

A common variant at the 14q32 endometrial cancer risk locus activates *AKT1* through YY1 binding

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ABSTRACT

A recent meta-analysis of multiple genome-wide association and follow-up endometrial cancer case-control datasets identified a novel genetic risk locus for this disease at chromosome 14q32.33. To prioritize the functional SNP(s) and target gene(s) at this locus we employed an *in silico* fine-mapping approach using genotyped and imputed SNP data for 6,608 endometrial cancer cases and 37,925 controls of European ancestry. Association and functional analyses provide evidence that the best candidate causal SNP is rs2494737. Multiple experimental analyses show that SNP rs2494737 maps to a silencer element located within *AKT1*, a member of the PI3K/AKT/MTOR intracellular signalling pathway activated in endometrial tumors. The rs2494737 risk *A* allele creates a YY1 transcription factor-binding site and abrogates the silencer activity in luciferase assays, an effect mimicked by transfection of YY1 siRNA. Our findings suggest YY1 is a positive regulator of *AKT1*, mediating the stimulatory effects of rs2494737 increasing endometrial cancer risk. Identification of an endometrial cancer risk allele within a member of the PI3K/AKT signaling pathway, more commonly activated in tumors by somatic alterations, raises the possibility that well tolerated inhibitors targeting this pathway could be candidates for evaluation as chemopreventive agents in individuals at high risk of developing endometrial cancer.

INTRODUCTION

Endometrial cancer [MIM: 608089] (cancer of the lining of the uterine corpus) is the fourth most diagnosed cancer in women in Europe and North America.^{1, 2} To date, analyses of multiple genome-wide association study (GWAS) and follow-up datasets, comprising up to 7,737 endometrial cancer cases and 37,144 controls, have identified seven risk loci at genome-wide significance for this disease, including *HNF1B* [MIM: 189907],^{3, 4} *CYP19A1* [MIM: 107910],⁵ and novel loci on chromosomes 13q22.1, 6q22.31, 8q24.21, 15q15.1 and 14q32.33.⁶ The lead SNP at the 14q32.33 locus, rs2498796, represents a single association signal located in the region of the *AKT1* [MIM: 164730] oncogene.⁶ *AKT1* is a member of the PI3K/AKT/MTOR intracellular signalling pathway affecting cell survival and proliferation.⁷ This gene is of particular interest for endometrial cancer as increased PI3K/AKT/MTOR signalling is a common occurrence in endometrial tumors, and in aggressive subtypes in particular.⁸ Somatic alterations in one or more members of the PI3K/AKT/MTOR signalling pathway are common, with *PTEN* [MIM: 601728] as the most frequently altered gene.⁹ Moreover, high *PIK3CA* [MIM: 171834] copy number and elevated levels of phosphorylated AKT have been associated with aggressive disease.^{8, 10, 11} Our previous bioinformatic analysis indicated that rs2498796 and other SNPs in high linkage disequilibrium (LD) with this SNP may also regulate other nearby genes *SIVA1* [MIM: 605567], *ZBTB42* [MIM: 613915], *ADSSL1* [MIM: 612498] and *INF2* [MIM: 610982].⁶ Here, we detail *in silico* fine-mapping and bioinformatic investigation of an expanded set of genotyped and imputed SNPs at 14q32.33, derived from the meta-analysis dataset described above, and multiple laboratory analyses to identify the functional SNP(s) and target gene(s) increasing endometrial cancer risk at this locus.

MATERIAL AND METHODS

Previously, meta-analysis of data for 7,737 endometrial cancer cases and 37,144 controls of European ancestry from three GWAS datasets (ANECS, SEARCH and NSECG) and two follow-up datasets (iCOGs and NSECG Phase 2) identified rs2498796 (OR=1.12 for the minor A allele, 95% CI:1.07-1.17, p-value= 3.55×10^{-8}) as the top SNP representing a single association signal at the 14q32.33 endometrial cancer risk locus.⁶ For the current study we employed an *in silico* fine-mapping approach¹² previously used to fine-map other endometrial cancer risk loci,^{4, 5, 13, 14} focussing on the 1Mb region surrounding rs2498796 (bases 104,743,220-105,743,220; NCBI build 37/hg19 assembly). The current analysis utilized genotyped and imputed SNP data for the three GWAS (ANECS, SEARCH and NSECG) and the iCOGs follow-up datasets and included a total of 6,608 endometrial cancer cases and 37,925 controls (details of these datasets can be found in ^{4,5}). The Cheng et al. analysis had included a total of 420 genotyped and imputed SNPs with minor allele frequencies (MAF) $\geq 1\%$ and information scores ≥ 0.9 per dataset within the focal region.⁶ To expand the search for potentially functional SNPs we considered all genotyped and imputed SNPs (N=2,922) with MAF $\geq 1\%$ and information scores ≥ 0.4 per dataset. As described previously⁴, regional imputation to the 1000 Genomes v3 2012 release was conducted separately for each of the four datasets, based on inference panels of SNPs typed for each dataset, using IMPUTE v2.¹⁵ Association testing was performed separately for each dataset using frequentist tests with a logistic regression model in SNPTEST v2.¹⁶, and standard fixed effects meta-analysis using the beta estimates and standard errors per dataset conducted using METAL.¹⁷ The regional association plot was created using LocusZoom.¹⁸ Log-likelihood tests were used to determine the most likely causal SNPs by comparing the log-likelihoods obtained from the meta-analysis of our top SNPs ($P < 10^{-6}$) with that of the most significantly associated SNP. SNPs with odds of 100:1 or better of being the top SNP were prioritized as potential causal candidates for bioinformatic and functional analyses.^{4, 19, 20} LD between SNPs was calculated from European Phase 3 1000 Genomes data and accessed from the National Cancer Institute LDlink tool.²¹

Bioinformatic analysis

Bioinformatic analyses on SNPs prioritized by the log-likelihood tests were performed using publically available datasets from ENCODE²², which includes information such as the location of promoter and enhancer histone marks, open chromatin, bound proteins and altered motifs for the Ishikawa endometrial cancer cell line. Data from Hnisz *et al.*²³ and PreSTIGE²⁴ was accessed to identify the location of likely enhancers and their gene targets in a cell-specific context.

Expression analyses

Expression quantitative trait locus (eQTL) analyses were conducted using uterine tissue-specific data (N=70) generated by the Genotype-Tissue Expression Project (GTEx)²⁵, and SNP (Affymetrix 6.0 arrays), RNA-Seq and copy number (CNV) data for endometrial carcinoma samples (N=526) and normal tissue samples adjacent to endometrial carcinoma (N=29) obtained from restricted (SNP and RNA-Seq) and public (CNV) data portals of The Cancer Genome Atlas (TCGA).²⁶ For the TCGA data, to investigate the expression of all *AKT1* isoforms, including unannotated transcripts, unprocessed RNA-Seq FASTQ files were

adapter trimmed using cutadapt (v1.8.1) and aligned to the Ensembl²⁷ GRCh37 reference (version 70) using STAR²⁸ (v2.4.2a). RNA-SeQC²⁹ (v1.1.8.1) was used to assess sequencing quality for all aligned data. Gene and transcript counts were estimated using RSEM³⁰ (v1.2.22). Genotypes for *AKT1* region SNPs present in the 1000 Genomes v3 2012 dataset which were not present on the Affymetrix 6.0 arrays were imputed using MaCH^{31, 32} and minimac^{33, 34} software. eQTL analyses were performed on transcripts expressed in >80% of samples using Kruskal-Wallis tests adjusting for copy number and sequencing method, with Bonferroni corrected p-values <0.006 (0.05/8 transcripts per SNP) considered statistically significant.

Cell lines

Endometrial cancer cell lines Ishikawa and EN-1078D (both heterozygous for the SNPs under investigation) were grown in DMEM medium with 10% FCS and antibiotics. Cell lines were maintained under standard conditions, routinely tested for *Mycoplasma* and short tandem repeat (STR) profiled to confirm cell line identity.

Chromatin conformation capture (3C)

3C libraries were generated using *NcoI* as described previously.³⁵ 3C interactions were quantitated by real-time PCR (qPCR) using primers designed within restriction fragments (**Table S1**). All qPCR was performed on a RotorGene 6000 using MyTaq HS DNA polymerase (Bioline) with the addition of 5 mM of Syto9, annealing temperature of 66°C and extension of 30 s. 3C analyses were performed in three independent 3C libraries from each cell line with each experiment quantified in duplicate. BAC clones covering the 14q32 region were used to create artificial libraries of ligation products in order to normalize for PCR efficiency. Data were normalized to the signal from the BAC clone library and, between cell lines, by reference to a region within *GAPDH* [MIM: 138400].³⁵ All qPCR products were electrophoresed on 2% agarose gels, gel purified and sequenced to verify the 3C product.

Electromobility shift assays (EMSAs)

Gel shift assays were performed with Ishikawa and EN-1078D nuclear lysates and biotinylated oligonucleotide duplexes (**Table S2**). Nuclear lysates were prepared using the NE-PER nuclear and cytoplasmic extraction reagents (Thermo Fisher Scientific) as per the manufacturer's instructions. Total protein concentrations in nuclear lysates were determined by Bradford's method. Duplexes were prepared by combining sense and antisense oligonucleotides in NEBuffer2 (New England Biolabs) and heat annealing at 80°C for 10 min and slow cooling to 25°C for 1 hr. Binding reactions were performed in binding buffer [10% (vol/vol) glycerol, 20 mM HEPES (pH 7.4), 1 mM DTT, protease inhibitor cocktail (Roche), 0.75 µg poly(dI:dC) (Sigma-Aldrich)] with 7.5 µg of nuclear lysate. For competition assays, binding reactions were pre-incubated with 1 pmol of competitor duplex (**Table S3**) at 25°C for 10 min before the addition of 10 fmol of biotinylated oligo duplex and a further incubation at 25°C for 15 min. For gel-supershift assays, 5 µg of rabbit polyclonal YY1 antibody (Santa Cruz H-414) or C/EBP antibody (Santa Cruz sc-150) was added immediately before probe addition. The rabbit pre-immune IgG (Santa Cruz sc-2027) was used as a negative control. Reactions were separated on 10% (wt/vol) Tris-Borate-EDTA (TBE)

polyacrylamide gels (Bio-Rad) in TBE buffer at 160 V for 40 min. Duplex-bound complexes were transferred onto Zeta-Probe positively-charged nylon membranes (Bio-Rad) by semi-dry transfer at 25 V for 20 min then cross-linked onto the membranes under 254 nm ultraviolet light for 10 min. Membranes were processed with the LightShift Chemiluminescent EMSA kit (Thermo Fisher Scientific) as per the manufacturer's instructions. Chemiluminescent signals were visualized with the C-DiGit blot scanner (LI-COR).

Plasmid construction and reporter assays

Promoter-driven luciferase reporter constructs were generated by the insertion of PCR amplified fragments containing *AKT1* canonical (can), *AKT1* alternative (alt) or *ZBTB42* promoters into the *Mlu*I and *Bgl*II sites of pGL3-Basic. A 2537 bp fragment containing a Putative Regulatory Element (PRE) identified by bioinformatic analysis was generated by PCR and cloned into *Bam*HI and *Sal*I sites of the modified pGL3-promoter constructs (**Table S4**). The minor (risk-increasing) alleles of individual SNPs were introduced into the PRE sequences by overlap extension PCR or gBlocks (Integrated DNA Technologies). Sequencing of all constructs confirmed variant incorporation (Australian Genome Research Facility). Ishikawa and EN-1078D cells were transfected with equimolar amounts of luciferase reporter plasmids and 50 ng of pRL-SV40 transfection control plasmid with Lipofectamine 2000. The total amount of transfected DNA was kept constant at 600 ng for each construct by the addition of pUC19 as a carrier plasmid. Luciferase activity was measured 24 hr post-transfection by the Dual-Glo Luciferase Assay System. To correct for any differences in transfection efficiency or cell lysate preparation, *Firefly* luciferase activity was normalized to *Renilla* luciferase, and the activity of each construct was measured relative to the promoter alone construct, which had a defined activity of 1. Statistical significance was tested by log transforming the data and performing 2-way ANOVA, followed by Dunnett's multiple comparisons test in GraphPad Prism.

siRNA silencing for reporter assays

Two Silencer Select siRNAs against YY1 (siYY1; s224779) and a Silencer Select nontargeting siRNA (siCON; 4390843) were purchased from Life Technologies (Thermo Fisher Scientific). For silencing, Ishikawa cells were co-transfected with the relevant luciferase reporter plasmids and 100 nM of either YY1 or non-targeting siRNAs with Lipofectamine 2000. Luciferase assays were performed as described above after 72 hr. qPCR was performed as described previously³⁶ to validate YY1 knockdown.

Chromatin Immunoprecipitation (ChIP)

Ishikawa cells were cross-linked with 1% formaldehyde at 37°C for 10 min, rinsed once with ice-cold PBS containing 5% BSA and once with PBS, and harvested in PBS containing 1X protease inhibitor cocktail (Roche). Harvested cells were centrifuged for 2 min at 3000rpm. Cell pellets were resuspended in 0.35 mL of lysis buffer (1% SDS, 10 mM EDTA, 50 mM Tris-HCl, pH 8.1, 1X protease inhibitor cocktail) and sonicated 3 times for 15 sec at 70% duty cycle (Branson SLPt) followed by centrifugation at 13000 rpm for 15 min. Supernatants were collected and diluted in dilution buffer (1% Triton X-100, 2 mM EDTA, 150 mM NaCl, 20 mM Tris-HCl, pH 8.1). Two micrograms of antibody was prebound for 6 h

to protein G Dynabeads (Life Technologies) and then added to the diluted chromatin for overnight immunoprecipitation. The magnetic bead-chromatin complexes were collected and washed six times in RIPA buffer (50 mM HEPES [pH 7.6], 1 mM EDTA, 0.7% Na deoxycholate, 1% NP-40, 0.5 M LiCl), then twice with TE buffer. To reverse the cross-linking, the magnetic bead complexes were incubated overnight at 65°C in elution buffer (1% SDS, 0.1 M NaHCO₃). DNA fragments were purified using a QIAquick Spin Kit (Qiagen). For qPCR, 2.0uL from a 100uL immunoprecipitated chromatin extraction and 40 cycles of amplification were used. All PCR products were sequenced by Sanger sequencing (AGRF). Antibodies used were anti-NFκB p50 (06-886), anti-YY1 (sc-1703-X) and control IgG (sc-2027). ChIP primers are listed in **Table S5**.

RESULTS

Association and likelihood testing at the 14q32.33 endometrial cancer risk locus prioritizes three SNPs for follow-up

A total of 2922 SNPs with MAF $\geq 1\%$ and information scores ≥ 0.4 per endometrial cancer dataset were included in the fine-mapping analysis, representing 76.6% of the SNPs with a MAF $\geq 1\%$ in the 1000 Genomes 2012 reference panel in this region (hg19 chr14: 104,743,220-105,743,220; **Table S6**). Considering SNPs correlated ($r^2 > 0.2$) with rs2498796, the previously reported top endometrial cancer risk SNP at this locus,⁶ coverage was good, with $>94\%$ of correlated SNPs in the same 1000 Genomes reference panel represented in each dataset.

Association and log-likelihood tests prioritized two SNPs for bioinformatic and functional follow-up: rs2498794 (OR=1.13, 95% CI 1.09-1.17, p-value 8.7×10^{-9}) and rs2494737 (OR=1.13, 95% CI 1.08-1.17, p-value 2.5×10^{-7} ; **Table 1** and **Table S7**). No other SNP was significant at $P < 1 \times 10^{-4}$ in analyses conditioning on rs2498794 or rs2494737 (r^2 to each other 0.54, Table S7), confirming the single association signal at this locus (**Figure 1**). As SNP rs2498796 (p-value 1.2×10^{-6} in the current analysis, r^2 to rs2498794 0.43, and to rs2494737 0.83; **Table 1**) was the original endometrial cancer risk SNP reported for this locus, it was also included in the bioinformatic and functional analyses detailed below. Neither rs2498794 nor rs2494737 had been reported in our previous genome-wide analysis because of the more stringent imputation threshold used in that study

The top candidate SNPs fall within a putative regulatory element (PRE) that frequently interacts with *AKT1* and *ZBTB42* promoter regions

Analysis of *cis* enhancer-gene interactions using data from Hnisz *et al*²³ and PreSTIGE²⁴ identified *AKT1*, *ZBTB42*, *SIVA1*, *ADSSL1* and *INF2* as potential candidate target genes of a PRE located in the region containing the top candidate SNPs (**Figure 2**). To determine the target gene(s) of the PRE, we performed chromosome conformation capture (3C) using an anchor primer within the PRE and primers within restriction fragments spanning all protein coding gene promoters within 2Mb of the PRE. The results showed that the PRE frequently interacted with a canonical and alternative promoter of *AKT1* and the *ZBTB42* promoter in both Ishikawa and EN-1078D endometrial cancer cells (**Figure 3a,b**). To assess any potential impact of SNP rs2494737 on chromatin looping, allele-specific 3C was performed in

heterozygous Ishikawa cell lines. A primer was designed to incorporate the rs2494737 into the 3C PCR products, which were then Sanger sequenced. The sequence profiles indicate that the cancer risk- and non-risk-associated rs2494737 alleles form loops with the *AKT1* and *ZBTB42* promoters with equal efficiencies (**Figure S1**). No significant interactions were detected between the PRE and other flanking genes including *SIVAI*, *ADSSL1*, *INF2* and *CEPB170B* (**Figure 3a** and **Figure S2**).

SNP rs2494737 affects the regulatory capability of the PRE on *AKT1* promoter regions

The regulatory capability of the PRE, combined with the effects of candidate SNPs, was examined in luciferase reporter assays in Ishikawa and EN-1078D cell lines. PRE constructs containing the reference (common, protective) alleles of the three candidate SNPs significantly reduced their associated target gene promoter activities, suggesting that the PRE can act as a transcriptional silencer (**Figure 4** and **Figure S3**). Inclusion of the minor (risk-increasing) allele of rs2494737 significantly increased the canonical and alternative *AKT1* promoter activities in both cell lines, but had no effect on the *ZBTB42* promoter. In contrast, inclusion of the minor (risk-increasing) alleles of SNPs rs2498796 and rs2498794 had no significant effects on *AKT1* or *ZBTB42* promoter activities (**Figure 4** and **Figure S3**).

The risk allele of SNP rs2494737 binds the YY1 transcription factor

We used bioinformatic analyses and functional studies to examine DNA-protein interactions for the three candidate SNPs. *In silico* prediction tools including HaploReg³⁷ and Alibaba2³⁸ predicted all three SNPs to alter transcription factor (TF) binding (**Table S8** and **Figure S4**). We performed electrophoretic mobility shift assays (EMSA) to assess binding of TFs to the common (protective) and minor (risk-increasing) alleles of each of these SNPs and showed allele-specific protein binding for rs2494737 and rs2498796 (**Figure 5a** and **Figure S5**). Competition with TF binding sites suggested that YY1 binds to the minor (risk-increasing) allele of rs2494737 and NF-κB binds to the common allele of rs2498796 (**Figure 5b** and **Figure S5**). No other predicted TFs were able to compete for binding at either site, including CEBPA, AP2 and CREB (**Figure S5**). Supershift assays using anti-YY1 antiserum indicated that the protein binding the minor allele of rs2494737 is likely to be YY1 (**Figure S6**). Chromatin immunoprecipitation (ChIP) in heterozygous Ishikawa cells confirmed occupancy of YY1 binding *in vivo* and showed it is preferentially recruited to the minor *A* (risk-increasing) allele of rs2494737 (**Figure 5c,d** and **Figure S7**). The importance of YY1 binding was confirmed in cotransfection assays that showed that two independent siRNAs against YY1 repressed the promoter activation in the presence of the minor *A* allele of rs2494737 (**Figure 5e** and **Figure S8**). We found no evidence of CEBPA binding to the rs2494737 site or NF-κB binding to the rs2498796 site *in vivo*.

Gene expression analysis in uterine tissue

Association between SNPs in the *AKT1* region and *AKT1* mRNA expression was investigated in both normal and endometrial tumor tissue. In the GTEx dataset, with the three candidate SNPs as input, rs2497896 was associated with increased *AKT1* expression in normal uterine tissue (sample N=70, $P=0.01$, **Figure S9**), but no eQTL effect was detected for rs2494737 or rs2498794, suggesting a stochastic effect due to the reasonably small sample size as these

SNPs are in moderate to high LD with each other. Performing an eQTL search for *AKT1* in uterine tissue returned no results. However, including all GTEx tissues revealed all three candidate SNPs, and others in moderate to high LD, to be highly significantly associated with *AKT1* expression in thyroid tissue (N=278; rs2494737=3.6x10⁻¹⁴, rs2498796=5.10x10⁻²⁵, and rs2498794=6.1x10⁻¹⁹; **Table S7**), indicating these SNPs are eQTLs for *AKT1* in some cellular contexts. In the TCGA datasets, no SNP in the *AKT1* region was associated with differential *AKT1* expression of any isoform in normal endometrial tissue (N=29) or in endometrial tumors (N=526; **Figure S10**).

DISCUSSION

In the largest association study for endometrial cancer to date, a recent meta-analysis of five GWAS and follow-up datasets revealed the presence of one multi-variant haplotype at the 14q32.33 chromosomal locus associated with the risk of this cancer.⁶ In consideration of the fact that our genotyping platforms were not specifically designed for fine-mapping of this region, we conducted *in silico* fine-mapping of the 14q32 region using SNPs with imputation scores down to 0.4. We identified two SNPs as most likely to be the causal SNPs increasing endometrial cancer risk in this region: SNPs rs2498794 and rs2494737, in moderate and high LD, respectively, with the original hit at this locus rs2498796.⁶ Multiple laboratory analyses then confirmed that rs2494737 has a functional impact on the *AKT1* oncogene, a gene of potential biological relevance to endometrial cancer risk as other PI3K pathway mutations have been detected in precursor lesions of complex atypical endometrial hyperplasia.³⁹

Our fine-mapping, together with multiple lines of bioinformatic and experimental evidence indicate that rs2494737 is the functional SNP most likely to be relevant for endometrial cancer at the 14q32 risk locus. However, additional bioinformatic analyses indicated multiple regulatory elements across the region that contained several less significantly risk-associated SNPs. Additionally, our SNP coverage of the region was not complete, although ~98% of SNPs in at least moderate LD ($r^2 > 0.2$), and 100% of SNPs in high LD ($r^2 > 0.8$), with rs2498796 in the 1000 Genomes 2012 panel were also present in our datasets, and imputed to high quality scores (>0.71). Therefore, we cannot rule out the possibility that additional SNPs exert effects on *AKT1* expression via alternative mechanisms. For example, at the well-characterized 8q24 risk locus, multiple risk-associated enhancers interact with *MYC* in a tissue-specific manner.⁴⁰ Furthermore, a few recent studies have indicated that risk-associated SNPs may also influence epigenetic features,^{41, 42} adding yet another layer of complexity to the control of gene expression.

Publicly available enhancer data from multiple cell types indicate that the region harboring rs2494737 may target a number of genes in the 14q32 region, some of which are highly plausible endometrial cancer candidate genes. Our 3C analyses show that in endometrial tumor cells the rs2494737 region specifically targets *AKT1* and *ZBTB42*, while luciferase assays showed that the rs2494737 minor *A* (risk-increasing) allele affects only *AKT1*, increasing the activity of both the canonical and an alternative promoter. Therefore, we expect the causal risk allele to result in increased expression of one or more *AKT1* isoforms *in vivo*. Although we observed no significant effect of the rs2494737 minor allele on overall

or isoform-specific *AKT1* expression in normal uterine or endometrial tumor tissue, there are multiple possible explanations. One reason could be that the risk allele affects *AKT1* expression in endometrial epithelial cells that represent only a fraction of the total cells in a normal uterine sample, which is comprised of substantially more endometrial stromal cells as well as underlying myometrium. Any effect on expression may also occur only in specific cellular contexts. Further, the lack of association in the normal tissue sample sets examined may also be due to low power, with only 47% and 23% power to detect an effect of a SNP (MAF 0.3) explaining even 5% of the variance in *AKT1* expression in the GTEx and TCGA datasets, respectively. We had 99.9% power to detect the same effect in the larger (N=526) endometrial tumor dataset, although here any eQTL effect may be difficult to detect due to the overall increase in *AKT1* expression seen in endometrial tumor cells in general. The apparent discrepancy between eQTL results and our *in vitro* findings is not unprecedented: functional SNPs in the *CCND1* [MIM: 168461]³⁶ and *MYC* [MIM: 190080]⁴³ genes show no association with gene expression in human tumor cells, although one *MYC* region SNP (rs6983267) has been demonstrated to have a functional effect *in vivo*.⁴³

AKT1, a serine/threonine kinase highly expressed in the endometrium,⁴⁴ regulates many processes including cell metabolism, proliferation, survival, growth and angiogenesis⁴⁵ and is already of considerable interest as a potential therapeutic target for endometrial cancer.^{9,46} Activation of the PI3K/AKT/mTOR intracellular signalling pathway, of which AKT1 is a member, occurs in numerous cancers^{9, 45} and up to 80% of endometrial tumors.⁴⁷ This pathway activation has been linked to somatic mutations and copy number alterations in various PI3K/AKT/mTOR pathway genes, including inactivating mutations and deletion of the *PTEN* tumor-suppressor gene and activating mutations or amplifications in the *PIK3RI* [MIM: 171833] and/or *PIK3CA* genes.⁴⁸ *AKT1* mutations are rare, with an oncogenic c.49G>A (p.Glu17Lys) mutation occurring in only ~2% of endometrial tumors,^{10, 11} and activation is thought to result from the concomitant loss or activation of upstream pathway proteins.⁴⁸

Our results indicate a possible additional mechanism whereby the presence of a common SNP allele results in increased *AKT1* transcriptional activity mediated through YY1 and results in an increased risk of endometrial cancer. YY1 is overexpressed in numerous cancers, including breast [MIM: 114480], prostate [MIM: 176807] and cervical cancers [MIM: 603956],⁴⁹ and was recently demonstrated to be over-expressed particularly in early stage (I and II) endometrial tumors, indicating this transcription factor could be a molecular marker of early tumor development.⁵⁰ Of note, YY1 knockdown using small interfering RNA (siRNA) and small hairpin RNA (shRNA) reduced YY1 protein levels, decreased cell proliferation and reduced cell motility of the AN3CA endometrial cancer cell line, while siYY1 injected directly into xenograft tumors in mice delayed endometrial tumor growth.⁵⁰ Although these data would suggest YY1 is a potential therapeutic target, transcription factors are notoriously hard to target with small molecules. The data presented here suggests that YY1 overexpression is oncogenic in part through upregulation of AKT expression, which is a signalling pathway that is more amenable to drug targeting.⁵¹

Activation of the AKT1 protein requires translocation to the plasma membrane followed by phosphorylation of the T308 and S473 residues: high levels of p-AKT1 are a marker of poor prognosis in endometrial and other cancers.^{8, 52, 53} A large number of inhibitors targeting mTOR and/or PI3K have been tested in early clinical trials in multiple tumor types, however, toxicity issues have complicated their ongoing development and many have not been taken forward into large phase III trials. Several AKT inhibitors are also in development, and initial clinical activity recently reported in several different solid tumor types including breast, lung and gynaecological tumors carrying the AKT1 c.49G>A (p.Glu17Lys) hotspot mutation.^{54, 55} There is a current emphasis on reducing systemic toxicities by optimising scheduling as well as evaluating nanoparticles to target these agents to tumors and reduce systemic exposure,⁵⁶ nonetheless it is unlikely that AKT inhibitors developed for treatment of metastatic disease will have an acceptable toxicity profile to be used as chemopreventive agents.

A promising alternative may be the re-positioning of the type 2 diabetes drug metformin. This drug has multiple mechanisms of action targeting both metabolism, by decreasing circulating glucose levels, as well as altering intracellular signalling by activating AMPK.⁵⁷ Activation of AMPK has been shown to inhibit mTOR, a downstream effector of PI3K/AKT signalling. Metformin is currently being evaluated in the adjuvant treatment of endometrial cancer⁵⁸ as well as large chemoprevention trials (e.g. the Diabetes Prevention Program Outcomes Study). It would be interesting to determine the outcome analyses from these large-scale chemoprevention trials if patients were genotyped and retrospectively stratified based on their germline *AKT1* risk alleles. Perhaps the ability of metformin to blunt mTOR signalling would be reflected in a greater decrease in endometrial cancer incidence in the *AKT1* SNP carriers treated with metformin.

Although our data indicate that *AKT1* is the likely target gene, it is possible that these SNPs also exert functional effects through long-range control of other genes under different conditions of cell activation or in other cell types, including nearby *SIVA1*, *ZBTB42*, *ADSSL1* and *INF2*. Notably, *SIVA1* is reported to activate and suppress apoptosis, a process dysregulated in cancer. Among other roles, *SIVA1* can inhibit p53 tumor suppressor functions and is mutated in up to 90% of aggressive endometrial tumors.^{26, 59} *ZBTB42* (zinc finger and BTB domain containing 42) is a poorly characterized member of the C₂H₂ zinc finger protein family⁶⁰. It is highly expressed in subsynaptic nuclei in skeletal muscles underlying the neuromuscular junctions,⁶⁰ and may be involved in muscle development.⁶¹ *ADSSL1* (Adenylosuccinate Synthase Like 1) is a muscle isozyme that is selectively deleted in carcinogen-induced mouse lung adenocarcinomas.⁶² While *INF2* (Inverted Formin 2) encodes a member of the diaphanous-related formin family, which is involved in remodelling the actin and microtubule cytoskeltons.⁶³ Mutations in this gene are reported to cause a form of autosomal-dominant focal and segmental glomerulosclerosis and Charcot-Marie-Tooth disease.^{64, 65}

In conclusion, we have identified a common SNP allele associated with endometrial cancer risk that functions to increase *AKT1* expression through YY1-mediated transcription. Identification of an endometrial cancer risk allele within a member of the PI3K/AKT

signaling pathway, more commonly activated in tumors by somatic alterations, raises the possibility that well tolerated inhibitors targeting this pathway could be candidates for evaluation as chemopreventive agents in individuals at high risk of developing endometrial cancer.

