774
Udt-gr	*SPRY2*	10253	13q31.1	Neutral:41.9354838709677	Amp:27.4193548387097	Del:30.6451612903226
Udt-gr	*ZIC2*	7546	13q32.3	Neutral:54.8387096774194	Amp:22.5806451612903	Del:22.5806451612903
Udt-gr	*ZIC5*	85416	13q32.3	Neutral:67.741935483871	Amp:14.5161290322581	Del:17.741935483871
Udt-gr	*ZMYM2*	7750	13q12.11	Neutral:59.6774193548387	Amp:4.83870967741935	Del:35.4838709677419
Udt-gr	*ZMYM5*	9205	13q12.11	Neutral:29.0322580645161	Amp:6.45161290322581	Del:64.5161290322581
Udt-gr	*FCF1*	51077	14q24.3	Neutral:37.0967741935484	Amp:8.06451612903226	Del:54.8387096774194
Udt-gr	*POTEM*	641455	14q11.2	Neutral:54.8387096774194	Amp:25.8064516129032	Del:19.3548387096774
Udt-gr	*YLPM1*	56252	14q24.3	Neutral:59.6774193548387	Amp:6.45161290322581	Del:33.8709677419355
Udt-gr	*ASB9P1*	728619	15q26.1	Neutral:59.6774193548387	Amp:9.67741935483871	Del:30.6451612903226
Udt-gr	*CHD2*	1106	15q26.1	Neutral:66.1290322580645	Amp:20.9677419354839	Del:12.9032258064516
Udt-gr	*FAM174B*	400451	15q26.1	Neutral:70.9677419354839	Amp:20.9677419354839	Del:8.06451612903226
Udt-gr	*GOLGA8A*	23015	15q14	Neutral:75.8064516129032	Amp:12.9032258064516	Del:11.2903225806452
Udt-gr	*BANP*	54971	16q24.2	Neutral:56.4516129032258	Amp:19.3548387096774	Del:24.1935483870968
Udt-gr	*CA5A*	763	16q24.2	Neutral:45.1612903225806	Amp:12.9032258064516	Del:41.9354838709677

Udt-gr	*CHST6*	4166	16q23.1	Neutral:40.3225806451613	Amp:17.741935483871	Del:41.9354838709677
Udt-gr	*LINC00273*	649159	16p11.2	Neutral:67.741935483871	Amp:12.9032258064516	Del:19.3548387096774
Udt-gr	*QPRT*	23475	16p11.2	Neutral:30.6451612903226	Amp:17.741935483871	Del:51.6129032258064
Udt-gr	*SLC7A5*	8140	16q24.2	Neutral:51.6129032258064	Amp:16.1290322580645	Del:32.258064516129
Udt-gr	*SLC7A5P1*	81893	16p11.2	Neutral:37.0967741935484	Amp:17.741935483871	Del:45.1612903225806
Udt-gr	*SPN*	6693	16p11.2	Neutral:27.4193548387097	Amp:20.9677419354839	Del:51.6129032258064
Udt-gr	*STX1B*	112755	16p11.2	Neutral:40.3225806451613	Amp:20.9677419354839	Del:38.7096774193548
Udt-gr	*STX4*	6810	16p11.2	Neutral:40.3225806451613	Amp:19.3548387096774	Del:40.3225806451613
Udt-gr	*TP53TG3B*	729355	16p11.2	Neutral:77.4193548387097	Amp:12.9032258064516	Del:9.67741935483871
Udt-gr	*TP53TG3C*	653550	16p11.2	Neutral:77.4193548387097	Amp:12.9032258064516	Del:9.67741935483871
Udt-gr	*UBE2MP1*	606551	16p11.2	Neutral:61.2903225806452	Amp:17.741935483871	Del:20.9677419354839
Udt-gr	*ARL17B*	100506084	17q21.31	Neutral:70.9677419354839	Amp:11.2903225806452	Del:17.741935483871
Udt-gr	*EVPLL*	645027	17p11.2	Neutral:45.1612903225806	Amp:17.741935483871	Del:37.0967741935484
Udt-gr	*KCNJ12*	3768	17p11.2	Neutral:62.9032258064516	Amp:25.8064516129032	Del:11.2903225806452
Udt-gr	*KCNJ2*	3759	17q24.3	Neutral:46.7741935483871	Amp:50	Del:3.2258064516129
Udt-gr	*LGALS9C*	654346	17p11.2	Neutral:67.741935483871	Amp:19.3548387096774	Del:12.9032258064516
Udt-gr	*LRRC37A*	9884	17q21.31	Neutral:70.9677419354839	Amp:12.9032258064516	Del:16.1290322580645
Udt-gr	*MAP2K3*	5606	17p11.2	Neutral:66.1290322580645	Amp:24.1935483870968	Del:9.67741935483871
Udt-gr	*MRPL45P2*	653479	17q21.32	Neutral:50	Amp:14.5161290322581	Del:35.4838709677419
Udt-gr	*NPEPPS*	9520	17q21.32	Neutral:56.4516129032258	Amp:11.2903225806452	Del:32.258064516129
Udt-gr	*SHMT1*	6470	17p11.2	Neutral:45.1612903225806	Amp:11.2903225806452	Del:43.5483870967742
Udt-gr	*SNORD65*	692106	17p11.2	Neutral:56.4516129032258	Amp:9.67741935483871	Del:33.8709677419355
Udt-gr	*SOX9*	6662	17q24.3	Neutral:58.0645161290323	Amp:40.3225806451613	Del:1.61290322580645
Udt-gr	*ZFP3*	124961	17p13.2	Neutral:48.3870967741936	Amp:8.06451612903226	Del:43.5483870967742
Udt-gr	*ZNF232*	7775	17p13.2	Neutral:66.1290322580645	Amp:9.67741935483871	Del:24.1935483870968
Udt-gr	*ABHD3*	171586	18q11.2	Neutral:54.8387096774194	Amp:4.83870967741935	Del:40.3225806451613
Udt-gr	*ADCYAP1*	116	18p11.32	Neutral:67.741935483871	Amp:16.1290322580645	Del:16.1290322580645
Udt-gr	*ATP9B*	374868	18q23	Neutral:67.741935483871	Amp:12.9032258064516	Del:19.3548387096774
Udt-gr	*ESCO1*	114799	18q11.2	Neutral:58.0645161290323	Amp:4.83870967741935	Del:37.0967741935484
Udt-gr	*GALR1*	2587	18q23	Neutral:51.6129032258064	Amp:19.3548387096774	Del:29.0322580645161
Udt-gr	*LINC00470*	56651	18p11.32	Neutral:62.9032258064516	Amp:20.9677419354839	Del:16.1290322580645
Udt-gr	*MBP*	4155	18q23	Neutral:58.0645161290323	Amp:27.4193548387097	Del:14.5161290322581
Udt-gr	*MIB1*	57534	18q11.2	Neutral:67.741935483871	Amp:12.9032258064516	Del:19.3548387096774
Udt-gr	*MIR320C1*	100302135	18q11.2	Neutral:54.8387096774194	Amp:4.83870967741935	Del:40.3225806451613
Udt-gr	*SALL3*	27164	18q23	Neutral:59.6774193548387	Amp:20.9677419354839	Del:19.3548387096774
Udt-gr	*SNRPD1*	6632	18q11.2	Neutral:51.6129032258064	Amp:4.83870967741935	Del:43.5483870967742
Udt-gr	*YES1*	7525	18p11.32	Neutral:58.0645161290323	Amp:9.67741935483871	Del:32.258064516129
Udt-gr	*GP6*	51206	19q13.42	Neutral:32.258064516129	Amp:17.741935483871	Del:50
Udt-gr	*LONP1*	9361	19p13.3	Neutral:40.3225806451613	Amp:17.741935483871	Del:41.9354838709677
Udt-gr	*MIDN*	90007	19p13.3	Neutral:37.0967741935484	Amp:38.7096774193548	Del:24.1935483870968
Udt-gr	*NLRP2*	55655	19q13.42	Neutral:32.258064516129	Amp:14.5161290322581	Del:53.2258064516129

Udt-gr	*NLRP7*	199713	19q13.42	Neutral:30.6451612903226	Amp:16.1290322580645	Del:53.2258064516129
Udt-gr	*SIGLEC14*	100049587	19q13.41	Neutral:61.2903225806452	Amp:24.1935483870968	Del:14.5161290322581
Udt-gr	*SIGLEC5*	8778	19q13.41	Neutral:61.2903225806452	Amp:25.8064516129032	Del:12.9032258064516
Udt-gr	*ZNF135*	7694	19q13.43	Neutral:53.2258064516129	Amp:19.3548387096774	Del:27.4193548387097
Udt-gr	*ZNF420*	147923	19q13.12	Neutral:62.9032258064516	Amp:11.2903225806452	Del:25.8064516129032
Udt-gr	*ZNF568*	374900	19q13.12	Neutral:56.4516129032258	Amp:12.9032258064516	Del:30.6451612903226
Udt-gr	*ZNF606*	80095	19q13.43	Neutral:50	Amp:12.9032258064516	Del:37.0967741935484
Udt-gr	*ZSCAN1*	284312	19q13.43	Neutral:50	Amp:19.3548387096774	Del:30.6451612903226
Udt-gr	*ABHD12*	26090	20p11.21	Neutral:69.3548387096774	Amp:20.9677419354839	Del:9.67741935483871
Udt-gr	*ACOT8*	10005	20q13.12	Neutral:50	Amp:19.3548387096774	Del:30.6451612903226
Udt-gr	*ADA*	100	20q13.12	Neutral:69.3548387096774	Amp:19.3548387096774	Del:11.2903225806452
Udt-gr	*ADRM1*	11047	20q13.33	Neutral:40.3225806451613	Amp:27.4193548387097	Del:32.258064516129
Udt-gr	*CD40*	958	20q13.12	Neutral:59.6774193548387	Amp:32.258064516129	Del:8.06451612903226
Udt-gr	*CDH22*	64405	20q13.12	Neutral:56.4516129032258	Amp:33.8709677419355	Del:9.67741935483871
Udt-gr	*CTSA*	5476	20q13.12	Neutral:43.5483870967742	Amp:20.9677419354839	Del:35.4838709677419
Udt-gr	*DBNDD2*	55861	20q13.12	Neutral:72.5806451612903	Amp:16.1290322580645	Del:11.2903225806452
Udt-gr	*DNTTIP1*	116092	20q13.12	Neutral:54.8387096774194	Amp:17.741935483871	Del:27.4193548387097
Udt-gr	*ELMO2*	63916	20q13.12	Neutral:56.4516129032258	Amp:38.7096774193548	Del:4.83870967741935
Udt-gr	*EYA2*	2139	20q13.12	Neutral:75.8064516129032	Amp:12.9032258064516	Del:11.2903225806452
Udt-gr	*FAM217B*	63939	20q13.33	Neutral:45.1612903225806	Amp:48.3870967741936	Del:6.45161290322581
Udt-gr	*FITM2*	128486	20q13.12	Neutral:56.4516129032258	Amp:16.1290322580645	Del:27.4193548387097
Udt-gr	*GDAP1L1*	78997	20q13.12	Neutral:64.5161290322581	Amp:16.1290322580645	Del:19.3548387096774
Udt-gr	*GINS1*	9837	20p11.21	Neutral:67.741935483871	Amp:11.2903225806452	Del:20.9677419354839
Udt-gr	*GTSF1L*	149699	20q13.12	Neutral:62.9032258064516	Amp:17.741935483871	Del:19.3548387096774
Udt-gr	*HNF4A*	3172	20q13.12	Neutral:66.1290322580645	Amp:16.1290322580645	Del:17.741935483871
Udt-gr	*IFT52*	51098	20q13.12	Neutral:51.6129032258064	Amp:9.67741935483871	Del:38.7096774193548
Udt-gr	*JPH2*	57158	20q13.12	Neutral:62.9032258064516	Amp:20.9677419354839	Del:16.1290322580645
Udt-gr	*KCNK15*	60598	20q13.12	Neutral:59.6774193548387	Amp:30.6451612903226	Del:9.67741935483871
Udt-gr	*KCNS1*	3787	20q13.12	Neutral:62.9032258064516	Amp:32.258064516129	Del:4.83870967741935
Udt-gr	*L3MBTL1*	26013	20q13.12	Neutral:67.741935483871	Amp:16.1290322580645	Del:16.1290322580645
Udt-gr	*LAMA5*	3911	20q13.33	Neutral:33.8709677419355	Amp:29.0322580645161	Del:37.0967741935484
Udt-gr	*MATN4*	8785	20q13.12	Neutral:62.9032258064516	Amp:17.741935483871	Del:19.3548387096774
Udt-gr	*MIR3616*	100500814	20q13.12	Neutral:69.3548387096774	Amp:12.9032258064516	Del:17.741935483871
Udt-gr	*MIR3646*	100500813	20q13.12	Neutral:66.1290322580645	Amp:19.3548387096774	Del:14.5161290322581
Udt-gr	*MKRN7P*	7686	20q13.12	Neutral:56.4516129032258	Amp:32.258064516129	Del:11.2903225806452
Udt-gr	*MMP9*	4318	20q13.12	Neutral:56.4516129032258	Amp:29.0322580645161	Del:14.5161290322581
Udt-gr	*MYBL2*	4605	20q13.12	Neutral:54.8387096774194	Amp:14.5161290322581	Del:30.6451612903226
Udt-gr	*NCOA3*	8202	20q13.12	Neutral:74.1935483870968	Amp:17.741935483871	Del:8.06451612903226
Udt-gr	*NCOA5*	57727	20q13.12	Neutral:46.7741935483871	Amp:45.1612903225806	Del:8.06451612903226
Udt-gr	*NEURL2*	140825	20q13.12	Neutral:41.9354838709677	Amp:22.5806451612903	Del:35.4838709677419
Udt-gr	*NKX2-2*	4821	20p11.22	Neutral:46.7741935483871	Amp:38.7096774193548	Del:14.5161290322581

Udt-gr	*PABPC1L*	80336	20q13.12	Neutral:66.1290322580645	Amp:16.1290322580645	Del:17.741935483871
Udt-gr	*PAX1*	5075	20p11.22	Neutral:48.3870967741936	Amp:40.3225806451613	Del:11.2903225806452
Udt-gr	*PCIF1*	63935	20q13.12	Neutral:54.8387096774194	Amp:22.5806451612903	Del:22.5806451612903
Udt-gr	*PI3*	5266	20q13.12	Neutral:59.6774193548387	Amp:35.4838709677419	Del:4.83870967741935
Udt-gr	*PIGT*	51604	20q13.12	Neutral:74.1935483870968	Amp:17.741935483871	Del:8.06451612903226
Udt-gr	*PKIG*	11142	20q13.12	Neutral:70.9677419354839	Amp:14.5161290322581	Del:14.5161290322581
Udt-gr	*PLTP*	5360	20q13.12	Neutral:43.5483870967742	Amp:20.9677419354839	Del:35.4838709677419
Udt-gr	*PPP1R3D*	5509	20q13.33	Neutral:40.3225806451613	Amp:45.1612903225806	Del:14.5161290322581
Udt-gr	*R3HDML*	140902	20q13.12	Neutral:58.0645161290323	Amp:16.1290322580645	Del:25.8064516129032
Udt-gr	*RBPJL*	11317	20q13.12	Neutral:69.3548387096774	Amp:16.1290322580645	Del:14.5161290322581
Udt-gr	*RIMS4*	140730	20q13.12	Neutral:61.2903225806452	Amp:32.258064516129	Del:6.45161290322581
Udt-gr	*SDC4*	6385	20q13.12	Neutral:74.1935483870968	Amp:16.1290322580645	Del:9.67741935483871
Udt-gr	*SEMG1*	6406	20q13.12	Neutral:59.6774193548387	Amp:30.6451612903226	Del:9.67741935483871
Udt-gr	*SEMG2*	6407	20q13.12	Neutral:54.8387096774194	Amp:32.258064516129	Del:12.9032258064516
Udt-gr	*SERINC3*	10955	20q13.12	Neutral:72.5806451612903	Amp:9.67741935483871	Del:17.741935483871
Udt-gr	*SGK2*	10110	20q13.12	Neutral:64.5161290322581	Amp:14.5161290322581	Del:20.9677419354839
Udt-gr	*SLC12A5*	57468	20q13.12	Neutral:54.8387096774194	Amp:38.7096774193548	Del:6.45161290322581
Udt-gr	*SLC13A3*	64849	20q13.12	Neutral:54.8387096774194	Amp:40.3225806451613	Del:4.83870967741935
Udt-gr	*SLC2A10*	81031	20q13.12	Neutral:62.9032258064516	Amp:29.0322580645161	Del:8.06451612903226
Udt-gr	*SLC35C2*	51006	20q13.12	Neutral:53.2258064516129	Amp:37.0967741935484	Del:9.67741935483871
Udt-gr	*SLPI*	6590	20q13.12	Neutral:56.4516129032258	Amp:30.6451612903226	Del:12.9032258064516
Udt-gr	*SNX21*	90203	20q13.12	Neutral:50	Amp:19.3548387096774	Del:30.6451612903226
Udt-gr	*SPATA25*	128497	20q13.12	Neutral:45.1612903225806	Amp:20.9677419354839	Del:33.8709677419355
Udt-gr	*SPINT3*	10816	20q13.12	Neutral:75.8064516129032	Amp:17.741935483871	Del:6.45161290322581
Udt-gr	*SPINT4*	391253	20q13.12	Neutral:59.6774193548387	Amp:9.67741935483871	Del:30.6451612903226
Udt-gr	*STK4*	6789	20q13.12	Neutral:70.9677419354839	Amp:20.9677419354839	Del:8.06451612903226
Udt-gr	*SULF2*	55959	20q13.12	Neutral:67.741935483871	Amp:24.1935483870968	Del:8.06451612903226
Udt-gr	*SYCP2*	10388	20q13.33	Neutral:37.0967741935484	Amp:40.3225806451613	Del:22.5806451612903
Udt-gr	*SYS1*	90196	20q13.12	Neutral:74.1935483870968	Amp:16.1290322580645	Del:9.67741935483871
Udt-gr	*SYS1-DBNDD2*	767557	20q13.12	Neutral:74.1935483870968	Amp:16.1290322580645	Del:9.67741935483871
Udt-gr	*TNNC2*	7125	20q13.12	Neutral:46.7741935483871	Amp:20.9677419354839	Del:32.258064516129
Udt-gr	*TOMM34*	10953	20q13.12	Neutral:72.5806451612903	Amp:19.3548387096774	Del:8.06451612903226
Udt-gr	*TOX2*	84969	20q13.12	Neutral:62.9032258064516	Amp:22.5806451612903	Del:14.5161290322581
Udt-gr	*TP53RK*	112858	20q13.12	Neutral:64.5161290322581	Amp:30.6451612903226	Del:4.83870967741935
Udt-gr	*TP53TG5*	27296	20q13.12	Neutral:72.5806451612903	Amp:16.1290322580645	Del:11.2903225806452
Udt-gr	*TTPAL*	79183	20q13.12	Neutral:74.1935483870968	Amp:12.9032258064516	Del:12.9032258064516
Udt-gr	*UBE2C*	11065	20q13.12	Neutral:51.6129032258064	Amp:19.3548387096774	Del:29.0322580645161
Udt-gr	*WFDC10A*	140832	20q13.12	Neutral:70.9677419354839	Amp:19.3548387096774	Del:9.67741935483871
Udt-gr	*WFDC10B*	280664	20q13.12	Neutral:67.741935483871	Amp:11.2903225806452	Del:20.9677419354839
Udt-gr	*WFDC11*	259239	20q13.12	Neutral:70.9677419354839	Amp:9.67741935483871	Del:19.3548387096774
Udt-gr	*WFDC12*	128488	20q13.12	Neutral:59.6774193548387	Amp:33.8709677419355	Del:6.45161290322581

Udt-gr	*WFDC13*	164237	20q13.12	Neutral:69.3548387096774	Amp:9.67741935483871	Del:20.9677419354839
Udt-gr	*WFDC2*	10406	20q13.12	Neutral:77.4193548387097	Amp:16.1290322580645	Del:6.45161290322581
Udt-gr	*WFDC3*	140686	20q13.12	Neutral:58.0645161290323	Amp:14.5161290322581	Del:27.4193548387097
Udt-gr	*WFDC5*	149708	20q13.12	Neutral:61.2903225806452	Amp:33.8709677419355	Del:4.83870967741935
Udt-gr	*WFDC6*	140870	20q13.12	Neutral:72.5806451612903	Amp:20.9677419354839	Del:6.45161290322581
Udt-gr	*WFDC8*	90199	20q13.12	Neutral:72.5806451612903	Amp:20.9677419354839	Del:6.45161290322581
Udt-gr	*WFDC9*	259240	20q13.12	Neutral:72.5806451612903	Amp:17.741935483871	Del:9.67741935483871
Udt-gr	*WISP2*	8839	20q13.12	Neutral:59.6774193548387	Amp:30.6451612903226	Del:9.67741935483871
Udt-gr	*YWHAB*	7529	20q13.12	Neutral:69.3548387096774	Amp:16.1290322580645	Del:14.5161290322581
Udt-gr	*ZMYND8*	23613	20q13.12	Neutral:74.1935483870968	Amp:9.67741935483871	Del:16.1290322580645
Udt-gr	*ZNF334*	55713	20q13.12	Neutral:51.6129032258064	Amp:38.7096774193548	Del:9.67741935483871
Udt-gr	*ZNF335*	63925	20q13.12	Neutral:53.2258064516129	Amp:25.8064516129032	Del:20.9677419354839
Udt-gr	*ZSWIM1*	90204	20q13.12	Neutral:45.1612903225806	Amp:20.9677419354839	Del:33.8709677419355
Udt-gr	*ZSWIM3*	140831	20q13.12	Neutral:45.1612903225806	Amp:20.9677419354839	Del:33.8709677419355
Udt-gr	*ANKRD30BP2*	149992	21q11.2	Neutral:64.5161290322581	Amp:9.67741935483871	Del:25.8064516129032
Udt-gr	*BAGE2*	85319	21p11.1	Neutral:67.741935483871	Amp:14.5161290322581	Del:17.741935483871
Udt-gr	*C21orf37*	100505929	21q21.1	Neutral:46.7741935483871	Amp:19.3548387096774	Del:33.8709677419355
Udt-gr	*CXADR*	1525	21q21.1	Neutral:59.6774193548387	Amp:12.9032258064516	Del:27.4193548387097
Udt-gr	*KRTAP10-12*	386685	21q22.3	Neutral:41.9354838709677	Amp:25.8064516129032	Del:32.258064516129
Udt-gr	*KRTAP10-4*	386672	21q22.3	Neutral:45.1612903225806	Amp:27.4193548387097	Del:27.4193548387097
Udt-gr	*KRTAP12-1*	353332	21q22.3	Neutral:45.1612903225806	Amp:24.1935483870968	Del:30.6451612903226
Udt-gr	*LINC00478*	388815	21q21.1	Neutral:46.7741935483871	Amp:35.4838709677419	Del:17.741935483871
Udt-gr	*MIR125B2*	406912	21q21.1	Neutral:43.5483870967742	Amp:30.6451612903226	Del:25.8064516129032
Udt-gr	*MIR3156-3*	100423018	21q11.2	Neutral:56.4516129032258	Amp:22.5806451612903	Del:20.9677419354839
Udt-gr	*TSPEAR*	54084	21q22.3	Neutral:48.3870967741936	Amp:24.1935483870968	Del:27.4193548387097
Udt-gr	*ATXN10*	25814	22q13.31	Neutral:54.8387096774194	Amp:30.6451612903226	Del:14.5161290322581
Udt-gr	*C22orf26*	55267	22q13.31	Neutral:74.1935483870968	Amp:11.2903225806452	Del:14.5161290322581
Udt-gr	*EP300*	2033	22q13.2	Neutral:51.6129032258064	Amp:8.06451612903226	Del:40.3225806451613
Udt-gr	*MIR1281*	100302237	22q13.2	Neutral:43.5483870967742	Amp:8.06451612903226	Del:48.3870967741936
Udt-gr	*MIR3619*	100500828	22q13.31	Neutral:74.1935483870968	Amp:11.2903225806452	Del:14.5161290322581
Udt-gr	*MIR4763*	100616143	22q13.31	Neutral:74.1935483870968	Amp:11.2903225806452	Del:14.5161290322581
Udt-gr	*MIRLET7A3*	406883	22q13.31	Neutral:74.1935483870968	Amp:11.2903225806452	Del:14.5161290322581
Udt-gr	*MIRLET7B*	406884	22q13.31	Neutral:74.1935483870968	Amp:11.2903225806452	Del:14.5161290322581
Udt-gr	*PPARA*	5465	22q13.31	Neutral:53.2258064516129	Amp:12.9032258064516	Del:33.8709677419355
Udt-gr	*RBX1*	9978	22q13.2	Neutral:45.1612903225806	Amp:11.2903225806452	Del:43.5483870967742
Udt-gr	*WNT7B*	7477	22q13.31	Neutral:74.1935483870968	Amp:11.2903225806452	Del:14.5161290322581
Udt-gr	*XPNPEP3*	63929	22q13.2	Neutral:50	Amp:11.2903225806452	Del:38.7096774193548

Table S12: Enriched KEGG pathways among CNA-affected genes

IDH-gr

None

KRAS-gr

P-value	Q-value	Pathway	Source	External ID	Members Input Overlap	Members Input Overlap (IDs)	Size	Effective Size
4.31E-11	3.02E-09	Natural killer cell mediated cytotoxicity	KEGG	path:hsa04650	NFATC1; IFNA8; IFNGR2; IFNAR2; IFNA1; PTK2B; TNFRSF10C; TNFRSF10B; TNFRSF10A; IFNAR1; SH3BP2; TNFRSF10D; PPP3CC	8793; 8794; 8795; 8797; 2185; 3439; 4772; 6452; 3445; 3454; 3455; 3460; 5533	135	134
1.25E-06	4.36E-05	Measles	KEGG	path:hsa05162	IFNAR2; IFNA8; IFNA1; TNFRSF10C; TNFRSF10B; TNFRSF10A; IFNAR1; IFNGR2; TNFRSF10D	8793; 8794; 8795; 8797; 3439; 3445; 3454; 3455; 3460	136	135
8.29E-06	0.000184768	Cytokine-cytokine receptor interaction	KEGG	path:hsa04060	IFNAR2; IFNA8; IL10RB; IFNA1; TNFRSF10C; TNFRSF10B; TNFRSF10A; IFNAR1; IFNGR2; TNFRSF10D; IFNE	3588; 8793; 8794; 8795; 8797; 3455; 3439; 3445; 3454; 3460; 338376	265	265
1.06E-05	0.000184768	Influenza A	KEGG	path:hsa05164	IFNAR2; IFNA8; IFNA1; TNFRSF10C; TNFRSF10B; TNFRSF10A; IFNAR1; IFNGR2; TNFRSF10D	8793; 8794; 8795; 8797; 3439; 3445; 3454; 3455; 3460	175	175
9.15E-05	0.001281322	Hepatitis C	KEGG	path:hsa05160	IFNAR2; IFNA8; CLDN17; IFNA1; PPP2R2A; CLDN8; IFNAR1	9073; 26285; 3439; 3445; 3454; 3455; 5520	133	133
0.000266659	0.003111016	Jak-STAT signaling pathway	KEGG	path:hsa04630	IFNA8; IL10RB; IFNA1; IFNAR2; IFNAR1; IFNGR2; IFNE	3588; 3439; 3445; 3454; 3455; 3460; 338376	158	158
0.000716291	0.007162907	Amyotrophic lateral sclerosis (ALS)	KEGG	path:hsa05014	NEFM; NEFL; PPP3CC; SOD1	4741; 4747; 5533; 6647	51	51
0.001096876	0.009597665	Hepatitis B	KEGG	path:hsa05161	NFATC1; IFNA8; EGR3; IFNA1; PTK2B; IFNAR1	2185; 4772; 3439; 3445; 3454; 1960	146	146
0.003946541	0.030695316	Osteoclast differentiation	KEGG	path:hsa04380	IFNAR2; NFATC1; IFNAR1; IFNGR2; PPP3CC	4772; 3454; 3455; 3460; 5533	132	131

TP53-gr

None

Udt-gr

P-value	Q-value	Pathway	Source	External ID	Members Input Overlap	Members Input Overlap (IDs)	Size	Effective Size
3.31E-05	0.005529661	Bacterial invasion of epithelial cells	KEGG	path:hsa05100	ITGB1; ARPC3; ARPC1B; PIK3CB; MET; CDC42; CAV2; ARPC1A; ELMO2; CAV1	4233; 857; 5291; 63916; 10552; 858; 998; 10094; 10095; 3688	78	78
0.000217995	0.013070107	SNARE interactions in vesicular transport	KEGG	path:hsa04130	STX1A; BET1; STX1B; VAMP4; STX4; YKT6	6804; 6810; 10652; 10282; 8674; 112755	34	34
0.000239755	0.013070107	Epstein-Barr virus infection	KEGG	path:hsa05169	EP300; RBPJL; HSPB1; CDKN1A; CD40; HLA-E; YWHAG; MAP2K3; SPN; YWHAB; PSMC2; POLR2J; PIK3CB; POLR2J2; POLR2J3	1026; 6693; 11317; 3133; 5701; 958; 5291; 3315; 548644; 5439; 7529; 7532; 246721; 5606; 2033	204	200
0.000313056	0.013070107	Proteoglycans in cancer	KEGG	path:hsa05205	ITGB1; CCND1; FZD9; CDKN1A; SDC4; CAMK2B; MET; CDC42; MMP9; CAV1; EGFR; WNT7B; CAV2; PIK3CB; WNT2	1026; 595; 3688; 8326; 4233; 5291; 4318; 6385; 7472; 816; 7477; 857; 858; 1956; 998	205	205
0.00089736	0.029971839	Leukocyte transendothelial migration	KEGG	path:hsa04670	ITGB1; NCF1; CLDN15; PIK3CB; MYL10; MYL7; MMP9; CLDN3; CLDN4; CDC42	653361; 24146; 3688; 58498; 5291; 4318; 93408; 1364; 1365; 998	116	116
0.001495311	0.041619483	Oocyte meiosis	KEGG	path:hsa04114	STAG3; SPDYE6; SPDYE1; CAMK2B; SPDYE2; SPDYE3; YWHAB; RBX1; YWHAG; ANAPC7	51434; 9978; 285955; 816; 7529; 7532; 441272; 441273; 10734; 729597	124	124

Table S13: Genome-wide DNA methylation analysis

Sample_ID	Driver Status	Source	Sentrix_ID	Sentrix_Position	Classification
120	IDH-gr	In House	8942297050	R04C01	iCCA
134	IDH-gr	In House	8942297043	R04C01	iCCA
137	IDH-gr	In House	8942297043	R01C02	iCCA
BR_1	IDH-gr	Jusakul et al. (PMID:28667006)	3999215224	R01C01	iCCA
FR_9	IDH-gr	Jusakul et al. (PMID:28667006)	3999215224	R06C02	iCCA
SG_28	IDH-gr	Jusakul et al. (PMID:28667006)	7927554089	R01C01	iCCA
TCGA-W5-AA2G	IDH-gr	TCGA	9996247050	R01C01	iCCA
TCGA-W5-AA34	IDH-gr	TCGA	9996247050	R04C02	iCCA
109	KRAS-gr	In House	8942297039	R05C01	iCCA
111	KRAS-gr	In House	8942297039	R01C02	iCCA
116	KRAS-gr	In House	8942297039	R06C02	iCCA
169	KRAS-gr	In House	8942297049	R06C02	iCCA
TCGA-ZH-A8Y8	KRAS-gr	TCGA	9996247047	R01C01	iCCA
TH_121	KRAS-gr	Jusakul et al. (PMID:28667006)	10005839063	R01C01	iCCA
TH_55	KRAS-gr	Jusakul et al. (PMID:28667006)	8691803053	R03C01	iCCA
TH_65	KRAS-gr	Jusakul et al. (PMID:28667006)	10005839063	R01C02	iCCA
118	TP53-gr	In House	8942297050	R02C01	iCCA
121	TP53-gr	In House	8942297050	R05C01	iCCA
125	TP53-gr	In House	8942297050	R02C02	iCCA
166	TP53-gr	In House	8942297049	R03C02	iCCA
FR_14	TP53-gr	Jusakul et al. (PMID:28667006)	3999215225	R05C02	iCCA
FR_3	TP53-gr	Jusakul et al. (PMID:28667006)	3999215225	R02C01	iCCA
sample11A	TP53-gr	In House	5935534001	R05C02	iCCA
sample15A	TP53-gr	In House	5935534013	R03C01	iCCA
sample16A	TP53-gr	In House	5935534013	R04C01	iCCA
sample19A	TP53-gr	In House	5935534013	R01C02	iCCA
SG_29	TP53-gr	Jusakul et al. (PMID:28667006)	3999215221	R06C02	iCCA
TCGA-W5-AA2I	TP53-gr	TCGA	9996247050	R06C01	iCCA
TCGA-ZH-A8Y5	TP53-gr	TCGA	3999997083	R04C01	iCCA
TH_28	TP53-gr	Jusakul et al. (PMID:28667006)	10005839066	R01C02	iCCA
TH_43	TP53-gr	Jusakul et al. (PMID:28667006)	10005839066	R03C02	iCCA
TH_78	TP53-gr	Jusakul et al. (PMID:28667006)	10005839063	R05C02	iCCA
TH_85	TP53-gr	Jusakul et al. (PMID:28667006)	10005839075	R04C01	iCCA
BR_2	Udt-gr	Jusakul et al. (PMID:28667006)	3999215224	R02C01	iCCA
FR_1	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R02C02	iCCA
FR_10	Udt-gr	Jusakul et al. (PMID:28667006)	3999215224	R05C02	iCCA
FR_11	Udt-gr	Jusakul et al. (PMID:28667006)	3999215224	R04C02	iCCA
FR_12	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R06C02	iCCA
FR_13	Udt-gr	Jusakul et al. (PMID:28667006)	3999215224	R03C02	iCCA
FR_15	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R03C02	iCCA
FR_16	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R04C02	iCCA

FR_2	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R01C02	iCCA
FR_4	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R03C01	iCCA
FR_5	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R04C01	iCCA
FR_6	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R05C01	iCCA
FR_7	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R06C01	iCCA
FR_8	Udt-gr	Jusakul et al. (PMID:28667006)	3999215225	R01C01	iCCA
KR_1	Udt-gr	Jusakul et al. (PMID:28667006)	3999215224	R03C01	iCCA
KR_2	Udt-gr	Jusakul et al. (PMID:28667006)	3999215224	R06C01	iCCA
RO_10	Udt-gr	Jusakul et al. (PMID:28667006)	10005839075	R05C01	iCCA
RO_38	Udt-gr	Jusakul et al. (PMID:28667006)	10005839075	R02C02	iCCA
SG_21	Udt-gr	Jusakul et al. (PMID:28667006)	3999215221	R05C01	iCCA
TCGA-3X-AAV9	Udt-gr	TCGA	9996247050	R02C01	iCCA
TCGA-3X-AAVA	Udt-gr	TCGA	3999997079	R05C02	iCCA
TCGA-3X-AAVE	Udt-gr	TCGA	9996247050	R04C01	iCCA
TCGA-4G-AAZO	Udt-gr	TCGA	3999997083	R05C01	iCCA
TCGA-4G-AAZT	Udt-gr	TCGA	9996247050	R01C02	iCCA
TCGA-W5-AA2Q	Udt-gr	TCGA	9996247047	R06C01	iCCA
TCGA-W5-AA2R	Udt-gr	TCGA	9996247061	R02C01	iCCA
TCGA-W5-AA2T	Udt-gr	TCGA	3999997083	R02C01	iCCA
TCGA-W5-AA2U	Udt-gr	TCGA	3999997079	R04C02	iCCA
TCGA-W5-AA2W	Udt-gr	TCGA	3999997083	R03C01	iCCA
TH_123	Udt-gr	Jusakul et al. (PMID:28667006)	3999215214	R01C01	iCCA
TH_27	Udt-gr	Jusakul et al. (PMID:28667006)	10005839066	R06C01	iCCA
TH_31	Udt-gr	Jusakul et al. (PMID:28667006)	3999215214	R06C01	iCCA
TH_59	Udt-gr	Jusakul et al. (PMID:28667006)	10005839063	R06C01	iCCA
TH_69	Udt-gr	Jusakul et al. (PMID:28667006)	10005839075	R01C01	iCCA
TH_75	Udt-gr	Jusakul et al. (PMID:28667006)	10005839063	R04C02	iCCA
TH_79	Udt-gr	Jusakul et al. (PMID:28667006)	3999215221	R04C01	iCCA
TCGA-W5-AA2I-11	-	TCGA	9996247047	R04C02	Surrounding Normal
TCGA-W5-AA2Q-11	-	TCGA	9996247050	R03C02	Surrounding Normal
TCGA-W5-AA2R-11	-	TCGA	3999997083	R06C01	Surrounding Normal
TCGA-W5-AA2U-11	-	TCGA	9996247047	R05C02	Surrounding Normal
TCGA-W5-AA30-11	-	TCGA	3999997083	R01C02	Surrounding Normal
TCGA-W5-AA31-11	-	TCGA	9996247050	R02C02	Surrounding Normal
TCGA-W5-AA34-11	-	TCGA	3999997083	R02C02	Surrounding Normal

IDH-gr: Differential methylated regions (DMRs)							
Location	**Epimutation**	**Chromosome**	**Start**	**End**	**Symbol**	**EntrezID**	**Combined FDR *P*-value**
Promoter	HYPER in CCA	chr11	116968654	116970653	*SIK3*	23387	0.000255716
Promoter	HYPER in CCA	chr20	5890576	5892575	*CHGB*	1114	0.001277982
Promoter	HYPER in CCA	chr2	177502160	177504159	*LINC01116*	375295	0.000821192
Promoter	HYPER in CCA	chr1	206807381	206809380	*DYRK3*	8444	0.001820747
Promoter	HYPER in CCA	chr19	42027850	42029849	*PLEKHA3P1*	NA	0.000340017
Promoter	HYPER in CCA	chr1	147734251	147736250	*RNU1-120P*	NA	0.002311143
Promoter	HYPER in CCA	chr2	219865437	219867436	*NA*	100129175	0.001273851
Promoter	HYPER in CCA	chr5	122425495	122427494	*NA*	NA	0.001418501
Promoter	HYPER in CCA	chr11	113345914	113357913	*DRD2*	1813	0.002418288
Promoter	HYPER in CCA	chr10	81663154	81665153	*MBL1P*	8512;100288974	0.001237546
Promoter	HYPER in CCA	chr7	102920358	102922357	*DPY19L2P2*	349152	0.000489645
Promoter	HYPER in CCA	chr13	79232815	79234814	*RNF219*	79596	0.002075183
Promoter	HYPER in CCA	chr20	30458051	30460050	*DUSP15*	128853	0.0007569
Promoter	HYPER in CCA	chr6	41206865	41208864	*RNA5SP207*	NA	0.000416055
Promoter	HYPER in CCA	chr1	204120808	204122807	*ETNK2*	55224	0.00034794
Promoter	HYPER in CCA	chr7	39871313	39873312	*NA*	NA	0.000100098
Promoter	HYPER in CCA	chr16	2246027	2248026	*CASKIN1*	57524	9.81E-05
Promoter	HYPER in CCA	chr17	79372040	79374039	*NA*	57597	0.00051514
Promoter	HYPER in CCA	chr11	72852807	72854806	*FCHSD2*	9873	0.000138435
Promoter	HYPER in CCA	chr2	71204010	71206009	*ANKRD53*	79998	0.000552887
Promoter	HYPER in CCA	chr18	18820703	18822702	*GREB1L*	80000	0.000233086
Promoter	HYPER in CCA	chr1	32169421	32171420	*COL16A1*	1307	0.000109753
Promoter	HYPER in CCA	chr2	197792021	197794020	*PGAP1*	80055	0.001836645
Promoter	HYPER in CCA	chr12	64062220	64064219	*DPY19L2*	283417	0.002159245
Promoter	HYPER in CCA	chr16	28890742	28892741	*NA*	100289092	0.00193174
Promoter	HYPER in CCA	chr10	112402044	112404043	*NA*	NA	0.001745891
Promoter	HYPER in CCA	chr6	34662594	34664593	*NA*	101929243	0.00028519
Promoter	HYPER in CCA	chr5	157097989	157099988	*SOX30*	11063	0.001797182
Promoter	HYPER in CCA	chr1	148759004	148761003	*NA*	NA	0.000438402
Promoter	HYPER in CCA	chr1	148760519	148762518	*NA*	NA	0.000438402
Promoter	HYPER in CCA	chr18	48084948	48086947	*MAPK4*	5596	0.000276344
Promoter	HYPER in CCA	chr15	45406043	45408042	*DUOX2*	50506	0.001692279

Promoter	HYPER in CCA	chr10	52749445	52751444	*PRKG1*	5592	0.000858674
Promoter	HYPER in CCA	chr16	8621805	8623804	*TMEM114*	283953	0.001591351
Promoter	HYPER in CCA	chr7	152132480	152134479	*FABP5P3*	220832	0.001283273
Promoter	HYPER in CCA	chr7	152132591	152134590	*KMT2C*	58508	0.001283273
Promoter	HYPER in CCA	chr1	149223722	149225721	*RNVU1-18*	6060;26863;26865;26866;26869;26870;26871	0.000232791
Promoter	HYPER in CCA	chr11	30607920	30609919	*MPPED2*	744	0.001217146
Promoter	HYPER in CCA	chr16	23764448	23766447	*CHP2*	63928	0.001062636
Promoter	HYPER in CCA	chr22	38850706	38852705	*KCNJ4*	3761	0.000568226
Promoter	HYPER in CCA	chr3	156534352	156536351	*LINC00886*	730091	0.001125439
Promoter	HYPER in CCA	chr2	27718209	27720208	*GCKR*	2646	0.001624424
Promoter	HYPER in CCA	chr12	6873182	6875181	*PTMS*	5763	0.002299619
Promoter	HYPER in CCA	chr16	31578538	31580537	*NA*	NA	0.000100719
Promoter	HYPER in CCA	chr1	53391401	53393400	*SCP2*	6342	0.001359968
Promoter	HYPER in CCA	chr10	102881036	102883035	*NA*	NA	9.07E-05
Promoter	HYPER in CCA	chr15	75017452	75019451	*CYP1A1*	1543	0.000472685
Promoter	HYPER in CCA	chr19	19006406	19008405	*GDF1*	2657	0.000171644
Promoter	HYPER in CCA	chr4	4228117	4230116	*OTOP1*	133060	0.001715521
Promoter	HYPER in CCA	chr1	202679046	202681045	*SYT2*	127833	0.00164386
Promoter	HYPER in CCA	chr6	35180690	35182689	*SCUBE3*	222663	0.000415957
Promoter	HYPER in CCA	chr20	3219337	3221336	*SLC4A11*	83959	0.000471808
Promoter	HYPER in CCA	chr15	22645103	22647102	*NA*	NA	0.001313523
Promoter	HYPER in CCA	chr4	185274631	185276630	*NA*	728175	0.001389401
Promoter	HYPER in CCA	chr4	185747473	185749472	*ACSL1*	2180	0.000350577
Promoter	HYPER in CCA	chr5	63984635	63986634	*FAM159B*	100132916	0.000517564
Promoter	HYPER in CCA	chr3	23243570	23245569	*UBE2E2-AS1*	NA	0.000592127
Promoter	HYPER in CCA	chr17	8066365	8068364	*VAMP2*	6844	0.000625488
Promoter	HYPER in CCA	chr12	71314124	71316123	*PTPRR*	5801	0.001754417
Promoter	HYPER in CCA	chr15	75198963	75200962	*FAM219B*	57184	0.000164103
Promoter	HYPER in CCA	chr1	22350962	22352961	*NA*	101928043	0.002309829
Promoter	HYPER in CCA	chr6	29795642	29797641	*HCG4P8*	NA	5.67E-05
Promoter	HYPER in CCA	chr1	149784737	149786736	*HIST2H3D*	126961;333932;653604	5.65E-05
Promoter	HYPER in CCA	chr12	115174009	115176008	*NA*	NA	0.001828136
Promoter	HYPER in CCA	chr19	707453	709452	*PALM*	5064	0.000773597
Promoter	HYPER in CCA	chr1	34641051	34643050	*NA*	NA	0.001202807

Promoter	HYPER in CCA	chr17	20686458	20688457	*SCDP1*	NA	0.00048336
Promoter	HYPER in CCA	chr17	8868530	8870529	*PIK3R5*	23533	0.001921433
Promoter	HYPER in CCA	chr10	23633275	23635274	*C10orf67*	256815	0.001857537
Promoter	HYPER in CCA	chr1	165511744	165513743	*LRRC52*	440699	0.00015286
Promoter	HYPER in CCA	chr20	35200391	35202390	*TGIF2*	60436	0.000819234
Promoter	HYPER in CCA	chr4	819487	821486	*CPLX1*	10815	0.001724835
Promoter	HYPER in CCA	chr20	61446096	61448095	*COL9A3*	1299	0.002181644
Promoter	HYPER in CCA	chr22	29075354	29077353	*TTC28*	23331	0.000411405
Promoter	HYPER in CCA	chr2	206812315	206814314	*NA*	NA	0.000847575
Promoter	HYPER in CCA	chr3	125897408	125899407	*ALDH1L1-AS2*	100862662	0.001091027
Promoter	HYPER in CCA	chr3	9957258	9959257	*IL17RC*	84818	6.61E-05
Promoter	HYPER in CCA	chr1	153497776	153697576	*C1orf233*	643988	0.002372008
Promoter	HYPER in CCA	chr1	172209975	172229974	*RNU1-2*	6060;26863;26865;26866;26869;26870;26871	0.000282508
Promoter	HYPER in CCA	chr2	26394460	26396459	*GAREML*	150946	0.000552898
Promoter	HYPER in CCA	chr19	38307441	38309440	*ZNF573*	126231	0.001400677
Promoter	HYPER in CCA	chr5	150472639	150474638	*TNIP1*	10318	0.000382178
Promoter	HYPER in CCA	chr1	161194293	161196292	*TOMM40L*	84134	0.000893451
Promoter	HYPER in CCA	chr11	112830497	112832496	*NCAM1*	4684	0.000385812
Promoter	HYPER in CCA	chr12	45444383	45446382	*DBX2*	440097	0.001756026
Promoter	HYPER in CCA	chr5	38257011	38259010	*EGFLAM*	133584	0.000188661
Promoter	HYPER in CCA	chr1	27112463	27114462	*PIGV*	55650	3.78E-05
Promoter	HYPER in CCA	chr7	108096662	108098661	*NRCAM*	4897	0.002337375
Promoter	HYPER in CCA	chr7	100316923	100318922	*EPO*	2056	0.001736622
Promoter	HYPER in CCA	chr3	75628651	75630650	*NA*	NA	0.001444406
Promoter	HYPER in CCA	chr3	158519225	158521224	*NA*	NA	0.000789905
Promoter	HYPER in CCA	chr8	22089355	22091354	*PHYHIP*	9796	9.84E-05
Promoter	HYPER in CCA	chr2	208633788	208635787	*FZD5*	7855	5.81E-05
Promoter	HYPER in CCA	chr11	63801942	63803941	*NA*	NA	0.001599924
Promoter	HYPER in CCA	chr2	99552223	99554222	*KIAA1211L*	343990	0.000343855
Promoter	HYPER in CCA	chr9	123690952	123692951	*TRAF1*	7185	0.000261763
Promoter	HYPER in CCA	chr22	30115204	30117203	*NA*	NA	0.00058384
Promoter	HYPER in CCA	chr1	91315816	91317815	*NA*	NA	0.001522581
Promoter	HYPER in CCA	chr11	46297712	46299711	*CREB3L1*	90993	0.002130055
Promoter	HYPER in CCA	chr19	40732098	40734097	*CNTD2*	79935	0.001097481

Promoter	HYPER in CCA	chr15	82943273	82945272	*NA*	NA	6.29E-05
Promoter	HYPER in CCA	chr1	92951934	92953933	*GFI1*	2672	0.000193097
Promoter	HYPER in CCA	chr11	79151493	79153492	*TENM4*	26011	0.001931798
Promoter	HYPER in CCA	chr19	33716257	33718256	*SLC7A10*	56301	0.002341486
Promoter	HYPER in CCA	chr13	111767526	111769525	*ARHGEF7-AS2*	NA	0.002175987
Promoter	HYPER in CCA	chr12	52299192	52301191	*ACVRL1*	94	0.00063399
Promoter	HYPER in CCA	chr10	126138254	126140253	*NKX1-2*	390010	0.000978211
Promoter	HYPER in CCA	chr6	44264959	44266958	*TCTE1*	202500	0.002339597
Promoter	HYPER in CCA	chr2	170645103	170647102	*NA*	NA	0.002271252
Promoter	HYPER in CCA	chr12	33592255	33594254	*SYT10*	341359	0.000793709
Promoter	HYPER in CCA	chr11	7533029	7535028	*PPFIBP2*	8495	3.69E-05
Promoter	HYPER in CCA	chr15	28344005	28346004	*OCA2*	4948	0.000553476
Promoter	HYPER in CCA	chr19	11591362	11593361	*ELAVL3*	1995;101928396	0.001639273
Promoter	HYPER in CCA	chr12	25100597	25102596	*NA*	NA	0.000566768
Promoter	HYPER in CCA	chr15	78236425	78238424	*NA*	NA	0.000559095
Promoter	HYPER in CCA	chr1	149398727	149400726	*HIST2H2BB*	NA	3.69E-05
Promoter	HYPER in CCA	chr1	149398563	149400562	*NA*	NA	3.69E-05
Promoter	HYPER in CCA	chr1	103573553	103575552	*COL11A1*	1301	0.000193189
Promoter	HYPER in CCA	chr6	29972860	29974859	*HLA-J*	3137	0.000347948
Promoter	HYPER in CCA	chr15	79573646	79575645	*ANKRD34C*	390616	0.001851807
Promoter	HYPER in CCA	chr3	38079196	38081195	*DLEC1*	9940	0.000156109
Promoter	HYPER in CCA	chr16	3066946	3068945	*TNFRSF12A*	51330	6.01E-05
Promoter	HYPER in CCA	chr5	156885527	156887526	*NIPAL4*	348938	0.00026018
Promoter	HYPER in CCA	chr1	1475334	1477333	*TMEM240*	339453	4.88E-05
Promoter	HYPER in CCA	chr20	21684797	21686796	*PAX1*	5075	0.001190724
Promoter	HYPER in CCA	chr13	20734689	20736688	*GJA3*	2700	0.000568987
Promoter	HYPER in CCA	chr19	42211004	42213003	*CEACAM5*	1048	0.000711438
Promoter	HYPER in CCA	chr7	95099647	95101646	*NA*	NA	0.001946539
Promoter	HYPER in CCA	chr20	44648856	44650855	*SLC12A5*	57468	0.000845109
Promoter	HYPER in CCA	chr8	143859141	143861140	*LYNX1*	66004	0.002390728
Promoter	HYPER in CCA	chr20	37432848	37434847	*PPP1R16B*	26051	0.000560028
Promoter	HYPER in CCA	chr8	57358794	57360793	*PENK*	5179	0.001537065
Promoter	HYPER in CCA	chr12	50354153	50356152	*AQP5*	362	0.000899587
Promoter	HYPER in CCA	chr1	207667992	207669991	*CR1*	1378	0.000127094

Promoter	HYPER in CCA	chr15	48483389	48485388	*NA*	NA	0.00195795
Promoter	HYPER in CCA	chr19	9608784	9610783	*ZNF560*	147741	0.0015776
Promoter	HYPER in CCA	chr5	75377497	75379496	*SV2C*	22987	0.002430971
Promoter	HYPER in CCA	chr5	141486570	141488569	*NDFIP1*	80762	7.53E-05
Promoter	HYPER in CCA	chr19	13213476	13215475	*LYL1*	4066	0.000647803
Promoter	HYPER in CCA	chr12	63544223	63546222	*AVPR1A*	552	0.001035815
Promoter	HYPER in CCA	chr2	87087523	87089522	*NA*	NA	0.001269618
Promoter	HYPER in CCA	chr5	157097061	157099060	*C5orf52*	100190949	0.002015651
Promoter	HYPER in CCA	chr6	100053106	100055105	*PRDM13*	59336	0.001884273
Promoter	HYPER in CCA	chr17	77774983	77776982	*CBX8*	57332	0.000466513
Promoter	HYPER in CCA	chr10	103535355	103537354	*FGF8*	2253	0.000621464
Promoter	HYPER in CCA	chr19	52955329	52957328	*ZNF578*	147660	0.00141662
Promoter	HYPER in CCA	chr3	193788260	193790259	*NA*	285389;100505902	0.000129032
Promoter	HYPER in CCA	chr2	102866216	102868215	*NA*	NA	0.000243972
Promoter	HYPER in CCA	chr3	132755735	132777734	*TMEM108*	66000	0.001766162
Promoter	HYPER in CCA	chr1	115631622	115633621	*TSPAN2*	10100	0.000924897
Promoter	HYPER in CCA	chr1	53066544	53068543	*GPX7*	2882	0.000718743
Promoter	HYPER in CCA	chr15	75918311	75920310	*SNUPN*	10073	0.000119478
Promoter	HYPER in CCA	chr5	176168706	176170705	*NA*	102577424	0.001878265
Promoter	HYPER in CCA	chr19	56878923	56880922	*NA*	NA	0.00075246
Promoter	HYPER in CCA	chr1	101701585	101703584	*NA*	101928370	0.000213986
Promoter	HYPER in CCA	chr15	100881711	100883710	*ADAMTS17*	170691	0.000856561
Promoter	HYPER in CCA	chr6	160767800	160769799	*SLC22A3*	6581	0.0004989
Promoter	HYPER in CCA	chr12	82152833	82154832	*PPFIA2*	8499	0.0008853
Promoter	HYPER in CCA	chr19	51070803	51072802	*LRRC4B*	94030	0.001138779
Promoter	HYPER in CCA	chr11	69633293	69635292	*FGF3*	2248	0.001934325
Promoter	HYPER in CCA	chr1	22350181	22352180	*LINC00339*	29092	0.001238648
Promoter	HYPER in CCA	chr1	37499231	37501230	*GRIK3*	2899	0.002058772
Promoter	HYPER in CCA	chr11	109291346	109293345	*C11orf87*	399947	0.002083984
Promoter	HYPER in CCA	chr1	99468332	99470331	*NA*	100129620	0.001336613
Promoter	HYPER in CCA	chr5	159342290	159344289	*ADRA1B*	147	0.001452775
Promoter	HYPER in CCA	chr7	100545687	100547686	*MUC3A*	4584;57876	0.000105377
Promoter	HYPER in CCA	chr7	100545757	100547756	*NA*	4584;100131514	0.000105377
Promoter	HYPER in CCA	chr1	165325453	165327452	*LMX1A*	4009	0.000929916

Promoter	HYPER in CCA	chr5	7394821	7396820	*ADCY2*	108	0.001522983
Promoter	HYPER in CCA	chr11	11392881	11393081	*ZBTB16*	7704	9.52E-05
Promoter	HYPER in CCA	chr19	31838287	31840286	*NA*	NA	0.000369063
Promoter	HYPER in CCA	chr19	849514	851513	*ELANE*	1991	0.000186044
Promoter	HYPER in CCA	chr2	89063824	89065823	*ANKRD36BP2*	645784	0.0001422
Promoter	HYPER in CCA	chr1	2461185	2463184	*HES5*	388585	0.001879333
Promoter	HYPER in CCA	chr19	9902797	9904796	*NA*	NA	0.001492154
Promoter	HYPER in CCA	chr19	9903357	9905356	*ZNF846*	162993;100505555	0.001492154
Promoter	HYPER in CCA	chr19	56877968	56879967	*ZNF542*	147947	0.00051342
Promoter	HYPER in CCA	chr1	113499136	113501135	*SLC16A1*	6566	0.00095681
Promoter	HYPER in CCA	chr3	137482079	137484078	*SOX14*	8403	0.001438795
Promoter	HYPER in CCA	chr19	5567546	5569545	*TINCR*	257000	0.0016335
Promoter	HYPER in CCA	chr15	76004690	76006689	*CSPG4*	1464	0.000767492
Promoter	HYPER in CCA	chr17	66193562	66195561	*NA*	440461	0.000901257
Promoter	HYPER in CCA	chr17	29297170	29299169	*NA*	NA	0.001950091
Promoter	HYPER in CCA	chr8	38008284	38010283	*STAR*	6770	0.000100907
Promoter	HYPER in CCA	chr11	1591083	1593082	*KRTAP5-AS1*	338651	0.001326091
Promoter	HYPER in CCA	chr6	28742193	28744192	*NA*	NA	0.000217829
Promoter	HYPER in CCA	chr6	27100042	27102041	*HIST1H2BJ*	8970	0.002219094
Promoter	HYPER in CCA	chr1	234350335	234352334	*NA*	NA	0.000111642
Promoter	HYPER in CCA	chr13	53382679	53384678	*MIR759*	100313778	0.000729045
Promoter	HYPER in CCA	chr7	69061935	69063934	*NA*	100507468	0.000146291
Promoter	HYPER in CCA	chr9	91793183	91795182	*SHC3*	53358	0.001423644
Promoter	HYPER in CCA	chr3	132755397	132757396	*NA*	NA	0.001738126
Promoter	HYPER in CCA	chr8	91802278	91804277	*NECAB1*	64168	0.00034919
Promoter	HYPER in CCA	chr17	21278009	21280008	*KCNJ12*	3768;100134444;100996843	0.001502848
Promoter	HYPER in CCA	chr14	36982535	36984534	*SFTA3*	253970	0.001020169
Promoter	HYPER in CCA	chr1	20913941	20915940	*CDA*	978	4.62E-06
Promoter	HYPER in CCA	chr9	139970453	139972452	*UAP1L1*	91373	0.000289146
Promoter	HYPER in CCA	chr22	48883772	48885771	*FAM19A5*	25817	0.002227426
Promoter	HYPER in CCA	chr10	101290435	101292434	*NA*	101927324	0.001331011
Promoter	HYPER in CCA	chr12	103351689	103353688	*PAH*	5053;101929036	0.000365022
Promoter	HYPER in CCA	chr5	71013490	71015489	*CARTPT*	9607	0.000596405
Promoter	HYPER in CCA	chr1	24513950	24515949	*IFNLR1*	163702	4.09E-05

Promoter	HYPER in CCA	chr17	42834899	42836898	*ADAM11*	4185	4.29E-05
Promoter	HYPER in CCA	chr22	30115349	30117348	*NA*	NA	0.000288384
Promoter	HYPER in CCA	chr11	63302781	63304780	*RARRES3*	5920	0.000696837
Promoter	HYPER in CCA	chr12	45443184	45445183	*NA*	NA	0.001178753
Promoter	HYPER in CCA	chr12	4917308	4919307	*NA*	NA	0.000213908
Promoter	HYPER in CCA	chr19	37802239	37804238	*HKR1*	284459;100507342	1.43E-05
Promoter	HYPER in CCA	chr21	22369133	22371132	*NCAM2*	4685	0.002295028
Promoter	HYPER in CCA	chr11	133937320	133939319	*JAM3*	83700	0.001482536
Promoter	HYPER in CCA	chr1	248098993	248100992	*OR2L13*	284521	4.12E-05
Promoter	HYPER in CCA	chr6	27597688	27599687	*TRNAI6*	NA	0.000321481
Promoter	HYPER in CCA	chr17	78451144	78453143	*NPTX1*	4884	0.001656631
Promoter	HYPER in CCA	chr11	117746883	117748882	*FXYD6-FXYD2*	100533181	0.000246499
Promoter	HYPER in CCA	chr16	22823998	22825997	*HS3ST2*	9956	0.001286606
Promoter	HYPER in CCA	chr15	48936648	48938647	*NA*	NA	0.000526521
Promoter	HYPER in CCA	chr17	45809110	45811109	*TBX21*	30009	0.001570002
Promoter	HYPER in CCA	chr10	23631386	23633385	*NA*	NA	0.000859453
Promoter	HYPER in CCA	chr11	128554930	128556929	*FLI1*	2313	0.002080186
Promoter	HYPER in CCA	chr12	103889250	103891249	*C12orf42*	374470	0.001710999
Promoter	HYPER in CCA	chr4	145565673	145567672	*HHIP*	64399	0.000627697
Promoter	HYPER in CCA	chr1	148853621	148855620	*NA*	NA	0.00226454
Promoter	HYPER in CCA	chr17	6657266	6659265	*XAF1*	54739	0.000264741
Promoter	HYPER in CCA	chr7	19150597	19152596	*NA*	NA	0.001718308
Promoter	HYPER in CCA	chr5	87970536	87972535	*NA*	NA	0.000512431
Promoter	HYPER in CCA	chr14	22004851	22006850	*SALL2*	6297	0.001142342
Promoter	HYPER in CCA	chr22	42094003	42096002	*MEI1*	150365	1.69E-05
Promoter	HYPER in CCA	chr12	323237	325236	*SLC6A12*	6539	5.15E-05
Promoter	HYPER in CCA	chr19	10396143	10398142	*ICAM4*	3386	0.000952967
Promoter	HYPER in CCA	chr17	79358661	79360660	*NA*	NA	5.59E-05
Promoter	HYPER in CCA	chr4	95678185	95680184	*NA*	100507012	0.001954925
Promoter	HYPER in CCA	chr10	124906138	124908137	*HMX2*	3167	0.000480184
Promoter	HYPER in CCA	chr2	45167402	45169401	*SIX3*	6496	0.001544812
Promoter	HYPER in CCA	chr12	14720784	14722783	*PLBD1*	79887	0.000227999
Promoter	HYPER in CCA	chr3	23243011	23245010	*UBE2E2*	7325	0.00015509
Promoter	HYPER in CCA	chr3	188664929	188666928	*TPRG1-AS1*	NA	0.000349359

Promoter	HYPER in CCA	chr16	31580297	31582296	*YBX3P1*	440359	3.52E-05
Promoter	HYPER in CCA	chr1	21040689	21040889	*SERTAD4-AS1*	574036	0.000996837
Promoter	HYPER in CCA	chr7	89747214	89749213	*DPY19L2P4*	442523	0.001427418
Promoter	HYPER in CCA	chr5	79865808	79867807	*ANKRD34B*	340120	0.000588782
Promoter	HYPER in CCA	chr7	128001240	128003239	*PRRT4*	401399	0.001366705
Promoter	HYPER in CCA	chr22	46544924	46546923	*PPARA*	5465	4.80E-05
Promoter	HYPER in CCA	chr7	41744434	41746433	*NA*	NA	6.16E-05
Promoter	HYPER in CCA	chr1	78693783	78695782	*NA*	149047	0.000537149
Promoter	HYPER in CCA	chr11	47207495	47209494	*PACSIN3*	29763	4.02E-05
Promoter	HYPER in CCA	chr12	55412229	55414228	*NEUROD4*	58158	0.000308916
Promoter	HYPER in CCA	chr1	3567584	3569583	*TP73*	7161	0.00067348
Promoter	HYPER in CCA	chr17	15244459	15246458	*TEKT3*	64518	0.000338762
Promoter	HYPER in CCA	chr6	117086387	117088386	*FAM162B*	221303	0.001748804
Promoter	HYPER in CCA	chr13	97646485	97648484	*OXGR1*	27199	0.001491121
Promoter	HYPER in CCA	chr2	130737540	130739539	*RAB6C-AS1*	100131320	0.00173203
Promoter	HYPER in CCA	chr17	1172353	1174352	*BHLHA9*	727857	5.08E-05
Promoter	HYPER in CCA	chr2	63275276	63277275	*NA*	100132215	0.001071466
Promoter	HYPER in CCA	chr7	18125072	18127071	*HDAC9*	9734	0.001272501
Promoter	HYPER in CCA	chr17	7940835	7942834	*ALOX15B*	247	0.000332582
Promoter	HYPER in CCA	chr15	89438358	89440357	*HAPLN3*	145864	0.000413574
Promoter	HYPER in CCA	chr10	20103668	20105667	*PLXDC2*	84898	0.002213329
Promoter	HYPER in CCA	chr1	1181603	1183602	*FAM132A*	388581	3.45E-05
Promoter	HYPER in CCA	chr19	15782067	15784066	*CYP4F12*	66002	0.000281295
Promoter	HYPER in CCA	chr1	150946980	150948979	*CERS2*	29956	5.31E-05
Promoter	HYPER in CCA	chr15	45995776	45997775	*NA*	NA	0.000212806
Promoter	HYPER in CCA	chr11	65777812	65779811	*CST6*	1474	3.05E-05
Promoter	HYPER in CCA	chr2	132217033	132219032	*RHOQP2*	NA	0.000194843
Promoter	HYPER in CCA	chr20	61808352	61810351	*MIR124-3*	406909	0.001835754
Promoter	HYPER in CCA	chr9	114361636	114363635	*PTGR1*	22949	0.000149576
Promoter	HYPER in CCA	chr4	6564828	6566827	*PPP2R2C*	5522	0.001160602
Promoter	HYPER in CCA	chr10	25462491	25464490	*GPR158*	57512	0.000680276
Promoter	HYPER in CCA	chr17	18087568	18089567	*NA*	101929865;101930243	0.001103894
Promoter	HYPER in CCA	chr1	67216642	67218641	*TCTEX1D1*	200132	0.000198266
Promoter	HYPER in CCA	chr7	28997435	28999434	*TRIL*	NA	0.002095222

Promoter	HYPER in CCA	chr13	24476295	24478294	*C1QTNF9B*	387911	0.000516108
Promoter	HYPER in CCA	chr3	98375146	98377145	*WWP1P1*	NA	0.000804986
Promoter	HYPER in CCA	chr7	100823058	100825057	*NAT16*	375607	0.000503581
Promoter	HYPER in CCA	chr11	8289764	8291763	*LMO1*	4004	0.000837184
Promoter	HYPER in CCA	chr17	29717142	29719141	*RAB11FIP4*	84440	0.000495765
Promoter	HYPER in CCA	chr15	61521019	61523018	*RORA*	6095	3.10E-05
Promoter	HYPER in CCA	chr11	128759751	128761750	*KCNJ5*	3762	0.002129091
Promoter	HYPER in CCA	chr13	70682092	70684091	*KLHL1*	57626	0.001339239
Promoter	HYPER in CCA	chr11	64057694	64059693	*NA*	NA	0.00018464
Promoter	HYPER in CCA	chr12	54446161	54448160	*NA*	3221	0.000858317
Promoter	HYPER in CCA	chr17	42246315	42248314	*ASB16*	92591	9.90E-05
Promoter	HYPER in CCA	chr2	73141889	73143888	*EMX1*	2016	0.001292747
Promoter	HYPER in CCA	chr12	130387712	130389711	*TMEM132D*	121256	0.002393693
Promoter	HYPER in CCA	chr19	56879253	56881252	*ZSCAN5A*	79149	0.000621066
Promoter	HYPER in CCA	chr17	44342903	44344902	*NA*	NA	0.000232081
Promoter	HYPER in CCA	chr17	27466001	27468000	*NA*	NA	0.000431468
Promoter	HYPER in CCA	chr2	238534719	238536718	*LRRFIP1*	9208	4.84E-05
Promoter	HYPER in CCA	chr15	88799500	88801499	*NTRK3*	4916	0.000240341
Promoter	HYPER in CCA	chr19	9607854	9609853	*NA*	NA	0.00145881
Promoter	HYPER in CCA	chr19	38345356	38347355	*NA*	100631378	0.001008894
Promoter	HYPER in CCA	chr16	23724322	23726321	*ERN2*	10595	0.000539219
Promoter	HYPER in CCA	chr12	52399224	52401223	*GRASP*	160622	0.000724932
Promoter	HYPER in CCA	chr15	66545586	66547585	*MEGF11*	84465	1.09E-06
Promoter	HYPER in CCA	chr1	77331626	77333625	*ST6GALNAC5*	81849	0.001871791
Promoter	HYPER in CCA	chr4	46994240	46996239	*GABRB1*	2560	4.31E-05
Promoter	HYPER in CCA	chr4	5894286	5896285	*CRMP1*	1400	0.000379454
Promoter	HYPER in CCA	chr20	4229222	4231221	*ADRA1D*	146	0.000163199
Promoter	HYPER in CCA	chr17	37393219	37395218	*NA*	NA	0.000476338
Promoter	HYPER in CCA	chr5	139025384	139027383	*CXXC5*	51523	5.59E-06
Promoter	HYPER in CCA	chr5	140623647	140625646	*PCDHB15*	56121	0.00035564
Promoter	HYPER in CCA	chr2	152953342	152955341	*NA*	NA	0.000295162
Promoter	HYPER in CCA	chr20	43729254	43731253	*KCNS1*	3787	0.000331535
Promoter	HYPER in CCA	chr2	207137887	207139886	*ZDBF2*	57683	0.000249055
Promoter	HYPER in CCA	chr19	13734305	13736304	*CACNA1A*	773;100507353	0.000835241

Promoter	HYPER in CCA	chr14	24833379	24835378	*NFATC4*	4776	1.77E-05
Promoter	HYPER in CCA	chr4	42154396	42156395	*BEND4*	389206	5.37E-05
Promoter	HYPER in CCA	chr22	37210870	37212869	*NA*	NA	0.001039138
Promoter	HYPER in CCA	chr7	35225435	35227434	*DPY19L2P1*	NA	9.43E-05
Promoter	HYPER in CCA	chr9	97402032	97404031	*FBP1*	2203	2.12E-05
Promoter	HYPER in CCA	chr22	20101961	20103960	*RANBP1*	5902	0.000378412
Promoter	HYPER in CCA	chr8	14592407	14592607	*NA*	NA	0.00129606
Promoter	HYPER in CCA	chr1	40419302	40421301	*MFSD2A*	84879	0.000323791
Promoter	HYPER in CCA	chr1	24780155	24780355	*NA*	NA	0.001431745
Promoter	HYPER in CCA	chr22	17600976	17602975	*NA*	NA	0.001856534
Promoter	HYPER in CCA	chr2	71113501	71115500	*LINC01143*	NA	0.00215176
Promoter	HYPER in CCA	chr6	13923177	13925176	*RNF182*	221687	5.08E-05
Promoter	HYPER in CCA	chr2	10710334	10710534	*NA*	NA	0.000158645
Promoter	HYPER in CCA	chr15	33602361	33604360	*NA*	101928134	0.002390766
Promoter	HYPER in CCA	chr1	11469604	11469804	*SYT6*	148281	0.000709505
Promoter	HYPER in CCA	chr19	46974321	46976320	*PNMAL1*	55228	0.001091714
Promoter	HYPER in CCA	chr22	19137297	19139296	*GSC2*	2928	0.002386955
Promoter	HYPER in CCA	chr8	14465464	14465664	*MROH6*	642475	1.89E-05
Promoter	HYPER in CCA	chr18	500223	502222	*COLEC12*	81035	0.002326126
Promoter	HYPER in CCA	chr1	47689969	47691968	*NA*	101930541	0.001269441
Promoter	HYPER in CCA	chr16	86608474	86610473	*FOXL1*	2300	0.00089357
Promoter	HYPER in CCA	chr18	5197003	5199002	*C18orf42*	642597	0.000332677
Promoter	HYPER in CCA	chr8	16859191	16861190	*FGF20*	26281	3.91E-05
Promoter	HYPER in CCA	chr7	116962844	116964843	*WNT2*	7472	0.001772728
Promoter	HYPER in CCA	chr12	114845748	114847747	*TBX5*	6910	0.001009148
Promoter	HYPER in CCA	chr15	41911922	41913921	*MGA*	23269	0.001660812
Promoter	HYPER in CCA	chr1	210110038	210112037	*SYT14*	255928	0.000962079
Promoter	HYPER in CCA	chr5	94954282	94956281	*GPR150*	285601	0.00049347
Promoter	HYPER in CCA	chr15	48937547	48939546	*FBN1*	2200	0.000219239
Promoter	HYPER in CCA	chr11	111409505	111411504	*LAYN*	143903	0.000612444
Promoter	HYPER in CCA	chr13	95354617	95356616	*LINC00391*	NA	0.001139094
Promoter	HYPER in CCA	chr5	167954621	167956620	*FBLL1*	NA	0.002134325
Promoter	HYPER in CCA	chr2	223535005	223537004	*MOGAT1*	116255	0.000743469
Promoter	HYPER in CCA	chr6	27774399	27776398	*HIST1H2AI*	8329;8330;8332;8336;8969;85235	0.00198113

Promoter	HYPER in CCA	chr5	139485862	139487861	*PURA*	5813	3.59E-05
Promoter	HYPER in CCA	chr3	115375880	115377879	*NA*	NA	2.41E-05
Promoter	HYPER in CCA	chr1	189560000	189570999	*PAX7*	5081	0.002159706
Promoter	HYPER in CCA	chr19	228168282	228368381	*C19orf35*	374872	0.001115601
Promoter	HYPER in CCA	chr2	241936755	241938754	*SNED1*	25992	0.000503593
Promoter	HYPER in CCA	chr4	121993677	121995676	*NDNF*	79625	0.001150417
Promoter	HYPER in CCA	chr11	571945554	571965553	*SLC43A3*	29015	0.000736818
Promoter	HYPER in CCA	chr5	128795883	128797882	*ADAMTS19-AS1*	NA	0.001713312
Promoter	HYPER in CCA	chr18	447750055	447770054	*SKOR2*	652991	0.00161191
Promoter	HYPER in CCA	chr5	146889120	146891119	*DPYSL3*	1809	0.002356557
Promoter	HYPER in CCA	chr12	8169957	8171956	*NA*	NA	0.00092624
Promoter	HYPER in CCA	chr17	42732262	42734261	*C17orf104*	284071	0.001163683
Promoter	HYPER in CCA	chr2	175547145	175549144	*WIPF1*	7456	0.000514647
Promoter	HYPER in CCA	chr1	53526354	53528353	*PODN*	127435	0.000121711
Promoter	HYPER in CCA	chr7	1082712	1084711	*GPR146*	115330	0.000276856
Promoter	HYPER in CCA	chr6	130686071	130688070	*SAMD3*	154075	0.000538591
Promoter	HYPER in CCA	chr5	160975551	160977550	*GABRB2*	2561	0.000919036
Promoter	HYPER in CCA	chr11	75379666	75381665	*MAP6*	4135	0.001424664
Promoter	HYPER in CCA	chr1	240774950	240776949	*GREM2*	64388	0.000354731
Promoter	HYPER in CCA	chr18	30348258	30350257	*NA*	NA	0.000553234
Promoter	HYPER in CCA	chr8	145924238	145926237	*NA*	100996662	0.00097402
Promoter	HYPER in CCA	chr1	226409819	226411818	*MIXL1*	83881	0.00015175
Promoter	HYPER in CCA	chr17	46801338	46803337	*MIR3185*	100422978	0.000267219
Promoter	HYPER in CCA	chr17	35077394	35079393	*NA*	NA	0.000213399
Promoter	HYPER in CCA	chr2	160818872	160838871	*MYCNOS*	10408	0.000865705
Promoter	HYPER in CCA	chr4	174450881	174452880	*HAND2*	9464	0.000629757
Promoter	HYPER in CCA	chr11	2291683	2293682	*ASCL2*	430	0.000226665
Promoter	HYPER in CCA	chr1	201251080	201253079	*PKP1*	5317	0.00039369
Promoter	HYPER in CCA	chr5	87989290	87991289	*NA*	NA	0.001575292
Promoter	HYPER in CCA	chr19	55660223	55662222	*TNNT1*	7138	0.001022325
Promoter	HYPER in CCA	chr17	46691979	46693978	*HOXB8*	3218	0.001306934
Promoter	HYPER in CCA	chr5	151066227	151088226	*SPARC*	6678	9.07E-05
Promoter	HYPER in CCA	chr19	19007037	19009036	*CERS1*	2657;10715	2.65E-05
Promoter	HYPER in CCA	chr19	55865683	55867682	*COX6B2*	125965	0.000759605

Promoter	HYPER in CCA	chr7	8009035	8011034	*NA*	NA	0.000768196
Promoter	HYPER in CCA	chr16	56227931	56229930	*NA*	26077	0.000746436
Promoter	HYPER in CCA	chr11	62341902	62343901	*EEF1G*	1937;100500804	4.42E-05
Promoter	HYPER in CCA	chr20	45087416	45089415	*ZNF663P*	NA	0.000142714
Promoter	HYPER in CCA	chr18	56885900	56887899	*GRP*	2922	0.001277857
Promoter	HYPER in CCA	chr5	140752151	140754150	*PCDHGA6*	56109	0.000302755
Promoter	HYPER in CCA	chr6	84561485	84563484	*RIPPLY2*	134701	0.001416384
Promoter	HYPER in CCA	chr3	33260208	33262207	*SUSD5*	26032	0.000630038
Promoter	HYPER in CCA	chr6	118227189	118229188	*SLC35F1*	222553	0.001400362
Promoter	HYPER in CCA	chr4	141419032	141421031	*NA*	152586	0.001924921
Promoter	HYPER in CCA	chr12	54384022	54386021	*MIR196A2*	406973	0.000318439
Promoter	HYPER in CCA	chr17	39648299	39650298	*KRT36*	8689	0.000304387
Promoter	HYPER in CCA	chr4	93224050	93226049	*GRID2*	2895	0.002150926
Promoter	HYPER in CCA	chr7	123670759	123672758	*NA*	NA	0.000294147
Promoter	HYPER in CCA	chr1	159824638	159826637	*C1orf204*	284677	0.000176201
Promoter	HYPER in CCA	chr16	2039859	2041858	*NA*	NA	1.02E-05
Promoter	HYPER in CCA	chr20	43933991	43935990	*RBPJL*	11317	2.98E-05
Promoter	HYPER in CCA	chr1	149604140	149606139	*NA*	NA	6.31E-05
Promoter	HYPER in CCA	chr19	47137443	47139442	*GNG8*	94235	0.000319431
Promoter	HYPER in CCA	chr2	197457917	197459916	*HECW2*	57520	0.000416751
Promoter	HYPER in CCA	chr2	133014154	133016153	*MIR663B*	100313824	0.000363558
Promoter	HYPER in CCA	chr6	142407870	142409869	*NA*	NA	0.000541611
Promoter	HYPER in CCA	chr12	2799867	2801866	*CACNA1C-AS1*	100652846	0.000938445
Promoter	HYPER in CCA	chr1	148852638	148854637	*NA*	NA	0.00091357
Promoter	HYPER in CCA	chr19	3931601	3933600	*NMRK2*	27231	0.000792342
Promoter	HYPER in CCA	chr19	35395462	35397461	*NA*	NA	0.000328132
Promoter	HYPER in CCA	chr1	101700944	101702943	*S1PR1*	1901	0.000105252
Promoter	HYPER in CCA	chr11	6341378	6343377	*PRKCDBP*	112464	6.45E-05
Promoter	HYPER in CCA	chr8	91803361	91805360	*TMEM64*	169200	0.000177002
Promoter	HYPER in CCA	chr6	100912306	100914305	*SIM1*	6492	0.000789954
Promoter	HYPER in CCA	chr8	11204512	11206511	*NA*	100129129	0.002022026
Promoter	HYPER in CCA	chr2	154726926	154728925	*GALNT13*	114805	0.0008188
Promoter	HYPER in CCA	chr20	57873982	57875981	*EDN3*	1908	0.001708366
Promoter	HYPER in CCA	chr17	38820934	38822933	*KRT222*	125113	0.00045806

Promoter	HYPER in CCA	chr17	38820894	38822893	*NA*	125113	0.00045806
Promoter	HYPER in CCA	chr2	21755 9749	21756 1748	*IGFBP5*	3488	6.69E-05
Promoter	HYPER in CCA	chr12	11341 4700	11341 6699	*OAS2*	4939	2.81E-05
Promoter	HYPER in CCA	chr19	33790685	33792684	*NA*	NA	0.001212923
Promoter	HYPER in CCA	chr5	17720 9900	17721 1899	*FAM153A*	285596	2.56E-05
Promoter	HYPER in CCA	chr3	35050 6	35250 5	*RPS8P6*	NA	8.96E-05
Promoter	HYPER in CCA	chr1	14778 9630	14779 1629	*NA*	NA	1.06E-05
Promoter	HYPER in CCA	chr4	93224830	93226829	*NA*	NA	0.001865438
Promoter	HYPER in CCA	chr17	47074355	47076354	*NA*	NA	0.000610027
Promoter	HYPER in CCA	chr12	14719184	14721183	*NA*	101928290	0.00028017
Promoter	HYPER in CCA	chr10	11616 4016	11616 6015	*AFAP1L2*	84632	6.21E-05
Promoter	HYPER in CCA	chr7	10729 9580	10730 1579	*SLC26A4*	5172	0.00024727
Promoter	HYPER in CCA	chr2	10860 1479	10860 3478	*SLC5A7*	60482	0.002203905
Promoter	HYPER in CCA	chr8	27489885	27491884	*SCARA3*	51435	0.000810515
Promoter	HYPER in CCA	chr6	10814 5022	10814 7021	*SCML4*	256380	5.84E-05
Promoter	HYPER in CCA	chr16	28074331	28076330	*GSG1L*	146395	0.000294419
Promoter	HYPER in CCA	chr13	34250406	34252405	*NA*	NA	0.000492458
Promoter	HYPER in CCA	chr11	11178 1960	11178 3959	*HSPB2-C11orf52*	3316;91894	2.90E-05
Promoter	HYPER in CCA	chr14	70652340	70654339	*NA*	NA	0.000136403
Promoter	HYPER in CCA	chr15	29075829	29077828	*NA*	NA	0.000246163
Promoter	HYPER in CCA	chr2	70994858	70996857	*ADD2*	119	0.002316286
Promoter	HYPER in CCA	chr17	59477105	59479104	*NA*	NA	0.000316352
Promoter	HYPER in CCA	chr12	54347118	54349117	*HOXC12*	3228	0.000789363
Promoter	HYPER in CCA	chr19	48389155	48391154	*SULT2A1*	6822	0.00107154
Promoter	HYPER in CCA	chr16	44522 5	44722 4	*NME4*	4833	0.000243
Promoter	HYPER in CCA	chr16	17564239	17566238	*XYLT1*	64131	9.76E-05
Promoter	HYPER in CCA	chr21	35015733	35017732	*CRYZL1*	9946	0.001105129
Promoter	HYPER in CCA	chr19	53757652	53759651	*ZNF677*	342926	0.000377637
Promoter	HYPER in CCA	chr2	18232 0429	18232 2428	*ITGA4*	3676	0.000243771
Promoter	HYPER in CCA	chr21	38376950	38378949	*RIPPLY3*	53820	0.000766593
Promoter	HYPER in CCA	chr17	48640645	48642644	*NA*	NA	2.69E-06
Promoter	HYPER in CCA	chr5	12662 5023	12662 7022	*MEGF10*	84466	8.16E-05
Promoter	HYPER in CCA	chr22	20791647	20793646	*SCARF2*	91179	0.002226088
Promoter	HYPER in CCA	chr6	27279450	27281449	*POM121L2*	94026	0.000743861