SUPPLEMENTARY TEXT

Supplementary text for online publication is provided in the additional file:
Painter_et al_Supplementary_Text.doc

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WEB RESOURCES

Online Mendelian Inheritance in Man (OMIM), <http://www.omim.org/>
National Cancer Institute LDlink tool, <http://analysistools.nci.nih.gov/LDlink/>
1000 Genomes, <http://browser.1000genomes.org/index.html>
Encyclopedia of DNA Elements at UCSC, <http://genome.ucsc.edu/ENCODE/>
Gene Expression Omnibus (GEO), <http://www.ncbi.nlm.nih.gov/geo/>
The Cancer Genome Atlas, www.cancergenome.nih.gov
PreSTIGE, <http://genetics.case.edu/prestige/>
LDlink, <http://analysistools.nci.nih.gov/LDlink/>
GTEx, www.gtexportal.org
QTL Genetic Power Calculator, <http://pngu.mgh.harvard.edu/~purcell/cgi-bin/qtlassoc.cgi>

REFERENCES

1. Ferlay J, S.I., Ervik M, Dikshit R, Eser S, Mathers C, Rebelo M, Parkin DM, Forman D, Bray, F. (2013). GLOBOCAN 2012 v1.0, Cancer Incidence and Mortality Worldwide: IARC CancerBase No. 11 [Internet]. Lyon, France: International Agency for Research on Cancer.
2. Ferlay, J., Soerjomataram, I., Dikshit, R., Eser, S., Mathers, C., Rebelo, M., Parkin, D.M., Forman, D., and Bray, F. (2015). Cancer incidence and mortality worldwide: sources, methods and major patterns in GLOBOCAN 2012. *Int J Cancer* 136, E359-386.
3. Spurdle, A.B., Thompson, D.J., Ahmed, S., Ferguson, K., Healey, C.S., O'Mara, T., Walker, L.C., Montgomery, S.B., Dermitzakis, E.T., Australian National Endometrial Cancer Study, G., et al. (2011). Genome-wide association study identifies a common variant associated with risk of endometrial cancer. *Nat Genet* 43, 451-454.
4. Painter, J.N., O'Mara, T.A., Batra, J., Cheng, T., Lose, F.A., Dennis, J., Michailidou, K., Tyrer, J.P., Ahmed, S., Ferguson, K., et al. (2015). Fine-mapping of the HNF1B

- multicancer locus identifies candidate variants that mediate endometrial cancer risk. *Hum Mol Genet* 24, 1478-1492.
5. Thompson, D.J., O'Mara, T.A., Glubb, D.M., Painter, J.N., Cheng, T., Folkerd, E., Doody, D., Dennis, J., Webb, P.M., Gorman, M., et al. (2015). CYP19A1 fine-mapping and Mendelian randomisation: estradiol is causal for endometrial cancer. *Endocr Relat Cancer*.
 6. Cheng, T., Thompson, D.J., O'Mara, T.A., Painter, J.N., Glubb, D.M., Flach, S., Lewis, A., French, J.D., Freeman-Mills, L., Church, D., et al. (2016). Five endometrial cancer risk loci identified through genome-wide association analysis. *Nat Genet* (DOI: 10.1038/ng.3562).
 7. Cantley, L.C. (2002). The phosphoinositide 3-kinase pathway. *Science* 296, 1655-1657.
 8. Salvesen, H.B., Carter, S.L., Mannelqvist, M., Dutt, A., Getz, G., Stefansson, I.M., Raeder, M.B., Sos, M.L., Engelsen, I.B., Trovik, J., et al. (2009). Integrated genomic profiling of endometrial carcinoma associates aggressive tumors with indicators of PI3 kinase activation. *Proc Natl Acad Sci U S A* 106, 4834-4839.
 9. Slomovitz, B.M., and Coleman, R.L. (2012). The PI3K/AKT/mTOR pathway as a therapeutic target in endometrial cancer. *Clin Cancer Res* 18, 5856-5864.
 10. Shoji, K., Oda, K., Nakagawa, S., Hosokawa, S., Nagae, G., Uehara, Y., Sone, K., Miyamoto, Y., Hiraike, H., Hiraike-Wada, O., et al. (2009). The oncogenic mutation in the pleckstrin homology domain of AKT1 in endometrial carcinomas. *Br J Cancer* 101, 145-148.
 11. Cohen, Y., Shalmon, B., Korach, J., Barshack, I., Fridman, E., and Rechavi, G. (2010). AKT1 pleckstrin homology domain E17K activating mutation in endometrial carcinoma. *Gynecol Oncol* 116, 88-91.
 12. Barrett, J.H., Taylor, J.C., Bright, C., Harland, M., Dunning, A.M., Akslen, L.A., Andresen, P.A., Avril, M.F., Azizi, E., Bianchi Scarra, G., et al. (2015). Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. *Int J Cancer* 136, 1351-1360.
 13. Carvajal-Carmona, L.G., O'Mara, T.A., Painter, J.N., Lose, F.A., Dennis, J., Michailidou, K., Tyrer, J.P., Ahmed, S., Ferguson, K., Healey, C.S., et al. (2015). Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. *Hum Genet* 134, 231-245.
 14. O'Mara, T.A., Glubb, D.M., Painter, J.N., Cheng, T., Dennis, J., Australian National Endometrial Cancer Study, G., Attia, J., Holliday, E.G., McEvoy, M., Scott, R.J., et al. (2015). Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. *Endocr Relat Cancer* 22, 851-861.
 15. Howie, B.N., Donnelly, P., and Marchini, J. (2009). A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. *PLoS Genet* 5, e1000529.
 16. Marchini, J., Howie, B., Myers, S., McVean, G., and Donnelly, P. (2007). A new multipoint method for genome-wide association studies by imputation of genotypes. *Nat Genet* 39, 906-913.

17. Willer, C.J., Li, Y., and Abecasis, G.R. (2010). METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics* 26, 2190-2191.
18. Pruim, R.J., Welch, R.P., Sanna, S., Teslovich, T.M., Chines, P.S., Gliedt, T.P., Boehnke, M., Abecasis, G.R., and Willer, C.J. (2010). LocusZoom: regional visualization of genome-wide association scan results. *Bioinformatics* 26, 2336-2337.
19. Edwards, S.L., Beesley, J., French, J.D., and Dunning, A.M. (2013). Beyond GWASs: illuminating the dark road from association to function. *Am J Hum Genet* 93, 779-797.
20. Udler, M.S., Tyrer, J., and Easton, D.F. (2010). Evaluating the power to discriminate between highly correlated SNPs in genetic association studies. *Genet Epidemiol* 34, 463-468.
21. Machiela, M.J., and Chanock, S.J. (2015). LDlink: a web-based application for exploring population-specific haplotype structure and linking correlated alleles of possible functional variants. *Bioinformatics*.
22. Consortium, E.P., Birney, E., Stamatoyannopoulos, J.A., Dutta, A., Guigo, R., Gingeras, T.R., Margulies, E.H., Weng, Z., Snyder, M., Dermitzakis, E.T., et al. (2007). Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* 447, 799-816.
23. Hnisz, D., Abraham, B.J., Lee, T.I., Lau, A., Saint-Andre, V., Sigova, A.A., Hoke, H.A., and Young, R.A. (2013). Super-enhancers in the control of cell identity and disease. *Cell* 155, 934-947.
24. Corradin, O., Saiakhova, A., Akhtar-Zaidi, B., Myeroff, L., Willis, J., Cowper-Salari, R., Lupien, M., Markowitz, S., and Scacheri, P.C. (2014). Combinatorial effects of multiple enhancer variants in linkage disequilibrium dictate levels of gene expression to confer susceptibility to common traits. *Genome Res* 24, 1-13.
25. Consortium, G.T. (2013). The Genotype-Tissue Expression (GTEx) project. *Nat Genet* 45, 580-585.
26. Cancer Genome Atlas Research, N., Kandoth, C., Schultz, N., Cherniack, A.D., Akbani, R., Liu, Y., Shen, H., Robertson, A.G., Pashtan, I., Shen, R., et al. (2013). Integrated genomic characterization of endometrial carcinoma. *Nature* 497, 67-73.
27. Flicek, P., Amode, M.R., Barrell, D., Beal, K., Billis, K., Brent, S., Carvalho-Silva, D., Clapham, P., Coates, G., Fitzgerald, S., et al. (2014). Ensembl 2014. *Nucleic Acids Res* 42, D749-755.
28. Dobin, A., Davis, C.A., Schlesinger, F., Drenkow, J., Zaleski, C., Jha, S., Batut, P., Chaisson, M., and Gingeras, T.R. (2013). STAR: ultrafast universal RNA-seq aligner. *Bioinformatics* 29, 15-21.
29. DeLuca, D.S., Levin, J.Z., Sivachenko, A., Fennell, T., Nazaire, M.D., Williams, C., Reich, M., Winckler, W., and Getz, G. (2012). RNA-SeQC: RNA-seq metrics for quality control and process optimization. *Bioinformatics* 28, 1530-1532.
30. Li, B., and Dewey, C.N. (2011). RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinformatics* 12, 323.
31. Li, Y., Willer, C., Sanna, S., and Abecasis, G. (2009). Genotype imputation. *Annu Rev Genomics Hum Genet* 10, 387-406.

32. Li, Y., Willer, C.J., Ding, J., Scheet, P., and Abecasis, G.R. (2010). MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. *Genet Epidemiol* 34, 816-834.
33. Fuchsberger, C., Abecasis, G.R., and Hinds, D.A. (2014). minimac2: faster genotype imputation. *Bioinformatics*.
34. Howie, B., Fuchsberger, C., Stephens, M., Marchini, J., and Abecasis, G.R. (2012). Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. *Nat Genet* 44, 955-959.
35. Ghousaini, M., Edwards, S.L., Michailidou, K., Nord, S., Cowper-Sal Lari, R., Desai, K., Kar, S., Hillman, K.M., Kaufmann, S., Glubb, D.M., et al. (2014). Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nat Commun* 4, 4999.
36. French, J.D., Ghousaini, M., Edwards, S.L., Meyer, K.B., Michailidou, K., Ahmed, S., Khan, S., Maranian, M.J., O'Reilly, M., Hillman, K.M., et al. (2013). Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. *Am J Hum Genet* 92, 489-503.
37. Ward, L.D., and Kellis, M. (2015). HaploReg v4: systematic mining of putative causal variants, cell types, regulators and target genes for human complex traits and disease. *Nucleic Acids Res*.
38. Grabe, N. (2002). AliBaba2: context specific identification of transcription factor binding sites. *In Silico Biol* 2, S1-15.
39. Hayes, M.P., Wang, H., Espinal-Witter, R., Douglas, W., Solomon, G.J., Baker, S.J., and Ellenson, L.H. (2006). PIK3CA and PTEN mutations in uterine endometrioid carcinoma and complex atypical hyperplasia. *Clin Cancer Res* 12, 5932-5935.
40. Ahmadiyeh, N., Pomerantz, M.M., Grisanzio, C., Herman, P., Jia, L., Almendro, V., He, H.H., Brown, M., Liu, X.S., Davis, M., et al. (2010). 8q24 prostate, breast, and colon cancer risk loci show tissue-specific long-range interaction with MYC. *Proc Natl Acad Sci U S A* 107, 9742-9746.
41. Voisin, S., Almen, M.S., Zheleznyakova, G.Y., Lundberg, L., Zarei, S., Castillo, S., Eriksson, F.E., Nilsson, E.K., Bluher, M., Bottcher, Y., et al. (2015). Many obesity-associated SNPs strongly associate with DNA methylation changes at proximal promoters and enhancers. *Genome Med* 7, 103.
42. Bell, C.G., Finer, S., Lindgren, C.M., Wilson, G.A., Rakyan, V.K., Teschendorff, A.E., Akan, P., Stupka, E., Down, T.A., Prokopenko, I., et al. (2010). Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. *PLoS One* 5, e14040.
43. Sur, I.K., Hallikas, O., Vaharautio, A., Yan, J., Turunen, M., Enge, M., Taipale, M., Karhu, A., Aaltonen, L.A., and Taipale, J. (2012). Mice lacking a Myc enhancer that includes human SNP rs6983267 are resistant to intestinal tumors. *Science* 338, 1360-1363.
44. Uhlen, M., Fagerberg, L., Hallstrom, B.M., Lindskog, C., Oksvold, P., Mardinoglu, A., Sivertsson, A., Kampf, C., Sjostedt, E., Asplund, A., et al. (2015). Proteomics. Tissue-based map of the human proteome. *Science* 347, 1260419.

45. Vivanco, I., and Sawyers, C.L. (2002). The phosphatidylinositol 3-Kinase AKT pathway in human cancer. *Nat Rev Cancer* 2, 489-501.
46. Salvesen, H.B., Haldorsen, I.S., and Trovik, J. (2012). Markers for individualised therapy in endometrial carcinoma. *Lancet Oncol* 13, e353-361.
47. Cheung, L.W., Hennessy, B.T., Li, J., Yu, S., Myers, A.P., Djordjevic, B., Lu, Y., Stemke-Hale, K., Dyer, M.D., Zhang, F., et al. (2011). High frequency of PIK3R1 and PIK3R2 mutations in endometrial cancer elucidates a novel mechanism for regulation of PTEN protein stability. *Cancer Discov* 1, 170-185.
48. Fabi, F., and Asselin, E. (2014). Expression, activation, and role of AKT isoforms in the uterus. *Reproduction* 148, R85-95.
49. Castellano, G., Torrisi, E., Ligresti, G., Malaponte, G., Militello, L., Russo, A.E., McCubrey, J.A., Canevari, S., and Libra, M. (2009). The involvement of the transcription factor Yin Yang 1 in cancer development and progression. *Cell Cycle* 8, 1367-1372.
50. Yang, Y., Zhou, L., Lu, L., Wang, L., Li, X., Jiang, P., Chan, L.K., Zhang, T., Yu, J., Kwong, J., et al. (2013). A novel miR-193a-5p-YY1-APC regulatory axis in human endometrioid endometrial adenocarcinoma. *Oncogene* 32, 3432-3442.
51. Courtney, K.D., Corcoran, R.B., and Engelman, J.A. (2010). The PI3K pathway as drug target in human cancer. *J Clin Oncol* 28, 1075-1083.
52. Gungorduk, K., Ertas, I.E., Sahbaz, A., Ozvural, S., Sarica, Y., Ozdemir, A., Sayhan, S., Gokcu, M., Yilmaz, B., Sancı, M., et al. (2014). Immunolocalization of ERK1/2 and p-AKT in normal endometrium, endometrial hyperplasia, and early and advanced stage endometrioid endometrial adenocarcinoma and their prognostic significance in malignant group. *Eur J Obstet Gynecol Reprod Biol* 179, 147-152.
53. Zhu, Z., Yu, W., Fu, X., Sun, M., Wei, Q., Li, D., Chen, H., Xiang, J., Li, H., Zhang, Y., et al. (2015). Phosphorylated AKT1 is associated with poor prognosis in esophageal squamous cell carcinoma. *J Exp Clin Cancer Res* 34, 95.
54. Hyman, D.M., Smyth, L., Bedard, P.L., Oza, A., Dean, E., Armstrong, A., Lima, J., Bando, H., Kabos, P., Perez-Fidalgo, J.A., et al. (2015). AZD5363, a catalytic pan-Akt inhibitor, in Akt1 E17K mutation positive advanced solid tumors
. Molecular Targets and Cancer Therapeutics Meeting Boston Clinical trial number NCT01226316.
55. Eathiraj, S., Schwartz, B., Yu, Y., Wick, M.J., Hall, T., Chai, F., Sachdev, J., and Abbadessa, G. (2015). Targeting PI3K pathway dependent endometrial tumors with allosteric AKT inhibitors, ARQ 092 and ARQ 751 Molecular Targets and Cancer Therapeutics Meeting Boston
56. Cadzow, L., Lam, M.H., Wang, H., DeWitt, D., Pucci, V., Mo, J.-R., Lewies-Clark, E., Ferguson, H., Gindy, M., Low, S., et al. (2015). Accurins improve the pharmacokinetics, pharmacodynamics, tolerability and anti-tumor activity of the AKT inhibitor MK-2206. Molecular Targets and Cancer Therapeutics Meeting Boston
57. Rena, G., Pearson, E.R., and Sakamoto, K. (2013). Molecular mechanism of action of metformin: old or new insights? *Diabetologia* 56, 1898-1906.
58. Porta, C., Paglino, C., and Mosca, A. (2014). Targeting PI3K/Akt/mTOR Signaling in Cancer. *Front Oncol* 4, 64.

59. Wang, X., Zha, M., Zhao, X., Jiang, P., Du, W., Tam, A.Y., Mei, Y., and Wu, M. (2013). Siva1 inhibits p53 function by acting as an ARF E3 ubiquitin ligase. *Nat Commun* 4, 1551.
60. Devaney, S.A., Mate, S.E., Devaney, J.M., and Hoffman, E.P. (2011). Characterization of the ZBTB42 gene in humans and mice. *Hum Genet* 129, 433-441.
61. Patel, N., Smith, L.L., Faqeih, E., Mohamed, J., Gupta, V.A., and Alkuraya, F.S. (2014). ZBTB42 mutation defines a novel lethal congenital contracture syndrome (LCCS6). *Hum Mol Genet* 23, 6584-6593.
62. Miller, J.C., Blake, D.C., Jr., and Herzog, C.R. (2009). Adenylosuccinate synthetase 1 gene is a novel target of deletion in lung adenocarcinoma. *Mol Carcinog* 48, 1116-1122.
63. Chesarone, M.A., DuPage, A.G., and Goode, B.L. (2010). Unleashing formins to remodel the actin and microtubule cytoskeletons. *Nat Rev Mol Cell Biol* 11, 62-74.
64. Barua, M., Brown, E.J., Charoonratana, V.T., Genovese, G., Sun, H., and Pollak, M.R. (2013). Mutations in the INF2 gene account for a significant proportion of familial but not sporadic focal and segmental glomerulosclerosis. *Kidney Int* 83, 316-322.
65. Boyer, O., Nevo, F., Plaisier, E., Funalot, B., Gribouval, O., Benoit, G., Huynh Cong, E., Arrondel, C., Tete, M.J., Montjean, R., et al. (2011). INF2 mutations in Charcot-Marie-Tooth disease with glomerulopathy. *N Engl J Med* 365, 2377-2388.

FIGURE LEGENDS

Figure 1. Regional association plot for the 14q32.33 endometrial cancer risk locus. The location (Build 19) and $-\log_{10}$ p-value of the original top SNP at this locus, rs2498796,⁶ is shown in purple, all other SNPs are shown in colors corresponding to their r^2 (linkage disequilibrium) value with rs2498796.

Figure 2. Regulatory landscape at the 14q32.33 endometrial cancer risk locus. (a) The location of the candidate SNPs are represented by black ticks, and the Putative Regulatory Element (PRE) is shown as a black box. Gene structures are depicted with exons (vertical boxes) joined by introns (lines). The subset of enhancers predicted in Hnisz *et al*²³ and PreSTIGE²⁴ which overlap the candidate causal SNPs are shown as colored bars, where the color matches its predicted gene target. Regions showing histone binding (H3K4Me1, indicative of regulatory regions; H3K4Me3, indicative of promoters; and H3K27Ac, indicative of active enhancers), DNaseI hypersensitivity (indicative of open chromatin, with darker shading indicating stronger experimental signal) and transcription factor (TF) binding in multiple ENCODE cell lines are indicated at the bottom of the panel. **(b)** Zoomed-in view of the location of candidate SNPs, PRE and nearby gene promoter regions.

Figure 3. Candidate causal SNPs are located within a PRE that interacts with the *AKT1* and *ZBTB42* promoter regions. (a) 3C interaction profiles between the PRE and local genes in Ishikawa and EN-1078D endometrial cancer cell lines. The 3C anchor (which contains the PRE) is shown as a grey box and significant interactions are outlined. **(b)** Zoomed-in view of significant interactions. *AKT1* Can and *AKT1* Alt denote a canonical and alternative *AKT1* promoter (prom) region, respectively. 3C libraries were generated with *NcoI*. Graphs represent three biological replicates. Error bars represent SD. Regions cloned into reporter gene constructs are shown as grey horizontal boxes.

Figure 4. The risk allele of SNP rs2494737 enhances *AKT1* promoter activity. Luciferase reporter assays following transient transfection of Ishikawa endometrial cancer cell lines. The putative regulatory element (PRE) containing the major SNP alleles were cloned downstream of target gene promoter-driven luciferase constructs. *AKT1* can and *AKT1* alt denote a canonical and alternative *AKT1* promoter (prom) region, respectively. Minor (risk-increasing) SNP alleles were engineered into the constructs and are designated by the rs ID of the corresponding SNP. Haplotype denotes a construct that contains the minor alleles of rs2498796 and rs2494737. Error bars denote 95% confidence intervals from three independent experiments performed in duplicate. P-values were determined by 2-way ANOVA followed by Dunnett's multiple comparisons test (**P<0.01, ****p<0.0001).

Figure 5. The risk allele of rs2494737 demonstrates allele-specific YY1 binding. (a) EMSAs to detect allele-specific binding of nuclear proteins. Oligonucleotides were incubated with Ishikawa nuclear extracts. Red arrowheads show bands of different mobility detected between the common (c) and minor (risk-increasing) (m) alleles for the candidate causal SNPs **(b)** Oligonucleotides for SNP rs2494737 were incubated with Ishikawa nuclear extracts. Red arrowhead indicates the band that was competed for complex formation on the minor

(m) allele. Competitor oligonucleotides are listed above each panel and were used at 100-fold molar excess: (-) no competitor; (Neg) a non-specific competitor; (YY1) consensus binding site; (YY1m) an identical oligonucleotide but with a mutated binding site. **(c)** ChIP-qPCR on SNP rs2494737 in heterozygous Ishikawa cell lines. ChIP assays were performed with YY1 antibody or non-immune IgG, a region 3.2kb upstream of the predicted YY1-binding site served as a negative control (Control). Graphs represent two biological replicates. Error bars denote SD. P-values were determined with a two-tailed t-test (**p<0.01). **(d)** Sanger sequencing of the PCR fragment generated using primers flanking SNP rs2494737 following YY1 ChIP-qPCR and the input DNA controls. **(e)** Luciferase assays in Ishikawa cells shows the effect of YY1 siRNA silencing on the activity of the *AKT1* canonical (can) and alternative (alt) promoter regions with the PRE containing the reference T allele (can+PRE; alt+PRE) or the risk A allele (rs2494737). Error bars denote 95% confidence intervals from three independent experiments performed in duplicate. P-values were determined by 2-way ANOVA followed by Dunnett's multiple comparisons test (**p<0.01, ***p<0.001). The level of YY1 silencing is shown in **Figure S8**.

1 **Table 1. Association of the top candidate causal SNPs at chromosome 14q32.33 with endometrial cancer risk.**

SNP	Position (Build 19)	Minor allele	Common allele	MAF ^a	OR (95% CI) ^b	P-value	<i>r</i> ² to rs2498796	Likelihood ratio ^c
rs2498794	105245251	G	A	0.48	1.13 (1.09-1.17)	8.7x10 ⁻⁹	0.43	1
rs2494737	105246325	A	T	0.30	1.13 (1.08-1.17)	2.5x10 ⁻⁷	0.83	26
rs2498796	105243220	A	G	0.30	1.11 (1.07-1.16)	1.2x10 ⁻⁶	--	120

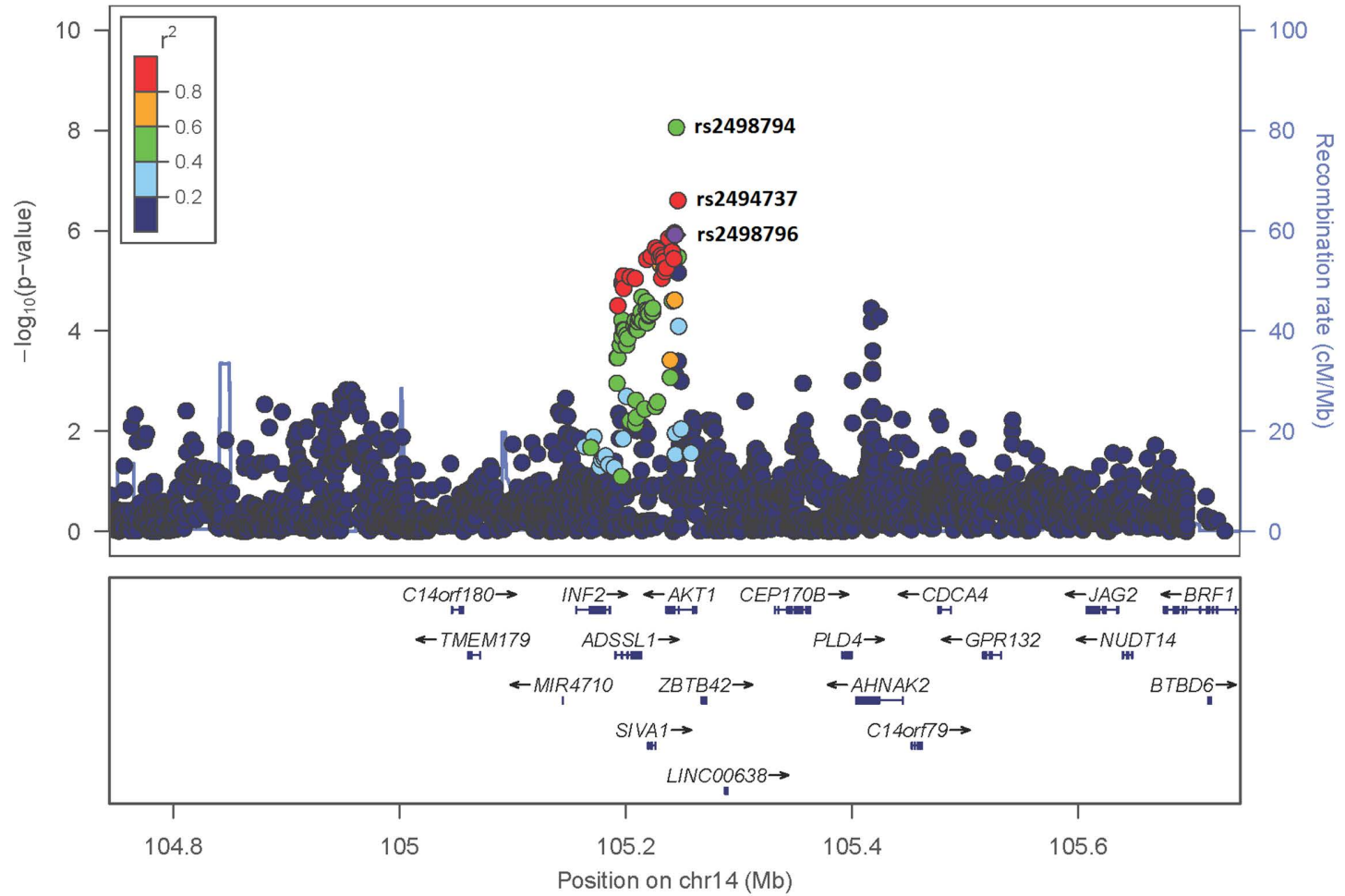
2

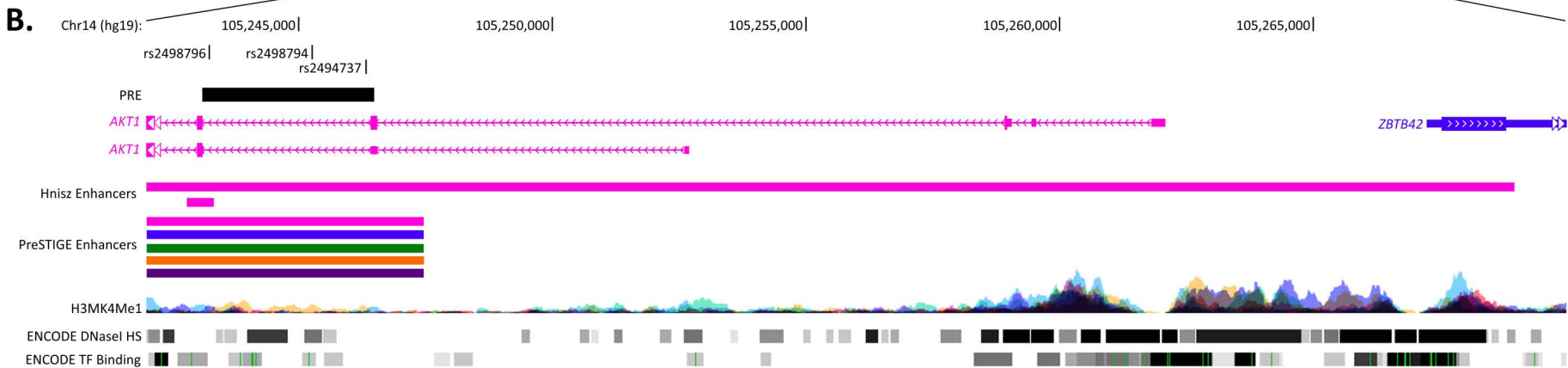
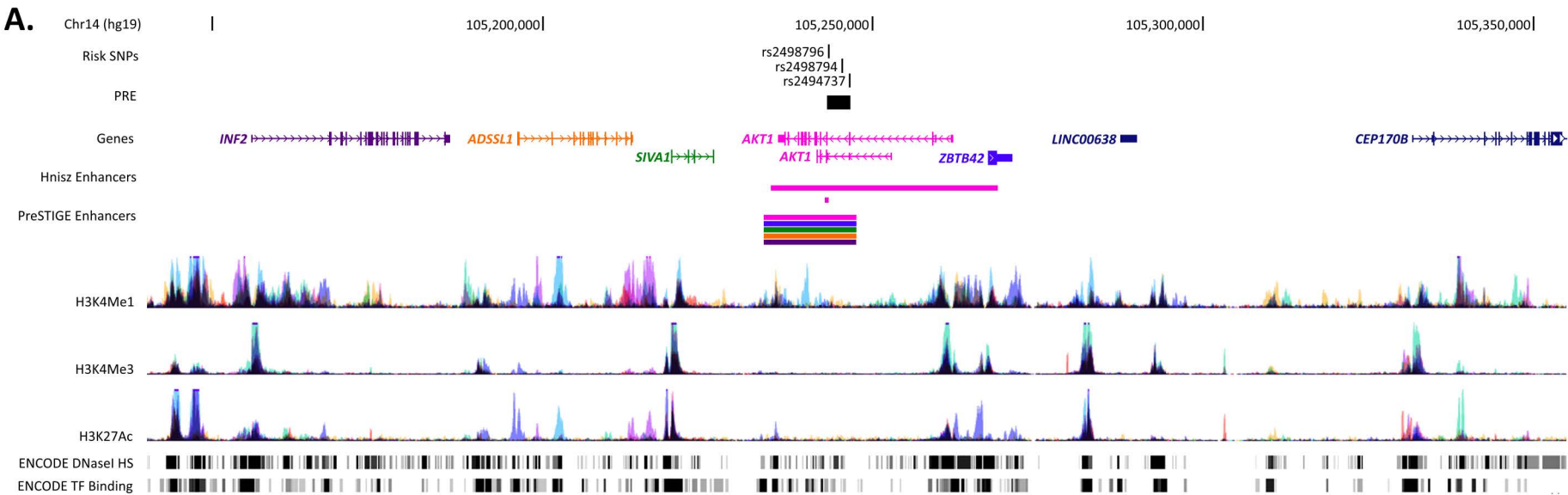
3 ^aMinor (risk-increasing) allele frequency