Promoter	HYPER in CCA	chr9	139689302	139691301	*CCDC183*	84960	1.71E-05
Promoter	HYPER in CCA	chr16	56671078	56673077	*MT1A*	4489	0.000169626
Promoter	HYPER in CCA	chr10	118897313	118899312	*VAX1*	11023	0.001710357
Promoter	HYPER in CCA	chr3	49459687	49461686	*AMT*	275	6.63E-06
Promoter	HYPER in CCA	chr7	45612239	45614238	*ADCY1*	107	0.000329134
Promoter	HYPER in CCA	chr19	23598378	23600377	*NA*	NA	0.002234454
Promoter	HYPER in CCA	chr4	101111440	101113439	*DDIT4L*	115265	0.000488953
Promoter	HYPER in CCA	chr6	390239	392238	*IRF4*	3662	0.000511364
Promoter	HYPER in CCA	chr13	26624670	26626669	*SHISA2*	387914	0.000193499
Promoter	HYPER in CCA	chr7	56160190	56162189	*PHKG1*	5260	3.90E-05
Promoter	HYPER in CCA	chr1	59521222	59523221	*NA*	NA	4.14E-05
Promoter	HYPER in CCA	chr7	64600103	64602102	*INTS4L1*	NA	2.98E-05
Promoter	HYPER in CCA	chr3	169530275	169532274	*LRRC34*	151827	3.06E-05
Promoter	HYPER in CCA	chr15	93631934	93633933	*RGMA*	56963	0.000773136
Promoter	HYPER in CCA	chr4	5020700	5022699	*CYTL1*	54360	0.000499988
Promoter	HYPER in CCA	chr4	154709773	154711772	*SFRP2*	6423	0.000468063
Promoter	HYPER in CCA	chr16	21831232	21833231	*RRN3P1*	NA	0.000100898
Promoter	HYPER in CCA	chr2	71679352	71681351	*DYSF*	8291	0.000153545
Promoter	HYPER in CCA	chr11	16633179	16635178	*C11orf58*	10944	5.40E-05
Promoter	HYPER in CCA	chr5	72676711	72678710	*NA*	NA	0.001707756
Promoter	HYPER in CCA	chr1	24647892	24649891	*NA*	NA	0.000334702
Promoter	HYPER in CCA	chr16	31708429	31710428	*NA*	NA	0.001197721
Promoter	HYPER in CCA	chr5	145717087	145719086	*POU4F3*	5459	0.000453958
Promoter	HYPER in CCA	chr22	17601758	17603757	*CECR6*	27439	0.001516883
Promoter	HYPER in CCA	chr15	92935558	92937557	*ST8SIA2*	8128	0.000787099
Promoter	HYPER in CCA	chr12	110210814	110212813	*FAM222A-AS1*	84983	0.000169677
Promoter	HYPER in CCA	chr10	26503736	26505735	*GAD2*	2572	0.00037924
Promoter	HYPER in CCA	chr4	16085502	16087501	*PROM1*	8842	0.000791583
Promoter	HYPER in CCA	chr5	124536081	124538080	*NA*	NA	7.09E-05
Promoter	HYPER in CCA	chr8	27346796	27348795	*EPHX2*	2053	0.000184953
Promoter	HYPER in CCA	chr17	77750431	77752430	*CBX2*	84733	8.67E-06
Promoter	HYPER in CCA	chr17	38820376	38822375	*NA*	NA	0.001513401
Promoter	HYPER in CCA	chr13	112720413	112722412	*SOX1*	6656	0.000843219
Promoter	HYPER in CCA	chr2	132762273	132764272	*ARHGAP42P2*	NA	1.99E-05

Promoter	HYPER in CCA	chr4	122686083	122688082	*TMEM155*	132332	0.000358351
Promoter	HYPER in CCA	chr3	62354506	62356505	*PTPRG-AS1*	100506994	0.000863449
Promoter	HYPER in CCA	chr6	29974394	29976393	*HCG4P3*	NA	7.19E-05
Promoter	HYPER in CCA	chr8	106329420	106331419	*ZFPM2*	23414	0.000342869
Promoter	HYPER in CCA	chr1	115880358	115882357	*NGF*	4803	0.000377994
Promoter	HYPER in CCA	chr2	945461	947460	*NA*	NA	0.001166356
Promoter	HYPER in CCA	chr4	2793250	2795249	*SH3BP2*	6452	8.03E-06
Promoter	HYPER in CCA	chr15	55880646	55882645	*PYGO1*	26108	5.25E-05
Promoter	HYPER in CCA	chr22	21332251	21334250	*LZTR1*	8216	0.0009233
Promoter	HYPER in CCA	chr13	46189375	46191374	*FAM194B*	220081	0.000247922
Promoter	HYPER in CCA	chr6	85473738	85475737	*TBX18*	9096	0.001952946
Promoter	HYPER in CCA	chr8	1763897	1765896	*MIR596*	693181	0.000606638
Promoter	HYPER in CCA	chr18	20713028	20715027	*CABLES1*	91768	0.000679018
Promoter	HYPER in CCA	chr5	131591864	131593863	*PDLIM4*	8572	0.000406607
Promoter	HYPER in CCA	chr17	36858085	36860084	*MIR4734*	100616203	0.000163473
Promoter	HYPER in CCA	chr22	21309880	21311879	*NA*	101928891	0.000196284
Promoter	HYPER in CCA	chr2	71017276	71019275	*FIGLA*	344018	6.49E-05
Promoter	HYPER in CCA	chr2	91634431	91636430	*NA*	NA	0.001267848
Promoter	HYPER in CCA	chr10	118999104	119001103	*SLC18A2*	6571	0.002052567
Promoter	HYPER in CCA	chr3	13973053	13975052	*FGD5P1*	100132526	0.000422741
Promoter	HYPER in CCA	chr17	32580804	32582803	*CCL2*	6347	0.000358044
Promoter	HYPER in CCA	chr17	37781493	37783492	*PPP1R1B*	84152	2.37E-05
Promoter	HYPER in CCA	chr17	53340873	53342872	*HLF*	3131	5.27E-05
Promoter	HYPER in CCA	chr8	65290206	65292205	*MIR124-2*	406908	0.00148014
Promoter	HYPER in CCA	chr11	64016467	64018466	*NA*	NA	1.05E-05
Promoter	HYPER in CCA	chr11	85862769	85864768	*RNU6-560P*	NA	4.45E-05
Promoter	HYPER in CCA	chr7	117853227	117855226	*ANKRD7*	56311	0.000435798
Promoter	HYPER in CCA	chr19	36449914	36451913	*NA*	NA	0.000262515
Promoter	HYPER in CCA	chr1	209847265	209849264	*G0S2*	50486	0.000186035
Promoter	HYPER in CCA	chr19	50192655	50194654	*CPT1C*	126129	0.000594695
Promoter	HYPER in CCA	chr10	118428114	118430113	*NA*	NA	7.61E-05
Promoter	HYPER in CCA	chr2	131511508	131513507	*AMER3*	205147	0.000305347
Promoter	HYPER in CCA	chr17	26903783	26905782	*ALDOC*	230	0.001955214
Promoter	HYPER in CCA	chr7	50342220	50344219	*IKZF1*	10320	0.000870304

Promoter	HYPER in CCA	chr8	72987353	72989352	*TRPA1*	8989	0.000405796
Promoter	HYPER in CCA	chr1	32409958	32411957	*PTP4A2*	8073	3.05E-05
Promoter	HYPER in CCA	chr10	23479756	23481755	*PTF1A*	256297	0.001009598
Promoter	HYPER in CCA	chr15	75637796	75639795	*NEIL1*	79661;693216	1.42E-05
Promoter	HYPER in CCA	chr7	27219381	27221380	*HOXA10*	3206	2.06E-05
Promoter	HYPER in CCA	chr10	135342162	135344161	*NA*	NA	0.002071857
Promoter	HYPER in CCA	chr9	72824	74823	*NA*	NA	0.000528737
Promoter	HYPER in CCA	chr10	54072556	54074555	*DKK1*	22943	0.000235416
Promoter	HYPER in CCA	chr14	23834462	23836461	*EFS*	10278	0.000555342
Promoter	HYPER in CCA	chr21	34442911	34444910	*NA*	NA	0.002142002
Promoter	HYPER in CCA	chr5	110557851	110559850	*CAMK4*	814	0.001490736
Promoter	HYPER in CCA	chr5	24644588	24646587	*CDH10*	1008	0.00086748
Promoter	HYPER in CCA	chr19	6107833	6109832	*NA*	NA	6.32E-05
Promoter	HYPER in CCA	chr6	62995633	62997632	*KHDRBS2*	202559	0.001555257
Promoter	HYPER in CCA	chr6	26519187	26521186	*RNU6-502P*	NA	0.001353154
Promoter	HYPER in CCA	chr2	96989569	96991568	*ITPRIPL1*	150771	0.001530398
Promoter	HYPER in CCA	chr8	22546163	22548162	*NA*	NA	7.56E-05
Promoter	HYPER in CCA	chr8	55368995	55370994	*SOX17*	64321	0.002226249
Promoter	HYPER in CCA	chr1	146554628	146556627	*NA*	NA	4.29E-05
Promoter	HYPER in CCA	chr14	60384931	60386930	*LRRC9*	NA	2.65E-05
Promoter	HYPER in CCA	chr17	79988000	79989999	*RAC3*	5881	0.000447299
Promoter	HYPER in CCA	chr15	33010709	33012708	*NA*	100131315	0.000437631
Promoter	HYPER in CCA	chr7	123673024	123675023	*TMEM229A*	730130	0.000566256
Promoter	HYPER in CCA	chr8	99955131	99957130	*OSR2*	116039	0.001182301
Promoter	HYPER in CCA	chr20	32899109	32901108	*AHCY*	191	5.88E-05
Promoter	HYPER in CCA	chr18	43606772	43608771	*NA*	NA	8.91E-05
Promoter	HYPER in CCA	chr4	66534179	66536178	*NA*	100144602	0.001117027
Promoter	HYPER in CCA	chr5	140478734	140480733	*PCDHB3*	56132	0.001513022
Promoter	HYPER in CCA	chr11	32456677	32458676	*WT1*	7490	0.001308012
Promoter	HYPER in CCA	chr11	111781466	111783465	*NA*	3316	1.42E-05
Promoter	HYPER in CCA	chr4	41748810	41750809	*NA*	NA	0.000864715
Promoter	HYPER in CCA	chr15	72489627	72491626	*GRAMD2*	196996	0.00031927
Promoter	HYPER in CCA	chr1	46667506	46669505	*LURAP1*	541468	0.000302196
Promoter	HYPER in CCA	chr3	195633447	195635446	*TNK2-AS1*	NA	0.000373946

Promoter	HYPER in CCA	chr16	72416	72616	*RHBDL1*	9028	0.001030523
Promoter	HYPER in CCA	chr12	49482	49484	*NA*	NA	0.000102937
Promoter	HYPER in CCA	chr12	53084	53086	*NA*	NA	0.000560352
Promoter	HYPER in CCA	chr22	30901	30903	*SEC14L4*	284904	0.000537975
Promoter	HYPER in CCA	chr16	56656	56676	*NA*	101926950	5.97E-08
Promoter	HYPER in CCA	chr17	46619	46621	*HOXB-AS1*	100874362	0.000151453
Promoter	HYPER in CCA	chr16	58718	58720	*SLC38A7*	55238	1.16E-06
Promoter	HYPER in CCA	chr17	46507	46509	*SKAP1*	8631	0.000463189
Promoter	HYPER in CCA	chr1	11872	11872	*SPAG17*	200162	5.74E-05
Promoter	HYPER in CCA	chr4	11022	11022	*NA*	NA	0.000401729
Promoter	HYPER in CCA	chr2	38301	38303	*CYP1B1-AS1*	285154	0.000297564
Promoter	HYPER in CCA	chr19	17958	17960	*JAK3*	3718	1.52E-05
Promoter	HYPER in CCA	chr8	77595	77597	*ZFHX4-AS1*	100192378	0.000131801
Promoter	HYPER in CCA	chr10	12953	12953	*FOXI2*	399823	0.002003569
Promoter	HYPER in CCA	chr3	12190	12190	*CASR*	846	0.001358231
Promoter	HYPER in CCA	chr7	10084	10084	*MOGAT3*	346606	0.000147618
Promoter	HYPER in CCA	chr6	28751	28753	*NA*	NA	0.00012367
Promoter	HYPER in CCA	chr11	10476	10477	*CASP12*	100506742	0.000293856
Promoter	HYPER in CCA	chr8	68615	68815	*ERICH1-AS1*	619343	0.001085534
Promoter	HYPER in CCA	chr10	11842	11843	*C10orf82*	143379	6.42E-05
Promoter	HYPER in CCA	chr2	10209	10209	*RFX8*	731220	0.000117265
Promoter	HYPER in CCA	chr4	48483	48485	*SLC10A4*	201780	0.00036688
Promoter	HYPER in CCA	chr14	36988	36990	*NA*	NA	0.000909664
Promoter	HYPER in CCA	chr14	22572	22574	*TRAV24*	NA	0.00027526
Promoter	HYPER in CCA	chr10	12574	12575	*YBX2P1*	NA	0.001576626
Promoter	HYPER in CCA	chr3	49458	49460	*NICN1-AS1*	NA	1.29E-05
Promoter	HYPER in CCA	chr22	17081	17083	*TPTEP1*	387590	0.001224679
Promoter	HYPER in CCA	chr5	15852	15852	*EBF1*	1879	0.001670447
Promoter	HYPER in CCA	chr7	92465	92467	*CDK6*	1021	0.000109154
Promoter	HYPER in CCA	chr4	19093	19093	*RNA5SP175*	NA	0.000636791
Promoter	HYPER in CCA	chr5	72743	72745	*FOXD1*	2297	0.00163353
Promoter	HYPER in CCA	chr5	72743	72745	*NA*	NA	0.00163353
Promoter	HYPER in CCA	chr15	62456	62458	*C2CD4B*	388125	1.08E-05
Promoter	HYPER in CCA	chr5	14078	14078	*PCDHGB6*	56100	0.001329424

Promoter	HYPER in CCA	chr1	79471904	79473903	*ELTD1*	64123	0.000216366
Promoter	HYPER in CCA	chr6	130685379	130687378	*TMEM200A*	114801	0.000144222
Promoter	HYPER in CCA	chr2	177014450	177016449	*HOXD4*	3233	0.000742696
Promoter	HYPER in CCA	chr3	139258172	139260171	*RBP1*	5947	0.00018476
Promoter	HYPER in CCA	chr2	37550983	37552982	*NA*	101929542	3.49E-06
Promoter	HYPER in CCA	chr12	58012922	58014921	*NA*	NA	0.000763598
Promoter	HYPER in CCA	chr17	33759803	33761802	*SLFN12*	55106	0.000978823
Promoter	HYPER in CCA	chr19	38746732	38748731	*PPP1R14A*	94274	0.000243664
Promoter	HYPER in CCA	chr10	104194769	104196768	*MIR146B*	574447	3.67E-05
Promoter	HYPER in CCA	chr6	27782108	27784107	*HIST1H2AJ*	8331	0.000308338
Promoter	HYPER in CCA	chr1	50512186	50514185	*ELAVL4*	1996	0.000170098
Promoter	HYPER in CCA	chr12	20520679	20522678	*PDE3A*	5139	6.33E-05
Promoter	HYPER in CCA	chr7	27219133	27221132	*NA*	NA	3.31E-05
Promoter	HYPER in CCA	chr12	66581159	66583158	*IRAK3*	11213	0.000502782
Promoter	HYPER in CCA	chr8	22733985	22735984	*NA*	101929237	7.34E-05
Promoter	HYPER in CCA	chr17	46806041	46808040	*HOXB13*	10481	0.000947514
Promoter	HYPER in CCA	chr3	127632575	127634574	*KBTBD12*	166348	1.82E-05
Promoter	HYPER in CCA	chr16	28549996	28551995	*NUPR1*	26471	2.06E-05
Promoter	HYPER in CCA	chr2	26043838	26045837	*PTGES3P2*	NA	0.001450672
Promoter	HYPER in CCA	chr10	43247094	43249093	*NA*	NA	0.001647592
Promoter	HYPER in CCA	chr5	1445046	1447045	*SLC6A3*	6531	0.001160573
Promoter	HYPER in CCA	chr12	78223185	78225184	*NAV3*	89795	0.000140854
Promoter	HYPER in CCA	chr16	56702226	56704225	*MT1H*	4496	0.000303299
Promoter	HYPER in CCA	chr16	31228181	31230180	*PYDC1*	260434	8.88E-05
Promoter	HYPER in CCA	chr4	113435041	113437040	*NA*	NA	0.000108414
Promoter	HYPER in CCA	chr9	110252264	110254263	*KLF4*	9314	4.62E-05
Promoter	HYPER in CCA	chr17	37123156	37125155	*FBXO47*	494188	7.20E-05
Promoter	HYPER in CCA	chr15	28753455	28755454	*ABCB10P4*	NA	3.07E-05
Promoter	HYPER in CCA	chr7	96636523	96638522	*DLX6-AS2*	NA	0.000122535
Promoter	HYPER in CCA	chr17	5018233	5020232	*USP6*	9098;84669	8.47E-05
Promoter	HYPER in CCA	chr1	248019001	248021000	*TRIM58*	25893	4.81E-05
Promoter	HYPER in CCA	chr5	33934991	33936990	*RXFP3*	51289	0.001291398
Promoter	HYPER in CCA	chr11	56947721	56949720	*LRRC55*	219527	0.000188495
Promoter	HYPER in CCA	chr17	38498889	38500888	*NA*	101929693	0.001304288

Promoter	HYPER in CCA	chr20	59054 3	59254 2	*TCF15*	6939	6.89E-05
Promoter	HYPER in CCA	chr2	13218 1941	13218 3940	*GNAQP1*	NA	0.001396538
Promoter	HYPER in CCA	chr11	64739 058	64741 057	*C11orf85*	283129	0.000216681
Promoter	HYPER in CCA	chr21	38073 365	38075 364	*NA*	NA	0.000144508
Promoter	HYPER in CCA	chr6	10653 2695	10653 4694	*PRDM1*	639	8.49E-06
Promoter	HYPER in CCA	chr14	52732 931	52734 930	*PTGDR*	5729	1.09E-05
Promoter	HYPER in CCA	chr11	71236 813	71238 812	*KRTAP5-7*	440050	4.42E-05
Promoter	HYPER in CCA	chr2	17519 8174	17520 0173	*SP9*	100131390	0.000137332
Promoter	HYPER in CCA	chr18	56302 00	56321 99	*EPB41L3*	23136	0.00013143
Promoter	HYPER in CCA	chr2	10710 2324	10710 4323	*CD8BP*	926	0.000125099
Promoter	HYPER in CCA	chr17	48043 041	48045 040	*RNU6-1313P*	NA	0.000908979
Promoter	HYPER in CCA	chr10	45495 837	45497 836	*C10orf25*	220979	0.000145827
Promoter	HYPER in CCA	chr2	17701 3531	17701 5530	*MIR10B*	406903	0.000287406
Promoter	HYPER in CCA	chr7	87935 707	87937 706	*STEAP4*	79689	8.06E-06
Promoter	HYPER in CCA	chr10	35103 754	35105 753	*PARD3*	56288	1.90E-05
Promoter	HYPER in CCA	chr17	46723 886	46725 885	*NA*	NA	0.000218143
Promoter	HYPER in CCA	chr8	18835 629	18837 628	*NA*	NA	0.000114495
Promoter	HYPER in CCA	chr6	13463 8751	13464 0750	*SGK1*	6446	0.000174207
Promoter	HYPER in CCA	chr19	38306 499	38308 498	*NA*	644554	0.000422866
Promoter	HYPER in CCA	chr20	27807 84	27827 83	*CPXM1*	56265	0.000661713
Promoter	HYPER in CCA	chr2	17700 1327	17700 3326	*HOXD-AS2*	100506783	0.000780785
Promoter	HYPER in CCA	chr19	58214 36	58234 35	*NA*	NA	4.59E-05
Promoter	HYPER in CCA	chr1	43919 161	43921 160	*HYI*	81888	0.000533794
Promoter	HYPER in CCA	chr12	54401 332	54403 331	*HOXC8*	3224	0.000221234
Promoter	HYPER in CCA	chr1	22095 8601	22096 0600	*Mar/01*	64757	6.83E-06
Promoter	HYPER in CCA	chr19	12935 025	12937 024	*NA*	NA	1.92E-05
Promoter	HYPER in CCA	chr10	88390 886	88392 885	*RPL7AP8*	NA	0.001294138
Promoter	HYPER in CCA	chr17	55173 287	55175 286	*NA*	NA	0.001128724
Promoter	HYPER in CCA	chr8	50820 849	50822 848	*SNTG1*	54212	0.000919323
Promoter	HYPER in CCA	chr12	54409 394	54411 393	*NA*	3222	0.000537928
Promoter	HYPER in CCA	chr15	90039 345	90041 344	*RHCG*	51458	0.001337577
Promoter	HYPER in CCA	chr17	88677 13	88697 12	*NA*	101928235	0.000537221
Promoter	HYPER in CCA	chr3	15782 2144	15782 4143	*RSRC1*	51319	0.001059286
Promoter	HYPER in CCA	chr3	17916 8879	17917 0878	*GNB4*	59345	0.001105419

Promoter	HYPER in CCA	chr20	53090636	53092635	*DOK5*	55816	0.00131937
Promoter	HYPER in CCA	chr17	16585252	16587251	*RNASEH1P2*	246243	5.12E-05
Promoter	HYPER in CCA	chr6	106546515	106548514	*NA*	NA	0.000191717
Promoter	HYPER in CCA	chr16	86600868	86602867	*NA*	NA	0.001284841
Promoter	HYPER in CCA	chr12	106975185	106977184	*RFX4*	5992	0.000858388
Promoter	HYPER in CCA	chr12	54409215	54411214	*HOXC4*	3221	0.000423086
Promoter	HYPER in CCA	chr6	1388569	1390568	*FOXF2*	2295	5.42E-05
Promoter	HYPER in CCA	chr19	51319437	51321436	*NA*	284365	0.000574829
Promoter	HYPER in CCA	chr1	67771547	67773546	*IL12RB2*	3595	2.08E-05
Promoter	HYPER in CCA	chr6	26612838	26614837	*NA*	NA	4.30E-05
Promoter	HYPER in CCA	chr12	57867728	57869727	*MARS*	4141;102465454	0.000185552
Promoter	HYPER in CCA	chr19	36909059	36911058	*ZFP82*	284406	6.45E-05
Promoter	HYPER in CCA	chr2	25391273	25393272	*POMC*	5443	6.07E-05
Promoter	HYPER in CCA	chr8	54163758	54165757	*OPRK1*	4986	0.001076958
Promoter	HYPER in CCA	chr12	54365410	54367409	*HOXC11*	3227	0.000167551
Promoter	HYPER in CCA	chr3	127793593	127795592	*RNU2-37P*	NA	0.000292347
Promoter	HYPER in CCA	chr9	137269757	137271756	*MIR4669*	100616236	0.001194531
Promoter	HYPER in CCA	chr14	60974169	60976168	*SIX6*	4990	0.000900731
Promoter	HYPER in CCA	chr14	103744060	103746059	*RAP2CP1*	NA	4.36E-07
Promoter	HYPER in CCA	chr15	60294921	60296920	*FOXB1*	27023	0.000421995
Promoter	HYPER in CCA	chr6	50784936	50786935	*TFAP2B*	7021	0.000389911
Promoter	HYPER in CCA	chr7	35293259	35295258	*TBX20*	57057	5.45E-05
Promoter	HYPER in CCA	chr11	789624	791623	*CEND1*	51286	3.82E-05
Promoter	HYPER in CCA	chr11	65816152	65818151	*GAL3ST3*	89792	8.68E-06
Promoter	HYPER in CCA	chr8	73448126	73450125	*KCNB2*	9312	0.00042955
Promoter	HYPER in CCA	chr7	5110256	5112255	*RBAKDN*	389458	0.000801415
Promoter	HYPER in CCA	chr6	105387903	105389902	*LINC00577*	100113403	2.15E-05
Promoter	HYPER in CCA	chr12	50297501	50299500	*FAIM2*	23017	0.000407834
Promoter	HYPER in CCA	chr7	139207102	139209101	*CLEC2L*	154790	0.001068507
Promoter	HYPER in CCA	chr7	97359720	97361719	*TAC1*	6863	0.000294539
Promoter	HYPER in CCA	chr1	179543903	179545902	*RNU5F-2P*	NA	8.12E-05
Promoter	HYPER in CCA	chr2	74208069	74210068	*DGUOK-AS1*	100874048	0.001357272
Promoter	HYPER in CCA	chr5	43042773	43044772	*ANXA2R*	389289	0.000121676
Promoter	HYPER in CCA	chr22	25678142	25680141	*NA*	101929416	0.000860779

Promoter	HYPER in CCA	chr1	248820160	248840150	*NA*	100506985	1.12E-06
Promoter	HYPER in CCA	chr1	248811020	248831010	*NCMAP*	400746	1.12E-06
Promoter	HYPER in CCA	chr5	140612438	140614437	*PCDHB18*	54660	2.00E-05
Promoter	HYPER in CCA	chr14	292335500	292355490	*FOXG1*	2290	0.000351477
Promoter	HYPER in CCA	chr11	942442470	942462460	*LINC01171*	NA	5.81E-05
Promoter	HYPER in CCA	chr20	558403530	558423520	*NA*	101927820	0.001330392
Promoter	HYPER in CCA	chr5	161803720	161823710	*Mar/11*	441061	0.001012057
Promoter	HYPER in CCA	chr14	103988949	103990948	*CKB*	1152	8.62E-05
Promoter	HYPER in CCA	chr19	141694720	141714710	*PALM3*	342979	0.000139062
Promoter	HYPER in CCA	chr5	114515744	114517743	*TRIM36*	55521	0.00036139
Promoter	HYPER in CCA	chr11	640572740	640592730	*KCNK4*	50801	2.49E-05
Promoter	HYPER in CCA	chr16	584952500	584972490	*NDRG4*	65009	0.000723333
Promoter	HYPER in CCA	chr20	225587810	225607800	*LINC00261*	140828	8.57E-05
Promoter	HYPER in CCA	chr6	104080730	104100720	*TFAP2A-AS1*	100130275	0.00039174
Promoter	HYPER in CCA	chr18	122528180	122548170	*CIDEA*	1149	0.000507023
Promoter	HYPER in CCA	chr2	220377392	220379391	*ASIC4*	55515	0.000462767
Promoter	HYPER in CCA	chr6	285834900	285854890	*SCAND3*	114821	0.001484215
Promoter	HYPER in CCA	chr19	505523460	505543450	*NA*	400710	3.54E-05
Promoter	HYPER in CCA	chr1	401372110	401392100	*NT5C1A*	84618	0.000414173
Promoter	HYPER in CCA	chr2	101814760	101834750	*KLF11*	8462	9.88E-05
Promoter	HYPER in CCA	chr1	150119873	150121872	*PLEKHO1*	51177	1.55E-05
Promoter	HYPER in CCA	chr5	173987279	173989278	*SUMO2P6*	NA	0.00046066
Promoter	HYPER in CCA	chr2	160760722	160762721	*LY75-CD302*	4065;9936;100526664	0.001352218
Promoter	HYPER in CCA	chr17	461141140	461161130	*MIR152*	406943	9.03E-05
Promoter	HYPER in CCA	chr10	157616250	157636240	*ITGA8*	8516	0.000106339
Promoter	HYPER in CCA	chr22	442578990	442598980	*SULT4A1*	25830	0.000737805
Promoter	HYPER in CCA	chr2	145281648	145283647	*ZEB2*	9839	5.98E-05
Promoter	HYPER in CCA	chr1	208084248	208086247	*CD34*	947	1.57E-05
Promoter	HYPER in CCA	chr11	324555640	324575630	*WT1-AS*	51352	0.000927479
Promoter	HYPER in CCA	chr19	381827390	381847380	*ZFP30*	22835	1.07E-05
Promoter	HYPER in CCA	chr19	381827240	381847230	*ZNF781*	163115	1.07E-05
Promoter	HYPER in CCA	chr1	196577856	196579855	*KCNT2*	343450	8.67E-07
Promoter	HYPER in CCA	chr5	156886587	156888586	*NA*	101927675	2.06E-05
Promoter	HYPER in CCA	chr20	442566650	442586640	*WFDC10A*	140832	1.12E-05

Promoter	HYPER in CCA	chr16	56657887	56659886	*MT1E*	4493	0.001358984
Promoter	HYPER in CCA	chr12	54387179	54389178	*HOXC9*	3225	5.82E-05
Promoter	HYPER in CCA	chr8	27849745	27851744	*SCARA5*	286133	0.000665738
Promoter	HYPER in CCA	chr15	76634483	76636482	*NA*	NA	8.69E-05
Promoter	HYPER in CCA	chr3	99355819	99357818	*COL8A1*	1295	0.00010689
Promoter	HYPER in CCA	chr6	26194294	26196293	*HIST1H1PS1*	NA	0.001303421
Promoter	HYPER in CCA	chr10	50602998	50604997	*DRGX*	644168	0.000683415
Promoter	HYPER in CCA	chr8	72756204	72758203	*MSC*	9242	0.000455302
Promoter	HYPER in CCA	chr10	103603178	103605177	*KCNIP2*	30819	0.000242308
Promoter	HYPER in CCA	chr19	35394719	35396718	*NA*	100652911	9.19E-05
Promoter	HYPER in CCA	chr7	27224343	27226342	*HOXA11*	3207	5.87E-05
Promoter	HYPER in CCA	chr10	129534470	129536469	*NA*	387720	0.001054112
Promoter	HYPER in CCA	chr1	4713292	4715291	*AJAP1*	55966	0.000418479
Promoter	HYPER in CCA	chr20	61637888	61639887	*BHLHE23*	128408	0.001101787
Promoter	HYPER in CCA	chr6	134208776	134210775	*TCF21*	6943	7.19E-06
Promoter	HYPER in CCA	chr8	104513405	104515404	*NA*	NA	3.12E-05
Promoter	HYPER in CCA	chr4	41258245	41260244	*UCHL1-AS1*	101410542	3.52E-05
Promoter	HYPER in CCA	chr14	48143500	48145499	*NA*	161357	0.000489139
Promoter	HYPER in CCA	chr19	4152098	4154097	*CREB3L3*	84699	0.000363263
Promoter	HYPER in CCA	chr5	169062751	169064750	*DOCK2*	1794	0.001300324
Promoter	HYPER in CCA	chr11	31839010	31841009	*PAX6*	5080	0.000317932
Promoter	HYPER in CCA	chr6	7100333	7120332	*NA*	NA	8.20E-06
Promoter	HYPER in CCA	chr14	104550516	104552515	*ASPG*	374569	1.74E-05
Promoter	HYPER in CCA	chr16	75150170	75152169	*LDHD*	197257	2.67E-05
Promoter	HYPER in CCA	chr2	17718893	17720892	*VSNL1*	7447	0.000296196
Promoter	HYPER in CCA	chr3	23677979	23877978	*CHL1*	10752	0.000120395
Promoter	HYPER in CCA	chr1	79084107	79086106	*IFI44L*	10964	4.91E-05
Promoter	HYPER in CCA	chr5	50678667	50680666	*NA*	642366	0.000512277
Promoter	HYPER in CCA	chr3	32858010	32860009	*TRIM71*	131405	0.000634371
Promoter	HYPER in CCA	chr2	127781287	127783286	*NA*	NA	6.45E-05
Promoter	HYPER in CCA	chr1	179544588	179546587	*NPHS2*	7827	5.53E-05
Promoter	HYPER in CCA	chr4	1399620	1401619	*NKX1-1*	NA	0.000284367
Promoter	HYPER in CCA	chr1	149400043	149402042	*HIST2H3PS2*	NA	2.31E-08
Promoter	HYPER in CCA	chr1	149400041	149402040	*NA*	NA	2.31E-08

Promoter	HYPER in CCA	chr12	52652152	52654151	*KRT121P*	NA	5.50E-06
Promoter	HYPER in CCA	chr2	119604755	119606754	*EN1*	2019	0.000273383
Promoter	HYPER in CCA	chr5	76935014	76937013	*OTP*	23440	7.97E-05
Promoter	HYPER in CCA	chr2	17699207	17701206	*RAD51AP2*	729475	0.000111564
Promoter	HYPER in CCA	chr3	187387688	187389687	*SST*	6750	0.000269826
Promoter	HYPER in CCA	chr6	104193	104213	*TFAP2A*	7020	0.000248302
Promoter	HYPER in CCA	chr19	44174200	44176199	*PLAUR*	5329	0.002163973
Promoter	HYPER in CCA	chr10	63212709	63214708	*TMEM26*	219623	9.38E-05
Promoter	HYPER in CCA	chr10	134775242	134777241	*LINC01167*	NA	0.001165765
Promoter	HYPER in CCA	chr19	45407511	45409510	*APOE*	348	1.14E-05
Promoter	HYPER in CCA	chr17	35300256	35302255	*NA*	NA	0.000171892
Promoter	HYPER in CCA	chr18	56940819	56942818	*RAX*	30062	0.000189382
Promoter	HYPER in CCA	chr2	45168513	45170512	*SIX3-AS1*	100506108	0.00017098
Promoter	HYPER in CCA	chr18	903444	905443	*ADCYAP1*	116	0.000185423
Promoter	HYPER in CCA	chr20	18038637	18040636	*NA*	NA	0.000819837
Promoter	HYPER in CCA	chr1	226150379	226152378	*NDUFA3P3*	NA	5.67E-05
Promoter	HYPER in CCA	chr8	58053748	58055747	*NA*	100507651;101929436	0.000121986
Promoter	HYPER in CCA	chr19	54411089	54413088	*CACNG7*	59284	0.000233314
Promoter	HYPER in CCA	chr10	124893978	124895977	*HMX3*	340784	0.00125894
Promoter	HYPER in CCA	chr3	128763106	128765105	*NA*	NA	4.12E-05
Promoter	HYPER in CCA	chr11	20181660	20183659	*DBX1*	120237	0.000140958
Promoter	HYPER in CCA	chr12	128750448	128752447	*TMEM132C*	92293	0.001302598
Promoter	HYPER in CCA	chr3	79816466	79818465	*ROBO1*	6091	0.000638489
Promoter	HYPER in CCA	chr7	27141931	27143930	*HOXA2*	3199	5.58E-05
Promoter	HYPER in CCA	chr6	27781322	27783321	*HIST1H2BM*	8342	0.000155072
Promoter	HYPER in CCA	chr1	26143631	26145630	*MTFR1L*	56181	0.000203235
Promoter	HYPER in CCA	chr6	38682494	38684493	*NA*	NA	6.50E-07
Promoter	HYPER in CCA	chr16	77468512	77470511	*ADAMTS18*	170692	0.000329641
Promoter	HYPER in CCA	chr7	12610518	12612517	*NA*	NA	0.00013633
Promoter	HYPER in CCA	chr8	57356866	57358865	*NA*	101929415	4.00E-05
Promoter	HYPER in CCA	chr12	54348818	54350817	*NA*	NA	6.74E-06
Promoter	HYPER in CCA	chr2	45180303	45182302	*NA*	NA	5.61E-05
Promoter	HYPER in CCA	chr7	19156796	19158795	*TWIST1*	7291	0.000332781
Promoter	HYPER in CCA	chr20	37351605	37353604	*SLC32A1*	140679	0.000205068

Promoter	HYPER in CCA	chr10	134597770	134599769	*NA*	NA	2.29E-05
Promoter	HYPER in CCA	chr7	101934869	101936868	*MIR4285*	100422858	0.000192703
Promoter	HYPER in CCA	chr2	114298014	114300013	*NA*	NA	0.001271756
Promoter	HYPER in CCA	chr5	140799262	140801261	*PCDHGA11*	5098;56105	0.00011905
Promoter	HYPER in CCA	chr14	52535213	52537212	*NID2*	22795	0.000202642
Promoter	HYPER in CCA	chr4	147558545	147560544	*POU4F2*	5458	1.74E-05
Promoter	HYPER in CCA	chr15	73661106	73663105	*HCN4*	10021	4.67E-06
Promoter	HYPER in CCA	chr2	89065335	89067334	*NA*	NA	7.37E-05
Promoter	HYPER in CCA	chr4	82135719	82137718	*PRKG2*	5593	0.001047197
Promoter	HYPER in CCA	chr2	149645852	149647851	*NA*	101928553	3.97E-06
Promoter	HYPER in CCA	chr5	1294685	1296684	*TERT*	7015	2.88E-06
Promoter	HYPER in CCA	chr9	95819489	95821488	*SUSD3*	203328	0.000583767
Promoter	HYPER in CCA	chr16	50726014	50728013	*NOD2*	64127	9.91E-06
Promoter	HYPER in CCA	chr6	105584550	105586549	*BVES*	11149	0.000150207
Promoter	HYPER in CCA	chr14	29233984	29235983	*NA*	NA	5.20E-05
Promoter	HYPER in CCA	chr7	157265503	157285502	*NA*	101927524	0.000752126
Promoter	HYPER in CCA	chr19	331670004	331690003	*ANKRD27*	84079	0.000913831
Promoter	HYPER in CCA	chr5	2737374	2739373	*NA*	NA	2.05E-05
Promoter	HYPER in CCA	chr10	88726449	88728448	*ADIRF*	10974	0.000129805
Promoter	HYPER in CCA	chr12	123257374	123259373	*CCDC62*	84660	9.97E-05
Promoter	HYPER in CCA	chr17	6678042	6680041	*FBXO39*	162517	0.000171041
Promoter	HYPER in CCA	chr5	178449253	178451252	*ZNF879*	345462	0.000367348
Promoter	HYPER in CCA	chr4	134069772	134071771	*NA*	101927359	0.002150519
Promoter	HYPER in CCA	chr5	72508274	72510273	*NA*	NA	6.31E-05
Promoter	HYPER in CCA	chr15	76633905	76635904	*NA*	NA	0.000143542
Promoter	HYPER in CCA	chr12	10022236	10024235	*CLEC2B*	9976	0.000486596
Promoter	HYPER in CCA	chr19	19647557	19649556	*CILP2*	148113	0.000180146
Promoter	HYPER in CCA	chr7	155301478	155303477	*NA*	NA	0.000315284
Promoter	HYPER in CCA	chr6	31275827	31277826	*NA*	NA	0.000261197
Promoter	HYPER in CCA	chr4	74863997	74865996	*CXCL5*	6374	0.000208429
Promoter	HYPER in CCA	chr2	176962958	176964957	*HOXD12*	3238	2.37E-05
Promoter	HYPER in CCA	chr11	41480824	41482823	*LRRC4C*	57689	0.000761175
Promoter	HYPER in CCA	chr17	35293461	35295460	*NA*	NA	0.000765362
Promoter	HYPER in CCA	chr2	162271105	162273104	*TBR1*	10716	1.80E-05

Promoter	HYPER in CCA	chr13	110956659	110958658	*COL4A2*	1284	0.000660551
Promoter	HYPER in CCA	chr6	24124850	24126849	*NRSN1*	140767	6.21E-07
Promoter	HYPER in CCA	chr22	46453541	46455540	*NA*	NA	2.66E-06
Promoter	HYPER in CCA	chr7	73440619	73442618	*ELN*	2006	9.28E-05
Promoter	HYPER in CCA	chr1	33801966	33803965	*RN7SKP16*	NA	6.35E-05
Promoter	HYPER in CCA	chr18	29302661	29304660	*LRRC37A7P*	NA	0.000126325
Promoter	HYPER in CCA	chr2	173539127	173541126	*NA*	NA	4.71E-05
Promoter	HYPER in CCA	chr12	56513224	56515223	*NA*	NA	3.75E-06
Promoter	HYPER in CCA	chr4	153600818	153602817	*TMEM154*	201799	1.27E-05
Promoter	HYPER in CCA	chr2	231915255	231917254	*NA*	NA	0.000412163
Promoter	HYPER in CCA	chr7	27169919	27171918	*HOXA4*	3201	0.000121039
Promoter	HYPER in CCA	chr8	48100895	48102894	*NA*	NA	0.000103163
Promoter	HYPER in CCA	chr17	46681855	46683854	*HOXB6*	3216	6.28E-05
Promoter	HYPER in CCA	chr1	50888673	50890672	*DMRTA2*	63950	0.000339712
Promoter	HYPER in CCA	chr2	224903537	224905536	*SERPINE2*	5270	3.99E-05
Promoter	HYPER in CCA	chr19	39694407	39696406	*SYCN*	342898	9.86E-06
Promoter	HYPER in CCA	chr6	2903015	2905014	*SERPINB9*	5272	8.83E-05
Promoter	HYPER in CCA	chr19	57828431	57830430	*NA*	NA	0.000101377
Promoter	HYPER in CCA	chr17	38598202	38600201	*IGFBP4*	3487	1.28E-05
Promoter	HYPER in CCA	chr6	27773353	27775352	*HIST1H4PS1*	NA	1.97E-05
Promoter	HYPER in CCA	chr5	44389309	44391308	*FGF10*	2255	0.000444313
Promoter	HYPER in CCA	chr3	181428214	181430213	*SOX2*	6657	0.000394908
Promoter	HYPER in CCA	chr2	182544893	182546892	*CERKL*	375298	0.000129748
Promoter	HYPER in CCA	chr2	182545104	182547103	*NEUROD1*	4760	0.000129748
Promoter	HYPER in CCA	chr6	27840790	27842789	*HIST1H4L*	8294;8359;8360;8361;8362;8363;8364;8365;8366;8367;8368;8370;121504;554313	0.000196845
Promoter	HYPER in CCA	chr9	34649199	34651198	*IL11RA*	3590	2.77E-05
Promoter	HYPER in CCA	chr4	110223314	110225313	*COL25A1*	84570	0.000114172
Promoter	HYPER in CCA	chr4	175443806	175445805	*HPGD*	3248	0.000369857
Promoter	HYPER in CCA	chr10	73976393	73978392	*ASCC1*	51008	0.000150802
Promoter	HYPER in CCA	chr8	38584204	38586203	*TACC1*	6867	4.02E-05
Promoter	HYPER in CCA	chr15	40379533	40381532	*NA*	NA	0.000223954
Promoter	HYPER in CCA	chr3	125427044	125447043	*RNU6-404P*	NA	9.28E-05
Promoter	HYPER in CCA	chr4	169753589	169755588	*NA*	NA	4.68E-05
Promoter	HYPER in CCA	chr12	2944211	2946210	*NRIP2*	83714	9.44E-05

Promoter	HYPER in CCA	chr17	46808953	46810952	*NA*	NA	8.49E-05
Promoter	HYPER in CCA	chr2	17698558	17698757	*HOXD9*	3235	0.000107652
Promoter	HYPER in CCA	chr8	82542870	82544869	*IMPA1P*	NA	3.70E-05
Promoter	HYPER in CCA	chr10	119304080	119306079	*EMX2OS*	196047	0.000252173
Promoter	HYPER in CCA	chr6	80656798	80658797	*ELOVL4*	6785	9.19E-06
Promoter	HYPER in CCA	chr1	100109999	100111998	*PALMD*	54873	0.000206962
Promoter	HYPER in CCA	chr2	5831299	5833298	*SOX11*	6664	1.13E-05
Promoter	HYPER in CCA	chr10	8094948	8096947	*GATA3-AS1*	399717	0.00072958
Promoter	HYPER in CCA	chr10	8094913	8096912	*NA*	399717	0.00072958
Promoter	HYPER in CCA	chr10	133109485	133111484	*TCERG1L*	256536	0.000467888
Promoter	HYPER in CCA	chr5	2750745	2752744	*C5orf38*	153571	0.000161385
Promoter	HYPER in CCA	chr7	150497949	150499948	*TMEM176B*	28959	1.34E-05
Promoter	HYPER in CCA	chr2	160760761	160762760	*LY75*	4065;9936;100526664	0.0009418
Promoter	HYPER in CCA	chr13	53422276	53424275	*PCDH8*	5100	0.000657518
Promoter	HYPER in CCA	chr17	79137807	79139806	*AATK-AS1*	388428	2.14E-07
Promoter	HYPER in CCA	chr16	1029752	1031751	*NA*	NA	2.63E-05
Promoter	HYPER in CCA	chr4	21949138	21951137	*NA*	NA	0.00021987
Promoter	HYPER in CCA	chr15	59155705	59157704	*ZNF444P1*	NA	3.41E-05
Promoter	HYPER in CCA	chr12	101109804	101111803	*ANO4*	121601	0.002163241
Promoter	HYPER in CCA	chr17	79374079	79376078	*MIR4740*	100616294	2.08E-05
Promoter	HYPER in CCA	chr7	142493182	142495181	*TRBJ2-4*	NA	1.59E-05
Promoter	HYPER in CCA	chr7	142493303	142495302	*TRBJ2-5*	NA	1.59E-05
Promoter	HYPER in CCA	chr7	142493423	142495422	*TRBJ2-6*	NA	1.59E-05
Promoter	HYPER in CCA	chr7	155173271	155175270	*NA*	NA	9.44E-05
Promoter	HYPER in CCA	chr15	83774659	83776658	*TM6SF1*	53346	0.001111331
Promoter	HYPER in CCA	chr11	30038071	30040070	*KCNA4*	3739	0.000178846
Promoter	HYPER in CCA	chr20	21490585	21492584	*NKX2-2-AS1*	NA	0.000457812
Promoter	HYPER in CCA	chr19	18528174	18530173	*SSBP4*	170463	3.65E-05
Promoter	HYPER in CCA	chr16	54972084	54974083	*NA*	NA	0.000144246
Promoter	HYPER in CCA	chr2	95691955	95693954	*NA*	NA	0.000220752
Promoter	HYPER in CCA	chr17	40931196	40933195	*WNK4*	65266	0.002101414
Promoter	HYPER in CCA	chr12	96388799	96390798	*NA*	NA	2.59E-07
Promoter	HYPER in CCA	chr19	57153013	57155012	*SMIM17*	147670	4.52E-05
Promoter	HYPER in CCA	chr5	95170251	95172250	*NA*	NA	6.98E-05

Promoter	HYPER in CCA	chr1	196152451	196172441	*AKR7A3*	22977	0.000398245
Promoter	HYPER in CCA	chr1	147752356	147754355	*NA*	NA	0.000217832
Promoter	HYPER in CCA	chr6	28413250	28415249	*COX11P1*	NA	0.000376947
Promoter	HYPER in CCA	chr22	45063093	45065092	*PRR5*	55615	0.000156872
Promoter	HYPER in CCA	chr13	24143009	24145008	*TNFRSF19*	55504	4.90E-06
Promoter	HYPER in CCA	chr4	21949923	21951922	*KCNIP4*	80333	0.000181542
Promoter	HYPER in CCA	chr12	22093837	22095836	*ABCC9*	10060	9.29E-06
Promoter	HYPER in CCA	chr1	53097516	53099515	*FAM159A*	348378	1.74E-06
Promoter	HYPER in CCA	chr6	133560236	133562235	*EYA4*	2070	5.87E-06
Promoter	HYPER in CCA	chr6	134212575	134214574	*NA*	100507308	0.000141598
Promoter	HYPER in CCA	chr18	70534123	70536122	*NA*	100505797	0.000782375
Promoter	HYPER in CCA	chr8	99954556	99956555	*STK3*	6788	8.38E-05
Promoter	HYPER in CCA	chr19	50553820	50555819	*NA*	NA	2.60E-05
Promoter	HYPER in CCA	chr4	100242059	100244058	*ADH1B*	125	2.31E-06
Promoter	HYPER in CCA	chr12	56039948	56041947	*OR10AE3P*	NA	1.20E-05
Promoter	HYPER in CCA	chr12	54332928	54334927	*HOXC13-AS*	100874366	0.000596841
Promoter	HYPER in CCA	chr10	74396024	74398023	*HMGN2P34*	NA	0.000333485
Promoter	HYPER in CCA	chr20	43438480	43440479	*RIMS4*	140730	0.001355548
Promoter	HYPER in CCA	chr4	109087181	109089180	*LEF1-AS1*	641518	0.001239551
Promoter	HYPER in CCA	chr2	201449091	201451090	*AOX1*	316	0.001092776
Promoter	HYPER in CCA	chr11	126147973	126149972	*RPL35AP26*	NA	4.33E-05
Promoter	HYPER in CCA	chr6	30922140	30924139	*HCG21*	NA	9.26E-05
Promoter	HYPER in CCA	chr5	129241111	129243110	*NA*	NA	0.000121531
Promoter	HYPER in CCA	chr17	38019942	38021941	*IKZF3*	22806	6.19E-06
Promoter	HYPER in CCA	chr8	24771731	24773730	*NA*	NA	1.16E-05
Promoter	HYPER in CCA	chr5	140733268	140735267	*PCDHGA4*	56111	1.03E-05
Promoter	HYPER in CCA	chr13	113758605	113760604	*F7*	2155	1.71E-05
Promoter	HYPER in CCA	chr1	228463268	228465267	*NA*	NA	0.000275786
Promoter	HYPER in CCA	chr16	89478473	89480472	*NA*	NA	2.74E-05
Promoter	HYPER in CCA	chr5	140012787	140014786	*CD14*	929	6.43E-07
Promoter	HYPER in CCA	chr4	174911513	174913512	*NA*	NA	0.000791773
Promoter	HYPER in CCA	chr2	172947968	172949967	*DLX1*	1745	2.42E-05
Promoter	HYPER in CCA	chr15	76627565	76629564	*ISL2*	64843	2.89E-05
Promoter	HYPER in CCA	chr22	37881940	37883939	*MFNG*	4242	0.001553139

Promoter	HYPER in CCA	chr5	50677421	50679420	*ISL1*	3670	0.000214387
Promoter	HYPER in CCA	chr18	31020566	31022565	*CCDC178*	374864	1.79E-05
Promoter	HYPER in CCA	chr4	184090071	184092070	*RNU7-158P*	NA	2.35E-05
Promoter	HYPER in CCA	chr15	93352615	93354614	*FAM174B*	400451	2.65E-07
Promoter	HYPER in CCA	chr3	112928350	112930349	*BOC*	91653	0.00015786
Promoter	HYPER in CCA	chr16	56640611	56642610	*MT2A*	4502	2.01E-06
Promoter	HYPER in CCA	chr6	27839600	27841599	*HIST1H3I*	8350;8351;8352;8353;8354;8355;8356;8357;8358;8968	0.000422662
Promoter	HYPER in CCA	chr8	81033587	81035586	*NA*	NA	1.01E-05
Promoter	HYPER in CCA	chr16	55364767	55366766	*NA*	NA	5.92E-05
Promoter	HYPER in CCA	chr8	67874326	67876325	*TCF24*	100129654	0.000597643
Promoter	HYPER in CCA	chr1	248100316	248102315	*NA*	NA	4.18E-06
Promoter	HYPER in CCA	chr12	120765093	120767092	*PLA2G1B*	5319	5.26E-06
Promoter	HYPER in CCA	chr10	135171030	135173029	*FUOM*	282969	1.56E-05
Promoter	HYPER in CCA	chr16	86599357	86601356	*FOXC2*	2303	0.000248873
Promoter	HYPER in CCA	chr19	39686101	39688100	*NCCRP1*	342897	2.88E-05
Promoter	HYPER in CCA	chr4	567702	569701	*NA*	NA	3.74E-05
Promoter	HYPER in CCA	chr19	7977904	7979903	*NA*	NA	6.01E-07
Promoter	HYPER in CCA	chr13	27976225	27978224	*RNY1P1*	NA	0.002230544
Promoter	HYPER in CCA	chr16	89508226	89510225	*RNU6-430P*	NA	0.002263229
Promoter	HYPER in CCA	chr8	41753781	41755780	*ANK1*	286	0.000827081
Promoter	HYPER in CCA	chr15	77859812	77861811	*NA*	NA	0.001689007
Promoter	HYPER in CCA	chr2	5834852	5836851	*NA*	NA	0.000205659
Promoter	HYPER in CCA	chr2	176967444	176969443	*HOXD11*	3237	0.000189
Promoter	HYPER in CCA	chr6	29892736	29894735	*HLA-K*	NA	0.000208308
Promoter	HYPER in CCA	chr7	54608518	54610517	*VSTM2A*	222008	1.34E-05
Promoter	HYPER in CCA	chr2	179914314	179916313	*CCDC141*	285025	0.001035482
Promoter	HYPER in CCA	chr1	98514920	98516919	*MIR137HG*	400765;406928;100616452	2.40E-05
Promoter	HYPER in CCA	chr4	75229360	75231359	*EREG*	2069	0.000280313
Promoter	HYPER in CCA	chr19	4534737	4536736	*PLIN5*	440503	0.001888414
Promoter	HYPER in CCA	chr10	134599057	134601056	*NKX6-2*	84504	0.000237415
Promoter	HYPER in CCA	chr2	162279589	162281588	*NA*	NA	1.63E-05
Promoter	HYPER in CCA	chr1	156388623	156390622	*MIR9-1*	407046	0.000224619
Promoter	HYPER in CCA	chr1	47601607	47603606	*CYP4A22*	1579;284541	4.00E-06
Promoter	HYPER in CCA	chr10	105035420	105037419	*INA*	9118	0.001216974

Promoter	HYPER in CCA	chr4	134068970	134070969	*PCDH10*	57575	0.0001199
Promoter	HYPER in CCA	chr2	73427886	73429885	*NOTO*	344022	2.40E-05
Promoter	HYPER in CCA	chr20	25129395	25131394	*NA*	284798	5.97E-07
Promoter	HYPER in CCA	chr18	19261971	19263970	*MIR320C1*	100302135	0.000148178
Promoter	HYPER in CCA	chr6	710906	712905	*NA*	NA	6.00E-06
Promoter	HYPER in CCA	chr11	66045497	66047496	*NA*	NA	0.00109654
Promoter	HYPER in CCA	chr7	19812722	19814721	*TMEM196*	256130	7.33E-06
Promoter	HYPER in CCA	chr16	56665651	56667650	*NA*	NA	8.67E-06
Promoter	HYPER in CCA	chr3	157823793	157825792	*SHOX2*	6474	7.85E-05
Promoter	HYPER in CCA	chr2	228734270	228736269	*DAW1*	164781	5.14E-05
Promoter	HYPER in CCA	chr6	168079451	168081450	*NA*	401286	0.000249344
Promoter	HYPER in CCA	chr7	142493031	142495030	*TRBJ2-3*	NA	1.11E-05
Promoter	HYPER in CCA	chr10	8094067	8096066	*GATA3*	2625	0.000493949
Promoter	HYPER in CCA	chr19	36736660	36738659	*ZNF565*	147929	2.31E-05
Promoter	HYPER in CCA	chr12	54368241	54370240	*HOTAIR*	100124700	8.08E-05
Promoter	HYPER in CCA	chr13	100623664	100625663	*ZIC5*	85416	2.07E-05
Promoter	HYPER in CCA	chr6	39758642	39760641	*DAAM2*	23500	0.000323239
Promoter	HYPER in CCA	chr5	158736441	158738440	*NA*	285626	0.000438097
Promoter	HYPER in CCA	chr12	85672385	85674384	*ALX1*	8092	0.000116162
Promoter	HYPER in CCA	chr20	20347265	20349264	*INSM1*	3642	0.000189471
Promoter	HYPER in CCA	chr14	102026269	102028268	*DIO3OS*	100302145	6.92E-05
Promoter	HYPER in CCA	chr2	127782800	127784799	*NA*	NA	2.66E-05
Promoter	HYPER in CCA	chr7	79082391	79084390	*MAGI2*	9863	0.000107715
Promoter	HYPER in CCA	chr17	46681775	46683774	*HOXB3*	3213	3.41E-05
Promoter	HYPER in CCA	chr2	176948142	176950141	*EVX2*	344191	8.79E-05
Promoter	HYPER in CCA	chr20	18039333	18041332	*OVOL2*	58495	0.000811983
Promoter	HYPER in CCA	chr20	56803210	56805209	*ANKRD60*	140731	2.22E-06
Promoter	HYPER in CCA	chr11	61062397	61064396	*VWCE*	220001	5.70E-07
Promoter	HYPER in CCA	chr17	42080414	42082413	*NAGS*	162417	3.64E-05
Promoter	HYPER in CCA	chr8	70983429	70985428	*PRDM14*	63978	3.61E-05
Promoter	HYPER in CCA	chr5	50263994	50265993	*NA*	NA	0.000118418
Promoter	HYPER in CCA	chr2	177053187	177055186	*HOXD-AS1*	401022	0.000573518
Promoter	HYPER in CCA	chr4	148558913	148560912	*NA*	NA	6.56E-06
Promoter	HYPER in CCA	chr1	40596936	40598935	*NA*	NA	1.08E-05

Promoter	HYPER in CCA	chr7	142493640	142495639	*TRBJ2-7*	NA	8.31E-06
Promoter	HYPER in CCA	chr10	119493324	119495323	*NA*	NA	0.000342284
Promoter	HYPER in CCA	chr14	48143658	48145657	*MDGA2*	161357	0.000314308
Promoter	HYPER in CCA	chr19	6670100	6672099	*TNFSF14*	8740	5.35E-06
Promoter	HYPER in CCA	chr12	53718149	53720148	*AAAS*	8086	6.31E-06
Promoter	HYPER in CCA	chr22	29874719	29876718	*NEFH*	4744	0.000312328
Promoter	HYPER in CCA	chr20	21376956	21378955	*NA*	NA	0.000138351
Promoter	HYPER in CCA	chr16	56223802	56225801	*GNAO1*	2775	0.000404093
Promoter	HYPER in CCA	chr1	26197245	26199244	*PAQR7*	164091	1.91E-06
Promoter	HYPER in CCA	chr9	126762449	126764448	*LHX2*	9355	0.001890257
Promoter	HYPER in CCA	chr11	86084278	86086277	*CCDC81*	60494	3.27E-06
Promoter	HYPER in CCA	chr12	9268326	9270325	*A2M*	2	3.90E-06
Promoter	HYPER in CCA	chr5	1882580	1884579	*NA*	NA	0.000472561
Promoter	HYPER in CCA	chr1	113497537	113499536	*SLC16A1-AS1*	100506392	4.82E-05
Promoter	HYPER in CCA	chr3	138665483	138667482	*FOXL2*	668	4.52E-05
Promoter	HYPER in CCA	chr19	12781671	12783670	*WDR83OS*	51398	2.55E-06
Promoter	HYPER in CCA	chr6	26234717	26236716	*HIST1H1D*	3007	0.000108655
Promoter	HYPER in CCA	chr6	73330020	73332019	*KCNQ5*	56479	1.95E-05
Promoter	HYPER in CCA	chr7	139167959	139169958	*KLRG2*	346689	0.000357174
Promoter	HYPER in CCA	chr11	63258167	63260166	*HRASLS5*	117245	1.98E-06
Promoter	HYPER in CCA	chr2	24231451	24233450	*MFSD2B*	388931	1.40E-05
Promoter	HYPER in CCA	chr16	1030308	1032307	*SOX8*	30812	4.46E-05
Promoter	HYPER in CCA	chr10	47082034	47084033	*NPY4R*	100996758	5.23E-06
Promoter	HYPER in CCA	chr17	58225797	58227796	*CA4*	762	9.08E-06
Promoter	HYPER in CCA	chr1	161207593	161209592	*NR1I3*	9970	2.24E-07
Promoter	HYPER in CCA	chr8	77591954	77593953	*ZFHX4*	79776	1.94E-05
Promoter	HYPER in CCA	chr14	22537320	22539319	*TRAV22*	NA	0.000382468
Promoter	HYPER in CCA	chr12	54745945	54747944	*NA*	NA	1.75E-06
Promoter	HYPER in CCA	chr2	237076513	237078512	*GBX2*	2637	0.000118595
Promoter	HYPER in CCA	chr19	18901624	18903623	*COMP*	1311	1.76E-07
Promoter	HYPER in CCA	chr19	59049779	59051778	*ZBTB45*	84878	8.07E-05
Promoter	HYPER in CCA	chr6	53881076	53883075	*ERHP2*	NA	1.37E-05
Promoter	HYPER in CCA	chr15	68549050	68551049	*CLN6*	54982	5.37E-06
Promoter	HYPER in CCA	chr1	116652876	116654875	*MAB21L3*	126868	2.16E-06

Promoter	HYPER in CCA	chr2	102299470	102319460	*NA*	NA	1.37E-05
Promoter	HYPER in CCA	chr9	130700264	130702263	*DPM2*	8818	6.20E-06
Promoter	HYPER in CCA	chr16	28751603	28753602	*NA*	NA	1.94E-05
Promoter	HYPER in CCA	chr10	102493860	102495859	*PAX2*	5076	2.32E-05
Promoter	HYPER in CCA	chr2	198650987	198652986	*BOLL*	66037	2.82E-05
Promoter	HYPER in CCA	chr1	111217156	111219155	*KCNA3*	3738	6.21E-05
Promoter	HYPER in CCA	chr20	62686656	62688655	*NA*	NA	1.35E-07
Promoter	HYPER in CCA	chr2	144693140	144695139	*NA*	NA	0.000135118
Promoter	HYPER in CCA	chr17	27891570	27893569	*TP53I13*	90313	2.46E-05
Promoter	HYPER in CCA	chr3	179754342	179756341	*PEX5L*	51555	4.85E-05
Promoter	HYPER in CCA	chr1	236046441	236048440	*LYST*	1130	0.000168638
Promoter	HYPER in CCA	chr20	30777831	30779830	*TSPY26P*	128854	4.65E-06
Promoter	HYPER in CCA	chr5	74162277	74164276	*FAM169A*	26049	1.80E-07
Promoter	HYPER in CCA	chr18	30352526	30354525	*KLHL14*	57565	1.13E-05
Promoter	HYPER in CCA	chr13	31505340	31507339	*TEX26*	122046	2.03E-06
Promoter	HYPER in CCA	chr8	104511476	104513475	*RIMS2*	9699	3.07E-05
Promoter	HYPER in CCA	chr2	119592187	119594186	*NA*	NA	1.08E-05
Promoter	HYPER in CCA	chr6	6006701	6008700	*NRN1*	51299	7.55E-06
Promoter	HYPER in CCA	chr2	219644972	219646971	*CYP27A1*	1593	0.000322395
Promoter	HYPER in CCA	chr1	71170636	71172635	*NA*	101927244	2.99E-05
Promoter	HYPER in CCA	chr2	223163216	223165215	*PAX3*	5077	2.99E-05
Promoter	HYPER in CCA	chr7	20826006	20828005	*SP8*	221833	1.65E-05
Promoter	HYPER in CCA	chr1	182911040	182913039	*HMGN1P4*	NA	9.37E-06
Promoter	HYPER in CCA	chr16	66611851	66613850	*CMTM2*	146225	1.04E-06
Promoter	HYPER in CCA	chr18	12909685	12911684	*NA*	NA	7.18E-06
Promoter	HYPER in CCA	chr10	73155191	73157190	*CDH23*	64072;100653137	6.23E-05
Promoter	HYPER in CCA	chr2	177040945	177042944	*NA*	NA	6.02E-06
Promoter	HYPER in CCA	chr1	196000189	196021888	*AKR7L*	NA	6.39E-05
Promoter	HYPER in CCA	chr7	8472085	8474084	*NXPH1*	30010	7.68E-05
Promoter	HYPER in CCA	chr19	23253779	23255778	*NA*	NA	0.000305285
Promoter	HYPER in CCA	chr2	162279343	162281342	*SLC4A10*	57282	6.91E-06
Promoter	HYPER in CCA	chr12	49739200	49741199	*DNAJC22*	79962	5.44E-05
Promoter	HYPER in CCA	chr8	144654160	144656159	*NA*	NA	8.39E-06
Promoter	HYPER in CCA	chr12	66628515	66630514	*RBMS1P1*	NA	0.000226754

Promoter	HYPER in CCA	chr6	87861051	87863050	*ZNF292*	23036	8.83E-08
Promoter	HYPER in CCA	chr1	47697393	47699392	*TAL1*	6886	6.11E-06
Promoter	HYPER in CCA	chr7	27196463	27198462	*NA*	NA	7.45E-05
Promoter	HYPER in CCA	chr7	12195 0246	12195 2245	*FEZF1*	389549	2.27E-05
Promoter	HYPER in CCA	chr1	23510 5310	23510 7309	*NA*	NA	3.20E-05
Promoter	HYPER in CCA	chr14	10202 6188	10202 8187	*DIO3*	1735	5.84E-05
Promoter	HYPER in CCA	chr17	79044 12	79064 11	*GUCY2D*	3000	1.29E-05
Promoter	HYPER in CCA	chr16	77469 500	77471 499	*NA*	NA	5.79E-05
Promoter	HYPER in CCA	chr18	20715 977	20717 976	*NA*	NA	4.43E-05
Promoter	HYPER in CCA	chr7	13753 1339	13753 3338	*DGKI*	9162	9.54E-06
Promoter	HYPER in CCA	chr8	12265 0033	12265 2032	*HAS2-AS1*	594842	1.26E-05
Promoter	HYPER in CCA	chr14	38068 746	38070 745	*FOXA1*	3169	0.000118804
Promoter	HYPER in CCA	chr19	30015 906	30017 905	*VSTM2B*	342865	0.000946166
Promoter	HYPER in CCA	chr6	10562 7371	10562 9370	*POPDC3*	64208	0.000135676
Promoter	HYPER in CCA	chr6	12606 7310	12606 9309	*HEY2*	23493	8.26E-07
Promoter	HYPER in CCA	chr5	72740 684	72742 683	*NA*	NA	8.71E-05
Promoter	HYPER in CCA	chr17	35292 584	35294 583	*LHX1*	3975	0.000552808
Promoter	HYPER in CCA	chr19	57182 136	57184 135	*NA*	NA	9.76E-05
Promoter	HYPER in CCA	chr19	57182 652	57184 651	*ZNF835*	90485	9.76E-05
Promoter	HYPER in CCA	chr2	13159 4068	13159 6067	*NA*	NA	0.001598246
Promoter	HYPER in CCA	chr2	10546 8243	10547 0242	*NA*	NA	0.000157144
Promoter	HYPER in CCA	chr17	11143 080	11145 079	*SHISA6*	388336	0.000182315
Promoter	HYPER in CCA	chr7	12833 5993	12833 7992	*RNA5SP242*	NA	0.000160451
Promoter	HYPER in CCA	chr7	12833 6264	12833 8263	*RNA5SP243*	NA	0.000160451
Promoter	HYPER in CCA	chr6	26239 061	26241 060	*HIST1H4F*	8294;8359;8360;8361;8362;8363;8364;8365;8366;8367;8368;8370;121504;554313	2.93E-06
Promoter	HYPER in CCA	chr6	16613 1327	16613 3326	*RNU6-730P*	NA	0.000246412
Promoter	HYPER in CCA	chr14	81425 362	81427 361	*CEP128*	145508	1.45E-06
Promoter	HYPER in CCA	chr3	12204 2591	12204 4590	*CSTA*	1475	1.35E-06
Promoter	HYPER in CCA	chr1	85463 330	85465 329	*WDR63*	126820	3.26E-06
Promoter	HYPER in CCA	chr1	16613 3833	16613 5832	*NA*	NA	2.86E-05
Promoter	HYPER in CCA	chr16	56224 507	56226 506	*NA*	283856	0.000299492
Promoter	HYPER in CCA	chr15	53096 640	53098 639	*NA*	101928499	0.000310569
Promoter	HYPER in CCA	chr7	10076 8870	10077 0869	*SERPINE1*	5054	0.000257296
Promoter	HYPER in CCA	chr6	26272 269	26274 268	*HIST1H2APS4*	NA	4.97E-06

Promoter	HYPER in CCA	chr7	27191718	27193717	*NA*	NA	6.90E-05
Promoter	HYPER in CCA	chr15	29033310	29035309	*NA*	646278;101929232	7.06E-06
Promoter	HYPER in CCA	chr1	14541595	14541594	*HFE2*	148738	1.54E-07
Promoter	HYPER in CCA	chr19	40788049	40790048	*MIR641*	693226	5.87E-06
Promoter	HYPER in CCA	chr14	36986983	36988982	*NKX2-1-AS1*	100506237	0.000171146
Promoter	HYPER in CCA	chr1	23720 4005	23720 6004	*RYR2*	6262	8.70E-06
Promoter	HYPER in CCA	chr4	18891 5425	18891 7424	*ZFP42*	132625	0.000489819
Promoter	HYPER in CCA	chr18	907182	909181	*NA*	NA	3.47E-05
Promoter	HYPER in CCA	chr18	70534882	70536881	*NETO1*	81832	3.56E-05
Promoter	HYPER in CCA	chr12	6880178	6882177	*LAG3*	3902	3.34E-07
Promoter	HYPER in CCA	chr1	15022 8054	15023 0053	*CA14*	23632	3.78E-07
Promoter	HYPER in CCA	chr16	3233519	3235518	*NA*	NA	3.82E-05
Promoter	HYPER in CCA	chr5	17616 5960	17616 7959	*NA*	NA	3.78E-06
Promoter	HYPER in CCA	chr19	14585675	14587674	*PTGER1*	5731	3.50E-07
Promoter	HYPER in CCA	chr5	13437 5238	13437 7237	*NA*	101927953	1.35E-06
Promoter	HYPER in CCA	chr7	27191701	27193700	*HOXA3*	3200	5.49E-05
Promoter	HYPER in CCA	chr7	27191681	27193680	*NA*	NA	5.49E-05
Promoter	HYPER in CCA	chr10	10306 9275	10307 1274	*NA*	NA	6.12E-06
Promoter	HYPER in CCA	chr6	10881675	10883674	*GCM2*	9247	7.78E-06
Promoter	HYPER in CCA	chr7	27133766	27135765	*HOTAIRM1*	100506311	6.42E-05
Promoter	HYPER in CCA	chr1	14971 8863	14972 0862	*NA*	NA	5.61E-07
Promoter	HYPER in CCA	chr6	26271113	26273112	*HIST1H3G*	8350;8351;8352;8353;8354;8355;8356;8357;8358;8968	1.43E-06
Promoter	HYPER in CCA	chr2	11187 2666	11187 4665	*NA*	400997	5.61E-06
Promoter	HYPER in CCA	chr9	11325 5	11525 4	*NA*	NA	6.87E-05
Promoter	HYPER in CCA	chr11	11670 8167	11671 0166	*APOA1*	335	5.25E-07
Promoter	HYPER in CCA	chr1	47406657	47408656	*CYP4A11*	1579;284541	1.68E-05
Promoter	HYPER in CCA	chr8	56013449	56015448	*XKR4*	114786	2.84E-05
Promoter	HYPER in CCA	chr4	90758967	90760966	*SNCA*	6622	0.000222212
Promoter	HYPER in CCA	chr20	21378167	21380166	*NKX2-4*	644524	0.000187009
Promoter	HYPER in CCA	chr16	24681884	24683883	*NA*	400511	2.61E-06
Promoter	HYPER in CCA	chr10	10521 2161	10521 4160	*CALHM2*	51063	1.09E-07
Promoter	HYPER in CCA	chr20	44745411	44747410	*CD40*	958	0.000347793
Promoter	HYPER in CCA	chr10	11930 0455	11930 2454	*EMX2*	2018	8.15E-06
Promoter	HYPER in CCA	chr2	85810031	85812030	*VAMP5*	10791	8.35E-05

Promoter	HYPER in CCA	chr7	155604468	155606467	*SHH*	6469	0.000127981
Promoter	HYPER in CCA	chr6	33159777	33161776	*COL11A2*	1302	4.47E-05
Promoter	HYPER in CCA	chr4	54969324	54971323	*NA*	NA	1.09E-05
Promoter	HYPER in CCA	chr16	19896990	19898989	*GPRC5B*	51704	2.76E-07
Promoter	HYPER in CCA	chr5	127872206	127874205	*SLC27A6*	28965	1.09E-05
Promoter	HYPER in CCA	chr2	130735735	130737734	*RAB6C*	84084;150786	1.08E-06
Promoter	HYPER in CCA	chr1	236227963	236229962	*NID1*	4811	0.000390947
Promoter	HYPER in CCA	chr19	35394600	35396599	*NA*	NA	1.51E-05
Promoter	HYPER in CCA	chr1	117664710	117666709	*TRIM45*	80263	3.39E-06
Promoter	HYPER in CCA	chr10	45494423	45496422	*ZNF22*	7570	5.55E-06
Promoter	HYPER in CCA	chr15	29032845	29034844	*NA*	NA	3.24E-06
Promoter	HYPER in CCA	chr13	46425372	46427371	*SIAH3*	283514	1.11E-06
Promoter	HYPER in CCA	chr19	30016160	30018159	*NA*	284395	0.000990093
Promoter	HYPER in CCA	chr3	138664576	138666575	*C3orf72*	401089	5.14E-05
Promoter	HYPER in CCA	chr16	20419356	20421355	*ACSM5*	54988	3.53E-08
Promoter	HYPER in CCA	chr8	99954323	99956322	*NA*	NA	2.78E-05
Promoter	HYPER in CCA	chr10	100995120	100997119	*HPSE2*	60495	1.63E-05
Promoter	HYPER in CCA	chr2	182546340	182548339	*NA*	NA	1.63E-05
Promoter	HYPER in CCA	chr16	22864 15	22884 14	*NA*	NA	2.15E-07
Promoter	HYPER in CCA	chr1	196945167	196947166	*CFHR5*	81494	2.54E-05
Promoter	HYPER in CCA	chr6	11042257	11044256	*ELOVL2-AS1*	100506409	2.97E-06
Promoter	HYPER in CCA	chr11	105479221	105481220	*GRIA4*	2893	2.08E-05
Promoter	HYPER in CCA	chr16	23845822	23847821	*PRKCB*	5579	6.80E-06
Promoter	HYPER in CCA	chr1	35586123	35588122	*EFCAB14P1*	NA	1.44E-05
Promoter	HYPER in CCA	chr19	31839954	31841953	*TSHZ3*	57616	0.000255689
Promoter	HYPER in CCA	chr2	54555671	54557670	*C2orf73*	129852	5.67E-05
Promoter	HYPER in CCA	chr4	122301715	122303714	*QRFPR*	84109	0.000539544
Promoter	HYPER in CCA	chr17	34328585	34330584	*CCL15*	6359	5.05E-05
Promoter	HYPER in CCA	chr2	176956119	176958118	*HOXD13*	3239	2.40E-06
Promoter	HYPER in CCA	chr17	14205671	14207670	*NA*	84815	2.59E-06
Promoter	HYPER in CCA	chr17	42003431	42005430	*NA*	NA	6.76E-07
Promoter	HYPER in CCA	chr5	140748331	140750330	*PCDHGB3*	56102	2.27E-05
Promoter	HYPER in CCA	chr5	79534909	79536908	*NA*	NA	0.000100334
Promoter	HYPER in CCA	chr17	15685102	15687101	*IL6STP1*	NA	2.58E-05

Promoter	HYPER in CCA	chr19	45428561	45430560	*APOC1P1*	342	3.66E-07
Promoter	HYPER in CCA	chr2	5830751	5832750	*NA*	NA	7.90E-07
Promoter	HYPER in CCA	chr2	5831121	5833120	*NA*	NA	6.74E-07
Promoter	HYPER in CCA	chr8	68862853	68864852	*PREX2*	80243	0.000542295
Promoter	HYPER in CCA	chr1	116105722	116107721	*CNOT7P2*	NA	7.68E-06
Promoter	HYPER in CCA	chr17	32581807	32583806	*NA*	NA	7.81E-05
Promoter	HYPER in CCA	chr7	27197056	27199055	*HOXA7*	3204	4.19E-05
Promoter	HYPER in CCA	chr15	100345728	100347727	*NA*	NA	4.16E-06
Promoter	HYPER in CCA	chr9	137032391	137034390	*NA*	NA	2.21E-06
Promoter	HYPER in CCA	chr19	39753522	39755521	*IFNL4P1*	NA	1.32E-05
Promoter	HYPER in CCA	chr11	118978542	118980541	*DPAGT1*	1798	6.19E-05
Promoter	HYPER in CCA	chr20	19738180	19740179	*NA*	101930064	0.0001688
Promoter	HYPER in CCA	chr9	95298438	95300437	*ECM2*	1842	1.20E-06
Promoter	HYPER in CCA	chr1	91182295	91184294	*BARHL2*	343472	1.41E-06
Promoter	HYPER in CCA	chr9	99447838	99449837	*NA*	100996557	0.001173507
Promoter	HYPER in CCA	chr5	170734788	170736787	*TLX3*	30012	3.66E-06
Promoter	HYPER in CCA	chr14	103564981	103566980	*EXOC3L4*	91828	7.73E-06
Promoter	HYPER in CCA	chr12	64784473	64786472	*C12orf56*	115749	0.000105395
Promoter	HYPER in CCA	chr19	41855258	41857257	*NA*	NA	6.32E-05
Promoter	HYPER in CCA	chr19	41855316	41857315	*TMEM91*	641649	6.32E-05
Promoter	HYPER in CCA	chr7	27222637	27224636	*HOXA11-AS*	221883	1.03E-06
Promoter	HYPER in CCA	chr1	235813555	235815554	*GNG4*	2786	1.66E-05
Promoter	HYPER in CCA	chr19	50310690	50312689	*NA*	NA	0.00032074
Promoter	HYPER in CCA	chr6	1384802	1386801	*NA*	NA	1.49E-05
Promoter	HYPER in CCA	chr16	52581215	52583214	*TOX3*	27324	3.34E-06
Promoter	HYPER in CCA	chr7	142492881	142494880	*TRBJ2-2P*	NA	1.92E-06
Promoter	HYPER in CCA	chr20	23014557	23016556	*SSTR4*	6754	8.61E-06
Promoter	HYPER in CCA	chr7	27236694	27238693	*HOTTIP*	100316868	7.89E-05
Promoter	HYPER in CCA	chr13	43565908	43567907	*EPSTI1*	94240	1.49E-05
Promoter	HYPER in CCA	chr1	217310598	217312597	*ESRRG*	2104	0.000156753
Promoter	HYPER in CCA	chr1	156597474	156797473	*MMP23B*	8510	4.44E-06
Promoter	HYPER in CCA	chr6	169653640	169655639	*THBS2*	7058	1.68E-07
Promoter	HYPER in CCA	chr14	51562280	51564279	*TRIM9*	114088	6.31E-06
Promoter	HYPER in CCA	chr9	35790651	35792650	*NPR2*	4882	7.31E-06

Promoter	HYPER in CCA	chr2	105483455	105485454	*NA*	NA	7.18E-05
Promoter	HYPER in CCA	chr15	75080599	75082598	*MIR4513*	100616183	4.46E-05
Promoter	HYPER in CCA	chr4	170896554	170898553	*NA*	100506085	1.79E-05
Promoter	HYPER in CCA	chr17	7346880	7348879	*CHRNB1*	1140	1.06E-06
Promoter	HYPER in CCA	chr5	190126	192125	*LRRC14B*	389257	1.71E-07
Promoter	HYPER in CCA	chr16	77465779	77467778	*NA*	NA	0.000386485
Promoter	HYPER in CCA	chr8	29210188	29212187	*NA*	NA	5.68E-07
Promoter	HYPER in CCA	chr5	176558526	176560525	*NSD1*	64324	7.33E-07
Promoter	HYPER in CCA	chr8	23563154	23565153	*NA*	NA	1.13E-05
Promoter	HYPER in CCA	chr8	24769087	24771086	*NA*	NA	6.33E-06
Promoter	HYPER in CCA	chr8	24769025	24771024	*NEFM*	4741	6.33E-06
Promoter	HYPER in CCA	chr17	59528265	59530264	*TBX4*	9496	0.000179895
Promoter	HYPER in CCA	chr17	14275956	14277955	*NA*	NA	1.32E-05
Promoter	HYPER in CCA	chr8	49468502	49470501	*NA*	NA	2.31E-05
Promoter	HYPER in CCA	chr2	45240308	45242307	*NA*	NA	3.63E-05
Promoter	HYPER in CCA	chr3	133463300	133465299	*TF*	7018	6.17E-07
Promoter	HYPER in CCA	chr1	228651828	228653827	*HIST3H2BA*	NA	5.93E-06
Promoter	HYPER in CCA	chr3	188663503	188665502	*TPRG1*	285386	9.53E-07
Promoter	HYPER in CCA	chr17	72320849	72322848	*KIF19*	124602	8.04E-07
Promoter	HYPER in CCA	chr2	145274164	145276163	*ZEB2-AS1*	100303491	0.000166798
Promoter	HYPER in CCA	chr7	27209618	27211617	*HOXA9*	3205;442920	5.57E-05
Promoter	HYPER in CCA	chr5	156991472	156993471	*NA*	NA	0.000179109
Promoter	HYPER in CCA	chr9	129884663	129886662	*ANGPTL2*	23452	1.36E-05
Promoter	HYPER in CCA	chr11	119241916	119243915	*NA*	NA	7.89E-07
Promoter	HYPER in CCA	chr2	177051807	177053806	*HOXD1*	3231	6.89E-05
Promoter	HYPER in CCA	chr6	108805513	108825512	*NA*	NA	3.12E-06
Promoter	HYPER in CCA	chr2	162279026	162281025	*NA*	NA	5.27E-06
Promoter	HYPER in CCA	chr15	95869859	95871858	*NA*	400456	1.84E-07
Promoter	HYPER in CCA	chr6	26250336	26252335	*HIST1H3F*	8350;8351;8352;8353;8354;8355;8356;8357;8358;8968	5.09E-06
Promoter	HYPER in CCA	chr1	227747382	227749381	*RNA5SP77*	NA	9.40E-07
Promoter	HYPER in CCA	chr11	116698922	116700921	*APOC3*	345	6.55E-07
Promoter	HYPER in CCA	chr7	150037360	150039359	*NA*	NA	0.00069144
Promoter	HYPER in CCA	chr11	110583413	110585412	*ARHGAP20*	57569	4.82E-07
Promoter	HYPER in CCA	chr7	150381285	150383284	*GIMAP2*	26157	5.41E-05

Promoter	HYPER in CCA	chr6	26250379	26252378	*HIST1H2BH*	8345	3.49E-06
Promoter	HYPER in CCA	chr3	13866236	13866436	*NA*	NA	6.67E-05
Promoter	HYPER in CCA	chr3	19729969	19730169	*BDH1*	622	4.07E-07
Promoter	HYPER in CCA	chr14	99727785	99729784	*NA*	NA	2.41E-05
Promoter	HYPER in CCA	chr2	22873486	22873686	*TDGF1P2*	NA	6.79E-06
Promoter	HYPER in CCA	chr19	2249138	2251137	*MIR4321*	100423031	1.85E-06
Promoter	HYPER in CCA	chr17	46709422	46711421	*MIR196A1*	406972	1.14E-05
Promoter	HYPER in CCA	chr5	1885946	1887945	*NA*	101929081	0.000323497
Promoter	HYPER in CCA	chr5	16292862	16293061	*MAT2B*	27430	3.00E-05
Promoter	HYPER in CCA	chr17	42081338	42083337	*PYY*	5697	4.06E-05
Promoter	HYPER in CCA	chr1	17955924	17956124	*TDRD5*	163589	2.51E-06
Promoter	HYPER in CCA	chr5	17010794	17010994	*NA*	NA	0.000110273
Promoter	HYPER in CCA	chr6	31971913	31973912	*CYP21A1P*	1590	2.47E-07
Promoter	HYPER in CCA	chr2	22316136	22316336	*CCDC140*	151278	1.18E-06
Promoter	HYPER in CCA	chr5	17678333	17678533	*RGS14*	10636	5.34E-07
Promoter	HYPER in CCA	chr3	19396393	19396593	*NA*	101929337	0.000107323
Promoter	HYPER in CCA	chr3	12969164	12969364	*TRH*	7200	3.90E-07
Promoter	HYPER in CCA	chr2	10267950	10268150	*IL1R1*	3554	0.000521708
Promoter	HYPER in CCA	chr16	48592072	48594071	*NA*	NA	0.000362071
Promoter	HYPER in CCA	chr3	14710970	14711170	*ZIC1*	7545	4.22E-07
Promoter	HYPER in CCA	chr4	16822944	16823144	*NA*	NA	1.68E-06
Promoter	HYPER in CCA	chr7	94022373	94024372	*COL1A2*	1278	3.11E-05
Promoter	HYPER in CCA	chr8	21888361	21890360	*NA*	NA	0.000399684
Promoter	HYPER in CCA	chr3	18619301	18619501	*NA*	NA	0.000339996
Promoter	HYPER in CCA	chr15	74656276	74658275	*NA*	NA	8.13E-08
Promoter	HYPER in CCA	chr5	50262343	50264342	*NA*	NA	1.08E-05
Promoter	HYPER in CCA	chr16	56664645	56666644	*MT1M*	4499	3.58E-06
Promoter	HYPER in CCA	chr3	16491439	16491639	*SLITRK3*	22865	5.50E-05
Promoter	HYPER in CCA	chr2	17360043	17360243	*RAPGEF4-AS1*	91149	1.36E-06
Promoter	HYPER in CCA	chr19	15343747	15345746	*EPHX3*	79852	6.25E-07
Promoter	HYPER in CCA	chr5	14073820	14074020	*PCDHGB2*	56103	2.35E-06
Promoter	HYPER in CCA	chr4	72669259	72671258	*GC*	2638	1.18E-05
Promoter	HYPER in CCA	chr5	78984200	78986199	*CMYA5*	202333	5.98E-05
Promoter	HYPER in CCA	chr16	67700669	67702668	*ENKD1*	84080	5.84E-06

Promoter	HYPER in CCA	chr2	200335490	200337489	*SATB2*	23314	6.58E-05
Promoter	HYPER in CCA	chr11	635793	637792	*DRD4*	1815	1.18E-06
Promoter	HYPER in CCA	chr16	56701478	56703477	*MT1G*	4495	6.74E-07
Promoter	HYPER in CCA	chr6	26271644	26273643	*HIST1H2BI*	8339;8343;8344;8346;8347	1.81E-06
Promoter	HYPER in CCA	chr2	170624810	170626809	*PTCHD3P2*	NA	1.48E-05
Promoter	HYPER in CCA	chr9	126794304	126796303	*NA*	NA	3.29E-07
Promoter	HYPER in CCA	chr12	121569122	121571121	*P2RX7*	5027	9.48E-07
Promoter	HYPER in CCA	chr7	27206738	27208737	*HOXA10-AS*	442920;100874323	2.86E-06
Promoter	HYPER in CCA	chr10	54530961	54532960	*MBL2*	4153	7.00E-07
Promoter	HYPER in CCA	chr8	105478782	105480781	*DPYS*	1807	1.92E-05
Promoter	HYPER in CCA	chr17	19651757	19653756	*ALDH3A1*	218	7.66E-06
Promoter	HYPER in CCA	chr5	140722101	140724100	*PCDHGA3*	56112	1.68E-06
Promoter	HYPER in CCA	chr8	142139561	142141560	*NA*	101927963	6.41E-08
Promoter	HYPER in CCA	chr16	49315243	49317242	*CBLN1*	869	2.93E-06
Promoter	HYPER in CCA	chr19	54484061	54486060	*MIR935*	100126325	9.59E-05
Promoter	HYPER in CCA	chr13	24900849	24902848	*NUS1P3*	NA	1.21E-06
Promoter	HYPER in CCA	chr7	142492744	142494743	*TRBJ2-2*	NA	6.44E-07
Promoter	HYPER in CCA	chr17	34328161	34330160	*CCL15-CCL14*	6358;6359	1.24E-05
Promoter	HYPER in CCA	chr18	76738775	76740774	*SALL3*	27164	0.000116516
Promoter	HYPER in CCA	chr6	43209918	43211917	*TTBK1*	84630	1.39E-06
Promoter	HYPER in CCA	chr7	27135116	27137115	*HOXA1*	3198	5.74E-06
Promoter	HYPER in CCA	chr1	196742425	196744424	*CFHR3*	10878	1.41E-07
Promoter	HYPER in CCA	chr3	187009311	187011310	*MASP1*	5648	0.000103775
Promoter	HYPER in CCA	chr19	46916342	46918341	*CCDC8*	83987	9.37E-06
Promoter	HYPER in CCA	chr17	46710435	46712434	*HOXB7*	3217	3.56E-06
Promoter	HYPER in CCA	chr12	86266573	86268572	*NTS*	4922	3.57E-06
Promoter	HYPER in CCA	chr16	227053	229052	*NA*	NA	5.93E-06
Promoter	HYPER in CCA	chr2	190044106	190046105	*COL5A2*	1290	5.75E-06
Promoter	HYPER in CCA	chr17	72857128	72859127	*GRIN2C*	2905	2.28E-06
Promoter	HYPER in CCA	chr10	28034490	28036489	*MKX*	283078	8.66E-06
Promoter	HYPER in CCA	chr1	3630363	3632362	*NA*	NA	4.32E-07
Promoter	HYPER in CCA	chr5	1886851	1888850	*IRX4*	50805	0.000162173
Promoter	HYPER in CCA	chr19	46996265	46998264	*NA*	NA	3.56E-05
Promoter	HYPER in CCA	chr11	43601444	43603443	*MIR129-2*	406918	7.04E-05

Promoter	HYPER in CCA	chr15	29031889	29033888	*NA*	100289656	5.78E-06
Promoter	HYPER in CCA	chr19	4517217	4519216	*PLIN4*	729359	8.99E-07
Promoter	HYPER in CCA	chr5	177017057	177019056	*COL23A1*	91522	5.44E-06
Promoter	HYPER in CCA	chr7	6702105	6704104	*NA*	NA	1.39E-06
Promoter	HYPER in CCA	chr14	70263507	70265506	*SLC10A1*	6554	3.14E-08
Promoter	HYPER in CCA	chr1	63789613	63791612	*NA*	NA	0.000127941
Promoter	HYPER in CCA	chr10	135159150	135161149	*PRAP1*	118471	5.48E-07
Promoter	HYPER in CCA	chr7	49811757	49813756	*VWC2*	375567	0.000720114
Promoter	HYPER in CCA	chr9	37001194	37003193	*NA*	NA	0.000704094
Promoter	HYPER in CCA	chr5	72414619	72416618	*TMEM171*	134285	2.14E-07
Promoter	HYPER in CCA	chr13	101241283	101243282	*GGACT*	87769	0.0019509
Promoter	HYPER in CCA	chr14	57276698	57278697	*OTX2*	5015	2.12E-06
Promoter	HYPER in CCA	chr8	21990398	21992397	*HR*	55806	0.00097615
Promoter	HYPER in CCA	chr1	205534344	205536343	*RNU2-19P*	NA	1.23E-05
Promoter	HYPER in CCA	chr2	176972018	176974017	*HOXD10*	3236	5.83E-06
Promoter	HYPER in CCA	chr8	40009489	40011488	*C8orf4*	56892	0.000722881
Promoter	HYPER in CCA	chr4	42398356	42400355	*SHISA3*	152573	1.99E-05
Promoter	HYPER in CCA	chr5	140742398	140744397	*PCDHGA5*	56110	1.91E-07
Promoter	HYPER in CCA	chr6	27234392	27236391	*NA*	NA	2.46E-05
Promoter	HYPER in CCA	chr2	160654254	160656253	*CD302*	9936	7.96E-05
Promoter	HYPER in CCA	chr22	30817026	30819025	*NA*	NA	3.67E-06
Promoter	HYPER in CCA	chr22	30817261	30819260	*RNF215*	200312	3.67E-06
Promoter	HYPER in CCA	chr5	3594668	3596667	*IRX1*	79192	1.31E-05
Promoter	HYPER in CCA	chr5	50265502	50267501	*NA*	100287592	1.05E-05
Promoter	HYPER in CCA	chr16	54967325	54969324	*NA*	NA	7.82E-06
Promoter	HYPER in CCA	chr3	52827284	52829283	*ITIH3*	3699	1.73E-07
Promoter	HYPER in CCA	chr19	11434618	11436617	*NA*	NA	0.002053883
Promoter	HYPER in CCA	chr18	56116806	56118805	*MIR122*	406906;100616357	2.16E-06
Promoter	HYPER in CCA	chr10	22632899	22634898	*SPAG6*	9576	2.63E-07
Promoter	HYPER in CCA	chr18	76738575	76740574	*NA*	NA	3.40E-05
Promoter	HYPER in CCA	chr10	63210897	63212896	*NA*	101928781	1.99E-07
Promoter	HYPER in CCA	chr6	27834860	27836859	*HIST1H1B*	3009	3.41E-06
Promoter	HYPER in CCA	chr3	46929672	46931671	*NA*	NA	4.40E-05
Promoter	HYPER in CCA	chr2	176992922	176994921	*HOXD8*	3234	9.69E-07

Promoter	HYPER in CCA	chr5	142814578	142816577	*NR3C1*	2908	2.17E-05
Promoter	HYPER in CCA	chr1	168106322	168108321	*GPR161*	23432	1.17E-05
Promoter	HYPER in CCA	chr13	79177174	79179173	*POU4F1*	5457	1.04E-05
Promoter	HYPER in CCA	chr7	24322282	24324281	*NPY*	4852	3.26E-05
Promoter	HYPER in CCA	chr2	176971871	176973870	*NA*	NA	3.78E-06
Promoter	HYPER in CCA	chr17	26699611	26701610	*SEBOX;VTN*	7448;645832	3.92E-06
Promoter	HYPER in CCA	chr17	40273256	40275255	*HSPB9*	94086	2.19E-06
Promoter	HYPER in CCA	chr7	27208684	27210683	*MIR196B*	442920	2.37E-05
Promoter	HYPER in CCA	chr20	25062497	25064496	*VSX1*	30813	4.13E-06
Promoter	HYPER in CCA	chr2	37570217	37572216	*QPCT*	25797	1.28E-06
Promoter	HYPER in CCA	chr12	54746076	54748075	*NA*	NA	3.19E-07
Promoter	HYPER in CCA	chr3	58612838	58614837	*FAM107A*	11170	6.80E-05
Promoter	HYPER in CCA	chr1	170630369	170632368	*PRRX1*	5396	3.41E-06
Promoter	HYPER in CCA	chr12	41580750	41582749	*PDZRN4*	29951	4.49E-06
Promoter	HYPER in CCA	chr5	176152745	176154744	*NA*	NA	4.52E-05
Promoter	HYPER in CCA	chr4	41256930	41258929	*UCHL1*	7345	2.46E-06
Promoter	HYPER in CCA	chr18	58999315	59001314	*CDH20*	28316	2.33E-06
Promoter	HYPER in CCA	chr2	105470469	105472468	*POU3F3*	5455	5.20E-05
Promoter	HYPER in CCA	chr5	140618018	140620017	*PCDHB19P*	84054	3.21E-06
Promoter	HYPER in CCA	chr5	54465951	54467950	*MIR449A*	554213	1.29E-05
Promoter	HYPER in CCA	chr5	54466071	54468070	*MIR449B*	693123	1.29E-05
Promoter	HYPER in CCA	chr19	4724186	4726185	*DPP9*	91039	0.000182486
Promoter	HYPER in CCA	chr1	53752196	53754195	*NA*	NA	4.74E-06
Promoter	HYPER in CCA	chr6	133034689	133036688	*VNN1*	8876	1.19E-06
Promoter	HYPER in CCA	chr14	76045432	76047431	*NA*	NA	1.41E-06
Promoter	HYPER in CCA	chr19	49258148	49260147	*FUT1*	2523	1.49E-08
Promoter	HYPER in CCA	chr11	6463348	6465347	*HPX*	3263	1.19E-07
Promoter	HYPER in CCA	chr17	19481756	19483755	*NA*	101060602	1.14E-05
Promoter	HYPER in CCA	chr5	140601431	140603430	*PCDHB14*	56122	3.78E-05
Promoter	HYPER in CCA	chr11	60719503	60721502	*SLC15A3*	51296	2.55E-06
Promoter	HYPER in CCA	chr11	66044161	66046160	*CNIH2*	254263	8.02E-05
Promoter	HYPER in CCA	chr12	49390650	49392649	*NA*	NA	1.64E-08
Promoter	HYPER in CCA	chr1	203320118	203322117	*FMOD*	2331	1.93E-06
Promoter	HYPER in CCA	chr10	96446411	96448410	*CYP2C19*	1557	1.45E-06

Promoter	HYPER in CCA	chr13	79168764	79170763	*NA*	NA	2.72E-06
Promoter	HYPER in CCA	chr5	16178847	16180846	*NA*	NA	0.000187349
Promoter	HYPER in CCA	chr12	53551870	53553869	*NA*	NA	1.30E-07
Promoter	HYPER in CCA	chr15	34782273	34784272	*HNRNPLP2*	NA	3.98E-05
Promoter	HYPER in CCA	chr19	1395967	1397966	*NA*	NA	1.51E-06
Promoter	HYPER in CCA	chr2	158112610	158114609	*GALNT5*	11227	7.43E-08
Promoter	HYPER in CCA	chr5	36301717	36303716	*RANBP3L*	202151	5.18E-08
Promoter	HYPER in CCA	chr2	95718422	95720421	*NA*	NA	2.00E-06
Promoter	HYPER in CCA	chr6	41515860	41517859	*NA*	101060264	4.02E-07
Promoter	HYPER in CCA	chr14	69401819	69403818	*BANF1P1*	NA	5.15E-09
Promoter	HYPER in CCA	chr21	44496554	44498553	*CBS*	875	9.41E-05
Promoter	HYPER in CCA	chr4	25622899	25624898	*NA*	NA	6.55E-07
Promoter	HYPER in CCA	chr5	135528323	135530322	*NA*	389332	1.69E-08
Promoter	HYPER in CCA	chr7	30590596	30592595	*GGCT*	79017	0.002388612
Promoter	HYPER in CCA	chr4	90756059	90758058	*NA*	644248	3.50E-07
Promoter	HYPER in CCA	chr8	23563612	23565611	*NKX2-6*	137814	2.86E-06
Promoter	HYPER in CCA	chr2	220298068	220300067	*SPEG*	10290;100996693	4.90E-08
Promoter	HYPER in CCA	chr12	123348382	123350381	*NA*	NA	1.58E-05
Promoter	HYPER in CCA	chr17	59540246	59542245	*NA*	NA	5.02E-07
Promoter	HYPER in CCA	chr11	57796902	57798901	*OR6Q1*	219952	1.79E-05
Promoter	HYPER in CCA	chr8	27558785	27560784	*MIR3622A;MIR3622B*	100500858;100500871	9.98E-06
Promoter	HYPER in CCA	chr5	140863241	140865240	*PCDHGC4*	56098	4.78E-07
Promoter	HYPER in CCA	chr20	56724460	56726459	*C20orf85*	128602	1.18E-07
Promoter	HYPER in CCA	chr7	131242477	131244476	*PODXL*	5420	1.38E-08
Promoter	HYPER in CCA	chr17	12875643	12877642	*RN7SL550P*	NA	6.91E-05
Promoter	HYPER in CCA	chr14	37125273	37127272	*PAX9*	5083	3.81E-05
Promoter	HYPER in CCA	chr2	132087931	132089930	*ARHGAP42P1*	NA	9.90E-06
Promoter	HYPER in CCA	chr22	50967986	50969985	*TYMP*	1890	0.000158165
Promoter	HYPER in CCA	chr6	52990445	52992444	*NA*	NA	4.82E-05
Promoter	HYPER in CCA	chr19	39522926	39524925	*FBXO27*	126433	1.94E-06
Promoter	HYPER in CCA	chr14	45380567	45382566	*NA*	101927418	2.45E-06
Promoter	HYPER in CCA	chr1	156356518	156358517	*NA*	NA	2.55E-05
Promoter	HYPER in CCA	chr17	16256471	16258470	*CENPV*	201161	8.71E-06
Promoter	HYPER in CCA	chr2	187713436	187715435	*ZSWIM2*	151112	2.70E-06

Promoter	HYPER in CCA	chr22	42527050	42529049	*NA*	NA	2.56E-09
Promoter	HYPER in CCA	chr7	12942526	12942 6525	*NA*	NA	3.73E-06
Promoter	HYPER in CCA	chr19	36288288	36290287	*NA*	644050	0.000244784
Promoter	HYPER in CCA	chr1	15437 8541	15438 0540	*NA*	101928101	2.67E-06
Promoter	HYPER in CCA	chr2	65214111	65216110	*SLC1A4*	6509	1.21E-05
Promoter	HYPER in CCA	chr17	33787070	33789069	*NA*	NA	2.05E-07
Promoter	HYPER in CCA	chr2	88427136	88429135	*FABP1*	2168	3.29E-08
Promoter	HYPER in CCA	chr19	15574883	15576882	*RASAL3*	64926	5.40E-08
Promoter	HYPER in CCA	chr10	10521 1103	10521 3102	*NA*	NA	1.20E-08
Promoter	HYPER in CCA	chr17	33823737	33825736	*NA*	NA	3.69E-07
Promoter	HYPER in CCA	chr2	17702 9945	17703 1944	*NA*	NA	2.36E-06
Promoter	HYPER in CCA	chr19	33360173	33362172	*SLC7A9*	11136	1.91E-08
Promoter	HYPER in CCA	chr22	41073254	41075253	*MCHR1*	2847	4.58E-09
Promoter	HYPER in CCA	chr3	12779 3153	12779 5152	*RUVBL1-AS1*	NA	1.73E-05
Promoter	HYPER in CCA	chr19	58543900	58545899	*ZSCAN1*	284312	3.95E-06
Promoter	HYPER in CCA	chr10	10289 8969	10290 0968	*NA*	NA	5.40E-06
Promoter	HYPER in CCA	chr17	37822734	37824733	*PNMT*	5409	1.11E-07
Promoter	HYPER in CCA	chr3	61724404	61726403	*NA*	NA	0.000340319
Promoter	HYPER in CCA	chr7	15358 2682	15358 4681	*DPP6*	1804	7.40E-06
Promoter	HYPER in CCA	chr5	43007146	43009145	*NA*	NA	4.24E-06
Promoter	HYPER in CCA	chr5	18052 7167	18052 9166	*FOXO1B*	NA	3.34E-06
Promoter	HYPER in CCA	chr4	54964190	54966189	*GSX2*	170825	1.21E-05
Promoter	HYPER in CCA	chr3	19407 1558	19407 3557	*CPN2*	1370	2.34E-09
Promoter	HYPER in CCA	chr11	67799864	67801863	*MIR4691*	100616403	1.04E-05
Promoter	HYPER in CCA	chr19	35628212	35630211	*FXYD1*	5348	1.50E-08
Promoter	HYPER in CCA	chr19	35628228	35630227	*NA*	NA	1.50E-08
Promoter	HYPER in CCA	chr3	12131 0466	12131 2465	*FBXO40*	51725	1.69E-07
Promoter	HYPER in CCA	chr7	39445446	39447445	*POU6F2-AS1*	100861520	4.23E-05
Promoter	HYPER in CCA	chr15	68123563	68125562	*NA*	NA	3.32E-06
Promoter	HYPER in CCA	chr17	41016439	41018438	*AOC4P*	90586	2.58E-07
Promoter	HYPER in CCA	chr20	30072081	30074080	*LINC00028*	140875	6.93E-08
Promoter	HYPER in CCA	chr2	24192 4990	24192 6989	*NA*	NA	8.60E-09
Promoter	HYPER in CCA	chr7	70595655	70597654	*WBSCR17*	64409	0.000160492
Promoter	HYPER in CCA	chr11	62476818	62478817	*BSCL2*	26580	6.50E-05

Promoter	HYPER in CCA	chr1	156609682	156611681	*BCAN*	63827	3.02E-06
Promoter	HYPER in CCA	chr1	150229182	150231181	*NA*	NA	6.23E-08
Promoter	HYPER in CCA	chr12	109552900	109554899	*ACACB*	32	1.71E-05
Promoter	HYPER in CCA	chr3	148939343	148941342	*CP*	1356	5.37E-06
Promoter	HYPER in CCA	chr22	36561726	36563725	*APOL3*	80833	6.96E-10
Promoter	HYPER in CCA	chr16	3236712	3238711	*NA*	NA	3.49E-05
Promoter	HYPER in CCA	chr7	27239226	27241225	*HOXA13*	3209	6.00E-07
Promoter	HYPER in CCA	chr8	54788710	54790709	*NA*	NA	1.92E-06
Promoter	HYPER in CCA	chr17	46799385	46801384	*PRAC1*	84366	1.32E-05
Promoter	HYPER in CCA	chr11	60622945	60624944	*PTGDR2*	11251	4.77E-08
Promoter	HYPER in CCA	chr12	54390070	54392069	*HOXC-AS2*	100874364	5.41E-07
Promoter	HYPER in CCA	chr15	54054901	54056900	*RNU6-449P*	NA	3.68E-06
Promoter	HYPER in CCA	chr15	54054576	54056575	*WDR72*	256764	3.68E-06
Promoter	HYPER in CCA	chr10	3107025	3109024	*PFKP*	5214	7.88E-07
Promoter	HYPER in CCA	chr2	132121232	132123231	*NA*	NA	1.77E-06
Promoter	HYPER in CCA	chr7	143132627	143134626	*TAS2R62P*	NA	1.19E-06
Promoter	HYPER in CCA	chr14	24803800	24805799	*ADCY4*	196883	9.23E-07
Promoter	HYPER in CCA	chr22	42526409	42528408	*CYP2D6*	1565;101929829	3.16E-09
Promoter	HYPER in CCA	chr1	178839688	178841687	*ANGPTL1*	9068	4.49E-05
Promoter	HYPER in CCA	chr11	116705333	116707332	*APOA1-AS*	NA	1.40E-08
Promoter	HYPER in CCA	chr19	6482069	6484068	*DENND1C*	79958	1.50E-06
Promoter	HYPER in CCA	chr17	46633124	46635123	*HOXB-AS2*	NA	2.02E-07
Promoter	HYPER in CCA	chr2	178968698	178970697	*CYCTP*	NA	8.81E-06
Promoter	HYPER in CCA	chr2	178968864	178970863	*NA*	NA	8.81E-06
Promoter	HYPER in CCA	chr9	104145302	104147301	*BAAT*	570	3.59E-09
Promoter	HYPER in CCA	chr17	40699732	40701731	*HSD17B1*	3292	3.79E-07
Promoter	HYPER in CCA	chr5	78364040	78366039	*BHMT2*	23743	3.40E-07
Promoter	HYPER in CCA	chr11	111384010	111386009	*C11orf88*	399949	3.62E-08
Promoter	HYPER in CCA	chr7	45960974	45962973	*IGFBP3*	3486	5.70E-07
Promoter	HYPER in CCA	chr7	27232568	27234567	*NA*	NA	2.04E-06
Promoter	HYPER in CCA	chr12	54412194	54414193	*NA*	NA	4.31E-06
Promoter	HYPER in CCA	chr7	27189723	27191722	*HOXA6*	3203	2.67E-06
Promoter	HYPER in CCA	chr14	101543748	101545747	*NA*	NA	7.14E-07
Promoter	HYPER in CCA	chr16	15700831	15702830	*NA*	NA	3.67E-05

Promoter	HYPER in CCA	chr14	69094663	69096662	*NA*	100996664	2.17E-06
Promoter	HYPER in CCA	chr12	54146642	54148641	*NA*	NA	4.17E-06
Promoter	HYPER in CCA	chr19	46798803	46800802	*HIF3A*	64344	9.53E-08
Promoter	HYPER in CCA	chr1	22105 2983	22105 4982	*HLA-AS1*	100873924	4.99E-08
Promoter	HYPER in CCA	chr21	36040188	36042187	*CLIC6*	54102	3.08E-07
Promoter	HYPER in CCA	chr7	10016 6254	10016 8253	*NA*	NA	2.72E-06
Promoter	HYPER in CCA	chr12	11436 8874	11437 0873	*NA*	NA	1.55E-06
Promoter	HYPER in CCA	chr17	43338980	43340979	*SPATA32*	124783	7.14E-08
Promoter	HYPER in CCA	chr17	4801213	4803212	*C17orf107*	100130311	5.83E-06
Promoter	HYPER in CCA	chr17	34308033	34310032	*CCL16*	6360	1.08E-07
Promoter	HYPER in CCA	chr19	45416004	45418003	*APOC1*	341	3.08E-09
Promoter	HYPER in CCA	chr11	69973903	69975902	*NA*	NA	0.000183623
Promoter	HYPER in CCA	chr8	10415 3204	10415 5203	*C8orf56*	NA	1.07E-07
Promoter	HYPER in CCA	chr8	13016187	13018186	*NA*	NA	2.12E-07
Promoter	HYPER in CCA	chr20	9495146	9497145	*NA*	101929329	6.17E-07
Promoter	HYPER in CCA	chr11	66044464	66046463	*NA*	NA	3.92E-05
Promoter	HYPER in CCA	chr2	10546 9142	10547 1141	*LINC01158*	100506421	2.43E-05
Promoter	HYPER in CCA	chr20	44517283	44519282	*CTSA*	5476	2.55E-08
Promoter	HYPER in CCA	chr9	12381 2055	12381 4054	*C5*	727	0.000105015
Promoter	HYPER in CCA	chr2	13674 3171	13674 5170	*DARS*	1615	5.43E-06
Promoter	HYPER in CCA	chr2	16292 8266	16293 0265	*NA*	NA	6.71E-07
Promoter	HYPER in CCA	chr7	10100 4601	10100 6600	*COL26A1*	136227	6.62E-08
Promoter	HYPER in CCA	chr12	85306895	85308894	*SLC6A15*	55117	1.62E-05
Promoter	HYPER in CCA	chr5	80689499	80691498	*ACOT12*	134526	1.40E-07
Promoter	HYPER in CCA	chr4	19096 0997	19096 2996	*AGGF1P1*	NA	3.61E-07
Promoter	HYPER in CCA	chr17	46659122	46661121	*MIR10A*	406902	9.50E-07
Promoter	HYPER in CCA	chr7	11456 0709	11456 2708	*MDFIC*	29969	1.86E-05
Promoter	HYPER in CCA	chr3	18643 3565	18643 5564	*KNG1*	3827	1.39E-08
Promoter	HYPER in CCA	chr2	44065505	44067504	*ABCG5*	64240	3.80E-09
Promoter	HYPER in CCA	chr22	24890543	24892542	*ADORA2A-AS1*	646023	1.23E-07
Promoter	HYPER in CCA	chr1	12586266	12588265	*NA*	NA	3.49E-06
Promoter	HYPER in CCA	chr4	22693037	22695036	*GBA3*	57733	2.25E-06
Promoter	HYPER in CCA	chr3	15414 7005	15414 9004	*GPR149*	344758	6.37E-07
Promoter	HYPER in CCA	chr7	14249 2549	14249 4548	*TRBJ2-1*	NA	9.08E-08

Promoter	HYPER in CCA	chr10	82048941	82050940	*MAT1A*	4143	2.18E-07
Promoter	HYPER in CCA	chr1	156610297	156612296	*NA*	NA	2.37E-07
Promoter	HYPER in CCA	chr1	26202487	26204486	*NA*	NA	1.07E-06
Promoter	HYPER in CCA	chr19	8426673	8428672	*ANGPTL4*	51129	4.09E-06
Promoter	HYPER in CCA	chr12	102873924	102875923	*IGF1*	3479	2.28E-07
Promoter	HYPER in CCA	chr2	44064603	44066602	*ABCG8*	64241	2.95E-09
Promoter	HYPER in CCA	chr8	59412296	59414295	*CYP7A1*	1581	1.72E-05
Promoter	HYPER in CCA	chr6	104259910	104279909	*NA*	NA	3.24E-07
Promoter	HYPER in CCA	chr2	176999840	177001839	*HOXD3*	3232;3233;401021	9.64E-06
Promoter	HYPER in CCA	chr20	19865665	19867664	*RIN2*	54453	3.04E-07
Promoter	HYPER in CCA	chr11	61596291	61598290	*FADS1*	3992;100302263	9.60E-08
Promoter	HYPER in CCA	chr14	37127507	37129506	*NA*	NA	8.74E-08
Promoter	HYPER in CCA	chr9	131681674	131683673	*PHYHD1*	254295	4.28E-10
Promoter	HYPER in CCA	chr6	26015107	26017106	*HIST1H1PS2*	NA	1.60E-07
Promoter	HYPER in CCA	chr3	184095433	184097432	*THPO*	7066	2.90E-08
Promoter	HYPER in CCA	chr16	56680660	56682659	*MT1CP*	NA	5.98E-09
Promoter	HYPER in CCA	chr16	56681293	56683292	*NA*	NA	5.98E-09
Promoter	HYPER in CCA	chr17	36887674	36889673	*RNA5SP440*	NA	6.20E-06
Promoter	HYPER in CCA	chr14	94918628	94920627	*SERPINA11*	256394	1.82E-06
Promoter	HYPER in CCA	chr2	99956666	99958665	*TXNDC9*	10190	2.56E-07
Promoter	HYPER in CCA	chr15	91425425	91427424	*FES*	2242	1.97E-08
Promoter	HYPER in CCA	chr6	160541321	160543320	*SLC22A1*	6580	2.54E-07
Promoter	HYPER in CCA	chr5	43017031	43019030	*NA*	NA	9.19E-08
Promoter	HYPER in CCA	chr17	46799030	46801029	*PRAC2*	100422978	5.90E-06
Promoter	HYPER in CCA	chr17	41042953	41044952	*RNU6-287P*	NA	1.83E-07
Promoter	HYPER in CCA	chr2	20864924	20866923	*GDF7*	151449	1.29E-06
Promoter	HYPER in CCA	chr3	47291617	47293616	*NA*	NA	3.09E-06
Promoter	HYPER in CCA	chr1	119869427	119871426	*NA*	NA	6.43E-07
Promoter	HYPER in CCA	chr1	119869299	119871298	*NA*	NA	6.43E-07
Promoter	HYPER in CCA	chr12	6664740	6666739	*IFFO1*	25900	2.07E-06
Promoter	HYPER in CCA	chr7	25989107	25991106	*MIR148A*	406940	6.17E-08
Promoter	HYPER in CCA	chr3	39195554	39197553	*CSRNP1*	64651	8.13E-07
Promoter	HYPER in CCA	chr17	6946743	6948742	*SLC16A11*	162515	2.45E-09
Promoter	HYPER in CCA	chr2	134325535	134327534	*NCKAP5*	344148	1.90E-07

Promoter	HYPER in CCA	chr1	31440584	31442583	*SNORD85*	692200	3.58E-09
Promoter	HYPER in CCA	chr12	47225692	47227691	*SLC38A4*	55089	7.83E-08
Promoter	HYPER in CCA	chr1	17105 8518	17106 0517	*FMO3*	2328	2.86E-08
Promoter	HYPER in CCA	chr17	37881248	37883247	*MIR4728*	100616132	6.85E-11
Promoter	HYPER in CCA	chr10	96696915	96698914	*CYP2C9*	1559	4.84E-10
Promoter	HYPER in CCA	chr3	12623 6117	12623 8116	*UROC1*	131669	3.29E-09
Promoter	HYPER in CCA	chr6	46759627	46761626	*MEP1A*	4224	5.19E-08
Promoter	HYPER in CCA	chr12	12424 5542	12424 7541	*DNAH10*	196385	1.03E-06
Promoter	HYPER in CCA	chr3	18648 9237	18649 1236	*RNU6-1105P*	NA	2.88E-08
Promoter	HYPER in CCA	chr4	69680211	69682210	*UGT2B10*	7365;101929773	3.76E-08
Promoter	HYPER in CCA	chr11	10145 3526	10145 5525	*NA*	NA	6.78E-08
Promoter	HYPER in CCA	chr1	65712402	65714401	*DNAJC6*	9829	1.23E-07
Promoter	HYPER in CCA	chr5	73832302	73834301	*NA*	NA	7.78E-07
Promoter	HYPER in CCA	chr16	72086991	72088990	*HP*	3240	8.84E-09
Promoter	HYPER in CCA	chr16	72087022	72089021	*HPR*	3250	8.84E-09
Promoter	HYPER in CCA	chr20	54985668	54987667	*CASS4*	57091	2.16E-08
Promoter	HYPER in CCA	chr14	85982779	85984778	*NA*	NA	9.82E-07
Promoter	HYPER in CCA	chr11	14925043	14927042	*CALCB*	797	1.29E-05
Promoter	HYPER in CCA	chr8	1918063	1920062	*KBTBD11-OT1*	NA	9.85E-07
Promoter	HYPER in CCA	chr7	27280664	27282663	*EVX1*	2128	2.08E-07
Promoter	HYPER in CCA	chr1	17388 6017	17388 8016	*SERPINC1*	462	1.11E-10
Promoter	HYPER in CCA	chr5	74658085	74660084	*NA*	NA	4.53E-07
Promoter	HYPER in CCA	chr17	68048070	68050069	*KCNJ16*	3773	9.23E-10
Promoter	HYPER in CCA	chr2	16988 7333	16988 9332	*ABCB11*	8647	1.11E-08
Promoter	HYPER in CCA	chr17	77996193	77998192	*NA*	NA	2.68E-09
Promoter	HYPER in CCA	chr6	38681617	38683616	*DNAH8*	1769	2.14E-09
Promoter	HYPER in CCA	chr15	83952967	83954966	*BNC1*	646	2.71E-08
Promoter	HYPER in CCA	chr12	66628903	66630902	*NA*	NA	0.000288332
Promoter	HYPER in CCA	chr16	51181650	51183649	*NA*	NA	3.46E-05
Promoter	HYPER in CCA	chr5	14992 2752	14992 4751	*NA*	NA	4.46E-07
Promoter	HYPER in CCA	chr19	11346678	11348677	*C19orf80*	55908	2.08E-08
Promoter	HYPER in CCA	chr19	35525738	35527737	*NA*	NA	2.93E-11
Promoter	HYPER in CCA	chr16	87969636	87971635	*CA5A*	763	7.81E-10
Promoter	HYPER in CCA	chr12	52415116	52417115	*NR4A1*	3164	2.36E-07

Promoter	HYPER in CCA	chr6	25930447	25932446	*SLC17A2*	10246	6.79E-08
Promoter	HYPER in CCA	chr5	82765784	82767783	*VCAN*	1462	1.35E-08
Promoter	HYPER in CCA	chr9	90338934	90340933	*CTSL*	1514	1.27E-07
Promoter	HYPER in CCA	chr3	42917134	42919133	*CYP8B1*	1582	1.74E-08
Promoter	HYPER in CCA	chr4	156774390	156776389	*TDO2*	6999	2.67E-08
Promoter	HYPER in CCA	chr14	57278401	57280400	*OTX2-AS1*	100309464	2.21E-06
Promoter	HYPER in CCA	chr11	914559	916558	*CHID1*	66005	1.84E-09
Promoter	HYPER in CCA	chr11	68611379	68613378	*CPT1A*	1374	7.59E-06
Promoter	HYPER in CCA	chr19	35629985	35631984	*NA*	NA	1.99E-09
Promoter	HYPER in CCA	chr14	100798627	100800626	*NA*	NA	2.31E-08
Promoter	HYPER in CCA	chr20	62365315	62367314	*LIME1*	54923	3.72E-09
Promoter	HYPER in CCA	chr1	230864126	230866125	*RN7SL467P*	NA	1.11E-07
Promoter	HYPER in CCA	chr1	170635022	170637021	*NA*	NA	9.60E-08
Promoter	HYPER in CCA	chr17	41362354	41364353	*TMEM106A*	113277	7.79E-06
Promoter	HYPER in CCA	chr9	104197606	104199605	*ALDOB*	229	5.26E-09
Promoter	HYPER in CCA	chr12	57827043	57829042	*INHBC*	3626	2.56E-10
Promoter	HYPER in CCA	chr5	179061286	179063285	*HNRNPH1*	3187	3.94E-10
Promoter	HYPER in CCA	chr21	31118994	31120993	*GRIK1-AS1*	642976	2.23E-06
Promoter	HYPER in CCA	chr21	45201504	45203503	*TMEM97P1*	NA	2.24E-08
Promoter	HYPER in CCA	chr3	186329212	186331211	*AHSG*	197	8.85E-11
Promoter	HYPER in CCA	chr11	118396687	118398686	*TTC36*	143941	4.12E-09
Promoter	HYPER in CCA	chr15	32607356	32609355	*NA*	NA	3.34E-06
Promoter	HYPER in CCA	chr16	71459868	71461867	*NA*	NA	1.08E-06
Promoter	HYPER in CCA	chr6	107230500	107232499	*MIR587*	693172	7.66E-08
Promoter	HYPER in CCA	chr17	53808983	53810982	*TMEM100*	55273	4.64E-09
Promoter	HYPER in CCA	chr17	30953257	30955256	*NA*	NA	1.97E-08
Promoter	HYPER in CCA	chr21	47574982	47576981	*FTCD*	10841	3.01E-09
Promoter	HYPER in CCA	chr11	77773407	77775406	*THRSP*	7069	1.30E-09
Promoter	HYPER in CCA	chr17	48987094	48989093	*NA*	NA	1.53E-07
Promoter	HYPER in CCA	chr6	160931657	160933656	*LPAL2*	80350	2.82E-07
Promoter	HYPER in CCA	chr6	151936515	151938514	*RNU6-813P*	NA	1.18E-06
Promoter	HYPER in CCA	chr1	244213085	244215084	*ZBTB18*	10472	1.74E-08
Promoter	HYPER in CCA	chr1	169429408	169431407	*CCDC181*	57821	2.24E-07
Promoter	HYPER in CCA	chr1	169429191	169431190	*NA*	101930556	2.24E-07

Promoter	HYPER in CCA	chr2	241806396	241808395	*AGXT*	189	2.48E-09
Promoter	HYPER in CCA	chr17	10631594	10633593	*NA*	101101775	5.34E-08
Promoter	HYPER in CCA	chr2	220968877	220970876	*NA*	NA	2.31E-07
Promoter	HYPER in CCA	chr1	165631425	165633424	*NA*	NA	1.83E-06
Promoter	HYPER in CCA	chr16	27225815	27227814	*NA*	NA	3.30E-09
Promoter	HYPER in CCA	chr5	78406102	78408101	*BHMT*	635	8.42E-09
Promoter	HYPER in CCA	chr3	110444368	110446367	*NA*	NA	6.59E-08
Promoter	HYPER in CCA	chr11	9448820	9450819	*SNORA23*	677808	7.21E-11
Promoter	HYPER in CCA	chr17	61507951	61509950	*NA*	NA	5.31E-06
Promoter	HYPER in CCA	chr14	60386558	60388557	*NA*	NA	3.53E-09
Promoter	HYPER in CCA	chr16	83980387	83982386	*OSGIN1*	29948	1.98E-09
Promoter	HYPER in CCA	chr10	30842913	30844912	*NA*	NA	6.07E-08
Promoter	HYPER in CCA	chr7	27280348	27282347	*NA*	NA	2.70E-08
Promoter	HYPER in CCA	chr2	172346432	172348431	*DAP3P2*	NA	3.67E-08
Promoter	HYPER in CCA	chr17	34326958	34328957	*NA*	NA	3.85E-07
Promoter	HYPER in CCA	chr19	45447743	45449742	*APOC2*	344	8.67E-09
Promoter	HYPER in CCA	chr10	74714037	74716036	*PLA2G12B*	84647	6.90E-10
Promoter	HYPER in CCA	chr1	11899574	11901573	*NPPA-AS1*	100379251	2.12E-07
Promoter	HYPER in CCA	chr1	53390596	53392595	*NA*	NA	1.56E-07
Promoter	HYPER in CCA	chr3	58522547	58524546	*ACOX2*	8309	2.15E-08
Promoter	HYPER in CCA	chr22	50643992	50645991	*NA*	NA	1.11E-09
Promoter	HYPER in CCA	chr2	237640525	237642524	*NA*	NA	2.41E-08
Promoter	HYPER in CCA	chr2	175189255	175191254	*NA*	285084	9.72E-08
Promoter	HYPER in CCA	chr2	37662252	37664251	*RNU6-1116P*	NA	4.93E-08
Promoter	HYPER in CCA	chr17	7018520	7020519	*ASGR2*	433	8.05E-09
Promoter	HYPER in CCA	chr4	57976052	57978051	*IGFBP7*	3490	8.51E-07
Promoter	HYPER in CCA	chr17	66951034	66953033	*ABCA8*	10351	4.10E-09
Promoter	HYPER in CCA	chr7	6055008	6057007	*NA*	NA	1.14E-08
Promoter	HYPER in CCA	chr20	62374542	62376541	*NA*	NA	2.19E-07
Promoter	HYPER in CCA	chr3	186488878	186490877	*NA*	NA	4.93E-09
Promoter	HYPER in CCA	chr1	78509333	78511332	*NA*	NA	6.72E-09
Promoter	HYPER in CCA	chr9	117090649	117092648	*ORM2*	5005	2.88E-08
Promoter	HYPER in CCA	chr2	173330251	173332250	*NA*	NA	1.17E-09
Promoter	HYPER in CCA	chr6	31893975	31895974	*CFB*	629	8.79E-09

Promoter	HYPER in CCA	chr6	31893975	31895974	*NA*	NA	8.79E-09
Promoter	HYPER in CCA	chr20	9493505	9495504	*LAMP5*	24141	5.37E-08
Promoter	HYPER in CCA	chr5	95581980	95583979	*NA*	NA	9.33E-08
Promoter	HYPER in CCA	chr16	14396324	14398323	*MIR193B*	574455	3.64E-10
Promoter	HYPER in CCA	chr6	135270761	135272760	*ALDH8A1*	64577	7.30E-09
Promoter	HYPER in CCA	chr10	96828755	96830754	*CYP2C8*	1558	2.33E-10
Promoter	HYPER in CCA	chr19	33794442	33796441	*NA*	NA	2.18E-09
Promoter	HYPER in CCA	chr12	1769047	1771046	*MIR3649*	100500816	1.26E-08
Promoter	HYPER in CCA	chr7	100239903	100241902	*TFR2*	7036	5.21E-10
Promoter	HYPER in CCA	chr17	33400894	33402893	*NA*	NA	3.47E-07
Promoter	HYPER in CCA	chr3	46537481	46539480	*RTP3*	83597	1.87E-08
Promoter	HYPER in CCA	chr1	53384594	53386593	*NA*	NA	4.68E-09
Promoter	HYPER in CCA	chr15	70371308	70373307	*MIR629*	693214	8.48E-11
Promoter	HYPER in CCA	chr1	243903624	243905623	*NA*	NA	5.64E-09
Promoter	HYPER in CCA	chr5	54804255	54806254	*MIR5687*	100847019	2.61E-07
Promoter	HYPER in CCA	chr4	74809542	74811541	*CXCL1P*	NA	9.62E-09
Promoter	HYPER in CCA	chr3	152555679	152557678	*NA*	NA	4.91E-08
Promoter	HYPER in CCA	chr1	156115657	156117656	*SEMA4A*	64218	7.47E-08
Promoter	HYPER in CCA	chr1	214203610	214205609	*NA*	NA	5.97E-10
Promoter	HYPER in CCA	chr5	135290224	135292223	*LECT2*	3950	3.84E-08
Promoter	HYPER in CCA	chr16	78539966	78541965	*NA*	NA	2.87E-08
Promoter	HYPER in CCA	chr1	36042831	36044830	*NA*	NA	3.30E-10
Promoter	HYPER in CCA	chr10	26725632	26727631	*APBB1IP*	54518	8.30E-09
Promoter	HYPER in CCA	chr2	240225657	240227656	*MIR4269*	100423043	9.15E-07
Promoter	HYPER in CCA	chr19	58220080	58222079	*ZNF154*	7710	7.81E-10
Promoter	HYPER in CCA	chr2	201541456	201543455	*AOX3P*	NA	1.19E-08
Promoter	HYPER in CCA	chr5	115152152	115154151	*CDO1*	1036	1.11E-11
Promoter	HYPER in CCA	chr2	201673817	201675816	*BZW1*	9689	1.54E-10
Promoter	HYPER in CCA	chr17	67137530	67139529	*ABCA6*	23460	2.68E-08
Promoter	HYPER in CCA	chr6	52608955	52610954	*GSTA7P*	NA	5.25E-07
Promoter	HYPER in CCA	chr17	28441039	28443038	*NSRP1*	84081	1.55E-05
Promoter	HYPER in CCA	chr18	12306168	12308167	*TUBB6*	84617	4.80E-08
Promoter	HYPER in CCA	chr16	2189304	2191303	*RAB26*	25837	1.57E-08
Promoter	HYPER in CCA	chr9	127710272	127712271	*GOLGA1*	2800	2.53E-07

Promoter	HYPER in CCA	chr2	55449916	55451915	*NA*	NA	8.89E-07
Promoter	HYPER in CCA	chr4	18401 5710	18401 7709	*NA*	NA	6.03E-07
Promoter	HYPER in CCA	chr18	21161586	21163585	*NA*	NA	1.75E-07
Promoter	HYPER in CCA	chr7	39649390	39651389	*NA*	NA	0.00048379
Promoter	HYPER in CCA	chr2	11136 6993	11136 8992	*NA*	NA	3.56E-10
Promoter	HYPER in CCA	chr13	34183604	34185603	*NA*	NA	1.84E-09
Promoter	HYPER in CCA	chr1	23549 8621	23550 0620	*NA*	NA	1.82E-08
Promoter	HYPER in CCA	chr15	64403269	64405268	*NA*	NA	1.42E-08
Promoter	HYPER in CCA	chr19	45115440	45117439	*IGSF23*	147710	5.29E-08
Promoter	HYPER in CCA	chr7	15679 7501	15679 9500	*MNX1-AS2*	NA	1.11E-08
Promoter	HYPER in CCA	chr18	21571237	21573236	*TTC39C*	125488	1.97E-10
Promoter	HYPER in CCA	chr15	81297874	81299873	*C15orf26*	161502	6.17E-07
Promoter	HYPER in CCA	chr10	75736 69	75756 68	*NA*	NA	8.13E-09
Promoter	HYPER in CCA	chr12	10949 1258	10949 3257	*USP30-AS1*	100131733	4.76E-09
Promoter	HYPER in CCA	chr2	47293461	47295460	*NA*	NA	4.02E-08
Promoter	HYPER in CCA	chr16	71610534	71612533	*TAT*	6898	3.93E-12
Promoter	HYPER in CCA	chr6	43276036	43278035	*CRIP3*	401262	2.29E-12
Promoter	HYPER in CCA	chr6	43276469	43278468	*NA*	NA	2.29E-12
Promoter	HYPER in CCA	chr3	17415 4863	17415 6862	*NAALADL2*	254827	4.62E-07
Promoter	HYPER in CCA	chr20	62368123	62370122	*NA*	NA	7.74E-13
Promoter	HYPER in CCA	chr6	13979 3693	13979 5692	*NA*	645434	1.08E-09
Promoter	HYPER in CCA	chr1	95584203	95586202	*NA*	NA	1.08E-08
Promoter	HYPER in CCA	chr7	25988524	25990523	*NA*	NA	7.38E-12
Promoter	HYPER in CCA	chr17	59477257	59486827	*TBX2*	6909	0.008602818
Promoter	HYPER in CCA	chr4	46920917	46996424	*GABRA4*	2557	0.004614406
Promoter	HYPER in CCA	chr5	15053 7667	15053 8023	*NA*	NA	0.005809526
Promoter	HYPER in CCA	chr4	13399 6466	13407 0271	*NA*	101927359	0.006205249
Promoter	HYPER in CCA	chr8	38001167	38008783	*STAR*	6770	0.00686242
Promoter	HYPER in CCA	chr1	14939 8877	14940 0540	*NA*	NA	0.001459877
Promoter	HYPER in CCA	chr12	10697 6685	10715 6581	*RFX4*	5992	0.007584399
Promoter	HYPER in CCA	chr16	20396 61	20442 76	*SYNGR3*	9143	0.004253187
Promoter	HYPER in CCA	chr1	20983 4709	20989 7470	*NA*	101930114;101930244	0.007144721
Promoter	HYPER in CCA	chr10	74034673	74035738	*NA*	NA	0.005013794
Promoter	HYPER in CCA	chr2	13127 8770	13128 5579	*CFC1B*	55997;653275	0.008755987

Promoter	HYPER in CCA	chr19	10203014	10213472	*ANGPTL6*	83854	0.003566703
Promoter	HYPER in CCA	chr11	11839 8187	11840 1912	*TTC36*	143941	0.007740886
Promoter	HYPER in CCA	chr1	11062 5310	11065 2341	*NA*	NA	0.003330228
Promoter	HYPER in CCA	chr19	38180 766	38210 089	*NA*	NA	0.002664647
Promoter	HYPER in CCA	chr19	45992 035	46005 768	*PPM1N*	147699	0.005960601
Promoter	HYPER in CCA	chr2	13150 1111	13151 3452	*NA*	NA	0.00541062
Promoter	HYPER in CCA	chr12	13050 9038	13052 9501	*NA*	NA	0.003322211
Promoter	HYPER in CCA	chr16	10257 61	10315 96	*NA*	64788	0.00403146
Promoter	HYPER in CCA	chr19	45988 547	46000 319	*RTN2*	6253	0.004405946
Promoter	HYPER in CCA	chr3	16880 1287	16938 1406	*MECOM*	2122	0.003435903
Promoter	HYPER in CCA	chr1	20805 7594	20808 4747	*CD34*	947	0.002821785
Promoter	HYPER in CCA	chr17	19398 698	19482 347	*SLC47A1*	55244	0.000900421
Promoter	HYPER in CCA	chr1	15982 4106	15983 2447	*VSIG8*	391123	0.008200685
Promoter	HYPER in CCA	chr5	74073 399	74162 776	*FAM169A*	26049	0.00296503
Promoter	HYPER in CCA	chr5	72416 119	72427 644	*TMEM171*	134285	0.003860016
Promoter	HYPER in CCA	chr8	14574 3376	14575 0557	*LRRC14*	9684	0.002313329
Promoter	HYPER in CCA	chr12	48577 366	48579 709	*C12orf68*	387856	0.006184324
Promoter	HYPER in CCA	chr18	43906 772	44043 103	*RNF165*	494470	0.005878761
Promoter	HYPER in CCA	chr4	11022 4191	11023 7291	*NA*	NA	0.005545825
Promoter	HYPER in CCA	chr12	21917 889	21928 515	*KCNJ8*	3764	0.007144721
Promoter	HYPER in CCA	chr12	10335 1464	10335 4294	*ASCL1*	429	0.006298063
Promoter	HYPER in CCA	chr16	23701 647	23724 821	*ERN2*	10595	0.003245753
Promoter	HYPER in CCA	chr19	39481 354	39523 425	*FBXO27*	126433	0.00677783
Promoter	HYPER in CCA	chr6	41470 182	41487 590	*NA*	NA	0.005291348
Promoter	HYPER in CCA	chr3	75589 200	75629 150	*NA*	NA	0.008755987
Promoter	HYPER in CCA	chr1	24809 9363	24810 0815	*NA*	NA	0.001570112
Promoter	HYPER in CCA	chr16	49311 828	49315 742	*CBLN1*	869	0.006847768
Promoter	HYPER in CCA	chr22	38203 912	38213 183	*GCAT*	23464	0.002646591
Promoter	HYPER in CCA	chr1	47681 962	47697 892	*TAL1*	6886	0.005406009
Promoter	HYPER in CCA	chr10	16555 742	16564 004	*C1QL3*	389941	0.006823109
Promoter	HYPER in CCA	chr21	36041 688	36090 525	*CLIC6*	54102	0.005547489
Promoter	HYPER in CCA	chr11	64058 774	64067 503	*KCNK4*	50801	0.005677903
Promoter	HYPER in CCA	chr17	46668 619	46671 323	*HOXB5*	3215	0.003095913
Promoter	HYPER in CCA	chr16	67197 288	67203 848	*HSF4*	3299	0.001929391

Promoter	HYPER in CCA	chr15	84721865	84748849	*NA*	NA	0.004743962
Promoter	HYPER in CCA	chr17	15164332	15169024	*NA*	NA	0.007685424
Promoter	HYPER in CCA	chr14	21756098	21819460	*RPGRIP1*	57096	0.001000313
Promoter	HYPER in CCA	chr12	49388932	49393092	*DDN*	23109	0.00072474
Promoter	HYPER in CCA	chr8	22545172	22550815	*EGR3*	1960	0.008605272
Promoter	HYPER in CCA	chr4	57975928	58071676	*IGFBP7-AS1*	255130	0.004874093
Promoter	HYPER in CCA	chr5	43014516	43067521	*NA*	648987	0.003498886
Promoter	HYPER in CCA	chr6	26501449	26510650	*BTN1A1*	696	0.004182322
Promoter	HYPER in CCA	chr7	92465797	92546501	*NA*	101927497	0.004655691
Promoter	HYPER in CCA	chr6	41604620	41621984	*MDFI*	4188	0.000814865
Promoter	HYPER in CCA	chr20	56793551	56803709	*ANKRD60*	140731	0.001100195
Promoter	HYPER in CCA	chr7	143076785	143077588	*NA*	NA	0.003791581
Promoter	HYPER in CCA	chr12	50260679	50298000	*FAIM2*	23017	0.004306029
Promoter	HYPER in CCA	chr7	113726382	114333827	*FOXP2*	93986	0.001062689
Promoter	HYPER in CCA	chr10	105036920	105050108	*INA*	9118	0.008612056
Promoter	HYPER in CCA	chr18	70535623	70548634	*NA*	100505797	0.003658954
Promoter	HYPER in CCA	chr17	37182968	37183363	*NA*	NA	9.92E-05
Promoter	HYPER in CCA	chr6	26183958	26184454	*HIST1H2BE*	8339;8343;8344;8346;8347	0.00446132
Promoter	HYPER in CCA	chr17	59537585	59540745	*NA*	NA	0.003566703
Promoter	HYPER in CCA	chr10	26727132	26856732	*APBB1IP*	54518	0.001914689
Promoter	HYPER in CCA	chr15	93349000	93351797	*NA*	NA	0.001714323
Promoter	HYPER in CCA	chr12	14656595	14721283	*PLBD1*	79887	0.007719905
Promoter	HYPER in CCA	chr6	708592	711405	*NA*	NA	0.00229249
Promoter	HYPER in CCA	chr20	44258165	44259835	*WFDC10A*	140832	0.001860082
Promoter	HYPER in CCA	chr9	14317084	14357907	*NA*	NA	0.005013794
Promoter	HYPER in CCA	chr10	105206543	105212660	*CALHM2*	51063	0.000373459
Promoter	HYPER in CCA	chr17	77774397	77776326	*NA*	NA	0.007259406
Promoter	HYPER in CCA	chr3	138666076	138672293	*C3orf72*	401089	0.008885066
Promoter	HYPER in CCA	chr15	78232253	78236924	*NA*	NA	0.003943244
Promoter	HYPER in CCA	chr6	29974360	29977733	*HLA-J*	3137	0.002427186
Promoter	HYPER in CCA	chr7	155174771	155189051	*NA*	NA	0.001195929
Promoter	HYPER in CCA	chr13	78493824	79191463	*RNF219-AS1*	100874222	0.004514523
Promoter	HYPER in CCA	chr1	151682909	151702070	*NA*	NA	0.004426946
Promoter	HYPER in CCA	chr1	151682909	151702281	*RIIAD1*	284485	0.004426946

Promoter	HYPER in CCA	chr14	102018558	102026768	*DIO3OS*	100302145	0.003907744
Promoter	HYPER in CCA	chr1	235093089	235105809	*NA*	NA	0.004331254
Promoter	HYPER in CCA	chr8	126010739	126034525	*SQLE*	6713	0.001062689
Promoter	HYPER in CCA	chr4	81104434	81111323	*NA*	NA	0.006725037
Promoter	HYPER in CCA	chr2	130724165	130738039	*RAB6C-AS1*	100131320	0.00201349
Promoter	HYPER in CCA	chr12	54144231	54145619	*NA*	102216268	0.00198579
Promoter	HYPER in CCA	chr2	145141648	145282147	*ZEB2*	9839	0.008771446
Promoter	HYPER in CCA	chr18	22641890	22932154	*ZNF521*	25925	0.002313329
Promoter	HYPER in CCA	chr5	139927251	139929163	*EIF4EBP3*	8637	0.004858689
Promoter	HYPER in CCA	chr8	131947655	131961911	*NA*	NA	0.002950098
Promoter	HYPER in CCA	chr3	125898908	125929012	*ALDH1L1-AS2*	100862662	0.001162659
Promoter	HYPER in CCA	chr12	54410894	54429145	*NA*	3222	0.005517512
Promoter	HYPER in CCA	chr12	75433857	75603648	*KCNC2*	3747	0.003340349
Promoter	HYPER in CCA	chr3	27757440	27764206	*EOMES*	8320	0.008978136
Promoter	HYPER in CCA	chr1	67218142	67244470	*TCTEX1D1*	200132	0.002396628
Promoter	HYPER in CCA	chr17	46698518	46703839	*HOXB9*	3219	0.007960883
Promoter	HYPER in CCA	chr9	19108373	19149288	*PLIN2*	123	0.003259664
Promoter	HYPER in CCA	chr19	50546453	50554319	*NA*	NA	0.003539244
Gene	HYPER in CCA	chr9	107543283	107690518	*ABCA1*	19	0.008271995
Gene	HYPER in CCA	chr6	5998232	6007200	*NRN1*	51299	0.007171856
Gene	HYPER in CCA	chr17	7942335	7952452	*ALOX15B*	247	0.003643677
Gene	HYPER in CCA	chr11	110447766	110583912	*ARHGAP20*	57569	0.002478367
Gene	HYPER in CCA	chr12	54332535	54340328	*HOXC13*	3229	0.007985018
Gene	HYPER in CCA	chr4	113434672	113437328	*NEUROG2*	63973	0.00783513
Gene	HYPER in CCA	chr19	8428173	8439257	*ANGPTL4*	51129	0.005474846
Gene	HYPER in CCA	chr19	9609354	9620755	*NA*	NA	0.005517512
Gene	HYPER in CCA	chr2	73143389	73162020	*EMX1*	2016	0.003668347
Gene	HYPER in CCA	chr6	137813336	137815531	*OLIG3*	167826	0.007144721
Gene	HYPER in CCA	chr2	162280843	162841792	*SLC4A10*	57282	0.004918263
Gene	HYPER in CCA	chr13	50069746	50103123	*PHF11*	51131	0.001349299
Gene	HYPER in CCA	chr19	15783567	15807984	*CYP4F12*	66002	0.00215972
Gene	HYPER in CCA	chr4	140187317	140201492	*MGARP*	84709	0.006511922
Gene	HYPER in CCA	chr12	54385522	54385631	*MIR196A2*	406973	0.003178282
Gene	HYPER in CCA	chr7	45951949	45961473	*IGFBP3*	3486	0.002621303

Gene	HYPER in CCA	chr10	119232726	119304579	*EMX2OS*	196047	0.007685424
Gene	HYPER in CCA	chr6	117586721	117594728	*VGLL2*	245806	0.006419517
Gene	HYPER in CCA	chr14	38723308	38725574	*CLEC14A*	161198	0.008473009
Gene	HYPER in CCA	chr10	101286107	101290934	*NA*	101927324	0.00815101
Gene	HYPER in CCA	chr15	41795836	41806085	*LTK*	4058	0.004840385
Gene	HYPER in CCA	chr12	56864736	56882198	*GLS2*	27165	0.007733554
Gene	HYPER in CCA	chr22	29876219	29887379	*NEFH*	4744	0.006390467
Gene	HYPER in CCA	chr16	57125125	57126215	*NA*	NA	0.001178088
Gene	HYPER in CCA	chr3	113251143	113348425	*SIDT1*	54847	0.001375761
Gene	HYPER in CCA	chr4	42112955	42154895	*BEND4*	389206	0.009056708
Gene	HYPER in CCA	chr17	56234389	56235161	*MSX2P1*	55545	0.005254942
Gene	HYPER in CCA	chr17	10602332	10633633	*TMEM220*	388335	0.00278238
Gene	HYPER in CCA	chr9	97365415	97402531	*FBP1*	2203	0.001385431
Gene	HYPER in CCA	chr16	2317788	2317881	*NA*	NA	0.000741742
Gene	HYPER in CCA	chr18	10125337	10144403	*NA*	NA	0.001953265
Gene	HYPER in CCA	chr7	103085654	103154454	*NA*	101927870	0.00895034
Gene	HYPER in CCA	chr12	49687035	49692465	*PRPH*	5630	0.007938272
Gene	HYPER in CCA	chr10	102989351	103029905	*LBX1-AS1*	NA	0.001937465
Gene	HYPER in CCA	chr9	129376722	129463311	*LMX1B*	4010	0.006044193
Gene	HYPER in CCA	chr6	100054606	100063454	*PRDM13*	59336	0.007938272
Gene	HYPER in CCA	chr12	54410715	54449813	*HOXC4*	3221	0.004695354
Gene	HYPER in CCA	chr1	234348352	234350834	*NA*	NA	0.002041324
Gene	HYPER in CCA	chr2	177494317	177502659	*LINC01116*	375295	0.00146551
Gene	HYPER in CCA	chr6	27858093	27860884	*HIST1H3J*	8350;8351;8352;8353;8354;8355;8356;8357;8358;8968	0.002929356
Gene	HYPER in CCA	chr12	20514666	20523196	*NA*	NA	0.003907744
Gene	HYPER in CCA	chr6	142379467	142409936	*NMBR*	4829	0.008201216
Gene	HYPER in CCA	chr1	181143620	181151344	*NA*	101928973	0.000937583
Gene	HYPER in CCA	chr6	44041650	44045689	*NA*	101929683	0.000681207
Gene	HYPER in CCA	chr1	36038971	36060929	*TFAP2E*	339488	0.000647186
Gene	HYPER in CCA	chr17	59529765	59562471	*TBX4*	9496	0.002600584
Gene	HYPER in CCA	chr5	72509774	72590761	*NA*	NA	0.001906047
Gene	HYPER in CCA	chr17	35218935	35293960	*NA*	NA	0.004769858
Gene	HYPER in CCA	chr17	46656992	46659621	*MIR10A*	406902	0.008623069
Gene	HYPER in CCA	chr15	83847934	84108197	*NA*	NA	0.001886694

Gene	HYPER in CCA	chr18	44746293	44775554	*SKOR2*	652991	0.004245835
Gene	HYPER in CCA	chr3	133464800	133497850	*TF*	7018	0.003414015
Gene	HYPER in CCA	chr1	170631869	170708560	*PRRX1*	5396	0.003539182
Gene	HYPER in CCA	chr4	175015811	175141549	*NA*	101928509	0.009006597
Gene	HYPER in CCA	chr10	63166401	63213208	*TMEM26*	219623	0.001602015
Gene	HYPER in CCA	chr2	172967734	172974710	*NA*	NA	0.006357947
Gene	HYPER in CCA	chr1	151300425	151300905	*NA*	NA	0.002929356
Gene	HYPER in CCA	chr2	130737235	130740311	*RAB6C*	84084;150786	0.001978906
Gene	HYPER in CCA	chr1	156213206	156217881	*PAQR6*	79957	0.005849921
Gene	HYPER in CCA	chr1	36035414	36043330	*NA*	NA	0.001188659
Gene	HYPER in CCA	chr17	35297346	35300755	*NA*	NA	0.004883386
Gene	HYPER in CCA	chr10	8092413	8095447	*GATA3-AS1*	399717	0.008628413
Gene	HYPER in CCA	chr4	1396720	1400119	*NKX1-1*	NA	0.008978136
Gene	HYPER in CCA	chr17	48046334	48052321	*DLX4*	1748	0.002965248
Gene	HYPER in CCA	chr17	43325292	43345997	*MAP3K14-AS1*	100133991	0.000299158
Gene	HYPER in CCA	chr8	32028898	32145082	*NRG1-IT2*	NA	0.002687934
Gene	HYPER in CCA	chr3	157154578	157161417	*PTX3*	5806	0.007264381
Gene	HYPER in CCA	chr7	19152097	19153894	*NA*	NA	0.004840385
Gene	HYPER in CCA	chr8	104495626	104513904	*NA*	NA	0.005056397
Gene	HYPER in CCA	chr6	19690056	19753344	*NA*	NA	0.00578599
Gene	HYPER in CCA	chr17	79880775	79882387	*NA*	NA	0.006996814
Gene	HYPER in CCA	chr6	3224495	3231964	*TUBB2B*	347733	0.004608232
Gene	HYPER in CCA	chr15	91426925	91439006	*FES*	2242	0.000342636
Gene	HYPER in CCA	chr17	46684594	46710934	*HOXB7*	3217	0.008227628
Gene	HYPER in CCA	chr14	36942412	36988726	*NA*	NA	0.00766202
Gene	HYPER in CCA	chr12	54379629	54428672	*NA*	NA	0.005602634
Gene	HYPER in CCA	chr18	52889562	53332018	*TCF4*	6925	0.003762244
Gene	HYPER in CCA	chr1	161274525	161279762	*MPZ*	4359	0.005265829
Gene	HYPER in CCA	chr20	54987168	55034396	*CASS4*	57091	0.002179346
Gene	HYPER in CCA	chr15	83924655	83953466	*BNC1*	646	0.006800271
Gene	HYPER in CCA	chr7	77045990	77054760	*NA*	101927243	0.001761471
Gene	HYPER in CCA	chr18	30252634	30353025	*KLHL14*	57565	0.008944369
Gene	HYPER in CCA	chr1	204159469	204165614	*KISS1*	3814	0.003474815
Gene	HYPER in CCA	chr4	145564074	145582509	*HHIP-AS1*	646576	0.007814097

Gene	HYPER in CCA	chr17	35294084	35301917	*LHX1*	3975	0.008271995
Gene	HYPER in CCA	chr2	101768122	101771872	*NA*	100506286	0.00213078
Gene	HYPER in CCA	chr20	44517264	44519926	*NEURL2*	140825	0.000442783
Gene	HYPER in CCA	chr18	904944	912173	*ADCYAP1*	116	0.004690004
Gene	HYPER in CCA	chr2	95691422	95719737	*MAL*	4118	0.006701259
Gene	HYPER in CCA	chr19	50553846	50570050	*NA*	400710	0.002482354
Gene	HYPER in CCA	chr7	35242042	35293758	*TBX20*	57057	0.002832472
Gene	HYPER in CCA	chr3	237441	239024	*CHL1-AS2*	NA	0.005227154
Gene	HYPER in CCA	chr6	26251879	26252303	*HIST1H2BH*	8345	0.001599073
Gene	HYPER in CCA	chr17	37824234	37826728	*PNMT*	5409	0.002390713
Gene	HYPER in CCA	chr3	139236276	139258671	*RBP1*	5947	0.00244766
Gene	HYPER in CCA	chr9	72701	88826	*NA*	NA	0.008063851
Gene	HYPER in CCA	chr7	129906667	129929638	*CPA2*	1358	0.002062244
Gene	HYPER in CCA	chr8	77403435	77595513	*ZFHX4-AS1*	100192378	0.00511771
Gene	HYPER in CCA	chr6	27782822	27783267	*HIST1H2BM*	8342	0.000576407
Gene	HYPER in CCA	chr18	43608272	43609795	*NA*	NA	0.001848735
Gene	HYPER in CCA	chr5	3596168	3601517	*IRX1*	79192	0.008907108
Gene	HYPER in CCA	chr2	68511303	68547183	*CNRIP1*	25927	0.004667463
Gene	HYPER in CCA	chr19	18893583	18902123	*COMP*	1311	0.003095913
Gene	HYPER in CCA	chr18	894436	907681	*NA*	NA	0.005775471
Gene	HYPER in CCA	chr10	118918167	118928570	*NA*	NA	0.006526978
Gene	HYPER in CCA	chr16	56703726	56705041	*MT1H*	4496	0.003027373
Gene	HYPER in CCA	chr7	87031013	87109751	*ABCB4*	5244	0.002333956
Gene	HYPER in CCA	chr20	25121425	25129894	*NA*	284798	0.000333956
Gene	HYPER in CCA	chr2	177001340	177037830	*HOXD3*	3232;3233;401021	0.007054155
Gene	HYPER in CCA	chr14	102027688	102029789	*DIO3*	1735	0.007893659
Gene	HYPER in CCA	chr6	99282580	99286660	*POU3F2*	5454	0.005758626
Gene	HYPER in CCA	chr19	56728537	56729146	*NA*	NA	0.006908905
Gene	HYPER in CCA	chr2	160628362	160761221	*LY75-CD302*	4065;9936;100526664	0.005758626
Gene	HYPER in CCA	chr1	209848765	209849733	*G0S2*	50486	0.005881545
Gene	HYPER in CCA	chr8	49464575	49469001	*NA*	NA	0.007938272
Gene	HYPER in CCA	chr12	54348618	54352740	*HOXC12*	3228	0.002636556
Gene	HYPER in CCA	chr2	182321929	182400914	*ITGA4*	3676	0.00212893
Gene	HYPER in CCA	chr11	63304281	63313934	*RARRES3*	5920	0.008137687

Gene	HYPER in CCA	chr8	24770525	24776607	*NEFM*	4741	0.002060306
Gene	HYPER in CCA	chr17	7342825	7349285	*NA*	NA	0.000885656
Gene	HYPER in CCA	chr18	56934267	56941318	*RAX*	30062	0.005935655
Gene	HYPER in CCA	chr19	10396477	10399695	*NA*	NA	0.003126994
Gene	HYPER in CCA	chr1	147789799	147790129	*NA*	NA	0.000412003
Gene	HYPER in CCA	chr3	52232102	52248343	*ALAS1*	211	0.000898004
Gene	HYPER in CCA	chr4	81105033	81125483	*PRDM8*	56978	0.006381518
Gene	HYPER in CCA	chr8	67858736	67874825	*TCF24*	100129654	0.005778315
Gene	HYPER in CCA	chr4	113436541	113468037	*NA*	NA	0.007347099
Gene	HYPER in CCA	chr17	66195062	66195737	*NA*	440461	0.000977127
Gene	HYPER in CCA	chr12	54384408	54424607	*HOXC6*	3223	0.005005111
Gene	HYPER in CCA	chr10	53990502	54073888	*PRKG1-AS1*	NA	0.001583689
Gene	HYPER in CCA	chr6	10393419	10419892	*TFAP2A*	7020	0.003265831
Gene	HYPER in CCA	chr17	46626232	46682274	*HOXB3*	3213	0.001809161
Gene	HYPER in CCA	chr10	45495923	45500774	*ZNF22*	7570	0.002737124
Gene	HYPER in CCA	chr10	21802407	21814611	*SKIDA1*	387640	0.003775465
Gene	HYPER in CCA	chr17	32582304	32584222	*CCL2*	6347	0.007210924
Gene	HYPER in CCA	chr6	108487262	108510013	*NR2E1*	7101	0.001705203
Gene	HYPER in CCA	chr22	46271879	46283628	*NA*	NA	0.00188509
Gene	HYPER in CCA	chr2	207139387	207179148	*ZDBF2*	57683	0.001515214
Gene	HYPER in CCA	chr8	122624356	122653630	*HAS2*	3037	0.004712957
Gene	HYPER in CCA	chr11	59436785	59443514	*NA*	NA	0.008709729
Gene	HYPER in CCA	chr5	2745959	2752969	*IRX2*	153572	0.006080176
Gene	HYPER in CCA	chr17	46626992	46683776	*HOXB-AS3*	404266	0.001779029
Gene	HYPER in CCA	chr4	41746099	41750987	*PHOX2B*	8929	0.006323107
Gene	HYPER in CCA	chr20	19738352	19790319	*NA*	NA	0.007366312
Gene	HYPER in CCA	chr17	19463424	19501235	*NA*	NA	0.001051085
Gene	HYPER in CCA	chr10	8095567	8117161	*GATA3*	2625	0.006275367
Gene	HYPER in CCA	chr14	24787555	24804299	*ADCY4*	196883	0.00122922
Gene	HYPER in CCA	chr1	165513244	165533198	*LRRC52*	440699	0.001464713
Gene	HYPER in CCA	chr8	104145191	104153703	*C8orf56*	NA	0.001553327
Gene	HYPER in CCA	chr11	65779312	65780976	*CST6*	1474	0.000381509
Gene	HYPER in CCA	chr11	31806340	31839509	*PAX6*	5080	0.002438533
Gene	HYPER in CCA	chr4	122685740	122687962	*NA*	NA	0.005481202

Gene	HYPER in CCA	chr16	31227283	31228680	*PYDC1*	260434	0.001793494
Gene	HYPER in CCA	chr2	12778 2787	12778 7262	*NA*	NA	0.002514211
Gene	HYPER in CCA	chr13	28536274	28545276	*CDX2*	1045	0.003711876
Gene	HYPER in CCA	chr1	11637 8998	11638 6538	*NHLH2*	4808	0.004614406
Gene	HYPER in CCA	chr1	95628775	95699538	*NA*	101928118	0.001597322
Gene	HYPER in CCA	chr2	98963458	98967603	*NA*	NA	0.008354365
Gene	HYPER in CCA	chr3	15781 4948	15782 4292	*SHOX2*	6474	0.003512478
Gene	HYPER in CCA	chr22	50986462	50989451	*KLHDC7B*	113730	0.000320534
Gene	HYPER in CCA	chr11	57093077	57095432	*NA*	NA	0.002208902
Gene	HYPER in CCA	chr9	88581 30	88622 55	*NA*	NA	0.006574535
Gene	HYPER in CCA	chr2	16062 8362	16076 1260	*LY75*	4065;9936;100526664	0.006095376
Gene	HYPER in CCA	chr14	61107448	61109307	*NA*	NA	0.008905533
Gene	HYPER in CCA	chr7	27145803	27192200	*HOXA3*	3200	0.00409291
Gene	HYPER in CCA	chr5	14056 0980	14056 5793	*PCDHB16*	57717	0.006140478
Gene	HYPER in CCA	chr17	46800530	46802819	*PRAC2*	100422978	0.005554919
Gene	HYPER in CCA	chr11	88237744	88257222	*GRM5-AS1*	100873989	0.007461992
Gene	HYPER in CCA	chr14	62570096	62583893	*NA*	NA	0.006976736
Gene	HYPER in CCA	chr16	28895 69	28927 45	*PRSS30P*	124221	0.002419257
Gene	HYPER in CCA	chr6	10873456	10882174	*GCM2*	9247	0.000417189
Gene	HYPER in CCA	chr10	95351444	95361501	*RBP4*	5950	0.002664075
Gene	HYPER in CCA	chr2	17701 5950	17701 7954	*HOXD4*	3233	0.005342113
Gene	HYPER in CCA	chr19	79810 30	79839 82	*TGFBR3L*	100507588	0.005602634
Gene	HYPER in CCA	chr2	89065324	89106126	*ANKRD36BP2*	645784	0.001477656
Gene	HYPER in CCA	chr16	56126899	56225006	*NA*	283856	0.004733121
Gene	HYPER in CCA	chr1	20330 9756	20332 0617	*FMOD*	2331	0.000751995
Gene	HYPER in CCA	chr10	11842 9614	11843 2250	*NA*	NA	0.008060518
Gene	HYPER in CCA	chr12	53183469	53189901	*KRT3*	3850	0.004253187
Gene	HYPER in CCA	chr14	57284288	57360428	*NA*	NA	0.000583836
Gene	HYPER in CCA	chr7	96584453	96643377	*DLX6-AS1*	285987	0.003968953
Gene	HYPER in CCA	chr3	13748 3579	13748 4396	*SOX14*	8403	0.005202684
Gene	HYPER in CCA	chr3	19420 8183	19423 9008	*LINC00884*	401106	0.000403621
Gene	HYPER in CCA	chr2	22306 4607	22316 3715	*PAX3*	5077	0.001500622
Gene	HYPER in CCA	chr17	48067369	48072588	*DLX3*	1747	0.005041259
Gene	HYPER in CCA	chr8	23564654	23647000	*NA*	NA	0.002658432

Gene	HYPER in CCA	chr13	108903588	108960832	*TNFSF13B*	10673	0.000267925
Gene	HYPER in CCA	chr4	135476 99	135494 25	*LINC01096*	NA	0.008261431
Gene	HYPER in CCA	chr15	101417919	101456831	*ALDH1A3*	220	0.002834459
Gene	HYPER in CCA	chr1	110602616	110613322	*ALX3*	257	0.000899885
Gene	HYPER in CCA	chr15	48938148	48944213	*NA*	NA	0.001937465
Gene	HYPER in CCA	chr17	16586752	16587541	*RNASEH1P2*	246243	0.001770187
Gene	HYPER in CCA	chr2	71127720	71160576	*VAX2*	25806	0.000728319
Gene	HYPER in CCA	chr1	91177096	91182794	*BARHL2*	343472	0.001794246
Gene	HYPER in CCA	chr2	7561392	7590385	*NA*	100506274	0.000375876
Gene	HYPER in CCA	chr10	99079022	99081672	*FRAT1*	10023	0.00025214
Gene	HYPER in CCA	chr1	53068044	53074723	*GPX7*	2882	0.003259664
Gene	HYPER in CCA	chr16	77467279	77478233	*NA*	NA	0.009021353
Gene	HYPER in CCA	chr7	150035408	150038763	*RARRES2*	5919	0.004758166
Gene	HYPER in CCA	chr16	31579707	31580796	*YBX3P1*	440359	0.001553327
Gene	HYPER in CCA	chr10	63212397	63241714	*NA*	101928781	0.001978906
Gene	HYPER in CCA	chr4	85413140	85419603	*NKX6-1*	4825	0.003057497
Gene	HYPER in CCA	chr14	60386141	60387057	*NA*	NA	0.000497462
Gene	HYPER in CCA	chr17	41831099	41836156	*SOST*	50964	0.001670905
Gene	HYPER in CCA	chr10	23481256	23483181	*PTF1A*	256297	0.007783658
Gene	HYPER in CCA	chr3	129693148	129696781	*TRH*	7200	0.003865065
Gene	HYPER in CCA	chr16	2285690	2286914	*NA*	NA	0.000602858
Gene	HYPER in CCA	chr12	54387594	54390569	*HOXC-AS2*	100874364	0.004194386
Gene	HYPER in CCA	chr19	33790840	33792074	*NA*	NA	0.008722993
Gene	HYPER in CCA	chr18	30349758	30354376	*NA*	NA	0.003849019
Gene	HYPER in CCA	chr10	119301955	119309056	*EMX2*	2018	0.00453211
Gene	HYPER in CCA	chr1	197881037	197904608	*LHX9*	56956	0.004426946
Gene	HYPER in CCA	chr2	182547840	182550434	*NA*	NA	0.003666388
Gene	HYPER in CCA	chr5	134363425	134370503	*PITX1*	5307	0.000563102
Gene	HYPER in CCA	chr7	87905744	87936206	*STEAP4*	79689	0.000338607
Gene	HYPER in CCA	chr7	19758933	19813221	*TMEM196*	256130	0.001948944
Gene	HYPER in CCA	chr15	76629065	76634817	*ISL2*	64843	0.003979816
Gene	HYPER in CCA	chr3	169511216	169530774	*LRRC34*	151827	0.000669972
Gene	HYPER in CCA	chr15	101402129	101425534	*NA*	NA	0.003184697
Gene	HYPER in CCA	chr17	46713285	46724385	*NA*	NA	0.005677903

Gene	HYPER in CCA	chr8	145698795	145701718	*FOXH1*	8928	0.003849019
Gene	HYPER in CCA	chr13	112721913	112726020	*SOX1*	6656	0.003895839
Gene	HYPER in CCA	chr12	63539014	63544722	*AVPR1A*	552	0.000770783
Gene	HYPER in CCA	chr2	5832799	5841516	*SOX11*	6664	0.0050615
Gene	HYPER in CCA	chr10	126085872	126107545	*OAT*	4942	0.001693422
Gene	HYPER in CCA	chr1	19609052	19615744	*AKR7A3*	22977	0.005384824
Gene	HYPER in CCA	chr7	100845043	100846807	*DGAT2L7P*	NA	0.005960601
Gene	HYPER in CCA	chr2	107099728	107103848	*NA*	NA	0.004304111
Gene	HYPER in CCA	chr10	91589267	91600618	*LINC00865*	643529	0.004041011
Gene	HYPER in CCA	chr10	118888032	118897812	*VAX1*	11023	0.004561709
Gene	HYPER in CCA	chr18	902767	906668	*NA*	NA	0.004187602
Gene	HYPER in CCA	chr7	156786745	156803345	*MNX1*	3110	0.000468979
Gene	HYPER in CCA	chr17	42081914	42086431	*NAGS*	162417	0.005474846
Gene	HYPER in CCA	chr4	54965690	54968672	*GSX2*	170825	0.006597726
Gene	HYPER in CCA	chr7	27185015	27190222	*HOXA6*	3203	0.005788917
Gene	HYPER in CCA	chr2	74740590	74744274	*TLX2*	3196	0.00557714
Gene	HYPER in CCA	chr2	234263220	234301045	*NA*	NA	0.000279283
Gene	HYPER in CCA	chr8	65486863	65494445	*NA*	401463	0.002658432
Gene	HYPER in CCA	chr7	48026745	48068716	*SUN3*	256979	0.002998638
Gene	HYPER in CCA	chr8	145747761	145752416	*LRRC24*	441381	0.000265344
Gene	HYPER in CCA	chr11	101322295	101743293	*TRPC6*	7225	0.000602858
Gene	HYPER in CCA	chr17	46802125	46806540	*HOXB13*	10481	0.002350683
Gene	HYPER in CCA	chr6	1610681	1614127	*FOXC1*	2296	0.007166659
Gene	HYPER in CCA	chr7	79082198	79100524	*MAGI2-AS3*	100505881	0.004847813
Gene	HYPER in CCA	chr7	27224137	27228912	*HOXA11-AS*	221883	0.00201349
Gene	HYPER in CCA	chr2	105469743	105542510	*NA*	NA	0.004005581
Gene	HYPER in CCA	chr17	46671639	46682354	*HOXB6*	3216	0.001671945
Gene	HYPER in CCA	chr2	127781828	127783299	*NA*	NA	0.002043396
Gene	HYPER in CCA	chr1	149400063	149429348	*NA*	NA	9.42E-06
Gene	HYPER in CCA	chr2	71004442	71017775	*FIGLA*	344018	0.002530078
Gene	HYPER in CCA	chr19	49570675	49576198	*KCNA7*	3743	0.000550722
Gene	HYPER in CCA	chr6	29795162	29796141	*HCG4P8*	NA	0.000133125
Gene	HYPER in CCA	chr15	62455734	62457482	*C2CD4B*	388125	0.001068322
Gene	HYPER in CCA	chr3	193723226	193788759	*NA*	285389;100505902	9.00E-05