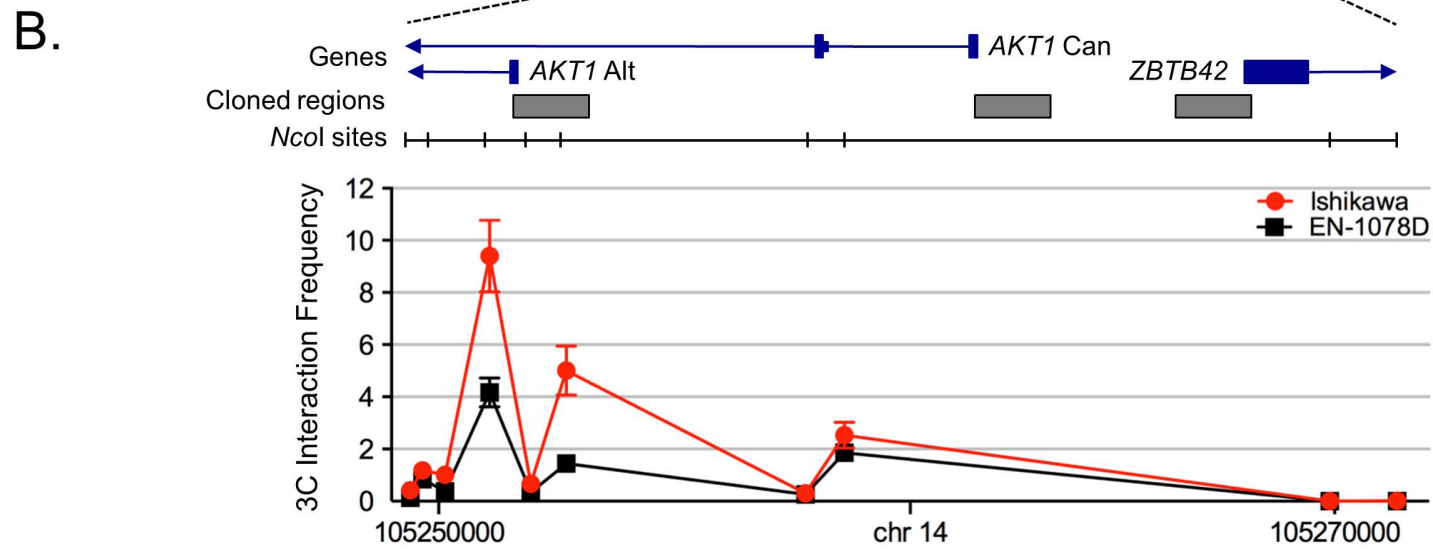
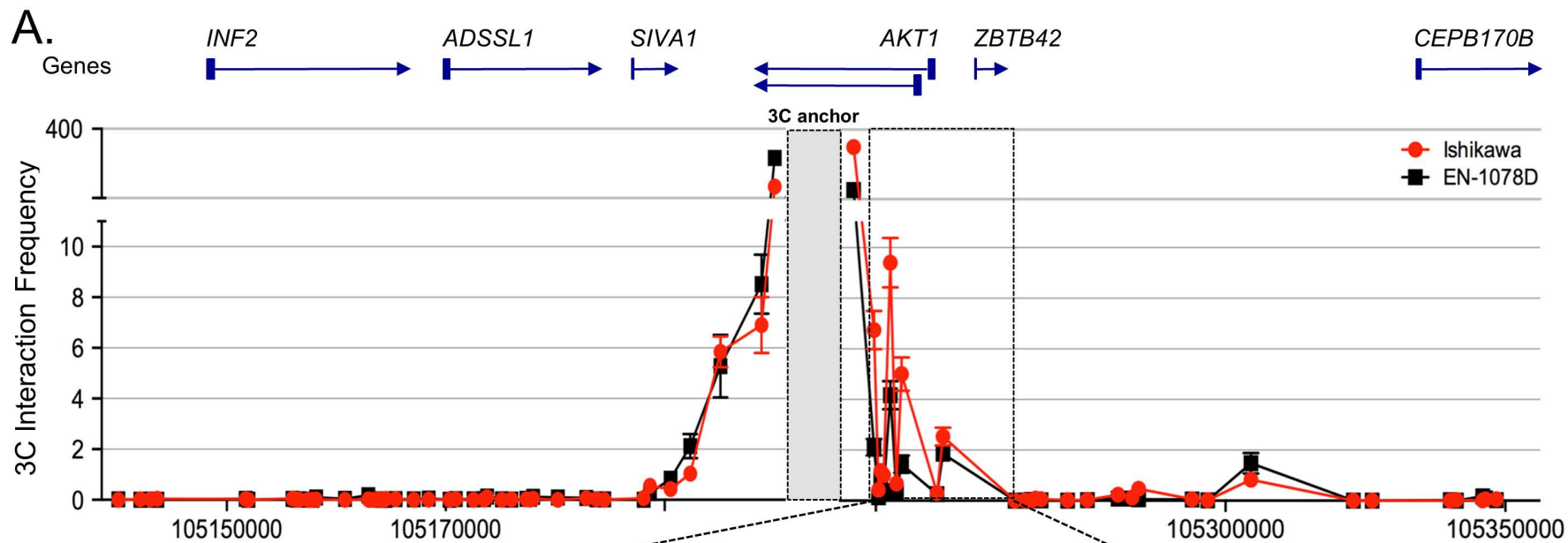
4 ^bOR for the effect allele

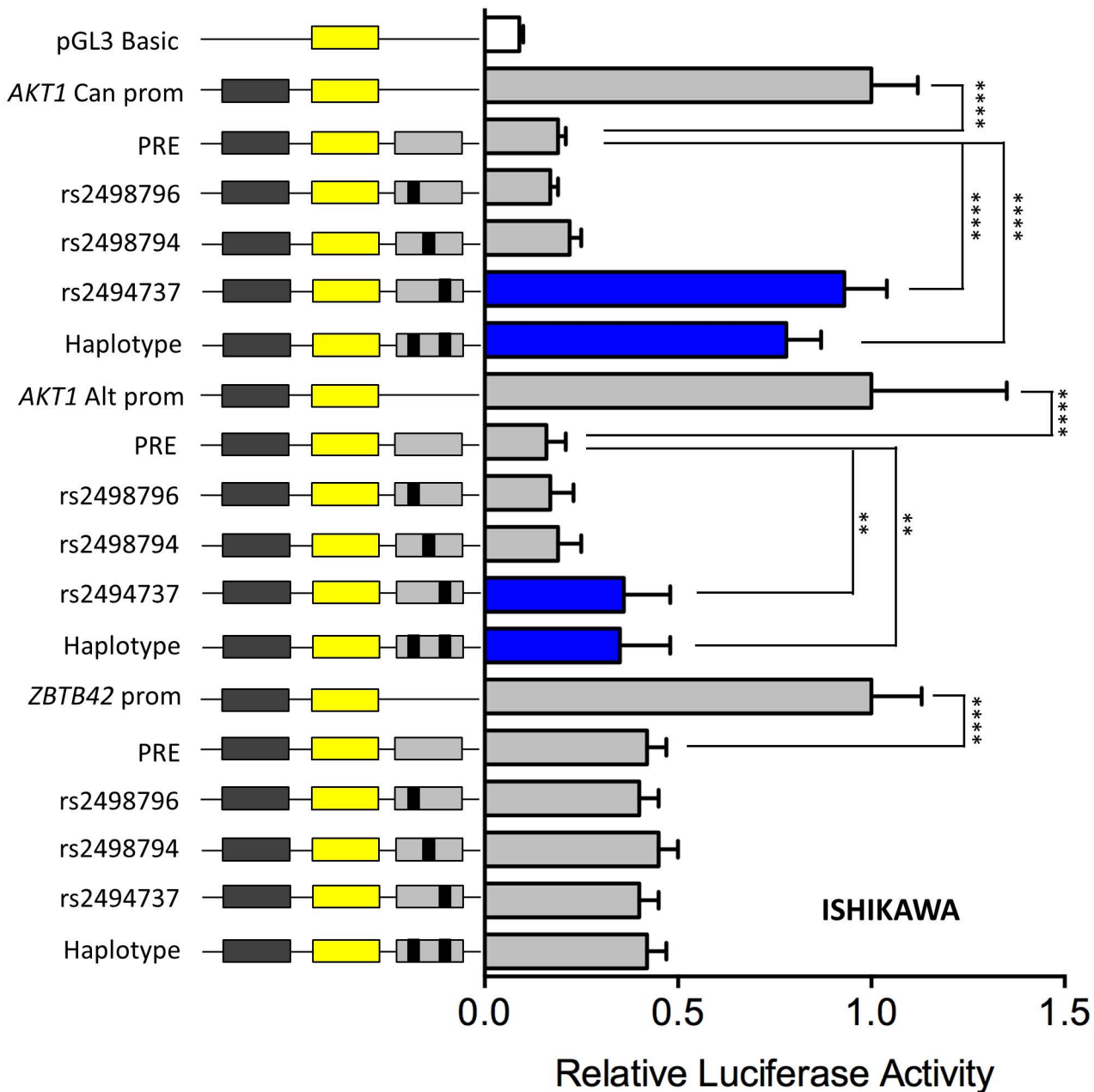
5 ^cRatio of the likelihood of rs2498794 to the likelihood of this SNP

Plotted SNPs

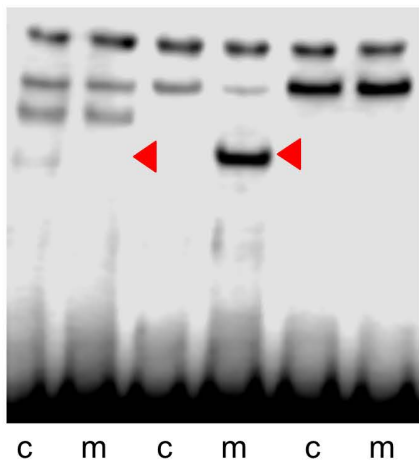




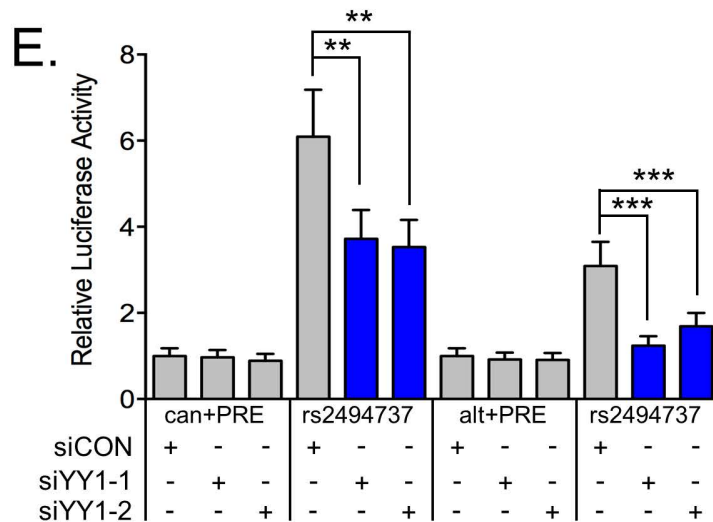
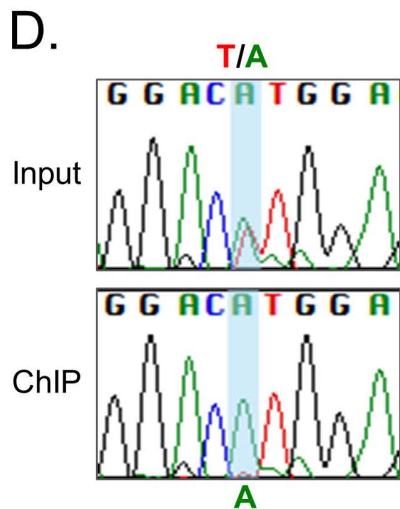
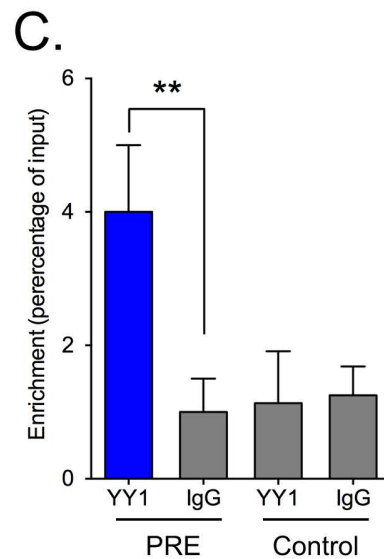
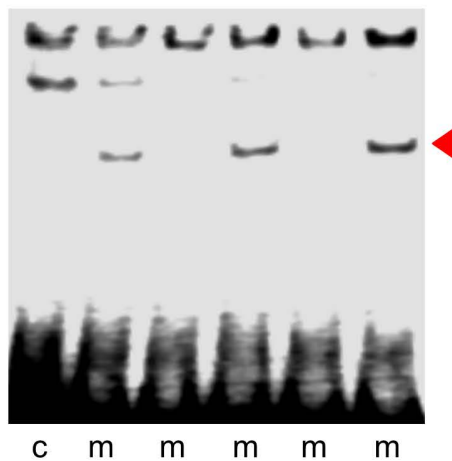




A. rs2498796 rs2494737 rs2498794



B. Self-A Neg YY1 YY1m



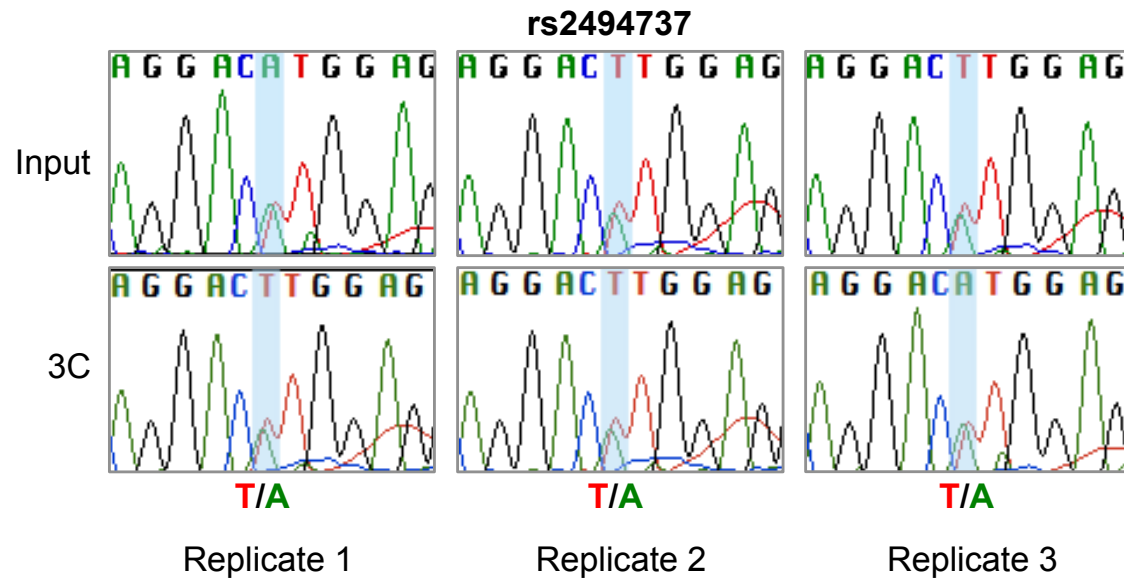


Figure S1. Allele-specific 3C in Ishikawa endometrial cancer cell lines. 3C followed by sequencing for the rs2494737-containing region in heterozygous Ishikawa endometrial cancer cells. Chromatograms represent three independent 3C libraries generated and sequenced. 3C libraries were generated with *NcoI*, with the anchor primer designed to incorporate the SNP into 3C PCR products.

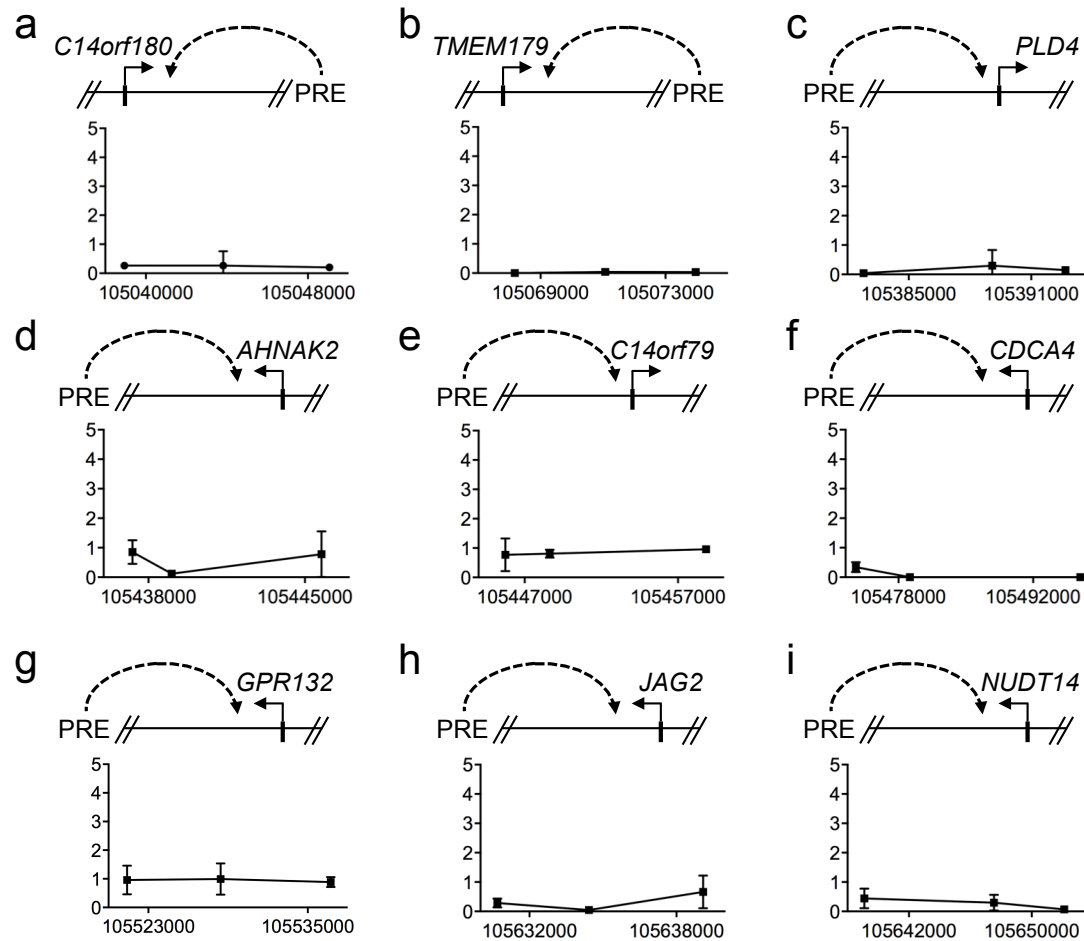


Figure S2. Chromatin interactions at 14q32 in Ishikawa endometrial cancer cell lines. 3C interaction profiles between the putative regulatory element (PRE; containing rs2498796, rs2498794 and rs2494737) and (a) *C14ORF180*, (b) *TMEM179*, (c) *PLD4*, (d) *AHNAK2*, (e) *C14ORF79*, (f) *CDCA4*, (g) *GPR132*, (h) *JAG2* and (i) *NUDT14* promoter regions. 3C libraries were generated with *Nco*I, with the anchor point set at the PRE. A physical map of the region interrogated by 3C is shown above. Graph represents three independent replicates. Error bars denote SD.

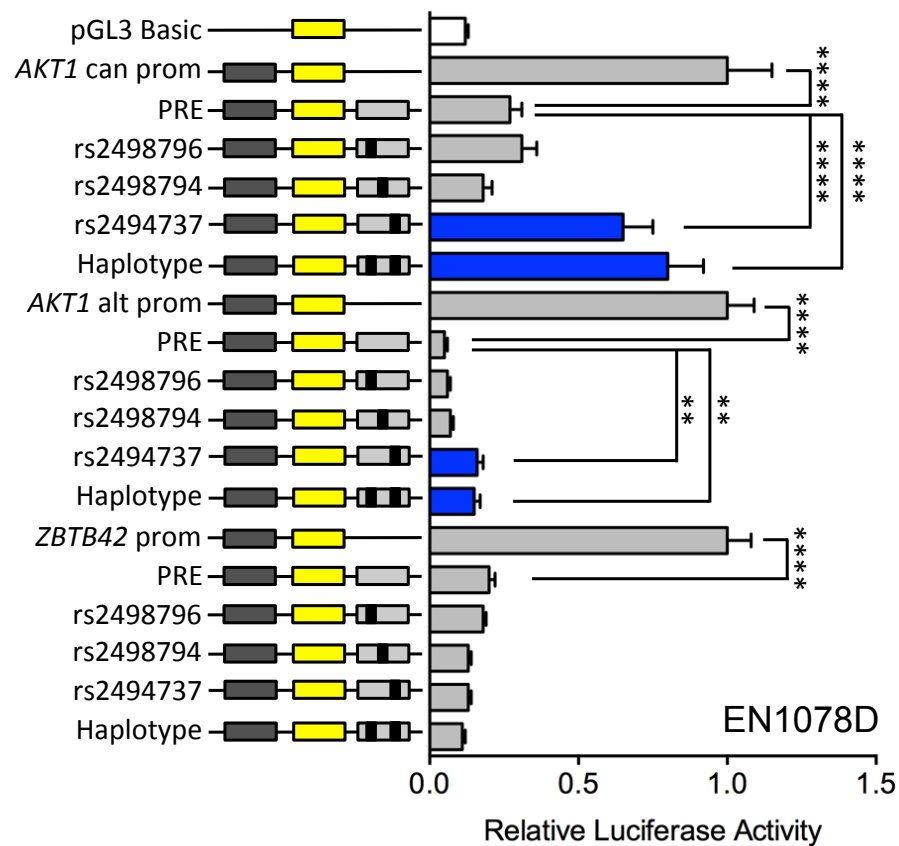


Figure S3. Luciferase reporter assays in EN-1078D endometrial cancer cells. The putative regulatory element (PRE) containing the major SNP alleles were cloned downstream of target gene promoter-driven luciferase constructs. *AKT1* can prom and *AKT1* alt prom denote a canonical and alternative *AKT1* promoter (prom) region, respectively. Minor SNP alleles were engineered into the constructs and are designated by the rs ID of the corresponding SNP. Haplotype denotes a construct that contains the minor alleles of rs2498796 and rs2494737. Error bars denote 95% confidence intervals from three independent experiments performed in duplicate. P-values were determined by 2-way ANOVA followed by Dunnett's multiple comparisons test (** $P < 0.01$, **** $P < 0.0001$).

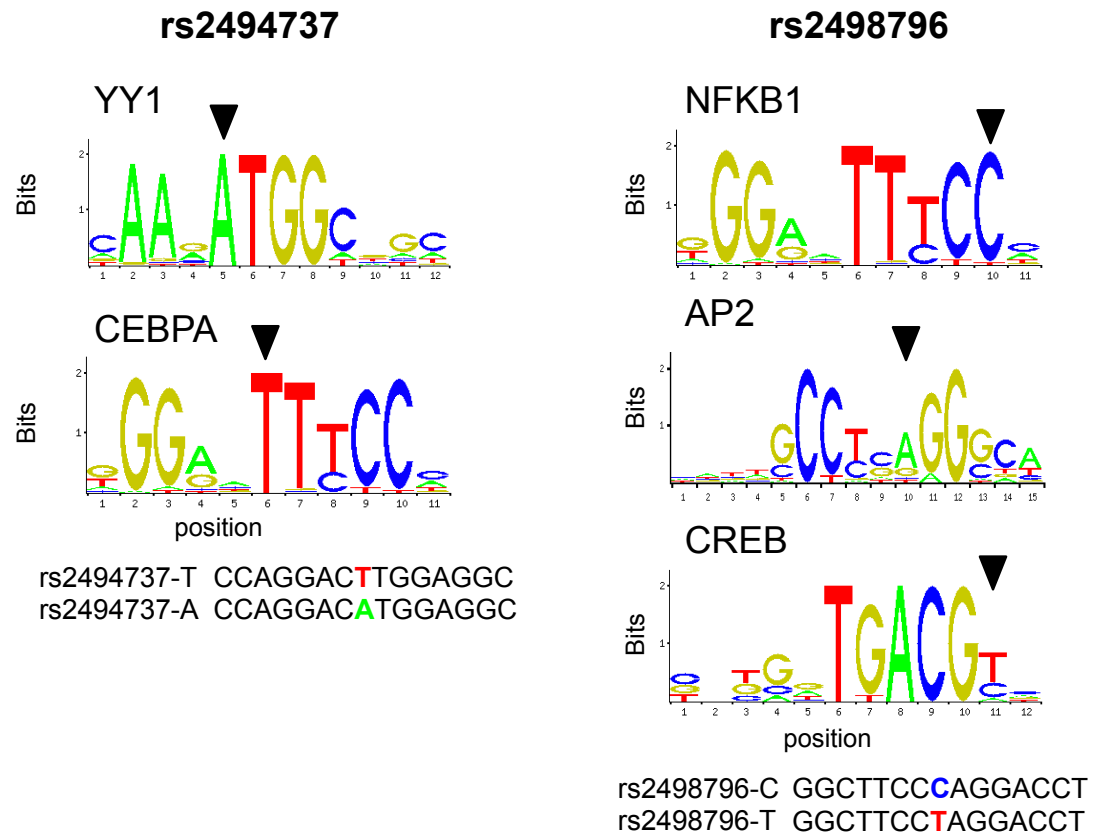


Figure S4. Transcription factor binding. Position weight matrix (PWM) of YY1, CEBPA, NFKB1, AP2 and CREB from JASPAR, with homology to the risk-associated alleles of rs2494737 and rs2498796 colored below. Predicted SNP changes are indicated by black arrowheads.

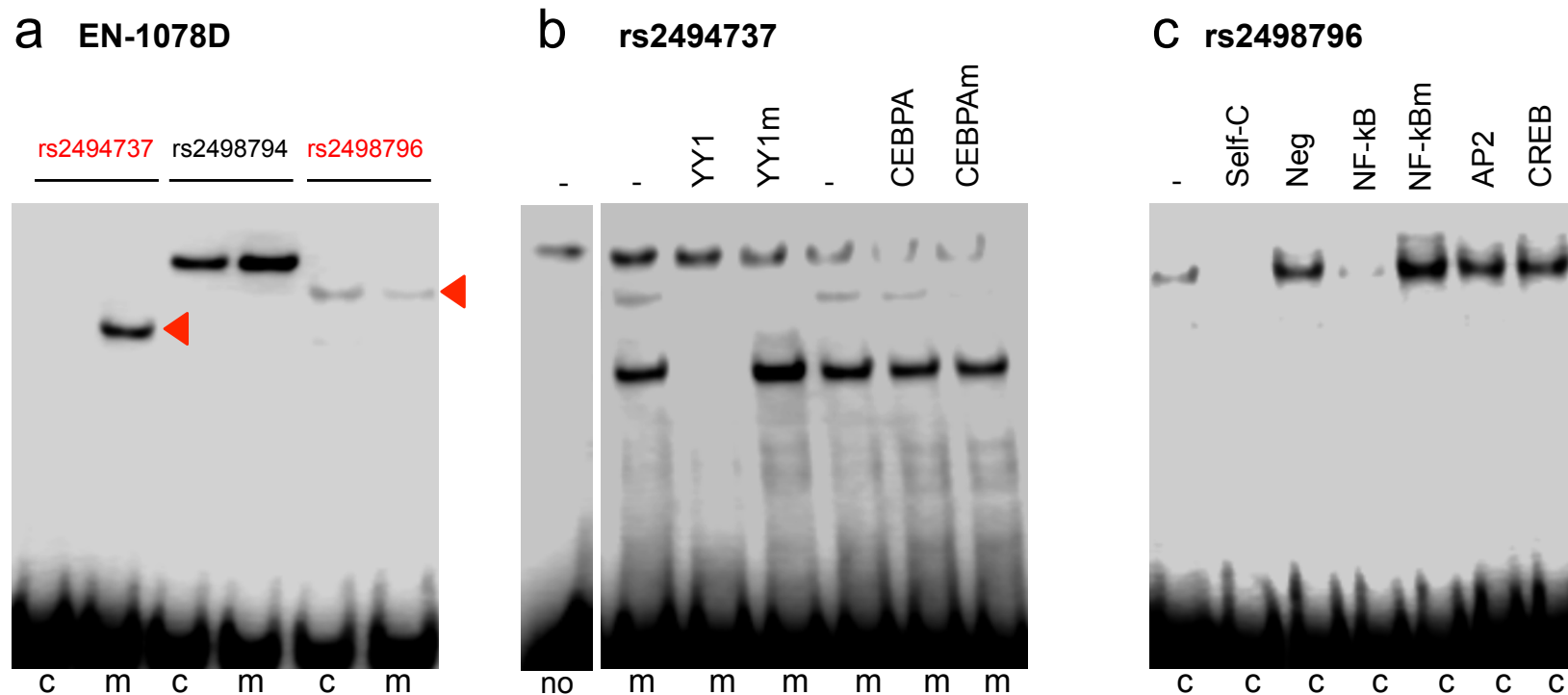


Figure S5. EMSAs for candidate causal SNPs to detect allele-specific binding of nuclear proteins. (a) Oligonucleotides were incubated with EN-1078D nuclear extracts. Red arrowheads show bands of different mobility or intensity detected between the common (c) and minor (m) alleles for the three candidate causal SNPs. Oligonucleotides for SNPs rs2494737 (b) and rs2498796 (c) were incubated with Ishikawa nuclear extracts. Competitor oligonucleotides are listed above each panel and were used at 100-fold molar excess: (no) no oligonucleotide; (-) no competitor; YY1 consensus binding site; YY1m, an identical oligonucleotide but with a mutated binding site (independent replicate of Figure 4a); CEBPA consensus binding site; CEBPAm, an identical oligonucleotide but with a mutated binding site; NF-kB consensus binding site; NF-kBm, an identical oligonucleotide but with a mutated binding site; AP2 and CREB consensus binding sites. Negative control (Neg) denotes a non-specific competitor.

rs2494737

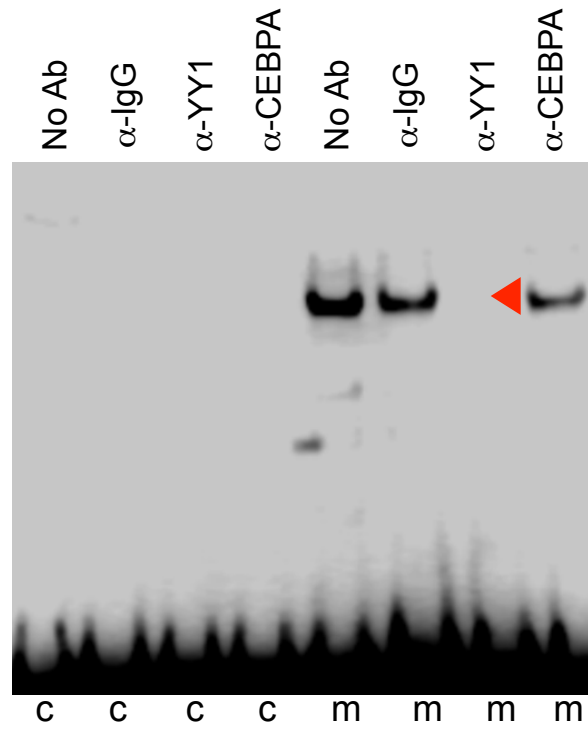


Figure S6. EMSA-supershift for candidate causal SNP rs2494737. Oligonucleotide duplexes for the common (c) or minor (m) alleles of SNP rs2494737 and antibodies against YY1 or CEPBA were incubated with Ishikawa nuclear extracts. Rabbit IgG was used as a negative control. The red arrowhead denotes the YY1 supershifted complex.

rs2494737 – YY1

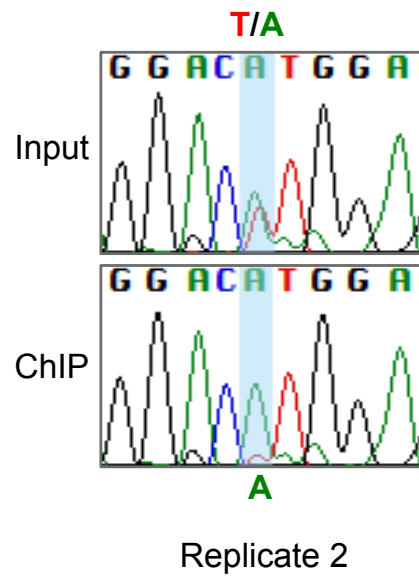


Figure S7. YY1 transcription factor binding *in vivo*. Sanger sequencing of the PCR fragment generated using primers flanking SNP rs2494737 in heterozygous Ishikawa endometrial cancer cells following YY1 ChIP-qPCR and the input DNA controls. Primers are listed in **Table S5**.

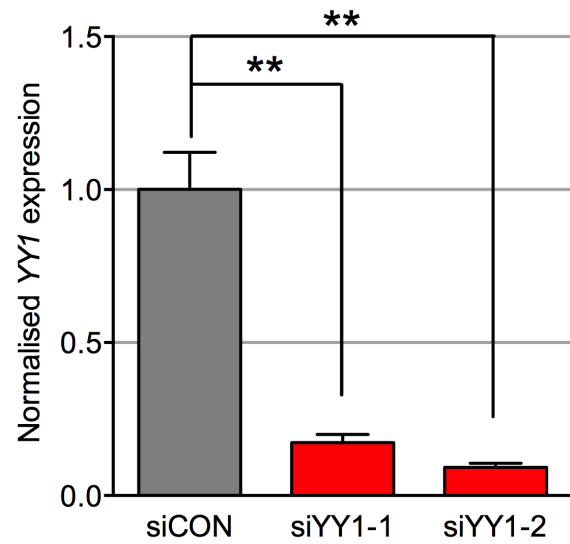


Figure S8. TaqMan real-time PCR assays confirming knockdown of *YY1* in Ishikawa cells. siCON is a nontargeting negative control and siYY1-1 and siYY1-2 are two independent siRNAs targeting *YY1*. Error bars denote the standard error of the mean from three experiments performed in duplicate. Statistical significance was determined by a paired t-test (** $P < 0.01$)

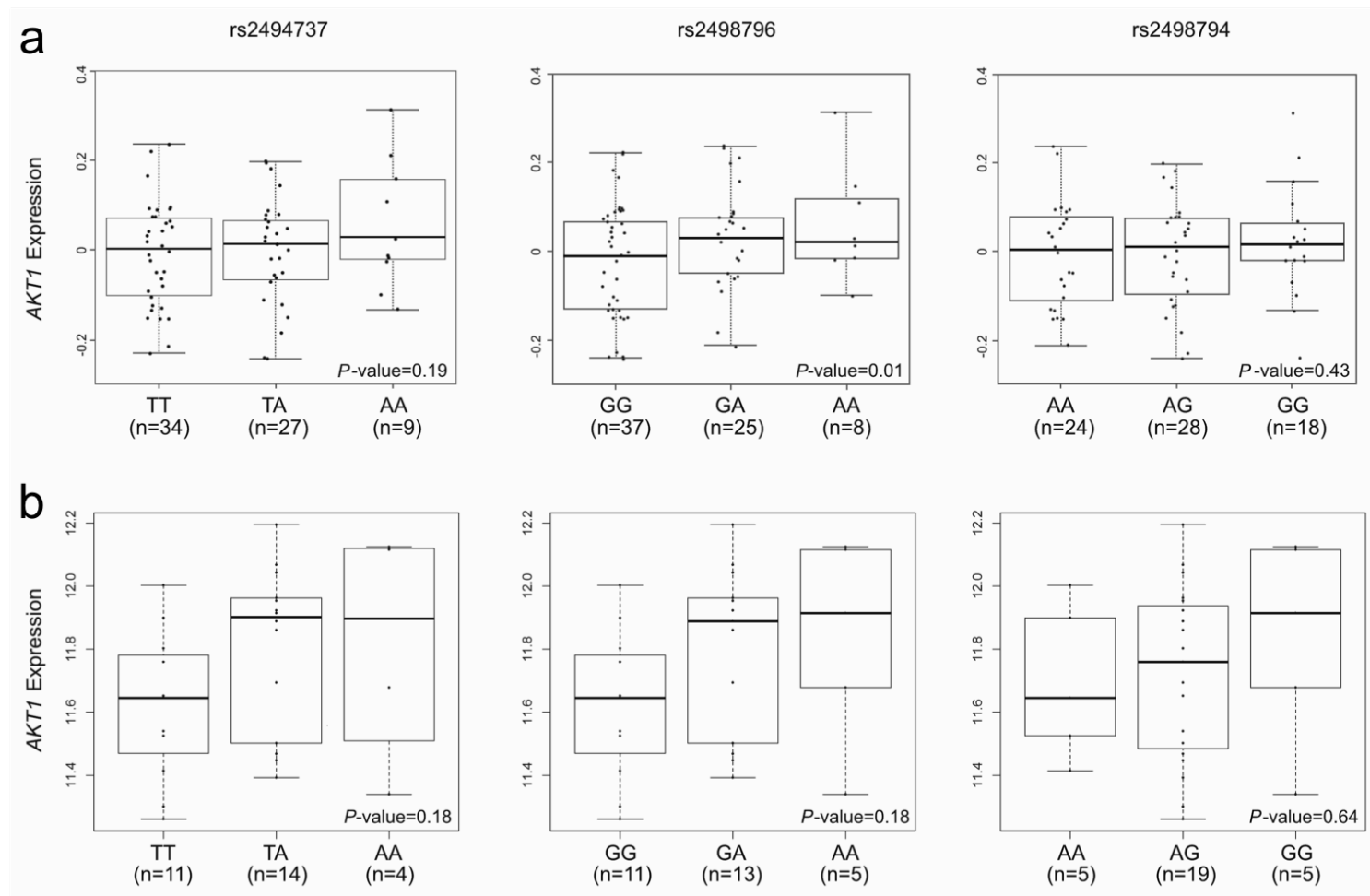


Figure S9. Associations of candidate causal SNPs with overall expression of *AKT1* in uterine samples from the **(A)** GTEx¹ database and **(B)** TCGA² dataset. The x-axis of each plot corresponds to the three observed SNP genotypes and the y-axis represents either log₂-normalized gene expression values (GTEx) or RSEM gene expression values (TCGA). For the TCGA data, prior to the eQTL, analyses the expression data were adjusted to account for copy-number at the *AKT1* locus, and the three candidate SNPs were imputed with the following RSQR quality scores: rs2494737=0.57, rs2498796=0.72 and rs2498794=0.46.

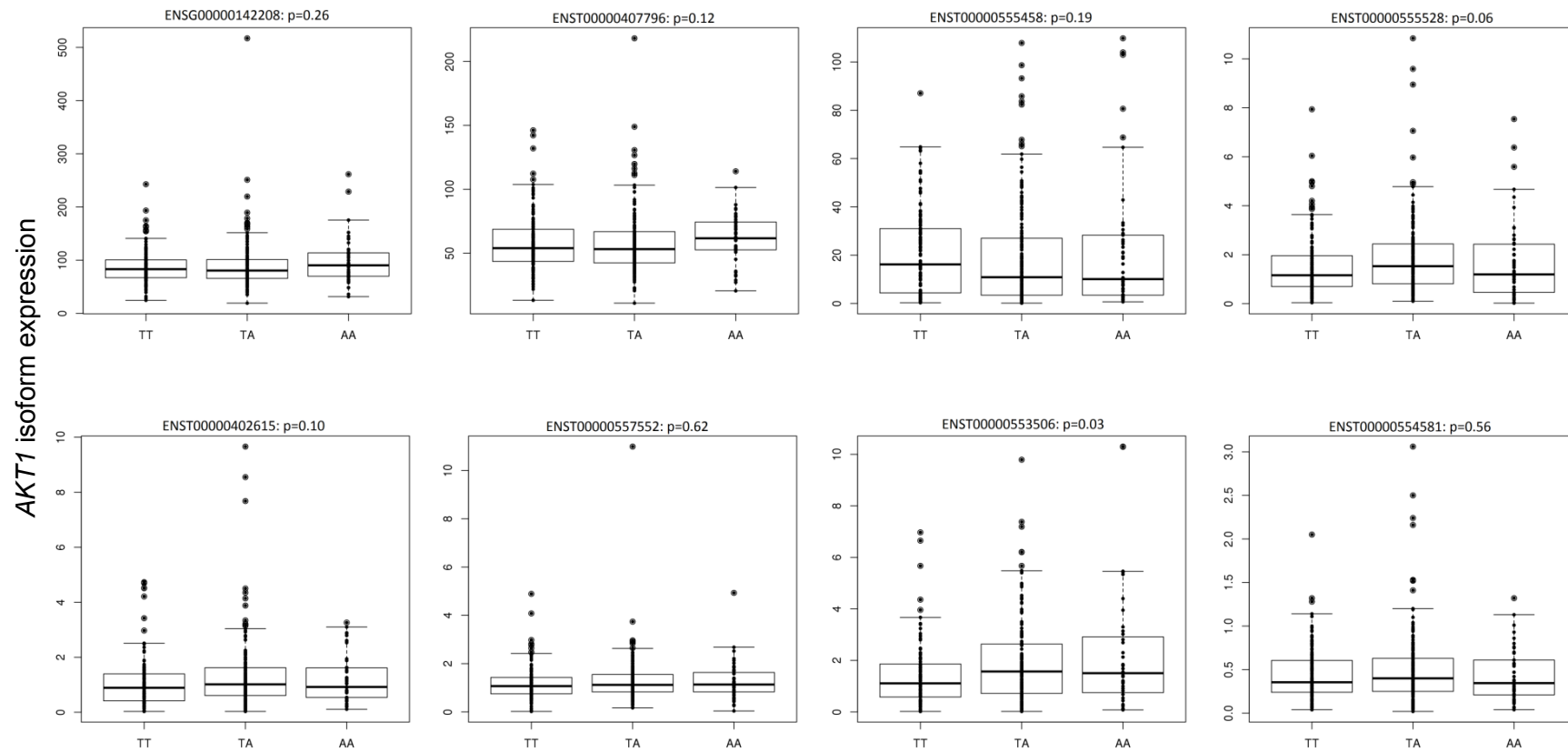


Figure S10. Associations of SNP rs2494737 with expression of *AKT1* isoforms in endometrial tumour samples from the TCGA dataset.² The x-axis of each plot corresponds to the three SNP genotypes and the y-axis represents the RSEM gene expression values for each isoform in 526 unique samples. Data was generated using single-read or paired-end RNA sequencing where SNP data was available. The main *AKT1* isoform is ENSG00000142208. Isoform ENST00000555380, corresponding to the ‘alt’ promoter examined in luciferase assays detailed above, was not expressed in the TCGA tumour or adjacent normal tissue datasets. Only isoforms for which expression was detected in >80% of samples are shown. Genotype at the risk SNP rs2494737 was not associated with differential expression for any isoform once multiple testing was taken into account (where the Bonferroni corrected P -value for a significant association was $0.05/8$ transcripts=0.006). Results for SNP rs2494737 in adjacent normal tissue, and for SNPs rs2498794 and rs2498796 in tumour and adjacent normal tissue were all not significant (data not shown).

Table S1. Oligonucleotides used in 3C assays.

3C Primer (<i>NcoI</i>)	Sequence (5' to 3')
PRE bait	CGCTACAGGTAAGGAATAAAGCCACAGCAGG
Allele-specific PRE bait	CCTTAGGACTCAGCCTGGAGACTCCCACC
Fragment 1	GCTGGCAGAGAGAAGCTGTGTATAAGCCTGG
Fragment 2	CCTGTGTGCACATAGCTCAGGGTTCTGC
Fragment 3	GCACAGTGTCTGGTTTCCTCCACTCAGC
Fragment 4	GCTGAGAAGTGGAGTGGGATAAGACGATGATAGG
Fragment 5	GGTGTGGGCGTTCTGAGAGAAATCCTCC
Fragment 6	TGCACAGACATGAGTGGCCTGAGAACG
Fragment 7	CAGTCTCACCCCTGAATCAGAGCCGTCC
Fragment 8	GGAGGATTCTGGTGACGAGCTCCTGG
Fragment 9	TGACACATGCTGGAGGCTCAAAGGAGC
Fragment 10	GAGCTCCCACACTGTGCTGTGGAAGG
Fragment 11	ATGTAGGCATTCGGATGGAGGTGCTGG
Fragment 12	GCCTCTGCTCGTGTTCCTGCCTTTGC
Fragment 13	ACCAGGAGGTCTTTGCCTCCCTGTTCC
Fragment 14	GTGAGCTGCTCCCCGGTGTCTGC
Fragment 15	CACTTCCTCCAGGGTGCATTCCTGG
Fragment 16	GACGCGCACACAAGTTCCATGTGC
Fragment 17	GACAGAGCACA ACTCTATGTGGGCGTCC
Fragment 18	GTTGAGGTT CAGGCTCTTCTTGGCATCG
Fragment 19	GTTTAGCCACTACTTGTCTGTGGCCTTGTGG
Fragment 20	GCAGGGTTTCCCCACGTAGTCATGG
Fragment 21	GACACGTT CAGCACCATGAAGGCTTTCC
Fragment 22	CATGTCCCCAGGAAGTCTGTGAGGAGACC
Fragment 23	CTGCCAGTGTCCACCACAGCTCTGC
Fragment 24	GTTGATGTGATGGCCAAGTTTCAGCTGC
Fragment 25	GCTGCACCTGAATCACTAACTCAGTGTGAGC
Fragment 26	ATCAGGTTCTTGCTTCAGAGCAGGGAGG
Fragment 27	CGAGGAGGCCAGACCTGCTTTGTCC
Fragment 28	CACATCACATCGTCTGCCTGTCTGTGC

Fragment 29	AGACATGCAGTCCGCTAACGCTGTGG
Fragment 30	CACTCAAGGCAGGTGTTCTGCACCATCC
Fragment 31	GCACTCACTCTGTCTTTCCTGCCTCATGG
Fragment 32	GATTCCCACAGCAAAGGCATCCAAGG
Fragment 33	AGGTAGGGAAACTGAGAGAAGGGAAGCCTATCC
Fragment 34	GCAGGAAACAAGGCCAAAGAGGCACC
Fragment 35	GAACACCCTTGGGGGCACACCTGATACTAGG
Fragment 36	GGCTTGAGAGGGTGCAGGGATACATATCG
Fragment 37	GGATCCGTGACCCTCACTTTCCTTGTGC
Fragment 38	ACGTGCACTTTCACCCACAGCACAGC
Fragment 39	TGCCTCCGGTGTGAAGAGGTGATGC
Fragment 40	GTGTGATTTACCTGGTGCCGCTTGTGC
Fragment 41	GAAGTGGCTCCATAGACCCAAAGCAAGC
Fragment 42	GCAGAAAGTAGGTAGAGGCCAGGAGGAAATGG
Fragment 43	GGTCTGTCTCATTCACTGCCCTACCCAGG
Fragment 44	AAGCAGCATCCTCAGAGCAGCTGGTCC
Fragment 45	TCCTCACGTGTGCACATCACCTTATAGTCACC
Fragment 46	CACACAAGCCACTGTCACCTGCTGTGC
Fragment 47	CCACCCGCTGCACATGTTTCAGACC
Fragment 48	GACCCTTAACCCTGTGACACTGCACCTATCC
Fragment 49	GGACCACATGGACAGTCACAGGCAGC
Fragment 50	AGGTGACCCTCAGAGGCAGATCATGACC
Fragment 51	AGTGCTGGCCTCTCAATCCCTGACACC
Fragment 52	GGAAGTCCCGTTGGAGATGAGGAAGTAAGG
Fragment 53	GCCTTCCAGGAAAGCCAGGAGAGAGG
Fragment 54	CCCTAACCTGATGCACCAGCTGACAGG
Fragment 55	GTTGGCCAAATGAATGAACCAGATTCAGACC
Fragment 56	GTTGTGGTCTCCACATTCTATTCATGTTTCGAGG
Fragment 57	CAGCTGACTGCTAGAGCTGTCGTGGAAGC
Fragment 58	CAATCCTGGCTGTCCCAGCTCTCAGG
Fragment 59	CTCACTCAGTGGAGCTTCAGTATCTGCACTTCC
Fragment 60	GGATGAACCCACACATTCCCTTCACTGC
Fragment 61	CTAATTCAGATGGCAATTTGATCACTGCTGTCC

Fragment 62	GACATCACACCATGTTCTGGCTGTAAGAATGG
Fragment 63	AGTGTGGGTGAGCACTGTCCAATCTGAGG
Fragment 64	TCGGAGCTGTGTTGTGAGCCACTAGTAATCC
Fragment 65	ATCTAGGCTCAAGTGGTGGCTGTTGGTGG
Fragment 66	CGTAGGCTTTGAAGATGCTTGTTTCAGAAACG
Fragment 67	AGAAGGGATGATATGCTCGGAATAACTGGAGG
Fragment 68	TTCCACTATGACCCTCAGCGAGTGTTTTCC
Fragment 69	TGAGATGTGCATGGCTGCTGGAATGG
Fragment 70	AGGAAAGGCTTTGAGGCAGGTGGTCC
Fragment 71	CACTCCCTCACTCCATTCATACCTCCACTTCC
Fragment 72	GCTGTAGAGGCCTCCTGGAGGCTTTGC
Fragment 73	CACGCCCAAGGTCTTCAGCTTTGAGG
Fragment 74	CCGAGTTTCTGCACCTGTCAGTGGAGC
Fragment 75	GAGAAGCCTCTAGGGCAGGTGCACAGG
Fragment 76	CTCGACTGTTCCCAAGGGCTCATGG
Fragment 77	CCAGGACTTCATGGCCCAGTGTCTGC
Fragment 78	TCAGAGGGGACAGAGATGAGTCTGATGACG

C14ORF180F1	CAACATAACATGACTGGCTGTGGCACTGG
C14ORF180F2	CCAGCCTAGCAGGAATGGATTCGTTACTCC
C14ORF180F3	GTGTAACCTGGAGGCCTCGTGACAGATGG
TMEM179F1	GGTTTGGCAACATGGGTGCAGATGACG
TMEM179F2	GGATTAGTGGTCTCATGGATTAATGGGTTGCC
TMEM179F3	GCCTTTGTAAGCACATGTTGATCAGTCACTGG

PLD4F1	GGAAAGCTTCCTGCATAATCACAGCTTCATTACC
PLD4F2	CCAGAGAGTCACACAGCCTCCAGCTAGTCC
PLD4F3	GCTCTTATCTGCCTCCTGTGGCAAGTGC
AHNAK2F1	ACAGGAAGGAGACGCTGGCACAGAGC
AHNAK2F2	GAGGTGCCACTTAAGGCTCCAAGCAGG
AHNAK2F3	CCTCTGTGTGGTGCCCAAGCTAGATCC
C14ORF79F1	CCTCTGTGTGGTGCCCAAGCTAGATCC
C14ORF79F2	CTGAGACAGTCCTAGATGCTCCCACCTCACC

C14ORF79F3	GTAGGAGGTAACAAGGACCTGAGACTGAGCTGG
CDCA4F1	GCCTTAGGGATCACACCCATTCCTTGG
CDCA4F2	CGAGACCAGCCTGGACAACATAGTGAGACC
CDCA4F3	GCTGGTCTCAAACCTCCTGAACTCAAGTGATCC
GPR132F1	CAGGGGACTCTGTTCTTGATCTGCTCTGAGG
GPR132F2	CAACAGTCAACCTGTCCTAGGAGGACCAGGAGAGC
GPR132F3	GGCAAGCTGAATCCCTCACCGTAAACC
JAG2F1	ACACCTTCCCAGTAGGGACCAGGAGAGC
JAG2F2	GAACATACTTTCCTGCAGCGTGCAGC
JAG2F3	GGAAGCAGTGACCCTGACCTGAGATGG
NUDT14F1	GGAAGCAGTGACCCTGACCTGAGATGG
NUDT14F2	GGAAGCTGTCCTGGCAGGAGGAGACC
NUDT14F3	GCTCCCTGCTGACGAGCTTACCTTCAGCGTGCAGC

Table S2. Oligonucleotides used in EMSAs.

SNP	allele ^a	Sequence (5' to 3') ^b
rs2498796	com	^{BIO} CACCCACCAGGTCCTGGGAAGCCCCATCTCT
	min	^{BIO} CACCCACCAGGTCCTAGGAAGCCCCATCTCT
rs2498794	com	^{BIO} AGACCTGCCTGAGACAGATCCCAGAGGCCTG
	min	^{BIO} AGACCTGCCTGAGACGGATCCCAGAGGCCTG
rs2494737	com	^{BIO} TTGCCAGCCCAGGACTTGGAGGCTCCAGGGG
	min	^{BIO} TTGCCAGCCCAGGACATGGAGGCTCCAGGGG

^a com: common allele, min: minor allele

^b BIO: 5' biotinylation (present on both the sense and antisense strands of the duplex)

Table S3. EMSA competitor duplexes and their target DNA binding proteins.

Competition Target	Sequence (5' to 3')
YY1 consensus FOR	CGCTCCCCGGCCATCTTGGCGGCTGGT
YY1 consensus REV	ACCAGCCGCCAAGATGGCCGGGGAGCG
YY1 mutated FOR (YY1m)	CGCTCCGCGATTATCTTGGCGGCTGGT
YY1 mutated REV (YY1m)	ACCAGCCGCCAAGATAATCGCGGAGCG
NFkB consensus FOR	AGTTGAGGGGACTTTCCCAGGC
NFkB consensus REV	GCCTGGGAAAGTCCCCTCAACT
NFkB mutated FOR (NFkBm)	AGTTGAATTGACTTTGCCAGGC
NFkB mutated REV (NFkBm)	GCCTGGCAAAGTCAATTCAACT
AP2 consensus FOR	GATCGAACTGACCGCCCGCGGCCCGT
AP2 consensus REV	ACGGGCCGCGGGCGGTCAGTTCGATC
CEBP consensus FOR	TGCAGATTGCGCAATCTGCA
CEBP consensus REV	TGCAGATTGCGCAATCTGCA
Negative Control FOR (Neg)	TGCAGAGACTAGTCTCTGCA
Negative Control REV (Neg)	TGCAGAGACTAGTCTCTGCA

Table S4. Oligonucleotides used in cloning luciferase constructs.

Primer	Sequence (5' to 3')
AKT CAN promoter FOR	<u>ACGCGT</u> GTCACTTTACAGACGGGGAAACTGAGG
AKT CAN promoter REV	AGATCTGGAAATGCCCAAGTACTTAGCAGG
AKT ALT promoter FOR	<u>ACGCGT</u> TCTAGGTGGCTTCAGTGTGAGACC
AKT ALT promoter FOR	AGATCTATGGGGACAGCACACAGTGC
ZBTB42 promoter FOR	<u>ACGCGT</u> AGGGCTGTGATCCAGGCAGG
ZBTB42 promoter REV	AGATCTCCGAGCTCCTCTCCGGTCG
PRE WT FOR	<u>GGATCC</u> CTCAAGAATGATGGCACCTTCATTGG
PRE WT REV	GTCGACGTGAGTGGAGTGTGTAGCCGCTGG

Table S5. Oligonucleotides used for ChIP analyses.

Primer name	Sequence (5' to 3')
SNPrs2494737FOR	AGGACTCAGCCTGGAGACTCC
SNPrs2494737REV	TCTCGGGATTCAGATTTGGG
SNPrs2498796FOR	TTCATCAGCTGGCACTCTGC
SNPrs2498796REV	GTAGAGTGTCTGAGCTGGAACAGG
NegControlFOR	CACAACAGGATCTTATGCGTGG
NegControlREV	CAGTCCCTGCTCATGATCTTGC

Table S6. Numbers of SNPs included in the *AKT1* fine-mapping region on chromosome 14 (bases 104,743,220-105,743,220) compared to SNPs present in the 1000Genomes 2012 reference panel. Linkage disequilibrium was calculated to the top hit previously published for this locus, which was drawn from a subset of risk SNPs selected on the basis of info score >0.9.³

SNP category	1000Genomes 2012 release	<i>AKT1</i> fine-mapping region	% of 1000G SNPs included in the fine-mapping dataset
SNPs with MAF \geq 1% in the 1000Genomes 2012 release ^a	3813	2922	76.6%
LD to rs2498796:			
\geq 0.8	26	26	100%
0.6-0.799	31	30	96.7%
0.4-0.599	16	16	100%
0.2-0.399	18	17	94.4%
<0.2/NA	3721	2832	76.1%

^a Minor allele frequencies (MAF) calculated for Europeans only (85 CEU individuals)

Table S7. See excel file.

Table S8. Predicted effects of candidate casual variants on transcription factor binding motifs.

rsID	Position (hg19; chr14)	TFBS^a	Motif change^b
rs2494737	105246325	YY1	++
		CEBPA	+
rs2498796	105243220	NF-kappaB	-
		AP2	-
		CREB	-
rs2498794	105245251	BCL	--
		GATA1	-
		AP1	+

^a Altered transcription factor binding site (TFBS) determined by HaploRegv3⁴ or AliBaba2⁵ (TRANSFAC and JASPAR matrices).

^b Degree of change to motif for minor allele: + increased agreement with consensus, - decreased.

Supplementary References

1. GTEx Consortium (2013). The Genotype-Tissue Expression (GTEx) project. *Nat Genet* 45, 580-585.
2. Cancer Genome Atlas Research, N., Kandoth, C., Schultz, N., Cherniack, A.D., Akbani, R., Liu, Y., Shen, H., Robertson, A.G., Pashtan, I., Shen, R., et al. (2013). Integrated genomic characterization of endometrial carcinoma. *Nature* 497, 67-73.
3. Cheng, T., Thompson, D.J., O'Mara, T.A., Painter, J.N., Glubb, D.M., Flach, S., Lewis, A., French, J.D., Freeman-Mills, L., Church, D., et al. (2016). Five endometrial cancer risk loci identified through genome-wide association analysis. *Nat Genet* (under re-review).
4. Ward, L.D. and Kellis, M. (2015). HaploReg v4: systematic mining of putative causal variants, cell types, regulators and target genes for human complex traits and disease. *Nucleic Acids Res* (doi: 10.1093/nar/gkv1340).
5. Grabe, N. (2002). AliBaba2: context specific identification of transcription factor binding sites. *In Silico Biol* 2, S1-15.

Table S7. Meta-analysis association results for genotyped and imputed SNPs at chromosome 14q32.33 across four endometrial cancer GWAS/follow-up studies.