Gene	HYPER in CCA	chr12	57610578	57620232	*NXPH4*	11247	0.001095339
Gene	HYPER in CCA	chr5	134869991	134871639	*NEUROG1*	4762	0.00553332
Gene	HYPER in CCA	chr18	14728271	14852737	*ANKRD30B*	374860	0.002720146
Gene	HYPER in CCA	chr3	138663066	138665982	*FOXL2*	668	0.005099126
Gene	HYPER in CCA	chr15	55831088	55881145	*PYGO1*	26108	0.00146086
Gene	HYPER in CCA	chr19	58193337	58228669	*ZNF551*	90233	0.000258387
Gene	HYPER in CCA	chr5	145718587	145720083	*POU4F3*	5459	0.002434551
Gene	HYPER in CCA	chr5	148206156	148208196	*ADRB2*	154	0.002929356
Gene	HYPER in CCA	chr5	58335588	58359330	*NA*	NA	0.002450587
Gene	HYPER in CCA	chr1	47691469	47696422	*NA*	101930541	0.00072674
Gene	HYPER in CCA	chr11	122848278	122852428	*BSX*	390259	0.003174603
Gene	HYPER in CCA	chr13	88324870	88331871	*SLITRK5*	26050	0.003192625
Gene	HYPER in CCA	chr10	8093504	8095047	*NA*	NA	0.002980238
Gene	HYPER in CCA	chr2	223162866	223169936	*CCDC140*	151278	0.001801114
Gene	HYPER in CCA	chr3	194014254	194030592	*LINC00887*	NA	0.003666388
Gene	HYPER in CCA	chr7	96649704	96654409	*DLX5*	1749	0.008601497
Gene	HYPER in CCA	chr4	111516671	111536614	*NA*	NA	0.007474873
Gene	HYPER in CCA	chr17	1173853	1174754	*BHLHA9*	727857	0.000591567
Gene	HYPER in CCA	chr15	29033389	29037148	*NA*	100289656	0.001162659
Gene	HYPER in CCA	chr12	45408455	45444882	*DBX2*	440097	0.002405754
Gene	HYPER in CCA	chr12	85673885	85695562	*ALX1*	8092	0.00513866
Gene	HYPER in CCA	chr9	1162377	1184177	*FOXD4*	2298	0.00025214
Gene	HYPER in CCA	chr2	105481955	105489053	*LINC01159*	NA	0.004714318
Gene	HYPER in CCA	chr5	50678921	50690564	*ISL1*	3670	0.006344316
Gene	HYPER in CCA	chr7	27168588	27192180	*NA*	NA	0.002719498
Gene	HYPER in CCA	chr13	21512703	21523738	*HNRNPA1P30*	101930748	0.000181229
Gene	HYPER in CCA	chr4	111538579	111563279	*PITX2*	5308	0.005053821
Gene	HYPER in CCA	chr6	29973898	29974893	*HCG4P3*	NA	0.003539182
Gene	HYPER in CCA	chr17	46114527	46114613	*MIR152*	406943	0.003717667
Gene	HYPER in CCA	chr11	105480721	105852819	*GRIA4*	2893	0.003517462
Gene	HYPER in CCA	chr19	35771619	35776046	*HAMP*	57817	0.000159702
Gene	HYPER in CCA	chr1	113550876	113589677	*NA*	NA	0.000628109
Gene	HYPER in CCA	chr5	134374528	134375737	*NA*	101927953	0.003318785
Gene	HYPER in CCA	chr10	8094205	8095412	*NA*	399717	0.004317015

Gene	HYPER in CCA	chr12	54356092	54368740	*HOTAIR*	100124700	0.001680787
Gene	HYPER in CCA	chr11	20177701	20182159	*DBX1*	120237	0.002350751
Gene	HYPER in CCA	chr17	33791268	33864880	*SLFN12L*	100506736	0.000669972
Gene	HYPER in CCA	chr7	27169596	27195542	*HOXA-AS3*	100133311	0.002438533
Gene	HYPER in CCA	chr4	75230860	75254468	*EREG*	2069	0.005303546
Gene	HYPER in CCA	chr2	17294 9468	17295 4405	*DLX1*	1745	0.006951963
Gene	HYPER in CCA	chr14	10191 3979	10192 3454	*NA*	NA	0.001827849
Gene	HYPER in CCA	chr1	50883222	50889172	*DMRTA2*	63950	0.001174535
Gene	HYPER in CCA	chr22	46451620	46454040	*NA*	NA	0.000238619
Gene	HYPER in CCA	chr15	60296421	60353929	*FOXB1*	27023	0.001623225
Gene	HYPER in CCA	chr19	33793763	33795960	*NA*	80054	0.000137409
Gene	HYPER in CCA	chr19	33793976	33795656	*CEBPA-AS1*	NA	0.000137409
Gene	HYPER in CCA	chr2	23191 6755	23191 7352	*NA*	NA	0.006822053
Gene	HYPER in CCA	chr17	79858621	79860781	*NPB*	256933	0.007331925
Gene	HYPER in CCA	chr2	17705 3307	17705 5688	*HOXD1*	3231	0.003717667
Gene	HYPER in CCA	chr2	21853420	21859181	*NA*	NA	0.006323107
Gene	HYPER in CCA	chr1	24865292	24882515	*NA*	100506985	3.52E-05
Gene	HYPER in CCA	chr15	43568478	43594453	*TGM7*	116179	0.002754261
Gene	HYPER in CCA	chr4	90645250	90759466	*SNCA*	6622	0.002153057
Gene	HYPER in CCA	chr3	51989330	51991509	*GPR62*	118442	0.000840799
Gene	HYPER in CCA	chr18	29304161	29306919	*LRRC37A7P*	NA	0.000638038
Gene	HYPER in CCA	chr5	18052 6140	18052 7666	*FOXO1B*	NA	0.002269692
Gene	HYPER in CCA	chr16	22858 17	22887 12	*DNASE1L2*	1775	0.000218962
Gene	HYPER in CCA	chr19	58238 13	58283 35	*NRTN*	4902	0.000473777
Gene	HYPER in CCA	chr5	72742083	72744352	*NA*	NA	0.008623069
Gene	HYPER in CCA	chr10	13459 8297	13459 9556	*NKX6-2*	84504	0.001162659
Gene	HYPER in CCA	chr17	46810453	46811250	*NA*	NA	0.002438533
Gene	HYPER in CCA	chr20	30522 66	30531 63	*OXT*	5020	0.00672494
Gene	HYPER in CCA	chr6	43274872	43337216	*ZNF318*	24149	0.000105686
Gene	HYPER in CCA	chr6	26234440	26235216	*HIST1H1D*	3007	0.00659808
Gene	HYPER in CCA	chr19	46913629	46916841	*CCDC8*	83987	0.000892453
Gene	HYPER in CCA	chr16	86598751	86601367	*NA*	NA	0.006190992
Gene	HYPER in CCA	chr18	53388294	53455992	*NA*	NA	0.001801114
Gene	HYPER in CCA	chr16	24672743	24682383	*NA*	400511	5.39E-05

Gene	HYPER in CCA	chr5	36248536	36302216	*RANBP3L*	202151	0.000149046
Gene	HYPER in CCA	chr20	26167556	26232162	*MIR663A*	284801;724033	0.000558885
Gene	HYPER in CCA	chr7	29603427	29606911	*PRR15*	222171	0.00072674
Gene	HYPER in CCA	chr19	54663846	54676944	*TMC4*	147798	0.003281453
Gene	HYPER in CCA	chr16	54968825	54988577	*NA*	NA	0.005751999
Gene	HYPER in CCA	chr2	132118066	132121731	*NA*	NA	0.001104958
Gene	HYPER in CCA	chr16	2075357	2089027	*SLC9A3R2*	9351	0.000602858
Gene	HYPER in CCA	chr6	10882013	10884582	*NA*	NA	0.002267789
Gene	HYPER in CCA	chr10	135043778	135045062	*UTF1*	8433	0.008726787
Gene	HYPER in CCA	chr17	46618256	46623441	*HOXB2*	3212	0.001000313
Gene	HYPER in CCA	chr2	145275664	145279058	*ZEB2-AS1*	100303491	0.003580703
Gene	HYPER in CCA	chr19	15337730	15344246	*EPHX3*	79852	0.001150301
Gene	HYPER in CCA	chr1	101003693	101007574	*GPR88*	54112	0.001694826
Gene	HYPER in CCA	chr6	28414750	28415584	*COX11P1*	NA	0.006440191
Gene	HYPER in CCA	chr2	200322423	200341658	*SATB2-AS1*	150538	0.000299158
Gene	HYPER in CCA	chr14	57267425	57277197	*OTX2*	5015	0.000433559
Gene	HYPER in CCA	chr12	56032696	56053579	*NA*	NA	0.000678214
Gene	HYPER in CCA	chr2	177037923	177053686	*HOXD-AS1*	401022	0.002410065
Gene	HYPER in CCA	chr14	29235050	29238870	*FOXG1*	2290	0.001593651
Gene	HYPER in CCA	chr2	176964458	176966408	*HOXD12*	3238	0.000478565
Gene	HYPER in CCA	chr15	45406519	45410619	*DUOXA2*	405753	0.000444522
Gene	HYPER in CCA	chr5	94955782	94957846	*GPR150*	285601	0.001538238
Gene	HYPER in CCA	chr4	141480588	141489959	*UCP1*	7350	0.000694111
Gene	HYPER in CCA	chr10	95326422	95364237	*FFAR4*	338557	0.001930301
Gene	HYPER in CCA	chr16	679239	684116	*WFIKKN1*	117166	0.000112898
Gene	HYPER in CCA	chr10	82031576	82049440	*MAT1A*	4143	0.000178067
Gene	HYPER in CCA	chr10	35894929	35897081	*NA*	NA	0.002269692
Gene	HYPER in CCA	chr8	97154562	97173020	*GDF6*	392255	0.003245753
Gene	HYPER in CCA	chr2	176942200	176948641	*EVX2*	344191	0.00270022
Gene	HYPER in CCA	chr8	23559964	23564111	*NKX2-6*	137814	0.001983775
Gene	HYPER in CCA	chr2	175199674	175203220	*SP9*	100131390	0.001051085
Gene	HYPER in CCA	chr17	46620913	46628610	*HOXB-AS1*	100874362	0.000320534
Gene	HYPER in CCA	chr11	18252896	18258440	*SAA4*	6291;100528017	0.000149046
Gene	HYPER in CCA	chr7	149119766	149121981	*NA*	NA	0.000732743

Gene	HYPER in CCA	chr10	94821021	94828454	*CYP26C1*	340665	0.000847751
Gene	HYPER in CCA	chr19	10397643	10399198	*ICAM4*	3386	0.000592663
Gene	HYPER in CCA	chr4	187900644	187943127	*NA*	NA	0.008473009
Gene	HYPER in CCA	chr9	132645972	132646449	*NA*	NA	0.004095403
Gene	HYPER in CCA	chr16	2521500	2524146	*NTN3*	4917	5.12E-05
Gene	HYPER in CCA	chr2	228735770	228789060	*DAW1*	164781	0.000802984
Gene	HYPER in CCA	chr19	14583278	14586174	*PTGER1*	5731	0.001628446
Gene	HYPER in CCA	chr10	135168658	135171529	*FUOM*	282969	0.001091984
Gene	HYPER in CCA	chr3	158519046	158519724	*NA*	NA	0.00072674
Gene	HYPER in CCA	chr8	55370495	55373448	*SOX17*	64321	0.003717667
Gene	HYPER in CCA	chr4	93218402	93225329	*NA*	NA	0.004536605
Gene	HYPER in CCA	chr3	23236561	23244069	*UBE2E2-AS1*	NA	0.000268029
Gene	HYPER in CCA	chr5	78293438	78531861	*DMGDH*	29958	0.000234487
Gene	HYPER in CCA	chr7	27221129	27224842	*HOXA11*	3207	0.000304894
Gene	HYPER in CCA	chr18	76736555	76739074	*NA*	NA	0.001979858
Gene	HYPER in CCA	chr7	142494531	142494579	*TRBJ2-3*	NA	0.001591316
Gene	HYPER in CCA	chr6	27774853	27775117	*HIST1H4PS1*	NA	0.000703797
Gene	HYPER in CCA	chr1	9732484	9747613	*NA*	101929074	0.002674121
Gene	HYPER in CCA	chr2	182537815	182545603	*NEUROD1*	4760	0.002386694
Gene	HYPER in CCA	chr6	29893760	29894750	*HCG4B*	80868	0.004751596
Gene	HYPER in CCA	chr6	134210276	134216691	*TCF21*	6943	0.001162659
Gene	HYPER in CCA	chr10	94178424	94180632	*MARK2P9*	100507674	6.61E-05
Gene	HYPER in CCA	chr12	54366910	54371427	*HOXC11*	3227	0.002127722
Gene	HYPER in CCA	chr10	45493146	45496336	*C10orf25*	220979	0.000707198
Gene	HYPER in CCA	chr10	91597369	91599091	*NA*	NA	0.001051085
Gene	HYPER in CCA	chr6	27100832	27103070	*HIST1H2AG*	8329;8330;8332;8336;8969;85235	0.000937583
Gene	HYPER in CCA	chr5	72740654	72744352	*FOXD1*	2297	0.003907744
Gene	HYPER in CCA	chr6	27840926	27841289	*HIST1H4L*	8294;8359;8360;8361;8362;8363;8364;8365;8366;8367;8368;8370;121504;554313	0.002813336
Gene	HYPER in CCA	chr7	96635695	96637022	*DLX6-AS2*	NA	0.002754261
Gene	HYPER in CCA	chr5	54515442	54523143	*MCIDAS*	345643	0.000233634
Gene	HYPER in CCA	chr2	45147332	45166338	*NA*	100130502	0.000584839
Gene	HYPER in CCA	chr14	37116288	37128006	*NA*	NA	0.001150301
Gene	HYPER in CCA	chr20	25051521	25062996	*VSX1*	30813	0.000428239
Gene	HYPER in CCA	chr17	42004931	42009990	*NA*	NA	0.000594159

Gene	HYPER in CCA	chr1	63788730	63790797	*FOXD3*	27022	0.006069879
Gene	HYPER in CCA	chr1	43919598	43922666	*HYI-AS1*	NA	0.002770152
Gene	HYPER in CCA	chr1	225997794	226033260	*EPHX1*	2052	0.000162076
Gene	HYPER in CCA	chr19	38879061	38886881	*SPRED3*	399473	0.002524643
Gene	HYPER in CCA	chr1	145413095	145417545	*HFE2*	148738	0.000120801
Gene	HYPER in CCA	chr2	176987088	176989853	*HOXD9*	3235	0.002098368
Gene	HYPER in CCA	chr16	56659387	56661024	*MT1E*	4493	0.007259406
Gene	HYPER in CCA	chr8	99956631	99964332	*OSR2*	116039	0.001167461
Gene	HYPER in CCA	chr1	20915441	20945401	*CDA*	978	3.81E-05
Gene	HYPER in CCA	chr1	149400131	149400542	*HIST2H3PS2*	NA	4.38E-06
Gene	HYPER in CCA	chr6	50786436	50815326	*TFAP2B*	7021	0.00034052
Gene	HYPER in CCA	chr2	176957619	176960666	*HOXD13*	3239	0.003575285
Gene	HYPER in CCA	chr1	204100190	204121307	*ETNK2*	55224	5.42E-05
Gene	HYPER in CCA	chr11	118382626	118401809	*NA*	NA	0.000210515
Gene	HYPER in CCA	chr2	19551246	19558414	*OSR1*	130497	0.000342636
Gene	HYPER in CCA	chr10	134774844	134775741	*LINC01167*	NA	0.003952329
Gene	HYPER in CCA	chr10	47379727	47420712	*FAM35DP*	NA	0.006599477
Gene	HYPER in CCA	chr10	47396223	47396822	*RHEBP2*	101060032	0.006599477
Gene	HYPER in CCA	chr1	46912345	46915376	*NA*	101929651	0.001953265
Gene	HYPER in CCA	chr14	101540206	101544247	*NA*	NA	7.59E-05
Gene	HYPER in CCA	chr1	156638555	156647189	*NES*	10763	0.000130961
Gene	HYPER in CCA	chr1	119911402	119936753	*HAO2*	51179	0.000440279
Gene	HYPER in CCA	chr8	24769678	24772230	*NA*	NA	0.000947387
Gene	HYPER in CCA	chr1	182584389	182585764	*NA*	284648	0.002438533
Gene	HYPER in CCA	chr11	66037303	66045996	*NA*	NA	0.004179738
Gene	HYPER in CCA	chr14	24801516	24806588	*NA*	NA	0.000736418
Gene	HYPER in CCA	chr16	56666145	56667898	*MT1M*	4499	0.001726043
Gene	HYPER in CCA	chr1	40598436	40599120	*NA*	NA	0.000497462
Gene	HYPER in CCA	chr6	26273144	26273622	*HIST1H2BI*	8339;8343;8344;8346;8347	0.001262624
Gene	HYPER in CCA	chr1	145438469	145442635	*TXNIP*	10628	0.002441456
Gene	HYPER in CCA	chr2	105471969	105476929	*POU3F3*	5455	0.00131648
Gene	HYPER in CCA	chr2	162280526	162285285	*NA*	NA	0.000811831
Gene	HYPER in CCA	chr10	124895478	124897257	*HMX3*	340784	0.002993172
Gene	HYPER in CCA	chr14	105119885	105122124	*NA*	NA	0.000805389

Gene	HYPER in CCA	chr17	19483256	19499371	*NA*	101060602	0.001928624
Gene	HYPER in CCA	chr7	27226192	27233067	*NA*	NA	0.000767055
Gene	HYPER in CCA	chr20	21376005	21378666	*NKX2-4*	644524	0.001608752
Gene	HYPER in CCA	chr19	50922195	50934570	*SPIB*	6689	0.000122555
Gene	HYPER in CCA	chr7	27193335	27197555	*HOXA7*	3204	0.001734841
Gene	HYPER in CCA	chr20	39314488	39317880	*MAFB*	9935	0.000840799
Gene	HYPER in CCA	chr5	16067248	16180871	*Mar/11*	441061	0.005751999
Gene	HYPER in CCA	chr5	138727635	138730885	*PROB1*	389333	0.002504812
Gene	HYPER in CCA	chr18	74962505	74980858	*GALR1*	2587	0.004987311
Gene	HYPER in CCA	chr12	102789645	102874423	*IGF1*	3479	0.000209996
Gene	HYPER in CCA	chr6	116575370	116577906	*NA*	100506496	0.00598285
Gene	HYPER in CCA	chr14	60975669	60979568	*SIX6*	4990	0.004690807
Gene	HYPER in CCA	chr13	95351948	95355116	*LINC00391*	NA	0.001653171
Gene	HYPER in CCA	chr5	74161718	74163679	*NA*	NA	2.94E-05
Gene	HYPER in CCA	chr11	111384768	111397480	*NA*	101928666	8.37E-05
Gene	HYPER in CCA	chr17	46652875	46657473	*HOXB4*	3214	0.000245153
Gene	HYPER in CCA	chr2	45168902	45173216	*SIX3*	6496	0.000133125
Gene	HYPER in CCA	chr2	175190755	175195371	*NA*	285084	0.000600457
Gene	HYPER in CCA	chr19	23251275	23254278	*NA*	NA	0.001268764
Gene	HYPER in CCA	chr1	79355449	79472403	*ELTD1*	64123	0.001460078
Gene	HYPER in CCA	chr11	82443053	82444906	*FAM181B*	220382	0.001204366
Gene	HYPER in CCA	chr2	162272605	162282381	*TBR1*	10716	0.0004287
Gene	HYPER in CCA	chr3	44039573	44040641	*NA*	NA	0.001789293
Gene	HYPER in CCA	chr2	176986339	177001826	*HOXD-AS2*	100506783	0.000797066
Gene	HYPER in CCA	chr6	43267448	43276535	*CRIP3*	401262	3.03E-05
Gene	HYPER in CCA	chr20	45947246	45949467	*NA*	NA	0.00176559
Gene	HYPER in CCA	chr7	27132612	27135615	*HOXA1*	3198	0.002524643
Gene	HYPER in CCA	chr18	53443958	53448952	*NA*	NA	0.00101667
Gene	HYPER in CCA	chr4	147560045	147563626	*POU4F2*	5458	0.000214374
Gene	HYPER in CCA	chr8	23583844	23600555	*NA*	NA	0.000747026
Gene	HYPER in CCA	chr20	61637331	61638387	*BHLHE23*	128408	0.000905398
Gene	HYPER in CCA	chr13	79172497	79177673	*POU4F1*	5457	0.000747026
Gene	HYPER in CCA	chr5	79535306	79535408	*NA*	NA	0.002719498
Gene	HYPER in CCA	chr5	140011313	140013286	*CD14*	929	0.000171524

Gene	HYPER in CCA	chr15	74657776	74659391	*NA*	NA	2.09E-05
Gene	HYPER in CCA	chr17	46706037	46712294	*HOXB-AS4*	NA	0.000624386
Gene	HYPER in CCA	chr1	156390123	156390230	*MIR9-1*	407046	0.007679667
Gene	HYPER in CCA	chr2	162279170	162280088	*NA*	NA	0.000277893
Gene	HYPER in CCA	chr17	6658766	6678966	*XAF1*	54739	0.000300364
Gene	HYPER in CCA	chr6	4774760	4775642	*NA*	101927913	0.002269692
Gene	HYPER in CCA	chr1	150229554	150237478	*CA14*	23632	0.000122555
Gene	HYPER in CCA	chr3	9944296	9958086	*IL17RE*	132014	1.16E-05
Gene	HYPER in CCA	chr11	6340176	6341877	*PRKCDBP*	112464	0.000299158
Gene	HYPER in CCA	chr5	50668570	50679166	*NA*	642366	0.001969727
Gene	HYPER in CCA	chr10	102095320	102106147	*NA*	NA	0.000126912
Gene	HYPER in CCA	chr10	28033715	28056723	*NA*	101929202	0.000774875
Gene	HYPER in CCA	chr22	50968139	50971009	*ODF3B*	440836	0.005587607
Gene	HYPER in CCA	chr7	27139721	27142430	*HOXA2*	3199	0.000137409
Gene	HYPER in CCA	chr6	28954577	28956313	*HCG16*	101929874	0.000440279
Gene	HYPER in CCA	chr7	129423210	129425025	*NA*	NA	0.000504343
Gene	HYPER in CCA	chr17	6944949	6947242	*SLC16A11*	162515	0.000117859
Gene	HYPER in CCA	chr2	177042445	177043736	*NA*	NA	0.000735819
Gene	HYPER in CCA	chr10	119494824	119495918	*NA*	NA	0.007404858
Gene	HYPER in CCA	chr13	53418109	53422775	*PCDH8*	5100	0.000478565
Gene	HYPER in CCA	chr20	21491648	21494664	*NKX2-2*	4821	0.003951171
Gene	HYPER in CCA	chr4	113704451	113705545	*MIR572*	693157	0.000530431
Gene	HYPER in CCA	chr10	114133776	114188138	*ACSL5*	51703	0.000179626
Gene	HYPER in CCA	chr2	177028892	177030444	*NA*	NA	0.001262624
Gene	HYPER in CCA	chr7	24323782	24331484	*NPY*	4852	0.001525978
Gene	HYPER in CCA	chr14	37126773	37148920	*PAX9*	5083	0.000309192
Gene	HYPER in CCA	chr6	27839623	27840099	*HIST1H3I*	8350;8351;8352;8353;8354;8355;8356;8357;8358;8968	0.004000174
Gene	HYPER in CCA	chr10	104196269	104196341	*MIR146B*	574447	0.000871944
Gene	HYPER in CCA	chr7	27186985	27192217	*NA*	NA	0.000878385
Gene	HYPER in CCA	chr1	156611182	156629324	*BCAN*	63827	3.17E-05
Gene	HYPER in CCA	chr2	119599747	119605254	*EN1*	2019	0.000594385
Gene	HYPER in CCA	chr16	28548606	28550495	*NUPR1*	26471	3.34E-05
Gene	HYPER in CCA	chr1	248020501	248041507	*TRIM58*	25893	0.000664266
Gene	HYPER in CCA	chr7	99691391	99691470	*MIR93*	407050	0.000191667

Gene	HYPER in CCA	chr2	175200601	175202151	*NA*	NA	0.000478565
Gene	HYPER in CCA	chr7	27210210	27219880	*HOXA10*	3206	0.000335254
Gene	HYPER in CCA	chr9	131683174	131704320	*PHYHD1*	254295	3.03E-05
Gene	HYPER in CCA	chr3	170374351	170379912	*NA*	101928583	0.00030943
Gene	HYPER in CCA	chr7	27202054	27210117	*HOXA9*	3205;442920	0.000396648
Gene	HYPER in CCA	chr4	185261909	185275130	*NA*	728175	0.002363864
Gene	HYPER in CCA	chr15	80487826	80544555	*NA*	100996492	0.000605196
Gene	HYPER in CCA	chr16	67197288	67199718	*NA*	NA	5.42E-05
Gene	HYPER in CCA	chr17	79374516	79374578	*MIR4740*	100616294	0.000745367
Gene	HYPER in CCA	chr19	17206228	17210117	*NA*	NA	0.006344316
Gene	HYPER in CCA	chr2	176968944	176974722	*HOXD11*	3237	0.001188423
Gene	HYPER in CCA	chr5	78365540	78385289	*BHMT2*	23743	0.000438487
Gene	HYPER in CCA	chr10	77036134	77036404	*HMGA1P5*	NA	0.00426437
Gene	HYPER in CCA	chr16	67700719	67702661	*C16orf86*	388284	0.000418779
Gene	HYPER in CCA	chr9	69199480	69202204	*FOXD4L6*	653404	8.76E-05
Gene	HYPER in CCA	chr20	21492085	21492947	*NKX2-2-AS1*	NA	0.004847117
Gene	HYPER in CCA	chr9	126793903	126794803	*NA*	NA	5.42E-05
Gene	HYPER in CCA	chr20	21378456	21381029	*NA*	NA	0.002929356
Gene	HYPER in CCA	chr7	20823906	20826505	*SP8*	221833	0.000820147
Gene	HYPER in CCA	chr8	72753784	72756703	*MSC*	9242	0.002131019
Gene	HYPER in CCA	chr13	100634026	100639018	*ZIC2*	7546	0.000602858
Gene	HYPER in CCA	chr13	79170264	79173754	*NA*	NA	0.000210515
Gene	HYPER in CCA	chr5	50265494	50266021	*NA*	NA	0.000477157
Gene	HYPER in CCA	chr20	62328021	62330037	*TNFRSF6B*	8771	0.000678214
Gene	HYPER in CCA	chr16	226679	227521	*HBA1*	3039;3040	0.000423527
Gene	HYPER in CCA	chr7	101936369	101936453	*MIR4285*	100422858	0.003907744
Gene	HYPER in CCA	chr16	56700643	56701977	*MT1G*	4495	1.65E-05
Gene	HYPER in CCA	chr10	135159258	135164230	*NA*	NA	8.22E-05
Gene	HYPER in CCA	chr13	28366780	28368905	*GSX1*	219409	0.001197292
Gene	HYPER in CCA	chr4	170712371	170712853	*PTGES3P3*	NA	0.001554689
Gene	HYPER in CCA	chr7	27203154	27219632	*NA*	NA	0.000279294
Gene	HYPER in CCA	chr19	13209847	13213975	*LYL1*	4066	0.000185333
Gene	HYPER in CCA	chr7	27233122	27239725	*HOXA13*	3209	0.000497462
Gene	HYPER in CCA	chr7	27238194	27246878	*HOTTIP*	100316868	0.00023934

Gene	HYPER in CCA	chr2	71115001	71117089	*LINC01143*	NA	5.32E-05
Gene	HYPER in CCA	chr11	11138 4164	11138 4240	*MIR34C*	407042	0.000222429
Gene	HYPER in CCA	chr5	17073 6288	17073 9138	*TLX3*	30012	0.000299158
Gene	HYPER in CCA	chr2	37552 483	37553 940	*NA*	101929542	0.000494587
Gene	HYPER in CCA	chr17	41052 814	41065 386	*G6PC*	2538	5.48E-05
Gene	HYPER in CCA	chr17	33640 521	33651 919	*NA*	NA	6.40E-05
Gene	HYPER in CCA	chr16	54971 698	54972 583	*NA*	NA	0.000798507
Gene	HYPER in CCA	chr3	58490 863	58523 046	*ACOX2*	8309	8.39E-05
Gene	HYPER in CCA	chr6	26272 421	26272 768	*HIST1H2APS4*	NA	5.75E-06
Gene	HYPER in CCA	chr1	22350 487	22351 461	*NA*	101928043	0.00022552
Gene	HYPER in CCA	chr21	40687 633	40695 144	*BRWD1-AS1*	100874093	0.001570112
Gene	HYPER in CCA	chr11	11670 6467	11670 8666	*APOA1*	335	1.47E-05
Gene	HYPER in CCA	chr1	53753 696	53755 378	*NA*	NA	0.000364227
Gene	HYPER in CCA	chr22	41074 754	41078 818	*MCHR1*	2847	1.26E-05
Gene	HYPER in CCA	chr3	12131 1966	12134 9139	*FBXO40*	51725	2.73E-05
Gene	HYPER in CCA	chr2	21986 6362	21986 6431	*MIR375*	494324	0.000168085
Gene	HYPER in CCA	chr22	18260 088	18262 247	*LINC00528*	200298	0.000927623
Gene	HYPER in CCA	chr7	27135 266	27139 884	*HOTAIRM1*	100506311	0.000299158
Gene	HYPER in CCA	chr5	50265 051	50266 001	*NA*	100287592	0.000647186
Gene	HYPER in CCA	chr1	15022 7489	15022 9681	*NA*	NA	2.09E-05
Gene	HYPER in CCA	chr17	27219 487	27220 360	*NA*	NA	0.001500622
Gene	HYPER in CCA	chr5	43376 747	43412 493	*CCL28*	56477	8.37E-06
Gene	HYPER in CCA	chr14	60386 431	60530 277	*LRRC9*	NA	3.34E-05
Gene	HYPER in CCA	chr3	18142 9714	18143 2221	*SOX2*	6657	0.000497462
Gene	HYPER in CCA	chr1	47881 744	47883 723	*FOXE3*	2301	0.001403161
Gene	HYPER in CCA	chr14	69403 319	69403 581	*BANF1P1*	NA	3.47E-06
Gene	HYPER in CCA	chr13	31506 840	31549 639	*TEX26*	122046	0.000136952
Gene	HYPER in CCA	chr17	41994 576	41995 326	*FAM215A*	NA	0.000591567
Gene	HYPER in CCA	chr11	57798 402	57799 403	*OR6Q1*	219952	0.000883476
Gene	HYPER in CCA	chr12	56039 979	56040 447	*OR10AE3P*	NA	0.000423028
Gene	HYPER in CCA	chr8	53850 991	53853 677	*NPBWR1*	2831	0.000372124
Gene	HYPER in CCA	chr8	41397 900	41402 563	*NA*	NA	0.000206773
Gene	HYPER in CCA	chr8	65291 706	65291 814	*MIR124-2*	406908	0.003895839
Gene	HYPER in CCA	chr17	39221 369	39222 131	*KRTAP2-4*	85294;730755	0.001978906

Gene	HYPER in CCA	chr19	36279778	36288787	*NA*	644050	0.004858707
Gene	HYPER in CCA	chr8	43102334	43102553	*NA*	NA	0.00120361
Gene	HYPER in CCA	chr18	12911185	12912022	*NA*	NA	0.000122555
Gene	HYPER in CCA	chr7	27282164	27290112	*EVX1*	2128	0.000405935
Gene	HYPER in CCA	chr6	10423373	10426409	*NA*	NA	3.96E-05
Gene	HYPER in CCA	chr5	115140430	115152651	*CDO1*	1036	4.06E-06
Gene	HYPER in CCA	chr8	29384829	29387840	*NA*	NA	5.32E-05
Gene	HYPER in CCA	chr11	57408671	57408759	*MIR130A*	406919	2.70E-05
Gene	HYPER in CCA	chr13	40918094	40924440	*NA*	NA	0.00025214
Gene	HYPER in CCA	chr17	39210750	39211482	*KRTAP2-2*	728279	1.28E-05
Gene	HYPER in CCA	chr16	72088491	72094954	*HP*	3240	0.000171524
Gene	HYPER in CCA	chr1	228651804	228652327	*HIST3H2BA*	NA	1.19E-05
Gene	HYPER in CCA	chr7	27208238	27211534	*HOXA10-AS*	442920;100874323	0.000514801
Gene	HYPER in CCA	chr7	27197963	27198595	*NA*	NA	0.000267925
Gene	HYPER in CCA	chr15	96592504	96607655	*NA*	NA	0.000434722
Gene	HYPER in CCA	chr3	188659504	188665428	*TPRG1-AS1*	NA	5.04E-05
Gene	HYPER in CCA	chr4	142161893	142199943	*NA*	NA	0.001871404
Gene	HYPER in CCA	chr14	69093883	69095162	*NA*	100996664	0.00188509
Gene	HYPER in CCA	chr1	180238788	180245359	*NA*	100527964	0.000438487
Gene	HYPER in CCA	chr17	3705459	3706676	*NA*	NA	1.28E-05
Gene	HYPER in CCA	chr19	39693471	39694906	*SYCN*	342898	6.76E-05
Gene	HYPER in CCA	chr12	47158546	47226191	*SLC38A4*	55089	5.05E-05
Gene	HYPER in CCA	chr11	313506	315272	*IFITM1*	8519	0.000102618
Gene	HYPER in CCA	chr16	15702331	15704420	*NA*	NA	0.001453842
Gene	HYPER in CCA	chr19	2249308	2252072	*AMH*	268;100423031	3.52E-05
Gene	HYPER in CCA	chr1	100111499	100160097	*PALMD*	54873	0.00188509
Gene	HYPER in CCA	chr11	43602944	43603033	*MIR129-2*	406918	0.000774309
Gene	HYPER in CCA	chr12	123349882	123351568	*NA*	NA	2.70E-05
Gene	HYPER in CCA	chr11	17716569	17719018	*NA*	NA	2.78E-05
Gene	HYPER in CCA	chr11	17716814	17718487	*NA*	NA	2.78E-05
Gene	HYPER in CCA	chr12	114370374	114375060	*NA*	NA	0.00016634
Gene	HYPER in CCA	chr5	50261521	50262842	*NA*	NA	0.00017809
Gene	HYPER in CCA	chr3	115377380	115380126	*NA*	NA	3.52E-05
Gene	HYPER in CCA	chr6	26017260	26018040	*HIST1H1A*	3024	0.000149046

Gene	HYPER in CCA	chr1	156611458	156614679	*NA*	NA	2.44E-05
Gene	HYPER in CCA	chr8	39972170	39984987	*NA*	NA	0.001597322
Gene	HYPER in CCA	chr7	155250824	155257526	*EN2*	2020	0.000105686
Gene	HYPER in CCA	chr16	65175659	65210616	*NA*	NA	0.000289453
Gene	HYPER in CCA	chr4	190962497	190964569	*AGGF1P1*	NA	0.000600457
Gene	HYPER in CCA	chr20	9495005	9511171	*LAMP5*	24141	3.75E-05
Gene	HYPER in CCA	chr16	78529823	78540465	*NA*	NA	2.99E-05
Gene	HYPER in CCA	chr5	43018531	43024349	*NA*	NA	1.93E-05
Gene	HYPER in CCA	chr3	186490378	186491265	*NA*	NA	1.22E-05
Gene	HYPER in CCA	chr7	27281048	27286848	*EVX1-AS*	NA	0.000105139
Gene	HYPER in CCA	chr19	35628549	35630484	*NA*	NA	3.39E-06
Gene	HYPER in CCA	chr2	187692562	187713935	*ZSWIM2*	151112	0.000329074
Gene	HYPER in CCA	chr10	35104695	35105314	*PARD3-AS1*	100505601	2.94E-05
Gene	HYPER in CCA	chr10	96443251	96495947	*CYP2C18*	1562	6.61E-05
Gene	HYPER in CCA	chr4	58292038	58332152	*NA*	101928851	0.002082787
Gene	HYPER in CCA	chr7	74021239	74021625	*NA*	NA	0.000576407
Gene	HYPER in CCA	chr6	168595038	168605181	*NA*	NA	0.005775471
Gene	HYPER in CCA	chr17	19622372	19625741	*NA*	NA	6.96E-05
Gene	HYPER in CCA	chr17	33825237	33826194	*NA*	NA	0.000207095
Gene	HYPER in CCA	chr2	88422510	88427635	*FABP1*	2168	5.75E-06
Gene	HYPER in CCA	chr1	169411876	169429690	*NA*	101930556	0.001570935
Gene	HYPER in CCA	chr6	26016607	26016829	*HIST1H1PS2*	NA	3.38E-05
Gene	HYPER in CCA	chr17	41795682	41797804	*NA*	NA	2.94E-05
Gene	HYPER in CCA	chr2	70351168	70352449	*NA*	100133985	4.77E-06
Gene	HYPER in CCA	chr6	26240561	26240976	*HIST1H4F*	8294;8359;8360;8361;8362;8363;8364;8365;8366;8367;8368;8370;121504;554313	2.63E-05
Gene	HYPER in CCA	chr19	58208735	58220579	*ZNF154*	7710	2.07E-05
Gene	HYPER in CCA	chr19	58907457	58908407	*NA*	646862	8.72E-06
Gene	HYPER in CCA	chr11	64658609	64658718	*MIR192*	406967	0.001223555
Gene	HYPER in CCA	chr17	40698782	40700724	*HSD17B1P1*	NA	3.52E-05
Gene	HYPER in CCA	chr6	26250370	26250835	*HIST1H3F*	8350;8351;8352;8353;8354;8355;8356;8357;8358;8968	9.92E-05
Gene	HYPER in CCA	chr9	139839698	139841426	*C8G*	733	1.34E-05
Gene	HYPER in CCA	chr1	173872947	173886516	*SERPINC1*	462	2.95E-06
Gene	HYPER in CCA	chr20	62340216	62370456	*NA*	54923	3.39E-06
Gene	HYPER in CCA	chr14	94896970	94931067	*NA*	NA	1.49E-05

Gene	HYPER in CCA	chr16	71599563	71611033	*TAT*	6898	3.29E-06
Gene	HYPER in CCA	chr17	43331760	43339479	*SPATA32*	124783	4.78E-05
Gene	HYPER in CCA	chr12	95782375	95799280	*NA*	NA	0.00068593
Gene	HYPER in CCA	chr2	17699422	17699742 3	*HOXD8*	3234	0.000110327
Gene	HYPER in CCA	chr17	73070401	73075644	*NA*	NA	1.05E-05
Gene	HYPER in CCA	chr14	94908801	94919127	*SERPINA11*	256394	1.22E-05
Gene	HYPER in CCA	chr19	45445495	45452820	*APOC4*	346	5.61E-06
Gene	HYPER in CCA	chr19	45445495	45452822	*APOC4-APOC2*	344;346	5.61E-06
Gene	HYPER in CCA	chr4	69681711	69696914	*UGT2B10*	7365;101929773	1.27E-05
Gene	HYPER in CCA	chr19	50312190	50312995	*NA*	NA	0.002751497
Gene	HYPER in CCA	chr1	95585703	95604110	*NA*	NA	3.29E-06
Gene	HYPER in CCA	chr17	68047418	68064236	*LINC01028*	101928141	1.50E-06
Gene	HYPER in CCA	chr17	14207171	14208822	*NA*	84815	1.19E-05
Gene	HYPER in CCA	chr5	72742184	72742811	*NA*	NA	0.000238489
Gene	HYPER in CCA	chr6	27834570	27835359	*HIST1H1B*	3009	4.90E-05
Gene	HYPER in CCA	chr16	51183150	51183730	*NA*	NA	0.001385431
Gene	HYPER in CCA	chr1	228462285	228463767	*NA*	NA	0.00282928
Gene	HYPER in CCA	chr8	109907258	110075646	*NA*	NA	1.39E-05
Gene	HYPER in CCA	chr9	117085336	117088755	*ORM1*	5004	0.000133125
Gene	HYPER in CCA	chr12	56754353	56756607	*APOF*	319	5.25E-06
Gene	HYPER in CCA	chr14	38025363	38036300	*NA*	NA	1.63E-07
Gene	HYPER in CCA	chr4	156750881	156787425	*ASIC5*	51802	1.05E-05
Gene	HYPER in CCA	chr8	29209937	29210687	*NA*	NA	4.11E-06
Gene	HYPER in CCA	chr15	41303795	41305498	*NA*	NA	0.000210774
Gene	HYPER in CCA	chr12	81329515	81329612	*MIR618*	693203	4.36E-06
Gene	HYPER in CCA	chr5	78407602	78428108	*BHMT*	635	3.29E-06
Gene	HYPER in CCA	chr13	94806447	94840245	*GPC6-AS1*	100873972	4.11E-06
Gene	HYPER in CCA	chr21	45203004	45203454	*TMEM97P1*	NA	9.25E-06
Gene	HYPER in CCA	chr17	32581900	32582306	*NA*	NA	0.000774928
Gene	HYPER in CCA	chr4	74861359	74864496	*CXCL5*	6374	0.000828009
Gene	HYPER in CCA	chr1	12587766	12588462	*NA*	NA	0.000130464
Gene	HYPER in CCA	chr5	43006835	43007645	*NA*	NA	7.10E-05
Gene	HYPER in CCA	chr12	57824899	57827718	*NA*	NA	4.67E-06
Gene	HYPER in CCA	chr10	54525140	54531460	*MBL2*	4153	0.000119924

Gene	HYPER in CCA	chr16	593277	593366	*MIR3176*	100423037	7.68E-05
Gene	HYPER in CCA	chr7	27278862	27280847	*NA*	NA	3.94E-05
Gene	HYPER in CCA	chr19	7983537	7984042	*NA*	NA	8.70E-05
Gene	HYPER in CCA	chr1	3701572	3702102	*NA*	NA	0.000364227
Gene	HYPER in CCA	chr8	54788710	54789209	*NA*	NA	2.29E-05
Gene	HYPER in CCA	chr17	46799084	46799884	*PRAC1*	84366	0.000137409
Gene	HYPER in CCA	chr20	9485827	9495645	*NA*	101929329	1.05E-05
Gene	HYPER in CCA	chr11	9450320	9450501	*SNORA23*	677808	3.61E-07
Gene	HYPER in CCA	chr4	74262831	74287129	*ALB*	213	1.22E-05
Gene	HYPER in CCA	chr1	197008321	197036397	*F13B*	2165	2.28E-06
Gene	HYPER in CCA	chr10	30842783	30843412	*NA*	NA	1.77E-05
Gene	HYPER in CCA	chr15	96571318	96590159	*NA*	NA	1.84E-05
Gene	HYPER in CCA	chr12	86268073	86276770	*NTS*	4922	9.25E-05
Gene	HYPER in CCA	chr17	12893466	12893927	*NA*	NA	1.88E-06
Gene	HYPER in CCA	chr10	29095050	29102387	*NA*	NA	0.000128432
Gene	HYPER in CCA	chr1	170636522	170638566	*NA*	NA	0.000434722
Gene	HYPER in CCA	chr17	67074843	67138029	*ABCA6*	23460	0.000179626
Gene	HYPER in CCA	chr10	135160650	135166187	*PRAP1*	118471	3.47E-06
Gene	HYPER in CCA	chr16	71599692	71612090	*NA*	100132529	3.61E-07
Gene	HYPER in CCA	chr2	173328990	173330750	*NA*	NA	1.73E-06
Gene	HYPER in CCA	chr11	77774907	77779397	*THRSP*	7069	1.50E-06
Gene	HYPER in CCA	chr3	46538981	46542439	*RTP3*	83597	6.91E-06
Gene	HYPER in CCA	chr4	100044808	100078949	*ADH4*	127	0.001000313
Gene	HYPER in CCA	chr7	114054299	114059930	*NA*	NA	1.94E-06
Gene	HYPER in CCA	chr7	156799001	156799826	*MNX1-AS2*	NA	3.24E-05
Gene	HYPER in CCA	chr12	54822087	54823187	*LINC01154*	NA	1.19E-05
Gene	HYPER in CCA	chr13	24902349	24903210	*NUS1P3*	NA	6.60E-06
Gene	HYPER in CCA	chr14	98602411	98605579	*NA*	NA	4.67E-06
Gene	HYPER in CCA	chr1	214202236	214204109	*NA*	NA	1.27E-06
Gene	HYPER in CCA	chr12	7276280	7281538	*RBP5*	83758	1.07E-06
Gene	HYPER in CCA	chr4	74809728	74810041	*CXCL1P*	NA	2.68E-06
Gene	HYPER in CCA	chr2	45240353	45240807	*NA*	NA	1.81E-06
Gene	HYPER in CCA	chr17	77997693	77999906	*NA*	NA	1.21E-06
Gene	HYPER in CCA	chr2	186897618	186947960	*NA*	101927217	3.52E-05

Gene	HYPER in CCA	chr22	50644014	50644491	*NA*	NA	1.28E-06
Gene	HYPER in CCA	chr20	62366815	62370456	*LIME1*	54923	1.03E-06
Gene	HYPER in CCA	chr10	75601591	75606324	*NA*	NA	5.73E-06
Gene	HYPER in CCA	chr13	34185104	34185659	*NA*	NA	2.28E-06
Gene	HYPER in CCA	chr7	29239156	29248586	*NA*	NA	5.12E-05
Gene	HYPER in CCA	chr5	142869420	142910915	*NA*	NA	2.28E-06
Gene	HYPER in CCA	chr17	41522075	41528568	*MIR2117*	100313779	1.47E-06
Gene	HYPER in CCA	chr1	161192082	161193421	*APOA2*	336	2.95E-06
Gene	HYPER in CCA	chr5	135527156	135528822	*NA*	389332	3.61E-07
Gene	HYPER in CCA	chr2	119591276	119592686	*NA*	NA	1.47E-06
Gene	HYPER in CCA	chr11	116969703	116978886	*NA*	NA	3.47E-06
Gene	HYPER in CCA	chr12	73004458	73005096	*CHCHD3P2*	NA	2.28E-06
Gene	HYPER in CCA	chr10	91406046	91410579	*NA*	NA	1.73E-06
Gene	HYPER in CCA	chr14	89816629	89831043	*NA*	101928817	0.000405935
Gene	HYPER in CCA	chr18	18820636	18821332	*NA*	NA	1.63E-05
Gene	HYPER in CCA	chr6	160693649	160697162	*NA*	NA	1.84E-05
Gene	HYPER in CCA	chr16	14397824	14397906	*MIR193B*	574455	2.73E-05
Gene	HYPER in CCA	chr7	69060944	69062434	*NA*	100507468	1.73E-06
Gene	HYPER in CCA	chr11	57243966	57245007	*NA*	NA	2.28E-06
Gene	HYPO in CCA	chr3	160393448	160395447	*ARL14*	80117	1.41E-10
Gene	HYPO in CCA	chr11	19400531	19402530	*NAV2-IT1*	NA	1.56E-08
Gene	HYPO in CCA	chr5	67729809	67731808	*NA*	NA	0.000102644
Gene	HYPO in CCA	chr1	204676059	204678058	*RNA5SP75*	NA	7.10E-08
Gene	HYPO in CCA	chr16	88717061	88719060	*CYBA*	1535	9.22E-10
Gene	HYPO in CCA	chr1	234699544	234701543	*NA*	NA	1.52E-07
Gene	HYPO in CCA	chr3	158389983	158391982	*LXN*	56925	3.01E-09
Gene	HYPO in CCA	chr8	125282424	125284423	*NA*	NA	1.79E-05
Gene	HYPO in CCA	chr17	55600459	55602458	*NA*	101927557	1.83E-09
Gene	HYPO in CCA	chr2	120996140	120998139	*RALB*	5899	1.08E-05
Gene	HYPO in CCA	chr19	47735524	47737523	*BBC3*	27113;100422832;100422899	7.34E-08
Gene	HYPO in CCA	chr5	166720779	166722778	*NA*	NA	3.42E-06
Gene	HYPO in CCA	chr12	90339970	90341969	*NA*	NA	1.26E-07
Gene	HYPO in CCA	chr6	43191099	43193098	*NA*	NA	7.21E-08
Gene	HYPO in CCA	chr11	119035777	119037776	*NLRX1*	79671	3.49E-07

Gene	HYPO in CCA	chr2	225874758	225876757	*MIR4439*	100616207	2.30E-06
Gene	HYPO in CCA	chr17	48769309	48771308	*NA*	NA	1.99E-07
Gene	HYPO in CCA	chr8	102062782	102064781	*NA*	441374	3.55E-07
Gene	HYPO in CCA	chr5	171172296	171192295	*NA*	NA	5.38E-07
Gene	HYPO in CCA	chr11	9159162	9161161	*SCUBE2*	57758	2.75E-08
Gene	HYPO in CCA	chr13	98859278	98861277	*MIR3170*	100422881	1.27E-07
Gene	HYPO in CCA	chr11	109203370	109223369	*NA*	NA	6.06E-05
Gene	HYPO in CCA	chr2	85133633	85135632	*TRABD2A*	129293	1.54E-07
Gene	HYPO in CCA	chr7	30842527	30844526	*NA*	NA	1.38E-05
Gene	HYPO in CCA	chr8	22931502	22933501	*NA*	NA	2.01E-08
Gene	HYPO in CCA	chr13	27892650	27894649	*NA*	NA	2.19E-06
Gene	HYPO in CCA	chr7	148427521	148429520	*NA*	NA	1.79E-07
Gene	HYPO in CCA	chr17	4760170	4762169	*ATP6V0CP1*	NA	4.73E-05
Gene	HYPO in CCA	chr6	3911714	3913713	*NA*	NA	6.74E-06
Gene	HYPO in CCA	chr10	87402330	87404329	*NA*	NA	1.13E-09
Gene	HYPO in CCA	chr14	101453967	101455966	*SNORD114-28*	767609	3.19E-08
Gene	HYPO in CCA	chr4	106472277	106474276	*ARHGEF38*	54848	3.88E-07
Gene	HYPO in CCA	chr11	128048822	128050821	*NA*	NA	4.16E-06
Gene	HYPO in CCA	chr4	106473013	106475012	*NA*	NA	3.73E-07
Gene	HYPO in CCA	chr1	43736108	43738107	*EBNA1BP2*	10969;102465439	1.69E-07
Gene	HYPO in CCA	chr8	74268197	74270196	*NA*	101926926	1.43E-05
Gene	HYPO in CCA	chr1	152019884	152021883	*S100A11*	6282	1.11E-07
Gene	HYPO in CCA	chr2	109294558	109296557	*NA*	NA	1.53E-05
Gene	HYPO in CCA	chr16	87359093	87361092	*NA*	NA	9.56E-06
Gene	HYPO in CCA	chr21	37801158	37803157	*NA*	NA	1.46E-08
Gene	HYPO in CCA	chr8	13372668	13374667	*DLC1*	10395	1.47E-05
Gene	HYPO in CCA	chr6	24355631	24357630	*KAAG1*	353219	4.02E-06
Gene	HYPO in CCA	chr17	9550478	9552477	*NA*	NA	8.27E-06
Gene	HYPO in CCA	chr10	43835734	43837733	*RNU6ATAC11P*	NA	6.20E-06
Gene	HYPO in CCA	chr22	38091511	38093510	*TRIOBP*	11078	2.44E-06
Gene	HYPO in CCA	chr11	6127414	6129413	*OR56B4*	196335	0.000111478
Gene	HYPO in CCA	chr11	128394537	128396536	*NA*	101929517	7.61E-05
Gene	HYPO in CCA	chr1	173834325	173836324	*SNORD78*	692198	1.13E-06
Gene	HYPO in CCA	chr12	124996268	124998267	*NA*	NA	3.94E-05

Gene	HYPO in CCA	chr1	156630717	156632716	*NA*	NA	8.21E-10
Gene	HYPO in CCA	chr11	85780425	85782424	*PICALM*	8301	7.09E-05
Gene	HYPO in CCA	chr3	149454002	149456001	*WWTR1*	25937	4.65E-05
Gene	HYPO in CCA	chr2	87753387	87755386	*LINC00152*	112597;541471	3.33E-06
Gene	HYPO in CCA	chr2	70483018	70485017	*PCYOX1*	51449	0.001621729
Gene	HYPO in CCA	chr3	97199851	97201850	*NA*	NA	8.48E-06
Gene	HYPO in CCA	chr15	81701358	81703357	*NA*	NA	8.96E-07
Gene	HYPO in CCA	chr17	73840299	73842298	*UNC13D*	201294	4.08E-07
Gene	HYPO in CCA	chr11	66622618	66624617	*LRFN4*	78999	2.87E-06
Gene	HYPO in CCA	chr5	141705521	141707520	*SPRY4*	81848	8.41E-08
Gene	HYPO in CCA	chr19	1257884	1259883	*CIRBP*	1153	1.85E-08
Gene	HYPO in CCA	chr17	38457957	38459956	*NA*	NA	6.02E-06
Gene	HYPO in CCA	chr3	73669364	73671363	*PDZRN3-AS1*	101927249	8.14E-05
Gene	HYPO in CCA	chr5	178805263	178807262	*NA*	NA	3.38E-05
Gene	HYPO in CCA	chr6	72112825	72114824	*MIR30A*	407029	1.81E-06
Gene	HYPO in CCA	chr8	35647865	35649864	*NA*	NA	1.36E-05
Gene	HYPO in CCA	chr17	43325704	43327703	*NA*	101927036	1.40E-05
Gene	HYPO in CCA	chr12	52585285	52587284	*KRT80*	144501	1.14E-05
Gene	HYPO in CCA	chr11	3069252	3071251	*RNU1-91P*	NA	0.000159091
Gene	HYPO in CCA	chr1	24644312	24646311	*GRHL3*	57822	5.96E-05
Gene	HYPO in CCA	chr7	100180105	100182104	*FBXO24*	26261	8.83E-08
Gene	HYPO in CCA	chr17	57917127	57919126	*MIR21*	406991	1.40E-05
Gene	HYPO in CCA	chr16	69163694	69165693	*CIRH1A*	84916	5.83E-05
Gene	HYPO in CCA	chr17	79520488	79522487	*C17orf70*	80233	0.000263287
Gene	HYPO in CCA	chr3	141085480	141087479	*NA*	NA	0.000327328
Gene	HYPO in CCA	chr1	161052755	161054754	*NA*	NA	5.51E-05
Gene	HYPO in CCA	chr1	27667013	27669012	*SYTL1*	84958	4.78E-06
Gene	HYPO in CCA	chr9	117567907	117569906	*TNFSF15*	9966	8.87E-06
Gene	HYPO in CCA	chr6	33243417	33245416	*B3GALT4*	8705	0.000241521
Gene	HYPO in CCA	chr18	8707120	8709119	*NA*	100287082	0.000121864
Gene	HYPO in CCA	chr1	32040675	32042674	*NA*	NA	0.000160222
Gene	HYPO in CCA	chr1	32040616	32042615	*TINAGL1*	64129	0.000160222
Gene	HYPO in CCA	chr4	129522063	129524062	*NA*	NA	4.76E-05
Gene	HYPO in CCA	chr2	262640	264639	*ACP1*	52	2.49E-06

Gene	HYPO in CCA	chr1	155947090	155949089	*NA*	NA	0.000110969
Gene	HYPO in CCA	chr12	76422774	76424773	*NA*	NA	0.000229351
Gene	HYPO in CCA	chr19	13907248	13909247	*NA*	NA	9.91E-05
Gene	HYPO in CCA	chr18	55862429	55864428	*NA*	NA	0.001849612
Gene	HYPO in CCA	chr16	29465786	29467785	*BOLA2*	552900;654483	0.001040911
Gene	HYPO in CCA	chr16	29464936	29466935	*NA*	NA	0.001040911
Gene	HYPO in CCA	chr16	29465473	29467472	*NA*	552900	0.001040911
Gene	HYPO in CCA	chr16	29464912	29466911	*SLX1B-SULT1A4*	100526831	0.001040911
Gene	HYPO in CCA	chr16	29465627	29467626	*SULT1A4*	6818;445329;101929857	0.001040911
Gene	HYPO in CCA	chr10	100174442	100176441	*PYROXD2*	84795	5.84E-05
Gene	HYPO in CCA	chr7	38402620	38404619	*TRGV2*	NA	0.001255892
Gene	HYPO in CCA	chr12	118499736	118501735	*WSB2*	55884	0.000129325
Gene	HYPO in CCA	chr17	28086621	28088620	*NA*	NA	0.000126789
Gene	HYPO in CCA	chr17	38463944	38465943	*RARA*	5914	0.000243506
Gene	HYPO in CCA	chr2	237642025	237663006	*NA*	NA	1.63E-07
Gene	HYPO in CCA	chr11	194020031	194065561	*NAV2-IT1*	NA	7.09E-06
Gene	HYPO in CCA	chr3	160394948	160396233	*ARL14*	80117	7.93E-07
Gene	HYPO in CCA	chr5	67726254	67730308	*NA*	NA	0.002751497
Gene	HYPO in CCA	chr15	63188011	63191742	*NA*	101928955	3.61E-07
Gene	HYPO in CCA	chr7	46184535	46185286	*NA*	NA	0.000471856
Gene	HYPO in CCA	chr4	88896819	88904562	*SPP1*	6696	0.003128196
Gene	HYPO in CCA	chr1	59304120	59316926	*NA*	NA	4.72E-05
Gene	HYPO in CCA	chr6	72113254	72113324	*MIR30A*	407029	8.72E-06
Gene	HYPO in CCA	chr8	125283924	125289825	*NA*	NA	0.000884492
Gene	HYPO in CCA	chr12	90341470	90343503	*NA*	NA	2.94E-05
Gene	HYPO in CCA	chr3	186504112	186504234	*NA*	NA	3.47E-06
Gene	HYPO in CCA	chr1	150209315	150209504	*RNU2-17P*	NA	0.0057017
Gene	HYPO in CCA	chr8	38401170	38410198	*NA*	NA	4.39E-05
Gene	HYPO in CCA	chr1	229228562	229230652	*NA*	NA	0.000120882
Gene	HYPO in CCA	chr8	102299673	102306011	*NA*	NA	0.000196218
Gene	HYPO in CCA	chr15	48095581	48138433	*NA*	101928442	0.000375876
Gene	HYPO in CCA	chr20	34556512	34618622	*CNBD2*	140894	2.80E-05
Gene	HYPO in CCA	chr4	106461347	106473512	*NA*	NA	4.86E-05
Gene	HYPO in CCA	chr5	6766004	6772066	*NA*	NA	0.000267495

Gene	HYPO in CCA	chr8	22928890	22932001	*NA*	NA	2.38E-06
Gene	HYPO in CCA	chr17	73679623	73680879	*NA*	NA	1.59E-05
Gene	HYPO in CCA	chr14	101456428	101456497	*SNORD114-29*	767610	0.000443073
Gene	HYPO in CCA	chr16	11290034	11318373	*NA*	NA	0.005103237
Gene	HYPO in CCA	chr11	128050322	128053449	*NA*	NA	0.000329074
Gene	HYPO in CCA	chr20	31175281	31196695	*NA*	NA	0.000132468
Gene	HYPO in CCA	chr16	2013746	2014096	*NA*	NA	0.00611252
Gene	HYPO in CCA	chr22	30580633	30603098	*NA*	NA	0.005596193
Gene	HYPO in CCA	chr17	9550337	9550977	*NA*	NA	0.001325847
Gene	HYPO in CCA	chr2	109293251	109295057	*NA*	NA	0.000795412
Gene	HYPO in CCA	chr3	109366954	109529708	*NA*	NA	0.001692112
Gene	HYPO in CCA	chr7	123977434	123989914	*NA*	101928211	0.006044132
Gene	HYPO in CCA	chr11	49119715	49122720	*NA*	NA	0.000747282
Gene	HYPO in CCA	chr1	248512077	248513015	*OR14C36*	127066	0.007633651
Gene	HYPO in CCA	chr1	155948590	155952777	*NA*	NA	0.000231121
Gene	HYPO in CCA	chr6	30734602	30760027	*HCG20*	NA	8.82E-05
Gene	HYPO in CCA	chr11	6128914	6130065	*OR56B4*	196335	0.001415982
Gene	HYPO in CCA	chr3	158363611	158390482	*LXN*	56925	0.000118533
Gene	HYPO in CCA	chr6	31804853	31804919	*SNORD52*	26797	0.007170852
Gene	HYPO in CCA	chr19	24216276	24312654	*ZNF254*	9534	0.000196292
Gene	HYPO in CCA	chr17	57918627	57918698	*MIR21*	406991	0.000133125
Gene	HYPO in CCA	chr1	45242162	45242265	*SNORD46*	94161	0.0001391
Gene	HYPO in CCA	chr1	153533584	153540366	*S100A2*	6273	0.000300364
Gene	HYPO in CCA	chr19	13907388	13907747	*NA*	NA	9.67E-05
Gene	HYPO in CCA	chr16	88709691	88717560	*CYBA*	1535	0.000255026
Gene	HYPO in CCA	chr3	158362067	158410364	*GFM1*	85476	0.000835942
Gene	HYPO in CCA	chr9	103189438	103213511	*MSANTD3*	91283	0.001583896
Gene	HYPO in CCA	chr3	181251965	181253669	*NA*	NA	0.001591342
Gene	HYPO in CCA	chr18	47018034	47018099	*SNORD58B*	26790	8.37E-05
Gene	HYPO in CCA	chr22	36134783	36424473	*RBFOX2*	23543	0.001474003

KRAS-gr: Differential methylated regions (DMRs)

Location	Epimutation	Chromosome	Start	End	Symbol	EntrezID	Combined FDR *P*-value
Promoter	HYPER in CCA	chr7	152132591	152134590	*KMT2C*	58508	0.003239759
Promote	HYPER in	chr7	15213248	15213447	*FABP5P3*	220832	0.003239759

r	CCA		0	9			
Promoter	HYPER in CCA	chr1	149398727	149400726	*HIST2H2BB*	NA	0.003496572
Promoter	HYPER in CCA	chr1	149398563	149400562	*NA*	NA	0.003496572
Promoter	HYPER in CCA	chr10	135171030	135173029	*FUOM*	282969	0.001224402
Promoter	HYPER in CCA	chr1	240774950	240776949	*GREM2*	64388	0.009261895
Promoter	HYPER in CCA	chr19	37802239	37804238	*HKR1*	284459;100507342	0.007704751
Promoter	HYPER in CCA	chr7	45612239	45614238	*ADCY1*	107	0.004600145
Promoter	HYPER in CCA	chr16	28751603	28753602	*NA*	NA	0.002521666
Promoter	HYPER in CCA	chr7	39871313	39873312	*NA*	NA	0.001140344
Promoter	HYPER in CCA	chr5	140513300	140515299	*PCDHB5*	26167	0.004537461
Promoter	HYPER in CCA	chr22	38850706	38852705	*KCNJ4*	3761	0.008089696
Promoter	HYPER in CCA	chr8	13422852	13424851	*C8orf48*	157773	0.003689674
Promoter	HYPER in CCA	chr19	21104528	21106527	*ZNF85*	7639	0.001988305
Promoter	HYPER in CCA	chr1	149400041	149402040	*NA*	NA	0.002740152
Promoter	HYPER in CCA	chr1	149400043	149402042	*HIST2H3PS2*	NA	0.002740152
Promoter	HYPER in CCA	chr1	563891	565890	*NA*	101928626	0.000117892
Promoter	HYPER in CCA	chr1	563520	565519	*MTND2P28*	NA	0.000117892
Promoter	HYPER in CCA	chr1	67216642	67218641	*TCTEX1D1*	200132	0.005809816
Promoter	HYPER in CCA	chr12	121569122	121571121	*P2RX7*	5027	0.001088767
Promoter	HYPER in CCA	chr19	38040808	38042807	*ZNF540*	163255	0.004938559
Promoter	HYPER in CCA	chr17	8868530	8870529	*PIK3R5*	23533	0.002332012
Promoter	HYPER in CCA	chr2	220173871	220175870	*PTPRN*	5798	0.002987493
Promoter	HYPER in CCA	chr2	132217033	132219032	*RHOQP2*	NA	0.002521666
Promoter	HYPER in CCA	chr5	140478734	140480733	*PCDHB3*	56132	0.006094176
Promoter	HYPER in CCA	chr1	78509333	78511332	*NA*	NA	0.006039433
Promoter	HYPER in CCA	chr5	2752470	2754469	*IRX2*	153572	0.007704751
Promoter	HYPER in CCA	chr3	75720042	75722041	*LINC00960*	401074	0.003906229
Promoter	HYPER in CCA	chr3	128211529	128213528	*GATA2*	2624	0.00367185
Promoter	HYPER in CCA	chr13	46425372	46427371	*SIAH3*	283514	0.006450264
Promoter	HYPER in CCA	chr19	36288288	36290287	*NA*	644050	0.005658494
Promoter	HYPER in CCA	chr13	53313448	53315447	*LECT1*	11061	0.004073389
Promoter	HYPER in CCA	chr16	55356172	55358171	*IRX6*	79190	0.007645375
Promoter	HYPER in CCA	chr14	104550516	104552515	*ASPG*	374569	0.000803722
Promoter	HYPER in CCA	chr16	31580297	31582296	*YBX3P1*	440359	0.001499609

Promoter	HYPER in CCA	chr3	62359500	62361499	*FEZF2*	55079	0.007741901
Promoter	HYPER in CCA	chr1	156610297	156612296	*NA*	NA	0.002402012
Promoter	HYPER in CCA	chr1	148853621	148855620	*NA*	NA	0.004447058
Promoter	HYPER in CCA	chr7	50342220	50344219	*IKZF1*	10320	0.003780253
Promoter	HYPER in CCA	chr12	54146642	54148641	*NA*	NA	0.006851386
Promoter	HYPER in CCA	chr20	54985668	54987667	*CASS4*	57091	0.008238851
Promoter	HYPER in CCA	chr5	71013490	71015489	*CARTPT*	9607	0.004048045
Promoter	HYPER in CCA	chr22	25678142	25680141	*NA*	101929416	0.006882453
Promoter	HYPER in CCA	chr19	15120056	15122055	*CCDC105*	126402	0.001441201
Promoter	HYPER in CCA	chr17	10631594	10633593	*NA*	101101775	0.000493729
Promoter	HYPER in CCA	chr16	31578538	31580537	*NA*	NA	0.003016101
Promoter	HYPER in CCA	chr1	34641051	34643050	*NA*	NA	0.005686998
Promoter	HYPER in CCA	chr15	98835907	98837906	*NA*	NA	0.002126684
Promoter	HYPER in CCA	chr5	140722101	140724100	*PCDHGA3*	56112	0.00589846
Promoter	HYPER in CCA	chr10	63212709	63214708	*TMEM26*	219623	0.00927624
Promoter	HYPER in CCA	chr1	147789630	147791629	*NA*	NA	0.005467168
Promoter	HYPER in CCA	chr1	33801966	33803965	*RN7SKP16*	NA	0.004526244
Promoter	HYPER in CCA	chr19	31838287	31840286	*NA*	NA	0.007389111
Promoter	HYPER in CCA	chr6	10880513	10882512	*NA*	NA	0.008403794
Promoter	HYPER in CCA	chr8	75895250	75897249	*CRISPLD1*	83690	0.004938559
Promoter	HYPER in CCA	chr17	14205671	14207670	*NA*	84815	0.000443593
Promoter	HYPER in CCA	chr6	28742193	28744192	*NA*	NA	0.002402551
Promoter	HYPER in CCA	chr15	28753455	28755454	*ABCB10P4*	NA	0.001441201
Promoter	HYPER in CCA	chr7	142493182	142495181	*TRBJ2-4*	NA	0.008141235
Promoter	HYPER in CCA	chr7	142493303	142495302	*TRBJ2-5*	NA	0.008141235
Promoter	HYPER in CCA	chr7	142493423	142495422	*TRBJ2-6*	NA	0.008141235
Promoter	HYPER in CCA	chr7	142493640	142495639	*TRBJ2-7*	NA	0.008164873
Promoter	HYPER in CCA	chr22	17081277	17083276	*TPTEP1*	387590	0.003769691
Promoter	HYPER in CCA	chr19	38307441	38309440	*ZNF573*	126231	0.001320558
Promoter	HYPER in CCA	chr19	22467710	22469709	*ZNF729*	100287226	0.004257718
Promoter	HYPER in CCA	chr12	54348818	54350817	*NA*	NA	0.004097167
Promoter	HYPER in CCA	chr11	113928815	113930814	*ZBTB16*	7704	0.004272846
Promoter	HYPER in CCA	chr19	51171152	51173151	*SYT3*	84258	0.005790141
Promoter	HYPER in CCA	chr5	140212469	140214468	*PCDHA7*	56141	0.000773152

Promoter	HYPER in CCA	chr2	238534719	238536718	*LRRFIP1*	9208	0.007627893
Promoter	HYPER in CCA	chr5	140752151	140754150	*PCDHGA6*	56109	0.002041375
Promoter	HYPER in CCA	chr19	51319437	51321436	*NA*	284365	0.003951802
Promoter	HYPER in CCA	chr6	11042257	11044256	*ELOVL2-AS1*	100506409	0.008127965
Promoter	HYPER in CCA	chr10	43247094	43249093	*NA*	NA	0.004874276
Promoter	HYPER in CCA	chr22	48883772	48885771	*FAM19A5*	25817	0.005506631
Promoter	HYPER in CCA	chr5	140234095	140236094	*PCDHA10*	56139	0.001602927
Promoter	HYPER in CCA	chr1	47697393	47699392	*TAL1*	6886	0.005076615
Promoter	HYPER in CCA	chr19	57828431	57830430	*NA*	NA	0.007646365
Promoter	HYPER in CCA	chr3	187387688	187389687	*SST*	6750	0.00682605
Promoter	HYPER in CCA	chr15	29033310	29035309	*NA*	646278;101929232	0.006361385
Promoter	HYPER in CCA	chr5	140500081	140502080	*PCDHB4*	56131	0.004272846
Promoter	HYPER in CCA	chr7	142493031	142495030	*TRBJ2-3*	NA	0.006714796
Promoter	HYPER in CCA	chr7	15726503	15728502	*NA*	101927524	0.00914645
Promoter	HYPER in CCA	chr7	150037360	150039359	*NA*	NA	0.008100486
Promoter	HYPER in CCA	chr12	2799867	2801866	*CACNA1C-AS1*	100652846	0.004003426
Promoter	HYPER in CCA	chr2	162279589	162281588	*NA*	NA	0.007095277
Promoter	HYPER in CCA	chr20	21086500	21088499	*LINC00237*	NA	0.007273899
Promoter	HYPER in CCA	chr1	177139133	177141132	*BRINP2*	57795	0.008381364
Promoter	HYPER in CCA	chr2	111366993	111368992	*NA*	NA	0.008100486
Promoter	HYPER in CCA	chr4	165304703	165306702	*Mar/01*	55016	0.005040804
Promoter	HYPER in CCA	chr1	247801551	247803550	*NA*	NA	0.003266708
Promoter	HYPER in CCA	chr5	76935014	76937013	*OTP*	23440	0.006450264
Promoter	HYPER in CCA	chr16	77469500	77471499	*NA*	NA	0.004003426
Promoter	HYPER in CCA	chr5	140808685	140810684	*PCDHGA12*	26025	0.005410651
Promoter	HYPER in CCA	chr2	130762273	130764272	*ARHGAP42P2*	NA	0.008592354
Promoter	HYPER in CCA	chr8	686151	688150	*ERICH1-AS1*	619343	0.005528197
Promoter	HYPER in CCA	chr10	118032480	118034479	*GFRA1*	2674	0.008691216
Promoter	HYPER in CCA	chr13	24900849	24902848	*NUS1P3*	NA	0.006108388
Promoter	HYPER in CCA	chr8	57358794	57360793	*PENK*	5179	0.002999329
Promoter	HYPER in CCA	chr12	75603149	75605148	*KCNC2*	3747	0.00880727
Promoter	HYPER in CCA	chr3	112928350	112930349	*BOC*	91653	0.002881624
Promoter	HYPER in CCA	chr12	123348382	123350381	*NA*	NA	0.005408261
Promoter	HYPER in CCA	chr16	22823998	22825997	*HS3ST2*	9956	0.005336685

Promoter	HYPER in CCA	chr19	37094219	37096218	*ZNF382*	84911	0.001145877
Promoter	HYPER in CCA	chr2	162279343	162281342	*SLC4A10*	57282	0.005815137
Promoter	HYPER in CCA	chr8	24771731	24773730	*NA*	NA	0.001089676
Promoter	HYPER in CCA	chr16	77465779	77467778	*NA*	NA	0.003006524
Promoter	HYPER in CCA	chr17	67137530	67139529	*ABCA6*	23460	0.004423628
Promoter	HYPER in CCA	chr5	1294685	1296684	*TERT*	7015	0.000693859
Promoter	HYPER in CCA	chr5	140253558	140255557	*PCDHA12*	56137	0.007903382
Promoter	HYPER in CCA	chr5	140742398	140744397	*PCDHGA5*	56110	0.000781328
Promoter	HYPER in CCA	chr15	95869859	95871858	*NA*	400456	0.003610885
Promoter	HYPER in CCA	chr1	50512186	50514185	*ELAVL4*	1996	0.008592354
Promoter	HYPER in CCA	chr20	21684797	21686796	*PAX1*	5075	0.004259376
Promoter	HYPER in CCA	chr8	65284385	65286384	*LINC00966*	100130155	0.007958823
Promoter	HYPER in CCA	chr20	56803210	56805209	*ANKRD60*	140731	0.005843585
Promoter	HYPER in CCA	chr12	5151585	5153584	*KCNA5*	3741	0.00524688
Promoter	HYPER in CCA	chr1	248098993	248100992	*OR2L13*	284521	0.000889999
Promoter	HYPER in CCA	chr4	154709773	154711772	*SFRP2*	6423	0.00655451
Promoter	HYPER in CCA	chr7	136551916	136553915	*CHRM2*	1129	0.005156499
Promoter	HYPER in CCA	chr7	64030316	64032315	*NA*	NA	0.003016101
Promoter	HYPER in CCA	chr16	14396324	14398323	*MIR193B*	574455	0.007083575
Promoter	HYPER in CCA	chr16	73515716	73517715	*NA*	NA	0.005735958
Promoter	HYPER in CCA	chr9	122131246	122133245	*BRINP1*	1620	0.003016101
Promoter	HYPER in CCA	chr6	6006701	6008700	*NRN1*	51299	0.009245869
Promoter	HYPER in CCA	chr7	142492881	142494880	*TRBJ2-2P*	NA	0.003438742
Promoter	HYPER in CCA	chr8	70983429	70985428	*PRDM14*	63978	0.004600462
Promoter	HYPER in CCA	chr4	156128281	156130280	*NPY2R*	4887	0.004055528
Promoter	HYPER in CCA	chr13	100623664	100625663	*ZIC5*	85416	0.001320558
Promoter	HYPER in CCA	chr19	29283279	29285278	*NA*	NA	0.000937519
Promoter	HYPER in CCA	chr1	210110038	210112037	*SYT14*	255928	0.008940381
Promoter	HYPER in CCA	chr1	149718863	149720862	*NA*	NA	0.002987493
Promoter	HYPER in CCA	chr19	22815626	22817625	*ZNF492*	57615	0.004423628
Promoter	HYPER in CCA	chr1	148852638	148854637	*NA*	NA	0.002372958
Promoter	HYPER in CCA	chr12	4917308	4919307	*NA*	NA	0.001863213
Promoter	HYPER in CCA	chr1	78693783	78695782	*NA*	149047	0.001957643
Promoter	HYPER in CCA	chr18	56940819	56942818	*RAX*	30062	0.005562991

Promoter	HYPER in CCA	chr6	100912306	100914305	*SIM1*	6492	0.008564442
Promoter	HYPER in CCA	chr10	106399359	106401358	*SORCS3*	22986	0.00598398
Promoter	HYPER in CCA	chr4	298611	300610	*ZNF732*	654254	0.002132274
Promoter	HYPER in CCA	chr13	95354617	95356616	*LINC00391*	NA	0.007497424
Promoter	HYPER in CCA	chr8	145924071	145926070	*NA*	NA	0.007790211
Promoter	HYPER in CCA	chr7	145811953	145813952	*CNTNAP2*	26047	0.00545419
Promoter	HYPER in CCA	chr18	44775055	44777054	*SKOR2*	652991	0.003663987
Promoter	HYPER in CCA	chr5	128794458	128796457	*ADAMTS19*	171019	0.004938815
Promoter	HYPER in CCA	chr10	57387203	57389202	*PCDH15*	65217	0.002753492
Promoter	HYPER in CCA	chr4	66534179	66536178	*NA*	100144602	0.005422479
Promoter	HYPER in CCA	chr2	71017276	71019275	*FIGLA*	344018	0.00061055
Promoter	HYPER in CCA	chr10	134597770	134599769	*NA*	NA	0.001605724
Promoter	HYPER in CCA	chr15	29075829	29077828	*NA*	NA	0.000570974
Promoter	HYPER in CCA	chr7	19812722	19814721	*TMEM196*	256130	0.006519359
Promoter	HYPER in CCA	chr6	105584550	105586549	*BVES*	11149	0.008234497
Promoter	HYPER in CCA	chr6	28583490	28585489	*SCAND3*	114821	0.004731612
Promoter	HYPER in CCA	chr16	77468512	77470511	*ADAMTS18*	170692	0.004271455
Promoter	HYPER in CCA	chr13	112720413	112722412	*SOX1*	6656	0.000662071
Promoter	HYPER in CCA	chr7	142492744	142494743	*TRBJ2-2*	NA	0.002601681
Promoter	HYPER in CCA	chr12	9268326	9270325	*A2M*	2	0.00085463
Promoter	HYPER in CCA	chr19	23253779	23255778	*NA*	NA	0.006614038
Promoter	HYPER in CCA	chr5	140748331	140750330	*PCDHGB3*	56102	0.000937519
Promoter	HYPER in CCA	chr16	49315243	49317242	*CBLN1*	869	0.002592831
Promoter	HYPER in CCA	chr4	147558545	147560544	*POU4F2*	5458	0.003493025
Promoter	HYPER in CCA	chr4	156129680	156131679	*NA*	NA	0.002694447
Promoter	HYPER in CCA	chr5	140612438	140614437	*PCDHB18*	54660	0.00732117
Promoter	HYPER in CCA	chr1	79471904	79473903	*ELTD1*	64123	0.001827691
Promoter	HYPER in CCA	chr10	105035420	105037419	*INA*	9118	0.004620565
Promoter	HYPER in CCA	chr19	36909059	36911058	*ZFP82*	284406	0.000241372
Promoter	HYPER in CCA	chr15	29031889	29033888	*NA*	100289656	0.005149404
Promoter	HYPER in CCA	chr5	50677421	50679420	*ISL1*	3670	0.007595477
Promoter	HYPER in CCA	chr14	29233984	29235983	*NA*	NA	0.00939691
Promoter	HYPER in CCA	chr1	221052983	221054982	*HLA-AS1*	100873924	0.001613415
Promoter	HYPER in CCA	chr6	28413250	28415249	*COX11P1*	NA	0.005688697

Promoter	HYPER in CCA	chr6	133560236	133562235	*EYA4*	2070	0.008861749
Promoter	HYPER in CCA	chr7	158937150	158939149	*VIPR2*	7434	0.003485415
Promoter	HYPER in CCA	chr10	118999104	119001103	*SLC18A2*	6571	0.005663081
Promoter	HYPER in CCA	chr2	130735735	130737734	*RAB6C*	84084;150786	7.67E-05
Promoter	HYPER in CCA	chr7	6702105	6704104	*NA*	NA	0.000174102
Promoter	HYPER in CCA	chr7	137531339	137533338	*DGKI*	9162	0.003006678
Promoter	HYPER in CCA	chr12	30352416	30354415	*NA*	NA	0.008192288
Promoter	HYPER in CCA	chr6	105627371	105629370	*POPDC3*	64208	0.006691178
Promoter	HYPER in CCA	chr10	18428106	18430105	*CACNB2*	783	0.009024114
Promoter	HYPER in CCA	chr1	224803423	224805422	*NA*	NA	0.004566461
Promoter	HYPER in CCA	chr8	145924238	145926237	*NA*	100996662	0.006395633
Promoter	HYPER in CCA	chr17	72320849	72322848	*KIF19*	124602	0.0060889
Promoter	HYPER in CCA	chr2	220298068	220300067	*SPEG*	10290;100996693	0.002694447
Promoter	HYPER in CCA	chr12	43945225	43947224	*ADAMTS20*	80070	0.004695401
Promoter	HYPER in CCA	chr6	100441624	100443623	*MCHR2*	84539	0.002863694
Promoter	HYPER in CCA	chr22	19137297	19139296	*GSC2*	2928	0.002801612
Promoter	HYPER in CCA	chr2	177001327	177003326	*HOXD-AS2*	100506783	0.001224402
Promoter	HYPER in CCA	chr6	126067310	126069309	*HEY2*	23493	0.004729517
Promoter	HYPER in CCA	chr5	2737374	2739373	*NA*	NA	0.002069054
Promoter	HYPER in CCA	chr18	74961005	74963004	*GALR1*	2587	0.006614038
Promoter	HYPER in CCA	chr5	16180372	16182371	*Mar/11*	441061	0.002507966
Promoter	HYPER in CCA	chr15	40379533	40381532	*NA*	NA	0.001058856
Promoter	HYPER in CCA	chr1	236046441	236048440	*LYST*	1130	0.000831114
Promoter	HYPER in CCA	chr2	162279026	162281025	*NA*	NA	0.004017767
Promoter	HYPER in CCA	chr18	500223	502222	*COLEC12*	81035	0.007764335
Promoter	HYPER in CCA	chr6	19836117	19838116	*ID4*	3400	0.009194146
Promoter	HYPER in CCA	chr2	154726926	154728925	*GALNT13*	114805	0.001154736
Promoter	HYPER in CCA	chr20	57088935	57090934	*APCDD1L-AS1*	149773	0.001790419
Promoter	HYPER in CCA	chr9	79633071	79635070	*FOXB2*	442425	0.00589846
Promoter	HYPER in CCA	chr17	46801338	46803337	*MIR3185*	100422978	0.00244882
Promoter	HYPER in CCA	chr20	21490585	21492584	*NKX2-2-AS1*	NA	0.003084696
Promoter	HYPER in CCA	chr7	19182416	19184415	*NA*	NA	0.004219973
Promoter	HYPER in CCA	chr1	47601607	47603606	*CYP4A22*	1579;284541	0.001267952
Promoter	HYPER in CCA	chr5	145717087	145719086	*POU4F3*	5459	0.001415818

Promoter	HYPER in CCA	chr6	41206865	41208864	*RNA5SP207*	NA	0.004474346
Promoter	HYPER in CCA	chr11	30038071	30040070	*KCNA4*	3739	0.005422479
Promoter	HYPER in CCA	chr5	72676711	72678710	*NA*	NA	0.000624034
Promoter	HYPER in CCA	chr7	27141931	27143930	*HOXA2*	3199	0.000781768
Promoter	HYPER in CCA	chr5	128795883	128797882	*ADAMTS19-AS1*	NA	0.004219973
Promoter	HYPER in CCA	chr19	52955329	52957328	*ZNF578*	147660	0.002881538
Promoter	HYPER in CCA	chr8	72756204	72758203	*MSC*	9242	0.003610885
Promoter	HYPER in CCA	chr3	187009311	187011310	*MASP1*	5648	0.004395689
Promoter	HYPER in CCA	chr13	79177174	79179173	*POU4F1*	5457	0.002901166
Promoter	HYPER in CCA	chr5	170734788	170736787	*TLX3*	30012	0.006326877
Promoter	HYPER in CCA	chr2	229045862	229047861	*SPHKAP*	80309	0.002987493
Promoter	HYPER in CCA	chr2	223163216	223165215	*PAX3*	5077	0.005562991
Promoter	HYPER in CCA	chr19	38345356	38347355	*NA*	100631378	0.003906229
Promoter	HYPER in CCA	chr1	150229182	150231181	*NA*	NA	0.000695701
Promoter	HYPER in CCA	chr10	8094067	8096066	*GATA3*	2625	0.008229941
Promoter	HYPER in CCA	chr2	105470469	105472468	*POU3F3*	5455	0.005817046
Promoter	HYPER in CCA	chr20	57089688	57091687	*APCDD1L*	164284	0.001399397
Promoter	HYPER in CCA	chr18	67066791	67068790	*DOK6*	220164	0.004636334
Promoter	HYPER in CCA	chr20	61338689	61340688	*NTSR1*	4923	0.003695875
Promoter	HYPER in CCA	chr20	61808352	61810351	*MIR124-3*	406909	0.005658494
Promoter	HYPER in CCA	chr16	56223802	56225801	*GNAO1*	2775	0.006008527
Promoter	HYPER in CCA	chr15	65336208	65338207	*SLC51B*	123264	0.00589846
Promoter	HYPER in CCA	chr16	71610534	71612533	*TAT*	6898	0.000174102
Promoter	HYPER in CCA	chr5	3599803	3601802	*NA*	NA	0.000217758
Promoter	HYPER in CCA	chr5	50265502	50267501	*NA*	100287592	0.002042219
Promoter	HYPER in CCA	chr17	46691979	46693978	*HOXB8*	3218	0.002909814
Promoter	HYPER in CCA	chr4	147558913	147560912	*NA*	NA	0.003316464
Promoter	HYPER in CCA	chr14	36986983	36988982	*NKX2-1-AS1*	100506237	0.008370512
Promoter	HYPER in CCA	chr12	56513224	56515223	*NA*	NA	7.77E-06
Promoter	HYPER in CCA	chr13	78492324	78494323	*RNF219-AS1*	100874222	0.002390849
Promoter	HYPER in CCA	chr16	86599357	86601356	*FOXC2*	2303	0.007813601
Promoter	HYPER in CCA	chr16	55364767	55366766	*NA*	NA	0.004423628
Promoter	HYPER in CCA	chr12	14995930	14997929	*ART4*	420	0.008141235
Promoter	HYPER in CCA	chr20	59825982	59827981	*CDH4*	1002	0.005325287

Promoter	HYPER in CCA	chr5	50263994	50265993	*NA*	NA	0.00217137
Promoter	HYPER in CCA	chr14	57276698	57278697	*OTX2*	5015	0.006519359
Promoter	HYPER in CCA	chr20	21378167	21380166	*NKX2-4*	644524	0.007127663
Promoter	HYPER in CCA	chr1	37499231	37501230	*GRIK3*	2899	0.00407977
Promoter	HYPER in CCA	chr18	70534123	70536122	*NA*	100505797	0.008788657
Promoter	HYPER in CCA	chr14	37127507	37129506	*NA*	NA	0.005298897
Promoter	HYPER in CCA	chr5	178017057	178019056	*COL23A1*	91522	0.00665337
Promoter	HYPER in CCA	chr17	53808983	53810982	*TMEM100*	55273	0.000822254
Promoter	HYPER in CCA	chr1	196742425	196744424	*CFHR3*	10878	0.002372958
Promoter	HYPER in CCA	chr11	20181660	20183659	*DBX1*	120237	0.00280262
Promoter	HYPER in CCA	chr8	687607	689606	*ERICH1*	157697;101927618	0.002704089
Promoter	HYPER in CCA	chr17	8867713	8869712	*NA*	101928235	0.000418843
Promoter	HYPER in CCA	chr10	134599057	134601056	*NKX6-2*	84504	0.004220443
Promoter	HYPER in CCA	chr16	56224507	56226506	*NA*	283856	0.004239527
Promoter	HYPER in CCA	chr7	27232568	27234567	*NA*	NA	0.005485404
Promoter	HYPER in CCA	chr15	30260569	30262568	*TJP1*	7082	0.009433736
Promoter	HYPER in CCA	chr14	24803800	24805799	*ADCY4*	196883	0.001863213
Promoter	HYPER in CCA	chr2	223161366	223163365	*CCDC140*	151278	0.001752672
Promoter	HYPER in CCA	chr4	81950619	81952618	*BMP3*	651	0.004172803
Promoter	HYPER in CCA	chr7	27189723	27191722	*HOXA6*	3203	0.006108388
Promoter	HYPER in CCA	chr14	45380567	45382566	*NA*	101927418	0.007437106
Promoter	HYPER in CCA	chr3	13973053	13975052	*FGD5P1*	100132526	0.000624034
Promoter	HYPER in CCA	chr5	1882580	1884579	*NA*	NA	0.005809816
Promoter	HYPER in CCA	chr3	133463300	133465299	*TF*	7018	0.000216852
Promoter	HYPER in CCA	chr9	96716379	96718378	*NA*	101928040	0.002909814
Promoter	HYPER in CCA	chr1	217310598	217312597	*ESRRG*	2104	0.007447112
Promoter	HYPER in CCA	chr7	19150597	19152596	*NA*	NA	0.007279409
Promoter	HYPER in CCA	chr3	46929672	46931671	*NA*	NA	0.00655451
Promoter	HYPER in CCA	chr7	19184545	19186544	*FERD3L*	222894	0.004872083
Promoter	HYPER in CCA	chr5	140618018	140620017	*PCDHB19P*	84054	0.002987493
Promoter	HYPER in CCA	chr5	87989290	87991289	*NA*	NA	0.008367393
Promoter	HYPER in CCA	chr3	179754342	179756341	*PEX5L*	51555	0.003529335
Promoter	HYPER in CCA	chr12	130387712	130389711	*TMEM132D*	121256	0.003584621
Promoter	HYPER in CCA	chr4	190937351	190939350	*RNA5SP175*	NA	0.00463954

Promoter	HYPER in CCA	chr7	19156796	19158795	*TWIST1*	7291	0.002843542
Promoter	HYPER in CCA	chr8	67874326	67876325	*TCF24*	100129654	0.008374648
Promoter	HYPER in CCA	chr12	54446161	54448160	*NA*	3221	0.001426494
Promoter	HYPER in CCA	chr14	60974169	60976168	*SIX6*	4990	0.005932896
Promoter	HYPER in CCA	chr1	2978460	2980459	*NA*	NA	0.001536756
Promoter	HYPER in CCA	chr7	35293259	35295258	*TBX20*	57057	0.000368165
Promoter	HYPER in CCA	chr19	35394600	35396599	*NA*	NA	0.004639987
Promoter	HYPER in CCA	chr5	140623647	140625646	*PCDHB15*	56121	0.001058856
Promoter	HYPER in CCA	chr10	26503736	26505735	*GAD2*	2572	0.004037686
Promoter	HYPER in CCA	chr6	105387903	105389902	*LINC00577*	100113403	0.000385985
Promoter	HYPER in CCA	chr19	35629985	35631984	*NA*	NA	0.001399397
Promoter	HYPER in CCA	chr1	53752196	53754195	*NA*	NA	0.003906229
Promoter	HYPER in CCA	chr2	133014154	133016153	*MIR663B*	100313824	0.000385985
Promoter	HYPER in CCA	chr13	53422276	53424275	*PCDH8*	5100	0.001310295
Promoter	HYPER in CCA	chr14	52535213	52537212	*NID2*	22795	0.006236203
Promoter	HYPER in CCA	chr5	134375238	134377237	*NA*	101927953	0.000605779
Promoter	HYPER in CCA	chr5	78406102	78408101	*BHMT*	635	0.000920569
Promoter	HYPER in CCA	chr14	48143500	48145499	*NA*	161357	0.006271894
Promoter	HYPER in CCA	chr6	52608955	52610954	*GSTA7P*	NA	0.002393193
Promoter	HYPER in CCA	chr5	72740684	72742683	*NA*	NA	0.001397726
Promoter	HYPER in CCA	chr12	6664740	6666739	*IFFO1*	25900	0.003610885
Promoter	HYPER in CCA	chr11	27014128	27016127	*FIBIN*	387758	0.004977679
Promoter	HYPER in CCA	chr1	18956000	18957999	*PAX7*	5081	0.008772793
Promoter	HYPER in CCA	chr2	945461	947460	*NA*	NA	0.001175063
Promoter	HYPER in CCA	chr7	142492549	142494548	*TRBJ2-1*	NA	0.000773152
Promoter	HYPER in CCA	chr16	51181650	51183649	*NA*	NA	0.006801705
Promoter	HYPER in CCA	chr4	44448522	44450521	*NA*	NA	0.006094176
Promoter	HYPER in CCA	chr3	58612838	58614837	*FAM107A*	11170	0.002287181
Promoter	HYPER in CCA	chr1	248019001	248021000	*TRIM58*	25893	2.47E-05
Promoter	HYPER in CCA	chr3	73673592	73675591	*PDZRN3*	23024	0.002265436
Promoter	HYPER in CCA	chr8	65280616	65282615	*NA*	NA	0.001668311
Promoter	HYPER in CCA	chr7	38670668	38672667	*AMPH*	273	0.003183434
Promoter	HYPER in CCA	chr1	47406657	47408656	*CYP4A11*	1579;284541	0.000220314
Promoter	HYPER in CCA	chr5	1445046	1447045	*SLC6A3*	6531	0.002420606

Promoter	HYPER in CCA	chr2	945054	947053	*SNTG2*	54221	0.004048045
Promoter	HYPER in CCA	chr4	174446921	174448920	*HAND2-AS1*	79804	0.001460594
Promoter	HYPER in CCA	chr2	176962958	176964957	*HOXD12*	3238	0.001154736
Promoter	HYPER in CCA	chr17	42732262	42734261	*C17orf104*	284071	0.000377873
Promoter	HYPER in CCA	chr16	71459868	71461867	*NA*	NA	0.005535115
Promoter	HYPER in CCA	chr2	5831299	5833298	*SOX11*	6664	0.000250517
Promoter	HYPER in CCA	chr20	25062497	25064496	*VSX1*	30813	0.005040561
Promoter	HYPER in CCA	chr8	23563154	23565153	*NA*	NA	0.001745809
Promoter	HYPER in CCA	chr14	48143658	48145657	*MDGA2*	161357	0.006250476
Promoter	HYPER in CCA	chr2	105483455	105485454	*NA*	NA	0.003752864
Promoter	HYPER in CCA	chr4	22693037	22695036	*GBA3*	57733	0.001702019
Promoter	HYPER in CCA	chr12	54365410	54367409	*HOXC11*	3227	0.005809816
Promoter	HYPER in CCA	chr17	46808953	46810952	*NA*	NA	0.003700445
Promoter	HYPER in CCA	chr11	110583413	110585412	*ARHGAP20*	57569	0.002843542
Promoter	HYPER in CCA	chr12	5017571	5019570	*KCNA1*	3736	0.008189651
Promoter	HYPER in CCA	chr9	113255	115254	*NA*	NA	0.00015652
Promoter	HYPER in CCA	chr1	170630369	170632368	*PRRX1*	5396	0.003465081
Promoter	HYPER in CCA	chr7	27206738	27208737	*HOXA10-AS*	442920;100874323	0.000416037
Promoter	HYPER in CCA	chr4	54969324	54971323	*NA*	NA	0.002011071
Promoter	HYPER in CCA	chr10	129533999	129535998	*FOXI2*	399823	0.004271455
Promoter	HYPER in CCA	chr12	130645504	130647503	*FZD10*	11211	0.007903382
Promoter	HYPER in CCA	chr8	69243227	69245226	*NA*	NA	0.002211526
Promoter	HYPER in CCA	chr8	55368995	55370994	*SOX17*	64321	0.003951802
Promoter	HYPER in CCA	chr1	227747382	227749381	*RNA5SP77*	NA	0.000425611
Promoter	HYPER in CCA	chr1	40596936	40598935	*NA*	NA	0.001089676
Promoter	HYPER in CCA	chr3	121310466	121312465	*FBXO40*	51725	0.000215895
Promoter	HYPER in CCA	chr5	178366692	178368691	*ZNF454*	285676	0.000288421
Promoter	HYPER in CCA	chr12	41580750	41582749	*PDZRN4*	29951	0.001576913
Promoter	HYPER in CCA	chr19	58569107	58571106	*ZNF135*	7694	0.000180597
Promoter	HYPER in CCA	chr18	906169	908168	*NA*	NA	0.005632842
Promoter	HYPER in CCA	chr10	119493324	119495323	*NA*	NA	0.002420606
Promoter	HYPER in CCA	chr7	27224343	27226342	*HOXA11*	3207	0.000628185
Promoter	HYPER in CCA	chr4	41256930	41258929	*UCHL1*	7345	0.004550797
Promoter	HYPER in CCA	chr1	50888673	50890672	*DMRTA2*	63950	0.001586908

Promoter	HYPER in CCA	chr12	130646302	130648301	*FZD10-AS1*	440119	0.008214439
Promoter	HYPER in CCA	chr10	22632899	22634898	*SPAG6*	9576	0.000242952
Promoter	HYPER in CCA	chr5	16178847	16180846	*NA*	NA	0.000271054
Promoter	HYPER in CCA	chr2	207505642	207507641	*NA*	NA	0.000410974
Promoter	HYPER in CCA	chr19	38182739	38184738	*ZFP30*	22835	0.000241674
Promoter	HYPER in CCA	chr19	38182724	38184723	*ZNF781*	163115	0.000241674
Promoter	HYPER in CCA	chr19	38306499	38308498	*NA*	644554	0.000271054
Promoter	HYPER in CCA	chr10	135042278	135044277	*UTF1*	8433	0.001133558
Promoter	HYPER in CCA	chr5	63257835	63259834	*HTR1A*	3350	0.000374776
Promoter	HYPER in CCA	chr4	174911513	174913512	*NA*	NA	0.00188347
Promoter	HYPER in CCA	chr8	54788710	54790709	*NA*	NA	0.004037686
Promoter	HYPER in CCA	chr3	52827284	52829283	*ITIH3*	3699	0.000126193
Promoter	HYPER in CCA	chr10	63210897	63212896	*NA*	101928781	0.000332417
Promoter	HYPER in CCA	chr1	91182295	91184294	*BARHL2*	343472	0.00162673
Promoter	HYPER in CCA	chr6	27234392	27236391	*NA*	NA	0.002231395
Promoter	HYPER in CCA	chr16	3233519	3235518	*NA*	NA	0.001001854
Promoter	HYPER in CCA	chr20	61637888	61639887	*BHLHE23*	128408	0.002623913
Promoter	HYPER in CCA	chr18	70534882	70536881	*NETO1*	81832	0.003695356
Promoter	HYPER in CCA	chr7	98245109	98247108	*NPTX2*	4885	0.004734729
Promoter	HYPER in CCA	chr12	85672385	85674384	*ALX1*	8092	0.005555101
Promoter	HYPER in CCA	chr17	46656974	46658973	*HOXB4*	3214	0.00062674
Promoter	HYPER in CCA	chr3	147109709	147111708	*ZIC1*	7545	0.001563952
Promoter	HYPER in CCA	chr3	75954346	75956345	*ROBO2*	6092	0.001050723
Promoter	HYPER in CCA	chr20	23014557	23016556	*SSTR4*	6754	0.00043339
Promoter	HYPER in CCA	chr5	1886851	1888850	*IRX4*	50805	0.00217137
Promoter	HYPER in CCA	chr4	190960997	190962996	*AGGF1P1*	NA	0.000118197
Promoter	HYPER in CCA	chr19	36736660	36738659	*ZNF565*	147929	0.000653762
Promoter	HYPER in CCA	chr6	31893975	31895974	*NA*	NA	0.000368355
Promoter	HYPER in CCA	chr6	31893975	31895974	*CFB*	629	0.000368355
Promoter	HYPER in CCA	chr20	37351605	37353604	*SLC32A1*	140679	0.000302404
Promoter	HYPER in CCA	chr10	7573669	7575668	*NA*	NA	0.00175311
Promoter	HYPER in CCA	chr3	129691648	129693647	*TRH*	7200	0.000953001
Promoter	HYPER in CCA	chr2	176956119	176958118	*HOXD13*	3239	0.001379359
Promoter	HYPER in CCA	chr8	23563612	23565611	*NKX2-6*	137814	0.000953982

Promoter	HYPER in CCA	chr11	101453526	101455525	*NA*	NA	0.003211828
Promoter	HYPER in CCA	chr2	176985588	176987587	*HOXD9*	3235	0.000622885
Promoter	HYPER in CCA	chr19	4724186	4726185	*DPP9*	91039	0.002008281
Promoter	HYPER in CCA	chr2	177029945	177031944	*NA*	NA	0.003314974
Promoter	HYPER in CCA	chr14	69401819	69403818	*BANF1P1*	NA	1.98E-05
Promoter	HYPER in CCA	chr19	57153013	57155012	*SMIM17*	147670	0.001318963
Promoter	HYPER in CCA	chr20	2780784	2782783	*CPXM1*	56265	0.004438224
Promoter	HYPER in CCA	chr10	133109485	133111484	*TCERG1L*	256536	0.000597278
Promoter	HYPER in CCA	chr2	37662252	37664251	*RNU6-1116P*	NA	0.002542642
Promoter	HYPER in CCA	chr15	83952967	83954966	*BNC1*	646	3.61E-05
Promoter	HYPER in CCA	chr11	20689617	20691616	*NELL1*	4745	0.003927752
Promoter	HYPER in CCA	chr10	129534470	129536469	*NA*	387720	0.003314721
Promoter	HYPER in CCA	chr19	37095679	37097678	*ZNF529*	57711	0.000108247
Promoter	HYPER in CCA	chr2	182546340	182548339	*NA*	NA	0.000292125
Promoter	HYPER in CCA	chr2	237076513	237078512	*GBX2*	2637	0.001490749
Promoter	HYPER in CCA	chr1	248100316	248102315	*NA*	NA	0.000559383
Promoter	HYPER in CCA	chr11	118396687	118398686	*TTC36*	143941	0.00016749
Promoter	HYPER in CCA	chr5	78364040	78366039	*BHMT2*	23743	0.000221368
Promoter	HYPER in CCA	chr7	27280664	27282663	*EVX1*	2128	0.000616121
Promoter	HYPER in CCA	chr8	65290206	65292205	*MIR124-2*	406908	0.001124511
Promoter	HYPER in CCA	chr1	111217156	111219155	*KCNA3*	3738	0.000135504
Promoter	HYPER in CCA	chr21	36040188	36042187	*CLIC6*	54102	0.000253072
Promoter	HYPER in CCA	chr19	39753522	39755521	*IFNL4P1*	NA	0.003016101
Promoter	HYPER in CCA	chr14	60386558	60388557	*NA*	NA	0.00227795
Promoter	HYPER in CCA	chr18	907182	909181	*NA*	NA	0.001573584
Promoter	HYPER in CCA	chr8	54163758	54165757	*OPRK1*	4986	0.001934349
Promoter	HYPER in CCA	chr4	174450881	174452880	*HAND2*	9464	0.003223157
Promoter	HYPER in CCA	chr5	3594668	3596667	*IRX1*	79192	0.000271054
Promoter	HYPER in CCA	chr19	35628212	35630211	*FXYD1*	5348	4.42E-05
Promoter	HYPER in CCA	chr19	35628228	35630227	*NA*	NA	4.42E-05
Promoter	HYPER in CCA	chr17	46704537	46706536	*HOXB-AS4*	NA	0.000854929
Promoter	HYPER in CCA	chr12	102873924	102875923	*IGF1*	3479	7.19E-05
Promoter	HYPER in CCA	chr10	102898969	102900968	*NA*	NA	0.001814953
Promoter	HYPER in CCA	chr19	30017356	30019355	*NA*	NA	0.003232949

Promoter	HYPER in CCA	chr17	46799385	46801384	*PRAC1*	84366	0.003529335
Promoter	HYPER in CCA	chr5	1885946	1887945	*NA*	101929081	0.001466358
Promoter	HYPER in CCA	chr5	140786270	140788269	*PCDHGB6*	56100	0.002249568
Promoter	HYPER in CCA	chr2	177013531	177015530	*MIR10B*	406903	0.000435283
Promoter	HYPER in CCA	chr2	198650987	198652986	*BOLL*	66037	0.001323561
Promoter	HYPER in CCA	chr1	53390596	53392595	*NA*	NA	0.000174102
Promoter	HYPER in CCA	chr8	57356866	57358865	*NA*	101929415	0.000129945
Promoter	HYPER in CCA	chr6	166581689	166583688	*T*	6862	0.005695657
Promoter	HYPER in CCA	chr9	131681674	131683673	*PHYHD1*	254295	1.10E-05
Promoter	HYPER in CCA	chr1	63789613	63791612	*NA*	NA	0.001530637
Promoter	HYPER in CCA	chr2	45240308	45242307	*NA*	NA	0.001527788
Promoter	HYPER in CCA	chr15	34782273	34784272	*HNRNPLP2*	NA	0.004921426
Promoter	HYPER in CCA	chr2	71502191	71504190	*ZNF638*	27332;100507113	0.003264183
Promoter	HYPER in CCA	chr7	27208684	27210683	*MIR196B*	442920	0.003984862
Promoter	HYPER in CCA	chr8	68862853	68864852	*PREX2*	80243	0.000271054
Promoter	HYPER in CCA	chr9	127710272	127712271	*GOLGA1*	2800	0.000153786
Promoter	HYPER in CCA	chr5	2750745	2752744	*C5orf38*	153571	0.00015195
Promoter	HYPER in CCA	chr6	139793693	139795692	*NA*	645434	0.002357067
Promoter	HYPER in CCA	chr10	125749926	125751925	*YBX2P1*	NA	0.000297988
Promoter	HYPER in CCA	chr12	114368874	114370873	*NA*	NA	2.70E-05
Promoter	HYPER in CCA	chr2	177014450	177016449	*HOXD4*	3233	0.000482102
Promoter	HYPER in CCA	chr7	27169919	27171918	*HOXA4*	3201	0.000288421
Promoter	HYPER in CCA	chr17	59528265	59530264	*TBX4*	9496	0.003634538
Promoter	HYPER in CCA	chr7	27280348	27282347	*NA*	NA	0.00027312
Promoter	HYPER in CCA	chr11	43601444	43603443	*MIR129-2*	406918	0.002051321
Promoter	HYPER in CCA	chr2	176972018	176974017	*HOXD10*	3236	9.34E-05
Promoter	HYPER in CCA	chr7	27182788	27184787	*HOXA5*	3202	0.000109869
Promoter	HYPER in CCA	chr17	35300256	35302255	*NA*	NA	0.001148028
Promoter	HYPER in CCA	chr11	32456677	32458676	*WT1*	7490	0.00217137
Promoter	HYPER in CCA	chr7	27196463	27198462	*NA*	NA	0.000654018
Promoter	HYPER in CCA	chr19	58543900	58545899	*ZSCAN1*	284312	0.000368165
Promoter	HYPER in CCA	chr3	186433565	186435564	*KNG1*	3827	1.21E-05
Promoter	HYPER in CCA	chr8	56013449	56015448	*XKR4*	114786	0.000648688
Promoter	HYPER in CCA	chr13	34183604	34185603	*NA*	NA	0.003439211

Promoter	HYPER in CCA	chr12	22093837	22095836	*ABCC9*	10060	0.00029699
Promoter	HYPER in CCA	chr6	151936515	151938514	*RNU6-813P*	NA	0.000309865
Promoter	HYPER in CCA	chr19	30015906	30017905	*VSTM2B*	342865	0.002069395
Promoter	HYPER in CCA	chr18	76738575	76740574	*NA*	NA	0.000707215
Promoter	HYPER in CCA	chr16	23845822	23847821	*PRKCB*	5579	0.000324272
Promoter	HYPER in CCA	chr2	169887333	169889332	*ABCB11*	8647	7.51E-06
Promoter	HYPER in CCA	chr3	152555679	152557678	*NA*	NA	0.003686899
Promoter	HYPER in CCA	chr4	188915425	188917424	*ZFP42*	132625	0.000919114
Promoter	HYPER in CCA	chr20	5296879	5298878	*PROKR2*	128674	0.001958118
Promoter	HYPER in CCA	chr5	127872206	127874205	*SLC27A6*	28965	0.000174102
Promoter	HYPER in CCA	chr20	30072081	30074080	*LINC00028*	140875	0.000359044
Promoter	HYPER in CCA	chr7	27168096	27170095	*HOXA-AS3*	100133311	2.22E-05
Promoter	HYPER in CCA	chr11	32455564	32457563	*WT1-AS*	51352	0.001563063
Promoter	HYPER in CCA	chr7	27197056	27199055	*HOXA7*	3204	0.000407872
Promoter	HYPER in CCA	chr9	37001194	37003193	*NA*	NA	0.006227472
Promoter	HYPER in CCA	chr3	174154863	174156862	*NAALADL2*	254827	0.001447009
Promoter	HYPER in CCA	chr2	176971871	176973870	*NA*	NA	6.39E-05
Promoter	HYPER in CCA	chr13	79168764	79170763	*NA*	NA	0.000161341
Promoter	HYPER in CCA	chr18	76738775	76740774	*SALL3*	27164	0.000648688
Promoter	HYPER in CCA	chr12	85306895	85308894	*SLC6A15*	55117	0.002046764
Promoter	HYPER in CCA	chr19	30016160	30018159	*NA*	284395	0.000976774
Promoter	HYPER in CCA	chr16	3236712	3238711	*NA*	NA	0.001167991
Promoter	HYPER in CCA	chr2	5831121	5833120	*NA*	NA	6.24E-05
Promoter	HYPER in CCA	chr17	66951034	66953033	*ABCA8*	10351	0.000203719
Promoter	HYPER in CCA	chr7	101004601	101006600	*COL26A1*	136227	1.86E-05
Promoter	HYPER in CCA	chr1	170635022	170637021	*NA*	NA	0.000522721
Promoter	HYPER in CCA	chr1	237204005	237206004	*RYR2*	6262	0.000242952
Promoter	HYPER in CCA	chr5	149922752	149924751	*NA*	NA	1.15E-05
Promoter	HYPER in CCA	chr16	87969636	87971635	*CA5A*	763	2.29E-06
Promoter	HYPER in CCA	chr19	45447743	45449742	*APOC2*	344	6.23E-06
Promoter	HYPER in CCA	chr18	21571237	21573236	*TTC39C*	125488	0.00102142
Promoter	HYPER in CCA	chr14	57278401	57280400	*OTX2-AS1*	100309464	0.004779659
Promoter	HYPER in CCA	chr19	57182652	57184651	*ZNF835*	90485	7.33E-05
Promoter	HYPER in CCA	chr19	57182136	57184135	*NA*	NA	7.33E-05

Promoter	HYPER in CCA	chr1	65712402	65714401	*DNAJC6*	9829	0.000179631
Promoter	HYPER in CCA	chr10	96828755	96830754	*CYP2C8*	1558	3.48E-05
Promoter	HYPER in CCA	chr2	176992922	176994921	*HOXD8*	3234	5.28E-05
Promoter	HYPER in CCA	chr7	27145896	27147895	*HOXA-AS2*	285943	8.55E-05
Promoter	HYPER in CCA	chr17	46799030	46801029	*PRAC2*	100422978	0.001081669
Promoter	HYPER in CCA	chr12	128750448	128752447	*TMEM132C*	92293	0.000270514
Promoter	HYPER in CCA	chr2	176999840	177001839	*HOXD3*	3232;3233;401021	7.26E-05
Promoter	HYPER in CCA	chr1	165631425	165633424	*NA*	NA	0.001067943
Promoter	HYPER in CCA	chr3	46537481	46539480	*RTP3*	83597	8.37E-06
Promoter	HYPER in CCA	chr14	19402765	19404764	*ARHGAP42P5*	NA	0.005658494
Promoter	HYPER in CCA	chr12	47225692	47227691	*SLC38A4*	55089	0.000189498
Promoter	HYPER in CCA	chr1	53384594	53386593	*NA*	NA	8.52E-06
Promoter	HYPER in CCA	chr2	5830751	5832750	*NA*	NA	7.32E-05
Promoter	HYPER in CCA	chr17	30953257	30955256	*NA*	NA	0.000150628
Promoter	HYPER in CCA	chr2	240225657	240227656	*MIR4269*	100423043	0.000129945
Promoter	HYPER in CCA	chr19	58220080	58222079	*ZNF154*	7710	0.000508585
Promoter	HYPER in CCA	chr12	54384022	54386021	*MIR196A2*	406973	0.000144322
Promoter	HYPER in CCA	chr3	58522547	58524546	*ACOX2*	8309	1.19E-05
Promoter	HYPER in CCA	chr11	914559	916558	*CHID1*	66005	3.55E-06
Promoter	HYPER in CCA	chr8	89337565	89339564	*NA*	NA	0.001026246
Promoter	HYPER in CCA	chr15	70371308	70373307	*MIR629*	693214	2.58E-06
Promoter	HYPER in CCA	chr7	153582682	153584681	*DPP6*	1804	5.40E-05
Promoter	HYPER in CCA	chr4	156774390	156776389	*TDO2*	6999	0.00010406
Promoter	HYPER in CCA	chr1	36042831	36044830	*NA*	NA	4.09E-05
Promoter	HYPER in CCA	chr7	27133766	27135765	*HOTAIRM1*	100506311	0.000108273
Promoter	HYPER in CCA	chr7	24322282	24324281	*NPY*	4852	0.000122628
Promoter	HYPER in CCA	chr7	6055008	6057007	*NA*	NA	2.22E-05
Promoter	HYPER in CCA	chr15	32607356	32609355	*NA*	NA	0.001669329
Promoter	HYPER in CCA	chr5	115152152	115154151	*CDO1*	1036	2.74E-05
Promoter	HYPER in CCA	chr7	27191718	27193717	*NA*	NA	2.70E-05
Promoter	HYPER in CCA	chr7	27191701	27193700	*HOXA3*	3200	3.52E-05
Promoter	HYPER in CCA	chr7	27191681	27193680	*NA*	NA	3.52E-05
Promoter	HYPER in CCA	chr17	46710435	46712434	*HOXB7*	3217	0.000189724
Promoter	HYPER in CCA	chr2	201541456	201543455	*AOX3P*	NA	0.000389469

Promoter	HYPER in CCA	chr22	50643992	50645991	*NA*	NA	1.43E-06
Promoter	HYPER in CCA	chr1	243903624	243905623	*NA*	NA	1.53E-05
Promoter	HYPER in CCA	chr7	27135116	27137115	*HOXA1*	3198	0.000145826
Promoter	HYPER in CCA	chr7	156797501	156799500	*MNX1-AS2*	NA	1.66E-05
Promoter	HYPER in CCA	chr5	135290224	135292223	*LECT2*	3950	2.05E-05
Promoter	HYPER in CCA	chr2	175189255	175191254	*NA*	285084	0.000390945
Promoter	HYPER in CCA	chr5	95581980	95583979	*NA*	NA	0.000139527
Promoter	HYPER in CCA	chr20	62374542	62376541	*NA*	NA	1.17E-05
Promoter	HYPER in CCA	chr15	64403269	64405268	*NA*	NA	3.26E-06
Promoter	HYPER in CCA	chr15	81297874	81299873	*C15orf26*	161502	0.000203719
Promoter	HYPER in CCA	chr1	235498621	235500620	*NA*	NA	2.53E-05
Promoter	HYPER in CCA	chr1	11899574	11901573	*NPPA-AS1*	100379251	6.23E-06
Promoter	HYPER in CCA	chr7	70595655	70597654	*WBSCR17*	64409	6.23E-06
Promoter	HYPER in CCA	chr12	109491258	109493257	*USP30-AS1*	100131733	0.000192692
Promoter	HYPER in CCA	chr17	46709422	46711421	*MIR196A1*	406972	1.66E-05
Promoter	HYPER in CCA	chr16	78539966	78541965	*NA*	NA	0.00010406
Promoter	HYPER in CCA	chr2	47293461	47295460	*NA*	NA	2.05E-05
Promoter	HYPER in CCA	chr1	95584203	95586202	*NA*	NA	1.98E-06
Gene	HYPER in CCA	chr19	9577183	9609283	*ZNF560*	147741	0.006235059
Gene	HYPER in CCA	chr19	15121556	15134081	*CCDC105*	126402	0.01063268
Gene	HYPER in CCA	chr17	41795682	41797804	*NA*	NA	0.006101603
Gene	HYPER in CCA	chr2	5758459	5831250	*NA*	NA	0.011047608
Gene	HYPER in CCA	chr6	10873456	10882174	*GCM2*	9247	0.013949775
Gene	HYPER in CCA	chr15	83847934	84108197	*NA*	NA	0.008924059
Gene	HYPER in CCA	chr8	26605667	26724790	*ADRA1A*	148	0.008847123
Gene	HYPER in CCA	chr7	39872813	39874544	*NA*	NA	0.003512468
Gene	HYPER in CCA	chr7	39872885	39873392	*NA*	NA	0.003897226
Gene	HYPER in CCA	chr1	113550876	113589677	*NA*	NA	0.00173
Gene	HYPER in CCA	chr12	102789645	102874423	*IGF1*	3479	0.006439717
Gene	HYPER in CCA	chr5	113696642	113832337	*KCNN2*	3781	0.011662611
Gene	HYPER in CCA	chr2	5742637	5831620	*NA*	NA	0.010048557
Gene	HYPER in CCA	chr17	42634925	42636907	*FZD2*	2535	0.010000467
Gene	HYPER in CCA	chr1	149398877	149400540	*NA*	NA	0.004983412
Gene	HYPER in CCA	chr16	2317788	2317881	*NA*	NA	0.002939885

Gene	HYPER in CCA	chr1	147718440	147718956	*NA*	NA	0.001120483
Gene	HYPER in CCA	chr20	62340216	62370456	*NA*	54923	0.005119511
Gene	HYPER in CCA	chr2	130737235	130740311	*RAB6C*	84084;150786	0.002304177
Gene	HYPER in CCA	chr1	36038971	36060929	*TFAP2E*	339488	0.005887408
Gene	HYPER in CCA	chr19	38039816	38078249	*ZNF571-AS1*	100507433	0.009946529
Gene	HYPER in CCA	chr1	149400131	149400542	*HIST2H3PS2*	NA	0.008185935
Gene	HYPER in CCA	chr13	53277399	53313947	*LECT1*	11061	0.010458558
Gene	HYPER in CCA	chr1	36035414	36043330	*NA*	NA	0.012788345
Gene	HYPER in CCA	chr10	105036920	105050108	*INA*	9118	0.001404937
Gene	HYPER in CCA	chr22	19136089	19137796	*GSC2*	2928	0.010409629
Gene	HYPER in CCA	chr11	73471608	73472115	*NA*	NA	0.000770269
Gene	HYPER in CCA	chr2	19551246	19558414	*OSR1*	130497	0.011912274
Gene	HYPER in CCA	chr7	150035408	150038763	*RARRES2*	5919	0.012194525
Gene	HYPER in CCA	chr19	57154513	57167134	*SMIM17*	147670	0.005313611
Gene	HYPER in CCA	chr1	149400063	149429348	*NA*	NA	0.003897226
Gene	HYPER in CCA	chr4	81104434	81111323	*NA*	NA	0.013181208
Gene	HYPER in CCA	chr10	91152303	91163745	*IFIT1*	3434	0.008101822
Gene	HYPER in CCA	chr5	16180347	16185694	*NA*	NA	0.012223361
Gene	HYPER in CCA	chr20	62366815	62370456	*LIME1*	54923	0.013181208
Gene	HYPER in CCA	chr10	63166401	63213208	*TMEM26*	219623	0.010332489
Gene	HYPER in CCA	chr2	130724165	130738039	*RAB6C-AS1*	100131320	0.001730751
Gene	HYPER in CCA	chr16	65175659	65210616	*NA*	NA	0.00738817
Gene	HYPER in CCA	chr2	132118066	132121731	*NA*	NA	0.00626626
Gene	HYPER in CCA	chr1	565020	566063	*MTND2P28*	NA	0.000188285
Gene	HYPER in CCA	chr7	156786745	156803345	*MNX1*	3110	0.001694731
Gene	HYPER in CCA	chr1	145413095	145417545	*HFE2*	148738	0.004208191
Gene	HYPER in CCA	chr6	10423373	10426409	*NA*	NA	0.004601005
Gene	HYPER in CCA	chr10	135160650	135166187	*PRAP1*	118471	0.007693645
Gene	HYPER in CCA	chr5	78293438	78531861	*DMGDH*	29958	0.006601636
Gene	HYPER in CCA	chr5	128795958	129074376	*ADAMTS19*	171019	0.011963331
Gene	HYPER in CCA	chr11	116706467	116708666	*APOA1*	335	0.012498483
Gene	HYPER in CCA	chr18	22641890	22932154	*ZNF521*	25925	0.008369157
Gene	HYPER in CCA	chr2	234263220	234301045	*NA*	NA	0.001721659
Gene	HYPER in CCA	chr14	94896970	94931067	*NA*	NA	0.009157195

Gene	HYPER in CCA	chr1	119425669	119532179	*TBX15*	6913	0.01246421
Gene	HYPER in CCA	chr20	23012179	23019873	*NA*	NA	0.003106913
Gene	HYPER in CCA	chr14	24801516	24806588	*NA*	NA	0.008695843
Gene	HYPER in CCA	chr15	29033389	29037148	*NA*	100289656	0.014070884
Gene	HYPER in CCA	chr5	54515442	54523143	*MCIDAS*	345643	0.006159992
Gene	HYPER in CCA	chr12	54410715	54449813	*HOXC4*	3221	0.007203811
Gene	HYPER in CCA	chr12	108168162	108170421	*ASCL4*	121549	0.011800363
Gene	HYPER in CCA	chr19	58193337	58228669	*ZNF551*	90233	0.007821587
Gene	HYPER in CCA	chr10	74034673	74035738	*NA*	NA	0.003987892
Gene	HYPER in CCA	chr15	34786621	34788101	*NA*	NA	0.009637114
Gene	HYPER in CCA	chr3	133464800	133497850	*TF*	7018	0.002443036
Gene	HYPER in CCA	chr2	233344537	233352538	*ECEL1*	9427	0.013727368
Gene	HYPER in CCA	chr6	116782533	116784934	*FAM26F*	441168	0.012788345
Gene	HYPER in CCA	chr19	52956829	53015407	*ZNF578*	147660	0.000798395
Gene	HYPER in CCA	chr2	71127720	71160576	*VAX2*	25806	0.009848695
Gene	HYPER in CCA	chr1	150227489	150229681	*NA*	NA	0.005004316
Gene	HYPER in CCA	chr6	43267448	43276535	*CRIP3*	401262	0.000893489
Gene	HYPER in CCA	chr17	46684594	46710934	*HOXB7*	3217	0.008771727
Gene	HYPER in CCA	chr10	94178424	94180632	*MARK2P9*	100507674	0.013642457
Gene	HYPER in CCA	chr1	67218142	67244470	*TCTEX1D1*	200132	0.002469545
Gene	HYPER in CCA	chr19	36874022	36909558	*ZFP82*	284406	0.001332186
Gene	HYPER in CCA	chr4	42112955	42154895	*BEND4*	389206	0.009487247
Gene	HYPER in CCA	chr6	27253682	27279949	*POM121L2*	94026	0.011765853
Gene	HYPER in CCA	chr10	63212397	63241714	*NA*	101928781	0.013181208
Gene	HYPER in CCA	chr8	57358366	57464626	*NA*	101929415	0.004636787
Gene	HYPER in CCA	chr8	57349233	57359293	*PENK*	5179	0.002998417
Gene	HYPER in CCA	chr19	36279778	36288787	*NA*	644050	0.007810993
Gene	HYPER in CCA	chr4	111286889	111486441	*ENPEP*	2028	0.004463206
Gene	HYPER in CCA	chr17	46698518	46703839	*HOXB9*	3219	0.002307415
Gene	HYPER in CCA	chr14	101540206	101544247	*NA*	NA	0.006941335
Gene	HYPER in CCA	chr5	134374528	134375737	*NA*	101927953	0.007974518
Gene	HYPER in CCA	chr2	182321929	182400914	*ITGA4*	3676	0.013949775
Gene	HYPER in CCA	chr18	44746293	44775554	*SKOR2*	652991	0.005373055
Gene	HYPER in CCA	chr2	114256661	114258728	*FOXD4L1*	200350	0.003087213

Gene	HYPER in CCA	chr8	75896750	75946793	*CRISPLD1*	83690	0.010787254
Gene	HYPER in CCA	chr18	63417488	63548638	*CDH7*	1005	0.01095688
Gene	HYPER in CCA	chr5	145583113	145718814	*RBM27*	54439	0.005793378
Gene	HYPER in CCA	chr12	54350318	54352745	*NA*	NA	0.00719211
Gene	HYPER in CCA	chr13	19864733	19918965	*ANKRD26P3*	NA	0.006796681
Gene	HYPER in CCA	chr1	156611182	156629324	*BCAN*	63827	0.002955657
Gene	HYPER in CCA	chr16	56126899	56225006	*NA*	283856	0.005602488
Gene	HYPER in CCA	chr17	46620913	46628610	*HOXB-AS1*	100874362	0.008350304
Gene	HYPER in CCA	chr16	2889569	2892745	*PRSS30P*	124221	0.005180144
Gene	HYPER in CCA	chr15	83924655	83953466	*BNC1*	646	0.013065558
Gene	HYPER in CCA	chr5	172659112	172662360	*NKX2-5*	1482	0.00857226
Gene	HYPER in CCA	chr10	101286107	101290934	*NA*	101927324	0.00697409
Gene	HYPER in CCA	chr1	75594119	75627218	*LHX8*	431707	0.012708424
Gene	HYPER in CCA	chr19	22469210	22499978	*ZNF729*	100287226	0.008490755
Gene	HYPER in CCA	chr7	27185015	27190222	*HOXA6*	3203	0.009558427
Gene	HYPER in CCA	chr4	81105033	81125483	*PRDM8*	56978	0.008998083
Gene	HYPER in CCA	chr20	54572496	54580528	*CBLN4*	140689	0.009906643
Gene	HYPER in CCA	chr12	58120054	58122139	*AGAP2-AS1*	NA	0.005445917
Gene	HYPER in CCA	chr19	2249308	2252072	*AMH*	268;100423031	0.00608464
Gene	HYPER in CCA	chr14	94908801	94919127	*SERPINA11*	256394	0.004599489
Gene	HYPER in CCA	chr19	38307999	38317278	*NA*	644554	0.002851865
Gene	HYPER in CCA	chr8	24770525	24776607	*NEFM*	4741	0.003577693
Gene	HYPER in CCA	chr19	38180766	38210089	*NA*	NA	0.001796659
Gene	HYPER in CCA	chr4	134070470	134129356	*PCDH10*	57575	0.012686475
Gene	HYPER in CCA	chr3	73670864	73675149	*PDZRN3-AS1*	101927249	0.00815962
Gene	HYPER in CCA	chr10	71331454	71332994	*NEUROG3*	50674	0.003492797
Gene	HYPER in CCA	chr3	26660821	26664181	*NA*	NA	0.010914742
Gene	HYPER in CCA	chr1	110602616	110613322	*ALX3*	257	0.005847523
Gene	HYPER in CCA	chr20	21686297	21696620	*PAX1*	5075	0.013612271
Gene	HYPER in CCA	chr9	116237	118417	*FOXD4*	2298	0.003446939
Gene	HYPER in CCA	chr1	119911402	119936753	*HAO2*	51179	0.006215687
Gene	HYPER in CCA	chr18	70409549	70535381	*NETO1*	81832	0.012239613
Gene	HYPER in CCA	chr8	72315675	72504260	*NA*	NA	0.009340534
Gene	HYPER in CCA	chr5	128795252	128796382	*ADAMTS19-AS1*	NA	0.011806852

Gene	HYPER in CCA	chr9	70917276	70920000	*FOXD4L3*	286380	0.000433857
Gene	HYPER in CCA	chr8	14423933 1	14424212 8	*LY6H*	4062	0.009634134
Gene	HYPER in CCA	chr5	14062514 7	14062779 9	*PCDHB15*	56121	0.006143328
Gene	HYPER in CCA	chr2	10546974 3	10554251 0	*NA*	NA	0.0105566
Gene	HYPER in CCA	chr11	12284827 8	12285242 8	*BSX*	390259	0.00843503
Gene	HYPER in CCA	chr19	21541732	21562104	*ZNF738*	NA	0.002727956
Gene	HYPER in CCA	chr4	41750310	41826136	*NA*	NA	0.014087362
Gene	HYPER in CCA	chr17	6588032	6616886	*SLC13A5*	284111	0.011108835
Gene	HYPER in CCA	chr18	12911185	12912022	*NA*	NA	0.007821587
Gene	HYPER in CCA	chr1	14778979 9	14779012 9	*NA*	NA	0.001730751
Gene	HYPER in CCA	chr18	49866542	51057784	*DCC*	1630	0.011084586
Gene	HYPER in CCA	chr19	56728537	56729146	*NA*	NA	0.00422729
Gene	HYPER in CCA	chr4	85413140	85419603	*NKX6-1*	4825	0.005252054
Gene	HYPER in CCA	chr22	41074754	41078818	*MCHR1*	2847	0.000550281
Gene	HYPER in CCA	chr14	37126773	37148920	*PAX9*	5083	0.013617848
Gene	HYPER in CCA	chr10	10129269 0	10129627 8	*NKX2-3*	159296	0.013065558
Gene	HYPER in CCA	chr5	2752245	2755508	*C5orf38*	153571	0.003888057
Gene	HYPER in CCA	chr19	38158652	38183223	*ZNF781*	163115	0.003653355
Gene	HYPER in CCA	chr17	46668619	46671323	*HOXB5*	3215	0.006652113
Gene	HYPER in CCA	chr6	13421027 6	13421669 1	*TCF21*	6943	0.009487247
Gene	HYPER in CCA	chr17	46688739	46692478	*HOXB8*	3218	0.013887026
Gene	HYPER in CCA	chr1	22956699 2	22956984 5	*ACTA1*	58	0.012977003
Gene	HYPER in CCA	chr19	36912438	36913436	*NA*	644189	0.002911558
Gene	HYPER in CCA	chr11	32409321	32457176	*WT1*	7490	0.012018138
Gene	HYPER in CCA	chr10	10128683 8	10128801 8	*NA*	NA	0.003802949
Gene	HYPER in CCA	chr2	22306460 7	22316371 5	*PAX3*	5077	0.006101603
Gene	HYPER in CCA	chr19	51320937	51322134	*NA*	284365	0.00843503
Gene	HYPER in CCA	chr8	65285885	65296344	*LINC00966*	100130155	0.009157195
Gene	HYPER in CCA	chr19	37095719	37119499	*ZNF382*	84911	0.000662696
Gene	HYPER in CCA	chr9	69199480	69202204	*FOXD4L6*	653404	0.002891026
Gene	HYPER in CCA	chr16	77467279	77478233	*NA*	NA	0.00697409
Gene	HYPER in CCA	chr2	11959974 7	11960525 4	*EN1*	2019	0.008899531
Gene	HYPER in CCA	chr9	10061553 6	10061898 6	*FOXE1*	2304	0.012018138
Gene	HYPER in CCA	chr7	96635695	96637022	*DLX6-AS2*	NA	0.007702729

Gene	HYPER in CCA	chr1	150229554	150237478	*CA14*	23632	0.001213961
Gene	HYPER in CCA	chr1	111214310	111217655	*KCNA3*	3738	0.001502501
Gene	HYPER in CCA	chr17	46626992	46683776	*HOXB-AS3*	404266	0.003902184
Gene	HYPER in CCA	chr12	48577366	48579709	*C12orf68*	387856	0.007480484
Gene	HYPER in CCA	chr17	35297346	35300755	*NA*	NA	0.005179278
Gene	HYPER in CCA	chr8	41397900	41402563	*NA*	NA	0.010525566
Gene	HYPER in CCA	chr7	27186985	27192217	*NA*	NA	0.011649992
Gene	HYPER in CCA	chr2	182547840	182550434	*NA*	NA	0.010000467
Gene	HYPER in CCA	chr10	124907638	124910188	*HMX2*	3167	0.006675285
Gene	HYPER in CCA	chr12	108233068	108258339	*NA*	NA	0.009555516
Gene	HYPER in CCA	chr14	52734431	52743442	*PTGDR*	5729	0.011735825
Gene	HYPER in CCA	chr17	46626232	46682274	*HOXB3*	3213	0.003630889
Gene	HYPER in CCA	chr1	248099363	248100815	*NA*	NA	0.001354877
Gene	HYPER in CCA	chr14	62570096	62583893	*NA*	NA	0.003837772
Gene	HYPER in CCA	chr10	35894929	35897081	*NA*	NA	0.008101014
Gene	HYPER in CCA	chr4	170712371	170712853	*PTGES3P3*	NA	0.001039735
Gene	HYPER in CCA	chr20	21376005	21378666	*NKX2-4*	644524	0.011804663
Gene	HYPER in CCA	chr7	35242042	35293758	*TBX20*	57057	0.001472859
Gene	HYPER in CCA	chr5	145686661	145756526	*NA*	NA	0.004206496
Gene	HYPER in CCA	chr12	54332535	54340328	*HOXC13*	3229	0.006374351
Gene	HYPER in CCA	chr11	109292846	109299840	*C11orf87*	399947	0.007367919
Gene	HYPER in CCA	chr14	51288598	51290219	*NA*	NA	0.000176466
Gene	HYPER in CCA	chr8	67858736	67874825	*TCF24*	100129654	0.000550281
Gene	HYPER in CCA	chr10	8093504	8095047	*NA*	NA	0.01063268
Gene	HYPER in CCA	chr10	102986733	102989551	*LBX1*	10660	0.010177998
Gene	HYPER in CCA	chr3	62355356	62359999	*FEZF2*	55079	0.012708424
Gene	HYPER in CCA	chr4	111516671	111536614	*NA*	NA	0.00692212
Gene	HYPER in CCA	chr4	156127681	156130179	*NA*	NA	0.005315727
Gene	HYPER in CCA	chr6	100441820	100524289	*MCHR2-AS1*	728012	0.005228094
Gene	HYPER in CCA	chr19	21106028	21133503	*ZNF85*	7639	0.002231089
Gene	HYPER in CCA	chr14	60863187	60982261	*C14orf39*	317761	0.010525566
Gene	HYPER in CCA	chr14	61107448	61109307	*NA*	NA	0.009954205
Gene	HYPER in CCA	chr8	97154562	97173020	*GDF6*	392255	0.007260537
Gene	HYPER in CCA	chr7	27210210	27219880	*HOXA10*	3206	0.002129535

Gene	HYPER in CCA	chr1	50883222	50889172	*DMRTA2*	63950	0.006235547
Gene	HYPER in CCA	chr7	19060614	19157295	*TWIST1*	7291	0.00719211
Gene	HYPER in CCA	chr13	88324870	88331871	*SLITRK5*	26050	0.005887668
Gene	HYPER in CCA	chr17	39221369	39222131	*KRTAP2-4*	85294;730755	0.012667079
Gene	HYPER in CCA	chr7	1272543	1276954	*UNCX*	340260	0.009222361
Gene	HYPER in CCA	chr18	904944	912173	*ADCYAP1*	116	0.009634134
Gene	HYPER in CCA	chr12	54375293	54379303	*HOXC-AS3*	NA	0.014000317
Gene	HYPER in CCA	chr7	27282164	27290112	*EVX1*	2128	0.011361354
Gene	HYPER in CCA	chr10	93388199	93392811	*PPP1R3C*	5507	0.000282533
Gene	HYPER in CCA	chr2	68511303	68547183	*CNRIP1*	25927	0.009946529
Gene	HYPER in CCA	chr17	46802125	46806540	*HOXB13*	10481	0.005565809
Gene	HYPER in CCA	chr9	131683174	131704320	*PHYHD1*	254295	0.000344997
Gene	HYPER in CCA	chr14	38723308	38725574	*CLEC14A*	161198	0.008771727
Gene	HYPER in CCA	chr12	113909808	113918429	*NA*	NA	0.006358337
Gene	HYPER in CCA	chr10	26505236	26593487	*GAD2*	2572	0.004136327
Gene	HYPER in CCA	chr14	57267425	57277197	*OTX2*	5015	0.006196012
Gene	HYPER in CCA	chr7	19758933	19813221	*TMEM196*	256130	0.012701526
Gene	HYPER in CCA	chr6	28414750	28415584	*COX11P1*	NA	0.007821587
Gene	HYPER in CCA	chr5	1877541	1887350	*IRX4*	50805	0.007658047
Gene	HYPER in CCA	chr18	14728271	14852737	*ANKRD30B*	374860	0.002288962
Gene	HYPER in CCA	chr20	36974759	37005665	*LBP*	3929	0.00040843
Gene	HYPER in CCA	chr18	894436	907681	*NA*	NA	0.012228169
Gene	HYPER in CCA	chr3	75721542	75728454	*LINC00960*	401074	0.002439935
Gene	HYPER in CCA	chr13	78469616	78493903	*EDNRB*	1910	0.00378943
Gene	HYPER in CCA	chr19	23258012	23330021	*ZNF730*	100129543	0.000975933
Gene	HYPER in CCA	chr2	45168902	45173216	*SIX3*	6496	0.00903026
Gene	HYPER in CCA	chr5	134869991	134871639	*NEUROG1*	4762	0.012362188
Gene	HYPER in CCA	chr11	115509281	115517680	*NA*	NA	0.002830276
Gene	HYPER in CCA	chr2	5832799	5841516	*SOX11*	6664	0.006796681
Gene	HYPER in CCA	chr2	182537815	182545603	*NEUROD1*	4760	0.012708424
Gene	HYPER in CCA	chr2	162279170	162280088	*NA*	NA	0.003375488
Gene	HYPER in CCA	chr5	63253720	63276870	*NA*	NA	0.001730751
Gene	HYPER in CCA	chr14	60386431	60530277	*LRRC9*	NA	0.005441917
Gene	HYPER in CCA	chr4	41752362	41759358	*NA*	NA	0.008532046

Gene	HYPER in CCA	chr5	78365540	78385289	*BHMT2*	23743	0.005004316
Gene	HYPER in CCA	chr19	30017406	30055386	*VSTM2B*	342865	0.003897226
Gene	HYPER in CCA	chr4	111538579	111563279	*PITX2*	5308	0.00422729
Gene	HYPER in CCA	chr2	31747550	31806136	*SRD5A2*	NA	0.003772109
Gene	HYPER in CCA	chr16	31579707	31580796	*YBX3P1*	440359	0.002543751
Gene	HYPER in CCA	chr15	41303795	41305498	*NA*	NA	0.006335698
Gene	HYPER in CCA	chr1	156611458	156614679	*NA*	NA	0.000276657
Gene	HYPER in CCA	chr11	12052422	12083332	*NA*	NA	0.000598155
Gene	HYPER in CCA	chr2	223162866	223169936	*CCDC140*	151278	0.006503303
Gene	HYPER in CCA	chr7	27145803	27192200	*HOXA3*	3200	0.002101608
Gene	HYPER in CCA	chr5	78407602	78428108	*BHMT*	635	0.003625329
Gene	HYPER in CCA	chr13	112721913	112726020	*SOX1*	6656	0.001226997
Gene	HYPER in CCA	chr10	134598297	134599556	*NKX6-2*	84504	0.001910695
Gene	HYPER in CCA	chr5	63256183	63258334	*HTR1A*	3350	0.001226997
Gene	HYPER in CCA	chr3	181429714	181432221	*SOX2*	6657	0.011970909
Gene	HYPER in CCA	chr2	131278770	131285579	*CFC1B*	55997;653275	0.001520425
Gene	HYPER in CCA	chr2	162280526	162285285	*NA*	NA	0.005935595
Gene	HYPER in CCA	chr11	32457064	32480315	*WT1-AS*	51352	0.010303184
Gene	HYPER in CCA	chr5	16067248	16180871	*Mar/11*	441061	0.000938708
Gene	HYPER in CCA	chr18	902767	906668	*NA*	NA	0.010878745
Gene	HYPER in CCA	chr20	61809852	61809938	*MIR124-3*	406909	0.010949784
Gene	HYPER in CCA	chr7	27281048	27286848	*EVX1-AS*	NA	0.004782137
Gene	HYPER in CCA	chr1	91177096	91182794	*BARHL2*	343472	0.005567622
Gene	HYPER in CCA	chr5	50668570	50679166	*NA*	642366	0.006050076
Gene	HYPER in CCA	chr1	63788730	63790797	*FOXD3*	27022	0.0029899
Gene	HYPER in CCA	chr2	177001340	177037830	*HOXD3*	3232;3233;401021	0.003802949
Gene	HYPER in CCA	chr19	57828576	57828930	*NA*	NA	0.007816947
Gene	HYPER in CCA	chr7	19152097	19153894	*NA*	NA	0.006941335
Gene	HYPER in CCA	chr7	99691391	99691470	*MIR93*	407050	0.000212232
Gene	HYPER in CCA	chr20	26167556	26232162	*MIR663A*	284801;724033	0.000594961
Gene	HYPER in CCA	chr3	58148274	58156363	*FLNB-AS1*	101929182	0.005154961
Gene	HYPER in CCA	chr13	28366780	28368905	*GSX1*	219409	0.007572198
Gene	HYPER in CCA	chr16	86598751	86601367	*NA*	NA	0.007359563
Gene	HYPER in CCA	chr12	14994026	14997642	*NA*	NA	0.011096743

Gene	HYPER in CCA	chr12	63539014	63544722	*AVPR1A*	552	0.002661693
Gene	HYPER in CCA	chr10	129535499	129539450	*FOXI2*	399823	0.005996136
Gene	HYPER in CCA	chr2	175190755	175195371	*NA*	285084	0.005861905
Gene	HYPER in CCA	chr13	79172497	79177673	*POU4F1*	5457	0.006101603
Gene	HYPER in CCA	chr12	123349882	123351568	*NA*	NA	0.000121986
Gene	HYPER in CCA	chr5	3596325	3600302	*NA*	NA	0.002096828
Gene	HYPER in CCA	chr17	34303529	34308532	*CCL16*	6360	0.000123063
Gene	HYPER in CCA	chr8	110986172	110987010	*NA*	NA	0.009995854
Gene	HYPER in CCA	chr19	23258003	23283163	*NA*	NA	0.000614238
Gene	HYPER in CCA	chr5	121646992	121647368	*NA*	NA	0.006937675
Gene	HYPER in CCA	chr6	168595038	168605181	*NA*	NA	0.004065526
Gene	HYPER in CCA	chr10	119494824	119495918	*NA*	NA	0.01140056
Gene	HYPER in CCA	chr2	105471969	105476929	*POU3F3*	5455	0.001774862
Gene	HYPER in CCA	chr10	135043778	135045062	*UTF1*	8433	0.004475665
Gene	HYPER in CCA	chr6	28954577	28956313	*HCG16*	101929874	0.001643387
Gene	HYPER in CCA	chr8	247696782	247722302	*NA*	NA	0.001750284
Gene	HYPER in CCA	chr19	29980682	30017855	*NA*	NA	0.009488266
Gene	HYPER in CCA	chr7	124869633	124904345	*NA*	101928254	0.003847763
Gene	HYPER in CCA	chr20	61637331	61638387	*BHLHE23*	128408	0.005021835
Gene	HYPER in CCA	chr11	201777012	201821594	*DBX1*	120237	0.005074343
Gene	HYPER in CCA	chr7	272261923	272330674	*NA*	NA	0.001396664
Gene	HYPER in CCA	chr17	338252373	338261944	*NA*	NA	0.009028288
Gene	HYPER in CCA	chr17	128934662	128939271	*NA*	NA	0.006424971
Gene	HYPER in CCA	chr8	235599641	235641113	*NKX2-6*	137814	0.002622133
Gene	HYPER in CCA	chr12	75433857	75603648	*KCNC2*	3747	0.002586638
Gene	HYPER in CCA	chr16	865441331	865480761	*FOXF1*	2294	0.00996659
Gene	HYPER in CCA	chr2	710044421	710177752	*FIGLA*	344018	0.001537555
Gene	HYPER in CCA	chr12	130647004	130650285	*FZD10*	11211	0.012128497
Gene	HYPER in CCA	chr1	537536962	537553784	*NA*	NA	0.005565809
Gene	HYPER in CCA	chr2	176942200	176948641	*EVX2*	344191	0.002997482
Gene	HYPER in CCA	chr16	3231233	3234018	*NA*	NA	0.009825395
Gene	HYPER in CCA	chr7	271352665	271398844	*HOTAIRM1*	100506311	0.004133972
Gene	HYPER in CCA	chr2	186897618	186947960	*NA*	101927217	0.00242761
Gene	HYPER in CCA	chr17	41052814	41065386	*G6PC*	2538	0.000404286

Gene	HYPER in CCA	chr13	31506840	31549639	*TEX26*	122046	0.000343959
Gene	HYPER in CCA	chr3	188659504	188665428	*TPRG1-AS1*	NA	0.001624073
Gene	HYPER in CCA	chr16	51183150	51183730	*NA*	NA	0.009273432
Gene	HYPER in CCA	chr20	9485827	9495645	*NA*	101929329	0.002428131
Gene	HYPER in CCA	chr14	29235050	29238870	*FOXG1*	2290	0.005441917
Gene	HYPER in CCA	chr5	3596168	3601517	*IRX1*	79192	0.000770269
Gene	HYPER in CCA	chr7	24323782	24331484	*NPY*	4852	0.003847763
Gene	HYPER in CCA	chr15	80487826	80544555	*NA*	100996492	0.00250921
Gene	HYPER in CCA	chr1	71172136	71252151	*NA*	101927244	0.005660086
Gene	HYPER in CCA	chr7	19183916	19185876	*NA*	NA	0.005883013
Gene	HYPER in CCA	chr7	56601923	56605823	*NA*	101928401	0.000881156
Gene	HYPER in CCA	chr7	64029806	64030815	*NA*	NA	0.001248566
Gene	HYPER in CCA	chr8	55370495	55373448	*SOX17*	64321	0.001854993
Gene	HYPER in CCA	chr4	190962497	190964569	*AGGF1P1*	NA	0.001036106
Gene	HYPER in CCA	chr7	27278862	27280847	*NA*	NA	0.005230144
Gene	HYPER in CCA	chr2	176964458	176966408	*HOXD12*	3238	0.00039394
Gene	HYPER in CCA	chr11	6452279	6463847	*HPX*	3263	7.98E-05
Gene	HYPER in CCA	chr4	147560045	147563626	*POU4F2*	5458	0.004506704
Gene	HYPER in CCA	chr11	116700422	116703788	*APOC3*	345	4.37E-05
Gene	HYPER in CCA	chr2	177015031	177015140	*MIR10B*	406903	0.001353637
Gene	HYPER in CCA	chr5	2745959	2752969	*IRX2*	153572	0.000738408
Gene	HYPER in CCA	chr16	67977450	67978423	*NA*	NA	5.11E-05
Gene	HYPER in CCA	chr7	27224137	27228912	*HOXA11-AS*	221883	0.001169047
Gene	HYPER in CCA	chr2	175200601	175202151	*NA*	NA	0.012788345
Gene	HYPER in CCA	chr17	46810453	46811250	*NA*	NA	0.005286215
Gene	HYPER in CCA	chr7	63642088	63643271	*NA*	NA	0.002117056
Gene	HYPER in CCA	chr4	174448421	174512475	*HAND2-AS1*	79804	0.003002074
Gene	HYPER in CCA	chr19	58208735	58220579	*ZNF154*	7710	0.00242761
Gene	HYPER in CCA	chr12	54356092	54368740	*HOTAIR*	100124700	0.002154375
Gene	HYPER in CCA	chr18	76736555	76739074	*NA*	NA	0.003212578
Gene	HYPER in CCA	chr20	39314488	39317880	*MAFB*	9935	0.005227318
Gene	HYPER in CCA	chr5	115140430	115152651	*CDO1*	1036	0.000217351
Gene	HYPER in CCA	chr6	137813336	137815531	*OLIG3*	167826	0.003897226
Gene	HYPER in CCA	chr20	37353105	37358015	*SLC32A1*	140679	0.00173

Gene	HYPER in CCA	chr16	28548606	28550495	*NUPR1*	26471	0.000189873
Gene	HYPER in CCA	chr7	27168588	27192180	*NA*	NA	0.000617284
Gene	HYPER in CCA	chr17	46656992	46659621	*MIR10A*	406902	0.001996998
Gene	HYPER in CCA	chr5	170736288	170739138	*TLX3*	30012	0.009954205
Gene	HYPER in CCA	chr5	145718587	145720083	*POU4F3*	5459	0.001300286
Gene	HYPER in CCA	chr20	21378456	21381029	*NA*	NA	0.000997534
Gene	HYPER in CCA	chr7	27203154	27219632	*NA*	NA	0.000836831
Gene	HYPER in CCA	chr19	35628549	35630484	*NA*	NA	0.00026291
Gene	HYPER in CCA	chr13	95351948	95355116	*LINC00391*	NA	0.000471577
Gene	HYPER in CCA	chr7	27169596	27195542	*HOXA-AS3*	100133311	0.000629014
Gene	HYPER in CCA	chr13	94806447	94840245	*GPC6-AS1*	100873972	0.000468966
Gene	HYPER in CCA	chr1	214202236	214204109	*NA*	NA	0.00051045
Gene	HYPER in CCA	chr2	176957619	176960666	*HOXD13*	3239	0.000799395
Gene	HYPER in CCA	chr2	176968944	176974722	*HOXD11*	3237	0.001083634
Gene	HYPER in CCA	chr3	121311966	121349139	*FBXO40*	51725	0.000168282
Gene	HYPER in CCA	chr18	74962505	74980858	*GALR1*	2587	0.002069234
Gene	HYPER in CCA	chr2	71115001	71117089	*LINC01143*	NA	0.002077072
Gene	HYPER in CCA	chr17	39210750	39211482	*KRTAP2-2*	728279	0.001075354
Gene	HYPER in CCA	chr1	40598436	40599120	*NA*	NA	0.000674978
Gene	HYPER in CCA	chr21	45203004	45203454	*TMEM97P1*	NA	0.002088208
Gene	HYPER in CCA	chr12	54413694	54416373	*NA*	NA	0.009511522
Gene	HYPER in CCA	chr4	174446120	174451380	*HAND2*	9464	0.001331146
Gene	HYPER in CCA	chr13	79170264	79173754	*NA*	NA	0.000578913
Gene	HYPER in CCA	chr14	69403319	69403581	*BANF1P1*	NA	4.39E-05
Gene	HYPER in CCA	chr1	79355449	79472403	*ELTD1*	64123	0.00090953
Gene	HYPER in CCA	chr1	12587766	12588462	*NA*	NA	0.000962033
Gene	HYPER in CCA	chr12	56754353	56756607	*APOF*	319	0.000212232
Gene	HYPER in CCA	chr3	58490863	58523046	*ACOX2*	8309	7.06E-05
Gene	HYPER in CCA	chr5	50265494	50266021	*NA*	NA	0.000608291
Gene	HYPER in CCA	chr4	74262831	74287129	*ALB*	213	0.002924395
Gene	HYPER in CCA	chr8	109907258	110075646	*NA*	NA	0.002765582
Gene	HYPER in CCA	chr16	593277	593366	*MIR3176*	100423037	0.000760496
Gene	HYPER in CCA	chr10	124895478	124897257	*HMX3*	340784	0.007480484
Gene	HYPER in CCA	chr19	45445495	45452820	*APOC4*	346	4.41E-05

Gene	HYPER in CCA	chr19	45445495	45452822	*APOC4-APOC2*	344;346	4.41E-05
Gene	HYPER in CCA	chr5	50265051	50266001	*NA*	100287592	0.001083634
Gene	HYPER in CCA	chr7	27202054	27210117	*HOXA9*	3205;442920	0.000693624
Gene	HYPER in CCA	chr2	17701595 0	17701795 4	*HOXD4*	3233	0.001163678
Gene	HYPER in CCA	chr2	945320	945960	*NA*	NA	0.005660086
Gene	HYPER in CCA	chr10	12575142 6	12575218 5	*YBX2P1*	NA	0.000863753
Gene	HYPER in CCA	chr10	54525140	54531460	*MBL2*	4153	0.005585786
Gene	HYPER in CCA	chr7	27197963	27198595	*NA*	NA	0.00052899
Gene	HYPER in CCA	chr13	53418109	53422775	*PCDH8*	5100	0.000544639
Gene	HYPER in CCA	chr2	13301453 9	13301465 3	*MIR663B*	100313824	0.005557174
Gene	HYPER in CCA	chr8	72753784	72756703	*MSC*	9242	0.000610746
Gene	HYPER in CCA	chr12	54385522	54385631	*MIR196A2*	406973	0.000375286
Gene	HYPER in CCA	chr7	27180671	27183287	*HOXA5*	3202	0.000468229
Gene	HYPER in CCA	chr2	17698708 8	17698985 3	*HOXD9*	3235	0.000955651
Gene	HYPER in CCA	chr1	16119208 2	16119342 1	*APOA2*	336	0.002970173
Gene	HYPER in CCA	chr16	71599692	71612090	*NA*	100132529	1.39E-05
Gene	HYPER in CCA	chr2	17698633 9	17700182 6	*HOXD-AS2*	100506783	0.000503552
Gene	HYPER in CCA	chr3	12969314 8	12969678 1	*TRH*	7200	0.00242761
Gene	HYPER in CCA	chr20	21491648	21494664	*NKX2-2*	4821	0.001936218
Gene	HYPER in CCA	chr7	35535631	35549873	*NA*	NA	5.11E-05
Gene	HYPER in CCA	chr12	95782375	95799280	*NA*	NA	0.002449027
Gene	HYPER in CCA	chr2	17702889 2	17703044 4	*NA*	NA	0.000738408
Gene	HYPER in CCA	chr14	60975669	60979568	*SIX6*	4990	0.001727656
Gene	HYPER in CCA	chr12	11437037 4	11437506 0	*NA*	NA	5.23E-05
Gene	HYPER in CCA	chr5	13950552 1	13950839 1	*IGIP*	492311	4.63E-06
Gene	HYPER in CCA	chr17	41522075	41528568	*MIR2117*	100313779	0.007018649
Gene	HYPER in CCA	chr7	19184405	19185044	*FERD3L*	222894	0.001694731
Gene	HYPER in CCA	chr2	20750714 2	20751417 3	*NA*	NA	0.000129241
Gene	HYPER in CCA	chr7	27208238	27211534	*HOXA10-AS*	442920;100874323	0.004287013
Gene	HYPER in CCA	chr4	15552528 6	15553411 9	*FGG*	2266	0.000871723
Gene	HYPER in CCA	chr13	34185104	34185659	*NA*	NA	0.00481158
Gene	HYPER in CCA	chr12	14978503	14996429	*ART4*	420	0.006467274
Gene	HYPER in CCA	chr1	19700832 1	19703639 7	*F13B*	2165	0.000164444
Gene	HYPER in CCA	chr11	9450320	9450501	*SNORA23*	677808	4.78E-05

Gene	HYPER in CCA	chr2	119591276	119592686	*NA*	NA	0.002152732
Gene	HYPER in CCA	chr20	21492085	21492947	*NKX2-2-AS1*	NA	0.002135334
Gene	HYPER in CCA	chr2	45240353	45240807	*NA*	NA	0.003676388
Gene	HYPER in CCA	chr17	14207171	14208822	*NA*	84815	4.41E-05
Gene	HYPER in CCA	chr7	27132612	27135615	*HOXA1*	3198	0.000770012
Gene	HYPER in CCA	chr3	170374351	170379912	*NA*	101928583	0.000900556
Gene	HYPER in CCA	chr7	27193335	27197555	*HOXA7*	3204	0.000475096
Gene	HYPER in CCA	chr1	3701572	3702102	*NA*	NA	0.000404286
Gene	HYPER in CCA	chr7	27168126	27170418	*HOXA4*	3201	4.78E-05
Gene	HYPER in CCA	chr11	43602944	43603033	*MIR129-2*	406918	0.004491197
Gene	HYPER in CCA	chr13	24902349	24903210	*NUS1P3*	NA	0.000829643
Gene	HYPER in CCA	chr14	19400329	19403264	*ARHGAP42P5*	NA	0.007807891
Gene	HYPER in CCA	chr7	156799001	156799826	*MNX1-AS2*	NA	0.000212232
Gene	HYPER in CCA	chr16	78529823	78540465	*NA*	NA	0.000515845
Gene	HYPER in CCA	chr16	71599563	71611033	*TAT*	6898	3.60E-06
Gene	HYPER in CCA	chr7	27209099	27209183	*MIR196B*	442920	0.005369366
Gene	HYPER in CCA	chr7	27139721	27142430	*HOXA2*	3199	7.49E-05
Gene	HYPER in CCA	chr12	57824899	57827718	*NA*	NA	3.60E-06
Gene	HYPER in CCA	chr8	43102334	43102553	*NA*	NA	0.001081161
Gene	HYPER in CCA	chr4	156750881	156787425	*ASIC5*	51802	0.000168486
Gene	HYPER in CCA	chr1	248020501	248041507	*TRIM58*	25893	3.60E-06
Gene	HYPER in CCA	chr1	95585703	95604110	*NA*	NA	9.38E-06
Gene	HYPER in CCA	chr17	46652875	46657473	*HOXB4*	3214	6.51E-05
Gene	HYPER in CCA	chr17	77997693	77999906	*NA*	NA	7.51E-06
Gene	HYPER in CCA	chr3	46538981	46542439	*RTP3*	83597	3.60E-06
Gene	HYPER in CCA	chr2	176994422	176997423	*HOXD8*	3234	0.000213693
Gene	HYPER in CCA	chr11	77774907	77779397	*THRSP*	7069	1.92E-06
Gene	HYPER in CCA	chr17	46706037	46712294	*HOXB-AS4*	NA	0.000146564
Gene	HYPER in CCA	chr16	14397824	14397906	*MIR193B*	574455	0.000515845
Gene	HYPER in CCA	chr12	7276280	7281538	*RBP5*	83758	3.60E-06
Gene	HYPER in CCA	chr17	46799084	46799884	*PRAC1*	84366	0.000253493
Gene	HYPER in CCA	chr22	50644014	50644491	*NA*	NA	4.59E-07
Gene	HYPER in CCA	chr5	142869420	142910915	*NA*	NA	0.00010177
Gene	HYPER in CCA	chr12	73004458	73005096	*CHCHD3P2*	NA	1.31E-05

Gene	HYPER in CCA	chr10	91406046	91410579	*NA*	NA	2.66E-05
Gene	HYPER in CCA	chr10	75601591	75606324	*NA*	NA	7.51E-06
Gene	HYPER in CCA	chr8	54788710	54789209	*NA*	NA	4.41E-05
Gene	HYPER in CCA	chr8	65291706	65291814	*MIR124-2*	406908	0.001154791
Gene	HYPER in CCA	chr6	160693649	160697162	*NA*	NA	3.60E-06
Gene	HYPER in CCA	chr17	46709852	46709921	*MIR196A1*	406972	8.34E-05
Promoter	HYPO in CCA	chr5	67729809	67731808	*NA*	NA	1.64E-05
Promoter	HYPO in CCA	chr22	40354901	40356900	*NA*	NA	1.98E-06
Promoter	HYPO in CCA	chr2	161991919	161993918	*TANK*	10010	3.68E-05
Promoter	HYPO in CCA	chr1	169071862	169073861	*NA*	101928596	0.000362056
Promoter	HYPO in CCA	chr1	173834325	173836324	*SNORD78*	692198	5.63E-06
Promoter	HYPO in CCA	chr15	96867667	96869666	*NR2F2*	7026	1.98E-06
Promoter	HYPO in CCA	chr6	43191099	43193098	*NA*	NA	1.42E-05
Promoter	HYPO in CCA	chr3	158389983	158391982	*LXN*	56925	1.11E-05
Promoter	HYPO in CCA	chr11	119035777	119037776	*NLRX1*	79671	0.000249881
Promoter	HYPO in CCA	chr15	91538360	91540359	*PRC1*	9055	0.000203638
Promoter	HYPO in CCA	chr20	39958263	39960262	*NA*	NA	9.34E-05
Promoter	HYPO in CCA	chr2	64870246	64872245	*NA*	NA	3.51E-05
Promoter	HYPO in CCA	chr2	85133633	85135632	*TRABD2A*	129293	5.63E-06
Promoter	HYPO in CCA	chr11	10920370	10922369	*NA*	NA	9.34E-05
Promoter	HYPO in CCA	chr17	79520488	79522487	*C17orf70*	80233	2.48E-05
Promoter	HYPO in CCA	chr16	88717061	88719060	*CYBA*	1535	4.26E-06
Promoter	HYPO in CCA	chr17	3623422	3625421	*NA*	NA	0.004846791
Promoter	HYPO in CCA	chr1	234699544	234701543	*NA*	NA	0.000965482
Promoter	HYPO in CCA	chr1	155909980	155911979	*RXFP4*	339403	5.28E-05
Promoter	HYPO in CCA	chr15	69371719	69373718	*NA*	NA	1.42E-05
Promoter	HYPO in CCA	chr2	109294558	109296557	*NA*	NA	6.53E-05
Promoter	HYPO in CCA	chr19	47735524	47737523	*BBC3*	27113;100422832;100422899	3.52E-05
Promoter	HYPO in CCA	chr7	30842527	30844526	*NA*	NA	0.001447701
Promoter	HYPO in CCA	chr14	55589328	55591327	*LGALS3*	3958	0.000678451
Promoter	HYPO in CCA	chr1	204676059	204678058	*RNA5SP75*	NA	0.001111032
Promoter	HYPO in CCA	chr8	22931502	22933501	*NA*	NA	1.01E-05
Promoter	HYPO in CCA	chr12	94954065	94956064	*MIR5700*	100847031	0.000174102
Promoter	HYPO in CCA	chr3	101658203	101660202	*NA*	152225	0.001512681

Promoter	HYPO in CCA	chr5	17117296	17119295	*NA*	NA	0.000410974
Promoter	HYPO in CCA	chr15	101707235	101709234	*NA*	NA	0.000102203
Promoter	HYPO in CCA	chr22	38091511	38093510	*TRIOBP*	11078	1.96E-05
Promoter	HYPO in CCA	chr11	85780425	85782424	*PICALM*	8301	0.000281728
Promoter	HYPO in CCA	chr15	22448320	22450319	*IGHV1OR15-1*	NA	0.003310504
Promoter	HYPO in CCA	chr1	228580491	228582490	*NA*	NA	4.68E-05
Promoter	HYPO in CCA	chr3	47023001	47025000	*CCDC12*	151903	0.003695939
Promoter	HYPO in CCA	chr2	70483018	70485017	*PCYOX1*	51449	0.000321091
Promoter	HYPO in CCA	chr6	35264095	35266094	*DEF6*	50619	0.000458795
Promoter	HYPO in CCA	chr1	43736108	43738107	*EBNA1BP2*	10969;102465439	3.67E-05
Promoter	HYPO in CCA	chr2	64832609	64834608	*NA*	339807	0.004883712
Promoter	HYPO in CCA	chr7	30026716	30028715	*NA*	NA	0.000349125
Promoter	HYPO in CCA	chr11	9159162	9161161	*SCUBE2*	57758	0.000220314
Promoter	HYPO in CCA	chr12	90339970	90341969	*NA*	NA	0.001258661
Promoter	HYPO in CCA	chr11	19400531	19402530	*NAV2-IT1*	NA	0.002287181
Promoter	HYPO in CCA	chr21	37801158	37803157	*NA*	NA	1.98E-06
Promoter	HYPO in CCA	chr1	26604167	26606166	*SH3BGRL3*	83442	6.78E-05
Promoter	HYPO in CCA	chr5	140097010	140099009	*VTRNA1-2*	56663	0.000677763
Promoter	HYPO in CCA	chr3	57092969	57094968	*SPATA12*	353324	0.000528832
Promoter	HYPO in CCA	chr3	97199851	97201850	*NA*	NA	0.001001854
Promoter	HYPO in CCA	chr3	149454002	149456001	*WWTR1*	25937	0.001453788
Promoter	HYPO in CCA	chr1	152019884	152021883	*S100A11*	6282	3.52E-05
Promoter	HYPO in CCA	chr2	241503721	241505720	*RNPEPL1*	57140	0.000383523
Promoter	HYPO in CCA	chr16	87359093	87361092	*NA*	NA	0.001426494
Promoter	HYPO in CCA	chr1	229546015	229548014	*RN7SKP276*	NA	0.000292125
Promoter	HYPO in CCA	chr8	1702444	1704443	*CLN8*	2055;101927714	0.000589871
Promoter	HYPO in CCA	chr1	27667013	27669012	*SYTL1*	84958	0.000173354
Promoter	HYPO in CCA	chr1	35729584	35731583	*RN7SL136P*	NA	5.42E-05
Promoter	HYPO in CCA	chr11	9780581	9782580	*NA*	440028	0.000220314
Promoter	HYPO in CCA	chr1	156630717	156632716	*NA*	NA	2.15E-06
Promoter	HYPO in CCA	chr8	125259140	125261139	*NA*	101927588	0.002694447
Promoter	HYPO in CCA	chr12	94676121	94678120	*NA*	NA	0.001604671
Promoter	HYPO in CCA	chr17	73840299	73842298	*UNC13D*	201294	0.000103183
Promoter	HYPO in CCA	chr6	149805698	149807697	*ZC3H12D*	340152	0.001653926