The SNPs considered for bioinformatic and functional follow-up are highlighted by blue shading. Results for analyses conditioning on the top 2 SNPs are also indicated.
 I=imputed SNP, G=genotyped SNP, G=genotyped in at least one GWAS study

SNP	BP	Effect allele	Other allele	Effect allele frequency	OR	StdErr	P	I2	r2 to rs2498796	1000G frequency	SNP genotyped or imputed in GWAS/iCOGs*	P conditioning on rs2498794		P conditioning on rs2494737		Average information score
												OR	P	OR	P	
rs2498794	105245251	G	A	0.48	1.13	0.02	8.7E-09	0	0.43	0.44	I/G	4.6E-02	0.37	2.5E-03	1.09	0.78
rs2494737	105246325	A	T	0.30	1.13	0.02	2.5E-07	0	0.83	0.32	I/I	1.5E-01	1.05	4.6E-02	0.37	0.82
rs3001371	105242831	T	C	0.31	1.11	0.02	1.1E-06	0	0.98	0.35	I/G	1.2E-01	1.05	4.9E-01	1.03	0.94
rs2498796	105243220	A	G	0.30	1.11	0.02	1.2E-06	0	1.00	0.35	I/I	1.3E-01	1.04	5.4E-01	1.03	0.93
rs2494731	105237680	C	G	0.33	1.11	0.02	1.4E-06	0	0.89	0.37	I/I	1.1E-01	1.04	5.2E-01	1.03	0.98
rs45607139	105226075	T	C	0.32	1.11	0.02	2.2E-06	0	0.89	0.37	I/I	1.3E-01	1.04	6.0E-01	1.02	0.99
rs73362602	105230595	C	T	0.49	1.10	0.02	2.4E-06	0	0.54	0.49	I/I	8.4E-01	0.99	6.3E-02	1.05	0.90
rs4983549	105228216	A	G	0.32	1.11	0.02	2.5E-06	0	0.89	0.37	I/I	1.4E-01	1.04	6.4E-01	1.02	0.99
rs2494733	105240784	G	C	0.32	1.11	0.02	2.6E-06	0	0.89	0.36	I/I	1.1E-01	1.04	5.4E-01	1.03	0.96
rs66464514	105231196	G	A	0.33	1.11	0.02	3.1E-06	0	0.89	0.37	I/I	1.6E-01	1.04	7.2E-01	1.02	0.99
rs1132975	105222037	T	C	0.32	1.11	0.02	3.2E-06	0	0.89	0.37	I/G	1.5E-01	1.04	7.1E-01	1.02	0.99
rs111268345	105245969	T	C	0.22	1.14	0.03	3.3E-06	0	0.56	0.24	I/I	1.1E-01	1.06	4.2E-01	1.04	0.68
rs7158655	105229646	C	T	0.31	1.11	0.02	3.4E-06	0	0.91	0.36	I/I	1.3E-01	1.04	6.0E-01	1.02	0.99
rs2498804	105233095	A	C	0.31	1.11	0.02	3.4E-06	0	0.89	0.36	G/G	1.3E-01	1.04	6.1E-01	1.02	1.00
rs2498797	105242228	C	T	0.33	1.11	0.02	3.6E-06	0	0.94	0.36	I/I	1.8E-01	1.04	8.4E-01	1.01	0.95
rs8006580	105218333	A	G	0.32	1.10	0.02	3.7E-06	0	0.87	0.36	I/I	1.6E-01	1.04	7.5E-01	1.01	0.99
rs2498803	105233408	A	G	0.31	1.10	0.02	4.1E-06	0	0.89	0.36	I/I	1.4E-01	1.04	6.5E-01	1.02	0.99
rs28368454	105230391	C	T	0.33	1.10	0.02	4.7E-06	0	0.88	0.37	I/I	1.8E-01	1.04	8.1E-01	1.01	0.96
rs2498801	105235558	C	T	0.33	1.10	0.02	5.5E-06	0	0.89	0.37	I/I	1.9E-01	1.04	8.6E-01	1.01	0.98
rs2494730	105233421	A	T	0.32	1.10	0.02	5.9E-06	0	0.89	0.36	I/I	1.6E-01	1.04	7.3E-01	1.01	0.99
rs2498802	105234442	C	G	0.34	1.10	0.02	6.5E-06	0	0.85	0.38	I/G	2.1E-01	1.03	9.1E-01	1.01	0.96
rs76347513	105246016	A	G	0.11	1.20	0.04	6.8E-06	0	<0.01	0.12	I/I	8.1E-03	1.12	3.0E-02	1.11	0.57
rs60798007	105197756	C	G	0.31	1.10	0.02	7.9E-06	0	0.85	0.36	I/I	1.7E-01	1.04	7.3E-01	1.01	0.97
rs7160733	105203678	A	G	0.32	1.10	0.02	8.3E-06	0	0.85	0.36	I/I	1.9E-01	1.04	8.2E-01	1.01	0.98
rs4983550	105231640	G	T	0.34	1.10	0.02	8.8E-06	0	0.88	0.38	I/I	2.4E-01	1.03	1.0E+00	1.00	0.96
rs4983384	105208057	T	C	0.31	1.10	0.02	8.9E-06	0	0.85	0.36	I/G	1.9E-01	1.04	8.4E-01	1.01	0.99
rs80097179	105196230	C	A	0.31	1.10	0.02	1.1E-05	0	0.85	0.36	I/I	1.9E-01	1.04	8.1E-01	1.01	0.97
rs60876857	105197354	G	C	0.31	1.10	0.02	1.2E-05	0	0.85	0.36	I/I	2.0E-01	1.03	8.4E-01	1.01	0.97
rs57098433	105197846	A	G	0.32	1.10	0.02	1.4E-05	0	0.85	0.36	I/I	2.0E-01	1.03	8.6E-01	1.01	0.96
rs4983544	105213978	G	T	0.45	1.09	0.02	2.1E-05	0	0.64	0.44	I/I	9.1E-01	1.00	3.5E-01	1.03	0.96
rs2494735	105242966	C	T	0.35	1.10	0.02	2.4E-05	0	0.84	0.39	I/I	3.4E-01	1.03	6.2E-01	0.98	0.88
rs2494734	105240885	G	C	0.45	1.09	0.02	2.5E-05	0	0.68	0.44	I/G	8.2E-01	0.99	4.0E-01	1.02	0.94
rs8011461	105217921	G	A	0.45	1.09	0.02	2.6E-05	0	0.66	0.44	I/I	8.3E-01	0.99	3.9E-01	1.02	0.96
rs72715972	105192685	A	G	0.32	1.10	0.02	3.1E-05	0	0.83	0.36	I/I	2.9E-01	1.03	9.0E-01	1.00	0.96
rs12590163	105223525	C	T	0.45	1.09	0.02	3.5E-05	0	0.68	0.44	I/G	7.8E-01	0.99	4.3E-01	1.02	0.97
rs180896416	105416838	A	C	0.03	0.63	0.11	3.5E-05	84.39	<0.01	0.01	I/I	4.3E-04	0.67	2.4E-04	0.66	0.45
rs8011779	105217982	T	C	0.44	1.09	0.02	3.8E-05	0	0.66	0.44	I/I	7.7E-01	0.99	4.4E-01	1.02	0.97
rs3809453	105219467	G	A	0.45	1.09	0.02	4.0E-05	0	0.68	0.44	I/I	7.8E-01	0.99	4.5E-01	1.02	0.95
rs6644	105213343	G	A	0.45	1.09	0.02	4.1E-05	0	0.63	0.44	I/I	7.3E-01	0.99	4.7E-01	1.02	0.97
rs12587551	105223457	T	C	0.44	1.09	0.02	4.2E-05	0	0.70	0.44	I/I	7.1E-01	0.99	4.8E-01	1.02	0.97
rs7151424	105220210	A	G	0.45	1.09	0.02	4.6E-05	0	0.67	0.44	I/I	6.9E-01	0.99	4.9E-01	1.02	0.97
rs12889167	105219976	C	T	0.45	1.09	0.02	4.9E-05	0	0.68	0.44	I/I	7.0E-01	0.99	5.0E-01	1.02	0.97
rs76650680	105423809	A	G	0.03	1.35	0.07	5.1E-05	0	<0.01	0.06	I/I	2.2E-04	1.31	7.9E-04	1.34	0.47
rs4983543	105212399	C	T	0.45	1.09	0.02	5.3E-05	0	0.63	0.44	I/I	6.7E-01	0.99	5.1E-01	1.02	0.97
rs7155192	105211426	A	G	0.45	1.09	0.02	5.5E-05	0	0.63	0.44	I/I	6.7E-01	0.99	5.2E-01	1.02	0.97
rs33958252	105196365	C	T	0.44	1.09	0.02	6.0E-05	0	0.63	0.44	I/I	7.9E-01	0.99	4.6E-01	1.02	0.97
rs4983539	105208037	C	A	0.45	1.09	0.02	6.2E-05	0	0.63	0.44	I/I	6.6E-01	0.99	5.3E-01	1.02	0.97
rs4983546	105214479	C	T	0.45	1.09	0.02	6.2E-05	0	0.64	0.44	I/I	6.1E-01	0.98	5.6E-01	1.02	0.97
rs145693791	105416839	T	G	0.03	0.64	0.11	6.4E-05	83.61	<0.01	0.01	I/I	7.0E-04	0.69	4.0E-04	0.68	0.44
rs7149551	105210759	A	G	0.45	1.09	0.02	6.5E-05	0	0.63	0.44	I/I	6.3E-01	0.99	5.5E-01	1.02	0.97
rs8006310	105218476	G	A	0.45	1.09	0.02	6.8E-05	0	0.66	0.44	I/I	5.8E-01	0.98	5.8E-01	1.02	0.96
rs3803307	105207134	G	A	0.45	1.08	0.02	7.8E-05	0	0.63	0.44	I/G	6.3E-01	0.99	5.7E-01	1.02	0.97
rs3730358	105246407	A	G	0.15	1.12	0.03	8.0E-05	0	0.43	0.19	I/G	1.4E-01	1.05	4.4E-01	1.03	0.82
rs4247034	105208879	G	C	0.45	1.08	0.02	9.1E-05	0	0.63	0.44	I/G	5.6E-01	0.98	6.2E-01	1.01	0.97
rs4983386	105210207	A	G	0.45	1.08	0.02	9.4E-05	0	0.63	0.44	I/G	5.5E-01	0.98	6.3E-01	1.01	0.97
rs11848612	105197567	G	C	0.44	1.08	0.02	9.4E-05	0	0.64	0.43	I/I	7.4E-01	0.99	4.7E-01	1.02	0.98
rs3402232	105198749	G	T	0.44	1.08	0.02	9.5E-05	0	0.64	0.43	I/I	7.4E-01	0.99	4.7E-01	1.02	0.98
rs34802997	105198822	T	C	0.44	1.08	0.02	9.6E-05	0	0.64	0.43	I/I	7.3E-01	0.99	4.8E-01	1.02	0.98
rs7142772	105200377	G	T	0.44	1.08	0.02	1.2E-04	0	0.63	0.43	G/G	7.0E-01	0.99	5.2E-01	1.02	1.00
rs34672588	105196235	A	G	0.44	1.08	0.02	1.3E-04	0	0.64	0.43	I/I	6.8E-01	0.99	5.5E-01	1.02	0.97
rs7149183	105201596	C	T	0.44	1.08	0.02	1.4E-04	0	0.61	0.43	I/I	6.5E-01	0.99	5.6E-01	1.02	0.97
rs7141697	105200505	G	C	0.45	1.08	0.02	1.9E-04	0	0.58	0.44	I/I	5.5E-01	0.98	6.6E-01	1.01	0.98
rs57430375	105194906	C	T	0.43	1.08	0.02	1.9E-04	0	0.64	0.42	I/I	6.2E-01	0.99	5.7E-01	1.02	0.96
rs191646265	105418110	T	C	0.14	1.16	0.04	2.5E-04	30.64	<0.01	0.14	I/I	1.3E-04	1.16	8.5E-04	1.17	0.52
rs35746773	105192684	C	T	0.43	1.08	0.02	3.4E-04	0	0.63	0.44	I/I	5.0E-01	0.98	7.3E-01	1.01	0.95
rs12887451	105192026	G	C	0.42	1.08	0.02	3.4E-04	0	0.64	0.43	I/I	5.8E-01	0.98	6.6E-01	1.01	0.94
rs3803304	105239146	G	C	0.26	1.09	0.02	3.8E-04	0	0.59	0.28	I/I	3.9E-01	1.02	9.6E-01	1.00	0.97
rs114064882	105245993	A	T	0.11	1.15	0.04	4.0E-04	26.75	<0.01	0.11	I/I	1.8E-01	1.06	4.4E-01	1.04	0.60
rs183215652	105417808	C	T	0.03	1.34	0.08	5.9E-04	64.2	<0.01	0.02	I/I	1.6E-03	1.31	6.7E-04	1.33	0.45
rs148787429	105416872	C	T	0.05	0.76	0.08	6.7E-04	60.76	0.02	0.04	I/I	2.6E-03	0.79	1.1E-03	0.77	0.47
rs188278119	105417867	A	G	0.08	1.19	0.05	6.9E-04	0	<0.01	0.09	I/I	1.2E-04	1.22	2.3E-04	1.21	0.47
rs149938880	105243623	G	C	0.08	1.16	0.04	7.3E-04	0	0.10	0.09	I/I	1.5E-01	1.07	3.3E-01	1.05	0.70
rs2494732	105239192	C	T	0.43	1.07	0.02	8.4E-04	0	0.61	0.47	I/G	3.2E-01	1.02	5.7E-01	0.98	0.89
rs184806471																

rs4983548	105216381	T	C	0.19	1.08	0.03	3.6E-03	0	0.51	0.25	/I	3.6E-01	1.03	8.9E-01	1.00	0.99
rs75207212	104929715	C	G	0.12	0.91	0.03	3.9E-03	0	<0.01	0.06	/I	5.3E-03	0.91	3.1E-03	0.91	0.94
rs77647965	104929714	A	G	0.12	0.91	0.03	3.9E-03	0	<0.01	0.06	/I	5.3E-03	0.91	3.1E-03	0.91	0.94
rs11346259	104811016	A	G	0.06	0.84	0.06	3.9E-03	11.12	<0.01	0.05	/I	8.8E-03	0.85	7.2E-03	0.85	0.72
rs141736470	105415346	C	T	0.29	1.09	0.03	3.9E-03	0	<0.01	0.31	/I	1.8E-04	1.12	2.7E-04	1.12	0.57
rs8012845	105140433	G	A	0.45	1.08	0.03	4.0E-03	0	0.07	0.44	/I	3.2E-02	1.06	2.5E-02	1.06	0.81
rs55653907	104895822	C	T	0.14	0.90	0.04	4.1E-03	8.96	<0.01	0.07	/I	5.5E-03	0.91	3.8E-03	0.90	0.79
rs34282498	104948316	C	A	0.11	0.91	0.03	4.2E-03	0	<0.01	0.05	/I	5.0E-03	0.91	3.2E-03	0.90	0.95
rs185730426	105427780	A	G	0.05	1.20	0.06	4.4E-03	0	0.02	0.06	/I	1.5E-02	1.17	1.5E-02	1.17	0.50
rs190981255	105427782	A	G	0.05	1.20	0.06	4.4E-03	0	0.02	0.06	/I	1.5E-02	1.17	1.5E-02	1.17	0.50
rs117165790	105193502	A	G	0.03	0.79	0.08	4.4E-03	0	0.02	0.02	/I	9.2E-02	0.87	3.2E-02	0.83	0.47
rs4247029	105142093	A	G	0.47	1.08	0.03	4.7E-03	0	0.07	0.45	/I	4.0E-02	1.06	2.9E-02	1.06	0.81
rs73366139	104765810	T	C	0.28	0.92	0.03	4.7E-03	0	<0.01	0.32	/I	6.3E-03	0.92	5.3E-03	0.92	0.84
rs35222345	104942054	A	G	0.12	0.91	0.03	4.9E-03	0	<0.01	0.06	/I	5.9E-03	0.91	3.8E-03	0.91	0.95
rs11628928	104965566	G	T	0.34	1.07	0.02	4.9E-03	0	<0.01	0.32	/I	8.4E-03	1.06	4.3E-03	1.07	0.94
rs4983523	105148241	G	A	0.25	1.08	0.03	5.0E-03	0	0.05	0.24	/I	2.6E-02	1.07	8.5E-03	1.08	0.78
rs56294432	105475491	T	C	0.11	1.13	0.04	5.2E-03	31.23	0.01	0.11	/I	1.9E-02	1.11	1.9E-02	1.11	0.60
rs4983541	105208986	A	G	0.19	1.07	0.03	5.3E-03	0	0.48	0.25	/I	4.4E-01	1.02	9.9E-01	1.00	0.99
rs2494747	105258437	T	G	0.38	0.94	0.02	5.4E-03	27.6	0.22	0.40	/I	2.6E-01	0.98	8.0E-01	0.99	0.89
rs56058013	105444012	T	C	0.39	1.07	0.02	5.8E-03	0	<0.01	0.39	/I	5.2E-03	1.07	2.7E-03	1.08	0.74
rs35252693	104930719	C	T	0.12	0.91	0.03	5.8E-03	0	<0.01	0.06	/I	7.5E-03	0.92	4.7E-03	0.91	0.95
rs113742549	105541730	A	T	0.01	1.35	0.11	6.0E-03	51.9	<0.01	0.02	/I	9.3E-03	1.32	1.5E-02	1.30	0.61
rs45490496	105272678	T	A	0.38	0.94	0.02	6.0E-03	12.16	0.22	0.40	/I	2.7E-01	0.98	7.9E-01	0.99	0.92
rs79414834	104931191	A	G	0.12	0.91	0.03	6.0E-03	0	<0.01	0.06	/I	7.8E-03	0.92	4.8E-03	0.91	0.95
rs34014106	104909092	C	G	0.10	0.90	0.04	6.0E-03	0	<0.01	0.07	/I	8.3E-03	0.90	5.4E-03	0.90	0.89
rs1866824	105358315	C	T	0.24	1.08	0.03	6.1E-03	51.82	<0.01	0.21	/I	2.6E-03	1.08	6.8E-03	1.07	0.88
rs12587476	105195476	A	C	0.06	1.12	0.04	6.1E-03	0	0.16	0.08	/I	2.3E-01	1.05	4.3E-01	1.04	0.95
rs75112537	105203500	T	C	0.19	1.07	0.03	6.2E-03	0	0.48	0.25	/I	4.7E-01	1.02	9.6E-01	1.00	0.98
rs11160819	105276883	T	G	0.38	0.94	0.02	6.2E-03	1.68	0.21	0.39	/I	2.5E-01	0.98	6.1E-01	0.99	0.97
rs2498786	105262368	G	C	0.38	0.94	0.02	6.6E-03	38.59	0.24	0.41	/I/G	2.8E-01	0.98	8.4E-01	0.99	0.89
rs182220262	105400373	G	C	0.20	1.10	0.04	6.8E-03	0	<0.01	0.23	/I	2.2E-03	1.11	1.3E-03	1.12	0.52
rs28734817	104940730	C	T	0.14	0.91	0.03	6.8E-03	0	<0.01	0.06	/I	8.3E-03	0.91	5.9E-03	0.91	0.83
rs75268661	105208393	A	G	0.18	1.07	0.03	7.2E-03	0	0.48	0.25	/I	5.2E-01	1.02	9.0E-01	1.00	0.99
rs67325187	105203105	C	T	0.06	1.12	0.04	7.3E-03	0	0.16	0.08	/I	2.6E-01	1.05	4.8E-01	1.03	0.96
rs17852251	105477990	T	C	0.02	1.32	0.10	7.4E-03	50.55	0.02	0.01	/I	4.1E-02	1.24	7.1E-02	1.21	0.55
rs76247235	104762528	G	T	0.28	0.92	0.03	7.9E-03	0	<0.01	0.32	/I	1.0E-02	0.92	8.6E-03	0.92	0.78
rs9783669	105215351	T	C	0.07	1.11	0.04	8.1E-03	0	0.14	0.08	G*/I	3.3E-01	1.04	5.7E-01	1.02	0.99
rs11628510	105275365	G	A	0.37	0.94	0.02	8.2E-03	8.83	0.24	0.39	/I	2.8E-01	0.98	7.6E-01	0.99	0.94
rs35054160	104917657	A	G	0.12	0.92	0.03	8.3E-03	0	<0.01	0.06	G*/I	1.0E-02	0.92	6.7E-03	0.91	0.93
rs35214721	104884523	G	A	0.19	0.92	0.03	8.4E-03	5.34	<0.01	0.14	/I	1.0E-02	0.92	1.2E-02	0.92	0.81
rs4983559	105277209	A	G	0.39	0.95	0.02	8.6E-03	0	0.20	0.39	G/G	3.0E-01	0.98	7.0E-01	0.99	1.00
rs12432802	105211221	T	C	0.06	1.12	0.04	8.8E-03	0	0.16	0.08	/I	2.9E-01	1.05	5.2E-01	1.03	0.98
rs117613328	105209258	A	G	0.04	0.82	0.08	9.0E-03	0	0.02	0.02	/I	1.7E-01	0.90	6.3E-02	0.86	0.48
rs11848899	105248660	T	G	0.16	1.08	0.03	9.0E-03	0	0.23	0.16	/I	6.6E-01	1.01	7.3E-01	0.99	0.76
rs75990247	105417358	C	T	0.22	1.09	0.03	9.1E-03	0	<0.01	0.24	/I	6.0E-04	1.12	1.3E-03	1.11	0.55
rs11629050	104974849	A	G	0.10	0.91	0.04	9.2E-03	0	<0.01	0.06	G*/I	1.2E-02	0.91	8.6E-03	0.91	0.94
rs76912402	105278363	A	G	0.10	1.13	0.05	9.4E-03	0	0.11	0.08	/I	8.1E-02	1.09	9.1E-02	1.08	0.52
rs12880001	104909461	A	G	0.12	0.92	0.03	9.4E-03	0	<0.01	0.06	/I	1.2E-02	0.92	7.6E-03	0.92	0.92
rs2494748	105258892	T	C	0.40	0.95	0.02	9.5E-03	16.74	0.22	0.47	/I/G	2.9E-01	0.98	8.6E-01	1.00	0.80
rs4587901	105209667	T	A	0.06	1.11	0.04	9.7E-03	0	0.16	0.08	/I	3.1E-01	1.05	5.4E-01	1.03	0.98
rs11622460	105541527	G	A	0.27	1.07	0.03	9.9E-03	57.31	<0.01	0.27	/I	1.4E-02	1.07	5.9E-03	1.08	0.81
rs34197832	104917800	T	C	0.12	0.92	0.03	9.9E-03	0	<0.01	0.06	/I	1.2E-02	0.92	8.0E-03	0.92	0.93
rs2251389	105352255	A	T	0.23	1.07	0.03	1.0E-02	63.1	<0.01	0.19	/I	3.4E-03	1.08	1.0E-02	1.07	0.89
rs12880721	104909952	A	G	0.12	0.92	0.03	1.1E-02	0	<0.01	0.07	/I	1.2E-02	0.92	7.7E-03	0.92	0.91
rs2582545	105354545	G	A	0.23	1.07	0.03	1.1E-02	61.7	<0.01	0.20	/I	3.7E-03	1.08	1.1E-02	1.07	0.90
rs3809454	105219069	C	A	0.06	1.11	0.04	1.1E-02	0	0.16	0.08	/I	3.0E-01	1.04	5.5E-01	1.03	0.98
rs57837762	105147219	T	C	0.19	1.09	0.03	1.1E-02	0	0.02	0.17	/I	1.0E-01	1.06	2.1E-02	1.08	0.82
rs35635404	105246681	A	G	0.02	0.77	0.10	1.1E-02	0	0.02	0.03	/I	4.9E-02	0.81	2.7E-02	0.79	0.59
rs148209792	105243605	C	G	0.13	1.10	0.04	1.1E-02	0	0.02	0.11	/I	9.6E-01	1.00	5.1E-01	0.97	0.66
rs2919629	105356137	C	G	0.23	1.07	0.03	1.1E-02	60.61	<0.01	0.20	/I	3.9E-03	1.08	1.2E-02	1.07	0.90
rs113335944	104775806	T	C	0.02	0.77	0.10	1.1E-02	0	<0.01	0.04	/I	9.2E-03	0.76	1.0E-02	0.77	0.75
rs2582548	105354293	G	A	0.23	1.07	0.03	1.1E-02	62.55	<0.01	0.20	/I	4.0E-03	1.08	1.2E-02	1.07	0.90
rs10047838	105218305	A	G	0.07	1.11	0.04	1.1E-02	0	0.16	0.08	/I	3.3E-01	1.04	5.4E-01	1.03	0.91
rs145013396	105243675	C	T	0.03	1.23	0.08	1.1E-02	0	<0.01	0.02	/I	2.0E-02	1.21	1.1E-02	1.23	0.45
rs28840384	104935015	A	G	0.16	0.93	0.03	1.2E-02	0	<0.01	0.13	/I	1.4E-02	0.93	8.4E-03	0.92	0.89
rs4983528	105151805	G	T	0.43	1.07	0.03	1.2E-02	42.87	0.09	0.44	/I	5.3E-01	1.02	3.3E-01	1.03	0.70
rs35466827	104908022	A	G	0.11	0.92	0.04	1.2E-02	0	<0.01	0.06	/I	1.3E-02	0.92	8.3E-03	0.91	0.89
rs10148026	105001976	T	A	0.40	1.08	0.03	1.3E-02	0	<0.01	0.32	/I	2.2E-02	1.07	2.9E-02	1.07	0.55
rs78116894	105418166	C	T	0.27	1.08	0.03	1.3E-02	16.46	<0.01	0.26	/I	2.3E-02	1.07	1.2E-02	1.08	0.60
rs35764643	104943312	C	T	0.13	0.92	0.03	1.3E-02	0	<0.01	0.07	/I	1.5E-02	0.92	1.0E-02	0.92	0.91
rs12890949	105415352	C	G	0.10	1.14	0.05	1.3E-02	37	<0.01	0.06	/I	1.3E-02	1.14	1.8E-02	1.13	0.47
rs2582549	105351637	G	A	0.23	1.07	0.03	1.3E-02	60.1	<0.01	0.19	/I	4.6E-03	1.08	1.4E-02	1.07	0.90
rs10136869	105153422	A	G	0.40	0.94	0.03	1.3E-02	52.17	0.07	0.43	/I	4.0E-01	0.98	3.1E-01	0.97	0.76
rs2289453	105355549	T	C	0.24	1.07	0.03	1.3E-02	59.91	<0.01	0.20	/I	4.8E-03	1.08	1.4E-02	1.07	0.90
rs56121689	105171482	A	G	0.23	1.07	0.03	1.3E-02	0	0.35	0.31	/I	4.1E-01	1.			

rs34504872	104943433	T	C	0.13	0.93	0.03	1.7E-02	0	<0.01	0.07	/I	2.1E-02	0.93	1.4E-02	0.92	0.93
rs9788594	105350868	T	C	0.23	1.06	0.03	1.7E-02	61.72	<0.01	0.20	/I	6.3E-03	1.07	1.8E-02	1.06	0.90
rs117276210	104929403	T	C	0.04	0.85	0.07	1.8E-02	0	<0.01	0.03	/I	3.2E-02	0.87	2.3E-02	0.86	0.72
rs74090038	105262781	T	C	0.29	1.06	0.02	1.8E-02	48.34	0.13	0.31	/I	1.8E-01	1.03	4.5E-01	1.02	0.87
rs11622483	105541534	T	C	0.38	1.07	0.03	1.8E-02	0	<0.01	0.39	/I	2.3E-02	1.07	1.2E-02	1.07	0.59
rs76927852	105099784	A	G	0.02	1.27	0.10	1.8E-02	0	0.01	0.02	/I	3.0E-02	1.24	4.6E-02	1.22	0.70
rs7145300	105147308	G	A	0.42	1.07	0.03	1.9E-02	0	0.04	0.45	/I	1.4E-01	1.04	6.7E-02	1.05	0.75
rs2494739	105246989	T	C	0.07	1.10	0.04	1.9E-02	3.98	0.15	0.08	/I	5.6E-01	1.02	9.9E-01	1.00	0.97
rs72709704	105667949	A	G	0.01	1.25	0.10	1.9E-02	0	0.01	0.02	/I	4.1E-02	1.22	5.2E-02	1.20	0.83
rs2498782	105280847	T	C	0.20	0.93	0.03	2.0E-02	70.25	<0.01	0.16	/I	1.0E-02	0.92	3.3E-02	0.93	0.64
rs6576058	105163560	C	T	0.34	1.06	0.02	2.0E-02	0	0.41	0.38	/I	8.1E-01	1.01	2.9E-01	0.97	0.88
rs2582558	105347488	T	C	0.43	1.05	0.02	2.0E-02	0	0.04	0.38	G/G	3.2E-03	1.06	5.6E-03	1.06	1.00
rs187903526	105356327	G	A	0.07	1.14	0.06	2.0E-02	0	<0.01	0.14	/I	2.3E-02	1.14	3.1E-02	1.13	0.50
rs111781133	105425903	A	G	0.03	1.17	0.07	2.0E-02	49.88	<0.01	0.05	/I	3.0E-02	1.16	3.2E-02	1.16	0.80
rs141600524	105418155	C	G	0.21	1.08	0.03	2.0E-02	0	<0.01	0.22	/I	2.7E-02	1.08	1.8E-02	1.08	0.58
rs79943085	104819295	C	T	0.02	0.76	0.12	2.1E-02	0	<0.01	0.04	/I	1.8E-02	0.76	1.9E-02	0.76	0.74
rs10142069	105252070	C	T	0.28	1.06	0.02	2.1E-02	38.46	0.13	0.31	/I	2.0E-01	1.03	4.8E-01	1.02	0.85
rs61759760	105256187	T	C	0.29	1.05	0.02	2.1E-02	37.58	0.13	0.31	/I	2.1E-01	1.03	5.0E-01	1.02	0.86
rs4380005	104992031	A	G	0.10	0.91	0.04	2.1E-02	0	<0.01	0.05	/I	2.0E-02	0.91	1.2E-02	0.90	0.85
rs28625715	104943599	T	C	0.13	0.93	0.03	2.1E-02	0	<0.01	0.07	/I	2.6E-02	0.93	1.7E-02	0.93	0.92
rs12588561	105168839	C	T	0.33	1.06	0.02	2.1E-02	0	0.43	0.36	/I	8.9E-01	1.00	2.9E-01	0.97	0.91
rs4983557	105277135	T	A	0.12	0.92	0.04	2.1E-02	7.82	0.09	0.13	/I	4.2E-01	0.97	8.2E-01	0.99	0.76
rs10139245	104959120	G	A	0.40	1.05	0.02	2.2E-02	0	<0.01	0.35	/I	3.7E-02	1.05	2.1E-02	1.05	0.96
rs34627241	104968147	A	G	0.11	0.92	0.04	2.2E-02	0	<0.01	0.06	/I	2.4E-02	0.92	1.7E-02	0.92	0.92
rs149617324	105553487	T	C	0.02	1.27	0.10	2.2E-02	0	0.02	0.01	/I	9.9E-02	1.19	1.6E-01	1.16	0.50
rs57421664	104863581	T	C	0.06	1.14	0.06	2.2E-02	0.12	<0.01	0.01	/I	1.8E-02	1.14	2.1E-02	1.14	0.61
rs147978925	105418149	T	A	0.21	1.08	0.03	2.2E-02	0	<0.01	0.22	/I	2.9E-02	1.07	2.1E-02	1.08	0.58
rs2841211	105315023	C	T	0.22	1.07	0.03	2.2E-02	73.2	<0.01	0.16	/I	6.1E-03	1.09	1.3E-02	1.08	0.74
rs11848805	105255658	A	G	0.29	1.05	0.02	2.2E-02	36.97	0.13	0.31	/I	2.1E-01	1.03	5.2E-01	1.02	0.86
rs2919620	105314007	G	A	0.22	1.07	0.03	2.3E-02	72.8	0.01	0.19	/I	1.6E-02	1.08	3.4E-02	1.07	0.76
rs10136000	105253581	A	G	0.28	1.05	0.02	2.3E-02	39.77	0.13	0.31	/I/G	2.0E-01	1.03	4.9E-01	1.02	0.86
rs1982231	105451642	T	C	0.48	1.06	0.02	2.3E-02	0	<0.01	0.48	/I	1.7E-02	1.06	4.5E-03	1.07	0.78
rs7493091	105214171	T	G	0.06	1.10	0.04	2.3E-02	0	0.15	0.07	/I	4.8E-01	1.03	7.7E-01	1.01	0.98
rs4983558	105277144	T	C	0.12	0.92	0.04	2.3E-02	7.02	0.09	0.13	/I	4.3E-01	0.97	8.4E-01	0.99	0.76
rs140572555	105217357	G	A	0.06	1.10	0.04	2.3E-02	0	0.15	0.07	/I	4.6E-01	1.03	7.5E-01	1.01	0.99
rs74504710	104964857	T	A	0.43	1.05	0.02	2.3E-02	0	<0.01	0.36	/I	3.5E-02	1.05	2.2E-02	1.05	0.88
rs76939505	104964854	G	A	0.43	1.05	0.02	2.3E-02	0	<0.01	0.36	/I	3.5E-02	1.05	2.2E-02	1.05	0.88
rs11626743	104990326	G	C	0.13	0.92	0.04	2.3E-02	0	<0.01	0.08	/I	2.5E-02	0.92	1.6E-02	0.92	0.88
rs7493507	104960774	C	T	0.42	1.05	0.02	2.4E-02	0	<0.01	0.38	/I	3.9E-02	1.05	2.2E-02	1.05	0.93
rs11844158	104987452	T	C	0.14	0.93	0.03	2.4E-02	0	<0.01	0.08	/I	2.6E-02	0.93	1.7E-02	0.92	0.88
rs4294750	104963113	T	C	0.40	1.05	0.02	2.4E-02	0	<0.01	0.35	G*/I	4.1E-02	1.05	2.3E-02	1.05	0.97
rs1130214	105259734	A	C	0.29	1.05	0.02	2.4E-02	36.32	0.13	0.31	/I	2.3E-01	1.03	5.4E-01	1.02	0.87
rs2247712	105359827	C	T	0.23	1.06	0.03	2.4E-02	51.2	<0.01	0.19	/I	1.1E-02	1.07	2.7E-02	1.06	0.89
rs36214921	105261414	C	G	0.29	1.05	0.02	2.4E-02	38.37	0.13	0.31	/I	2.3E-01	1.03	5.2E-01	1.02	0.87
rs28562073	104944346	T	C	0.13	0.93	0.03	2.4E-02	0	<0.01	0.07	/I	2.9E-02	0.93	1.9E-02	0.93	0.92
rs188407491	104927991	C	A	0.07	1.14	0.06	2.4E-02	15.15	<0.01	0.05	/I	2.4E-02	1.14	2.2E-02	1.14	0.59
rs752265	105361934	C	T	0.23	1.06	0.03	2.5E-02	56.94	<0.01	0.19	/I	1.1E-02	1.07	2.7E-02	1.06	0.89
rs57414669	105415293	T	C	0.27	1.07	0.03	2.5E-02	0	<0.01	0.26	/I	8.0E-03	1.08	1.2E-02	1.08	0.63
rs28566061	104962704	A	G	0.40	1.05	0.02	2.5E-02	0	<0.01	0.35	/I	4.2E-02	1.04	2.4E-02	1.05	0.97
rs2819435	105416220	A	T	0.23	1.07	0.03	2.5E-02	4.36	<0.01	0.21	/I	1.1E-02	1.08	1.2E-02	1.08	0.73
rs11847866	105255205	A	G	0.28	1.05	0.02	2.5E-02	40.9	0.13	0.31	/I	2.2E-01	1.03	5.2E-01	1.02	0.86
rs12385898	104959641	A	T	0.40	1.05	0.02	2.5E-02	0	<0.01	0.35	/I	4.3E-02	1.04	2.4E-02	1.05	0.97
rs78809671	104964849	T	C	0.43	1.05	0.02	2.5E-02	0	<0.01	0.36	/I	3.8E-02	1.05	2.4E-02	1.05	0.88
rs113861864	104811549	A	G	0.02	0.77	0.12	2.6E-02	0	<0.01	0.04	/I	2.3E-02	0.76	2.4E-02	0.76	0.75
rs11848695	105255405	A	G	0.28	1.05	0.02	2.6E-02	40.81	0.13	0.31	/I	2.3E-01	1.03	5.3E-01	1.02	0.86
rs11628199	104961972	G	A	0.40	1.05	0.02	2.6E-02	0	<0.01	0.35	G*/I	4.4E-02	1.04	2.5E-02	1.05	0.97
rs28449913	104962667	C	G	0.40	1.05	0.02	2.6E-02	0	<0.01	0.35	/I	4.4E-02	1.04	2.5E-02	1.05	0.97
rs7149036	104967813	A	G	0.49	1.06	0.03	2.6E-02	0	<0.01	0.42	/I	4.4E-02	1.05	2.6E-02	1.06	0.68
rs3001410	105313998	C	T	0.26	1.06	0.03	2.6E-02	69.19	<0.01	0.23	/I	9.9E-03	1.08	2.0E-02	1.07	0.76
rs61758556	105256575	T	A	0.15	1.07	0.03	2.6E-02	0	0.27	0.15	/I	9.3E-01	1.00	5.3E-01	0.98	0.82
rs28714324	104962678	A	G	0.40	1.05	0.02	2.6E-02	0	<0.01	0.35	G*/I	4.5E-02	1.04	2.6E-02	1.05	0.97
rs10140805	104962372	C	T	0.40	1.05	0.02	2.6E-02	0	<0.01	0.35	G*/I	4.5E-02	1.04	2.6E-02	1.05	0.97
rs10151834	104962454	A	G	0.40	1.05	0.02	2.6E-02	0	<0.01	0.35	G*/I	4.5E-02	1.04	2.6E-02	1.05	0.97
rs10138337	104962178	C	T	0.40	1.05	0.02	2.6E-02	0	<0.01	0.35	G*/I	4.5E-02	1.04	2.6E-02	1.05	0.97
rs10149078	104962055	T	C	0.40	1.05	0.02	2.6E-02	0	<0.01	0.35	G*/I	4.5E-02	1.04	2.6E-02	1.05	0.97
rs12590313	104961635	A	G	0.40	1.05	0.02	2.7E-02	0	<0.01	0.35	G*/I	4.6E-02	1.04	2.6E-02	1.05	0.97
rs11160809	104964027	A	G	0.40	1.05	0.02	2.7E-02	0	<0.01	0.35	/I	4.6E-02	1.04	2.6E-02	1.05	0.96
rs12879055	104909124	T	C	0.12	0.93	0.03	2.7E-02	0	<0.01	0.06	/I	3.3E-02	0.93	2.2E-02	0.93	0.91
rs10142313	104959891	G	A	0.40	1.05	0.02	2.7E-02	0	<0.01	0.35	/I	4.6E-02	1.04	2.7E-02	1.05	0.97
rs61758466	105257354	A	G	0.15	1.07	0.03	2.7E-02	0	0.27	0.15	/I	9.4E-01	1.00	5.2E-01	0.98	0.82
rs67110142	105274945	A	G	0.26	1.06	0.02	2.7E-02	0	0.10	0.28	/I	2.5E-01	1.03	5.2E-01	1.02	0.88
rs4372620	104963414	C	T	0.40	1.05	0.02	2.7E-02	0	<0.01	0.35	/I	4.6E-02	1.04	2.6E-02	1.05	0.97
rs61999508	105630471	T	C	0.24	1.07	0.03	2.7E-02	0	<0.01	0.29	/I	2.0E-02	1.07	2.3E-02	1.07	0.82
rs11620654	104963006	T	C	0.40	1.05	0.02	2.8E-02	0	<0.01	0.35	G*/I	4.7E-02	1.04	2.7E-02	1.05	0.97
rs11625393	104962984	A	T	0.40	1.05	0.02	2.8E-02	0	<0.01	0.35	G*/I	4.7E-02	1.04	2.7E-02	1.05	0.97
rs35148920	104962															

rs4247030	105181848	G	A	0.23	0.95	0.03	3.1E-02	0	0.38	0.30	/I	5.8E-01	0.99	8.1E-01	1.01	0.95
rs56256371	105563060	A	C	0.45	1.05	0.02	3.1E-02	0	<0.01	0.45	/I	3.2E-02	1.05	1.8E-02	1.06	0.84
rs74212664	104965084	C	A	0.40	1.05	0.02	3.2E-02	0	<0.01	0.35	/I	5.3E-02	1.04	3.0E-02	1.05	0.94
rs72708091	104965112	C	T	0.40	1.05	0.02	3.2E-02	0	<0.01	0.35	/I	5.3E-02	1.04	3.0E-02	1.05	0.94
rs10138387	105315682	G	T	0.20	1.07	0.03	3.2E-02	74.1	0.01	0.17	/I	1.7E-02	1.07	3.7E-02	1.07	0.80
rs7153573	104973839	C	G	0.23	0.94	0.03	3.3E-02	73.72	<0.01	0.19	/I	1.9E-02	0.93	2.1E-02	0.93	0.86
rs4274376	104963402	A	T	0.40	1.05	0.02	3.3E-02	0	<0.01	0.35	/I	5.5E-02	1.04	3.2E-02	1.05	0.97
rs9672043	105180484	T	C	0.23	0.95	0.03	3.3E-02	0	0.38	0.30	/I	5.9E-01	0.99	8.0E-01	1.01	0.95
rs67183455	105281420	A	C	0.19	0.93	0.03	3.4E-02	74.83	<0.01	0.16	/I	2.4E-02	0.93	5.0E-02	0.94	0.65
rs7141960	104966414	A	C	0.40	1.05	0.02	3.4E-02	0	<0.01	0.35	G*/I	5.9E-02	1.04	3.2E-02	1.05	0.92
rs12886273	104976393	T	C	0.23	0.94	0.03	3.4E-02	73.14	<0.01	0.18	/I	2.0E-02	0.93	2.2E-02	0.93	0.86
rs77667449	105417353	G	T	0.22	1.07	0.03	3.4E-02	0	<0.01	0.22	/I	3.0E-03	1.11	5.9E-03	1.10	0.55
rs61996214	105678818	T	C	0.16	1.07	0.03	3.4E-02	0	<0.01	0.18	/I	4.9E-02	1.07	6.4E-02	1.07	0.77
rs4983535	105180565	C	T	0.23	0.95	0.03	3.4E-02	0	0.38	0.30	/I	6.0E-01	0.99	7.8E-01	1.01	0.95
rs10140224	104975015	C	T	0.23	0.94	0.03	3.4E-02	73.23	<0.01	0.18	/I	2.0E-02	0.93	2.2E-02	0.93	0.86
rs72715996	105277950	A	G	0.21	0.93	0.03	3.5E-02	53.52	0.03	0.22	/I	1.1E-01	0.95	5.4E-01	0.98	0.59
rs34552840	104909981	C	T	0.12	0.93	0.03	3.5E-02	0	<0.01	0.06	/I	4.3E-02	0.94	2.9E-02	0.93	0.91
rs2841244	105360746	C	T	0.23	1.06	0.03	3.5E-02	49.78	<0.01	0.19	/I	1.4E-02	1.07	3.6E-02	1.06	0.87
rs28562928	105316950	G	C	0.20	1.07	0.03	3.5E-02	75.16	0.01	0.17	/I	1.9E-02	1.07	4.0E-02	1.06	0.80
rs9805957	105437057	C	A	0.37	1.05	0.02	3.5E-02	0	<0.01	0.37	/I	2.9E-02	1.05	1.1E-02	1.06	0.92
rs117987592	105152336	A	G	0.12	1.08	0.04	3.5E-02	0	<0.01	0.12	/I	7.6E-01	1.01	4.3E-01	1.03	0.74
rs72707701	105661036	T	C	0.02	1.20	0.09	3.5E-02	9.14	0.02	0.03	/I	6.7E-02	1.17	8.2E-02	1.16	0.79
rs189195328	105321409	A	G	0.08	1.12	0.05	3.6E-02	33.09	<0.01	0.08	/I	2.6E-02	1.13	1.4E-02	1.14	0.47
rs187630833	105415394	C	T	0.24	1.07	0.03	3.7E-02	0	<0.01	0.26	/I	1.8E-03	1.11	5.0E-03	1.10	0.55
rs4983534	105178478	C	T	0.23	0.95	0.03	3.7E-02	0	0.38	0.30	/I	6.1E-01	0.99	7.6E-01	1.01	0.94
rs28375558	104939327	G	A	0.39	0.96	0.02	3.8E-02	0	<0.01	0.35	/I	6.3E-02	0.96	3.8E-02	0.96	0.95
rs74090040	105274801	A	C	0.28	1.05	0.02	3.8E-02	12.04	0.11	0.28	/I	2.6E-01	1.03	5.6E-01	1.02	0.86
rs2494736	105243565	G	A	0.07	1.09	0.04	3.8E-02	0	0.17	0.09	I/G	7.3E-01	1.02	9.3E-01	1.00	0.86
rs10873547	104949875	A	T	0.40	1.05	0.02	3.8E-02	0	<0.01	0.35	G*/I	6.3E-02	1.04	3.8E-02	1.05	0.97
rs4073164	104947517	T	C	0.40	1.05	0.02	3.8E-02	0	<0.01	0.35	G*/I	6.3E-02	1.04	3.8E-02	1.05	0.96
rs2582516	105314093	T	G	0.20	1.07	0.03	3.8E-02	72.84	0.01	0.17	/I	1.9E-02	1.07	4.3E-02	1.06	0.80
rs73352180	104910564	C	G	0.12	0.94	0.03	3.9E-02	0	<0.01	0.06	/I	4.7E-02	0.94	3.2E-02	0.93	0.91
rs187206356	105356468	T	A	0.10	0.90	0.05	3.9E-02	33.46	<0.01	0.08	/I	3.1E-02	0.90	2.1E-02	0.89	0.51
rs4577018	105480240	A	G	0.29	1.05	0.02	3.9E-02	0	<0.01	0.28	/I	4.3E-02	1.05	1.8E-02	1.06	0.99
rs6576069	105480130	C	T	0.29	1.05	0.02	3.9E-02	0	<0.01	0.28	/I	4.4E-02	1.05	1.8E-02	1.06	0.99
rs115474770	104942888	C	T	0.01	0.75	0.14	3.9E-02	7.48	<0.01	0.01	/I	5.7E-02	0.77	5.5E-02	0.77	0.68
rs4570772	105480250	G	T	0.29	1.05	0.02	3.9E-02	0	<0.01	0.28	/I	4.4E-02	1.05	1.8E-02	1.06	0.99
rs4577017	105480237	A	G	0.29	1.05	0.02	3.9E-02	0	<0.01	0.28	/I	4.4E-02	1.05	1.8E-02	1.06	0.99
rs4983563	104973165	G	A	0.23	0.94	0.03	3.9E-02	73.48	<0.01	0.19	/I	2.3E-02	0.93	2.6E-02	0.94	0.85
rs7150546	105493110	G	C	0.33	1.05	0.02	3.9E-02	0	<0.01	0.31	/I	3.6E-02	1.05	1.3E-02	1.06	0.97
rs11160820	105290070	G	A	0.20	0.94	0.03	3.9E-02	68.43	0.02	0.16	/I	1.4E-02	0.92	3.3E-02	0.93	0.69
rs35183811	105275924	A	G	0.27	1.05	0.02	4.0E-02	13.93	0.10	0.28	/I	2.8E-01	1.03	5.8E-01	1.01	0.90
rs28403559	104948334	T	G	0.40	1.05	0.02	4.0E-02	0	<0.01	0.35	G*/I	6.6E-02	1.04	4.0E-02	1.05	0.97
rs3902821	104948075	A	G	0.40	1.05	0.02	4.0E-02	0	<0.01	0.35	/I	6.7E-02	1.04	4.0E-02	1.05	0.97
rs879210	105420927	G	A	0.46	1.05	0.02	4.0E-02	33.6	<0.01	0.45	/I	3.3E-02	1.05	2.8E-02	1.05	0.84
rs78026692	105189968	A	G	0.08	1.09	0.04	4.0E-02	15.87	0.16	0.11	/I	5.8E-01	1.02	8.5E-01	1.01	0.91
rs10144833	105474840	G	A	0.29	1.05	0.02	4.0E-02	0	<0.01	0.28	/I	4.5E-02	1.05	1.9E-02	1.06	0.99
rs28715110	104941016	A	G	0.40	1.05	0.02	4.0E-02	0	<0.01	0.34	/I	6.3E-02	1.04	3.9E-02	1.05	0.93
rs7146925	105480025	A	G	0.29	1.05	0.02	4.1E-02	0	<0.01	0.28	/I	4.5E-02	1.05	1.9E-02	1.06	0.99
rs4075087	105479655	T	C	0.29	1.05	0.02	4.1E-02	0	<0.01	0.28	/I	4.5E-02	1.05	1.9E-02	1.06	0.99
rs11621569	104862889	T	C	0.16	0.93	0.03	4.1E-02	0	<0.01	0.12	/I	5.9E-02	0.94	4.5E-02	0.93	0.76
rs78413415	104943792	A	G	0.01	0.75	0.14	4.1E-02	6.6	<0.01	0.01	/I	5.9E-02	0.77	5.7E-02	0.77	0.68
rs10147672	105481186	A	G	0.29	1.05	0.02	4.1E-02	0	<0.01	0.28	/I	4.5E-02	1.05	1.9E-02	1.06	0.99
rs879209	105421050	G	T	0.46	1.05	0.02	4.1E-02	33.46	<0.01	0.45	/I	3.3E-02	1.05	2.8E-02	1.05	0.84
rs72713895	105151205	C	A	0.12	1.08	0.04	4.1E-02	0	0.14	0.12	/I	8.1E-01	1.01	4.4E-01	1.03	0.73
rs35511641	105430162	A	G	0.02	0.82	0.10	4.1E-02	0	<0.01	0.01	/I	4.5E-02	0.82	4.0E-02	0.82	0.61
rs2819429	105414280	G	T	0.16	1.07	0.03	4.1E-02	0	0.01	0.16	/I	2.0E-02	1.08	1.1E-02	1.09	0.80
rs193251778	105107977	G	T	0.04	0.85	0.08	4.2E-02	0	0.02	0.06	/I	6.9E-02	0.86	5.6E-02	0.85	0.44
rs117324809	105533420	A	G	0.04	1.17	0.08	4.2E-02	0	0.02	0.06	/I	1.2E-01	1.13	7.6E-02	1.15	0.50
rs145335724	104886007	A	G	0.02	1.20	0.09	4.2E-02	12.43	<0.01	0.03	/I	4.6E-02	1.20	5.2E-02	1.20	0.76
rs112040506	105316251	T	C	0.01	1.26	0.11	4.2E-02	4.39	<0.01	0.01	/I	1.3E-01	1.19	9.0E-02	1.21	0.66
rs78641964	104877106	A	G	0.02	1.20	0.09	4.3E-02	9.25	<0.01	0.03	/I	4.7E-02	1.20	5.4E-02	1.19	0.74
rs11160831	105482276	T	C	0.29	1.05	0.02	4.4E-02	0	<0.01	0.28	/I	4.9E-02	1.05	2.1E-02	1.05	0.99
rs55862960	105430738	A	G	0.37	1.05	0.02	4.4E-02	0	<0.01	0.38	/I	3.6E-02	1.05	1.4E-02	1.06	0.92
rs117623208	104882923	G	C	0.02	1.20	0.09	4.4E-02	15.13	<0.01	0.03	/I	4.8E-02	1.20	5.4E-02	1.19	0.76
rs79518131	105044745	A	G	0.02	1.22	0.10	4.4E-02	27.02	<0.01	0.02	/I	2.8E-02	1.24	2.0E-02	1.26	0.45
rs148561059	105230714	T	C	0.02	0.81	0.10	4.4E-02	8.46	0.01	0.02	/I	3.8E-01	0.91	1.9E-01	0.87	0.45
rs74090022	105245223	T	C	0.05	1.11	0.05	4.4E-02	21.86	0.11	0.05	/I	5.7E-01	1.03	8.3E-01	1.01	0.68
rs55791176	105418344	G	T	0.48	1.05	0.02	4.5E-02	63.92	<0.01	0.49	/I	3.2E-02	1.05	3.4E-02	1.05	0.87
rs117608670	104867949	G	A	0.02	1.21	0.09	4.5E-02	12.95	<0.01	0.03	/I	4.9E-02	1.20	5.6E-02	1.20	0.72
rs4983591	105002781	C	T	0.15	1.07	0.03	4.5E-02	63.77	<0.01	0.14	G*/I	6.8E-02	1.07	1.0E-01	1.06	0.87
rs28654371	105430927	G	T	0.36	1.05	0.02	4.5E-02	0	<0.01	0.36	/I	3.6E-02	1.05	1.4E-02	1.06	0.92
rs4247032	105184689	G	A	0.23	0.95	0.03	4.6E-02	0	0.39	0.29	/I	6.9E-01	0.99	6.7E-01	1.01	0.97
rs4983388	105318117	A	G	0.28	1.05	0.03	4.6E-02	80.11	0.01	0.25	/I	1.0E-02	1.07	1.3E-02	1.07	0.82
rs2582515	105314262	C	T	0.20	1.06	0.03	4.6E-									

rs116886725	104862877	A	G	0.03	0.87	0.08	5.4E-02	0	<0.01	0.03	/I	9.1E-02	0.88	7.0E-02	0.87	0.68
rs1160841	105673042	A	G	0.27	1.05	0.03	5.4E-02	0	<0.01	0.32	/I	6.0E-02	1.05	7.2E-02	1.05	0.89
rs33925946	105271836	T	G	0.28	1.05	0.02	5.5E-02	3.44	0.10	0.28	/I	3.2E-01	1.02	6.5E-01	1.01	0.89
rs117206535	104937693	T	C	0.04	1.12	0.06	5.5E-02	0	<0.01	0.01	/I	4.1E-02	1.13	4.6E-02	1.13	0.80
rs146460135	105464288	A	G	0.02	0.81	0.11	5.5E-02	28.22	0.01	0.01	/I	4.8E-02	0.81	6.3E-02	0.82	0.60
rs12887693	104976429	C	T	0.22	0.94	0.03	5.6E-02	75.03	0.01	0.18	/I	3.3E-02	0.94	3.7E-02	0.94	0.86
rs74409343	104821531	A	G	0.02	0.80	0.11	5.6E-02	0	<0.01	0.04	/I	4.9E-02	0.80	5.2E-02	0.80	0.74
rs4488389	104830428	T	C	0.23	0.94	0.03	5.7E-02	0	<0.01	0.28	/I	8.5E-02	0.95	7.5E-02	0.95	0.85
rs7146045	104915383	A	C	0.34	0.96	0.02	5.7E-02	0	<0.01	0.36	/G	7.8E-02	0.96	5.1E-02	0.96	0.96
rs59751257	104824825	T	C	0.02	0.81	0.11	5.7E-02	0	<0.01	0.04	/I	5.0E-02	0.80	5.3E-02	0.80	0.74
rs75288492	104825284	T	C	0.02	0.81	0.11	5.7E-02	0	<0.01	0.04	/I	5.0E-02	0.80	5.3E-02	0.80	0.74
rs187750084	105412328	T	C	0.23	1.06	0.03	5.8E-02	0	<0.01	0.21	/I	2.6E-02	1.07	2.4E-02	1.08	0.58
rs192308340	105412330	T	A	0.23	1.06	0.03	5.8E-02	0	<0.01	0.21	/I	2.6E-02	1.07	2.4E-02	1.08	0.58
rs4591063	104825323	G	T	0.23	0.94	0.03	5.8E-02	0	<0.01	0.28	/I	8.6E-02	0.95	7.7E-02	0.95	0.85
rs11625007	105418391	T	C	0.50	1.04	0.02	5.9E-02	56.84	<0.01	0.50	/I	4.3E-02	1.05	4.0E-02	1.05	0.84
rs3803300	105269779	C	T	0.09	0.93	0.04	5.9E-02	0	0.09	0.10	/I	5.9E-01	0.98	9.7E-01	1.00	0.95
rs111243858	104820457	T	G	0.02	0.80	0.12	5.9E-02	0	<0.01	0.04	/I	5.3E-02	0.80	5.5E-02	0.80	0.75
rs35914118	105290216	C	G	0.29	1.05	0.03	6.0E-02	71.64	<0.01	0.25	/I	1.7E-02	1.07	2.9E-02	1.06	0.71
rs34251364	105180785	T	C	0.08	1.07	0.04	6.1E-02	21.66	0.16	0.11	/I	7.5E-01	1.01	9.9E-01	1.00	0.95
rs2841215	105318852	A	G	0.06	1.12	0.06	6.1E-02	1.35	<0.01	0.02	/I	5.5E-02	1.12	8.4E-02	1.11	0.57
rs12896097	105015096	C	T	0.14	1.08	0.04	6.1E-02	0	<0.01	0.14	/I	6.4E-02	1.08	6.0E-02	1.08	0.56
rs57714398	104908584	A	G	0.13	0.94	0.03	6.1E-02	0	<0.01	0.06	/I	6.9E-02	0.94	4.9E-02	0.94	0.90
rs10254	105213376	T	C	0.04	1.12	0.06	6.1E-02	18.34	0.10	0.05	/I	5.4E-01	1.04	8.1E-01	1.02	0.72
rs12147772	105156756	G	A	0.48	1.05	0.02	6.1E-02	0	0.10	0.49	/I	5.1E-01	0.98	9.9E-01	1.00	0.88
rs2582497	105431949	C	A	0.29	1.05	0.02	6.2E-02	0	0.02	0.31	/I	5.7E-02	1.05	2.9E-02	1.06	0.93
rs5969979	105148770	G	T	0.06	1.09	0.05	6.2E-02	38.13	0.02	0.06	/I	2.7E-02	1.11	5.1E-02	1.09	0.91
rs7150255	104912876	T	C	0.35	0.96	0.02	6.2E-02	0	<0.01	0.36	/I	8.6E-02	0.96	5.7E-02	0.96	0.93
rs28548671	104971836	T	A	0.19	1.06	0.03	6.3E-02	17.43	<0.01	0.22	/I	8.7E-02	1.06	8.8E-02	1.06	0.79
rs61996004	105356290	G	A	0.22	1.07	0.04	6.3E-02	26.1	<0.01	0.23	/I	1.2E-02	1.09	1.9E-02	1.09	0.48
rs6576053	105081882	C	T	0.38	0.95	0.03	6.3E-02	0	<0.01	0.44	/I	6.5E-02	0.95	7.8E-02	0.96	0.85
rs112150875	104838133	A	G	0.06	0.90	0.06	6.3E-02	38.8	<0.01	0.05	/I	1.1E-01	0.91	9.9E-02	0.91	0.73
rs6576037	104870913	T	C	0.05	0.89	0.06	6.3E-02	46.9	<0.01	0.05	/I	4.5E-02	0.88	5.0E-02	0.89	0.67
rs12878750	105309608	T	C	0.20	1.06	0.03	6.3E-02	71.22	0.01	0.17	/I	3.6E-02	1.07	7.6E-02	1.06	0.78
rs4994392	105149702	G	A	0.15	1.08	0.04	6.3E-02	21.66	<0.01	0.13	/I	5.3E-01	1.03	3.8E-01	1.04	0.51
rs2582544	105374900	C	T	0.21	1.05	0.03	6.3E-02	56.64	0.01	0.19	/I	3.7E-02	1.06	5.6E-02	1.05	0.94
rs57609341	104816372	A	C	0.24	0.94	0.03	6.4E-02	0	<0.01	0.28	/I	9.1E-02	0.95	8.1E-02	0.95	0.85
rs7141547	104914539	C	T	0.35	0.96	0.02	6.4E-02	0	<0.01	0.36	/I	8.7E-02	0.96	5.8E-02	0.96	0.93
rs2841284	105312054	G	A	0.20	1.06	0.03	6.4E-02	72.14	0.01	0.17	/I	3.5E-02	1.07	7.5E-02	1.06	0.79
rs146449084	105415281	C	G	0.29	1.05	0.03	6.4E-02	0	<0.01	0.27	/I	2.0E-02	1.07	2.8E-02	1.06	0.65
rs3001409	105313861	G	A	0.23	1.06	0.03	6.4E-02	71.82	0.01	0.18	/I	3.1E-02	1.07	5.0E-02	1.06	0.74
rs77747991	104810541	A	G	0.21	0.94	0.03	6.4E-02	0	<0.01	0.24	/I	9.8E-02	0.95	8.6E-02	0.95	0.83
rs9652309	105486280	A	C	0.32	1.04	0.02	6.4E-02	0	<0.01	0.30	/I	6.1E-02	1.04	2.4E-02	1.05	0.98
rs35855714	105567150	G	C	0.34	1.05	0.02	6.4E-02	55.18	<0.01	0.31	/I	6.8E-02	1.05	3.8E-02	1.05	0.90
rs7150715	105493175	T	C	0.30	1.04	0.02	6.4E-02	0	<0.01	0.29	/I	7.0E-02	1.04	3.2E-02	1.05	0.99
rs12431529	104980330	T	C	0.23	0.95	0.03	6.4E-02	76.5	<0.01	0.19	/I	3.9E-02	0.94	4.3E-02	0.94	0.85
rs3924892	105494262	A	G	0.29	1.04	0.02	6.5E-02	0	<0.01	0.29	G*/I	7.2E-02	1.04	7.2E-02	1.05	0.99
rs6576038	104911441	G	A	0.35	0.96	0.02	6.5E-02	0	<0.01	0.36	/I	9.0E-02	0.96	5.9E-02	0.96	0.93
rs10130149	105309966	A	G	0.20	1.06	0.03	6.5E-02	72.21	0.01	0.17	/I	3.7E-02	1.07	7.8E-02	1.06	0.78
rs18665513	105635321	A	C	0.02	1.19	0.10	6.5E-02	67.94	<0.01	0.02	/I	9.6E-02	1.17	1.1E-01	1.16	0.54
rs2919621	105310498	C	T	0.20	1.06	0.03	6.5E-02	72.21	0.01	0.17	/I	3.6E-02	1.07	7.6E-02	1.06	0.79
rs11629188	105293940	G	C	0.20	0.94	0.03	6.5E-02	73.1	0.01	0.18	/I	3.9E-02	0.94	8.6E-02	0.95	0.73
rs45529634	105362199	T	C	0.03	1.14	0.07	6.6E-02	0	<0.01	0.04	/I	8.2E-02	1.13	1.0E-01	1.12	0.74
rs112235149	104917060	A	G	0.02	1.20	0.10	6.6E-02	0	<0.01	0.02	/I	8.0E-02	1.19	4.5E-02	1.22	0.46
rs141884370	105156001	A	G	0.13	1.07	0.04	6.6E-02	0	0.14	0.13	/I	9.8E-01	1.00	5.3E-01	1.02	0.77
rs72702010	105369308	C	T	0.03	1.13	0.07	6.7E-02	0	<0.01	0.06	/I	5.3E-02	1.13	8.0E-02	1.12	0.68
rs56729078	104815572	A	G	0.24	0.94	0.03	6.7E-02	0	<0.01	0.28	/I	9.6E-02	0.95	8.5E-02	0.95	0.85
rs28461670	104908412	C	T	0.13	0.94	0.03	6.8E-02	0	<0.01	0.06	/I	7.5E-02	0.94	5.3E-02	0.94	0.89
rs10147484	105481158	A	C	0.32	1.04	0.02	6.8E-02	0	<0.01	0.30	/I	6.7E-02	1.04	2.7E-02	1.05	0.99
rs11160832	105482352	A	G	0.32	1.04	0.02	6.9E-02	0	<0.01	0.30	/I	6.7E-02	1.04	2.7E-02	1.05	0.99
rs12101186	105308519	G	A	0.20	0.95	0.03	6.9E-02	73.47	<0.01	0.18	/I	4.5E-02	0.94	8.7E-02	0.95	0.77
rs11850821	105175085	G	A	0.09	1.07	0.04	6.9E-02	26.63	0.14	0.12	/I	8.0E-01	1.01	9.3E-01	1.00	0.95
rs12100484	104814471	G	A	0.24	0.95	0.03	6.9E-02	0	<0.01	0.28	/I	9.9E-02	0.95	8.9E-02	0.95	0.84
rs6576071	105495886	C	T	0.29	1.04	0.02	6.9E-02	0	<0.01	0.29	/I	7.6E-02	1.04	3.4E-02	1.05	0.99
rs11160821	105290076	G	A	0.07	0.90	0.06	6.9E-02	0	<0.01	0.10	/I	1.3E-02	0.87	1.6E-02	0.87	0.49
rs12884362	105545230	T	C	0.38	1.05	0.03	7.0E-02	17.45	<0.01	0.29	/I	6.6E-02	1.05	2.5E-02	1.06	0.64
rs183418924	105356323	G	A	0.07	1.11	0.06	7.0E-02	20.55	<0.01	0.10	/I	3.8E-02	1.13	3.3E-02	1.13	0.50
rs2498795	105243435	T	G	0.05	1.09	0.05	7.0E-02	0	0.10	0.05	/G	6.9E-01	1.02	9.0E-01	1.01	0.91
rs11628912	104896200	C	A	0.12	0.92	0.05	7.0E-02	11.93	<0.01	0.03	/I	9.7E-02	0.92	8.3E-02	0.92	0.52
rs3923888	105480587	T	C	0.32	1.04	0.02	7.0E-02	0	<0.01	0.30	/I	6.8E-02	1.04	2.8E-02	1.05	0.99
rs4983399	105003568	A	C	0.15	1.07	0.04	7.0E-02	42.77	<0.01	0.14	/I	8.8E-02	1.06	1.4E-01	1.05	0.82
rs3803294	105478102	A	G	0.32	1.04	0.02	7.1E-02	0	<0.01	0.30	/I	6.9E-02	1.04	2.8E-02	1.05	0.99
rs12431580	105478881	G	T	0.32	1.04	0.02	7.1E-02	0	<0.01	0.30	/I	6.9E-02	1.04	2.8E-02	1.05	0.99
rs4906452	104808535	G	A	0.29	0.95	0.03	7.1E-02	0	<0.01	0.25	/I	8.6E-02	0.95	7.8E-02	0.95	0.79
rs11851580	104908722	T	G	0.13	0.94	0.03	7.2E-02	0	<0.01	0.06	/I	8.0E-02	0.95	5.6E-02	0.94	0.90
rs2582506	105416685	G	C	0.36	1.05	0.02	7.2E-02									