Promoter	HYPO in CCA	chr16	87839583	87841582	*NA*	NA	0.001912975
Promoter	HYPO in CCA	chr7	142986208	142988207	*RN7SL535P*	NA	0.000211022
Promoter	HYPO in CCA	chr4	43898974	43900973	*NA*	NA	0.001673597
Promoter	HYPO in CCA	chr3	183542883	183544882	*MAP6D1*	79929	0.000128069
Promoter	HYPO in CCA	chr21	45579460	45581459	*NA*	101928576	0.00048152
Promoter	HYPO in CCA	chr3	46447154	46449153	*CCRL2*	9034	0.001267952
Promoter	HYPO in CCA	chr9	101864820	101866819	*TGFBR1*	7046	0.00506367
Promoter	HYPO in CCA	chr7	100180105	100182104	*FBXO24*	26261	0.000100611
Promoter	HYPO in CCA	chr17	43325704	43327703	*NA*	101927036	0.000416037
Promoter	HYPO in CCA	chr2	87753387	87755386	*LINC00152*	112597;541471	0.000320314
Promoter	HYPO in CCA	chr17	75275151	75277150	*Sep/09*	10801	0.001680929
Promoter	HYPO in CCA	chr2	220116465	220118464	*TUBA4B*	80086	1.98E-05
Promoter	HYPO in CCA	chr15	81701358	81703357	*NA*	NA	1.22E-05
Promoter	HYPO in CCA	chr16	69760355	69762354	*NQO1*	1728	2.63E-05
Promoter	HYPO in CCA	chr6	33243417	33245416	*B3GALT4*	8705	0.000248542
Promoter	HYPO in CCA	chr1	30181895	30183894	*NA*	NA	0.008238851
Promoter	HYPO in CCA	chr19	54367977	54369976	*MYADM*	91663	0.000445119
Promoter	HYPO in CCA	chr1	24644312	24646311	*GRHL3*	57822	0.000730854
Promoter	HYPO in CCA	chr16	69163694	69165693	*CIRH1A*	84916	0.000114765
Promoter	HYPO in CCA	chr17	27965145	27967144	*NA*	NA	0.000493729
Promoter	HYPO in CCA	chr3	46448051	46450050	*NA*	NA	0.002741067
Promoter	HYPO in CCA	chr12	124996268	124998267	*NA*	NA	0.005990826
Promoter	HYPO in CCA	chr1	248510577	248512576	*OR14C36*	127066	0.00899332
Promoter	HYPO in CCA	chr17	73027170	73029169	*KCTD2*	23510;101928375	0.000100611
Promoter	HYPO in CCA	chr9	117567907	117569906	*TNFSF15*	9966	0.000123446
Promoter	HYPO in CCA	chr10	88730569	88732568	*ADIRF-AS1*	NA	0.000516694
Promoter	HYPO in CCA	chr17	61915843	61917842	*RN7SL805P*	NA	0.001903664
Promoter	HYPO in CCA	chr14	105143587	105145586	*MIR4710*	100616300	9.84E-05
Promoter	HYPO in CCA	chr5	141705521	141707520	*SPRY4*	81848	0.000189498
Promoter	HYPO in CCA	chr19	14489813	14491812	*CD97*	976	0.00497805
Promoter	HYPO in CCA	chr11	71565823	71567822	*NA*	NA	0.007399367
Promoter	HYPO in CCA	chr15	85873066	85875065	*ADAMTS7P4*	NA	0.001694613
Promoter	HYPO in CCA	chr17	73082322	73084321	*SLC16A5*	9121	0.009252237
Promoter	HYPO in CCA	chr16	69759416	69761415	*NA*	NA	6.07E-05

Promoter	HYPO in CCA	chr10	106027131	106029130	*GSTO2*	119391	0.000615542
Promoter	HYPO in CCA	chr12	118499736	118501735	*WSB2*	55884	0.000359802
Promoter	HYPO in CCA	chr1	159879660	159881659	*NA*	NA	0.000619209
Promoter	HYPO in CCA	chr10	106027678	106029677	*MIR4482-1*	100616323	0.00089893
Promoter	HYPO in CCA	chr14	24808752	24810751	*RIPK3*	11035	0.001168536
Promoter	HYPO in CCA	chr20	33758376	33760375	*PROCR*	10544	0.003610885
Promoter	HYPO in CCA	chr12	29470282	29472281	*NA*	100506606	0.002438997
Promoter	HYPO in CCA	chr1	45242015	45244014	*SNORD38A*	94162	0.000159913
Promoter	HYPO in CCA	chr2	239198244	239200243	*PER2*	8864	0.002828757
Promoter	HYPO in CCA	chr8	22455614	22457613	*C8orf58*	541565	0.001124511
Promoter	HYPO in CCA	chr10	99471430	99473429	*MARVELD1*	83742	0.001683662
Promoter	HYPO in CCA	chr21	32931791	32933790	*TIAM1*	7074	0.004003426
Promoter	HYPO in CCA	chr1	235116052	235118051	*NA*	NA	7.32E-05
Promoter	HYPO in CCA	chr18	55862429	55864428	*NA*	NA	0.000271054
Promoter	HYPO in CCA	chr19	1257884	1259883	*CIRBP*	1153	6.78E-05
Promoter	HYPO in CCA	chr1	1369454	1371453	*NA*	NA	0.001941738
Promoter	HYPO in CCA	chr8	38409699	38411698	*NA*	NA	0.002282983
Promoter	HYPO in CCA	chr19	13907248	13909247	*NA*	NA	0.001240004
Promoter	HYPO in CCA	chr17	15554468	15556467	*NA*	NA	0.000942209
Promoter	HYPO in CCA	chr17	15553404	15555403	*NA*	NA	0.000942209
Promoter	HYPO in CCA	chr12	7339781	7341780	*PEX5*	5830	0.000100611
Promoter	HYPO in CCA	chr10	88730084	88732083	*NA*	NA	0.003660492
Promoter	HYPO in CCA	chr17	20370353	20372352	*LGALS9B*	284194	0.002196737
Promoter	HYPO in CCA	chr21	46349528	46351527	*NA*	NA	0.000962188
Promoter	HYPO in CCA	chr16	125506	127505	*MPG*	4350	0.000410974
Promoter	HYPO in CCA	chr7	87847174	87849173	*NA*	NA	0.006932924
Promoter	HYPO in CCA	chr11	66622618	66624617	*LRFN4*	78999	0.006715553
Promoter	HYPO in CCA	chr15	74726309	74728308	*SEMA7A*	8482	0.000473065
Promoter	HYPO in CCA	chr16	29464936	29466935	*NA*	NA	0.000297988
Promoter	HYPO in CCA	chr16	29465473	29467472	*NA*	552900	0.000297988
Promoter	HYPO in CCA	chr16	29465786	29467785	*BOLA2*	552900;654483	0.000297988
Promoter	HYPO in CCA	chr16	29464912	29466911	*SLX1B-SULT1A4*	100526831	0.000297988
Promoter	HYPO in CCA	chr16	29465627	29467626	*SULT1A4*	6818;445329;101929857	0.000297988
Promoter	HYPO in CCA	chr5	131630509	131632508	*P4HA2*	8974;101927705	0.005000971

Promoter	HYPO in CCA	chr6	52224719	52226718	*PAQR8*	85315	0.000854929
Promoter	HYPO in CCA	chr1	32040675	32042674	*NA*	NA	0.007127673
Promoter	HYPO in CCA	chr1	32040616	32042615	*TINAGL1*	64129	0.007127673
Promoter	HYPO in CCA	chr7	1781428	1783427	*NA*	101927125	0.001444041
Promoter	HYPO in CCA	chr16	29818554	29820553	*NA*	NA	0.003612353
Promoter	HYPO in CCA	chr18	29265300	29267299	*B4GALT6*	9331	0.00589846
Promoter	HYPO in CCA	chr10	102754875	102756874	*LZTS2*	84445	0.000304401
Promoter	HYPO in CCA	chr1	2142462	2144461	*NA*	NA	0.000472801
Promoter	HYPO in CCA	chr11	63751825	63753824	*OTUB1*	55611;101927673	0.000321091
Promoter	HYPO in CCA	chr14	100202530	100204529	*EML1*	2009	0.002132842
Promoter	HYPO in CCA	chr1	151812534	151814533	*C2CD4D*	100191040	0.006630264
Promoter	HYPO in CCA	chr5	40839786	40841785	*CARD6*	84674	0.004963
Promoter	HYPO in CCA	chr14	61789037	61791036	*NA*	NA	0.004255713
Promoter	HYPO in CCA	chr6	32920400	32922399	*NA*	NA	0.00524688
Promoter	HYPO in CCA	chr3	119041108	119043107	*ARHGAP31-AS1*	NA	0.000174102
Promoter	HYPO in CCA	chr1	155947090	155949089	*NA*	NA	0.000919114
Promoter	HYPO in CCA	chr6	26194294	26196293	*HIST1H1PS1*	NA	0.001043135
Promoter	HYPO in CCA	chr16	66636277	66638276	*CMTM3*	123920	0.000409069
Promoter	HYPO in CCA	chr9	140170701	140172700	*TOR4A*	54863	0.001548666
Promoter	HYPO in CCA	chr11	6341378	6343377	*PRKCDBP*	112464	0.001654514
Promoter	HYPO in CCA	chr22	36850492	36852491	*NA*	NA	0.000622885
Promoter	HYPO in CCA	chr16	21170263	21172262	*DNAH3*	55567	0.005114941
Promoter	HYPO in CCA	chr3	52566529	52568528	*SMIM4*	440957	0.002860779
Promoter	HYPO in CCA	chr2	262640	264639	*ACP1*	52	0.003917012
Promoter	HYPO in CCA	chr9	120465110	120467109	*TLR4*	7099	0.002486647
Promoter	HYPO in CCA	chr12	56325903	56327902	*WIBG*	84305	0.000304401
Promoter	HYPO in CCA	chr6	43042506	43044505	*PTK7*	5754	0.002830128
Gene	HYPO in CCA	chr5	67726254	67730308	*NA*	NA	3.60E-05
Gene	HYPO in CCA	chr22	30580633	30603098	*NA*	NA	3.60E-06
Gene	HYPO in CCA	chr2	237642025	237663006	*NA*	NA	0.00051045
Gene	HYPO in CCA	chr4	88896819	88904562	*SPP1*	6696	8.34E-05
Gene	HYPO in CCA	chr1	150209315	150209504	*RNU2-17P*	NA	0.000539964
Gene	HYPO in CCA	chr1	185527504	185597659	*NA*	101929093	0.001565737
Gene	HYPO in CCA	chr20	31175281	31196695	*NA*	NA	0.000134278
Gene	HYPO in CCA	chr10	119184705	119249930	*NA*	NA	0.000134278

Gene	HYPO in CCA	chr4	143487172	143582103	*NA*	NA	0.00400114
Gene	HYPO in CCA	chr5	6766004	6772066	*NA*	NA	0.000137938
Gene	HYPO in CCA	chr8	22928890	22932001	*NA*	NA	9.09E-05
Gene	HYPO in CCA	chr6	31804853	31804919	*SNORD52*	26797	0.000316709
Gene	HYPO in CCA	chr15	55665138	55665232	*MIR628*	693213	0.005373055
Gene	HYPO in CCA	chr8	62671653	62678528	*NA*	101929610	4.41E-05
Gene	HYPO in CCA	chr14	101459573	101459647	*SNORD114-31*	767612	6.08E-05
Gene	HYPO in CCA	chr21	37504748	37505330	*RPS9P1*	NA	1.24E-05
Gene	HYPO in CCA	chr19	3558013	3558484	*NA*	NA	0.005887668
Gene	HYPO in CCA	chr8	38401170	38410198	*NA*	NA	0.000442631
Gene	HYPO in CCA	chr11	72121760	72123123	*NA*	NA	0.002851865
Gene	HYPO in CCA	chr2	109293251	109295057	*NA*	NA	0.00011294
Gene	HYPO in CCA	chr16	2013746	2014096	*NA*	NA	0.000233325
Gene	HYPO in CCA	chr2	43268332	43270921	*NA*	NA	0.000719403
Gene	HYPO in CCA	chr15	63188011	63191742	*NA*	101928955	7.98E-05
Gene	HYPO in CCA	chr9	74920346	74958126	*NA*	100507540	0.004944408
Gene	HYPO in CCA	chr14	101455467	101455538	*SNORD114-28*	767609	0.000136503
Gene	HYPO in CCA	chr3	160394948	160396233	*ARL14*	80117	0.000811613
Gene	HYPO in CCA	chr1	222001008	222014008	*NA*	101929771	0.005887668
Gene	HYPO in CCA	chr14	103587184	103589344	*LINC00677*	NA	0.000179829
Gene	HYPO in CCA	chr12	91311800	91342446	*LINC00615*	439916	0.012106289
Gene	HYPO in CCA	chr17	73679623	73680879	*NA*	NA	0.006057868
Gene	HYPO in CCA	chr12	90341470	90343503	*NA*	NA	0.001896894
Gene	HYPO in CCA	chr15	77817882	77826452	*NA*	101929457	0.012391974
Gene	HYPO in CCA	chr11	19402031	19406561	*NAV2-IT1*	NA	0.003290099
Gene	HYPO in CCA	chr19	13947401	13947473	*MIR23A*	407010	2.75E-05
Gene	HYPO in CCA	chr3	133774100	133776492	*NA*	100507210	0.003173826
Gene	HYPO in CCA	chr7	87845975	87848541	*NA*	NA	0.007656913
Gene	HYPO in CCA	chr14	32395007	32399352	*NA*	NA	0.002326804
Gene	HYPO in CCA	chr16	72038936	72040442	*ATP5A1P3*	NA	0.000329852
Gene	HYPO in CCA	chr16	11290034	11318373	*NA*	NA	0.011963331
Gene	HYPO in CCA	chr1	155948590	155952777	*NA*	NA	5.23E-05
Gene	HYPO in CCA	chr12	94671534	94676620	*NA*	NA	0.001392768
Gene	HYPO in CCA	chr20	47896856	47896946	*SNORD12B*	100113393	0.005159898
Gene	HYPO in CCA	chr1	1252961	1254069	*NA*	NA	0.000134278
Gene	HYPO in CCA	chr17	9550337	9550977	*NA*	NA	0.002490309
Gene	HYPO in CCA	chr15	48095581	48138433	*NA*	101928442	0.001201697
Gene	HYPO in CCA	chr8	142363503	142365465	*NA*	NA	0.007969512
Gene	HYPO in CCA	chr1	32037186	32041174	*NA*	NA	0.006350434

Gene	HYPO in CCA	chr19	13945330	13947173	*MIR24-2*	284454;407013	0.003414658
Gene	HYPO in CCA	chr19	41931264	41934635	*B3GNT8*	374907	5.54E-05
Gene	HYPO in CCA	chr18	29265618	29266786	*NA*	NA	0.001564395
Gene	HYPO in CCA	chr17	80172103	80175228	*NA*	NA	0.003847763
Gene	HYPO in CCA	chr7	46300662	46334067	*NA*	NA	0.004385622
Gene	HYPO in CCA	chr16	28873487	28874661	*NA*	NA	0.012518488
Gene	HYPO in CCA	chr7	46184535	46185286	*NA*	NA	0.001868397
Gene	HYPO in CCA	chr1	2143610	2144013	*NA*	NA	0.000186579
Gene	HYPO in CCA	chr14	102196774	102198859	*NA*	NA	0.000881156
Gene	HYPO in CCA	chr4	10117380	10117508	*RNA5SP155*	NA	0.000963046
Gene	HYPO in CCA	chr22	40297086	40369725	*GRAP2*	9402	0.000631692
Gene	HYPO in CCA	chr1	153533584	153540366	*S100A2*	6273	0.000723258
Gene	HYPO in CCA	chr21	45578623	45579959	*NA*	101928576	0.003534436
Gene	HYPO in CCA	chr1	45242162	45242265	*SNORD46*	94161	0.000183641
Gene	HYPO in CCA	chr19	42637597	42637665	*MIR4323*	100422980	0.002129535
Gene	HYPO in CCA	chr15	78285747	78287631	*NA*	NA	0.001207539
Gene	HYPO in CCA	chr11	49119715	49122720	*NA*	NA	0.000760496
Gene	HYPO in CCA	chr3	158363611	158390482	*LXN*	56925	0.000189873
Gene	HYPO in CCA	chr6	30734602	30760027	*HCG20*	NA	0.000183641
Gene	HYPO in CCA	chr1	15490840	15497813	*C1orf195*	727684	0.002851865
Gene	HYPO in CCA	chr1	61005921	61106163	*NA*	NA	0.00051045
Gene	HYPO in CCA	chr1	30181698	30182394	*NA*	NA	0.011251141
Gene	HYPO in CCA	chr6	26195794	26195999	*HIST1H1PS1*	NA	0.000411251
Gene	HYPO in CCA	chr4	43900474	43901368	*NA*	NA	0.001798775
Gene	HYPO in CCA	chr17	27966645	27967843	*NA*	NA	0.000770269
Gene	HYPO in CCA	chr2	43254992	43266686	*NA*	NA	0.000510134
Gene	HYPO in CCA	chr19	52645879	52647409	*NA*	NA	0.001226997
Gene	HYPO in CCA	chr3	149086809	149095652	*TM4SF1*	4071	0.001641855
Gene	HYPO in CCA	chr17	79336072	79348014	*NA*	NA	0.003270988
Gene	HYPO in CCA	chr19	13907388	13907747	*NA*	NA	0.000510134
Gene	HYPO in CCA	chr19	54368017	54369394	*NA*	NA	0.002281516
Gene	HYPO in CCA	chr21	32931558	32932800	*NA*	150051	0.005883013
Gene	HYPO in CCA	chr1	234859789	234867390	*LINC01132*	100506810	0.002583914
Gene	HYPO in CCA	chr11	67351066	67354131	*GSTP1*	2950	0.002468278
Gene	HYPO in CCA	chr19	36158850	36164193	*UPK1A-AS1*	100862728	0.004667472
Gene	HYPO in CCA	chr3	46448654	46454488	*CCRL2*	9034	0.006794385
Gene	HYPO in CCA	chr4	123372625	123377880	*IL2*	3558	0.001431971
Gene	HYPO in CCA	chr21	46222492	46224632	*NA*	101928689	0.00040843
Gene	HYPO in CCA	chr16	57655946	57665559	*NA*	NA	0.00287829
Gene	HYPO in CCA	chr15	90207596	90222658	*PLIN1*	5346	0.000581314

Gene	HYPO in CCA	chr1	24634046	24648391	*NA*	NA	0.003802949
Gene	HYPO in CCA	chr17	20352708	20370852	*LGALS9B*	284194	0.003145573
Gene	HYPO in CCA	chr10	120968043	120971272	*GRK5-IT1*	101927868	0.012766327
Gene	HYPO in CCA	chr19	13890884	13900972	*NA*	NA	0.010019944
Gene	HYPO in CCA	chr3	158362067	158410364	*GFM1*	85476	0.002682499
Gene	HYPO in CCA	chr16	29465822	29469540	*SLX1B*	79008;548593	0.000504701
Gene	HYPO in CCA	chr1	161110998	161111126	*NA*	NA	0.008140199
Gene	HYPO in CCA	chr1	8935847	8938066	*ENO1-IT1*	NA	0.000750221
Gene	HYPO in CCA	chr20	32254304	32256331	*ACTL10*	170487	0.012099599
Gene	HYPO in CCA	chr19	24216276	24312654	*ZNF254*	9534	0.011885055
Gene	HYPO in CCA	chr1	185286911	185287662	*NA*	NA	0.004263938
Gene	HYPO in CCA	chr3	185224050	185270401	*LIPH*	200879	0.00242761
Gene	HYPO in CCA	chr14	24805227	24809251	*RIPK3*	11035	0.004667472
Gene	HYPO in CCA	chr1	224407315	224415745	*NA*	101927164	0.012708424
Gene	HYPO in CCA	chr2	27440258	27466811	*CAD*	790	0.001580843
Gene	HYPO in CCA	chr14	105144031	105144086	*MIR4710*	100616300	0.000134278
Gene	HYPO in CCA	chr16	69740899	69760854	*NQO1*	1728	0.000738408
Gene	HYPO in CCA	chr10	88730498	88769883	*NA*	NA	0.001727656
Gene	HYPO in CCA	chr15	42184991	42190773	*NA*	NA	0.005154961
Gene	HYPO in CCA	chr14	74178494	74181128	*PNMA1*	9240	0.003375488
Gene	HYPO in CCA	chr17	70117161	70122561	*SOX9*	6662	0.007068796
Gene	HYPO in CCA	chr12	7319270	7341665	*NA*	NA	0.00039394
Gene	HYPO in CCA	chr14	106110833	106115394	*NA*	NA	0.00358847
Gene	HYPO in CCA	chr3	119033140	119041607	*ARHGAP31-AS1*	NA	0.000770269
Gene	HYPO in CCA	chr16	88709691	88717560	*CYBA*	1535	0.000748085
Gene	HYPO in CCA	chr19	54357835	54372361	*NA*	NA	0.005887668
Gene	HYPO in CCA	chr4	152328703	152329987	*NA*	NA	0.008811024
Gene	HYPO in CCA	chr5	40841286	40860275	*CARD6*	84674	0.011026151
Gene	HYPO in CCA	chr5	112043195	112181936	*APC*	324	0.005154961
Gene	HYPO in CCA	chr8	38409766	38416538	*NA*	NA	0.012915215
Gene	HYPO in CCA	chr16	89778264	89784573	*VPS9D1-AS1*	100128881	0.001996998
Gene	HYPO in CCA	chr4	6689175	6692246	*NA*	339988	0.00098283
Gene	HYPO in CCA	chr19	1238178	1239521	*NA*	NA	0.003837772
Gene	HYPO in CCA	chr22	39410088	39416357	*APOBEC3C*	27350	0.002051826
Gene	HYPO in CCA	chr19	46142252	46142345	*MIR330*	442902	0.000408002
Gene	HYPO in CCA	chr12	70037140	70093256	*BEST3*	144453	0.00040843
Gene	HYPO in CCA	chr2	166651361	166666520	*NA*	NA	0.001286079
Gene	HYPO in CCA	chr21	37502669	37504208	*MEMO1P1*	NA	7.83E-05
Gene	HYPO in CCA	chr18	20837128	20840318	*NA*	NA	0.006240338

Gene	HYPO in CCA	chr2	192542794	192561385	*NABP1*	64859	0.000811613
Gene	HYPO in CCA	chr9	103189438	103213511	*MSANTD3*	91283	0.011526426
Gene	HYPO in CCA	chr12	98879322	98897633	*NA*	643770	0.00442454
Gene	HYPO in CCA	chr18	55857066	55862928	*NA*	NA	0.003606849

TP53-gr: Differential methylated regions (DMRs)

Location	Epimutation	Chromosome	Start	End	Symbol	EntrezID	Combined FDR *P*-value
Promoter	HYPER in CCA	chr2	47293461	47295460	*NA*	NA	1.28E-06
Promoter	HYPER in CCA	chr1	235498621	235500620	*NA*	NA	0.000128842
Promoter	HYPER in CCA	chr1	95584203	95586202	*NA*	NA	0.000475705
Promoter	HYPER in CCA	chr1	11899574	11901573	*NPPA-AS1*	100379251	3.76E-08
Promoter	HYPER in CCA	chr15	81297874	81299873	*C15orf26*	161502	1.34E-05
Promoter	HYPER in CCA	chr22	24384181	24386180	*GSTT1*	2952	0.000204181
Promoter	HYPER in CCA	chr15	34782273	34784272	*HNRNPLP2*	NA	0.000226649
Promoter	HYPER in CCA	chr3	174154863	174156862	*NAALADL2*	254827	0.000403688
Promoter	HYPER in CCA	chr16	78539966	78541965	*NA*	NA	0.000485714
Promoter	HYPER in CCA	chr12	109491258	109493257	*USP30-AS1*	100131733	0.000509031
Promoter	HYPER in CCA	chr5	95581980	95583979	*NA*	NA	0.000126323
Promoter	HYPER in CCA	chr5	16178847	16180846	*NA*	NA	4.85E-05
Promoter	HYPER in CCA	chr5	1886851	1888850	*IRX4*	50805	8.56E-05
Promoter	HYPER in CCA	chr5	1885946	1887945	*NA*	101929081	0.000215018
Promoter	HYPER in CCA	chr14	57278401	57280400	*OTX2-AS1*	100309464	0.001342581
Promoter	HYPER in CCA	chr19	30016160	30018159	*NA*	284395	0.001342581
Promoter	HYPER in CCA	chr6	139793693	139795692	*NA*	645434	0.000301972
Promoter	HYPER in CCA	chr19	30015906	30017905	*VSTM2B*	342865	0.001251416
Promoter	HYPER in CCA	chr15	32607356	32609355	*NA*	NA	0.001105465
Promoter	HYPER in CCA	chr7	24322282	24324281	*NPY*	4852	0.001914639
Promoter	HYPER in CCA	chr7	56296976	56298975	*CCNJP1*	NA	0.000599821
Promoter	HYPER in CCA	chr5	2750745	2752744	*C5orf38*	153571	3.96E-05
Promoter	HYPER in CCA	chr7	70595655	70597654	*WBSCR17*	64409	0.002451632
Promoter	HYPER in CCA	chr9	127710272	127712271	*GOLGA1*	2800	6.84E-06
Promoter	HYPER in CCA	chr18	76738775	76740774	*SALL3*	27164	0.000141326
Promoter	HYPER in CCA	chr17	46709422	46711421	*MIR196A1*	406972	0.000258992
Promoter	HYPER in CCA	chr2	177014450	177016449	*HOXD4*	3233	3.60E-05
Promoter	HYPER in CCA	chr2	176999840	177001839	*HOXD3*	3232;3233;401021	0.000258552

Promoter	HYPER in CCA	chr10	135042278	135044277	*UTF1*	8433	5.53E-05
Promoter	HYPER in CCA	chr7	153582682	153584681	*DPP6*	1804	0.000916284
Promoter	HYPER in CCA	chr19	58543900	58545899	*ZSCAN1*	284312	5.97E-05
Promoter	HYPER in CCA	chr19	4724186	4726185	*DPP9*	91039	0.000178458
Promoter	HYPER in CCA	chr19	57182652	57184651	*ZNF835*	90485	0.000583461
Promoter	HYPER in CCA	chr19	57182136	57184135	*NA*	NA	0.000583461
Promoter	HYPER in CCA	chr2	177013531	177015530	*MIR10B*	406903	4.85E-05
Promoter	HYPER in CCA	chr18	76738575	76740574	*NA*	NA	0.000192949
Promoter	HYPER in CCA	chr10	63210897	63212896	*NA*	101928781	0.000157506
Promoter	HYPER in CCA	chr2	198650987	198652986	*BOLL*	66037	0.002115614
Promoter	HYPER in CCA	chr5	127872206	127874205	*SLC27A6*	28965	0.001155856
Promoter	HYPER in CCA	chr19	36736660	36738659	*ZNF565*	147929	0.000204181
Promoter	HYPER in CCA	chr4	188915425	188917424	*ZFP42*	132625	0.00155071
Promoter	HYPER in CCA	chr8	54163758	54165757	*OPRK1*	4986	0.002663592
Promoter	HYPER in CCA	chr9	37001194	37003193	*NA*	NA	0.002050163
Promoter	HYPER in CCA	chr12	85306895	85308894	*SLC6A15*	55117	0.003114075
Promoter	HYPER in CCA	chr3	147109709	147111708	*ZIC1*	7545	0.000292885
Promoter	HYPER in CCA	chr1	237204005	237206004	*RYR2*	6262	0.004213448
Promoter	HYPER in CCA	chr19	53757652	53759651	*ZNF677*	342926	0.000296863
Promoter	HYPER in CCA	chr20	61637888	61639887	*BHLHE23*	128408	0.000141326
Promoter	HYPER in CCA	chr19	35394600	35396599	*NA*	NA	0.000993773
Promoter	HYPER in CCA	chr12	22093837	22095836	*ABCC9*	10060	0.004378568
Promoter	HYPER in CCA	chr2	177029945	177031944	*NA*	NA	0.001305519
Promoter	HYPER in CCA	chr1	111217156	111219155	*KCNA3*	3738	0.001891078
Promoter	HYPER in CCA	chr5	140786270	140788269	*PCDHGB6*	56100	0.002137062
Promoter	HYPER in CCA	chr3	58522547	58524546	*ACOX2*	8309	5.89E-05
Promoter	HYPER in CCA	chr2	176992922	176994921	*HOXD8*	3234	0.00011061
Promoter	HYPER in CCA	chr10	119493324	119495323	*NA*	NA	0.003078963
Promoter	HYPER in CCA	chr19	38306499	38308498	*NA*	644554	0.000546647
Promoter	HYPER in CCA	chr6	28413250	28415249	*COX11P1*	NA	9.97E-05
Promoter	HYPER in CCA	chr5	3594668	3596667	*IRX1*	79192	0.000278819
Promoter	HYPER in CCA	chr6	27234392	27236391	*NA*	NA	0.003505168
Promoter	HYPER in CCA	chr10	22632899	22634898	*SPAG6*	9576	1.81E-05
Promoter	HYPER in CCA	chr8	57356866	57358865	*NA*	101929415	0.000155741

Promoter	HYPER in CCA	chr5	16180372	16182371	*Mar/11*	441061	0.001406453
Promoter	HYPER in CCA	chr6	105387903	105389902	*LINC00577*	100113403	6.51E-05
Promoter	HYPER in CCA	chr15	83774659	83776658	*TM6SF1*	53346	0.00410737
Promoter	HYPER in CCA	chr20	61808352	61810351	*MIR124-3*	406909	0.00059646
Promoter	HYPER in CCA	chr10	102898969	102900968	*NA*	NA	7.42E-05
Promoter	HYPER in CCA	chr13	53422276	53424275	*PCDH8*	5100	0.001697946
Promoter	HYPER in CCA	chr17	46710435	46712434	*HOXB7*	3217	0.000625716
Promoter	HYPER in CCA	chr5	180527167	180529166	*FOXO1B*	NA	0.000538826
Promoter	HYPER in CCA	chr5	178366692	178368691	*ZNF454*	285676	0.000598788
Promoter	HYPER in CCA	chr4	1399620	1401619	*NKX1-1*	NA	0.000148272
Promoter	HYPER in CCA	chr8	73163301	73165300	*NA*	NA	0.003926479
Promoter	HYPER in CCA	chr8	55368995	55370994	*SOX17*	64321	0.001116223
Promoter	HYPER in CCA	chr8	56013449	56015448	*XKR4*	114786	0.002244501
Promoter	HYPER in CCA	chr11	43601444	43603443	*MIR129-2*	406918	0.001470952
Promoter	HYPER in CCA	chr7	19184545	19186544	*FERD3L*	222894	0.003171499
Promoter	HYPER in CCA	chr2	5830751	5832750	*NA*	NA	0.001660355
Promoter	HYPER in CCA	chr12	128750448	128752447	*TMEM132C*	92293	0.003493932
Promoter	HYPER in CCA	chr19	23253779	23255778	*NA*	NA	0.003577283
Promoter	HYPER in CCA	chr2	132087931	132089930	*ARHGAP42P1*	NA	0.002354047
Promoter	HYPER in CCA	chr2	5831121	5833120	*NA*	NA	0.00147399
Promoter	HYPER in CCA	chr16	23845822	23847821	*PRKCB*	5579	0.001859038
Promoter	HYPER in CCA	chr13	84456029	84458028	*SLITRK1*	114798	0.003742612
Promoter	HYPER in CCA	chr21	45768546	45770545	*TRPM2*	7226	0.000617349
Promoter	HYPER in CCA	chr17	46659122	46661121	*MIR10A*	406902	0.004201295
Promoter	HYPER in CCA	chr5	140808685	140810684	*PCDHGA12*	26025	0.002680544
Promoter	HYPER in CCA	chr1	248100316	248102315	*NA*	NA	0.001425692
Promoter	HYPER in CCA	chr1	4713292	4715291	*AJAP1*	55966	0.002321361
Promoter	HYPER in CCA	chr7	27280348	27282347	*NA*	NA	0.001201397
Promoter	HYPER in CCA	chr7	27208684	27210683	*MIR196B*	442920	4.85E-05
Promoter	HYPER in CCA	chr7	27197056	27199055	*HOXA7*	3204	0.000583965
Promoter	HYPER in CCA	chr3	179754342	179756341	*PEX5L*	51555	0.001477078
Promoter	HYPER in CCA	chr6	38681617	38683616	*DNAH8*	1769	0.000524038
Promoter	HYPER in CCA	chr1	247801551	247803550	*NA*	NA	0.002990889
Promoter	HYPER in CCA	chr2	237076513	237078512	*GBX2*	2637	0.00079945

Promoter	HYPER in CCA	chr2	177040945	177042944	*NA*	NA	0.00236695
Promoter	HYPER in CCA	chr19	38182739	38184738	*ZFP30*	22835	0.000485714
Promoter	HYPER in CCA	chr19	38182724	38184723	*ZNF781*	163115	0.000485714
Promoter	HYPER in CCA	chr18	74961005	74963004	*GALR1*	2587	0.002129458
Promoter	HYPER in CCA	chr2	95718422	95720421	*NA*	NA	0.000724158
Promoter	HYPER in CCA	chr17	35300256	35302255	*NA*	NA	0.00388434
Promoter	HYPER in CCA	chr1	37499231	37501230	*GRIK3*	2899	0.00258742
Promoter	HYPER in CCA	chr18	70534882	70536881	*NETO1*	81832	0.005461822
Promoter	HYPER in CCA	chr7	27133766	27135765	*HOTAIRM1*	100506311	0.003976231
Promoter	HYPER in CCA	chr7	101004601	101006600	*COL26A1*	136227	0.000604866
Promoter	HYPER in CCA	chr3	129691648	129693647	*TRH*	7200	0.000712276
Promoter	HYPER in CCA	chr1	91182295	91184294	*BARHL2*	343472	0.002126521
Promoter	HYPER in CCA	chr1	217310598	217312597	*ESRRG*	2104	0.003742612
Promoter	HYPER in CCA	chr20	37351605	37353604	*SLC32A1*	140679	0.001467317
Promoter	HYPER in CCA	chr1	50512186	50514185	*ELAVL4*	1996	0.000317009
Promoter	HYPER in CCA	chr7	27206738	27208737	*HOXA10-AS*	442920;100874323	0.000204181
Promoter	HYPER in CCA	chr2	176972018	176974017	*HOXD10*	3236	0.002383256
Promoter	HYPER in CCA	chr19	58569107	58571106	*ZNF135*	7694	0.001974773
Promoter	HYPER in CCA	chr10	15761625	15763624	*ITGA8*	8516	0.002050163
Promoter	HYPER in CCA	chr11	105479221	105481220	*GRIA4*	2893	0.005332616
Promoter	HYPER in CCA	chr15	28753455	28755454	*ABCB10P4*	NA	9.04E-05
Promoter	HYPER in CCA	chr20	23014557	23016556	*SSTR4*	6754	0.001025925
Promoter	HYPER in CCA	chr1	18956000	18957999	*PAX7*	5081	0.005219966
Promoter	HYPER in CCA	chr14	60974169	60976168	*SIX6*	4990	0.004694561
Promoter	HYPER in CCA	chr6	101845164	101847163	*GRIK2*	2898	0.003870558
Promoter	HYPER in CCA	chr7	27280664	27282663	*EVX1*	2128	0.002155601
Promoter	HYPER in CCA	chr10	23479756	23481755	*PTF1A*	256297	0.005268785
Promoter	HYPER in CCA	chr2	176971871	176973870	*NA*	NA	0.003416828
Promoter	HYPER in CCA	chr8	687607	689606	*ERICH1*	157697;101927618	0.000993773
Promoter	HYPER in CCA	chr22	17081277	17083276	*TPTEP1*	387590	0.001404354
Promoter	HYPER in CCA	chr19	35394719	35396718	*NA*	100652911	0.002552084
Promoter	HYPER in CCA	chr20	30072081	30074080	*LINC00028*	140875	0.003475584
Promoter	HYPER in CCA	chr6	100912306	100914305	*SIM1*	6492	0.000346168
Promoter	HYPER in CCA	chr15	83952967	83954966	*BNC1*	646	0.001470952

Promoter	HYPER in CCA	chr13	112720413	112722412	*SOX1*	6656	0.000249275
Promoter	HYPER in CCA	chr19	35629985	35631984	*NA*	NA	0.001342581
Promoter	HYPER in CCA	chr4	147558913	147560912	*NA*	NA	0.00381015
Promoter	HYPER in CCA	chr7	158937150	158939149	*VIPR2*	7434	0.001966967
Promoter	HYPER in CCA	chr7	27209618	27211617	*HOXA9*	3205;442920	0.001472939
Promoter	HYPER in CCA	chr18	70534123	70536122	*NA*	100505797	0.003416828
Promoter	HYPER in CCA	chr6	105584550	105586549	*BVES*	11149	0.002296522
Promoter	HYPER in CCA	chr19	9607854	9609853	*NA*	NA	0.001863149
Promoter	HYPER in CCA	chr5	1445046	1447045	*SLC6A3*	6531	0.001160522
Promoter	HYPER in CCA	chr19	54464794	54466793	*CACNG8*	59283	0.005211684
Promoter	HYPER in CCA	chr12	30352416	30354415	*NA*	NA	0.004202919
Promoter	HYPER in CCA	chr21	34396653	34398652	*OLIG2*	10215	0.003606632
Promoter	HYPER in CCA	chr17	46799030	46801029	*PRAC2*	100422978	0.00314546
Promoter	HYPER in CCA	chr5	115152152	115154151	*CDO1*	1036	0.003639235
Promoter	HYPER in CCA	chr8	145924071	145926070	*NA*	NA	0.002155601
Promoter	HYPER in CCA	chr8	145924238	145926237	*NA*	100996662	0.002155601
Promoter	HYPER in CCA	chr10	105035420	105037419	*INA*	9118	0.001324887
Promoter	HYPER in CCA	chr15	40379533	40381532	*NA*	NA	0.001008565
Promoter	HYPER in CCA	chr7	27196463	27198462	*NA*	NA	0.001342581
Promoter	HYPER in CCA	chr1	149718863	149720862	*NA*	NA	0.00020547
Promoter	HYPER in CCA	chr6	390239	392238	*IRF4*	3662	0.002214775
Promoter	HYPER in CCA	chr5	170734788	170736787	*TLX3*	30012	0.001694083
Promoter	HYPER in CCA	chr2	5831299	5833298	*SOX11*	6664	0.001789387
Promoter	HYPER in CCA	chr4	298611	300610	*ZNF732*	654254	0.001346613
Promoter	HYPER in CCA	chr9	113255	115254	*NA*	NA	4.43E-05
Promoter	HYPER in CCA	chr4	66534179	66536178	*NA*	100144602	0.004383911
Promoter	HYPER in CCA	chr2	154726926	154728925	*GALNT13*	114805	0.001914639
Promoter	HYPER in CCA	chr14	36986983	36988982	*NKX2-1-AS1*	100506237	0.002683831
Promoter	HYPER in CCA	chr12	54384022	54386021	*MIR196A2*	406973	0.00373755
Promoter	HYPER in CCA	chr17	6678042	6680041	*FBXO39*	162517	0.004404929
Promoter	HYPER in CCA	chr7	27191718	27193717	*NA*	NA	0.004579565
Promoter	HYPER in CCA	chr7	35293259	35295258	*TBX20*	57057	0.002527056
Promoter	HYPER in CCA	chr1	248019001	248021000	*TRIM58*	25893	0.000828694
Promoter	HYPER in CCA	chr4	147558545	147560544	*POU4F2*	5458	0.004450326

Promoter	HYPER in CCA	chr2	162279026	162281025	*NA*	NA	0.000769191
Promoter	HYPER in CCA	chr20	21376956	21378955	*NA*	NA	0.002374174
Promoter	HYPER in CCA	chr2	176985588	176987587	*HOXD9*	3235	0.002194275
Promoter	HYPER in CCA	chr19	52955329	52957328	*ZNF578*	147660	0.002990889
Promoter	HYPER in CCA	chr18	44775055	44777054	*SKOR2*	652991	0.002969774
Promoter	HYPER in CCA	chr19	22467710	22469709	*ZNF729*	100287226	0.004083428
Promoter	HYPER in CCA	chr20	25062497	25064496	*VSX1*	30813	0.000387186
Promoter	HYPER in CCA	chr6	55037550	55039549	*HCRTR2*	3062	0.004199395
Promoter	HYPER in CCA	chr1	224803423	224805422	*NA*	NA	0.003114075
Promoter	HYPER in CCA	chr15	95869859	95871858	*NA*	400456	0.000342149
Promoter	HYPER in CCA	chr2	176962958	176964957	*HOXD12*	3238	0.003187092
Promoter	HYPER in CCA	chr22	19137297	19139296	*GSC2*	2928	0.00370175
Promoter	HYPER in CCA	chr12	4917308	4919307	*NA*	NA	0.00086505
Promoter	HYPER in CCA	chr10	50816847	50818846	*SLC18A3*	6572	0.005186051
Promoter	HYPER in CCA	chr7	6702105	6704104	*NA*	NA	6.04E-05
Promoter	HYPER in CCA	chr18	56940819	56942818	*RAX*	30062	0.002709436
Promoter	HYPER in CCA	chr22	29874719	29876718	*NEFH*	4744	0.001342581
Promoter	HYPER in CCA	chr5	72676711	72678710	*NA*	NA	0.002186545
Promoter	HYPER in CCA	chr8	49468502	49470501	*NA*	NA	0.003982484
Promoter	HYPER in CCA	chr6	123315616	123317615	*CLVS2*	134829	0.003504721
Promoter	HYPER in CCA	chr19	35395462	35397461	*NA*	NA	0.005287327
Promoter	HYPER in CCA	chr3	172165747	172167746	*GHSR*	2693	0.005187826
Promoter	HYPER in CCA	chr10	118897313	118899312	*VAX1*	11023	0.003642716
Promoter	HYPER in CCA	chr20	57089688	57091687	*APCDD1L*	164284	0.005415644
Promoter	HYPER in CCA	chr19	9608784	9610783	*ZNF560*	147741	0.002374282
Promoter	HYPER in CCA	chr9	96716379	96718378	*NA*	101928040	0.003891954
Promoter	HYPER in CCA	chr16	22823998	22825997	*HS3ST2*	9956	0.004087146
Promoter	HYPER in CCA	chr16	49315243	49317242	*CBLN1*	869	0.00297177
Promoter	HYPER in CCA	chr8	105478782	105480781	*DPYS*	1807	0.003947144
Promoter	HYPER in CCA	chr4	122686083	122688082	*TMEM155*	132332	0.002115614
Promoter	HYPER in CCA	chr19	38307441	38309440	*ZNF573*	126231	0.002186545
Promoter	HYPER in CCA	chr7	27224343	27226342	*HOXA11*	3207	0.001966967
Promoter	HYPER in CCA	chr1	148852638	148854637	*NA*	NA	0.001800153
Promoter	HYPER in CCA	chr3	112928350	112930349	*BOC*	91653	0.00283731

Promoter	HYPER in CCA	chr20	590543	592542	*TCF15*	6939	0.001131203
Promoter	HYPER in CCA	chr4	104640474	104642473	*TACR3*	6870	0.005156918
Promoter	HYPER in CCA	chr1	150229182	150231181	*NA*	NA	0.005284302
Promoter	HYPER in CCA	chr6	28742193	28744192	*NA*	NA	0.003654098
Gene	HYPER in CCA	chr6	160693649	160697162	*NA*	NA	1.22E-07
Gene	HYPER in CCA	chr10	75601591	75606324	*NA*	NA	1.27E-08
Gene	HYPER in CCA	chr5	142869420	142910915	*NA*	NA	9.11E-06
Gene	HYPER in CCA	chr12	73004458	73005096	*CHCHD3P2*	NA	4.38E-07
Gene	HYPER in CCA	chr22	50644014	50644491	*NA*	NA	1.22E-07
Gene	HYPER in CCA	chr10	91406046	91410579	*NA*	NA	1.27E-05
Gene	HYPER in CCA	chr11	77774907	77779397	*THRSP*	7069	2.77E-08
Gene	HYPER in CCA	chr12	57824899	57827718	*NA*	NA	5.13E-08
Gene	HYPER in CCA	chr8	65291706	65291814	*MIR124-2*	406908	0.010550357
Gene	HYPER in CCA	chr14	19400329	19403264	*ARHGAP42P5*	NA	0.000940074
Gene	HYPER in CCA	chr16	71599563	71611033	*TAT*	6898	5.13E-08
Gene	HYPER in CCA	chr12	54413694	54416373	*NA*	NA	0.000160339
Gene	HYPER in CCA	chr13	94806447	94840245	*GPC6-AS1*	100873972	1.46E-05
Gene	HYPER in CCA	chr12	7276280	7281538	*RBP5*	83758	5.02E-05
Gene	HYPER in CCA	chr16	14397824	14397906	*MIR193B*	574455	0.002646
Gene	HYPER in CCA	chr1	214202236	214204109	*NA*	NA	0.000121294
Gene	HYPER in CCA	chr5	139505521	139508391	*IGIP*	492311	3.93E-07
Gene	HYPER in CCA	chr8	54788710	54789209	*NA*	NA	0.003065233
Gene	HYPER in CCA	chr1	95585703	95604110	*NA*	NA	3.33E-05
Gene	HYPER in CCA	chr17	46799084	46799884	*PRAC1*	84366	0.000395214
Gene	HYPER in CCA	chr1	197008321	197036397	*F13B*	2165	0.000702199
Gene	HYPER in CCA	chr2	176994422	176997423	*HOXD8*	3234	0.000183536
Gene	HYPER in CCA	chr12	14978503	14996429	*ART4*	420	0.011282142
Gene	HYPER in CCA	chr1	3701572	3702102	*NA*	NA	0.001262067
Gene	HYPER in CCA	chr3	46538981	46542439	*RTP3*	83597	0.000370846
Gene	HYPER in CCA	chr12	95782375	95799280	*NA*	NA	0.00160732
Gene	HYPER in CCA	chr2	45240353	45240807	*NA*	NA	0.000457733
Gene	HYPER in CCA	chr11	75115465	75115610	*SNORD15B*	114599	0.003165413
Gene	HYPER in CCA	chr7	19184405	19185044	*FERD3L*	222894	0.001920308
Gene	HYPER in CCA	chr1	148250249	148347506	*NBPF20*	25832;343505;100132406;101060226	0.000337557

Gene	HYPER in CCA	chr10	65132717	65132808	*MIR1296*	100302150	0.000483248
Gene	HYPER in CCA	chr4	74262831	74287129	*ALB*	213	0.001181013
Gene	HYPER in CCA	chr11	9450320	9450501	*SNORA23*	677808	0.000184239
Gene	HYPER in CCA	chr8	43102334	43102553	*NA*	NA	0.004901708
Gene	HYPER in CCA	chr10	119494824	119495918	*NA*	NA	0.002546242
Gene	HYPER in CCA	chr1	248020501	248041507	*TRIM58*	25893	4.90E-05
Gene	HYPER in CCA	chr2	133014539	133014653	*MIR663B*	100313824	0.000656381
Gene	HYPER in CCA	chr1	161192082	161193421	*APOA2*	336	0.001320131
Gene	HYPER in CCA	chr12	114370374	114375060	*NA*	NA	3.83E-05
Gene	HYPER in CCA	chr16	15702331	15704420	*NA*	NA	0.002866352
Gene	HYPER in CCA	chr17	77997693	77999906	*NA*	NA	0.002585863
Gene	HYPER in CCA	chr7	27168126	27170418	*HOXA4*	3201	2.93E-05
Gene	HYPER in CCA	chr12	56754353	56756607	*APOF*	319	5.77E-05
Gene	HYPER in CCA	chr1	71172136	71252151	*NA*	101927244	0.006358859
Gene	HYPER in CCA	chr5	16067248	16180871	*Mar/11*	441061	0.000219548
Gene	HYPER in CCA	chr16	71599692	71612090	*NA*	100132529	1.05E-05
Gene	HYPER in CCA	chr8	79672377	79674666	*PRKRIRP7*	NA	0.010550357
Gene	HYPER in CCA	chr17	14207171	14208822	*NA*	84815	6.77E-05
Gene	HYPER in CCA	chr16	78529823	78540465	*NA*	NA	0.000611829
Gene	HYPER in CCA	chr16	593277	593366	*MIR3176*	100423037	0.003956057
Gene	HYPER in CCA	chr2	177028892	177030444	*NA*	NA	0.001920308
Gene	HYPER in CCA	chr13	53418109	53422775	*PCDH8*	5100	0.000276419
Gene	HYPER in CCA	chr20	61809852	61809938	*MIR124-3*	406909	0.000797715
Gene	HYPER in CCA	chr3	75721542	75728454	*LINC00960*	401074	0.000124719
Gene	HYPER in CCA	chr17	46706037	46712294	*HOXB-AS4*	NA	0.000696605
Gene	HYPER in CCA	chr11	43602944	43603033	*MIR129-2*	406918	0.001702584
Gene	HYPER in CCA	chr6	28414750	28415584	*COX11P1*	NA	0.000160339
Gene	HYPER in CCA	chr7	19183916	19185876	*NA*	NA	0.004380253
Gene	HYPER in CCA	chr17	12893466	12893927	*NA*	NA	0.001603159
Gene	HYPER in CCA	chr7	27180671	27183287	*HOXA5*	3202	6.30E-05
Gene	HYPER in CCA	chr7	27139721	27142430	*HOXA2*	3199	0.000470599
Gene	HYPER in CCA	chr7	27197963	27198595	*NA*	NA	0.000328612
Gene	HYPER in CCA	chr4	155525286	155534119	*FGG*	2266	0.003233085
Gene	HYPER in CCA	chr1	79355449	79472403	*ELTD1*	64123	0.001920308

Gene	HYPER in CCA	chr14	60975669	60979568	*SIX6*	4990	0.001953932
Gene	HYPER in CCA	chr7	27208238	27211534	*HOXA10-AS*	442920;100874323	7.11E-05
Gene	HYPER in CCA	chr19	23258012	23330021	*ZNF730*	100129543	0.00236658
Gene	HYPER in CCA	chr7	63642088	63643271	*NA*	NA	0.000868618
Gene	HYPER in CCA	chr13	95351948	95355116	*LINC00391*	NA	0.001707914
Gene	HYPER in CCA	chr5	50265051	50266001	*NA*	100287592	0.004489699
Gene	HYPER in CCA	chr2	207507142	207514173	*NA*	NA	0.000666201
Gene	HYPER in CCA	chr7	27132612	27135615	*HOXA1*	3198	0.001085744
Gene	HYPER in CCA	chr14	69403319	69403581	*BANF1P1*	NA	0.000286721
Gene	HYPER in CCA	chr19	29980682	30017855	*NA*	NA	0.005171141
Gene	HYPER in CCA	chr3	170374351	170379912	*NA*	101928583	0.008130752
Gene	HYPER in CCA	chr2	176987088	176989853	*HOXD9*	3235	0.000636911
Gene	HYPER in CCA	chr3	121311966	121349139	*FBXO40*	51725	0.000304052
Gene	HYPER in CCA	chr5	2745959	2752969	*IRX2*	153572	0.000595283
Gene	HYPER in CCA	chr2	177042445	177043736	*NA*	NA	0.005623844
Gene	HYPER in CCA	chr4	156750881	156787425	*ASIC5*	51802	0.005171141
Gene	HYPER in CCA	chr12	75433857	75603648	*KCNC2*	3747	0.002133082
Gene	HYPER in CCA	chr4	147560045	147563626	*POU4F2*	5458	0.003048594
Gene	HYPER in CCA	chr20	61637331	61638387	*BHLHE23*	128408	0.000543949
Gene	HYPER in CCA	chr3	58490863	58523046	*ACOX2*	8309	8.43E-05
Gene	HYPER in CCA	chr2	176986339	177001826	*HOXD-AS2*	100506783	0.000696605
Gene	HYPER in CCA	chr17	33825237	33826194	*NA*	NA	0.00471346
Gene	HYPER in CCA	chr1	40598436	40599120	*NA*	NA	0.000274822
Gene	HYPER in CCA	chr19	35628549	35630484	*NA*	NA	0.000334452
Gene	HYPER in CCA	chr19	23258003	23283163	*NA*	NA	0.003664523
Gene	HYPER in CCA	chr5	50265494	50266021	*NA*	NA	0.004006311
Gene	HYPER in CCA	chr7	27193335	27197555	*HOXA7*	3204	0.002201147
Gene	HYPER in CCA	chr13	88324870	88331871	*SLITRK5*	26050	0.000516654
Gene	HYPER in CCA	chr20	21492085	21492947	*NKX2-2-AS1*	NA	0.004247124
Gene	HYPER in CCA	chr10	135043778	135045062	*UTF1*	8433	0.001128218
Gene	HYPER in CCA	chr12	123349882	123351568	*NA*	NA	0.000954256
Gene	HYPER in CCA	chr19	58208735	58220579	*ZNF154*	7710	0.011772766
Gene	HYPER in CCA	chr2	177015031	177015140	*MIR10B*	406903	0.000124719
Gene	HYPER in CCA	chr7	27209099	27209183	*MIR196B*	442920	0.002103623

Gene	HYPER in CCA	chr2	177015950	177017954	*HOXD4*	3233	0.000522661
Gene	HYPER in CCA	chr5	170736288	170739138	*TLX3*	30012	0.004585072
Gene	HYPER in CCA	chr17	50939481	50976948	*NA*	NA	0.008392253
Gene	HYPER in CCA	chr7	24323782	24331484	*NPY*	4852	0.006500389
Gene	HYPER in CCA	chr8	72753784	72756703	*MSC*	9242	0.009256576
Gene	HYPER in CCA	chr2	68511303	68547183	*CNRIP1*	25927	0.002087888
Gene	HYPER in CCA	chr11	12052422	12083332	*NA*	NA	0.002675254
Gene	HYPER in CCA	chr7	27202054	27210117	*HOXA9*	3205;442920	0.000198827
Gene	HYPER in CCA	chr18	74962505	74980858	*GALR1*	2587	0.002866352
Gene	HYPER in CCA	chr18	14728271	14852737	*ANKRD30B*	374860	0.001560636
Gene	HYPER in CCA	chr5	21616371	21779631	*NA*	NA	0.004425603
Gene	HYPER in CCA	chr6	137813336	137815531	*OLIG3*	167826	0.002724024
Gene	HYPER in CCA	chr7	27168588	27192180	*NA*	NA	0.00058454
Gene	HYPER in CCA	chr9	69199480	69202204	*FOXD4L6*	653404	0.002453116
Gene	HYPER in CCA	chr1	147789799	147790129	*NA*	NA	8.43E-05
Gene	HYPER in CCA	chr22	24376133	24384680	*GSTT1*	2952	0.00643883
Gene	HYPER in CCA	chr16	28548606	28550495	*NUPR1*	26471	0.000364206
Gene	HYPER in CCA	chr8	110986172	110987010	*NA*	NA	0.007943719
Gene	HYPER in CCA	chr2	71115001	71117089	*LINC01143*	NA	0.004275564
Gene	HYPER in CCA	chr7	27169596	27195542	*HOXA-AS3*	100133311	0.000813888
Gene	HYPER in CCA	chr5	3596168	3601517	*IRX1*	79192	0.006280701
Gene	HYPER in CCA	chr10	93388199	93392811	*PPP1R3C*	5507	0.0002853
Gene	HYPER in CCA	chr17	39210750	39211482	*KRTAP2-2*	728279	0.000797487
Gene	HYPER in CCA	chr8	55370495	55373448	*SOX17*	64321	0.003837821
Gene	HYPER in CCA	chr8	41397900	41402563	*NA*	NA	0.004969555
Gene	HYPER in CCA	chr13	28366780	28368905	*GSX1*	219409	0.004698392
Gene	HYPER in CCA	chr13	84451344	84456528	*SLITRK1*	114798	0.006374999
Gene	HYPER in CCA	chr19	21106028	21133503	*ZNF85*	7639	0.007167552
Gene	HYPER in CCA	chr7	64029806	64030815	*NA*	NA	0.001740616
Gene	HYPER in CCA	chr7	95212811	95225803	*PDK4*	5166	2.45E-05
Gene	HYPER in CCA	chr1	53753696	53755378	*NA*	NA	0.003960505
Gene	HYPER in CCA	chr19	23251275	23254278	*NA*	NA	0.008812223
Gene	HYPER in CCA	chr1	63788730	63790797	*FOXD3*	27022	0.009883832
Gene	HYPER in CCA	chr2	124774435	124782750	*NA*	NA	0.001337331

Gene	HYPER in CCA	chr2	176968944	176974722	*HOXD11*	3237	0.005036403
Gene	HYPER in CCA	chr1	228651804	228652327	*HIST3H2BA*	NA	0.001982071
Gene	HYPER in CCA	chr6	84262599	84419410	*SNAP91*	9892	0.011312292
Gene	HYPER in CCA	chr7	27145803	27192200	*HOXA3*	3200	0.001378976
Gene	HYPER in CCA	chr2	162280526	162285285	*NA*	NA	0.00080767
Gene	HYPER in CCA	chr21	34398153	34401504	*OLIG2*	10215	0.003656154
Gene	HYPER in CCA	chr3	188659504	188665428	*TPRG1-AS1*	NA	0.001745474
Gene	HYPER in CCA	chr1	101003693	101007574	*GPR88*	54112	0.007399623
Gene	HYPER in CCA	chr2	176964458	176966408	*HOXD12*	3238	0.002535625
Gene	HYPER in CCA	chr9	131683174	131704320	*PHYHD1*	254295	1.53E-05
Gene	HYPER in CCA	chr13	31506840	31549639	*TEX26*	122046	0.000854946
Gene	HYPER in CCA	chr20	21378456	21381029	*NA*	NA	0.007149037
Gene	HYPER in CCA	chr10	129535499	129539450	*FOXI2*	399823	0.008881485
Gene	HYPER in CCA	chr12	119210837	119212942	*NA*	NA	0.012428423
Gene	HYPER in CCA	chr4	1396720	1400119	*NKX1-1*	NA	0.002507842
Gene	HYPER in CCA	chr1	119911402	119936753	*HAO2*	51179	0.006518764
Gene	HYPER in CCA	chr17	46656992	46659621	*MIR10A*	406902	0.010765124
Gene	HYPER in CCA	chr14	57267425	57277197	*OTX2*	5015	0.005955127
Gene	HYPER in CCA	chr5	1877541	1887350	*IRX4*	50805	0.008751596
Gene	HYPER in CCA	chr18	76736555	76739074	*NA*	NA	0.004919055
Gene	HYPER in CCA	chr20	26167556	26232162	*MIR663A*	284801;724033	0.000324723
Gene	HYPER in CCA	chr20	21491648	21494664	*NKX2-2*	4821	0.010667461
Gene	HYPER in CCA	chr5	134869991	134871639	*NEUROG1*	4762	0.003342578
Gene	HYPER in CCA	chr2	177001340	177037830	*HOXD3*	3232;3233;401021	0.002087888
Gene	HYPER in CCA	chr13	112721913	112726020	*SOX1*	6656	0.00216554
Gene	HYPER in CCA	chr4	122685740	122687962	*NA*	NA	0.002262432
Gene	HYPER in CCA	chr19	56988619	57012035	*ZNF667-AS1*	100128252	0.009426579
Gene	HYPER in CCA	chr13	79172497	79177673	*POU4F1*	5457	0.007109277
Gene	HYPER in CCA	chr5	71014990	71016875	*CARTPT*	9607	0.010269607
Gene	HYPER in CCA	chr6	55299167	55444012	*HMGCLL1*	54511	0.010204246
Gene	HYPER in CCA	chr16	31579707	31580796	*YBX3P1*	440359	0.002079067
Gene	HYPER in CCA	chr4	41752362	41759358	*NA*	NA	0.007326971
Gene	HYPER in CCA	chr10	23481256	23483181	*PTF1A*	256297	0.008643121
Gene	HYPER in CCA	chr7	27203154	27219632	*NA*	NA	0.000854946

Gene	HYPER in CCA	chr5	63253720	63276870	*NA*	NA	0.007467774
Gene	HYPER in CCA	chr10	50818347	50820765	*SLC18A3*	6572	0.00146125
Gene	HYPER in CCA	chr4	190962497	190964569	*AGGF1P1*	NA	0.006342703
Gene	HYPER in CCA	chr19	38307999	38317278	*NA*	644554	0.001501248
Gene	HYPER in CCA	chr1	50883222	50889172	*DMRTA2*	63950	0.002591931
Gene	HYPER in CCA	chr8	24769678	24772230	*NA*	NA	0.008316776
Gene	HYPER in CCA	chr2	176942200	176948641	*EVX2*	344191	0.011093675
Gene	HYPER in CCA	chr19	35395296	35395961	*NA*	NA	0.00677389
Gene	HYPER in CCA	chr20	21376005	21378666	*NKX2-4*	644524	0.003002612
Gene	HYPER in CCA	chr3	129693148	129696781	*TRH*	7200	0.005340235
Gene	HYPER in CCA	chr6	391739	411447	*IRF4*	3662	0.006342703
Gene	HYPER in CCA	chr12	63539014	63544722	*AVPR1A*	552	0.002601354
Gene	HYPER in CCA	chr5	63256183	63258334	*HTR1A*	3350	0.008743909
Gene	HYPER in CCA	chr20	37353105	37358015	*SLC32A1*	140679	0.010019575
Gene	HYPER in CCA	chr10	124907638	124910188	*HMX2*	3167	0.006363582
Gene	HYPER in CCA	chr19	22235254	22274282	*ZNF257*	113835	0.001652469
Gene	HYPER in CCA	chr6	1384025	1385301	*NA*	NA	0.009536726
Gene	HYPER in CCA	chr19	38158652	38183223	*ZNF781*	163115	0.004488263
Gene	HYPER in CCA	chr2	71004442	71017775	*FIGLA*	344018	0.003008423
Gene	HYPER in CCA	chr10	74034673	74035738	*NA*	NA	0.003489416
Gene	HYPER in CCA	chr14	60863187	60982261	*C14orf39*	317761	0.009868721
Gene	HYPER in CCA	chr2	105471969	105476929	*POU3F3*	5455	0.005912398
Gene	HYPER in CCA	chr14	29235050	29238870	*FOXG1*	2290	0.011853912
Gene	HYPER in CCA	chr5	78407602	78428108	*BHMT*	635	0.003656154
Gene	HYPER in CCA	chr19	22715428	22716296	*NA*	100128139	0.006073216
Gene	HYPER in CCA	chr19	9609354	9620755	*NA*	NA	0.002795954
Gene	HYPER in CCA	chr8	67858736	67874825	*TCF24*	100129654	0.002695838
Gene	HYPER in CCA	chr11	105480721	105852819	*GRIA4*	2893	0.011770068
Gene	HYPER in CCA	chr6	85397069	85474237	*TBX18*	9096	0.010847067
Gene	HYPER in CCA	chr16	2317788	2317881	*NA*	NA	2.33E-06
Gene	HYPER in CCA	chr18	902767	906668	*NA*	NA	0.009400725
Gene	HYPER in CCA	chr1	67218142	67244470	*TCTEX1D1*	200132	0.006342703
Gene	HYPER in CCA	chr3	126111875	126113694	*NA*	100506907	0.0049635
Gene	HYPER in CCA	chr4	174446120	174451380	*HAND2*	9464	0.010598368

Gene	HYPER in CCA	chr19	30017406	30055386	*VSTM2B*	342865	0.00724688
Gene	HYPER in CCA	chr7	1272543	1276954	*UNCX*	340260	0.010019575
Gene	HYPER in CCA	chr9	79634571	79635869	*FOXB2*	442425	0.005351121
Gene	HYPER in CCA	chr4	111286889	111486441	*ENPEP*	2028	0.003427931
Gene	HYPER in CCA	chr18	44746293	44775554	*SKOR2*	652991	0.002335863
Gene	HYPER in CCA	chr12	54385522	54385631	*MIR196A2*	406973	0.007399623
Gene	HYPER in CCA	chr20	54572496	54580528	*CBLN4*	140689	0.011480908
Gene	HYPER in CCA	chr6	50786436	50815326	*TFAP2B*	7021	0.010695076
Gene	HYPER in CCA	chr19	54216601	54216688	*MIR519D*	574480	0.001358423
Gene	HYPER in CCA	chr8	24814135	24814624	*NA*	NA	0.012719651
Gene	HYPER in CCA	chr19	22469210	22499978	*ZNF729*	100287226	0.01047256
Gene	HYPER in CCA	chr17	66195062	66195737	*NA*	440461	0.000958516
Gene	HYPER in CCA	chr1	229566992	229569845	*ACTA1*	58	0.002628581
Gene	HYPER in CCA	chr11	32409321	32457176	*WT1*	7490	0.009735372
Gene	HYPER in CCA	chr14	61107448	61109307	*NA*	NA	0.00283366
Gene	HYPER in CCA	chr6	105544697	105585049	*BVES*	11149	0.009523671
Gene	HYPER in CCA	chr19	7983537	7984042	*NA*	NA	0.008497291
Gene	HYPER in CCA	chr11	17716569	17719018	*NA*	NA	0.00530846
Gene	HYPER in CCA	chr11	17716814	17718487	*NA*	NA	0.00530846
Gene	HYPER in CCA	chr18	894436	907681	*NA*	NA	0.011312292
Gene	HYPER in CCA	chr7	27224137	27228912	*HOXA11-AS*	221883	0.003904366
Gene	HYPER in CCA	chr10	63212397	63241714	*NA*	101928781	0.011695136
Gene	HYPER in CCA	chr4	170712371	170712853	*PTGES3P3*	NA	0.00409517
Gene	HYPER in CCA	chr8	97154562	97173020	*GDF6*	392255	0.011516527
Gene	HYPER in CCA	chr6	43267448	43276535	*CRIP3*	401262	7.36E-05
Gene	HYPER in CCA	chr19	36912438	36913436	*NA*	644189	0.003904366
Gene	HYPER in CCA	chr7	35242042	35293758	*TBX20*	57057	0.007718839
Gene	HYPER in CCA	chr5	16180347	16185694	*NA*	NA	0.00887526
Gene	HYPER in CCA	chr7	27226192	27233067	*NA*	NA	0.003548058
Gene	HYPER in CCA	chr1	150229554	150237478	*CA14*	23632	0.003392507
Gene	HYPER in CCA	chr10	134598297	134599556	*NKX6-2*	84504	0.012032942
Gene	HYPER in CCA	chr17	46626232	46682274	*HOXB3*	3213	0.009400725
Gene	HYPER in CCA	chr10	101286838	101288018	*NA*	NA	0.007602323
Gene	HYPER in CCA	chr2	31747550	31806136	*SRD5A2*	NA	0.011719413

Gene	HYPER in CCA	chr17	46626992	46683776	*HOXB-AS3*	404266	0.009907671
Gene	HYPER in CCA	chr7	27281048	27286848	*EVX1-AS*	NA	0.011963765
Gene	HYPER in CCA	chr7	96635695	96637022	*DLX6-AS2*	NA	0.007997317
Gene	HYPER in CCA	chr2	176973518	176984670	*HOXD10*	3236	0.010667461
Gene	HYPER in CCA	chr17	35297346	35300755	*NA*	NA	0.008636187
Gene	HYPER in CCA	chr22	29876219	29887379	*NEFH*	4744	0.000517392
Gene	HYPER in CCA	chr3	133464800	133497850	*TF*	7018	0.00440195
Gene	HYPER in CCA	chr19	53731577	53758151	*ZNF677*	342926	0.004380253
Gene	HYPER in CCA	chr19	28926295	29218684	*NA*	NA	0.008812223
Gene	HYPER in CCA	chr4	122680088	122686582	*TMEM155*	132332	0.010670509
Gene	HYPER in CCA	chr2	119591276	119592686	*NA*	NA	0.004425603
Gene	HYPER in CCA	chr16	86598751	86601367	*NA*	NA	0.006202835
Gene	HYPER in CCA	chr4	111516671	111536614	*NA*	NA	0.007653406
Gene	HYPER in CCA	chr11	20691971	20692843	*NA*	NA	0.010894198
Gene	HYPER in CCA	chr10	71331454	71332994	*NEUROG3*	50674	0.003884898
Gene	HYPER in CCA	chr19	29777918	30016659	*NA*	284395	0.009330215
Gene	HYPER in CCA	chr13	58205944	58303445	*PCDH17*	27253	0.010748743
Gene	HYPER in CCA	chr8	49464575	49469001	*NA*	NA	0.009035621
Gene	HYPER in CCA	chr1	110602616	110613322	*ALX3*	257	0.0038347
Gene	HYPER in CCA	chr10	101286107	101290934	*NA*	101927324	0.007568166
Gene	HYPER in CCA	chr19	21541732	21562104	*ZNF738*	NA	0.001920308
Gene	HYPER in CCA	chr18	70409549	70535381	*NETO1*	81832	0.009928036
Gene	HYPER in CCA	chr10	63166401	63213208	*TMEM26*	219623	0.006374999
Gene	HYPER in CCA	chr19	38180766	38210089	*NA*	NA	0.002516687
Gene	HYPER in CCA	chr19	53611132	53636330	*ZNF415*	55786	0.009540342
Gene	HYPER in CCA	chr4	81105033	81125483	*PRDM8*	56978	0.009151291
Gene	HYPER in CCA	chr1	149400131	149400542	*HIST2H3PS2*	NA	0.002739391
Gene	HYPER in CCA	chr6	117073363	117086886	*FAM162B*	221303	0.005161331
Gene	HYPER in CCA	chr19	20959110	20991922	*ZNF66*	NA	0.001246882
Gene	HYPER in CCA	chr19	21753624	21770124	*NA*	NA	0.002419094
Gene	HYPER in CCA	chr6	123317116	123394072	*CLVS2*	134829	0.010765124
Gene	HYPER in CCA	chr17	1173853	1174754	*BHLHA9*	727857	0.00409517
Gene	HYPER in CCA	chr11	17741115	17743678	*MYOD1*	4654	0.008928179
Gene	HYPER in CCA	chr1	119425669	119532179	*TBX15*	6913	0.007109277

Gene	HYPER in CCA	chr9	96713905	96717654	*BARX1*	56033	0.01074028
Gene	HYPER in CCA	chr15	22646603	22647417	*NA*	NA	0.003410423
Gene	HYPER in CCA	chr17	16586752	16587541	*RNASEH1P2*	246243	0.007426361
Gene	HYPER in CCA	chr1	248099363	248100815	*NA*	NA	0.006470334
Gene	HYPER in CCA	chr12	48577366	48579709	*C12orf68*	387856	0.009413989
Gene	HYPER in CCA	chr5	180526140	180527666	*FOXO1B*	NA	0.012052957
Gene	HYPER in CCA	chr15	34786621	34788101	*NA*	NA	0.00409517
Gene	HYPER in CCA	chr15	29033389	29037148	*NA*	100289656	0.006470334
Gene	HYPER in CCA	chr5	63986135	64013917	*FAM159B*	100132916	0.004275564
Gene	HYPER in CCA	chr6	142379467	142409936	*NMBR*	4829	0.011939262
Gene	HYPER in CCA	chr20	61798149	61812255	*NA*	NA	0.010159334
Gene	HYPER in CCA	chr19	23945807	24010937	*RPSAP58*	NA	0.009744435
Gene	HYPER in CCA	chr8	57358366	57464626	*NA*	101929415	0.009786525
Gene	HYPER in CCA	chr19	56728537	56729146	*NA*	NA	0.001358423
Gene	HYPER in CCA	chr18	22641890	22932154	*ZNF521*	25925	0.004138429
Gene	HYPER in CCA	chr3	172162923	172166246	*GHSR*	2693	0.008476759
Gene	HYPER in CCA	chr4	81104434	81111323	*NA*	NA	0.011973848
Gene	HYPER in CCA	chr10	102986733	102989551	*LBX1*	10660	0.007568166
Gene	HYPER in CCA	chr8	99956631	99964332	*OSR2*	116039	0.006518764
Gene	HYPER in CCA	chr2	19551246	19558414	*OSR1*	130497	0.008716704
Gene	HYPER in CCA	chr13	19864733	19918965	*ANKRD26P3*	NA	0.008743956
Gene	HYPER in CCA	chr12	103351464	103354294	*ASCL1*	429	0.007718839
Gene	HYPER in CCA	chr19	38039816	38078249	*ZNF571-AS1*	100507433	0.001547244
Gene	HYPER in CCA	chr10	105036920	105050108	*INA*	9118	0.009107098
Gene	HYPER in CCA	chr19	9577183	9609283	*ZNF560*	147741	0.003904366
Gene	HYPER in CCA	chr8	57349233	57359293	*PENK*	5179	0.005499988
Gene	HYPER in CCA	chr2	162280843	162841792	*SLC4A10*	57282	0.010115953
Gene	HYPER in CCA	chr2	200322423	200341658	*SATB2-AS1*	150538	0.005135978
Gene	HYPER in CCA	chr3	75718082	75719336	*NA*	NA	8.43E-05
Gene	HYPER in CCA	chr19	52956829	53015407	*ZNF578*	147660	0.005499988
Gene	HYPER in CCA	chr2	74740590	74744274	*TLX2*	3196	0.012236079
Gene	HYPER in CCA	chr2	233344537	233352538	*ECEL1*	9427	0.002293044
Gene	HYPER in CCA	chr8	26605667	26724790	*ADRA1A*	148	0.007672684
Gene	HYPER in CCA	chr1	149400063	149429348	*NA*	NA	0.004598052

Gene	HYPER in CCA	chr6	10423373	10426409	*NA*	NA	0.011939262
Gene	HYPER in CCA	chr1	145413095	145417545	*HFE2*	148738	0.005038304
Gene	HYPER in CCA	chr1	149398877	149400540	*NA*	NA	0.0049635
Gene	HYPER in CCA	chr20	25051521	25062996	*VSX1*	30813	0.006239106
Promoter	HYPO in CCA	chr22	36850492	36852491	*NA*	NA	6.35E-06
Promoter	HYPO in CCA	chr14	100202530	100204529	*EML1*	2009	0.000211094
Promoter	HYPO in CCA	chr12	7339781	7341780	*PEX5*	5830	5.42E-05
Promoter	HYPO in CCA	chr1	155947090	155949089	*NA*	NA	0.000110255
Promoter	HYPO in CCA	chr5	141705521	141707520	*SPRY4*	81848	0.00011061
Promoter	HYPO in CCA	chr12	29470282	29472281	*NA*	100506606	0.001131203
Promoter	HYPO in CCA	chr14	105143587	105145586	*MIR4710*	100616300	0.000996922
Promoter	HYPO in CCA	chr10	102754875	102756874	*LZTS2*	84445	5.42E-05
Promoter	HYPO in CCA	chr15	74726309	74728308	*SEMA7A*	8482	5.89E-05
Promoter	HYPO in CCA	chr16	69163694	69165693	*CIRH1A*	84916	0.002730368
Promoter	HYPO in CCA	chr16	29818554	29820553	*NA*	NA	0.000104572
Promoter	HYPO in CCA	chr17	61915843	61917842	*RN7SL805P*	NA	0.001597508
Promoter	HYPO in CCA	chr8	22455614	22457613	*C8orf58*	541565	0.00010965
Promoter	HYPO in CCA	chr3	183542883	183544882	*MAP6D1*	79929	0.005139579
Promoter	HYPO in CCA	chr16	69759416	69761415	*NA*	NA	9.33E-06
Promoter	HYPO in CCA	chr21	42732370	42734369	*MX2*	4600	0.003749938
Promoter	HYPO in CCA	chr2	239198244	239200243	*PER2*	8864	0.001846694
Promoter	HYPO in CCA	chr9	117567907	117569906	*TNFSF15*	9966	5.43E-05
Promoter	HYPO in CCA	chr21	37801158	37803157	*NA*	NA	0.001113383
Promoter	HYPO in CCA	chr2	220116465	220118464	*TUBA4B*	80086	3.77E-06
Promoter	HYPO in CCA	chr1	24644312	24646311	*GRHL3*	57822	0.000346168
Promoter	HYPO in CCA	chr3	46447154	46449153	*CCRL2*	9034	0.002460867
Promoter	HYPO in CCA	chr15	81701358	81703357	*NA*	NA	5.47E-07
Promoter	HYPO in CCA	chr7	100180105	100182104	*FBXO24*	26261	2.60E-05
Promoter	HYPO in CCA	chr1	156630717	156632716	*NA*	NA	5.31E-06
Promoter	HYPO in CCA	chr7	142986208	142988207	*RN7SL535P*	NA	0.000408701
Promoter	HYPO in CCA	chr6	33243417	33245416	*B3GALT4*	8705	0.00064289
Promoter	HYPO in CCA	chr17	73840299	73842298	*UNC13D*	201294	6.74E-06
Promoter	HYPO in CCA	chr16	69760355	69762354	*NQO1*	1728	1.72E-06
Promoter	HYPO in CCA	chr6	35264095	35266094	*DEF6*	50619	0.000816166

Promoter	HYPO in CCA	chr1	27667013	27669012	*SYTL1*	84958	1.24E-05
Promoter	HYPO in CCA	chr19	14489813	14491812	*CD97*	976	0.001114012
Promoter	HYPO in CCA	chr2	87753387	87755386	*LINC00152*	112597;541471	1.46E-05
Promoter	HYPO in CCA	chr5	17117296	17119295	*NA*	NA	0.002944927
Promoter	HYPO in CCA	chr21	45579460	45581459	*NA*	101928576	3.21E-05
Promoter	HYPO in CCA	chr16	87839583	87841582	*NA*	NA	0.00040854
Promoter	HYPO in CCA	chr3	158389983	158391982	*LXN*	56925	0.002899463
Promoter	HYPO in CCA	chr1	152019884	152021883	*S100A11*	6282	2.34E-07
Promoter	HYPO in CCA	chr1	26604167	26606166	*SH3BGRL3*	83442	0.000254915
Promoter	HYPO in CCA	chr2	109294558	109296557	*NA*	NA	0.000209061
Promoter	HYPO in CCA	chr14	32412559	32414558	*NA*	NA	0.00260345
Promoter	HYPO in CCA	chr22	38091511	38093510	*TRIOBP*	11078	4.60E-05
Promoter	HYPO in CCA	chr11	85780425	85782424	*PICALM*	8301	0.000387186
Promoter	HYPO in CCA	chr1	43736108	43738107	*EBNA1BP2*	10969;102465439	8.13E-07
Promoter	HYPO in CCA	chr12	94676121	94678120	*NA*	NA	0.000108562
Promoter	HYPO in CCA	chr15	96867667	96869666	*NR2F2*	7026	0.0007648
Promoter	HYPO in CCA	chr8	22931502	22933501	*NA*	NA	2.60E-06
Promoter	HYPO in CCA	chr2	85133633	85135632	*TRABD2A*	129293	4.06E-08
Promoter	HYPO in CCA	chr2	64832609	64834608	*NA*	339807	0.001477078
Promoter	HYPO in CCA	chr19	47735524	47737523	*BBC3*	27113;100422832;100422899	3.30E-06
Promoter	HYPO in CCA	chr17	79520488	79522487	*C17orf70*	80233	6.96E-07
Promoter	HYPO in CCA	chr12	48274932	48276931	*NA*	NA	0.004965211
Promoter	HYPO in CCA	chr16	88717061	88719060	*CYBA*	1535	3.94E-06
Promoter	HYPO in CCA	chr8	23192184	23194183	*NA*	100507156	4.37E-05
Promoter	HYPO in CCA	chr22	40354901	40356900	*NA*	NA	0.001008565
Promoter	HYPO in CCA	chr1	173834325	173836324	*SNORD78*	692198	5.87E-07
Promoter	HYPO in CCA	chr6	43191099	43193098	*NA*	NA	3.84E-07
Promoter	HYPO in CCA	chr5	67729809	67731808	*NA*	NA	9.65E-07
Gene	HYPO in CCA	chr14	105144031	105144086	*MIR4710*	100616300	0.006125989
Gene	HYPO in CCA	chr19	47278140	47291851	*SLC1A5*	6510	0.000618914
Gene	HYPO in CCA	chr11	66097713	66104311	*RIN1*	9610	0.000888494
Gene	HYPO in CCA	chr22	39410088	39416357	*APOBEC3C*	27350	0.006332718
Gene	HYPO in CCA	chr16	89778264	89784573	*VPS9D1-AS1*	100128881	0.003170455
Gene	HYPO in CCA	chr12	7319270	7341665	*NA*	NA	0.000337557