rs75573399	105147285	A	G	0.06	1.10	0.05	7.8E-02	0	0.04	0.06	/I	3.1E-01	1.06	3.0E-01	1.06	0.79
rs7157970	105463936	C	T	0.32	1.04	0.02	7.9E-02	0	<0.01	0.29	G/G	7.7E-02	1.04	3.2E-02	1.05	1.00
rs28592881	104942599	T	C	0.18	0.95	0.03	7.9E-02	0	<0.01	0.09	/I	1.0E-01	0.96	7.6E-02	0.95	0.94
rs61997789	105541708	T	C	0.32	1.04	0.02	7.9E-02	23.49	<0.01	0.29	/I	9.0E-02	1.04	4.3E-02	1.05	0.88
rs56855842	105562601	A	G	0.07	0.91	0.05	7.9E-02	86.23	<0.01	0.05	/I	7.7E-02	0.91	7.0E-02	0.91	0.86
rs116975471	104843658	A	G	0.05	1.12	0.07	7.9E-02	58.06	<0.01	0.05	/I	7.8E-02	1.13	7.4E-02	1.13	0.49
rs8017794	105468764	A	T	0.21	1.05	0.03	7.9E-02	0	<0.01	0.19	/I	1.1E-01	1.04	6.3E-02	1.05	0.91
rs60916402	104815412	G	T	0.25	0.95	0.03	7.9E-02	0	<0.01	0.29	/I	1.1E-01	0.95	9.7E-02	0.95	0.85
rs7158370	105276053	G	A	0.12	0.94	0.04	8.0E-02	0	0.09	0.13	/I	5.9E-01	0.98	5.9E-01	1.00	0.71
rs34752012	105416734	G	T	0.01	1.26	0.13	8.0E-02	0	<0.01	0.02	/I	1.0E-01	1.24	8.1E-02	1.26	0.48
rs141756656	105195873	G	T	0.27	1.05	0.03	8.0E-02	0	<0.01	0.28	/I	1.7E-01	0.96	6.8E-02	0.94	0.78
rs2582577	105450112	T	C	0.19	0.95	0.03	8.0E-02	0	<0.01	0.16	/I	6.3E-02	0.95	3.7E-02	0.94	0.90
rs73357594	105443654	T	C	0.04	0.86	0.08	8.1E-02	41.53	0.01	0.02	/I	8.4E-02	0.87	6.5E-02	0.86	0.60
rs10146201	104978518	G	A	0.22	0.95	0.03	8.1E-02	74.59	<0.01	0.17	/I	4.9E-02	0.94	5.5E-02	0.94	0.86
rs192814484	105320781	G	A	0.09	0.91	0.05	8.1E-02	0	<0.01	0.06	/I	2.0E-01	0.93	2.4E-01	0.94	0.50
rs59478060	104813284	C	T	0.25	0.95	0.03	8.1E-02	0	<0.01	0.29	/I	1.1E-01	0.95	1.0E-01	0.95	0.84
rs12100485	104814453	T	C	0.25	0.95	0.03	8.1E-02	0	<0.01	0.28	/I	1.1E-01	0.95	1.0E-01	0.95	0.85
rs117034570	105174722	A	G	0.08	1.07	0.04	8.1E-02	26.59	0.16	0.11	/I	8.1E-01	1.01	9.4E-01	1.00	0.97
rs60377306	104815365	T	C	0.25	0.95	0.03	8.2E-02	0	<0.01	0.28	/I	1.1E-01	0.95	1.0E-01	0.95	0.85
rs6576063	105365456	G	C	0.21	1.05	0.03	8.2E-02	59.06	<0.01	0.18	/I	4.8E-02	1.06	7.2E-02	1.05	0.94
rs2582519	105312593	C	T	0.20	1.05	0.03	8.3E-02	74.22	<0.01	0.18	/I	5.3E-02	1.06	1.0E-01	1.05	0.78
rs141316041	105196796	T	C	0.07	1.07	0.04	8.3E-02	8.25	0.04	0.04	/I	8.9E-01	1.01	9.0E-01	0.99	0.94
rs2816666	105599946	G	A	0.23	1.05	0.03	8.3E-02	0	<0.01	0.25	/I	1.0E-01	1.05	7.0E-02	1.06	0.88
rs61996162	105665478	T	C	0.07	1.09	0.05	8.3E-02	0	<0.01	0.08	/I	1.2E-01	1.08	1.6E-01	1.07	0.69
rs11621606	105565770	T	C	0.34	1.04	0.02	8.3E-02	53.06	<0.01	0.31	/I	8.7E-02	1.04	5.0E-02	1.05	0.90
rs72713898	105157228	G	A	0.13	1.06	0.04	8.3E-02	0	0.14	0.13	/I	9.5E-01	1.00	6.2E-01	1.02	0.77
rs10142116	105285423	A	C	0.29	1.05	0.03	8.4E-02	76.74	<0.01	0.25	/I	2.2E-02	1.07	3.9E-02	1.06	0.71
rs12893998	105690946	C	T	0.28	1.04	0.03	8.4E-02	8.17	<0.01	0.32	/I	9.1E-02	1.04	1.0E-01	1.04	0.91
rs77971640	105445428	G	A	0.15	0.94	0.04	8.5E-02	2.03	0.01	0.12	/I	1.7E-01	0.95	7.0E-02	0.94	0.66
rs67906390	105292650	A	C	0.20	0.95	0.03	8.5E-02	75.6	0.01	0.17	/I	5.1E-02	0.94	1.1E-01	0.95	0.73
rs149534442	105469592	C	T	0.25	1.05	0.03	8.5E-02	51.26	<0.01	0.26	/I	1.7E-01	1.04	1.0E-01	1.05	0.66
rs9324080	105483700	C	T	0.32	1.04	0.02	8.5E-02	0	<0.01	0.30	/I	8.2E-02	1.04	3.4E-02	1.05	0.98
rs57515560	105148831	A	G	0.05	1.08	0.05	8.5E-02	50.4	0.01	0.06	/I	3.6E-02	1.10	6.5E-02	1.09	0.95
rs59509782	104813283	G	T	0.24	0.95	0.03	8.5E-02	0	<0.01	0.29	/I	1.2E-01	0.95	1.1E-01	0.95	0.84
rs7152944	105166002	G	A	0.09	1.06	0.04	8.5E-02	56.14	0.14	0.12	G*/I	8.0E-01	1.01	9.3E-01	1.00	0.99
rs2919630	105319292	A	C	0.37	1.04	0.02	8.6E-02	0	0.04	0.33	/I	3.4E-02	1.05	5.2E-02	1.04	0.91
rs117737288	104972672	A	G	0.01	0.80	0.13	8.6E-02	0	<0.01	0.01	/I	9.7E-02	0.80	1.0E-01	0.81	0.63
rs2241866	105455877	G	C	0.10	0.93	0.04	8.6E-02	0	<0.01	0.09	/I	1.1E-01	0.94	8.1E-02	0.93	0.76
rs12892016	105077624	C	T	0.39	0.96	0.03	8.6E-02	0	<0.01	0.44	/I	8.5E-02	0.96	1.0E-01	0.96	0.86
rs76136813	105167112	T	C	0.09	1.06	0.04	8.6E-02	54.45	0.14	0.12	/I	8.0E-01	1.01	9.3E-01	1.00	0.99
rs66987285	105292245	A	G	0.20	0.95	0.03	8.6E-02	75.64	0.01	0.17	/I	5.2E-02	0.94	1.2E-01	0.95	0.73
rs7150778	105566446	A	G	0.34	1.04	0.02	8.6E-02	52.3	<0.01	0.31	/I	8.9E-02	1.04	5.1E-02	1.05	0.90
rs2498807	105284772	A	T	0.29	0.95	0.03	8.7E-02	76.76	<0.01	0.25	/I	2.3E-02	0.94	4.0E-02	0.94	0.70
rs7153151	105166122	G	A	0.09	1.06	0.04	8.7E-02	56.02	0.14	0.12	G*/I	8.0E-01	1.01	9.3E-01	1.00	0.99
rs7150306	105454226	A	G	0.16	0.95	0.03	8.7E-02	0	<0.01	0.16	/I	8.1E-02	0.95	5.3E-02	0.94	0.93
rs73345582	105165872	C	G	0.09	1.06	0.04	8.7E-02	56.08	0.14	0.12	G*/I	8.0E-01	1.01	9.3E-01	1.00	0.99
rs78139891	105183474	T	C	0.02	1.18	0.10	8.7E-02	0	<0.01	0.05	/I	7.5E-03	1.30	1.7E-02	1.27	0.57
rs7153623	105166106	A	G	0.09	1.06	0.04	8.7E-02	56.02	0.14	0.12	G*/I	8.1E-01	1.01	9.2E-01	1.00	0.99
rs10145119	105349877	T	C	0.35	1.04	0.02	8.7E-02	0	0.04	0.32	/I	2.3E-02	1.05	4.7E-02	1.04	0.96
rs192581462	105356498	G	C	0.09	0.92	0.05	8.8E-02	49.29	<0.01	0.06	/I	1.3E-01	0.93	1.7E-01	0.93	0.47
rs760269	105608403	G	A	0.06	1.09	0.05	8.9E-02	0	<0.01	0.05	/I	7.4E-02	1.10	6.2E-02	1.10	0.86
rs12588024	105162493	A	T	0.06	1.08	0.05	8.9E-02	47.22	0.08	0.08	/I	6.4E-01	1.02	8.4E-01	1.01	0.86
rs61995965	105272806	G	A	0.09	0.94	0.04	8.9E-02	0.7	0.10	0.10	/I	7.3E-01	0.99	8.8E-01	1.01	0.90
rs56140783	105363410	T	C	0.31	1.04	0.02	8.9E-02	58.48	<0.01	0.27	/I	2.5E-02	1.06	3.5E-02	1.05	0.91
rs7159328	105460429	A	G	0.32	1.04	0.02	9.0E-02	0.38	<0.01	0.29	/I	8.6E-02	1.04	3.6E-02	1.05	1.00
rs8018607	105572749	C	T	0.34	1.04	0.02	9.0E-02	46.17	<0.01	0.32	/I	1.0E-01	1.04	5.2E-02	1.05	0.89
rs11847667	105167020	T	A	0.09	1.06	0.04	9.0E-02	54.87	0.14	0.12	/I	8.2E-01	1.01	9.1E-01	1.00	0.99
rs8018522	105162343	C	T	0.01	0.77	0.15	9.0E-02	0	<0.01	0.01	/I	2.4E-01	0.84	1.6E-01	0.81	0.47
rs10129625	105573654	C	T	0.34	1.04	0.02	9.0E-02	45.14	<0.01	0.32	/I	1.0E-01	1.04	5.2E-02	1.05	0.90
rs2582520	105312067	C	T	0.20	1.05	0.03	9.1E-02	74.22	<0.01	0.18	/I	5.8E-02	1.06	1.1E-01	1.05	0.78
rs139774148	105162977	A	G	0.01	0.77	0.16	9.1E-02	0	<0.01	0.01	/I	2.6E-01	0.84	1.7E-01	0.81	0.47
rs8017662	105162561	T	C	0.01	0.77	0.16	9.1E-02	0	<0.01	0.01	/I	2.6E-01	0.84	1.7E-01	0.81	0.47
rs4353429	105499828	G	C	0.28	1.05	0.03	9.1E-02	0	<0.01	0.29	/I	9.9E-02	1.05	4.9E-02	1.06	0.57
rs2819457	105448233	C	G	0.20	0.95	0.03	9.1E-02	14.08	<0.01	0.18	/I	7.6E-02	0.95	4.3E-02	0.94	0.90
rs7156965	105567506	A	G	0.34	1.04	0.02	9.1E-02	51.84	<0.01	0.31	/I	9.4E-02	1.04	5.4E-02	1.05	0.90
rs7156642	105567491	T	C	0.34	1.04	0.02	9.1E-02	51.85	<0.01	0.31	/I	9.4E-02	1.04	5.4E-02	1.05	0.90
rs34284721	105267934	A	G	0.12	1.06	0.03	9.2E-02	58.35	0.21	0.12	/I	7.8E-01	0.99	3.5E-01	0.97	0.77
rs77250823	105487819	T	C	0.04	1.10	0.06	9.2E-02	36.29	<0.01	0.02	/I	1.2E-01	1.09	1.3E-01	1.09	0.82
rs12889599	105302878	G	A	0.19	0.95	0.03	9.2E-02	71.5	0.01	0.17	/I	6.0E-02	0.94	1.1E-01	0.95	0.76
rs62638758	105167744	A	G	0.01	0.77	0.16	9.2E-02	0	<0.01	0.01	/I	2.6E-01	0.84	1.7E-01	0.81	0.48
rs4635277	105488267	C	G	0.32	1.04	0.02	9.2E-02	0	<0.01	0.30	/I	9.0E-02	1.04	3.8E-02	1.05	0.99
rs2816637	105611775	G	A	0.06	1.09	0.05	9.3E-02	0	<0.01	0.05	/I	7.8E-02	1.10	6.6E-02	1.10	0.86
rs141430061	105069922	C	T	0.11	1.07	0.04	9.3E-02	25.14	<0.01	0.11	/I	1.0E-01	1.07	1.1E-01	1.06	0.80
rs8016434	105468785	G	A	0.21	1.05	0.03	9.3E-02	0	<0.01	0.20	/I	1.2E-01	1.04	6.9E-02	1.05	0.89
rs6576062	105360355	T	C	0.31</												

rs10144463	105575294	A	G	0.37	1.04	0.03	9.8E-02	54.83	<0.01	0.36	/I	8.5E-02	1.04	5.0E-02	1.05	0.83
rs9743945	105564147	A	G	0.34	1.04	0.02	9.9E-02	52.41	<0.01	0.31	/I	1.0E-01	1.04	5.9E-02	1.05	0.90
rs10145122	105349886	T	C	0.34	1.04	0.02	9.9E-02	0	0.04	0.32	/I	2.6E-02	1.05	5.3E-02	1.04	0.97
rs2819460	105448809	G	A	0.20	0.96	0.03	9.9E-02	10.62	<0.01	0.18	/I	8.2E-02	0.95	4.6E-02	0.95	0.91
rs4983524	105148597	A	G	0.04	1.10	0.06	9.9E-02	0	<0.01	0.03	/I	8.8E-02	1.10	1.2E-01	1.09	0.91
rs3957307	105382578	T	G	0.21	1.05	0.03	9.9E-02	53.04	<0.01	0.19	/I	6.3E-02	1.05	8.8E-02	1.05	0.92
rs2582547	105319231	C	G	0.37	1.04	0.02	9.9E-02	0	0.04	0.33	/I	4.0E-02	1.05	6.1E-02	1.04	0.92
rs2816662	105596604	A	G	0.23	1.05	0.03	1.0E-01	0	<0.01	0.26	G*/I	1.2E-01	1.05	8.7E-02	1.05	0.89
rs62641737	105352651	T	C	0.03	1.15	0.09	1.0E-01	0	<0.01	0.04	/I	6.2E-02	1.18	1.0E-01	1.15	0.53
rs61996057	105469368	T	G	0.32	1.04	0.02	1.0E-01	3.58	<0.01	0.29	/I	9.9E-02	1.04	4.2E-02	1.05	0.98
rs17846832	105238636	C	G	0.07	1.07	0.04	1.0E-01	0	<0.01	0.04	/I	9.8E-01	1.00	8.2E-01	0.99	0.96
rs4457931	104831411	C	G	0.30	0.95	0.03	1.0E-01	0	<0.01	0.33	/I	1.2E-01	0.96	1.3E-01	0.96	0.84
rs4983525	105148632	C	G	0.05	1.08	0.05	1.0E-01	46.28	<0.01	0.06	/I	4.5E-02	1.10	7.7E-02	1.08	1.00
rs2735801	105598048	A	T	0.23	1.05	0.03	1.0E-01	0	<0.01	0.25	/I	1.3E-01	1.05	8.8E-02	1.05	0.88
rs2498778	105283159	T	C	0.25	0.95	0.03	1.0E-01	76.3	<0.01	0.22	/I	5.2E-02	0.94	1.0E-01	0.95	0.70
rs77422581	105122086	A	G	0.06	1.09	0.05	1.0E-01	0	0.03	0.07	/I	3.6E-01	1.05	3.6E-01	1.05	0.82
rs2498779	105283406	A	G	0.25	0.95	0.03	1.0E-01	76.28	<0.01	0.22	/I	5.3E-02	0.94	1.0E-01	0.95	0.70
rs2498809	105283166	T	C	0.25	0.95	0.03	1.0E-01	76.31	<0.01	0.22	/I	5.3E-02	0.94	1.0E-01	0.95	0.70
rs2919622	105382003	C	T	0.21	1.05	0.03	1.0E-01	56.7	0.01	0.19	/I	6.4E-02	1.05	9.1E-02	1.05	0.94
rs4983526	105148655	T	C	0.05	1.08	0.05	1.0E-01	46.71	0.01	0.06	G/G	4.6E-02	1.09	7.9E-02	1.08	1.00
rs6576041	104919290	A	T	0.40	0.97	0.02	1.0E-01	0	<0.01	0.38	/I	1.5E-01	0.97	1.0E-01	0.97	0.95
rs117379881	105415745	G	C	0.48	1.04	0.02	1.0E-01	0	<0.01	0.48	/I	2.4E-02	1.06	3.2E-02	1.05	0.78
rs3001421	105381763	C	T	0.21	1.05	0.03	1.0E-01	56.71	0.01	0.19	G*/I	6.5E-02	1.05	9.2E-02	1.05	0.94
rs3002452	105283727	C	T	0.25	0.95	0.03	1.0E-01	76.32	<0.01	0.22	/I	5.3E-02	0.94	1.1E-01	0.95	0.70
rs7160811	105564734	A	G	0.34	1.04	0.02	1.0E-01	52.31	<0.01	0.31	G*/I	1.1E-01	1.04	6.1E-02	1.05	0.90
rs12147672	105663187	A	G	0.30	1.04	0.03	1.0E-01	0	<0.01	0.31	/I	1.1E-01	1.04	3.6E-01	1.04	0.88
rs60754080	105414238	A	C	0.44	1.04	0.02	1.0E-01	7.69	<0.01	0.45	/I	5.8E-02	1.05	8.7E-02	1.04	0.79
rs11538811	105171022	A	C	0.08	1.06	0.04	1.0E-01	29.74	0.16	0.11	/I	8.8E-01	1.01	8.7E-01	0.99	0.98
rs7153342	104782659	C	T	0.36	0.96	0.03	1.0E-01	15.49	<0.01	0.38	/I	1.1E-01	0.96	8.9E-02	0.96	0.88
rs10162501	105486749	A	G	0.30	1.04	0.02	1.0E-01	0	<0.01	0.31	/I	1.3E-01	1.04	6.2E-02	1.04	0.96
rs12885315	105562697	G	C	0.34	1.04	0.02	1.0E-01	51.61	<0.01	0.31	/I	1.1E-01	1.04	6.3E-02	1.05	0.90
rs10139525	105285159	G	A	0.29	1.05	0.03	1.0E-01	74.35	<0.01	0.25	/I	2.5E-02	1.06	5.2E-02	1.06	0.71
rs12435117	105570924	G	T	0.34	1.04	0.02	1.1E-01	50.52	<0.01	0.32	/I	1.1E-01	1.04	6.3E-02	1.05	0.90
rs11620979	105648277	G	C	0.35	1.04	0.03	1.1E-01	0	<0.01	0.39	/I	1.1E-01	1.04	1.1E-01	1.04	0.81
rs4448870	105571894	T	C	0.34	1.04	0.02	1.1E-01	50.77	<0.01	0.32	/I	1.1E-01	1.04	6.4E-02	1.05	0.90
rs4497620	105571959	A	G	0.34	1.04	0.02	1.1E-01	50.76	<0.01	0.32	/I	1.1E-01	1.04	6.4E-02	1.05	0.90
rs11623028	105596992	A	G	0.23	1.05	0.03	1.1E-01	0	<0.01	0.25	/I	1.4E-01	1.04	9.5E-02	1.05	0.88
rs73350354	105278492	T	C	0.02	0.84	0.11	1.1E-01	0	<0.01	0.01	/I	9.3E-02	0.83	6.2E-02	0.82	0.55
rs1554960	105599634	C	T	0.23	1.05	0.03	1.1E-01	0	<0.01	0.25	/I	1.3E-01	1.05	9.3E-02	1.05	0.88
rs142317644	105665739	T	C	0.02	1.16	0.09	1.1E-01	74.88	<0.01	0.02	/I	9.6E-02	1.17	1.1E-01	1.16	0.54
rs6576074	105569170	C	T	0.34	1.04	0.02	1.1E-01	48.5	<0.01	0.32	/I	1.1E-01	1.04	6.5E-02	1.05	0.90
rs11622579	105689647	A	G	0.28	1.04	0.03	1.1E-01	11.11	<0.01	0.32	/I	1.1E-01	1.04	1.3E-01	1.04	0.92
rs79009899	105304385	C	G	0.19	0.95	0.03	1.1E-01	73.03	0.01	0.16	/I	6.4E-02	0.94	1.2E-01	0.95	0.77
rs2816665	105599938	C	T	0.23	1.05	0.03	1.1E-01	0	<0.01	0.25	/I	1.3E-01	1.05	9.4E-02	1.05	0.88
rs10130501	105570615	G	A	0.34	1.04	0.02	1.1E-01	48.33	<0.01	0.32	/I	1.1E-01	1.04	6.5E-02	1.05	0.90
rs10130930	105570821	A	G	0.34	1.04	0.02	1.1E-01	50.23	<0.01	0.32	/I	1.1E-01	1.04	6.5E-02	1.05	0.90
rs2013462	105416959	G	A	0.49	1.04	0.03	1.1E-01	2.22	<0.01	0.50	/I	3.7E-02	1.05	5.2E-02	1.05	0.70
rs66802074	104835864	T	C	0.23	0.95	0.03	1.1E-01	0	<0.01	0.26	/I	1.5E-01	0.96	1.4E-01	0.95	0.85
rs28391579	105470463	G	T	0.32	1.04	0.02	1.1E-01	0	<0.01	0.29	/I	1.0E-01	1.04	4.6E-02	1.05	0.99
rs8015942	105568787	C	T	0.34	1.04	0.02	1.1E-01	47.94	<0.01	0.32	/I	1.1E-01	1.04	6.6E-02	1.05	0.90
rs33997228	105679373	T	G	0.28	1.04	0.02	1.1E-01	0	<0.01	0.32	/I	1.2E-01	1.04	1.3E-01	1.04	0.93
rs7157947	105569365	T	C	0.34	1.04	0.02	1.1E-01	47.91	<0.01	0.32	/I	1.1E-01	1.04	6.6E-02	1.05	0.90
rs7158905	105569998	G	A	0.34	1.04	0.02	1.1E-01	47.9	<0.01	0.32	/I	1.1E-01	1.04	6.6E-02	1.05	0.90
rs7159054	105570049	G	A	0.34	1.04	0.02	1.1E-01	47.89	<0.01	0.32	/I	1.1E-01	1.04	6.6E-02	1.05	0.90
rs12896149	105570102	T	G	0.34	1.04	0.02	1.1E-01	47.88	<0.01	0.32	/I	1.1E-01	1.04	6.6E-02	1.05	0.90
rs4464011	105589636	C	T	0.11	0.94	0.04	1.1E-01	0	<0.01	0.14	/I	1.1E-01	0.94	1.0E-01	0.93	0.85
rs7140735	105237401	G	A	0.07	1.07	0.04	1.1E-01	0	0.04	0.04	/I	9.7E-01	1.00	7.8E-01	0.99	0.95
rs56069762	105560437	T	C	0.34	1.04	0.02	1.1E-01	51.27	<0.01	0.31	/I	1.2E-01	1.04	6.7E-02	1.05	0.89
rs4357873	105574565	C	T	0.34	1.04	0.02	1.1E-01	45.22	<0.01	0.32	/I	1.2E-01	1.04	6.5E-02	1.05	0.91
rs72703887	105527735	T	C	0.10	0.93	0.05	1.1E-01	0	<0.01	0.11	/I	1.1E-01	0.93	1.2E-01	0.93	0.63
rs10144185	105575159	G	C	0.35	1.04	0.02	1.1E-01	47.53	<0.01	0.34	/I	1.2E-01	1.04	6.9E-02	1.05	0.90
rs57718059	105171619	C	T	0.08	1.06	0.04	1.1E-01	29.94	0.16	0.11	/I	9.1E-01	1.00	8.4E-01	0.99	0.98
rs3891052	105672895	T	C	0.28	1.04	0.03	1.1E-01	0	<0.01	0.30	/I	1.3E-01	1.04	1.5E-01	1.04	0.88
rs28626414	105587664	A	G	0.11	0.94	0.04	1.1E-01	0	<0.01	0.14	G*/I	1.0E-01	0.93	1.0E-01	0.93	0.86
rs4377097	105560678	G	A	0.34	1.04	0.02	1.1E-01	49.81	<0.01	0.31	/I	1.2E-01	1.04	6.8E-02	1.05	0.90
rs186344496	105427668	G	A	0.02	1.15	0.09	1.1E-01	0	<0.01	0.02	/I	2.7E-01	1.10	2.3E-01	1.11	0.78
rs115602636	105156076	A	G	0.08	1.06	0.04	1.1E-01	41.13	0.14	0.12	/I	9.2E-01	1.00	9.6E-01	1.00	0.89
rs2028415	105349220	G	T	0.35	1.03	0.02	1.1E-01	0	0.04	0.31	/I	3.1E-02	1.05	5.9E-02	1.04	0.99
rs12885324	105562765	G	A	0.36	1.04	0.02	1.1E-01	57.14	<0.01	0.33	/I	1.1E-01	1.04	7.4E-02	1.05	0.85
rs2582492	105443695	T	C	0.29	0.96	0.03	1.1E-01	0	<0.01	0.32	/I	1.2E-01	0.96	6.4E-02	0.95	0.84
rs12886857	105279618	T	C	0.17	1.06	0.03	1.1E-01	77.87	0.02	0.13	/I	6.0E-02	1.07	1.2E-01	1.06	0.66
rs2582574	105454529	G	A	0.19	0.96	0.03	1.1E-01	29.68	<0.01	0.18	/I	9.3E-02	0.95	5.5E-02	0.95	0.93
rs72702011	105370802	G	A	0.03	1.11	0.07	1.1E-01	0	0.01	0.05	/I	1.1E-01	1.11	1.3E-01	1.10	0.71
rs4983529	105155355	C	T	0.48	1.04	0.02	1.1E-01	0	0.09	0.48	/I	4.4E-01	0.98	8.6E-01	1.00	0.84
rs2841277	105391005	T	C	0.47	0.97	0.02	1.1E-01	54.84	<0.01	0.48	G/G					