Gene	HYPO in CCA	chr19	47567444	47617009	*ZC3H4*	23211	0.000367933
Gene	HYPO in CCA	chr16	31213206	31214773	*C16orf98*	NA	0.002913961
Gene	HYPO in CCA	chr18	47018034	47018099	*SNORD58B*	26790	0.000222819
Gene	HYPO in CCA	chr2	202098166	202152434	*CASP8*	841	0.00053645
Gene	HYPO in CCA	chr16	29465822	29469540	*SLX1B*	79008;548593	0.003801761
Gene	HYPO in CCA	chr2	27440258	27466811	*CAD*	790	0.001116693
Gene	HYPO in CCA	chr1	244232122	244256328	*NA*	NA	0.010598368
Gene	HYPO in CCA	chr19	46142252	46142345	*MIR330*	442902	8.70E-07
Gene	HYPO in CCA	chr16	31212806	31214771	*PYCARD*	29108	0.002405714
Gene	HYPO in CCA	chr1	185286911	185287662	*NA*	NA	0.007718839
Gene	HYPO in CCA	chr16	69740899	69760854	*NQO1*	1728	0.000395361
Gene	HYPO in CCA	chr6	43968317	43973695	*C6orf223*	221416	0.004840801
Gene	HYPO in CCA	chr1	61005921	61106163	*NA*	NA	0.005221953
Gene	HYPO in CCA	chr17	27041299	27045447	*RAB34*	83871;100861437	0.005171141
Gene	HYPO in CCA	chr19	1238178	1239521	*NA*	NA	7.11E-05
Gene	HYPO in CCA	chr16	88709691	88717560	*CYBA*	1535	0.002646
Gene	HYPO in CCA	chr3	185224050	185270401	*LIPH*	200879	0.00045683
Gene	HYPO in CCA	chr2	43254992	43266686	*NA*	NA	0.00963733
Gene	HYPO in CCA	chr3	46448654	46454488	*CCRL2*	9034	0.007977024
Gene	HYPO in CCA	chr14	91709103	91717426	*NA*	NA	0.006719902
Gene	HYPO in CCA	chr9	5299868	5304969	*RLN2*	6019	0.003801761
Gene	HYPO in CCA	chr17	79336072	79348014	*NA*	NA	0.010683459
Gene	HYPO in CCA	chr3	149086809	149095652	*TM4SF1*	4071	0.001547244
Gene	HYPO in CCA	chr19	13907388	13907747	*NA*	NA	0.001347053
Gene	HYPO in CCA	chr15	42184991	42190773	*NA*	NA	0.001113111
Gene	HYPO in CCA	chr1	24634046	24648391	*NA*	NA	0.001920308
Gene	HYPO in CCA	chr2	64412212	64432619	*LINC00309*	150992	0.007182032
Gene	HYPO in CCA	chr15	78285747	78287631	*NA*	NA	0.000405417
Gene	HYPO in CCA	chr19	13890884	13900972	*NA*	NA	0.001196898
Gene	HYPO in CCA	chr11	49119715	49122720	*NA*	NA	0.006227715
Gene	HYPO in CCA	chr5	138855119	138862520	*TMEM173*	340061	0.01226362
Gene	HYPO in CCA	chr19	41931264	41934635	*B3GNT8*	374907	0.001992128
Gene	HYPO in CCA	chr17	27966645	27967843	*NA*	NA	0.001740616
Gene	HYPO in CCA	chr17	80172103	80175228	*NA*	NA	0.010148518

Gene	HYPO in CCA	chr6	30734602	30760027	*HCG20*	NA	1.26E-05
Gene	HYPO in CCA	chr19	13945330	13947173	*MIR24-2*	284454;407013	0.003218254
Gene	HYPO in CCA	chr1	153533584	153540366	*S100A2*	6273	0.000196065
Gene	HYPO in CCA	chr19	36158850	36164193	*UPK1A-AS1*	100862728	0.001262067
Gene	HYPO in CCA	chr17	9550337	9550977	*NA*	NA	0.008869597
Gene	HYPO in CCA	chr12	90341470	90343503	*NA*	NA	0.010159334
Gene	HYPO in CCA	chr22	40297086	40369725	*GRAP2*	9402	0.008869597
Gene	HYPO in CCA	chr15	74781943	74809300	*NA*	NA	0.000715099
Gene	HYPO in CCA	chr12	122501212	122506522	*NA*	100506691	0.002365699
Gene	HYPO in CCA	chr15	77817882	77826452	*NA*	101929457	0.004376699
Gene	HYPO in CCA	chr4	10117380	10117508	*RNA5SP155*	NA	0.000520594
Gene	HYPO in CCA	chr16	11290034	11318373	*NA*	NA	0.010400642
Gene	HYPO in CCA	chr1	2143610	2144013	*NA*	NA	0.00030556
Gene	HYPO in CCA	chr19	35861831	35863855	*GPR42*	NA	0.004846203
Gene	HYPO in CCA	chr1	45242162	45242265	*SNORD46*	94161	1.26E-05
Gene	HYPO in CCA	chr19	13947401	13947473	*MIR23A*	407010	9.13E-05
Gene	HYPO in CCA	chr19	42637597	42637665	*MIR4323*	100422980	0.000388126
Gene	HYPO in CCA	chr14	103587184	103589344	*LINC00677*	NA	1.46E-05
Gene	HYPO in CCA	chr16	49476821	49487989	*NA*	NA	0.005973852
Gene	HYPO in CCA	chr7	46300662	46334067	*NA*	NA	0.002319766
Gene	HYPO in CCA	chr17	77910551	77910992	*NA*	NA	0.000262447
Gene	HYPO in CCA	chr2	109293251	109295057	*NA*	NA	0.000328612
Gene	HYPO in CCA	chr21	45578623	45579959	*NA*	101928576	0.000218679
Gene	HYPO in CCA	chr6	43690523	43705571	*NA*	NA	0.000675872
Gene	HYPO in CCA	chr1	155948590	155952777	*NA*	NA	5.25E-06
Gene	HYPO in CCA	chr6	31804853	31804919	*SNORD52*	26797	0.005017486
Gene	HYPO in CCA	chr11	19402031	19406561	*NAV2-IT1*	NA	0.002069819
Gene	HYPO in CCA	chr9	74920346	74958126	*NA*	100507540	0.001227877
Gene	HYPO in CCA	chr22	43608680	43609667	*NA*	NA	0.000675872
Gene	HYPO in CCA	chr12	94671534	94676620	*NA*	NA	2.42E-05
Gene	HYPO in CCA	chr15	55665138	55665232	*MIR628*	693213	0.006202835
Gene	HYPO in CCA	chr10	119184705	119249930	*NA*	NA	0.000491326
Gene	HYPO in CCA	chr20	31175281	31196695	*NA*	NA	0.000107175
Gene	HYPO in CCA	chr8	38401170	38410198	*NA*	NA	0.001473144

Gene	HYPO in CCA	chr19	3558013	3558484	*NA*	NA	0.009101741
Gene	HYPO in CCA	chr16	2013746	2014096	*NA*	NA	6.25E-05
Gene	HYPO in CCA	chr6	138723722	138724697	*MARCKSL1P2*	NA	0.000424613
Gene	HYPO in CCA	chr5	6766004	6772066	*NA*	NA	2.22E-05
Gene	HYPO in CCA	chr2	237642025	237663006	*NA*	NA	0.000269322
Gene	HYPO in CCA	chr4	88896819	88904562	*SPP1*	6696	0.000162246
Gene	HYPO in CCA	chr1	150209315	150209504	*RNU2-17P*	NA	0.000530524
Gene	HYPO in CCA	chr22	30580633	30603098	*NA*	NA	5.77E-05
Gene	HYPO in CCA	chr5	67726254	67730308	*NA*	NA	1.77E-06

Udt-gr: Differential methylated regions (DMRs)

Location	Epimutation	Chromosome	Start	End	Symbol	EntrezID	Combined FDR *P*-value
Promoter	HYPER in CCA	chr1	95584203	95586202	*NA*	NA	2.45E-13
Promoter	HYPER in CCA	chr2	47293461	47295460	*NA*	NA	3.43E-09
Promoter	HYPER in CCA	chr3	174154863	174156862	*NAALADL2*	254827	7.08E-10
Promoter	HYPER in CCA	chr14	57278401	57280400	*OTX2-AS1*	100309464	4.79E-10
Promoter	HYPER in CCA	chr15	34782273	34784272	*HNRNPLP2*	NA	2.73E-08
Promoter	HYPER in CCA	chr1	11899574	11901573	*NPPA-AS1*	100379251	1.20E-14
Promoter	HYPER in CCA	chr15	81297874	81299873	*C15orf26*	161502	3.43E-09
Promoter	HYPER in CCA	chr1	165631425	165633424	*NA*	NA	7.08E-10
Promoter	HYPER in CCA	chr5	135290224	135292223	*LECT2*	3950	1.65E-12
Promoter	HYPER in CCA	chr10	96828755	96830754	*CYP2C8*	1558	2.70E-08
Promoter	HYPER in CCA	chr22	50643992	50645991	*NA*	NA	1.20E-14
Promoter	HYPER in CCA	chr5	115152152	115154151	*CDO1*	1036	1.65E-12
Promoter	HYPER in CCA	chr2	176999840	177001839	*HOXD3*	3232;3233;401021	1.19E-08
Promoter	HYPER in CCA	chr6	139793693	139795692	*NA*	645434	4.98E-07
Promoter	HYPER in CCA	chr2	175189255	175191254	*NA*	285084	4.31E-07
Promoter	HYPER in CCA	chr6	151936515	151938514	*RNU6-813P*	NA	1.13E-07
Promoter	HYPER in CCA	chr16	78539966	78541965	*NA*	NA	2.52E-05
Promoter	HYPER in CCA	chr7	153582682	153584681	*DPP6*	1804	3.44E-10
Promoter	HYPER in CCA	chr20	62365315	62367314	*LIME1*	54923	1.34E-13
Promoter	HYPER in CCA	chr7	70595655	70597654	*WBSCR17*	64409	2.22E-08
Promoter	HYPER in CCA	chr7	6055008	6057007	*NA*	NA	5.28E-11
Promoter	HYPER in CCA	chr1	170635022	170637021	*NA*	NA	8.60E-08
Promote	HYPER in	chr12	10949125	10949325	*USP30-AS1*	100131733	9.11E-05

r	CCA		8	7			
Promoter	HYPER in CCA	chr19	30016160	30018159	*NA*	284395	2.59E-07
Promoter	HYPER in CCA	chr5	95581980	95583979	*NA*	NA	1.13E-08
Promoter	HYPER in CCA	chr17	30953257	30955256	*NA*	NA	8.97E-08
Promoter	HYPER in CCA	chr18	21161586	21163585	*NA*	NA	5.54E-06
Promoter	HYPER in CCA	chr2	37662252	37664251	*RNU6-1116P*	NA	3.05E-06
Promoter	HYPER in CCA	chr1	36042831	36044830	*NA*	NA	1.48E-11
Promoter	HYPER in CCA	chr9	127710272	127712271	*GOLGA1*	2800	2.16E-08
Promoter	HYPER in CCA	chr17	46709422	46711421	*MIR196A1*	406972	2.27E-09
Promoter	HYPER in CCA	chr18	21571237	21573236	*TTC39C*	125488	7.32E-06
Promoter	HYPER in CCA	chr4	188915425	188917424	*ZFP42*	132625	3.99E-07
Promoter	HYPER in CCA	chr5	1885946	1887945	*NA*	101929081	2.15E-08
Promoter	HYPER in CCA	chr5	1886851	1888850	*IRX4*	50805	5.77E-09
Promoter	HYPER in CCA	chr17	46633124	46635123	*HOXB-AS2*	NA	5.04E-08
Promoter	HYPER in CCA	chr11	43601444	43603443	*MIR129-2*	406918	3.34E-10
Promoter	HYPER in CCA	chr17	46659122	46661121	*MIR10A*	406902	5.52E-10
Promoter	HYPER in CCA	chr3	58522547	58524546	*ACOX2*	8309	7.67E-10
Promoter	HYPER in CCA	chr9	37001194	37003193	*NA*	NA	5.26E-11
Promoter	HYPER in CCA	chr16	87969636	87971635	*CA5A*	763	1.53E-11
Promoter	HYPER in CCA	chr19	30015906	30017905	*VSTM2B*	342865	3.81E-07
Promoter	HYPER in CCA	chr12	85306895	85308894	*SLC6A15*	55117	6.15E-06
Promoter	HYPER in CCA	chr6	27234392	27236391	*NA*	NA	1.24E-07
Promoter	HYPER in CCA	chr17	46799030	46801029	*PRAC2*	100422978	7.68E-08
Promoter	HYPER in CCA	chr2	201541456	201543455	*AOX3P*	NA	9.11E-05
Promoter	HYPER in CCA	chr7	156797501	156799500	*MNX1-AS2*	NA	1.24E-08
Promoter	HYPER in CCA	chr7	24322282	24324281	*NPY*	4852	1.21E-06
Promoter	HYPER in CCA	chr12	22093837	22095836	*ABCC9*	10060	5.76E-10
Promoter	HYPER in CCA	chr6	31893975	31895974	*NA*	NA	1.83E-08
Promoter	HYPER in CCA	chr6	31893975	31895974	*CFB*	629	1.83E-08
Promoter	HYPER in CCA	chr2	177029945	177031944	*NA*	NA	5.13E-10
Promoter	HYPER in CCA	chr16	51181650	51183649	*NA*	NA	8.78E-05
Promoter	HYPER in CCA	chr5	149922752	149924751	*NA*	NA	1.14E-07
Promoter	HYPER in CCA	chr7	25988524	25990523	*NA*	NA	0.000109272
Promoter	HYPER in CCA	chr6	28413250	28415249	*COX11P1*	NA	4.15E-09

Promoter	HYPER in CCA	chr2	132087931	132089930	*ARHGAP42P1*	NA	4.29E-10
Promoter	HYPER in CCA	chr7	27208684	27210683	*MIR196B*	442920	1.65E-12
Promoter	HYPER in CCA	chr11	118396687	118398686	*TTC36*	143941	2.53E-10
Promoter	HYPER in CCA	chr19	35629985	35631984	*NA*	NA	4.04E-10
Promoter	HYPER in CCA	chr5	50265502	50267501	*NA*	100287592	5.68E-08
Promoter	HYPER in CCA	chr11	914559	916558	*CHID1*	66005	4.32E-12
Promoter	HYPER in CCA	chr16	23845822	23847821	*PRKCB*	5579	1.14E-07
Promoter	HYPER in CCA	chr2	176992922	176994921	*HOXD8*	3234	5.26E-10
Promoter	HYPER in CCA	chr3	46537481	46539480	*RTP3*	83597	1.20E-07
Promoter	HYPER in CCA	chr7	27280348	27282347	*NA*	NA	1.19E-07
Promoter	HYPER in CCA	chr12	128750448	128752447	*TMEM132C*	92293	3.81E-07
Promoter	HYPER in CCA	chr17	46710435	46712434	*HOXB7*	3217	3.16E-09
Promoter	HYPER in CCA	chr2	177014450	177016449	*HOXD4*	3233	4.36E-07
Promoter	HYPER in CCA	chr13	79168764	79170763	*NA*	NA	1.42E-07
Promoter	HYPER in CCA	chr16	3236712	3238711	*NA*	NA	1.28E-06
Promoter	HYPER in CCA	chr5	16178847	16180846	*NA*	NA	9.85E-07
Promoter	HYPER in CCA	chr8	68862853	68864852	*PREX2*	80243	5.75E-07
Promoter	HYPER in CCA	chr10	102898969	102900968	*NA*	NA	1.16E-08
Promoter	HYPER in CCA	chr7	27135116	27137115	*HOXA1*	3198	3.04E-08
Promoter	HYPER in CCA	chr1	227747382	227749381	*RNA5SP77*	NA	2.92E-09
Promoter	HYPER in CCA	chr6	52608955	52610954	*GSTA7P*	NA	0.000820957
Promoter	HYPER in CCA	chr14	57276698	57278697	*OTX2*	5015	1.54E-07
Promoter	HYPER in CCA	chr9	131681674	131683673	*PHYHD1*	254295	2.17E-12
Promoter	HYPER in CCA	chr4	184015710	184017709	*NA*	NA	0.000136377
Promoter	HYPER in CCA	chr1	63789613	63791612	*NA*	NA	7.41E-08
Promoter	HYPER in CCA	chr2	169887333	169889332	*ABCB11*	8647	2.04E-07
Promoter	HYPER in CCA	chr10	63210897	63212896	*NA*	101928781	3.11E-09
Promoter	HYPER in CCA	chr17	35300256	35302255	*NA*	NA	7.40E-08
Promoter	HYPER in CCA	chr8	57356866	57358865	*NA*	101929415	6.70E-10
Promoter	HYPER in CCA	chr19	57182652	57184651	*ZNF835*	90485	4.34E-06
Promoter	HYPER in CCA	chr19	57182136	57184135	*NA*	NA	4.34E-06
Promoter	HYPER in CCA	chr5	78406102	78408101	*BHMT*	635	1.02E-06
Promoter	HYPER in CCA	chr1	71170636	71172635	*NA*	101927244	6.08E-12
Promoter	HYPER in CCA	chr8	23563612	23565611	*NKX2-6*	137814	1.27E-08

Promoter	HYPER in CCA	chr15	83952967	83954966	*BNC1*	646	2.42E-08
Promoter	HYPER in CCA	chr2	17701353	17701553	*MIR10B*	406903	6.25E-07
Promoter	HYPER in CCA	chr6	38681617	38683616	*DNAH8*	1769	2.18E-05
Promoter	HYPER in CCA	chr10	11949332	11949532	*NA*	NA	1.47E-08
Promoter	HYPER in CCA	chr19	35628212	35630211	*FXYD1*	5348	2.86E-11
Promoter	HYPER in CCA	chr19	35628228	35630227	*NA*	NA	2.86E-11
Promoter	HYPER in CCA	chr4	15677439	15677638	*TDO2*	6999	8.04E-06
Promoter	HYPER in CCA	chr5	14078627	14078826	*PCDHGB6*	56100	4.51E-05
Promoter	HYPER in CCA	chr7	27191718	27193717	*NA*	NA	1.69E-08
Promoter	HYPER in CCA	chr5	54804255	54806254	*MIR5687*	100847019	3.33E-05
Promoter	HYPER in CCA	chr7	27133766	27135765	*HOTAIRM1*	100506311	9.65E-08
Promoter	HYPER in CCA	chr15	32607356	32609355	*NA*	NA	0.000355358
Promoter	HYPER in CCA	chr8	65290206	65292205	*MIR124-2*	406908	1.53E-06
Promoter	HYPER in CCA	chr1	17063036	17063236	*PRRX1*	5396	2.80E-06
Promoter	HYPER in CCA	chr7	27191701	27193700	*HOXA3*	3200	1.62E-08
Promoter	HYPER in CCA	chr7	27191681	27193680	*NA*	NA	1.62E-08
Promoter	HYPER in CCA	chr3	12131046	12131246	*FBXO40*	51725	2.49E-08
Promoter	HYPER in CCA	chr12	85672385	85674384	*ALX1*	8092	1.08E-06
Promoter	HYPER in CCA	chr18	76738775	76740774	*SALL3*	27164	2.72E-07
Promoter	HYPER in CCA	chr4	12230171	12230371	*QRFPR*	84109	2.20E-06
Promoter	HYPER in CCA	chr7	27280664	27282663	*EVX1*	2128	4.59E-07
Promoter	HYPER in CCA	chr3	14710970	14711170	*ZIC1*	7545	3.96E-08
Promoter	HYPER in CCA	chr2	17704094	17704294	*NA*	NA	6.43E-07
Promoter	HYPER in CCA	chr19	30017356	30019355	*NA*	NA	9.27E-06
Promoter	HYPER in CCA	chr17	46799385	46801384	*PRAC1*	84366	1.29E-06
Promoter	HYPER in CCA	chr5	2737374	2739373	*NA*	NA	7.82E-07
Promoter	HYPER in CCA	chr12	10287392	10287592	*IGF1*	3479	7.40E-08
Promoter	HYPER in CCA	chr18	76738575	76740574	*NA*	NA	2.07E-07
Promoter	HYPER in CCA	chr4	17491151	17491351	*NA*	NA	5.25E-07
Promoter	HYPER in CCA	chr8	56013449	56015448	*XKR4*	114786	1.70E-07
Promoter	HYPER in CCA	chr8	55368995	55370994	*SOX17*	64321	7.68E-08
Promoter	HYPER in CCA	chr7	27197056	27199055	*HOXA7*	3204	1.17E-07
Promoter	HYPER in CCA	chr19	58220080	58222079	*ZNF154*	7710	0.001068566
Promoter	HYPER in CCA	chr19	35394600	35396599	*NA*	NA	3.52E-07

Promoter	HYPER in CCA	chr10	129534470	129536469	*NA*	387720	5.90E-07
Promoter	HYPER in CCA	chr2	176956119	176958118	*HOXD13*	3239	4.63E-08
Promoter	HYPER in CCA	chr1	116105722	116107721	*CNOT7P2*	NA	2.92E-09
Promoter	HYPER in CCA	chr1	228651828	228653827	*HIST3H2BA*	NA	8.17E-06
Promoter	HYPER in CCA	chr8	24769087	24771086	*NA*	NA	1.95E-08
Promoter	HYPER in CCA	chr8	24769025	24771024	*NEFM*	4741	1.95E-08
Promoter	HYPER in CCA	chr13	79177174	79179173	*POU4F1*	5457	3.72E-06
Promoter	HYPER in CCA	chr6	28751282	28753281	*NA*	NA	2.16E-06
Promoter	HYPER in CCA	chr15	29031889	29033888	*NA*	100289656	8.05E-07
Promoter	HYPER in CCA	chr17	59528265	59530264	*TBX4*	9496	3.50E-06
Promoter	HYPER in CCA	chr1	217310598	217312597	*ESRRG*	2104	1.36E-06
Promoter	HYPER in CCA	chr2	176967444	176969443	*HOXD11*	3237	1.15E-05
Promoter	HYPER in CCA	chr20	61637888	61639887	*BHLHE23*	128408	2.14E-08
Promoter	HYPER in CCA	chr7	27206738	27208737	*HOXA10-AS*	442920;100874323	1.38E-09
Promoter	HYPER in CCA	chr5	178366692	178368691	*ZNF454*	285676	5.99E-08
Promoter	HYPER in CCA	chr1	111217156	111219155	*KCNA3*	3738	4.11E-07
Promoter	HYPER in CCA	chr7	27209618	27211617	*HOXA9*	3205;442920	1.80E-07
Promoter	HYPER in CCA	chr17	33823737	33825736	*NA*	NA	8.78E-08
Promoter	HYPER in CCA	chr20	30072081	30074080	*LINC00028*	140875	3.70E-07
Promoter	HYPER in CCA	chr2	176972018	176974017	*HOXD10*	3236	5.25E-08
Promoter	HYPER in CCA	chr2	237076513	237078512	*GBX2*	2637	2.04E-07
Promoter	HYPER in CCA	chr22	17081277	17083276	*TPTEP1*	387590	1.16E-10
Promoter	HYPER in CCA	chr8	59412296	59414295	*CYP7A1*	1581	8.23E-05
Promoter	HYPER in CCA	chr5	170734788	170736787	*TLX3*	30012	5.93E-10
Promoter	HYPER in CCA	chr8	67874326	67876325	*TCF24*	100129654	1.17E-06
Promoter	HYPER in CCA	chr7	27169919	27171918	*HOXA4*	3201	8.67E-09
Promoter	HYPER in CCA	chr10	105035420	105037419	*INA*	9118	3.61E-09
Promoter	HYPER in CCA	chr14	45380567	45382566	*NA*	101927418	3.62E-09
Promoter	HYPER in CCA	chr2	240225657	240227656	*MIR4269*	100423043	0.002044588
Promoter	HYPER in CCA	chr11	14925043	14927042	*CALCB*	797	0.000350793
Promoter	HYPER in CCA	chr3	187009311	187011310	*MASP1*	5648	0.000100583
Promoter	HYPER in CCA	chr10	28034490	28036489	*MKX*	283078	5.34E-07
Promoter	HYPER in CCA	chr8	23563154	23565153	*NA*	NA	7.32E-08
Promoter	HYPER in CCA	chr17	46656974	46658973	*HOXB4*	3214	3.40E-06

Promoter	HYPER in CCA	chr2	177001327	177003326	*HOXD-AS2*	100506783	1.20E-06
Promoter	HYPER in CCA	chr19	56988935	56990934	*ZNF667*	63934	0.000754327
Promoter	HYPER in CCA	chr4	190960997	190962996	*AGGF1P1*	NA	3.03E-08
Promoter	HYPER in CCA	chr1	53752196	53754195	*NA*	NA	1.55E-06
Promoter	HYPER in CCA	chr13	53422276	53424275	*PCDH8*	5100	3.59E-07
Promoter	HYPER in CCA	chr20	43438480	43440479	*RIMS4*	140730	1.42E-05
Promoter	HYPER in CCA	chr19	54411089	54413088	*CACNG7*	59284	4.84E-07
Promoter	HYPER in CCA	chr12	47225692	47227691	*SLC38A4*	55089	6.48E-06
Promoter	HYPER in CCA	chr3	75954346	75956345	*ROBO2*	6092	6.65E-07
Promoter	HYPER in CCA	chr19	53757652	53759651	*ZNF677*	342926	1.81E-07
Promoter	HYPER in CCA	chr6	96462360	96464359	*FUT9*	10690	1.44E-05
Promoter	HYPER in CCA	chr8	54788710	54790709	*NA*	NA	2.35E-06
Promoter	HYPER in CCA	chr2	176971871	176973870	*NA*	NA	2.03E-07
Promoter	HYPER in CCA	chr4	42398356	42400355	*SHISA3*	152573	3.03E-05
Promoter	HYPER in CCA	chr7	27196463	27198462	*NA*	NA	3.59E-07
Promoter	HYPER in CCA	chr16	227053	229052	*NA*	NA	1.27E-07
Promoter	HYPER in CCA	chr5	3594668	3596667	*IRX1*	79192	9.11E-09
Promoter	HYPER in CCA	chr5	50263994	50265993	*NA*	NA	1.82E-06
Promoter	HYPER in CCA	chr8	104511476	104513475	*RIMS2*	9699	7.57E-05
Promoter	HYPER in CCA	chr1	237204005	237206004	*RYR2*	6262	1.55E-05
Promoter	HYPER in CCA	chr2	105483455	105485454	*NA*	NA	1.28E-06
Promoter	HYPER in CCA	chr8	69243227	69245226	*NA*	NA	2.16E-05
Promoter	HYPER in CCA	chr15	28753455	28755454	*ABCB10P4*	NA	1.65E-12
Promoter	HYPER in CCA	chr3	46929672	46931671	*NA*	NA	0.000107625
Promoter	HYPER in CCA	chr1	91182295	91184294	*BARHL2*	343472	1.02E-07
Promoter	HYPER in CCA	chr3	179754342	179756341	*PEX5L*	51555	1.45E-08
Promoter	HYPER in CCA	chr7	97359720	97361719	*TAC1*	6863	4.91E-06
Promoter	HYPER in CCA	chr19	38306499	38308498	*NA*	644554	3.62E-06
Promoter	HYPER in CCA	chr10	135042278	135044277	*UTF1*	8433	2.72E-07
Promoter	HYPER in CCA	chr12	54412194	54414193	*NA*	NA	2.71E-06
Promoter	HYPER in CCA	chr5	127872206	127874205	*SLC27A6*	28965	2.36E-05
Promoter	HYPER in CCA	chr7	27232568	27234567	*NA*	NA	5.23E-05
Promoter	HYPER in CCA	chr7	19184545	19186544	*FERD3L*	222894	4.71E-06
Promoter	HYPER in CCA	chr3	129691648	129693647	*TRH*	7200	9.16E-09

Promoter	HYPER in CCA	chr11	30038071	30040070	*KCNA4*	3739	4.24E-06
Promoter	HYPER in CCA	chr4	22693037	22695036	*GBA3*	57733	0.000103427
Promoter	HYPER in CCA	chr12	54390070	54392069	*HOXC-AS2*	100874364	1.62E-05
Promoter	HYPER in CCA	chr7	19150597	19152596	*NA*	NA	7.91E-06
Promoter	HYPER in CCA	chr19	39753522	39755521	*IFNL4P1*	NA	1.67E-05
Promoter	HYPER in CCA	chr12	41580750	41582749	*PDZRN4*	29951	2.66E-06
Promoter	HYPER in CCA	chr10	23479756	23481755	*PTF1A*	256297	4.14E-07
Promoter	HYPER in CCA	chr20	37351605	37353604	*SLC32A1*	140679	2.27E-09
Promoter	HYPER in CCA	chr10	22632899	22634898	*SPAG6*	9576	5.93E-10
Promoter	HYPER in CCA	chr2	130735735	130737734	*RAB6C*	84084;150786	9.80E-10
Promoter	HYPER in CCA	chr2	5834852	5836851	*NA*	NA	0.0011848
Promoter	HYPER in CCA	chr2	223161366	223163365	*CCDC140*	151278	4.59E-07
Promoter	HYPER in CCA	chr4	66534179	66536178	*NA*	100144602	3.15E-06
Promoter	HYPER in CCA	chr12	30352416	30354415	*NA*	NA	3.23E-08
Promoter	HYPER in CCA	chr1	248100316	248102315	*NA*	NA	1.07E-05
Promoter	HYPER in CCA	chr20	25062497	25064496	*VSX1*	30813	3.44E-08
Promoter	HYPER in CCA	chr16	55364767	55366766	*NA*	NA	9.22E-07
Promoter	HYPER in CCA	chr15	35045785	35047784	*NA*	101928174	1.51E-05
Promoter	HYPER in CCA	chr11	32455564	32457563	*WT1-AS*	51352	3.56E-05
Promoter	HYPER in CCA	chr2	5830751	5832750	*NA*	NA	4.13E-06
Promoter	HYPER in CCA	chr17	42732262	42734261	*C17orf104*	284071	1.72E-08
Promoter	HYPER in CCA	chr6	28583490	28585489	*SCAND3*	114821	7.03E-08
Promoter	HYPER in CCA	chr2	176985588	176987587	*HOXD9*	3235	1.07E-07
Promoter	HYPER in CCA	chr1	79471904	79473903	*ELTD1*	64123	1.72E-08
Promoter	HYPER in CCA	chr6	105582683	105584682	*BVES-AS1*	154442	2.58E-06
Promoter	HYPER in CCA	chr2	198650987	198652986	*BOLL*	66037	1.94E-06
Promoter	HYPER in CCA	chr14	52535213	52537212	*NID2*	22795	1.88E-06
Promoter	HYPER in CCA	chr5	140808685	140810684	*PCDHGA12*	26025	0.000294223
Promoter	HYPER in CCA	chr2	108601479	108603478	*SLC5A7*	60482	7.55E-07
Promoter	HYPER in CCA	chr8	54163758	54165757	*OPRK1*	4986	4.93E-05
Promoter	HYPER in CCA	chr2	17718893	17720892	*VSNL1*	7447	0.000101053
Promoter	HYPER in CCA	chr16	49315243	49317242	*CBLN1*	869	4.99E-06
Promoter	HYPER in CCA	chr20	23014557	23016556	*SSTR4*	6754	1.40E-08
Promoter	HYPER in CCA	chr8	65280616	65282615	*NA*	NA	1.47E-06

Promoter	HYPER in CCA	chr20	61808352	61810351	*MIR124-3*	406909	1.47E-07
Promoter	HYPER in CCA	chr1	50888673	50890672	*DMRTA2*	63950	1.61E-06
Promoter	HYPER in CCA	chr17	48987094	48989093	*NA*	NA	0.000713119
Promoter	HYPER in CCA	chr13	84456029	84458028	*SLITRK1*	114798	2.51E-05
Promoter	HYPER in CCA	chr16	86599357	86601356	*FOXC2*	2303	1.68E-06
Promoter	HYPER in CCA	chr10	129533999	129535998	*FOXI2*	399823	4.54E-06
Promoter	HYPER in CCA	chr2	223163216	223165215	*PAX3*	5077	2.48E-06
Promoter	HYPER in CCA	chr4	1399620	1401619	*NKX1-1*	NA	1.70E-07
Promoter	HYPER in CCA	chr2	105470469	105472468	*POU3F3*	5455	6.38E-05
Promoter	HYPER in CCA	chr6	62995633	62997632	*KHDRBS2*	202559	9.52E-05
Promoter	HYPER in CCA	chr10	133109485	133111484	*TCERG1L*	256536	0.000119912
Promoter	HYPER in CCA	chr4	134068970	134070969	*PCDH10*	57575	6.68E-05
Promoter	HYPER in CCA	chr2	132121232	132123231	*NA*	NA	8.78E-08
Promoter	HYPER in CCA	chr19	21646211	21648210	*NA*	101928983	5.64E-05
Promoter	HYPER in CCA	chr15	29032845	29034844	*NA*	NA	4.95E-07
Promoter	HYPER in CCA	chr20	54985668	54987667	*CASS4*	57091	4.27E-06
Promoter	HYPER in CCA	chr11	105479221	105481220	*GRIA4*	2893	6.59E-05
Promoter	HYPER in CCA	chr16	54967325	54969324	*NA*	NA	1.32E-06
Promoter	HYPER in CCA	chr7	19156796	19158795	*TWIST1*	7291	1.29E-06
Promoter	HYPER in CCA	chr2	5831121	5833120	*NA*	NA	8.80E-06
Promoter	HYPER in CCA	chr14	37127507	37129506	*NA*	NA	1.87E-07
Promoter	HYPER in CCA	chr8	73163301	73165300	*NA*	NA	1.98E-05
Promoter	HYPER in CCA	chr6	108805132	108825121	*NA*	NA	6.10E-06
Promoter	HYPER in CCA	chr5	140618018	140620017	*PCDHB19P*	84054	0.000346038
Promoter	HYPER in CCA	chr6	105387903	105389902	*LINC00577*	100113403	1.57E-07
Promoter	HYPER in CCA	chr5	140623647	140625646	*PCDHB15*	56121	1.03E-05
Promoter	HYPER in CCA	chr1	248019001	248021000	*TRIM58*	25893	6.32E-10
Promoter	HYPER in CCA	chr8	65284385	65286384	*LINC00966*	100130155	4.01E-05
Promoter	HYPER in CCA	chr15	29033310	29035309	*NA*	646278;101929232	2.52E-06
Promoter	HYPER in CCA	chr6	123315616	123317615	*CLVS2*	134829	3.55E-07
Promoter	HYPER in CCA	chr18	70534882	70536881	*NETO1*	81832	8.50E-05
Promoter	HYPER in CCA	chr4	134069772	134071771	*NA*	101927359	0.001077113
Promoter	HYPER in CCA	chr11	32456677	32458676	*WT1*	7490	8.07E-05
Promoter	HYPER in CCA	chr4	147558913	147560912	*NA*	NA	2.19E-06

Promoter	HYPER in CCA	chr5	73832302	73834301	*NA*	NA	0.000973215
Promoter	HYPER in CCA	chr14	29254494	29256493	*NA*	NA	1.29E-05
Promoter	HYPER in CCA	chr2	16227902	16228102	*NA*	NA	1.57E-08
Promoter	HYPER in CCA	chr5	18052716	18052916	*FOXO1B*	NA	8.80E-06
Promoter	HYPER in CCA	chr3	13866236	13866436	*NA*	NA	9.28E-05
Promoter	HYPER in CCA	chr18	907182	909181	*NA*	NA	1.19E-05
Promoter	HYPER in CCA	chr2	17696295	17696495	*HOXD12*	3238	1.97E-07
Promoter	HYPER in CCA	chr11	11670533	11670733	*APOA1-AS*	NA	8.05E-07
Promoter	HYPER in CCA	chr4	298611	300610	*ZNF732*	654254	2.16E-06
Promoter	HYPER in CCA	chr2	10527429	10527629	*NA*	NA	2.12E-06
Promoter	HYPER in CCA	chr14	48143658	48145657	*MDGA2*	161357	3.14E-05
Promoter	HYPER in CCA	chr17	33815528	33817527	*NA*	NA	7.72E-06
Promoter	HYPER in CCA	chr19	35394719	35396718	*NA*	100652911	3.62E-06
Promoter	HYPER in CCA	chr1	50512186	50514185	*ELAVL4*	1996	3.39E-07
Promoter	HYPER in CCA	chr2	15472692	15472892	*GALNT13*	114805	2.56E-07
Promoter	HYPER in CCA	chr8	72756204	72758203	*MSC*	9242	0.000226905
Promoter	HYPER in CCA	chr6	10881675	10883674	*GCM2*	9247	2.13E-06
Promoter	HYPER in CCA	chr12	13064630	13064830	*FZD10-AS1*	440119	2.12E-05
Promoter	HYPER in CCA	chr1	14971886	14972086	*NA*	NA	5.14E-08
Promoter	HYPER in CCA	chr19	4724186	4726185	*DPP9*	91039	0.000198067
Promoter	HYPER in CCA	chr1	78509333	78511332	*NA*	NA	0.000102546
Promoter	HYPER in CCA	chr6	10558455	10558654	*BVES*	11149	8.80E-06
Promoter	HYPER in CCA	chr9	79633071	79635070	*FOXB2*	442425	3.22E-06
Promoter	HYPER in CCA	chr2	13076227	13076427	*ARHGAP42P2*	NA	1.28E-07
Promoter	HYPER in CCA	chr15	35046667	35048666	*GJD2*	57369	3.85E-05
Promoter	HYPER in CCA	chr2	95718422	95720421	*NA*	NA	2.85E-05
Promoter	HYPER in CCA	chr11	20181660	20183659	*DBX1*	120237	3.00E-06
Promoter	HYPER in CCA	chr16	14396324	14398323	*MIR193B*	574455	0.000539428
Promoter	HYPER in CCA	chr18	70534123	70536122	*NA*	100505797	0.000140621
Promoter	HYPER in CCA	chr16	71459868	71461867	*NA*	NA	1.98E-05
Promoter	HYPER in CCA	chr8	687607	689606	*ERICH1*	157697;101927618	1.18E-05
Promoter	HYPER in CCA	chr14	37125273	37127272	*PAX9*	5083	2.01E-05
Promoter	HYPER in CCA	chr7	35293259	35295258	*TBX20*	57057	6.12E-07
Promoter	HYPER in CCA	chr1	19674242	19674442	*CFHR3*	10878	1.53E-08

Promoter	HYPER in CCA	chr6	166581689	166583688	*T*	6862	5.10E-05
Promoter	HYPER in CCA	chr10	118897313	118899312	*VAX1*	11023	4.14E-07
Promoter	HYPER in CCA	chr8	49468502	49470501	*NA*	NA	0.000110935
Promoter	HYPER in CCA	chr19	23253779	23255778	*NA*	NA	2.84E-05
Promoter	HYPER in CCA	chr19	37095679	37097678	*ZNF529*	57711	0.000565203
Promoter	HYPER in CCA	chr17	50236878	50238877	*CA10*	56934	2.63E-05
Promoter	HYPER in CCA	chr5	63257835	63259834	*HTR1A*	3350	1.38E-05
Promoter	HYPER in CCA	chr5	16180372	16182371	*Mar/11*	441061	4.70E-05
Promoter	HYPER in CCA	chr18	74961005	74963004	*GALR1*	2587	1.08E-05
Promoter	HYPER in CCA	chr3	112928350	112930349	*BOC*	91653	3.38E-05
Promoter	HYPER in CCA	chr1	119531680	119533679	*TBX15*	6913	1.71E-06
Promoter	HYPER in CCA	chr6	107230500	107232499	*MIR587*	693172	0.000358171
Promoter	HYPER in CCA	chr4	41256930	41258929	*UCHL1*	7345	0.000481773
Promoter	HYPER in CCA	chr4	174450881	174452880	*HAND2*	9464	2.93E-05
Promoter	HYPER in CCA	chr17	46808953	46810952	*NA*	NA	8.04E-06
Promoter	HYPER in CCA	chr19	58543900	58545899	*ZSCAN1*	284312	0.001746167
Promoter	HYPER in CCA	chr6	101845164	101847163	*GRIK2*	2898	1.05E-05
Promoter	HYPER in CCA	chr3	138664576	138666575	*C3orf72*	401089	0.0001138
Promoter	HYPER in CCA	chr1	221052983	221054982	*HLA-AS1*	100873924	3.72E-06
Promoter	HYPER in CCA	chr20	590543	592542	*TCF15*	6939	9.16E-09
Promoter	HYPER in CCA	chr11	20689617	20691616	*NELL1*	4745	6.15E-05
Promoter	HYPER in CCA	chr18	58999315	59001314	*CDH20*	28316	2.91E-06
Promoter	HYPER in CCA	chr7	27141931	27143930	*HOXA2*	3199	3.38E-05
Promoter	HYPER in CCA	chr4	147558545	147560544	*POU4F2*	5458	2.91E-06
Promoter	HYPER in CCA	chr6	1384802	1386801	*NA*	NA	3.13E-05
Promoter	HYPER in CCA	chr5	76935014	76937013	*OTP*	23440	2.13E-06
Promoter	HYPER in CCA	chr4	190937351	190939350	*RNA5SP175*	NA	0.000135277
Promoter	HYPER in CCA	chr19	57153013	57155012	*SMIM17*	147670	1.44E-05
Promoter	HYPER in CCA	chr11	101453526	101455525	*NA*	NA	0.0019828
Promoter	HYPER in CCA	chr20	9493505	9495504	*LAMP5*	24141	0.000356555
Promoter	HYPER in CCA	chr5	1882580	1884579	*NA*	NA	0.000441814
Promoter	HYPER in CCA	chr12	130387712	130389711	*TMEM132D*	121256	1.67E-05
Promoter	HYPER in CCA	chr10	50602998	50604997	*DRGX*	644168	4.17E-05
Promoter	HYPER in CCA	chr17	53808983	53810982	*TMEM100*	55273	0.000476058

Promoter	HYPER in CCA	chr19	22467710	22469709	*ZNF729*	100287226	2.68E-05
Promoter	HYPER in CCA	chr3	133463300	133465299	*TF*	7018	2.15E-06
Promoter	HYPER in CCA	chr19	15574883	15576882	*RASAL3*	64926	6.15E-05
Promoter	HYPER in CCA	chr18	903444	905443	*ADCYAP1*	116	7.60E-06
Promoter	HYPER in CCA	chr8	70983429	70985428	*PRDM14*	63978	3.72E-06
Promoter	HYPER in CCA	chr14	60974169	60976168	*SIX6*	4990	7.09E-06
Promoter	HYPER in CCA	chr16	3233519	3235518	*NA*	NA	0.001175415
Promoter	HYPER in CCA	chr12	130645504	130647503	*FZD10*	11211	6.10E-05
Promoter	HYPER in CCA	chr7	6702105	6704104	*NA*	NA	2.00E-09
Promoter	HYPER in CCA	chr14	36986983	36988982	*NKX2-1-AS1*	100506237	1.24E-05
Promoter	HYPER in CCA	chr5	160975551	160977550	*GABRB2*	2561	5.78E-05
Promoter	HYPER in CCA	chr2	229045862	229047861	*SPHKAP*	80309	4.62E-05
Promoter	HYPER in CCA	chr6	100441624	100443623	*MCHR2*	84539	7.81E-06
Promoter	HYPER in CCA	chr21	45768546	45770545	*TRPM2*	7226	5.69E-05
Promoter	HYPER in CCA	chr17	8867713	8869712	*NA*	101928235	9.07E-05
Promoter	HYPER in CCA	chr4	41748810	41750809	*NA*	NA	2.07E-05
Promoter	HYPER in CCA	chr5	80689499	80691498	*ACOT12*	134526	0.000135854
Promoter	HYPER in CCA	chr19	22815626	22817625	*ZNF492*	57615	3.85E-05
Promoter	HYPER in CCA	chr9	113255	115254	*NA*	NA	1.95E-08
Promoter	HYPER in CCA	chr6	6006701	6008700	*NRN1*	51299	0.000114085
Promoter	HYPER in CCA	chr5	72676711	72678710	*NA*	NA	8.05E-07
Promoter	HYPER in CCA	chr22	19137297	19139296	*GSC2*	2928	5.15E-05
Promoter	HYPER in CCA	chr8	145924071	145926070	*NA*	NA	8.05E-07
Promoter	HYPER in CCA	chr8	145924238	145926237	*NA*	100996662	8.05E-07
Promoter	HYPER in CCA	chr20	21376956	21378955	*NA*	NA	1.22E-06
Promoter	HYPER in CCA	chr16	22823998	22825997	*HS3ST2*	9956	2.52E-07
Promoter	HYPER in CCA	chr20	21378167	21380166	*NKX2-4*	644524	4.92E-06
Promoter	HYPER in CCA	chr5	140612438	140614437	*PCDHB18*	54660	5.25E-05
Promoter	HYPER in CCA	chr2	163694741	163696740	*KCNH7*	90134	1.04E-05
Promoter	HYPER in CCA	chr2	176948142	176950141	*EVX2*	344191	1.47E-05
Promoter	HYPER in CCA	chr13	112720413	112722412	*SOX1*	6656	2.69E-07
Promoter	HYPER in CCA	chr14	48143500	48145499	*NA*	161357	8.37E-05
Promoter	HYPER in CCA	chr7	19182416	19184415	*NA*	NA	2.94E-05
Promoter	HYPER in CCA	chr8	99954323	99956322	*NA*	NA	0.000224405

Promoter	HYPER in CCA	chr12	6664740	6666739	*IFFO1*	25900	0.000361667
Promoter	HYPER in CCA	chr7	27224343	27226342	*HOXA11*	3207	7.73E-07
Promoter	HYPER in CCA	chr3	13973053	13975052	*FGD5P1*	100132526	0.000102546
Promoter	HYPER in CCA	chr17	35293461	35295460	*NA*	NA	0.000224538
Promoter	HYPER in CCA	chr4	21949138	21951137	*NA*	NA	0.000166612
Promoter	HYPER in CCA	chr4	90756059	90758058	*NA*	644248	3.93E-05
Promoter	HYPER in CCA	chr19	52955329	52957328	*ZNF578*	147660	2.93E-06
Promoter	HYPER in CCA	chr12	54393295	54395294	*HOXC-AS1*	100874363	0.000300408
Promoter	HYPER in CCA	chr4	104640474	104642473	*TACR3*	6870	2.51E-05
Promoter	HYPER in CCA	chr12	114845748	114847747	*TBX5*	6910	4.58E-05
Promoter	HYPER in CCA	chr16	86600868	86602867	*NA*	NA	6.78E-05
Promoter	HYPER in CCA	chr7	64030316	64032315	*NA*	NA	0.000338794
Promoter	HYPER in CCA	chr7	98245109	98247108	*NPTX2*	4885	0.000489711
Promoter	HYPER in CCA	chr19	38182739	38184738	*ZFP30*	22835	0.000355782
Promoter	HYPER in CCA	chr19	38182724	38184723	*ZNF781*	163115	0.000355782
Promoter	HYPER in CCA	chr2	190044106	190046105	*COL5A2*	1290	1.89E-05
Promoter	HYPER in CCA	chr8	41753781	41755780	*ANK1*	286	0.000356678
Promoter	HYPER in CCA	chr2	177053187	177055186	*HOXD-AS1*	401022	0.000562531
Promoter	HYPER in CCA	chr5	87989290	87991289	*NA*	NA	2.90E-05
Promoter	HYPER in CCA	chr3	138665483	138667482	*FOXL2*	668	0.000139532
Promoter	HYPER in CCA	chr12	43945225	43947224	*ADAMTS20*	80070	6.36E-06
Promoter	HYPER in CCA	chr5	1445046	1447045	*SLC6A3*	6531	2.55E-05
Promoter	HYPER in CCA	chr1	47697393	47699392	*TAL1*	6886	1.47E-06
Promoter	HYPER in CCA	chr12	54384022	54386021	*MIR196A2*	406973	5.22E-05
Promoter	HYPER in CCA	chr14	29233984	29235983	*NA*	NA	1.18E-05
Promoter	HYPER in CCA	chr1	235813555	235815554	*GNG4*	2786	0.000918899
Promoter	HYPER in CCA	chr10	125424371	125426370	*GPR26*	2849	0.0001806
Promoter	HYPER in CCA	chr10	124893978	124895977	*HMX3*	340784	0.00185497
Promoter	HYPER in CCA	chr1	18956000	18957999	*PAX7*	5081	5.75E-05
Promoter	HYPER in CCA	chr2	5831299	5833298	*SOX11*	6664	6.23E-05
Promoter	HYPER in CCA	chr2	182546340	182548339	*NA*	NA	8.80E-06
Promoter	HYPER in CCA	chr7	19812722	19814721	*TMEM196*	256130	5.76E-05
Promoter	HYPER in CCA	chr10	15761625	15763624	*ITGA8*	8516	6.21E-06
Promoter	HYPER in CCA	chr1	98514920	98516919	*MIR137HG*	400765;406928;100616452	8.07E-05

Promoter	HYPER in CCA	chr9	96716379	96718378	*NA*	101928040	6.95E-06
Promoter	HYPER in CCA	chr1	150229182	150231181	*NA*	NA	5.57E-05
Promoter	HYPER in CCA	chr6	100440320	100442319	*MCHR2-AS1*	728012	1.29E-05
Promoter	HYPER in CCA	chr7	158937150	158939149	*VIPR2*	7434	0.000406762
Promoter	HYPER in CCA	chr12	5017571	5019570	*KCNA1*	3736	2.84E-05
Promoter	HYPER in CCA	chr19	36736660	36738659	*ZNF565*	147929	2.19E-05
Promoter	HYPER in CCA	chr4	54969324	54971323	*NA*	NA	0.002097454
Promoter	HYPER in CCA	chr11	86084278	86086277	*CCDC81*	60494	4.99E-06
Promoter	HYPER in CCA	chr7	100941394	100943393	*NA*	101927721	3.75E-05
Promoter	HYPER in CCA	chr20	5296879	5298878	*PROKR2*	128674	7.59E-05
Promoter	HYPER in CCA	chr19	52871670	52873669	*ZNF880*	400713	0.001216847
Promoter	HYPER in CCA	chr2	182544893	182546892	*CERKL*	375298	2.13E-06
Promoter	HYPER in CCA	chr2	182545104	182547103	*NEUROD1*	4760	2.13E-06
Promoter	HYPER in CCA	chr19	46996265	46998264	*NA*	NA	2.12E-05
Promoter	HYPER in CCA	chr12	54446161	54448160	*NA*	3221	2.08E-05
Promoter	HYPER in CCA	chr8	57358794	57360793	*PENK*	5179	2.46E-06
Promoter	HYPER in CCA	chr19	9607854	9609853	*NA*	NA	4.21E-06
Promoter	HYPER in CCA	chr20	21490585	21492584	*NKX2-2-AS1*	NA	3.35E-05
Promoter	HYPER in CCA	chr5	169062751	169064750	*DOCK2*	1794	0.000643174
Promoter	HYPER in CCA	chr7	27189723	27191722	*HOXA6*	3203	6.31E-05
Promoter	HYPER in CCA	chr18	12909685	12911684	*NA*	NA	4.66E-06
Promoter	HYPER in CCA	chr22	29874719	29876718	*NEFH*	4744	1.84E-05
Promoter	HYPER in CCA	chr17	48043041	48045040	*RNU6-1313P*	NA	9.97E-05
Promoter	HYPER in CCA	chr13	100623664	100625663	*ZIC5*	85416	8.08E-06
Promoter	HYPER in CCA	chr19	23185479	23187478	*ZNF728*	388523	2.03E-05
Promoter	HYPER in CCA	chr11	65599612	65601611	*SNX32*	254122	4.60E-06
Promoter	HYPER in CCA	chr13	24900849	24902848	*NUS1P3*	NA	0.000407141
Promoter	HYPER in CCA	chr1	247801551	247803550	*NA*	NA	3.87E-05
Promoter	HYPER in CCA	chr15	95869859	95871858	*NA*	400456	5.75E-07
Promoter	HYPER in CCA	chr2	162279333	162281332	*SLC4A10*	57282	5.14E-08
Promoter	HYPER in CCA	chr5	2750745	2752744	*C5orf38*	153571	0.000179149
Promoter	HYPER in CCA	chr5	134375238	134377237	*NA*	101927953	1.88E-05
Promoter	HYPER in CCA	chr4	21949923	21951922	*KCNIP4*	80333	0.000249091
Promoter	HYPER in CCA	chr8	50820849	50822848	*SNTG1*	54212	0.00015456

Promoter	HYPER in CCA	chr10	50816847	50818846	*SLC18A3*	6572	4.27E-06
Promoter	HYPER in CCA	chr20	61338689	61340688	*NTSR1*	4923	4.36E-05
Promoter	HYPER in CCA	chr16	71610534	71612533	*TAT*	6898	0.001298355
Promoter	HYPER in CCA	chr19	57828431	57830430	*NA*	NA	1.15E-06
Promoter	HYPER in CCA	chr2	145274164	145276163	*ZEB2-AS1*	100303491	0.001985996
Promoter	HYPER in CCA	chr8	69241457	69243456	*C8orf34*	116328	0.000101225
Promoter	HYPER in CCA	chr19	46916342	46918341	*CCDC8*	83987	0.000383864
Promoter	HYPER in CCA	chr16	73515716	73517715	*NA*	NA	1.59E-05
Promoter	HYPER in CCA	chr4	154709773	154711772	*SFRP2*	6423	9.31E-05
Promoter	HYPER in CCA	chr3	128763106	128765105	*NA*	NA	7.46E-05
Promoter	HYPER in CCA	chr17	46691979	46693978	*HOXB8*	3218	5.72E-05
Promoter	HYPER in CCA	chr19	54464794	54466793	*CACNG8*	59283	0.000315473
Promoter	HYPER in CCA	chr5	145717087	145719086	*POU4F3*	5459	1.77E-05
Promoter	HYPER in CCA	chr11	123299558	123301557	*NA*	NA	8.72E-05
Promoter	HYPER in CCA	chr2	107102324	107104323	*CD8BP*	926	7.03E-05
Promoter	HYPER in CCA	chr5	140722101	140724100	*PCDHGA3*	56112	0.000139964
Promoter	HYPER in CCA	chr1	156356518	156358517	*NA*	NA	0.000132368
Promoter	HYPER in CCA	chr19	35395462	35397461	*NA*	NA	1.90E-05
Promoter	HYPER in CCA	chr10	63212709	63214708	*TMEM26*	219623	2.30E-05
Promoter	HYPER in CCA	chr7	129424526	129426525	*NA*	NA	0.000124667
Promoter	HYPER in CCA	chr7	137531339	137533338	*DGKI*	9162	7.59E-06
Promoter	HYPER in CCA	chr16	77468512	77470511	*ADAMTS18*	170692	0.000148887
Promoter	HYPER in CCA	chr14	292335509	292355498	*FOXG1*	2290	7.52E-05
Promoter	HYPER in CCA	chr2	182320429	182322428	*ITGA4*	3676	0.000128657
Promoter	HYPER in CCA	chr20	982408	984407	*RSPO4*	343637	5.04E-05
Promoter	HYPER in CCA	chr20	2780784	2782783	*CPXM1*	56265	4.00E-05
Promoter	HYPER in CCA	chr8	105478782	105480781	*DPYS*	1807	0.000431624
Promoter	HYPER in CCA	chr8	686151	688150	*ERICH1-AS1*	619343	7.12E-06
Promoter	HYPER in CCA	chr7	145811953	145813952	*CNTNAP2*	26047	0.000631486
Promoter	HYPER in CCA	chr18	44775055	44777054	*SKOR2*	652991	0.000110632
Promoter	HYPER in CCA	chr7	136551916	136553915	*CHRM2*	1129	0.000100583
Promoter	HYPER in CCA	chr2	945461	947460	*NA*	NA	0.000359392
Promoter	HYPER in CCA	chr3	187387688	187389687	*SST*	6750	2.12E-05
Promoter	HYPER in CCA	chr14	23834462	23836461	*EFS*	10278	3.96E-05

Promoter	HYPER in CCA	chr19	53811398	53813397	*FAM90A28P*	NA	0.000322617
Promoter	HYPER in CCA	chr2	162279589	162281588	*NA*	NA	1.89E-07
Promoter	HYPER in CCA	chr17	35292584	35294583	*LHX1*	3975	0.000731839
Promoter	HYPER in CCA	chr7	15726503	15728502	*NA*	101927524	0.000388429
Promoter	HYPER in CCA	chr15	83774659	83776658	*TM6SF1*	53346	0.001175415
Promoter	HYPER in CCA	chr7	19158056	19160055	*NA*	NA	0.000114706
Promoter	HYPER in CCA	chr2	220298068	220300067	*SPEG*	10290;100996693	9.44E-06
Promoter	HYPER in CCA	chr5	128794458	128796457	*ADAMTS19*	171019	0.000859179
Promoter	HYPER in CCA	chr17	47074355	47076354	*NA*	NA	0.000230423
Promoter	HYPER in CCA	chr1	37499231	37501230	*GRIK3*	2899	5.24E-05
Promoter	HYPER in CCA	chr6	100912306	100914305	*SIM1*	6492	1.11E-05
Promoter	HYPER in CCA	chr7	54608518	54610517	*VSTM2A*	222008	3.19E-05
Promoter	HYPER in CCA	chr21	27945104	27947103	*CYYR1*	116159	8.75E-06
Promoter	HYPER in CCA	chr16	54972084	54974083	*NA*	NA	3.35E-05
Promoter	HYPER in CCA	chr19	29283279	29285278	*NA*	NA	3.49E-05
Promoter	HYPER in CCA	chr2	71017276	71019275	*FIGLA*	344018	3.83E-08
Promoter	HYPER in CCA	chr2	175198174	175200173	*SP9*	100131390	1.17E-06
Promoter	HYPER in CCA	chr10	119300455	119302454	*EMX2*	2018	7.69E-05
Promoter	HYPER in CCA	chr3	62354506	62356505	*PTPRG-AS1*	100506994	9.75E-05
Promoter	HYPER in CCA	chr10	134599057	134601056	*NKX6-2*	84504	0.000177632
Promoter	HYPER in CCA	chr19	56879253	56881252	*ZSCAN5A*	79149	0.000267073
Promoter	HYPER in CCA	chr4	165304703	165306702	*Mar/01*	55016	9.52E-05
Promoter	HYPER in CCA	chr10	57387203	57389202	*PCDH15*	65217	0.000101025
Promoter	HYPER in CCA	chr21	34396653	34398652	*OLIG2*	10215	0.000271711
Promoter	HYPER in CCA	chr8	72987353	72989352	*TRPA1*	8989	0.00026011
Promoter	HYPER in CCA	chr20	41818111	41820110	*PTPRT*	11122	8.79E-05
Promoter	HYPER in CCA	chr1	119869427	119871426	*NA*	NA	0.000574715
Promoter	HYPER in CCA	chr1	119869299	119871298	*NA*	NA	0.000574715
Promoter	HYPER in CCA	chr1	224803423	224805422	*NA*	NA	9.31E-05
Promoter	HYPER in CCA	chr2	208649239	208669238	*GDF7*	151449	0.000154648
Promoter	HYPER in CCA	chr4	122686083	122688082	*TMEM155*	132332	2.85E-05
Promoter	HYPER in CCA	chr2	145281648	145283647	*ZEB2*	9839	2.07E-05
Promoter	HYPER in CCA	chr6	13885695	13905694	*FOXF2*	2295	0.000219129
Promoter	HYPER in CCA	chr16	56224507	56226506	*NA*	283856	0.0006198

Promoter	HYPER in CCA	chr2	45180303	45182302	*NA*	NA	0.000100583
Promoter	HYPER in CCA	chr7	155301478	155303477	*NA*	NA	9.11E-05
Promoter	HYPER in CCA	chr13	95354617	95356616	*LINC00391*	NA	1.98E-05
Promoter	HYPER in CCA	chr11	110583413	110585412	*ARHGAP20*	57569	1.97E-05
Promoter	HYPER in CCA	chr2	45240308	45242307	*NA*	NA	0.000160979
Promoter	HYPER in CCA	chr10	134597770	134599769	*NA*	NA	1.96E-06
Promoter	HYPER in CCA	chr12	4917308	4919307	*NA*	NA	2.59E-07
Promoter	HYPER in CCA	chr2	945054	947053	*SNTG2*	54221	0.001078348
Promoter	HYPER in CCA	chr4	41750862	41752861	*NA*	NA	0.000289735
Promoter	HYPER in CCA	chr17	10631594	10633593	*NA*	101101775	0.001077341
Promoter	HYPER in CCA	chr8	24771731	24773730	*NA*	NA	0.000589128
Promoter	HYPER in CCA	chr17	6678042	6680041	*FBXO39*	162517	0.002013556
Promoter	HYPER in CCA	chr8	9762377	9764376	*LINC00599*	157627;406907	0.000336136
Promoter	HYPER in CCA	chr9	100614036	100616035	*FOXE1*	2304	0.001599089
Promoter	HYPER in CCA	chr11	27743106	27745105	*BDNF*	627	0.000983347
Promoter	HYPER in CCA	chr4	41750488	41752487	*PHOX2B*	8929	0.000300408
Promoter	HYPER in CCA	chr5	140478734	140480733	*PCDHB3*	56132	0.000211838
Promoter	HYPER in CCA	chr6	55037550	55039549	*HCRTR2*	3062	4.16E-05
Promoter	HYPER in CCA	chr5	134871140	134873139	*NEUROG1*	4762	0.000806912
Promoter	HYPER in CCA	chr19	22714788	22716787	*ZNF98*	148198	2.18E-05
Promoter	HYPER in CCA	chr19	22713928	22715927	*NA*	100128139	2.18E-05
Promoter	HYPER in CCA	chr12	50297501	50299500	*FAIM2*	23017	0.001976272
Promoter	HYPER in CCA	chr16	31580297	31582296	*YBX3P1*	440359	1.44E-06
Promoter	HYPER in CCA	chr10	119099104	119001103	*SLC18A2*	6571	0.000780988
Promoter	HYPER in CCA	chr11	69633293	69635292	*FGF3*	2248	3.19E-05
Promoter	HYPER in CCA	chr6	55443513	55445512	*HMGCLL1*	54511	0.001119498
Promoter	HYPER in CCA	chr6	85473738	85475737	*TBX18*	9096	0.000440208
Promoter	HYPER in CCA	chr20	43933991	43935990	*RBPJL*	11317	7.15E-06
Promoter	HYPER in CCA	chr1	240774950	240776949	*GREM2*	64388	0.00037966
Promoter	HYPER in CCA	chr4	567702	569701	*NA*	NA	0.002034629
Promoter	HYPER in CCA	chr6	26612838	26614837	*NA*	NA	8.74E-07
Promoter	HYPER in CCA	chr11	9024209	9026208	*NA*	NA	0.001388669
Promoter	HYPER in CCA	chr6	105627371	105629370	*POPDC3*	64208	0.001775942
Promoter	HYPER in CCA	chr6	137815032	137817031	*OLIG3*	167826	4.34E-05

Promoter	HYPER in CCA	chr17	72320849	72322848	*KIF19*	124602	4.21E-05
Promoter	HYPER in CCA	chr7	79082391	79084390	*MAGI2*	9863	0.000111715
Promoter	HYPER in CCA	chr5	146889120	146891119	*DPYSL3*	1809	0.000705533
Promoter	HYPER in CCA	chr10	100995120	100997119	*HPSE2*	60495	6.00E-05
Promoter	HYPER in CCA	chr19	38307441	38309440	*ZNF573*	126231	5.23E-05
Promoter	HYPER in CCA	chr18	12252818	12254817	*CIDEA*	1149	6.27E-05
Promoter	HYPER in CCA	chr6	169653640	169655639	*THBS2*	7058	0.000100583
Promoter	HYPER in CCA	chr6	80656798	80658797	*ELOVL4*	6785	0.000381779
Promoter	HYPER in CCA	chr10	106399359	106401358	*SORCS3*	22986	0.001730972
Promoter	HYPER in CCA	chr18	56940819	56942818	*RAX*	30062	0.000492328
Promoter	HYPER in CCA	chr2	38301291	38303290	*CYP1B1-AS1*	285154	3.03E-05
Promoter	HYPER in CCA	chr6	11042257	11044256	*ELOVL2-AS1*	100506409	0.000573766
Promoter	HYPER in CCA	chr19	9608784	9610783	*ZNF560*	147741	7.47E-06
Promoter	HYPER in CCA	chr14	36982535	36984534	*SFTA3*	253970	1.97E-05
Promoter	HYPER in CCA	chr6	50784936	50786935	*TFAP2B*	7021	0.001508037
Promoter	HYPER in CCA	chr1	75598244	75600243	*NA*	NA	0.001451381
Promoter	HYPER in CCA	chr3	172165747	172167746	*GHSR*	2693	6.66E-05
Promoter	HYPER in CCA	chr17	11143080	11145079	*SHISA6*	388336	0.000268496
Promoter	HYPER in CCA	chr7	101004601	101006600	*COL26A1*	136227	2.38E-05
Promoter	HYPER in CCA	chr4	172731905	172733904	*GALNTL6*	442117	0.000491886
Promoter	HYPER in CCA	chr1	114696042	114698041	*SYT6*	148281	1.74E-05
Promoter	HYPER in CCA	chr19	36288288	36290287	*NA*	644050	4.21E-06
Promoter	HYPER in CCA	chr9	77113544	77115543	*NA*	NA	0.00011789
Promoter	HYPER in CCA	chr19	56987119	56989118	*ZNF667-AS1*	100128252	0.001306265
Promoter	HYPER in CCA	chr12	33592255	33594254	*SYT10*	341359	0.000397953
Promoter	HYPER in CCA	chr7	8472085	8474084	*NXPH1*	30010	0.000673367
Promoter	HYPER in CCA	chr1	100109999	100111998	*PALMD*	54873	0.001111251
Promoter	HYPER in CCA	chr8	109095414	109097413	*RSPO2*	340419	0.000317235
Promoter	HYPER in CCA	chr13	70682092	70684091	*KLHL1*	57626	0.000287971
Promoter	HYPER in CCA	chr19	38746732	38748731	*PPP1R14A*	94274	0.000556036
Promoter	HYPER in CCA	chr17	16585252	16587251	*RNASEH1P2*	246243	0.000223729
Promoter	HYPER in CCA	chr1	47132924	47152923	*AJAP1*	55966	0.000791465
Promoter	HYPER in CCA	chr1	115880358	115882357	*NGF*	4803	8.31E-05
Promoter	HYPER in CCA	chr8	104513405	104515404	*NA*	NA	0.000454349

Promoter	HYPER in CCA	chr1	21011003	21011203	*SYT14*	255928	5.49E-05
Promoter	HYPER in CCA	chr18	63415988	63417987	*CDH7*	1005	0.000124674
Promoter	HYPER in CCA	chr4	56684669	56686668	*NA*	644145	0.000255059
Promoter	HYPER in CCA	chr9	975464	977463	*DMRT3*	58524	0.000821961
Promoter	HYPER in CCA	chr4	17444692	17444892	*HAND2-AS1*	79804	0.00034002
Promoter	HYPER in CCA	chr12	11484449	11484649	*TBX5-AS1*	255480	0.001241588
Promoter	HYPER in CCA	chr4	14556567	14556767	*HHIP*	64399	0.000210654
Promoter	HYPER in CCA	chr4	46994240	46996239	*GABRB1*	2560	1.88E-06
Promoter	HYPER in CCA	chr3	33260208	33262207	*SUSD5*	26032	0.000255571
Promoter	HYPER in CCA	chr2	20033549	20033748	*SATB2*	23314	2.76E-05
Promoter	HYPER in CCA	chr20	57089688	57091687	*APCDD1L*	164284	8.32E-05
Promoter	HYPER in CCA	chr22	25678142	25680141	*NA*	101929416	0.000107088
Promoter	HYPER in CCA	chr15	93631934	93633933	*RGMA*	56963	0.001265545
Promoter	HYPER in CCA	chr1	17713913	17714113	*BRINP2*	57795	0.000543914
Promoter	HYPER in CCA	chr2	70994858	70996857	*ADD2*	119	0.000929105
Promoter	HYPER in CCA	chr6	13420877	13421077	*TCF21*	6943	2.66E-05
Promoter	HYPER in CCA	chr4	11022331	11022531	*COL25A1*	84570	0.000773125
Promoter	HYPER in CCA	chr19	56877968	56879967	*ZNF542*	147947	0.00034002
Promoter	HYPER in CCA	chr5	75379512	75381511	*NA*	NA	0.000219197
Promoter	HYPER in CCA	chr3	27763707	27765706	*EOMES*	8320	0.000547932
Promoter	HYPER in CCA	chr10	23982175	23984174	*KIAA1217*	56243	0.000346038
Promoter	HYPER in CCA	chr10	50886197	50888196	*C10orf53*	282966	0.000570644
Promoter	HYPER in CCA	chr11	11138401	11138600	*C11orf88*	399949	0.000497133
Promoter	HYPER in CCA	chr3	13748929	13749129	*NA*	100507274	0.000680287
Promoter	HYPER in CCA	chr19	22193252	22195251	*ZNF208*	7757	0.000539428
Promoter	HYPER in CCA	chr22	44257899	44259898	*SULT4A1*	25830	0.000133691
Promoter	HYPER in CCA	chr1	75592619	75594618	*LHX8*	431707	0.001564394
Promoter	HYPER in CCA	chr1	14885263	14885463	*NA*	NA	0.000217824
Promoter	HYPER in CCA	chr21	34442911	34444910	*NA*	NA	0.000510636
Promoter	HYPER in CCA	chr12	11941780	11941979	*SRRM4*	84530	0.000585746
Promoter	HYPER in CCA	chr13	78492324	78494323	*RNF219-AS1*	100874222	0.00087975
Promoter	HYPER in CCA	chr5	3599803	3601802	*NA*	NA	2.21E-05
Promoter	HYPER in CCA	chr15	29075829	29077828	*NA*	NA	1.08E-05
Promoter	HYPER in CCA	chr6	43209918	43211917	*TTBK1*	84630	0.001079864

Promoter	HYPER in CCA	chr5	162928620	162930619	*MAT2B*	27430	0.001282913
Promoter	HYPER in CCA	chr16	31578538	31580537	*NA*	NA	2.90E-05
Promoter	HYPER in CCA	chr11	94134086	94136085	*GPR83*	10888	0.00015432
Promoter	HYPER in CCA	chr8	106329420	106331419	*ZFPM2*	23414	0.001050117
Promoter	HYPER in CCA	chr20	57088935	57090934	*APCDD1L-AS1*	149773	0.000106759
Promoter	HYPER in CCA	chr16	1029752	1031751	*NA*	NA	0.001892577
Promoter	HYPER in CCA	chr14	52732931	52734930	*PTGDR*	5729	0.000265357
Promoter	HYPER in CCA	chr1	179544588	179546587	*NPHS2*	7827	0.001389656
Promoter	HYPER in CCA	chr12	54332928	54334927	*HOXC13-AS*	100874366	0.000447965
Promoter	HYPER in CCA	chr7	27222637	27224636	*HOXA11-AS*	221883	0.000825774
Promoter	HYPER in CCA	chr12	45443184	45445183	*NA*	NA	0.000713331
Promoter	HYPER in CCA	chr12	75603149	75605148	*KCNC2*	3747	8.98E-05
Promoter	HYPER in CCA	chr20	21086500	21088499	*LINC00237*	NA	9.77E-05
Promoter	HYPER in CCA	chr5	71013490	71015489	*CARTPT*	9607	0.000206797
Promoter	HYPER in CCA	chr2	207505642	207507641	*NA*	NA	0.00015432
Promoter	HYPER in CCA	chr1	179543903	179545902	*RNU5F-2P*	NA	0.001509716
Promoter	HYPER in CCA	chr6	38682494	38684493	*NA*	NA	0.000643174
Promoter	HYPER in CCA	chr19	56878923	56880922	*NA*	NA	0.000441431
Promoter	HYPER in CCA	chr20	56803210	56805209	*ANKRD60*	140731	8.71E-06
Promoter	HYPER in CCA	chr17	46801338	46803337	*MIR3185*	100422978	0.000104537
Promoter	HYPER in CCA	chr7	1271043	1273042	*UNCX*	340260	2.01E-05
Promoter	HYPER in CCA	chr2	71113501	71115500	*LINC01143*	NA	0.001306265
Promoter	HYPER in CCA	chr5	128795883	128797882	*ADAMTS19-AS1*	NA	0.002080349
Promoter	HYPER in CCA	chr15	60294921	60296920	*FOXB1*	27023	0.000346038
Promoter	HYPER in CCA	chr3	127632575	127634574	*KBTBD12*	166348	4.28E-05
Promoter	HYPER in CCA	chr2	107103349	107105348	*NA*	NA	0.000124581
Promoter	HYPER in CCA	chr11	9025097	9027096	*NRIP3*	56675	0.001436653
Promoter	HYPER in CCA	chr20	41817362	41819361	*NA*	NA	0.000221168
Promoter	HYPER in CCA	chr8	140714800	140716799	*KCNK9*	51305	5.04E-05
Promoter	HYPER in CCA	chr19	53540652	53542651	*ZNF702P*	79986	0.001217081
Promoter	HYPER in CCA	chr17	47073274	47075273	*IGF2BP1*	10642	0.000745905
Promoter	HYPER in CCA	chr7	121950246	121952245	*FEZF1*	389549	0.001029845
Promoter	HYPER in CCA	chr3	22414313	22416312	*ZNF385D*	79750	0.000746397
Promoter	HYPER in CCA	chr5	180076125	180078124	*FLT4*	2324	0.000215577

Promoter	HYPER in CCA	chr6	28742193	28744192	*NA*	NA	2.03E-05
Promoter	HYPER in CCA	chr15	89345174	89347173	*ACAN*	176	0.000263458
Promoter	HYPER in CCA	chr4	48986764	48988763	*CWH43*	80157	9.86E-05
Promoter	HYPER in CCA	chr5	126625023	126627022	*MEGF10*	84466	6.82E-05
Promoter	HYPER in CCA	chr11	31839010	31841009	*PAX6*	5080	0.000722344
Promoter	HYPER in CCA	chr10	25464706	25466705	*GPR158-AS1*	100128811	2.85E-05
Promoter	HYPER in CCA	chr12	2799867	2801866	*CACNA1C-AS1*	100652846	2.31E-06
Promoter	HYPER in CCA	chr12	132905436	132907435	*GALNT9*	50614	0.000940434
Promoter	HYPER in CCA	chr12	132904936	132906935	*NA*	101928416	0.000940434
Promoter	HYPER in CCA	chr18	56885900	56887899	*GRP*	2922	3.06E-05
Promoter	HYPER in CCA	chr4	111536115	111538114	*NA*	NA	0.00068781
Promoter	HYPER in CCA	chr19	29218185	29220184	*NA*	NA	0.001456076
Promoter	HYPER in CCA	chr12	54348818	54350817	*NA*	NA	8.02E-06
Promoter	HYPER in CCA	chr12	54365410	54367409	*HOXC11*	3227	0.001828448
Promoter	HYPER in CCA	chr4	42154396	42156395	*BEND4*	389206	4.89E-05
Promoter	HYPER in CCA	chr1	67216642	67218641	*TCTEX1D1*	200132	1.90E-05
Promoter	HYPER in CCA	chr14	104550516	104552515	*ASPG*	374569	4.57E-06
Promoter	HYPER in CCA	chr5	177209900	177211899	*FAM153A*	285596	4.39E-07
Promoter	HYPER in CCA	chr1	99468332	99470331	*NA*	100129620	8.78E-05
Promoter	HYPER in CCA	chr11	124733782	124735781	*ROBO3*	64221	4.24E-05
Promoter	HYPER in CCA	chr17	46619413	46621412	*HOXB-AS1*	100874362	0.000187874
Promoter	HYPER in CCA	chr18	5197003	5199002	*C18orf42*	642597	0.001202588
Promoter	HYPER in CCA	chr5	178771932	178773931	*ADAMTS2*	9509	0.001255974
Promoter	HYPER in CCA	chr4	110222691	110224690	*NA*	NA	0.000767217
Promoter	HYPER in CCA	chr10	135342162	135344161	*NA*	NA	0.000417466
Promoter	HYPER in CCA	chr5	38257011	38259010	*EGFLAM*	133584	0.000539192
Promoter	HYPER in CCA	chr1	229569346	229571345	*ACTA1*	58	0.001144171
Promoter	HYPER in CCA	chr9	122131246	122133245	*BRINP1*	1620	0.000379096
Promoter	HYPER in CCA	chr10	99790086	99792085	*CRTAC1*	55118	0.000101176
Promoter	HYPER in CCA	chr6	134212575	134214574	*NA*	100507308	0.000441431
Promoter	HYPER in CCA	chr11	109291346	109293345	*C11orf87*	399947	3.59E-05
Promoter	HYPER in CCA	chr15	92935558	92937557	*ST8SIA2*	8128	0.001553945
Promoter	HYPER in CCA	chr3	26662797	26664796	*LRRC3B*	116135	0.00068792
Promoter	HYPER in CCA	chr6	27597688	27599687	*TRNAI6*	NA	0.000411634

Promoter	HYPER in CCA	chr19	51171152	51173151	*SYT3*	84258	0.000183785
Promoter	HYPER in CCA	chr16	56223802	56225801	*GNAO1*	2775	0.001487731
Promoter	HYPER in CCA	chr8	75895250	75897249	*CRISPLD1*	83690	0.000260189
Promoter	HYPER in CCA	chr8	35091475	35093474	*UNC5D*	137970	0.000519412
Promoter	HYPER in CCA	chr18	906169	908168	*NA*	NA	0.000709264
Promoter	HYPER in CCA	chr7	139207102	139209101	*CLEC2L*	154790	0.000110981
Promoter	HYPER in CCA	chr6	133560236	133562235	*EYA4*	2070	0.001684646
Promoter	HYPER in CCA	chr1	248098993	248100992	*OR2L13*	284521	0.000131487
Promoter	HYPER in CCA	chr1	86622127	86624126	*COL24A1*	255631	0.001405964
Promoter	HYPER in CCA	chr12	71314124	71316123	*PTPRR*	5801	0.000517773
Promoter	HYPER in CCA	chr14	42073560	42075559	*NA*	NA	0.002067316
Promoter	HYPER in CCA	chr10	101290435	101292434	*NA*	101927324	0.000327607
Promoter	HYPER in CCA	chr12	5151585	5153584	*KCNA5*	3741	0.000970826
Promoter	HYPER in CCA	chr10	124906128	124908127	*HMX2*	3167	0.000488426
Promoter	HYPER in CCA	chr1	148853621	148855620	*NA*	NA	0.000380511
Promoter	HYPER in CCA	chr10	26503736	26505735	*GAD2*	2572	0.001759268
Promoter	HYPER in CCA	chr7	152132591	152134590	*KMT2C*	58508	5.96E-11
Promoter	HYPER in CCA	chr7	152132480	152134479	*FABP5P3*	220832	5.96E-11
Promoter	HYPER in CCA	chr22	48883772	48885771	*FAM19A5*	25817	0.001836614
Promoter	HYPER in CCA	chr1	103573553	103575552	*COL11A1*	1301	0.000236608
Promoter	HYPER in CCA	chr2	45168513	45170512	*SIX3-AS1*	100506108	0.000565203
Promoter	HYPER in CCA	chr10	119304080	119306079	*EMX2OS*	196047	0.000526224
Promoter	HYPER in CCA	chr5	140733268	140735267	*PCDHGA4*	56111	0.00052949
Promoter	HYPER in CCA	chr4	37244342	37246341	*KIAA1239*	57495	0.00155894
Promoter	HYPER in CCA	chr5	161272697	161274696	*GABRA1*	2554	0.001948138
Promoter	HYPER in CCA	chr18	500223	502222	*COLEC12*	81035	0.001080821
Promoter	HYPER in CCA	chr1	34641051	34643050	*NA*	NA	2.76E-05
Promoter	HYPER in CCA	chr3	132755397	132757396	*NA*	NA	0.000490274
Promoter	HYPER in CCA	chr2	111366993	111368992	*NA*	NA	0.002098991
Promoter	HYPER in CCA	chr12	45444383	45446382	*DBX2*	440097	0.000477592
Promoter	HYPER in CCA	chr2	239755173	239757172	*TWIST2*	117581	0.000138939
Promoter	HYPER in CCA	chr15	88799500	88801499	*NTRK3*	4916	0.001963449
Promoter	HYPER in CCA	chr20	55840353	55842352	*NA*	101927820	0.001952406
Promoter	HYPER in CCA	chr6	117086387	117088386	*FAM162B*	221303	0.000702697

Promoter	HYPER in CCA	chr11	44331217	44333216	*ALX4*	60529	0.000148129
Promoter	HYPER in CCA	chr11	49578598	49580597	*NA*	440040	8.80E-06
Promoter	HYPER in CCA	chr6	100053106	100055105	*PRDM13*	59336	0.000621523
Promoter	HYPER in CCA	chr18	15197275	15199274	*NA*	NA	0.001098778
Promoter	HYPER in CCA	chr21	38073365	38075364	*NA*	NA	0.001884046
Promoter	HYPER in CCA	chr2	95689922	95691921	*MAL*	4118	0.000556036
Promoter	HYPER in CCA	chr3	73673592	73675591	*PDZRN3*	23024	0.001966933
Promoter	HYPER in CCA	chr21	22369133	22371132	*NCAM2*	4685	0.001939944
Promoter	HYPER in CCA	chr5	36301717	36303716	*RANBP3L*	202151	0.001953609
Promoter	HYPER in CCA	chr17	78451144	78453143	*NPTX1*	4884	0.0006898
Promoter	HYPER in CCA	chr3	132755735	132757734	*TMEM108*	66000	0.000820114
Promoter	HYPER in CCA	chr7	121942212	121944211	*FEZF1-AS1*	154860	0.000545021
Promoter	HYPER in CCA	chr12	14132554	14134553	*GRIN2B*	2904	0.000414318
Promoter	HYPER in CCA	chr22	42094003	42096002	*MEI1*	150365	1.94E-05
Promoter	HYPER in CCA	chr15	22645103	22647102	*NA*	NA	1.42E-05
Promoter	HYPER in CCA	chr17	8868530	8870529	*PIK3R5*	23533	0.000881727
Promoter	HYPER in CCA	chr15	66545586	66547585	*MEGF11*	84465	2.85E-05
Promoter	HYPER in CCA	chr2	173600435	173602434	*RAPGEF4-AS1*	91149	0.001960676
Promoter	HYPER in CCA	chr4	135122404	135124403	*PABPC4L*	132430	0.000556723
Promoter	HYPER in CCA	chr9	96717155	96719154	*BARX1*	56033	0.000102251
Promoter	HYPER in CCA	chr4	156129680	156131679	*NA*	NA	0.001797423
Promoter	HYPER in CCA	chr20	4229222	4231221	*ADRA1D*	146	0.00037847
Promoter	HYPER in CCA	chr14	36989855	36991854	*NKX2-1*	7080	0.001337386
Promoter	HYPER in CCA	chr16	82658908	82660907	*CDH13*	1012	7.50E-05
Promoter	HYPER in CCA	chr2	48982381	48984380	*LHCGR*	3973	0.000435617
Promoter	HYPER in CCA	chr11	20619446	20621445	*SLC6A5*	9152	0.001842902
Promoter	HYPER in CCA	chr7	43150698	43152697	*HECW1*	23072	4.58E-05
Promoter	HYPER in CCA	chr11	17739615	17741614	*MYOD1*	4654	0.000833011
Promoter	HYPER in CCA	chr11	128554930	128556929	*FLI1*	2313	0.001429632
Promoter	HYPER in CCA	chr11	66186975	66188974	*NPAS4*	266743	0.000720685
Promoter	HYPER in CCA	chr1	149400041	149402040	*NA*	NA	1.57E-05
Promoter	HYPER in CCA	chr1	149400043	149402042	*HIST2H3PS2*	NA	1.57E-05
Promoter	HYPER in CCA	chr5	129241111	129243110	*NA*	NA	0.002019841
Promoter	HYPER in CCA	chr20	54580029	54582028	*CBLN4*	140689	3.51E-07

Promoter	HYPER in CCA	chr9	32781997	32783996	*TMEM215*	401498	0.000184571
Promoter	HYPER in CCA	chr2	220173871	220175870	*PTPRN*	5798	0.000201297
Promoter	HYPER in CCA	chr5	75377497	75379496	*SV2C*	22987	0.001307712
Promoter	HYPER in CCA	chr7	89747214	89749213	*DPY19L2P4*	442523	0.000781967
Promoter	HYPER in CCA	chr10	23631386	23633385	*NA*	NA	0.001839432
Promoter	HYPER in CCA	chr11	88798614	88800613	*GRM5*	2915	1.52E-05
Promoter	HYPER in CCA	chr16	55356172	55358171	*IRX6*	79190	0.001101246
Promoter	HYPER in CCA	chr11	18813769	18815768	*PTPN5*	84867	0.000334169
Promoter	HYPER in CCA	chr15	98835907	98837906	*NA*	NA	0.000292066
Promoter	HYPER in CCA	chr7	18125072	18127071	*HDAC9*	9734	0.001759268
Promoter	HYPER in CCA	chr10	135171030	135173029	*FUOM*	282969	0.000174257
Promoter	HYPER in CCA	chr12	103351689	103353688	*PAH*	5053;101929036	0.001358986
Promoter	HYPER in CCA	chr7	100316923	100318922	*EPO*	2056	0.001351026
Promoter	HYPER in CCA	chr1	66256697	66258696	*PDE4B*	5142	0.000220894
Promoter	HYPER in CCA	chr14	62582697	62584696	*LINC00643*	646113	0.000990562
Promoter	HYPER in CCA	chr2	130737540	130739539	*RAB6C-AS1*	100131320	5.23E-05
Promoter	HYPER in CCA	chr15	79573646	79575645	*ANKRD34C*	390616	0.001451381
Promoter	HYPER in CCA	chr14	62583394	62585393	*NA*	NA	0.001029839
Promoter	HYPER in CCA	chr10	103535355	103537354	*FGF8*	2253	0.000112377
Promoter	HYPER in CCA	chr7	45612239	45614238	*ADCY1*	107	0.000621122
Promoter	HYPER in CCA	chr16	86318533	86320532	*NA*	146513	0.001746167
Promoter	HYPER in CCA	chr7	4998345	5000344	*MMD2*	221938	0.000312444
Promoter	HYPER in CCA	chr7	35225435	35227434	*DPY19L2P1*	NA	0.000359392
Promoter	HYPER in CCA	chr10	102987851	102989850	*LBX1-AS1*	NA	0.000492408
Promoter	HYPER in CCA	chr3	137482079	137484078	*SOX14*	8403	0.000842435
Promoter	HYPER in CCA	chr2	87087523	87089522	*NA*	NA	9.53E-05
Promoter	HYPER in CCA	chr7	4922851	4924850	*RADIL*	55698	0.000718723
Promoter	HYPER in CCA	chr1	177133610	177135609	*ASTN1*	460	0.000162956
Gene	HYPER in CCA	chr6	160693649	160697162	*NA*	NA	8.98E-13
Gene	HYPER in CCA	chr10	75601591	75606324	*NA*	NA	4.63E-16
Gene	HYPER in CCA	chr5	142869420	142910915	*NA*	NA	4.69E-13
Gene	HYPER in CCA	chr10	91406046	91410579	*NA*	NA	2.81E-10
Gene	HYPER in CCA	chr22	50644014	50644491	*NA*	NA	1.51E-15
Gene	HYPER in CCA	chr8	65291706	65291814	*MIR124-2*	406908	6.82E-06

Gene	HYPER in CCA	chr1	71172136	71252151	*NA*	101927244	6.91E-09
Gene	HYPER in CCA	chr8	54788710	54789209	*NA*	NA	4.64E-09
Gene	HYPER in CCA	chr8	43102334	43102553	*NA*	NA	4.61E-11
Gene	HYPER in CCA	chr16	14397824	14397906	*MIR193B*	574455	3.95E-05
Gene	HYPER in CCA	chr1	3701572	3702102	*NA*	NA	8.64E-07
Gene	HYPER in CCA	chr17	46799084	46799884	*PRAC1*	84366	2.61E-09
Gene	HYPER in CCA	chr11	77774907	77779397	*THRSP*	7069	4.63E-16
Gene	HYPER in CCA	chr2	176994422	176997423	*HOXD8*	3234	2.81E-10
Gene	HYPER in CCA	chr12	57824899	57827718	*NA*	NA	2.16E-18
Gene	HYPER in CCA	chr17	77997693	77999906	*NA*	NA	7.06E-08
Gene	HYPER in CCA	chr2	45240353	45240807	*NA*	NA	9.85E-11
Gene	HYPER in CCA	chr12	73004458	73005096	*CHCHD3P2*	NA	3.00E-09
Gene	HYPER in CCA	chr12	7276280	7281538	*RBP5*	83758	5.15E-14
Gene	HYPER in CCA	chr1	197008321	197036397	*F13B*	2165	1.75E-10
Gene	HYPER in CCA	chr17	46709852	46709921	*MIR196A1*	406972	7.25E-05
Gene	HYPER in CCA	chr1	95585703	95604110	*NA*	NA	4.41E-14
Gene	HYPER in CCA	chr16	71599563	71611033	*TAT*	6898	8.48E-15
Gene	HYPER in CCA	chr5	50265051	50266001	*NA*	100287592	1.69E-08
Gene	HYPER in CCA	chr13	24902349	24903210	*NUS1P3*	NA	1.20E-05
Gene	HYPER in CCA	chr5	50265494	50266021	*NA*	NA	2.67E-08
Gene	HYPER in CCA	chr7	27208238	27211534	*HOXA10-AS*	442920;100874323	2.92E-12
Gene	HYPER in CCA	chr1	149146714	149146879	*RNU1-114P*	NA	1.31E-06
Gene	HYPER in CCA	chr1	248020501	248041507	*TRIM58*	25893	1.74E-12
Gene	HYPER in CCA	chr12	95782375	95799280	*NA*	NA	8.26E-07
Gene	HYPER in CCA	chr3	46538981	46542439	*RTP3*	83597	1.70E-07
Gene	HYPER in CCA	chr11	43602944	43603033	*MIR129-2*	406918	1.34E-09
Gene	HYPER in CCA	chr7	19184405	19185044	*FERD3L*	222894	4.13E-07
Gene	HYPER in CCA	chr1	161192082	161193421	*APOA2*	336	7.15E-05
Gene	HYPER in CCA	chr12	81329515	81329612	*MIR618*	693203	6.64E-08
Gene	HYPER in CCA	chr16	51183150	51183730	*NA*	NA	0.000113273
Gene	HYPER in CCA	chr6	28414750	28415584	*COX11P1*	NA	7.77E-09
Gene	HYPER in CCA	chr17	46652875	46657473	*HOXB4*	3214	6.91E-09
Gene	HYPER in CCA	chr17	46706037	46712294	*HOXB-AS4*	NA	1.44E-08
Gene	HYPER in CCA	chr2	177028892	177030444	*NA*	NA	7.88E-10

Gene	HYPER in CCA	chr10	119494824	119495918	*NA*	NA	3.50E-06
Gene	HYPER in CCA	chr1	214202236	214204109	*NA*	NA	1.52E-06
Gene	HYPER in CCA	chr4	100044808	100078949	*ADH4*	127	0.000617381
Gene	HYPER in CCA	chr1	228651804	228652327	*HIST3H2BA*	NA	3.31E-07
Gene	HYPER in CCA	chr1	79355449	79472403	*ELTD1*	64123	1.34E-09
Gene	HYPER in CCA	chr19	35628549	35630484	*NA*	NA	9.77E-11
Gene	HYPER in CCA	chr4	74262831	74287129	*ALB*	213	2.75E-05
Gene	HYPER in CCA	chr17	33825237	33826194	*NA*	NA	1.36E-07
Gene	HYPER in CCA	chr2	177042445	177043736	*NA*	NA	2.80E-06
Gene	HYPER in CCA	chr1	12587766	12588462	*NA*	NA	3.61E-05
Gene	HYPER in CCA	chr7	27139721	27142430	*HOXA2*	3199	4.85E-08
Gene	HYPER in CCA	chr19	45445495	45452820	*APOC4*	346	1.17E-08
Gene	HYPER in CCA	chr19	45445495	45452822	*APOC4-APOC2*	344;346	1.17E-08
Gene	HYPER in CCA	chr7	27132612	27135615	*HOXA1*	3198	3.31E-07
Gene	HYPER in CCA	chr4	156750881	156787425	*ASIC5*	51802	1.12E-05
Gene	HYPER in CCA	chr2	176986339	177001826	*HOXD-AS2*	100506783	1.48E-08
Gene	HYPER in CCA	chr7	156799001	156799826	*MNX1-AS2*	NA	2.95E-07
Gene	HYPER in CCA	chr7	27193335	27197555	*HOXA7*	3204	7.06E-08
Gene	HYPER in CCA	chr7	27209099	27209183	*MIR196B*	442920	3.29E-07
Gene	HYPER in CCA	chr3	58148274	58156363	*FLNB-AS1*	101929182	5.27E-06
Gene	HYPER in CCA	chr5	170736288	170739138	*TLX3*	30012	7.38E-09
Gene	HYPER in CCA	chr2	176987088	176989853	*HOXD9*	3235	7.38E-09
Gene	HYPER in CCA	chr16	71599692	71612090	*NA*	100132529	2.23E-10
Gene	HYPER in CCA	chr7	27278862	27280847	*NA*	NA	1.06E-05
Gene	HYPER in CCA	chr8	109907258	110075646	*NA*	NA	0.00023061
Gene	HYPER in CCA	chr7	124869633	124904345	*NA*	101928254	4.97E-05
Gene	HYPER in CCA	chr13	53418109	53422775	*PCDH8*	5100	4.38E-09
Gene	HYPER in CCA	chr9	69199480	69202204	*FOXD4L6*	653404	1.80E-07
Gene	HYPER in CCA	chr16	72088491	72094954	*HP*	3240	1.94E-05
Gene	HYPER in CCA	chr20	21492085	21492947	*NKX2-2-AS1*	NA	5.77E-06
Gene	HYPER in CCA	chr2	105481865	105483954	*NA*	NA	5.77E-06
Gene	HYPER in CCA	chr7	19152097	19153894	*NA*	NA	1.98E-05
Gene	HYPER in CCA	chr20	61637331	61638387	*BHLHE23*	128408	1.90E-08
Gene	HYPER in CCA	chr16	78529823	78540465	*NA*	NA	1.70E-05

Gene	HYPER in CCA	chr13	95351948	95355116	*LINC00391*	NA	3.77E-08
Gene	HYPER in CCA	chr7	27168126	27170418	*HOXA4*	3201	3.56E-08
Gene	HYPER in CCA	chr17	46656992	46659621	*MIR10A*	406902	2.12E-06
Gene	HYPER in CCA	chr2	71115001	71117089	*LINC01143*	NA	1.53E-07
Gene	HYPER in CCA	chr3	121311966	121349139	*FBXO40*	51725	1.61E-08
Gene	HYPER in CCA	chr7	27202054	27210117	*HOXA9*	3205;442920	8.65E-10
Gene	HYPER in CCA	chr2	119591276	119592686	*NA*	NA	4.75E-07
Gene	HYPER in CCA	chr7	27197963	27198595	*NA*	NA	1.64E-07
Gene	HYPER in CCA	chr5	115140430	115152651	*CDO1*	1036	2.61E-09
Gene	HYPER in CCA	chr13	31506840	31549639	*TEX26*	122046	2.41E-06
Gene	HYPER in CCA	chr1	100111499	100160097	*PALMD*	54873	9.82E-05
Gene	HYPER in CCA	chr5	78407602	78428108	*BHMT*	635	4.59E-06
Gene	HYPER in CCA	chr7	27180671	27183287	*HOXA5*	3202	1.30E-09
Gene	HYPER in CCA	chr14	60975669	60979568	*SIX6*	4990	1.53E-07
Gene	HYPER in CCA	chr1	53753696	53755378	*NA*	NA	2.40E-06
Gene	HYPER in CCA	chr2	177015950	177017954	*HOXD4*	3233	9.11E-08
Gene	HYPER in CCA	chr3	170374351	170379912	*NA*	101928583	3.75E-06
Gene	HYPER in CCA	chr10	124895478	124897257	*HMX3*	340784	6.86E-06
Gene	HYPER in CCA	chr12	85673885	85695562	*ALX1*	8092	1.75E-05
Gene	HYPER in CCA	chr8	72753784	72756703	*MSC*	9242	4.70E-05
Gene	HYPER in CCA	chr4	147560045	147563626	*POU4F2*	5458	2.30E-07
Gene	HYPER in CCA	chr7	27203154	27219632	*NA*	NA	2.58E-08
Gene	HYPER in CCA	chr18	12911185	12912022	*NA*	NA	3.66E-07
Gene	HYPER in CCA	chr8	24769678	24772230	*NA*	NA	4.10E-10
Gene	HYPER in CCA	chr18	74962505	74980858	*GALR1*	2587	2.54E-07
Gene	HYPER in CCA	chr17	14207171	14208822	*NA*	84815	1.11E-05
Gene	HYPER in CCA	chr13	79170264	79173754	*NA*	NA	1.27E-06
Gene	HYPER in CCA	chr16	226679	227521	*HBA1*	3039;3040	2.06E-07
Gene	HYPER in CCA	chr5	16067248	16180871	*Mar/11*	441061	6.47E-06
Gene	HYPER in CCA	chr2	176957619	176960666	*HOXD13*	3239	3.29E-07
Gene	HYPER in CCA	chr7	19183916	19185876	*NA*	NA	1.03E-05
Gene	HYPER in CCA	chr7	24323782	24331484	*NPY*	4852	1.68E-05
Gene	HYPER in CCA	chr8	55370495	55373448	*SOX17*	64321	1.15E-07
Gene	HYPER in CCA	chr2	105471969	105476929	*POU3F3*	5455	1.83E-08

Gene	HYPER in CCA	chr2	176968944	176974722	*HOXD11*	3237	3.11E-06
Gene	HYPER in CCA	chr13	112721913	112726020	*SOX1*	6656	1.71E-07
Gene	HYPER in CCA	chr20	9485827	9495645	*NA*	101929329	1.74E-06
Gene	HYPER in CCA	chr19	29980682	30017855	*NA*	NA	8.71E-06
Gene	HYPER in CCA	chr10	129534323	129534969	*NA*	387720	2.56E-06
Gene	HYPER in CCA	chr6	28743693	28743800	*NA*	NA	0.000988115
Gene	HYPER in CCA	chr17	50939481	50976948	*NA*	NA	0.000638617
Gene	HYPER in CCA	chr17	39210750	39211482	*KRTAP2-2*	728279	7.53E-11
Gene	HYPER in CCA	chr20	61809852	61809938	*MIR124-3*	406909	1.05E-07
Gene	HYPER in CCA	chr5	50261521	50262842	*NA*	NA	2.18E-05
Gene	HYPER in CCA	chr13	79172497	79177673	*POU4F1*	5457	4.59E-06
Gene	HYPER in CCA	chr4	90757559	90763129	*NA*	644248	0.000170215
Gene	HYPER in CCA	chr2	162280526	162285285	*NA*	NA	5.92E-08
Gene	HYPER in CCA	chr10	23481256	23483181	*PTF1A*	256297	3.03E-07
Gene	HYPER in CCA	chr7	27135266	27139884	*HOTAIRM1*	100506311	3.07E-06
Gene	HYPER in CCA	chr2	175200601	175202151	*NA*	NA	1.67E-06
Gene	HYPER in CCA	chr7	1272543	1276954	*UNCX*	340260	1.64E-07
Gene	HYPER in CCA	chr10	28033715	28056723	*NA*	101929202	2.58E-06
Gene	HYPER in CCA	chr19	39693471	39694906	*SYCN*	342898	7.67E-06
Gene	HYPER in CCA	chr18	76736555	76739074	*NA*	NA	1.11E-05
Gene	HYPER in CCA	chr5	145718587	145720083	*POU4F3*	5459	2.60E-06
Gene	HYPER in CCA	chr7	27169596	27195542	*HOXA-AS3*	100133311	3.03E-07
Gene	HYPER in CCA	chr7	100942894	100944551	*NA*	101927721	1.18E-05
Gene	HYPER in CCA	chr7	27168588	27192180	*NA*	NA	2.82E-07
Gene	HYPER in CCA	chr19	7983537	7984042	*NA*	NA	5.44E-06
Gene	HYPER in CCA	chr1	101003693	101007574	*GPR88*	54112	4.52E-05
Gene	HYPER in CCA	chr6	137813336	137815531	*OLIG3*	167826	1.06E-06
Gene	HYPER in CCA	chr7	27281048	27286848	*EVX1-AS*	NA	4.67E-06
Gene	HYPER in CCA	chr15	80487826	80544555	*NA*	100996492	0.000788268
Gene	HYPER in CCA	chr2	177015031	177015140	*MIR10B*	406903	5.67E-06
Gene	HYPER in CCA	chr14	57267425	57277197	*OTX2*	5015	6.89E-08
Gene	HYPER in CCA	chr17	46620913	46628610	*HOXB-AS1*	100874362	3.29E-07
Gene	HYPER in CCA	chr4	155525286	155534119	*FGG*	2266	0.000664767
Gene	HYPER in CCA	chr7	97361220	97369784	*TAC1*	6863	1.46E-05

Gene	HYPER in CCA	chr4	190962497	190964569	*AGGF1P1*	NA	6.84E-06
Gene	HYPER in CCA	chr16	86598751	86601367	*NA*	NA	2.78E-06
Gene	HYPER in CCA	chr12	75433857	75603648	*KCNC2*	3747	8.49E-07
Gene	HYPER in CCA	chr2	176964458	176966408	*HOXD12*	3238	1.33E-07
Gene	HYPER in CCA	chr2	182537815	182545603	*NEUROD1*	4760	1.24E-06
Gene	HYPER in CCA	chr17	41994576	41995326	*FAM215A*	NA	0.000355579
Gene	HYPER in CCA	chr5	3596325	3600302	*NA*	NA	4.06E-06
Gene	HYPER in CCA	chr12	130647004	130650285	*FZD10*	11211	8.87E-06
Gene	HYPER in CCA	chr5	3596168	3601517	*IRX1*	79192	9.71E-07
Gene	HYPER in CCA	chr10	93388199	93392811	*PPP1R3C*	5507	3.56E-08
Gene	HYPER in CCA	chr16	54971698	54972583	*NA*	NA	2.37E-05
Gene	HYPER in CCA	chr1	63788730	63790797	*FOXD3*	27022	7.65E-08
Gene	HYPER in CCA	chr6	50786436	50815326	*TFAP2B*	7021	6.76E-06
Gene	HYPER in CCA	chr10	8093504	8095047	*NA*	NA	9.23E-06
Gene	HYPER in CCA	chr9	131683174	131704320	*PHYHD1*	254295	6.35E-09
Gene	HYPER in CCA	chr2	133014539	133014653	*MIR663B*	100313824	7.66E-06
Gene	HYPER in CCA	chr2	175199674	175203220	*SP9*	100131390	3.56E-06
Gene	HYPER in CCA	chr13	28366780	28368905	*GSX1*	219409	1.89E-05
Gene	HYPER in CCA	chr17	33817028	33818257	*NA*	NA	1.08E-05
Gene	HYPER in CCA	chr4	41746099	41750987	*PHOX2B*	8929	1.17E-05
Gene	HYPER in CCA	chr3	129693148	129696781	*TRH*	7200	1.20E-06
Gene	HYPER in CCA	chr20	21491648	21494664	*NKX2-2*	4821	3.61E-05
Gene	HYPER in CCA	chr2	175190755	175195371	*NA*	285084	2.03E-05
Gene	HYPER in CCA	chr2	68511303	68547183	*CNRIP1*	25927	6.46E-06
Gene	HYPER in CCA	chr5	50668570	50679166	*NA*	642366	0.00018502
Gene	HYPER in CCA	chr20	21378456	21381029	*NA*	NA	1.11E-05
Gene	HYPER in CCA	chr17	46618256	46623441	*HOXB2*	3212	1.55E-06
Gene	HYPER in CCA	chr4	111538579	111563279	*PITX2*	5308	7.29E-06
Gene	HYPER in CCA	chr5	134869991	134871639	*NEUROG1*	4762	7.88E-07
Gene	HYPER in CCA	chr12	63539014	63544722	*AVPR1A*	552	2.97E-08
Gene	HYPER in CCA	chr4	41752362	41759358	*NA*	NA	2.75E-05
Gene	HYPER in CCA	chr2	108602979	108630450	*SLC5A7*	60482	1.32E-07
Gene	HYPER in CCA	chr11	17716569	17719018	*NA*	NA	0.000196177
Gene	HYPER in CCA	chr11	17716814	17718487	*NA*	NA	0.000196177

Gene	HYPER in CCA	chr14	29235050	29238870	*FOXG1*	2290	2.23E-06
Gene	HYPER in CCA	chr4	111516671	111536614	*NA*	NA	1.72E-05
Gene	HYPER in CCA	chr2	177001340	177037830	*HOXD3*	3232;3233;401021	4.26E-06
Gene	HYPER in CCA	chr16	31579707	31580796	*YBX3P1*	440359	2.92E-06
Gene	HYPER in CCA	chr5	63253720	63276870	*NA*	NA	3.58E-06
Gene	HYPER in CCA	chr11	82443053	82444906	*FAM181B*	220382	5.85E-05
Gene	HYPER in CCA	chr2	177053307	177055688	*HOXD1*	3231	5.70E-05
Gene	HYPER in CCA	chr4	174446120	174451380	*HAND2*	9464	3.73E-05
Gene	HYPER in CCA	chr1	50883222	50889172	*DMRTA2*	63950	6.95E-06
Gene	HYPER in CCA	chr20	37353105	37358015	*SLC32A1*	140679	6.30E-07
Gene	HYPER in CCA	chr4	90645250	90759466	*SNCA*	6622	9.96E-05
Gene	HYPER in CCA	chr2	207507142	207514173	*NA*	NA	2.17E-05
Gene	HYPER in CCA	chr2	223162866	223169936	*CCDC140*	151278	4.53E-06
Gene	HYPER in CCA	chr11	20177701	20182159	*DBX1*	120237	2.55E-05
Gene	HYPER in CCA	chr19	56988619	57012035	*ZNF667-AS1*	100128252	0.000395889
Gene	HYPER in CCA	chr19	30017406	30055386	*VSTM2B*	342865	7.24E-07
Gene	HYPER in CCA	chr8	23559964	23564111	*NKX2-6*	137814	3.46E-07
Gene	HYPER in CCA	chr19	23251275	23254278	*NA*	NA	2.34E-05
Gene	HYPER in CCA	chr6	26272421	26272768	*HIST1H2APS4*	NA	0.001525717
Gene	HYPER in CCA	chr2	176942200	176948641	*EVX2*	344191	4.56E-05
Gene	HYPER in CCA	chr17	46810453	46811250	*NA*	NA	1.12E-05
Gene	HYPER in CCA	chr7	27145803	27192200	*HOXA3*	3200	3.13E-06
Gene	HYPER in CCA	chr7	27282164	27290112	*EVX1*	2128	1.05E-05
Gene	HYPER in CCA	chr2	5832799	5841516	*SOX11*	6664	0.000335173
Gene	HYPER in CCA	chr2	124774435	124782750	*NA*	NA	0.000196177
Gene	HYPER in CCA	chr1	91177096	91182794	*BARHL2*	343472	4.26E-07
Gene	HYPER in CCA	chr17	35297346	35300755	*NA*	NA	5.98E-07
Gene	HYPER in CCA	chr7	27226192	27233067	*NA*	NA	6.44E-07
Gene	HYPER in CCA	chr8	67858736	67874825	*TCF24*	100129654	1.33E-07
Gene	HYPER in CCA	chr2	71004442	71017775	*FIGLA*	344018	4.44E-07
Gene	HYPER in CCA	chr10	8094205	8095412	*NA*	399717	9.76E-05
Gene	HYPER in CCA	chr21	34398153	34401504	*OLIG2*	10215	1.68E-05
Gene	HYPER in CCA	chr8	97154562	97173020	*GDF6*	392255	2.21E-06
Gene	HYPER in CCA	chr1	47881744	47883723	*FOXE3*	2301	0.000194763

Gene	HYPER in CCA	chr7	27210210	27219880	*HOXA10*	3206	1.72E-05
Gene	HYPER in CCA	chr6	10882013	10884582	*NA*	NA	6.65E-06
Gene	HYPER in CCA	chr8	65285885	65296344	*LINC00966*	100130155	4.25E-05
Gene	HYPER in CCA	chr20	26167556	26232162	*MIR663A*	284801;724033	1.05E-07
Gene	HYPER in CCA	chr10	135043778	135045062	*UTF1*	8433	3.90E-06
Gene	HYPER in CCA	chr12	45408455	45444882	*DBX2*	440097	1.91E-05
Gene	HYPER in CCA	chr19	35395296	35395961	*NA*	NA	2.51E-05
Gene	HYPER in CCA	chr13	84451344	84456528	*SLITRK1*	114798	9.82E-05
Gene	HYPER in CCA	chr1	147789799	147790129	*NA*	NA	3.22E-08
Gene	HYPER in CCA	chr6	85397069	85474237	*TBX18*	9096	4.45E-05
Gene	HYPER in CCA	chr2	186897618	186947960	*NA*	101927217	0.001304871
Gene	HYPER in CCA	chr3	188659504	188665428	*TPRG1-AS1*	NA	0.000227946
Gene	HYPER in CCA	chr10	50818347	50820765	*SLC18A3*	6572	1.41E-07
Gene	HYPER in CCA	chr1	119542967	119544015	*NA*	NA	7.74E-05
Gene	HYPER in CCA	chr2	45168902	45173216	*SIX3*	6496	2.92E-06
Gene	HYPER in CCA	chr14	29252697	29254993	*NA*	NA	2.96E-05
Gene	HYPER in CCA	chr17	46626232	46682274	*HOXB3*	3213	3.81E-06
Gene	HYPER in CCA	chr7	27186985	27192217	*NA*	NA	3.33E-05
Gene	HYPER in CCA	chr14	29241910	29282493	*C14orf23*	NA	1.63E-05
Gene	HYPER in CCA	chr5	63256183	63258334	*HTR1A*	3350	4.27E-06
Gene	HYPER in CCA	chr4	85413140	85419603	*NKX6-1*	4825	5.45E-06
Gene	HYPER in CCA	chr8	57025501	57026541	*MOS*	4342	4.88E-05
Gene	HYPER in CCA	chr18	902767	906668	*NA*	NA	1.03E-05
Gene	HYPER in CCA	chr20	21376005	21378666	*NKX2-4*	644524	1.25E-06
Gene	HYPER in CCA	chr2	119599747	119605254	*EN1*	2019	0.000142263
Gene	HYPER in CCA	chr17	46626992	46683776	*HOXB-AS3*	404266	4.75E-06
Gene	HYPER in CCA	chr18	14728271	14852737	*ANKRD30B*	374860	4.46E-05
Gene	HYPER in CCA	chr16	86600857	86602539	*FOXC2*	2303	8.98E-05
Gene	HYPER in CCA	chr4	1396720	1400119	*NKX1-1*	NA	8.76E-06
Gene	HYPER in CCA	chr6	1384025	1385301	*NA*	NA	1.04E-06
Gene	HYPER in CCA	chr2	176973518	176984670	*HOXD10*	3236	1.91E-05
Gene	HYPER in CCA	chr8	99956631	99964332	*OSR2*	116039	3.65E-05
Gene	HYPER in CCA	chr4	174448421	174512475	*HAND2-AS1*	79804	2.82E-05
Gene	HYPER in CCA	chr7	64029806	64030815	*NA*	NA	0.000155189

Gene	HYPER in CCA	chr7	19060614	19157295	*TWIST1*	7291	4.70E-06
Gene	HYPER in CCA	chr7	96635695	96637022	*DLX6-AS2*	NA	4.40E-05
Gene	HYPER in CCA	chr5	161494546	161582542	*GABRG2*	2566	0.00065928
Gene	HYPER in CCA	chr2	107099728	107103848	*NA*	NA	0.000186131
Gene	HYPER in CCA	chr12	54385522	54385631	*MIR196A2*	406973	0.000124043
Gene	HYPER in CCA	chr7	96649704	96654409	*DLX5*	1749	5.70E-05
Gene	HYPER in CCA	chr2	162272605	162282381	*TBR1*	10716	1.38E-05
Gene	HYPER in CCA	chr16	49311828	49315742	*CBLN1*	869	9.27E-05
Gene	HYPER in CCA	chr2	162279170	162280088	*NA*	NA	1.29E-05
Gene	HYPER in CCA	chr4	66185281	66536213	*EPHA5*	2044	6.04E-05
Gene	HYPER in CCA	chr19	53802304	53811897	*FAM90A28P*	NA	0.000595325
Gene	HYPER in CCA	chr14	38723308	38725574	*CLEC14A*	161198	9.90E-05
Gene	HYPER in CCA	chr5	1877541	1887350	*IRX4*	50805	0.000162005
Gene	HYPER in CCA	chr17	46802125	46806540	*HOXB13*	10481	3.72E-05
Gene	HYPER in CCA	chr7	27224137	27228912	*HOXA11-AS*	221883	2.62E-06
Gene	HYPER in CCA	chr2	105469743	105542510	*NA*	NA	7.92E-06
Gene	HYPER in CCA	chr5	2745959	2752969	*IRX2*	153572	7.68E-05
Gene	HYPER in CCA	chr15	29033389	29037148	*NA*	100289656	1.45E-05
Gene	HYPER in CCA	chr12	54356092	54368740	*HOTAIR*	100124700	4.97E-05
Gene	HYPER in CCA	chr3	137483579	137484396	*SOX14*	8403	6.26E-05
Gene	HYPER in CCA	chr4	122685740	122687962	*NA*	NA	3.22E-05
Gene	HYPER in CCA	chr4	122250467	122302214	*QRFPR*	84109	1.44E-05
Gene	HYPER in CCA	chr3	181429714	181432221	*SOX2*	6657	0.000333093
Gene	HYPER in CCA	chr16	3231233	3234018	*NA*	NA	0.00042803
Gene	HYPER in CCA	chr7	27185015	27190222	*HOXA6*	3203	0.000186131
Gene	HYPER in CCA	chr1	75595659	75598261	*NA*	NA	7.50E-05
Gene	HYPER in CCA	chr19	2249308	2252072	*AMH*	268;100423031	4.27E-06
Gene	HYPER in CCA	chr3	138663066	138665982	*FOXL2*	668	4.45E-05
Gene	HYPER in CCA	chr13	70681345	70713561	*ATXN8OS*	6315	1.62E-05
Gene	HYPER in CCA	chr18	53443958	53448952	*NA*	NA	3.60E-05
Gene	HYPER in CCA	chr7	35242042	35293758	*TBX20*	57057	4.93E-06
Gene	HYPER in CCA	chr3	146627472	147088443	*NA*	NA	5.57E-05
Gene	HYPER in CCA	chr2	105481955	105489053	*LINC01159*	NA	6.73E-05
Gene	HYPER in CCA	chr11	32457064	32480315	*WT1-AS*	51352	9.16E-05

Gene	HYPER in CCA	chr10	101286838	101288018	*NA*	NA	4.05E-05
Gene	HYPER in CCA	chr17	35294084	35301917	*LHX1*	3975	3.73E-05
Gene	HYPER in CCA	chr4	134070470	134129356	*PCDH10*	57575	5.45E-06
Gene	HYPER in CCA	chr2	223064607	223163715	*PAX3*	5077	9.03E-06
Gene	HYPER in CCA	chr7	96584453	96643377	*DLX6-AS1*	285987	5.60E-05
Gene	HYPER in CCA	chr10	124907638	124910188	*HMX2*	3167	1.70E-05
Gene	HYPER in CCA	chr6	100441820	100524289	*MCHR2-AS1*	728012	2.55E-05
Gene	HYPER in CCA	chr4	135476990	135494250	*LINC01096*	NA	0.000256612
Gene	HYPER in CCA	chr10	129535499	129539450	*FOXI2*	399823	4.28E-05
Gene	HYPER in CCA	chr10	134598297	134599556	*NKX6-2*	84504	1.29E-06
Gene	HYPER in CCA	chr17	33791268	33864880	*SLFN12L*	100506736	4.05E-05
Gene	HYPER in CCA	chr2	98963458	98967603	*NA*	NA	0.000102694
Gene	HYPER in CCA	chr14	36942412	36988726	*NA*	NA	1.68E-05
Gene	HYPER in CCA	chr14	94908801	94919127	*SERPINA11*	256394	0.000186374
Gene	HYPER in CCA	chr5	50678921	50690564	*ISL1*	3670	0.00036454
Gene	HYPER in CCA	chr2	45147332	45166338	*NA*	100130502	2.60E-05
Gene	HYPER in CCA	chr16	86544133	86548076	*FOXF1*	2294	0.000101763
Gene	HYPER in CCA	chr1	75594119	75627218	*LHX8*	431707	5.50E-05
Gene	HYPER in CCA	chr1	150229554	150237478	*CA14*	23632	1.63E-05
Gene	HYPER in CCA	chr18	894436	907681	*NA*	NA	2.31E-05
Gene	HYPER in CCA	chr19	38307999	38317278	*NA*	644554	2.78E-05
Gene	HYPER in CCA	chr19	22469210	22499978	*ZNF729*	100287226	0.00016381
Gene	HYPER in CCA	chr18	44746293	44775554	*SKOR2*	652991	3.97E-07
Gene	HYPER in CCA	chr19	56879468	56891197	*ZNF542*	147947	0.000217049
Gene	HYPER in CCA	chr10	118888032	118897812	*VAX1*	11023	0.000153193
Gene	HYPER in CCA	chr14	94896970	94931067	*NA*	NA	0.00058518
Gene	HYPER in CCA	chr14	60863187	60982261	*C14orf39*	317761	1.65E-05
Gene	HYPER in CCA	chr18	904944	912173	*ADCYAP1*	116	2.45E-05
Gene	HYPER in CCA	chr1	119543241	119544028	*NA*	NA	0.001547221
Gene	HYPER in CCA	chr14	37126773	37148920	*PAX9*	5083	2.79E-05
Gene	HYPER in CCA	chr19	9609354	9620755	*NA*	NA	3.91E-06
Gene	HYPER in CCA	chr14	61107448	61109307	*NA*	NA	5.70E-05
Gene	HYPER in CCA	chr20	9495005	9511171	*LAMP5*	24141	0.001266865
Gene	HYPER in CCA	chr12	85253492	85307394	*SLC6A15*	55117	0.000109737

Gene	HYPER in CCA	chr19	22715428	22716296	*NA*	100128139	0.000106028
Gene	HYPER in CCA	chr11	10548072	10585281	*GRIA4*	2893	0.000115432
Gene	HYPER in CCA	chr4	81105033	81125483	*PRDM8*	56978	7.96E-05
Gene	HYPER in CCA	chr7	12942321	12942502	*NA*	NA	6.52E-05
Gene	HYPER in CCA	chr1	75593515	75598743	*NA*	NA	0.000250669
Gene	HYPER in CCA	chr12	11921083	11921294	*NA*	NA	0.000463846
Gene	HYPER in CCA	chr13	88324870	88331871	*SLITRK5*	26050	2.78E-05
Gene	HYPER in CCA	chr14	62570096	62583893	*NA*	NA	2.20E-06
Gene	HYPER in CCA	chr11	66326337	66327855	*NA*	NA	5.83E-06
Gene	HYPER in CCA	chr6	10554469	10558504	*BVES*	11149	7.19E-05
Gene	HYPER in CCA	chr20	62366815	62370456	*LIME1*	54923	0.00050399
Gene	HYPER in CCA	chr2	18232192	18240091	*ITGA4*	3676	1.64E-07
Gene	HYPER in CCA	chr1	67218142	67244470	*TCTEX1D1*	200132	1.25E-06
Gene	HYPER in CCA	chr20	54572496	54580528	*CBLN4*	140689	9.45E-06
Gene	HYPER in CCA	chr4	41750310	41826136	*NA*	NA	0.000187247
Gene	HYPER in CCA	chr15	60296421	60353929	*FOXB1*	27023	5.79E-05
Gene	HYPER in CCA	chr10	63212397	63241714	*NA*	101928781	2.55E-05
Gene	HYPER in CCA	chr6	391739	411447	*IRF4*	3662	0.000266477
Gene	HYPER in CCA	chr2	15433385	15433532	*RPRM*	56475	0.000119566
Gene	HYPER in CCA	chr8	23583844	23600555	*NA*	NA	0.000775725
Gene	HYPER in CCA	chr20	39314488	39317880	*MAFB*	9935	8.21E-05
Gene	HYPER in CCA	chr11	11670646	11670866	*APOA1*	335	0.000248295
Gene	HYPER in CCA	chr10	11413377	11418813	*ACSL5*	51703	0.000186802
Gene	HYPER in CCA	chr6	50681541	50740701	*TFAP2D*	83741	3.16E-05
Gene	HYPER in CCA	chr6	11657537	11657790	*NA*	100506496	0.001304871
Gene	HYPER in CCA	chr5	14568666	14575652	*NA*	NA	6.44E-05
Gene	HYPER in CCA	chr1	40598436	40599120	*NA*	NA	0.000824367
Gene	HYPER in CCA	chr6	26043455	26043885	*HIST1H2BB*	3018	0.00058621
Gene	HYPER in CCA	chr1	11060261	11061332	*ALX3*	257	6.95E-06
Gene	HYPER in CCA	chr16	54968825	54988577	*NA*	NA	0.000132935
Gene	HYPER in CCA	chr6	27253682	27279949	*POM121L2*	94026	0.000209127
Gene	HYPER in CCA	chr2	17703792	17705368	*HOXD-AS1*	401022	0.000534911
Gene	HYPER in CCA	chr12	47158546	47226191	*SLC38A4*	55089	0.001565871
Gene	HYPER in CCA	chr12	11484599	11485063	*TBX5-AS1*	255480	0.000136094

Gene	HYPER in CCA	chr2	132118066	132121731	*NA*	NA	1.35E-06
Gene	HYPER in CCA	chr4	175015811	175141549	*NA*	101928509	0.000256612
Gene	HYPER in CCA	chr3	154055461	154147504	*GPR149*	344758	0.000412731
Gene	HYPER in CCA	chr7	27238194	27246878	*HOTTIP*	100316868	0.000390892
Gene	HYPER in CCA	chr9	100615536	100618986	*FOXE1*	2304	0.000770394
Gene	HYPER in CCA	chr1	229566992	229569845	*ACTA1*	58	9.01E-05
Gene	HYPER in CCA	chr3	62355356	62359999	*FEZF2*	55079	0.000591037
Gene	HYPER in CCA	chr7	155250824	155257526	*EN2*	2020	0.000104113
Gene	HYPER in CCA	chr10	101286107	101290934	*NA*	101927324	5.12E-05
Gene	HYPER in CCA	chr14	29198289	29234483	*NA*	NA	0.00023061
Gene	HYPER in CCA	chr12	25055243	25057615	*NA*	NA	0.000269315
Gene	HYPER in CCA	chr12	54366910	54371427	*HOXC11*	3227	0.001235979
Gene	HYPER in CCA	chr8	24770525	24776607	*NEFM*	4741	1.00E-05
Gene	HYPER in CCA	chr19	36279778	36288787	*NA*	644050	5.99E-06
Gene	HYPER in CCA	chr18	70409549	70535381	*NETO1*	81832	0.000647007
Gene	HYPER in CCA	chr19	22817126	22850472	*ZNF492*	57615	0.000578599
Gene	HYPER in CCA	chr2	131278770	131285579	*CFC1B*	55997;653275	0.000761742
Gene	HYPER in CCA	chr10	101292690	101296278	*NKX2-3*	159296	0.000200644
Gene	HYPER in CCA	chr17	46688739	46692478	*HOXB8*	3218	0.000196695
Gene	HYPER in CCA	chr6	117586721	117594728	*VGLL2*	245806	0.000355921
Gene	HYPER in CCA	chr16	65175659	65210616	*NA*	NA	0.001202746
Gene	HYPER in CCA	chr8	57358366	57464626	*NA*	101929415	5.71E-06
Gene	HYPER in CCA	chr17	16586752	16587541	*RNASEH1P2*	246243	0.000273684
Gene	HYPER in CCA	chr3	75721542	75728454	*LINC00960*	401074	0.000135097
Gene	HYPER in CCA	chr2	105424030	105469641	*LINC01158*	100506421	7.30E-05
Gene	HYPER in CCA	chr5	2752245	2755508	*C5orf38*	153571	0.000359895
Gene	HYPER in CCA	chr6	104233736	104264097	*NA*	NA	9.19E-05
Gene	HYPER in CCA	chr6	123317116	123394072	*CLVS2*	134829	3.57E-05
Gene	HYPER in CCA	chr2	74740590	74744274	*TLX2*	3196	9.13E-06
Gene	HYPER in CCA	chr9	79634571	79635869	*FOXB2*	442425	8.66E-05
Gene	HYPER in CCA	chr5	134374528	134375737	*NA*	101927953	0.000137715
Gene	HYPER in CCA	chr6	100054606	100063454	*PRDM13*	59336	5.69E-05
Gene	HYPER in CCA	chr4	145564074	145582509	*HHIP-AS1*	646576	0.00058657
Gene	HYPER in CCA	chr18	53388294	53455992	*NA*	NA	0.000101887

Gene	HYPER in CCA	chr3	26660821	26664181	*NA*	NA	0.000137123
Gene	HYPER in CCA	chr11	10929284	10929984	*C11orf87*	399947	6.86E-05
Gene	HYPER in CCA	chr14	52734431	52743442	*PTGDR*	5729	0.00023061
Gene	HYPER in CCA	chr8	72315675	72504260	*NA*	NA	4.88E-05
Gene	HYPER in CCA	chr20	62340216	62370456	*NA*	54923	3.69E-05
Gene	HYPER in CCA	chr1	11942566	11953217	*TBX15*	6913	6.51E-05
Gene	HYPER in CCA	chr2	20032242	20034165	*SATB2-AS1*	150538	1.75E-05
Gene	HYPER in CCA	chr3	14710383	14712464	*ZIC4*	84107	0.000132349
Gene	HYPER in CCA	chr12	54410715	54449813	*HOXC4*	3221	5.69E-05
Gene	HYPER in CCA	chr14	37116288	37128006	*NA*	NA	0.000159469
Gene	HYPER in CCA	chr6	13421027	13421669	*TCF21*	6943	0.000114292
Gene	HYPER in CCA	chr12	21917889	21928515	*KCNJ8*	3764	0.000196695
Gene	HYPER in CCA	chr8	10449562	10451390	*NA*	NA	0.001192674
Gene	HYPER in CCA	chr8	57349233	57359293	*PENK*	5179	1.90E-06
Gene	HYPER in CCA	chr11	12284827	12285242	*BSX*	390259	0.000223517
Gene	HYPER in CCA	chr1	46912345	46915376	*NA*	101929651	0.000248295
Gene	HYPER in CCA	chr8	49464575	49469001	*NA*	NA	0.000654198
Gene	HYPER in CCA	chr17	46713285	46724385	*NA*	NA	0.000186374
Gene	HYPER in CCA	chr2	23707387	23707701	*GBX2*	2637	0.001337789
Gene	HYPER in CCA	chr4	12268008	12268658	*TMEM155*	132332	0.000440495
Gene	HYPER in CCA	chr10	13534102	13534266	*NA*	NA	0.000942486
Gene	HYPER in CCA	chr4	10450718	10464097	*TACR3*	6870	0.000104711
Gene	HYPER in CCA	chr17	46684594	46710934	*HOXB7*	3217	0.000216431
Gene	HYPER in CCA	chr2	18254784	18255043	*NA*	NA	0.000301967
Gene	HYPER in CCA	chr5	1884080	1884763	*NA*	NA	0.000478609
Gene	HYPER in CCA	chr7	10031842	10032132	*EPO*	2056	0.000256612
Gene	HYPER in CCA	chr7	8473585	8792593	*NXPH1*	30010	0.000129667
Gene	HYPER in CCA	chr10	71331454	71332994	*NEUROG3*	50674	1.36E-05
Gene	HYPER in CCA	chr17	56234389	56235161	*MSX2P1*	55545	0.001079288
Gene	HYPER in CCA	chr4	81104434	81111323	*NA*	NA	0.000285452
Gene	HYPER in CCA	chr16	2317788	2317881	*NA*	NA	1.75E-10
Gene	HYPER in CCA	chr11	31806340	31839509	*PAX6*	5080	0.000155189
Gene	HYPER in CCA	chr6	11707336	11708688	*FAM162B*	221303	0.000561626
Gene	HYPER in CCA	chr9	12676394	12679558	*LHX2*	9355	0.000244858

Gene	HYPER in CCA	chr1	145413095	145417545	*HFE2*	148738	5.23E-05
Gene	HYPER in CCA	chr4	188916925	188926204	*ZFP42*	132625	4.76E-05
Gene	HYPER in CCA	chr6	5998232	6007200	*NRN1*	51299	0.000179013
Gene	HYPER in CCA	chr5	140560980	140565793	*PCDHB16*	57717	0.000988115
Gene	HYPER in CCA	chr22	29876219	29887379	*NEFH*	4744	3.10E-06
Gene	HYPER in CCA	chr11	32409321	32457176	*WT1*	7490	0.000352556
Gene	HYPER in CCA	chr18	49866542	51057784	*DCC*	1630	0.000560246
Gene	HYPER in CCA	chr1	149400131	149400542	*HIST2H3PS2*	NA	3.49E-06
Gene	HYPER in CCA	chr2	130724165	130738039	*RAB6C-AS1*	100131320	8.15E-07
Gene	HYPER in CCA	chr19	46913629	46916841	*CCDC8*	83987	0.000100828
Gene	HYPER in CCA	chr17	47072628	47074854	*NA*	NA	0.00054602
Gene	HYPER in CCA	chr19	21627043	21646710	*NA*	101928983	0.000412731
Gene	HYPER in CCA	chr1	111214310	111217655	*KCNA3*	3738	2.88E-05
Gene	HYPER in CCA	chr8	72740402	73030628	*NA*	100132891	0.000788454
Gene	HYPER in CCA	chr17	46668619	46671323	*HOXB5*	3215	5.59E-05
Gene	HYPER in CCA	chr10	119301955	119309056	*EMX2*	2018	0.000238893
Gene	HYPER in CCA	chr19	21541732	21562104	*ZNF738*	NA	0.000151201
Gene	HYPER in CCA	chr1	47691469	47696422	*NA*	101930541	5.69E-05
Gene	HYPER in CCA	chr21	27838528	27945603	*CYYR1*	116159	0.000161876
Gene	HYPER in CCA	chr13	37005967	37017019	*CCNA1*	8900	0.000835292
Gene	HYPER in CCA	chr2	19551246	19558414	*OSR1*	130497	9.57E-05
Gene	HYPER in CCA	chr6	19690056	19753344	*NA*	NA	4.89E-05
Gene	HYPER in CCA	chr10	63166401	63213208	*TMEM26*	219623	1.53E-05
Gene	HYPER in CCA	chr16	77467279	77478233	*NA*	NA	0.001035443
Gene	HYPER in CCA	chr14	36942493	36983034	*SFTA3*	253970	9.05E-05
Gene	HYPER in CCA	chr6	43267448	43276535	*CRIP3*	401262	5.37E-08
Gene	HYPER in CCA	chr17	1173853	1174754	*BHLHA9*	727857	3.10E-06
Gene	HYPER in CCA	chr18	63417488	63548638	*CDH7*	1005	0.000196181
Gene	HYPER in CCA	chr5	54515442	54523143	*MCIDAS*	345643	1.87E-05
Gene	HYPER in CCA	chr13	78469616	78493903	*EDNRB*	1910	0.000850249
Gene	HYPER in CCA	chr8	37820516	37824483	*ADRB3*	155	0.000203768
Gene	HYPER in CCA	chr6	29795162	29796141	*HCG4P8*	NA	5.69E-05
Gene	HYPER in CCA	chr18	56934267	56941318	*RAX*	30062	0.000229496
Gene	HYPER in CCA	chr7	79082198	79100524	*MAGI2-AS3*	100505881	0.000377088

Gene	HYPER in CCA	chr7	96634860	96640351	*DLX6*	1750	0.000566497
Gene	HYPER in CCA	chr10	8092413	8095447	*GATA3-AS1*	399717	0.001052195
Gene	HYPER in CCA	chr14	36985602	36990354	*NKX2-1*	7080	0.000470122
Gene	HYPER in CCA	chr8	75896750	75946793	*CRISPLD1*	83690	0.000696844
Gene	HYPER in CCA	chr12	54384408	54424607	*HOXC6*	3223	0.000870817
Gene	HYPER in CCA	chr9	96713905	96717654	*BARX1*	56033	0.000282162
Gene	HYPER in CCA	chr8	65486863	65494445	*NA*	401463	0.000770862
Gene	HYPER in CCA	chr13	58205944	58303445	*PCDH17*	27253	0.000149726
Gene	HYPER in CCA	chr5	87972036	88018648	*NA*	NA	0.000275741
Gene	HYPER in CCA	chr4	55944644	55991756	*KDR*	3791	0.000241821
Gene	HYPER in CCA	chr11	118382626	118401809	*NA*	NA	5.74E-06
Gene	HYPER in CCA	chr6	1390069	1395832	*FOXF2*	2295	0.000642628
Gene	HYPER in CCA	chr2	80515483	80531874	*LRRTM1*	347730	0.000448587
Gene	HYPER in CCA	chr12	33527173	33592754	*SYT10*	341359	0.001070768
Gene	HYPER in CCA	chr7	27221129	27224842	*HOXA11*	3207	0.000784137
Gene	HYPER in CCA	chr19	57828576	57828930	*NA*	NA	0.001125092
Gene	HYPER in CCA	chr12	102789645	102874423	*IGF1*	3479	0.000153115
Gene	HYPER in CCA	chr2	130737235	130740311	*RAB6C*	84084;150786	1.35E-06
Gene	HYPER in CCA	chr19	18893583	18902123	*COMP*	1311	0.000792704
Gene	HYPER in CCA	chr19	29777918	30016659	*NA*	284395	0.000182818
Gene	HYPER in CCA	chr7	54610018	54638773	*VSTM2A*	222008	0.000249005
Gene	HYPER in CCA	chr7	19758933	19813221	*TMEM196*	256130	0.001039536
Gene	HYPER in CCA	chr2	71127720	71160576	*VAX2*	25806	0.000102986
Gene	HYPER in CCA	chr4	113436541	113468037	*NA*	NA	0.001425883
Gene	HYPER in CCA	chr7	155213901	155249794	*NA*	NA	0.000738239
Gene	HYPER in CCA	chr10	94178424	94180632	*MARK2P9*	100507674	0.000701915
Gene	HYPER in CCA	chr12	113909808	113918429	*NA*	NA	0.000364963
Gene	HYPER in CCA	chr19	38879061	38886881	*SPRED3*	399473	0.000310159
Gene	HYPER in CCA	chr12	48577366	48579709	*C12orf68*	387856	8.95E-05
Gene	HYPER in CCA	chr1	248099363	248100815	*NA*	NA	0.000170215
Gene	HYPER in CCA	chr17	46698518	46703839	*HOXB9*	3219	0.000283666
Gene	HYPER in CCA	chr20	25051521	25062996	*VSX1*	30813	4.38E-05
Gene	HYPER in CCA	chr8	69215703	69243726	*NA*	NA	0.000203661
Gene	HYPER in CCA	chr2	31747550	31806136	*SRD5A2*	NA	0.000407702

Gene	HYPER in CCA	chr16	55293881	55367500	*NA*	NA	0.000706876
Gene	HYPER in CCA	chr3	172162923	172166246	*GHSR*	2693	1.09E-05
Gene	HYPER in CCA	chr15	89911248	89911337	*MIR9-3*	407051	5.14E-05
Gene	HYPER in CCA	chr19	22235254	22274282	*ZNF257*	113835	0.000454751
Gene	HYPER in CCA	chr5	33936491	33939023	*RXFP3*	51289	0.000449818
Gene	HYPER in CCA	chr11	111384768	111397480	*NA*	101928666	0.000887866
Gene	HYPER in CCA	chr15	34786621	34788101	*NA*	NA	2.74E-05
Gene	HYPER in CCA	chr10	102986733	102989551	*LBX1*	10660	7.74E-05
Gene	HYPER in CCA	chr19	52956829	53015407	*ZNF578*	147660	6.11E-06
Gene	HYPER in CCA	chr11	123301058	123306427	*NA*	NA	0.000368177
Gene	HYPER in CCA	chr13	78493824	79191463	*RNF219-AS1*	100874222	0.000361253
Gene	HYPER in CCA	chr1	156611182	156629324	*BCAN*	63827	0.000282436
Gene	HYPER in CCA	chr1	170631869	170708560	*PRRX1*	5396	0.000798922
Gene	HYPER in CCA	chr11	69587797	69590171	*FGF4*	2249	0.001054616
Gene	HYPER in CCA	chr4	42112955	42154895	*BEND4*	389206	6.74E-05
Gene	HYPER in CCA	chr6	62389865	62996132	*KHDRBS2*	202559	0.000636727
Gene	HYPER in CCA	chr12	54379629	54428672	*NA*	NA	0.001346519
Gene	HYPER in CCA	chr2	162280843	162841792	*SLC4A10*	57282	4.05E-05
Gene	HYPER in CCA	chr5	145583113	145718814	*RBM27*	54439	0.000283104
Gene	HYPER in CCA	chr12	54410894	54429145	*NA*	3222	0.000294533
Gene	HYPER in CCA	chr4	133996466	134070271	*NA*	101927359	0.000582244
Gene	HYPER in CCA	chr12	54332535	54340328	*HOXC13*	3229	0.000251148
Gene	HYPER in CCA	chr16	73517216	73521643	*NA*	NA	0.00025075
Gene	HYPER in CCA	chr11	17741115	17743678	*MYOD1*	4654	0.000291567
Gene	HYPER in CCA	chr5	180526140	180527666	*FOXO1B*	NA	0.000391915
Gene	HYPER in CCA	chr10	102989351	103029905	*LBX1-AS1*	NA	0.000195907
Gene	HYPER in CCA	chr10	105036920	105050108	*INA*	9118	2.22E-06
Gene	HYPER in CCA	chr5	172659112	172662360	*NKX2-5*	1482	0.000125463
Gene	HYPER in CCA	chr6	100367786	100442123	*MCHR2*	84539	0.000273276
Gene	HYPER in CCA	chr1	53308183	53360670	*ZYG11A*	440590	1.87E-06
Gene	HYPER in CCA	chr2	220192131	220197899	*RESP18*	389075	0.000362106
Gene	HYPER in CCA	chr3	138654031	138662862	*NA*	NA	0.000102552
Gene	HYPER in CCA	chr5	161803470	161856946	*NA*	NA	0.000766809
Gene	HYPER in CCA	chr2	89065324	89106126	*ANKRD36BP2*	645784	0.000276579

Gene	HYPER in CCA	chr4	46920917	46996424	*GABRA4*	2557	3.11E-05
Gene	HYPER in CCA	chr9	841690	969090	*DMRT1*	1761	0.00121235
Gene	HYPER in CCA	chr15	22646603	22647417	*NA*	NA	1.92E-05
Gene	HYPER in CCA	chr17	66195062	66195737	*NA*	440461	4.98E-05
Gene	HYPER in CCA	chr3	179512746	179754841	*PEX5L*	51555	3.70E-05
Gene	HYPER in CCA	chr10	119232726	119304579	*EMX2OS*	196047	0.001085176
Gene	HYPER in CCA	chr20	61798149	61812255	*NA*	NA	5.90E-05
Gene	HYPER in CCA	chr15	76629065	76634817	*ISL2*	64843	0.000492174
Gene	HYPER in CCA	chr1	204100190	204121307	*ETNK2*	55224	1.41E-05
Gene	HYPER in CCA	chr6	10873456	10882174	*GCM2*	9247	0.000199697
Gene	HYPER in CCA	chr18	22641890	22932154	*ZNF521*	25925	0.000302016
Gene	HYPER in CCA	chr14	57284288	57360428	*NA*	NA	9.13E-06
Gene	HYPER in CCA	chr20	21686297	21696620	*PAX1*	5075	0.000921921
Gene	HYPER in CCA	chr12	116019866	116077539	*NA*	NA	0.00046982
Gene	HYPER in CCA	chr12	54348618	54352740	*HOXC12*	3228	0.000256991
Gene	HYPER in CCA	chr20	21068245	21086999	*LINC00237*	NA	0.001070666
Gene	HYPER in CCA	chr11	20691971	20692843	*NA*	NA	7.90E-05
Gene	HYPER in CCA	chr1	152078793	152086556	*TCHH*	7062	0.000850249
Gene	HYPER in CCA	chr22	19136089	19137796	*GSC2*	2928	0.001404225
Gene	HYPER in CCA	chr5	72509774	72590761	*NA*	NA	0.000270596
Gene	HYPER in CCA	chr8	72932152	72987852	*TRPA1*	8989	0.001105662
Gene	HYPER in CCA	chr14	101540206	101544247	*NA*	NA	3.48E-06
Gene	HYPER in CCA	chr3	187386694	187388187	*SST*	6750	0.000617381
Gene	HYPER in CCA	chr6	142379477	142409936	*NMBR*	4829	0.000248295
Gene	HYPER in CCA	chr11	125773271	125793158	*DDX25*	29118	7.27E-05
Gene	HYPER in CCA	chr5	76924538	76935513	*OTP*	23440	0.000721677
Gene	HYPER in CCA	chr5	87803363	87986858	*LINC00461*	407047;645323	0.001235979
Gene	HYPER in CCA	chr6	105584183	105617820	*BVES-AS1*	154442	0.000224388
Gene	HYPER in CCA	chr19	53731577	53758151	*ZNF677*	342926	5.34E-05
Gene	HYPER in CCA	chr17	42634925	42636907	*FZD2*	2535	5.07E-05
Gene	HYPER in CCA	chr7	156786745	156803345	*MNX1*	3110	0.000139875
Gene	HYPER in CCA	chr1	149400063	149429348	*NA*	NA	2.11E-05
Gene	HYPER in CCA	chr14	23825611	23834961	*EFS*	10278	0.000690183
Gene	HYPER in CCA	chr12	56864736	56882198	*GLS2*	27165	0.000280138

Gene	HYPER in CCA	chr17	59529765	59562471	*TBX4*	9496	0.000280005
Gene	HYPER in CCA	chr5	12759360 1	12799487 8	*FBN2*	2201	0.000986097
Gene	HYPER in CCA	chr8	14423933 1	14424212 8	*LY6H*	4062	0.00025538
Gene	HYPER in CCA	chr8	80523049	80578410	*STMN2*	11075	0.00027414
Gene	HYPER in CCA	chr15	10091314 4	10097811 9	*NA*	NA	0.001090664
Gene	HYPER in CCA	chr11	10922581 2	10945463 3	*NA*	NA	0.000362231
Gene	HYPER in CCA	chr11	31833939	32127301	*RCN1*	5954;440034	0.000459926
Gene	HYPER in CCA	chr21	38071433	38122218	*SIM2*	6493	0.000915421
Gene	HYPER in CCA	chr2	11991381 9	11991646 5	*C1QL2*	165257	0.00022875
Gene	HYPER in CCA	chr8	92967203	93115514	*RUNX1T1*	862	0.001051275
Gene	HYPER in CCA	chr10	10288925 7	10289754 5	*TLX1*	3195	0.001166218
Gene	HYPER in CCA	chr12	13050903 8	13052950 1	*NA*	NA	0.000721713
Gene	HYPER in CCA	chr19	56728537	56729146	*NA*	NA	0.000382226
Gene	HYPER in CCA	chr19	23945807	24010937	*RPSAP58*	NA	0.000849229
Gene	HYPER in CCA	chr8	14450135 2	14451257 6	*MAFA*	389692	0.000984408
Gene	HYPER in CCA	chr12	10335146 4	10335429 4	*ASCL1*	429	0.001553106
Gene	HYPER in CCA	chr5	15852749 1	15854448 6	*NA*	101927740	0.000681634
Gene	HYPER in CCA	chr12	54329112	54333427	*HOXC13-AS*	100874366	0.000704005
Gene	HYPER in CCA	chr11	71950121	71956708	*PHOX2A*	401	0.000249005
Gene	HYPER in CCA	chr6	26183958	26184454	*HIST1H2BE*	8339;8343;8344;8346;8347	0.000432653
Gene	HYPER in CCA	chr6	99282580	99286660	*POU3F2*	5454	0.000155189
Gene	HYPER in CCA	chr5	87988468	87988676	*NA*	NA	0.001528831
Gene	HYPER in CCA	chr1	14939887 7	14940054 0	*NA*	NA	0.000360479
Gene	HYPER in CCA	chr19	9577183	9609283	*ZNF560*	147741	0.000311495
Gene	HYPER in CCA	chr12	11389983 9	11391008 5	*LHX5*	64211	0.001309765
Gene	HYPER in CCA	chr7	87031013	87109751	*ABCB4*	5244	0.000280116
Gene	HYPER in CCA	chr10	50817141	50901925	*CHAT*	1103	0.000707308
Gene	HYPER in CCA	chr17	47300724	47308128	*PHOSPHO1*	162466	0.001231821
Gene	HYPER in CCA	chr9	32783497	32787397	*TMEM215*	401498	7.68E-05
Gene	HYPER in CCA	chr5	11369664 2	11383233 7	*KCNN2*	3781	0.000420465
Gene	HYPER in CCA	chr2	15472842 6	15531036 1	*GALNT13*	114805	0.00017584
Gene	HYPER in CCA	chr2	23334453 7	23335253 8	*ECEL1*	9427	0.000455376
Gene	HYPER in CCA	chr6	10848726 2	10851001 3	*NR2E1*	7101	0.001507002
Gene	HYPER in CCA	chr4	48485360	48491213	*SLC10A4*	201780	0.000401339

Gene	HYPER in CCA	chr15	68112042	68126899	*SKOR1*	390598	0.001003076
Gene	HYPER in CCA	chr1	20915441	20945401	*CDA*	978	7.63E-05
Gene	HYPER in CCA	chr7	89748613	89752204	*NA*	NA	0.000502905
Gene	HYPER in CCA	chr12	30353916	30370849	*NA*	NA	0.00024876
Gene	HYPER in CCA	chr15	83847934	84108197	*NA*	NA	0.001064658
Gene	HYPER in CCA	chr14	62581071	62584284	*NA*	NA	0.000761742
Gene	HYPER in CCA	chr8	113235157	114449328	*CSMD3*	114788	0.000681353
Gene	HYPER in CCA	chr17	48046334	48052321	*DLX4*	1748	0.000223324
Gene	HYPER in CCA	chr19	49570675	49576198	*KCNA7*	3743	7.51E-06
Gene	HYPER in CCA	chr16	56126899	56225006	*NA*	283856	0.000430168
Gene	HYPER in CCA	chr18	12254318	12277594	*CIDEA*	1149	0.000367533
Gene	HYPER in CCA	chr13	70274726	70682591	*KLHL1*	57626	0.000647007
Gene	HYPER in CCA	chr8	68864353	69149265	*PREX2*	80243	0.000227946
Gene	HYPER in CCA	chr2	237076090	237203570	*NA*	NA	0.001138906
Gene	HYPER in CCA	chr6	42694972	42695438	*ATP6V0CP3*	NA	0.000610622
Gene	HYPER in CCA	chr19	15121556	15134081	*CCDC105*	126402	0.000185972
Gene	HYPER in CCA	chr8	22545172	22550815	*EGR3*	1960	0.000647926
Promoter	HYPO in CCA	chr3	52566529	52568528	*SMIM4*	440957	0.000460595
Promoter	HYPO in CCA	chr3	119041108	119043107	*ARHGAP31-AS1*	NA	6.92E-06
Promoter	HYPO in CCA	chr13	33924268	33926267	*STARD13*	90627	0.000946383
Promoter	HYPO in CCA	chr2	262640	264639	*ACP1*	52	2.04E-07
Promoter	HYPO in CCA	chr12	7339781	7341780	*PEX5*	5830	0.000120017
Promoter	HYPO in CCA	chr12	118499736	118501735	*WSB2*	55884	0.000270898
Promoter	HYPO in CCA	chr1	155947090	155949089	*NA*	NA	7.11E-08
Promoter	HYPO in CCA	chr1	161052755	161054754	*NA*	NA	0.001035721
Promoter	HYPO in CCA	chr12	29470282	29472281	*NA*	100506606	0.000109261
Promoter	HYPO in CCA	chr19	13907248	13909247	*NA*	NA	0.000268007
Promoter	HYPO in CCA	chr16	29818554	29820553	*NA*	NA	0.000260274
Promoter	HYPO in CCA	chr17	20370353	20372352	*LGALS9B*	284194	0.000173157
Promoter	HYPO in CCA	chr8	22455614	22457613	*C8orf58*	541565	0.000460595
Promoter	HYPO in CCA	chr1	32040675	32042674	*NA*	NA	6.26E-06
Promoter	HYPO in CCA	chr1	32040616	32042615	*TINAGL1*	64129	6.26E-06
Promoter	HYPO in CCA	chr17	61915843	61917842	*RN7SL805P*	NA	0.000318667
Promoter	HYPO in CCA	chr11	3069252	3071251	*RNU1-91P*	NA	0.000947762

Promoter	HYPO in CCA	chr1	35729584	35731583	*RN7SL136P*	NA	0.001153899
Promoter	HYPO in CCA	chr16	69759416	69761415	*NA*	NA	1.09E-05
Promoter	HYPO in CCA	chr21	45579460	45581459	*NA*	101928576	0.000219197
Promoter	HYPO in CCA	chr19	1257884	1259883	*CIRBP*	1153	3.20E-10
Promoter	HYPO in CCA	chr5	141705521	141707520	*SPRY4*	81848	5.38E-07
Promoter	HYPO in CCA	chr17	43325704	43327703	*NA*	101927036	2.16E-07
Promoter	HYPO in CCA	chr16	69163694	69165693	*CIRH1A*	84916	8.61E-07
Promoter	HYPO in CCA	chr9	117567907	117569906	*TNFSF15*	9966	3.04E-09
Promoter	HYPO in CCA	chr11	66622618	66624617	*LRFN4*	78999	2.59E-07
Promoter	HYPO in CCA	chr7	100180105	100182104	*FBXO24*	26261	5.77E-09
Promoter	HYPO in CCA	chr16	69760355	69762354	*NQO1*	1728	1.83E-05
Promoter	HYPO in CCA	chr1	24644312	24646311	*GRHL3*	57822	1.95E-08
Promoter	HYPO in CCA	chr21	32930058	32932057	*NA*	150051	0.000502921
Promoter	HYPO in CCA	chr15	81701358	81703357	*NA*	NA	8.53E-09
Promoter	HYPO in CCA	chr12	66429515	66431514	*NA*	NA	1.03E-05
Promoter	HYPO in CCA	chr21	37801158	37803157	*NA*	NA	6.48E-06
Promoter	HYPO in CCA	chr17	73840299	73842298	*UNC13D*	201294	1.02E-08
Promoter	HYPO in CCA	chr6	33243417	33245416	*B3GALT4*	8705	7.39E-05
Promoter	HYPO in CCA	chr1	156630717	156632716	*NA*	NA	5.44E-09
Promoter	HYPO in CCA	chr1	229546015	229548014	*RN7SKP276*	NA	0.000171007
Promoter	HYPO in CCA	chr1	27667013	27669012	*SYTL1*	84958	1.16E-09
Promoter	HYPO in CCA	chr12	124996268	124998267	*NA*	NA	1.67E-05
Promoter	HYPO in CCA	chr21	32931791	32933790	*TIAM1*	7074	6.38E-05
Promoter	HYPO in CCA	chr19	14489813	14491812	*CD97*	976	0.001266056
Promoter	HYPO in CCA	chr16	87839583	87841582	*NA*	NA	0.000527854
Promoter	HYPO in CCA	chr11	85780425	85782424	*PICALM*	8301	2.27E-05
Promoter	HYPO in CCA	chr11	9780581	9782580	*NA*	440028	1.50E-05
Promoter	HYPO in CCA	chr19	17401918	17403917	*MRPL34*	64981	0.001821806
Promoter	HYPO in CCA	chr17	79520488	79522487	*C17orf70*	80233	2.96E-06
Promoter	HYPO in CCA	chr1	152019884	152021883	*S100A11*	6282	5.26E-13
Promoter	HYPO in CCA	chr6	149353210	149355209	*NA*	NA	5.69E-05
Promoter	HYPO in CCA	chr5	140097010	140099009	*VTRNA1-2*	56663	2.12E-05
Promoter	HYPO in CCA	chr2	85133633	85135632	*TRABD2A*	129293	6.08E-12
Promoter	HYPO in CCA	chr2	109294558	109296557	*NA*	NA	2.92E-07

Promoter	HYPO in CCA	chr5	17117296	17119295	*NA*	NA	1.21E-06
Promoter	HYPO in CCA	chr22	38091511	38093510	*TRIOBP*	11078	3.55E-08
Promoter	HYPO in CCA	chr8	23192184	23194183	*NA*	100507156	0.001437621
Promoter	HYPO in CCA	chr1	43736108	43738107	*EBNA1BP2*	10969;102465439	3.52E-13
Promoter	HYPO in CCA	chr3	158389983	158391982	*LXN*	56925	4.38E-06
Promoter	HYPO in CCA	chr2	70483018	70485017	*PCYOX1*	51449	4.98E-06
Promoter	HYPO in CCA	chr8	22931502	22933501	*NA*	NA	3.52E-13
Promoter	HYPO in CCA	chr1	228580491	228582490	*NA*	NA	2.08E-05
Promoter	HYPO in CCA	chr1	234699544	234701543	*NA*	NA	1.15E-05
Promoter	HYPO in CCA	chr19	47735524	47737523	*BBC3*	27113;100422832;100422899	1.87E-09
Promoter	HYPO in CCA	chr22	40354901	40356900	*NA*	NA	3.86E-05
Promoter	HYPO in CCA	chr5	166720779	166722778	*NA*	NA	2.69E-07
Promoter	HYPO in CCA	chr11	9159162	9161161	*SCUBE2*	57758	4.09E-11
Promoter	HYPO in CCA	chr11	19400531	19402530	*NAV2-IT1*	NA	2.16E-08
Promoter	HYPO in CCA	chr6	43191099	43193098	*NA*	NA	2.15E-08
Promoter	HYPO in CCA	chr11	119035777	119037776	*NLRX1*	79671	8.72E-08
Promoter	HYPO in CCA	chr16	88717061	88719060	*CYBA*	1535	2.08E-11
Promoter	HYPO in CCA	chr1	204676059	204678058	*RNA5SP75*	NA	1.43E-07
Promoter	HYPO in CCA	chr1	169071862	169073861	*NA*	101928596	2.12E-05
Promoter	HYPO in CCA	chr1	173834325	173836324	*SNORD78*	692198	1.52E-09
Promoter	HYPO in CCA	chr5	67729809	67731808	*NA*	NA	1.86E-06
Gene	HYPO in CCA	chr12	70037140	70093256	*BEST3*	144453	4.93E-06
Gene	HYPO in CCA	chr3	119033140	119041607	*ARHGAP31-AS1*	NA	6.03E-06
Gene	HYPO in CCA	chr17	70117161	70122561	*SOX9*	6662	0.000584646
Gene	HYPO in CCA	chr19	47567444	47617009	*ZC3H4*	23211	5.97E-07
Gene	HYPO in CCA	chr17	57918627	57918698	*MIR21*	406991	0.000124043
Gene	HYPO in CCA	chr18	47018034	47018099	*SNORD58B*	26790	5.11E-07
Gene	HYPO in CCA	chr3	158362067	158410364	*GFM1*	85476	0.001515287
Gene	HYPO in CCA	chr6	43968317	43973695	*C6orf223*	221416	0.000631757
Gene	HYPO in CCA	chr16	69740899	69760854	*NQO1*	1728	6.97E-05
Gene	HYPO in CCA	chr1	24634046	24648391	*NA*	NA	2.11E-06
Gene	HYPO in CCA	chr17	20352708	20370852	*LGALS9B*	284194	0.000217037
Gene	HYPO in CCA	chr3	158363611	158390482	*LXN*	56925	0.000741817
Gene	HYPO in CCA	chr16	88709691	88717560	*CYBA*	1535	4.00E-06
Gene	HYPO in CCA	chr19	24216276	24312654	*ZNF254*	9534	4.82E-05
Gene	HYPO in CCA	chr19	13907388	13907747	*NA*	NA	3.68E-05

Gene	HYPO in CCA	chr14	24391456	24403777	*LINC00596*	NA	0.000888037
Gene	HYPO in CCA	chr1	8935847	8938066	*ENO1-IT1*	NA	1.25E-05
Gene	HYPO in CCA	chr21	45578623	45579959	*NA*	101928576	0.000727644
Gene	HYPO in CCA	chr1	153533584	153540366	*S100A2*	6273	5.13E-07
Gene	HYPO in CCA	chr6	30734602	30760027	*HCG20*	NA	1.69E-08
Gene	HYPO in CCA	chr15	78285747	78287631	*NA*	NA	8.57E-06
Gene	HYPO in CCA	chr12	90341470	90343503	*NA*	NA	0.001145353
Gene	HYPO in CCA	chr3	109366954	109529708	*NA*	NA	5.27E-06
Gene	HYPO in CCA	chr14	103587184	103589344	*LINC00677*	NA	1.56E-05
Gene	HYPO in CCA	chr1	2143610	2144013	*NA*	NA	0.000121263
Gene	HYPO in CCA	chr20	34556512	34618622	*CNBD2*	140894	5.12E-05
Gene	HYPO in CCA	chr12	94671534	94676620	*NA*	NA	1.45E-05
Gene	HYPO in CCA	chr17	9550337	9550977	*NA*	NA	0.000232752
Gene	HYPO in CCA	chr1	155948590	155952777	*NA*	NA	2.75E-10
Gene	HYPO in CCA	chr15	48095581	48138433	*NA*	101928442	1.11E-05
Gene	HYPO in CCA	chr1	45242162	45242265	*SNORD46*	94161	1.74E-12
Gene	HYPO in CCA	chr1	32037186	32041174	*NA*	NA	8.34E-07
Gene	HYPO in CCA	chr14	32395007	32399352	*NA*	NA	4.83E-05
Gene	HYPO in CCA	chr21	32931558	32932800	*NA*	150051	9.45E-06
Gene	HYPO in CCA	chr8	22928890	22932001	*NA*	NA	1.34E-08
Gene	HYPO in CCA	chr2	109293251	109295057	*NA*	NA	4.53E-07
Gene	HYPO in CCA	chr22	43608680	43609667	*NA*	NA	4.29E-07
Gene	HYPO in CCA	chr17	73679623	73680879	*NA*	NA	9.13E-06
Gene	HYPO in CCA	chr20	31175281	31196695	*NA*	NA	3.24E-06
Gene	HYPO in CCA	chr3	133774100	133776492	*NA*	100507210	2.55E-05
Gene	HYPO in CCA	chr8	102299673	102306011	*NA*	NA	3.97E-05
Gene	HYPO in CCA	chr6	31804853	31804919	*SNORD52*	26797	2.48E-05
Gene	HYPO in CCA	chr16	11290034	11318373	*NA*	NA	9.52E-07
Gene	HYPO in CCA	chr22	30580633	30603098	*NA*	NA	9.20E-05
Gene	HYPO in CCA	chr16	2013746	2014096	*NA*	NA	2.34E-05
Gene	HYPO in CCA	chr5	6766004	6772066	*NA*	NA	3.94E-07
Gene	HYPO in CCA	chr7	46184535	46185286	*NA*	NA	1.76E-07
Gene	HYPO in CCA	chr8	38401170	38410198	*NA*	NA	6.00E-06
Gene	HYPO in CCA	chr11	19402031	19406561	*NAV2-IT1*	NA	3.95E-08
Gene	HYPO in CCA	chr4	88896819	88904562	*SPP1*	6696	2.00E-09
Gene	HYPO in CCA	chr5	67726254	67730308	*NA*	NA	2.80E-06
Gene	HYPO in CCA	chr2	237642025	237663006	*NA*	NA	3.48E-10

Table S14: Enriched KEGG pathways among differentially methylated regions

IDH-gr

P-value	Q-value	Pathway	Source
9.22E-09	2.03E-06	PPAR signaling pathway	KEGG
7.22E-07	7.94E-05	Alcoholism	KEGG
9.69E-05	0.00699	GABAergic synapse	KEGG
0.000127	0.00699	Transcriptional misregulation in cancer	KEGG
0.000399	0.0133	Primary bile acid biosynthesis	KEGG
0.000399	0.0133	Bile secretion	KEGG
0.000482	0.0133	Morphine addiction	KEGG
0.000507	0.0133	Cholinergic synapse	KEGG
0.000543	0.0133	Systemic lupus erythematosus	KEGG
0.00114	0.0251	Complement and coagulation cascades	KEGG
0.00146	0.0275	Retrograde endocannabinoid signaling	KEGG
0.00157	0.0275	Serotonergic synapse	KEGG
0.00163	0.0275	Chemical carcinogenesis	KEGG
0.00199	0.0313	Thyroid hormone synthesis	KEGG
0.00247	0.0363	Circadian entrainment	KEGG
0.0034	0.0448	Fat digestion and absorption	KEGG
0.00346	0.0448	Drug metabolism - cytochrome P450	KEGG

KRAS-gr

P-value	Q-value	Pathway	Source
0.000457	0.0474	Maturity onset diabetes of the young	KEGG
0.000787	0.0474	Neuroactive ligand-receptor interaction	KEGG
0.000929	0.0474	Complement and coagulation cascades	KEGG

TP53-gr

P-value	Q-value	Pathway	Source
4.51E-05	0.00284	Neuroactive ligand-receptor interaction	KEGG

Udt-gr

P-value	Q-value	Pathway	Source
3.18E-09	5.00E-07	Neuroactive ligand-receptor interaction	KEGG
1.15E-05	0.000903	Maturity onset diabetes of the young	KEGG
1.93E-05	0.00101	GABAergic synapse	KEGG
2.89E-05	0.00113	Nicotine addiction	KEGG
7.74E-05	0.00243	Retrograde endocannabinoid signaling	KEGG
0.000131	0.00343	Morphine addiction	KEGG
0.0002	0.00449	cAMP signaling pathway	KEGG
0.00215	0.0422	Proteoglycans in cancer	KEGG

METTL13 amplification			
***P*-value**	**Q-value**	**Pathway**	**Source**
1.09E-21	2.62E-19	Neuroactive ligand-receptor interaction	KEGG
1.62E-11	1.67E-09	Retrograde endocannabinoid signaling	KEGG
2.07E-11	1.67E-09	Nicotine addiction	KEGG
1.05E-10	6.34E-09	Morphine addiction	KEGG
2.18E-10	1.05E-08	GABAergic synapse	KEGG
2.54E-09	1.02E-07	Glutamatergic synapse	KEGG
4.36E-08	1.50E-06	Alcoholism	KEGG
6.68E-07	2.01E-05	Circadian entrainment	KEGG
2.23E-06	5.97E-05	cAMP signaling pathway	KEGG
3.38E-06	8.14E-05	Calcium signaling pathway	KEGG
7.87E-06	0.000172	Oxytocin signaling pathway	KEGG
1.76E-05	0.000353	Transcriptional misregulation in cancer	KEGG
3.45E-05	0.00064	Cholinergic synapse	KEGG
5.29E-05	0.000911	Rap1 signaling pathway	KEGG
0.000115	0.00185	Serotonergic synapse	KEGG
0.00023	0.00346	Systemic lupus erythematosus	KEGG
0.000414	0.00586	Bile secretion	KEGG
0.000892	0.0119	Taste transduction	KEGG
0.000978	0.0124	Cocaine addiction	KEGG
0.00141	0.017	Maturity onset diabetes of the young	KEGG
0.0016	0.0179	PI3K-Akt signaling pathway	KEGG
0.00163	0.0179	Taurine and hypotaurine metabolism	KEGG
0.00184	0.0193	Pathways in cancer	KEGG
0.002	0.0198	Dilated cardiomyopathy	KEGG
0.00205	0.0198	Long-term depression	KEGG
0.00226	0.0201	Salivary secretion	KEGG
0.00226	0.0201	Protein digestion and absorption	KEGG
0.00234	0.0201	Amphetamine addiction	KEGG
0.00331	0.0275	Regulation of lipolysis in adipocytes	KEGG
0.00387	0.0311	Cell adhesion molecules (CAMs)	KEGG
0.00445	0.0346	Gap junction	KEGG
0.00546	0.0411	ECM-receptor interaction	KEGG
0.00594	0.0434	Gastric acid secretion	KEGG
0.00664	0.0471	Ras signaling pathway	KEGG
0.00926	0.0638	Melanoma	KEGG
0.0104	0.0678	PPAR signaling pathway	KEGG
0.0104	0.0678	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	KEGG
0.0116	0.0735	Ovarian steroidogenesis	KEGG

0.0176	0.109	Insulin secretion	KEGG
0.0192	0.116	Breast cancer	KEGG
0.0211	0.124	Vascular smooth muscle contraction	KEGG
0.0235	0.135	Axon guidance	KEGG
0.0256	0.144	Proteoglycans in cancer	KEGG
0.0274	0.15	Malaria	KEGG
0.0287	0.154	Inflammatory mediator regulation of TRP channels	KEGG
0.0301	0.158	MAPK signaling pathway	KEGG
0.0315	0.161	Hypertrophic cardiomyopathy (HCM)	KEGG
0.0324	0.162	Focal adhesion	KEGG
0.0337	0.162	Melanogenesis	KEGG
0.0337	0.162	Long-term potentiation	KEGG
0.0346	0.163	Amyotrophic lateral sclerosis (ALS)	KEGG
0.0391	0.181	Regulation of actin cytoskeleton	KEGG
0.0398	0.181	Dopaminergic synapse	KEGG
0.0448	0.2	Pancreatic secretion	KEGG