rs12885406	105450109	C	T	0.19	0.96	0.03	1.2E-01	0	<0.01	0.18	/I	9.3E-02	0.95	5.7E-02	0.95	0.91
rs2494750	105262912	C	G	0.07	0.94	0.04	1.2E-01	0	0.07	0.08	/I	7.1E-01	0.98	9.5E-01	1.00	0.91
rs7155121	105563519	C	T	0.34	1.04	0.02	1.2E-01	51.82	<0.01	0.31	/I	1.2E-01	1.04	7.2E-02	1.05	0.90
rs74629810	105469336	A	T	0.33	1.04	0.02	1.2E-01	5.16	<0.01	0.32	/I	1.2E-01	1.04	5.5E-02	1.04	0.95
rs8014250	105575693	G	C	0.33	1.04	0.02	1.2E-01	0	<0.01	0.32	/I	1.4E-01	1.04	7.5E-02	1.05	0.90
rs28600075	105408315	C	T	0.47	1.03	0.02	1.2E-01	57.91	<0.01	0.48	/I	7.4E-02	1.04	9.7E-02	1.04	0.97
rs11624762	105312935	T	C	0.13	0.94	0.04	1.2E-01	65.35	0.02	0.14	G*/I	7.0E-02	0.94	1.1E-01	0.94	0.90
rs28454709	105405942	A	G	0.47	1.03	0.02	1.2E-01	57.58	<0.01	0.48	/I	7.4E-02	1.04	9.7E-02	1.04	0.97
rs34274508	105004581	C	T	0.14	1.06	0.04	1.2E-01	42.66	<0.01	0.14	/I	1.5E-01	1.05	2.2E-01	1.04	0.83
rs2494744	105255814	G	A	0.08	0.94	0.04	1.2E-01	0	0.07	0.08	/G	7.9E-01	0.99	8.6E-01	1.01	0.88
rs80022508	105182891	A	G	0.04	0.89	0.08	1.2E-01	53.39	0.03	0.06	/I	5.9E-01	0.96	3.9E-01	0.94	0.53
rs2819426	105412259	C	G	0.27	1.05	0.03	1.2E-01	3.17	<0.01	0.25	/I	8.6E-02	1.05	1.1E-01	1.05	0.61
rs10083496	105402786	A	G	0.47	1.03	0.02	1.2E-01	57.01	<0.01	0.48	/I	7.3E-02	1.04	9.6E-02	1.04	0.97
rs4983565	104975650	G	A	0.21	0.95	0.03	1.2E-01	75.55	<0.01	0.18	G*/I	7.1E-02	0.95	8.2E-02	0.95	0.88
rs11624956	105184631	A	G	0.01	0.80	0.15	1.2E-01	0	0.01	0.02	/I	3.5E-01	0.87	2.4E-01	0.84	0.49
rs55797226	105413223	G	A	0.47	1.03	0.02	1.2E-01	52.12	<0.01	0.49	/I	8.1E-02	1.04	9.9E-02	1.04	0.93
rs2841223	105334196	A	C	0.36	1.03	0.02	1.2E-01	0	0.04	0.33	/I	4.2E-02	1.04	7.4E-02	1.04	1.00
rs736066	105435649	G	A	0.29	1.04	0.03	1.2E-01	0	0.01	0.29	G*/I	1.2E-01	1.04	7.2E-02	1.05	0.94
rs11627133	105541463	C	T	0.31	1.04	0.02	1.2E-01	5.59	<0.01	0.28	/I	1.4E-01	1.04	7.4E-02	1.04	0.91
rs7146406	104972592	C	A	0.33	0.96	0.03	1.2E-01	60.32	<0.01	0.31	/I	9.7E-02	0.96	1.1E-01	0.96	0.80
rs2498784	105264963	G	A	0.07	0.94	0.04	1.2E-01	0	0.07	0.08	/I	7.8E-01	0.99	8.8E-01	1.01	0.94
rs56116208	105191538	G	C	0.04	0.90	0.07	1.2E-01	61.3	0.03	0.06	/I	6.4E-01	0.97	4.1E-01	0.95	0.56
rs76959031	105210447	G	T	0.07	1.06	0.04	1.2E-01	0	0.04	0.04	/I	9.1E-01	1.00	7.1E-01	0.98	0.96
rs2028414	105349388	C	A	0.35	1.03	0.02	1.2E-01	0	0.04	0.31	/I	3.6E-02	1.05	6.6E-02	1.04	0.99
rs61996161	105639175	C	G	0.35	1.04	0.03	1.2E-01	0	<0.01	0.38	/I	1.4E-01	1.04	1.3E-01	1.04	0.83
rs79405222	105214669	A	C	0.08	0.94	0.04	1.2E-01	0	0.05	0.09	/I	9.4E-01	1.00	5.9E-01	0.98	0.68
rs12884027	105450002	A	C	0.16	0.96	0.03	1.2E-01	0	<0.01	0.16	/I	1.2E-01	0.95	7.7E-02	0.95	0.92
rs2494741	105249322	T	C	0.08	1.06	0.04	1.2E-01	0	0.07	0.08	/I	7.9E-01	1.01	8.4E-01	0.99	0.85
rs35960466	105064771	A	G	0.38	0.96	0.03	1.3E-01	0	<0.01	0.44	/I	1.3E-01	0.96	1.6E-01	0.97	0.89
rs118109748	105291862	A	G	0.04	0.90	0.07	1.3E-01	0	<0.01	0.05	/I	1.4E-01	0.90	1.5E-01	0.91	0.63
rs66481343	104983421	A	G	0.15	0.95	0.03	1.3E-01	0	<0.01	0.09	/I	1.3E-01	0.95	9.6E-02	0.95	0.89
rs56159244	105519559	G	A	0.32	1.04	0.02	1.3E-01	0	<0.01	0.28	/I	1.5E-01	1.04	7.8E-02	1.04	0.85
rs34344799	105324484	T	C	0.36	1.03	0.02	1.3E-01	0	0.04	0.33	/I	4.3E-02	1.04	7.5E-02	1.04	0.97
rs8008615	105486729	A	G	0.11	0.95	0.03	1.3E-01	0	0.01	0.11	/I	1.0E-01	0.95	6.8E-02	0.94	0.96
rs117278745	105178151	A	G	0.01	0.80	0.15	1.3E-01	0	<0.01	0.02	/I	3.7E-01	0.87	2.5E-01	0.84	0.49
rs2582561	105345331	C	T	0.35	1.03	0.02	1.3E-01	0	0.04	0.31	/I	3.7E-02	1.05	6.8E-02	1.04	0.99
rs28627825	105084117	A	C	0.07	0.93	0.05	1.3E-01	0	<0.01	0.06	/I	9.1E-02	0.92	1.0E-01	0.92	0.76
rs28477712	105670559	C	T	0.16	0.95	0.03	1.3E-01	0	<0.01	0.15	/I	1.3E-01	0.95	1.4E-01	0.95	0.80
rs138919548	105179463	G	C	0.01	0.80	0.15	1.3E-01	0	<0.01	0.02	/I	3.7E-01	0.88	2.5E-01	0.84	0.49
rs28520026	105587513	T	C	0.11	0.94	0.04	1.3E-01	0	<0.01	0.14	/I	1.2E-01	0.94	1.2E-01	0.94	0.86
rs113524219	105640986	A	G	0.02	1.15	0.09	1.3E-01	0	<0.01	0.02	/I	2.0E-01	1.13	2.5E-01	1.11	0.79
rs61996017	105360947	A	G	0.01	1.21	0.13	1.3E-01	21.97	0.01	0.02	/I	4.2E-02	1.30	6.6E-02	1.26	0.51
rs11850453	105684721	C	T	0.28	1.04	0.02	1.3E-01	0	<0.01	0.32	/I	1.4E-01	1.04	1.6E-01	1.04	0.93
rs4329859	104803674	C	T	0.30	0.96	0.03	1.3E-01	0	<0.01	0.25	/I	1.5E-01	0.96	1.4E-01	0.96	0.81
rs4334223	105490896	A	G	0.11	0.95	0.03	1.3E-01	0	<0.01	0.12	/I	1.2E-01	0.95	7.1E-02	0.94	0.96
rs117057128	105103972	T	C	0.03	1.12	0.07	1.3E-01	37.96	0.01	0.03	/I	6.1E-02	1.15	9.9E-02	1.13	0.76
rs11625588	105298315	C	G	0.19	0.95	0.03	1.3E-01	71.99	0.01	0.16	/I	8.3E-02	0.95	1.7E-01	0.96	0.74
rs117457867	105180652	T	C	0.01	0.80	0.15	1.3E-01	0	<0.01	0.02	/I	3.7E-01	0.88	2.5E-01	0.84	0.49
rs45463395	105207642	T	C	0.07	1.06	0.04	1.3E-01	0	0.04	0.04	/I	9.0E-01	0.99	7.0E-01	0.98	0.95
rs4073804	104808801	T	C	0.21	0.95	0.03	1.3E-01	0	<0.01	0.23	/I	1.9E-01	0.96	1.6E-01	0.96	0.82
rs188729656	105351271	T	C	0.03	0.87	0.09	1.3E-01	46.84	<0.01	0.01	/I	3.2E-02	0.82	3.5E-02	0.82	0.50
rs4492978	105482485	C	G	0.11	0.95	0.03	1.3E-01	0	<0.01	0.11	/I	1.1E-01	0.95	6.8E-02	0.94	0.97
rs12587575	105223420	A	G	0.07	1.06	0.04	1.3E-01	0	0.04	0.04	/I	8.9E-01	0.99	6.9E-01	0.98	0.97
rs12890396	105516226	T	C	0.32	1.03	0.02	1.3E-01	0	<0.01	0.32	/I	1.1E-01	1.04	4.3E-02	1.05	0.95
rs61997108	104782996	A	C	0.22	0.95	0.03	1.3E-01	21.3	<0.01	0.26	/I	1.6E-01	0.96	1.3E-01	0.95	0.84
rs12433815	105412542	G	A	0.33	1.04	0.03	1.3E-01	0	<0.01	0.31	/I	5.4E-02	1.05	8.7E-02	1.05	0.65
rs118097302	105183329	T	C	0.01	0.80	0.15	1.3E-01	0	<0.01	0.02	/I	3.8E-01	0.88	2.5E-01	0.84	0.49
rs61996163	105671276	A	G	0.02	1.15	0.10	1.3E-01	0	<0.01	0.03	/I	1.0E-01	1.17	9.2E-02	1.17	0.54
rs8013710	105065267	A	G	0.08	0.93	0.05	1.3E-01	0	<0.01	0.06	/I	8.9E-02	0.92	1.2E-01	0.93	0.79
rs28480267	105339284	C	T	0.49	1.03	0.02	1.3E-01	0	0.02	0.48	/I	6.7E-02	1.04	5.7E-02	1.04	0.87
rs7155738	105184116	A	G	0.01	0.80	0.15	1.3E-01	0	<0.01	0.02	/I	3.8E-01	0.88	2.6E-01	0.84	0.49
rs2841235	105348733	T	G	0.40	1.03	0.02	1.3E-01	0	0.05	0.35	/I	2.8E-02	1.05	4.2E-02	1.04	0.98
rs6576067	105473903	T	C	0.11	0.95	0.03	1.3E-01	0	<0.01	0.11	/I	1.1E-01	0.95	7.0E-02	0.94	0.98
rs2494749	105258893	G	A	0.10	0.95	0.04	1.3E-01	0	0.06	0.14	/I	6.5E-01	0.98	9.8E-01	1.00	0.74
rs7157045	105184269	A	T	0.01	0.80	0.15	1.3E-01	0	<0.01	0.02	/I	3.8E-01	0.88	2.6E-01	0.84	0.49
rs11715233	105589675	C	T	0.02	1.17	0.10	1.3E-01	44.22	<0.01	0.02	/I	1.2E-01	1.18	6.6E-02	1.21	0.49
rs4983520	105141027	C	T	0.43	1.04	0.03	1.3E-01	0	0.02	0.44	/I	2.4E-01	1.03	2.1E-01	1.03	0.85
rs117387615	104943168	A	G	0.06	1.10	0.06	1.4E-01	0	0.01	0.09	/I	8.5E-02	1.11	9.7E-02	1.11	0.47
rs111666304	104930755	G	A	0.06	1.07	0.05	1.4E-01	0	0.01	0.03	/I	1.1E-01	1.08	1.2E-01	1.08	0.81
rs7145565	105477613	C	T	0.11	0.95	0.03	1.4E-01	0	<0.01	0.11	G*/I	1.2E-01	0.95	7.1E-02	0.94	0.98
rs34527763	105062190	A	G	0.38	0.96	0.03	1.4E-01	0	<0.01	0.44	/I	1.5E-01	0.96	1.7E-01	0.97	0.88
rs8004004	105142574	G	A	0.42	1.04	0.03	1.4E-01	0	0.02	0.44	/I	2.4E-01	1.03	2.1E-01	1.03	0.84
rs12433813	105132581	C	T	0.45	1.04	0.03	1.4E-01	22.01	0.04	0.46	/I	2.6E-01	1.03	2.4E-01	1.03	0.82
rs8023004	105116232	T	G	0.45	1.04	0.03	1.4E-01	0	0.05	0.48	G*/I	2.2E-01	1.04	4.4E-01	1.02	0.86
rs28615744	105074753	A	G	0.08	0.93	0.05	1.4E-01	0	<0.01	0.06	/I	9.2E-02	0.92			

rs8014717	105296055	C	T	0.02	0.85	0.11	1.4E-01	0	<0.01	0.05	/I	8.2E-02	0.83	1.1E-01	0.84	0.47
rs35040216	104943086	G	A	0.20	0.96	0.03	1.4E-01	0	<0.01	0.09	/I	1.7E-01	0.96	1.3E-01	0.96	0.94
rs12433837	105412541	T	C	0.33	1.04	0.03	1.4E-01	0	<0.01	0.31	/I	5.6E-02	1.05	9.2E-02	1.05	0.65
rs112894309	105629943	A	C	0.03	1.13	0.08	1.4E-01	21.83	<0.01	0.02	/I	1.5E-01	1.13	1.5E-01	1.13	0.60
rs11845844	105484039	A	G	0.11	0.95	0.03	1.4E-01	0	<0.01	0.11	/I	1.2E-01	0.95	7.4E-02	0.94	0.97
rs1022431	105603415	A	C	0.11	0.94	0.04	1.4E-01	0	<0.01	0.12	/I	1.4E-01	0.94	1.4E-01	0.94	0.84
rs151018124	105304019	T	C	0.13	0.95	0.04	1.4E-01	70.1	0.02	0.14	/I	8.3E-02	0.94	1.4E-01	0.95	0.85
rs28459454	104942628	A	G	0.20	0.96	0.03	1.4E-01	0	<0.01	0.09	/I	1.7E-01	0.96	1.3E-01	0.96	0.94
rs4983521	105142946	C	T	0.42	1.04	0.03	1.4E-01	0	0.02	0.44	/I	2.5E-01	1.03	2.2E-01	1.03	0.84
rs56166764	104983966	A	G	0.15	0.95	0.03	1.4E-01	0	<0.01	0.09	/I	1.4E-01	0.95	1.1E-01	0.95	0.89
rs4553558	105140132	C	T	0.43	1.04	0.03	1.4E-01	0	0.02	0.44	/I	2.5E-01	1.03	2.2E-01	1.03	0.86
rs4077520	105153469	G	A	0.32	1.04	0.03	1.4E-01	8.93	<0.01	0.34	/I	9.4E-01	1.00	2.1E-01	1.03	0.82
rs12883995	105449928	G	C	0.19	0.96	0.03	1.4E-01	0	<0.01	0.17	/I	1.2E-01	0.96	7.1E-02	0.95	0.91
rs28675197	105489565	T	C	0.11	0.95	0.03	1.4E-01	0	<0.01	0.11	/I	1.2E-01	0.95	7.6E-02	0.94	0.97
rs80205198	105203855	C	G	0.09	0.94	0.04	1.4E-01	0	0.05	0.10	/I	7.8E-01	1.01	7.1E-01	0.99	0.71
rs28405640	104775852	G	C	0.35	0.96	0.03	1.4E-01	1.75	<0.01	0.37	/I	1.5E-01	0.96	1.3E-01	0.96	0.88
rs10139323	104989158	T	C	0.36	0.96	0.03	1.4E-01	22.55	<0.01	0.39	/I	1.1E-01	0.96	1.3E-01	0.96	0.85
rs4247027	105139894	G	A	0.42	1.04	0.03	1.4E-01	0	0.02	0.44	G*/I	2.5E-01	1.03	2.2E-01	1.03	0.87
rs10148938	105493605	C	A	0.11	0.95	0.03	1.4E-01	0	<0.01	0.11	/I	1.2E-01	0.95	7.7E-02	0.94	0.97
rs79062923	105443997	T	C	0.04	1.11	0.07	1.4E-01	18.79	<0.01	0.05	/I	2.5E-01	1.09	2.0E-01	1.09	0.51
rs34252654	105477180	G	A	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	G*/I	1.2E-01	0.95	7.8E-02	0.94	0.98
rs10138346	105472922	T	A	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	/I	1.2E-01	0.95	7.7E-02	0.94	0.98
rs28707248	105487997	G	T	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	/I	1.3E-01	0.95	7.8E-02	0.94	0.97
rs144714404	105005308	G	A	0.02	1.14	0.09	1.5E-01	53.73	<0.01	0.02	/I	1.6E-01	1.13	8.6E-02	1.17	0.60
rs141772799	105364764	A	T	0.03	0.87	0.10	1.5E-01	37.08	<0.01	0.04	/I	2.7E-01	0.90	1.8E-01	0.88	0.62
rs8181961	105314642	C	T	0.28	1.04	0.03	1.5E-01	73.31	<0.01	0.25	/I	4.0E-02	1.06	6.3E-02	1.05	0.76
rs116882956	105183403	A	G	0.01	0.81	0.15	1.5E-01	0	<0.01	0.02	/I	4.1E-01	0.89	2.8E-01	0.85	0.49
rs10138366	104971184	A	G	0.28	0.96	0.03	1.5E-01	11.54	<0.01	0.28	/I	1.4E-01	0.96	1.1E-01	0.96	0.86
rs2841221	105331466	C	G	0.36	1.03	0.02	1.5E-01	0	0.05	0.31	/I	5.2E-02	1.04	9.2E-02	1.04	0.97
rs113203583	105592294	T	C	0.12	1.06	0.04	1.5E-01	0	<0.01	0.12	/I	1.8E-01	1.05	2.5E-01	1.04	0.88
rs10083374	105402994	C	T	0.47	1.03	0.02	1.5E-01	57.29	<0.01	0.48	/I	9.3E-02	1.04	1.2E-01	1.03	0.97
rs61996045	105417103	A	G	0.41	1.04	0.03	1.5E-01	0	<0.01	0.43	/I	4.3E-02	1.05	6.2E-02	1.05	0.67
rs11848041	105485849	G	A	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	/I	1.2E-01	0.95	7.8E-02	0.94	0.97
rs7146817	105170175	G	T	0.22	0.96	0.03	1.5E-01	0	0.10	0.21	/I	1.0E-01	0.96	9.2E-01	1.00	0.91
rs4461008	105019987	G	A	0.06	1.08	0.05	1.5E-01	3.33	<0.01	0.06	/I	7.5E-02	1.10	9.3E-02	1.09	0.70
rs10137527	105600664	T	C	0.11	0.94	0.04	1.5E-01	0	<0.01	0.12	/I	1.4E-01	0.94	1.4E-01	0.94	0.85
rs117572009	105162807	A	C	0.07	1.06	0.04	1.5E-01	30.87	0.14	0.11	/I	9.9E-01	1.00	7.5E-01	0.99	0.98
rs10140601	104840805	T	G	0.22	0.96	0.03	1.5E-01	0	0.01	0.23	/I	1.9E-01	0.96	1.4E-01	0.96	0.83
rs12891996	105484622	T	G	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	/I	1.3E-01	0.95	7.9E-02	0.94	0.97
rs11848239	105486157	A	G	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	/I	1.3E-01	0.95	7.9E-02	0.94	0.97
rs8008344	105486758	T	C	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	/I	1.3E-01	0.95	7.9E-02	0.94	0.97
rs116886213	105279615	A	G	0.02	0.85	0.12	1.5E-01	0	<0.01	0.04	/I	2.3E-01	0.87	1.8E-01	0.86	0.59
rs72700159	105339984	A	G	0.02	1.14	0.09	1.5E-01	0	<0.01	0.03	/I	1.1E-01	1.16	1.4E-01	1.15	0.55
rs7145851	105170222	A	G	0.22	0.96	0.03	1.5E-01	0	0.10	0.21	/I	1.1E-01	0.96	9.1E-01	1.00	0.91
rs61997771	105497911	T	C	0.32	1.03	0.02	1.5E-01	0	<0.01	0.31	/I	1.4E-01	1.03	6.6E-02	1.04	0.99
rs7158955	105546369	C	T	0.15	1.05	0.04	1.5E-01	0	<0.01	0.18	/I	1.6E-01	1.05	9.0E-02	1.06	0.75
rs2248966	105417102	C	T	0.47	1.04	0.03	1.5E-01	22.28	<0.01	0.47	/I	4.6E-02	1.05	7.5E-02	1.05	0.67
rs12432572	105152344	A	G	0.48	1.04	0.03	1.5E-01	53.22	0.01	0.46	/I	4.0E-01	1.02	4.0E-01	1.02	0.65
rs2819422	105408955	G	A	0.46	1.03	0.02	1.5E-01	63.04	<0.01	0.48	/I	9.6E-02	1.04	1.2E-01	1.03	0.97
rs117117106	105028257	A	G	0.02	1.13	0.08	1.5E-01	45.88	<0.01	0.02	/I	3.3E-01	1.09	3.2E-01	1.09	0.71
rs12323856	105293185	T	G	0.08	1.07	0.05	1.5E-01	67.58	<0.01	0.08	/I	1.2E-01	1.08	1.3E-01	1.08	0.63
rs12895272	105141783	C	T	0.12	1.06	0.04	1.5E-01	0	<0.01	0.08	/I	4.1E-01	1.03	1.3E-01	1.06	0.82
rs2494752	105263608	G	A	0.08	0.95	0.04	1.5E-01	0	0.07	0.08	/I	7.4E-01	0.99	8.8E-01	1.01	0.91
rs4533207	105019970	T	C	0.06	1.08	0.05	1.5E-01	21.69	<0.01	0.06	/I	8.2E-02	1.10	9.9E-02	1.09	0.71
rs7154620	104973914	C	T	0.21	0.96	0.03	1.5E-01	75.67	<0.01	0.18	/I	9.1E-02	0.95	1.0E-01	0.95	0.87
rs59729652	104756479	T	C	0.15	1.06	0.04	1.5E-01	0	<0.01	0.14	/I	1.6E-01	1.06	1.9E-01	1.05	0.60
rs10143367	105486513	T	C	0.11	0.95	0.03	1.5E-01	0	<0.01	0.11	/I	1.3E-01	0.95	8.2E-02	0.94	0.97
rs2819421	105408811	G	A	0.49	1.03	0.02	1.5E-01	39.76	<0.01	0.48	/I	9.1E-02	1.04	1.3E-01	1.03	0.86
rs11160812	105064457	T	C	0.37	0.96	0.03	1.5E-01	0	<0.01	0.44	G*/I	1.6E-01	0.96	1.9E-01	0.97	0.88
rs7158479	105552083	C	T	0.33	1.04	0.02	1.5E-01	65.08	<0.01	0.31	G*/I	1.6E-01	1.04	9.7E-02	1.04	0.90
rs2919618	105323300	C	T	0.35	1.03	0.02	1.5E-01	0	0.05	0.32	/I	5.6E-02	1.04	9.5E-02	1.04	0.97
rs3803316	105060368	C	A	0.38	0.96	0.03	1.6E-01	0	<0.01	0.43	/I	1.6E-01	0.97	1.9E-01	0.97	0.88
rs72703900	105541302	A	G	0.05	0.92	0.06	1.6E-01	40.85	<0.01	0.04	/I	2.2E-01	0.93	2.0E-01	0.93	0.80
rs10142723	105107922	A	C	0.45	1.04	0.03	1.6E-01	0	0.05	0.48	/I	2.5E-01	1.03	4.8E-01	1.02	0.84
rs2028417	105324800	T	C	0.44	1.03	0.02	1.6E-01	30.5	0.04	0.41	/I	3.3E-02	1.05	4.1E-02	1.04	0.96
rs7148960	105068247	C	T	0.23	0.96	0.03	1.6E-01	0	<0.01	0.26	/I	1.5E-01	0.96	2.1E-01	0.97	0.91
rs113514625	105174598	T	C	0.14	1.05	0.03	1.6E-01	0	0.15	0.19	/I	5.0E-01	1.02	9.9E-01	1.00	0.91
rs10144190	105179081	A	G	0.45	0.97	0.02	1.6E-01	0	0.08	0.48	/I	6.9E-01	1.01	7.0E-01	0.99	0.90
rs7149763	104969416	T	G	0.23	0.96	0.03	1.6E-01	77.7	<0.01	0.21	/I	1.0E-01	0.95	1.0E-01	0.95	0.80
rs60520694	105391712	G	T	0.03	1.09	0.06	1.6E-01	0	<0.01	0.03	/I	1.9E-01	1.08	2.6E-01	1.07	0.83
rs76386715	105171208	T	C	0.14	1.05	0.03	1.6E-01	0	0.15	0.19	/I	5.0E-01	1.02	1.0E+00	1.00	0.91
rs79559717	105172315	A	G	0.14	1.05	0.03	1.6E-01	0	0.15	0.19	/I	5.0E-01	1.02	1.0E+00	1.00	0.91
rs10144804	105068206	C	G	0.24	0.96	0.03	1.6E-01	0	<0.01	0.26	/I	1.5E-01	0.96	2.2E-01	0.97	0.91
rs145596224	105172546	T	C	0.01	0.81	0.15	1.6E-01	0	<0.01	0.01	/I	3.6E-01	0.87	3.0E-01	0.86	0.47
rs10873548	105068500	A	G	0.23	0.96	0.03	1.6E-01	0	<0.01	0.26	/I	1.5E-01	0.96	2.2E-01	0.97	0.91
rs426																

rs3001412	105323157	G	A	0.35	1.03	0.02	1.7E-01	0	0.05	0.32	/I	6.1E-02	1.04	1.0E-01	1.04	0.97
rs2494742	105251196	C	G	0.08	1.05	0.04	1.7E-01	0	0.08	0.08	/G	9.5E-01	1.00	7.0E-01	0.98	0.89
rs3001413	105323216	G	C	0.35	1.03	0.02	1.7E-01	0	0.05	0.32	/I	6.1E-02	1.04	1.0E-01	1.04	0.97
rs7161438	105564595	A	T	0.35	1.03	0.02	1.7E-01	55.49	<0.01	0.32	/I	1.9E-01	1.03	1.1E-01	1.04	0.89
rs4983576	105554527	A	G	0.11	1.06	0.04	1.7E-01	0	<0.01	0.12	/I	2.0E-01	1.05	1.4E-01	1.06	0.87
rs12882641	105432044	A	G	0.18	0.96	0.03	1.7E-01	0	<0.01	0.22	/I	1.4E-01	0.96	1.0E-01	0.95	0.87
rs61997814	105553403	T	C	0.27	1.04	0.03	1.7E-01	57.15	<0.01	0.24	/I	1.7E-01	1.04	1.2E-01	1.05	0.68
rs12433626	104904929	A	G	0.09	0.94	0.04	1.7E-01	8.31	<0.01	0.13	/I	2.2E-01	0.95	1.8E-01	0.94	0.72
rs8008126	105331457	G	A	0.40	1.03	0.02	1.7E-01	50.11	0.05	0.34	/I	5.3E-02	1.04	8.1E-02	1.04	0.91
rs61997788	105541701	G	A	0.32	1.03	0.02	1.7E-01	34.77	<0.01	0.30	/I	1.8E-01	1.03	9.6E-02	1.04	0.90
rs11849430	104827325	C	T	0.31	0.96	0.03	1.7E-01	0	<0.01	0.34	/I	2.0E-01	0.96	2.1E-01	0.96	0.84
rs2841220	105329758	C	G	0.35	1.03	0.02	1.7E-01	0	0.05	0.32	/I	6.3E-02	1.04	1.1E-01	1.04	0.99
rs7151310	104970219	A	G	0.24	0.96	0.03	1.7E-01	77.66	<0.01	0.21	/I	1.1E-01	0.95	1.1E-01	0.95	0.79
rs2582565	105330036	T	A	0.35	1.03	0.02	1.7E-01	0	0.05	0.32	/I	6.3E-02	1.04	1.1E-01	1.04	0.99
rs4983378	105145568	A	G	0.06	1.07	0.05	1.7E-01	44.05	0.01	0.06	/I	1.0E-01	1.08	1.6E-01	1.07	0.93
rs28591099	104939147	C	G	0.06	1.06	0.04	1.7E-01	24.49	0.01	0.02	/I	1.3E-01	1.07	1.4E-01	1.07	0.89
rs10137404	105485036	G	C	0.11	0.95	0.03	1.7E-01	0	<0.01	0.11	/I	1.4E-01	0.95	9.2E-02	0.94	0.96
rs7145815	105170163	A	G	0.23	0.96	0.03	1.7E-01	0	0.10	0.22	/I	1.4E-01	0.96	8.2E-01	1.01	0.90
rs7147450	105488819	T	G	0.19	1.04	0.03	1.7E-01	0	<0.01	0.17	/I	2.1E-01	1.03	1.3E-01	1.04	0.97
rs2841231	105340643	T	C	0.36	1.03	0.02	1.7E-01	0	0.04	0.34	G/G	6.2E-02	1.04	1.1E-01	1.04	1.00
rs61995985	105330676	A	C	0.44	1.03	0.02	1.7E-01	38	0.04	0.41	/I	3.9E-02	1.04	4.7E-02	1.04	0.97
rs4575477	104830600	G	A	0.31	0.96	0.03	1.8E-01	0	<0.01	0.34	/I	2.1E-01	0.96	2.2E-01	0.97	0.84
rs3742935	105405599	C	G	0.47	1.03	0.02	1.8E-01	58.81	<0.01	0.48	/I	1.1E-01	1.03	1.4E-01	1.03	0.97
rs2735799	105622583	C	T	0.02	0.86	0.11	1.8E-01	0	0.02	0.03	/I	1.0E-01	0.83	1.1E-01	0.83	0.70
rs7146692	105575208	T	C	0.07	0.93	0.05	1.8E-01	85.57	<0.01	0.05	/I	1.7E-01	0.93	1.6E-01	0.93	0.84
rs3803313	105070791	T	G	0.23	0.96	0.03	1.8E-01	0	<0.01	0.26	/I	1.6E-01	0.96	2.3E-01	0.97	0.91
rs55671614	105053022	A	G	0.27	1.04	0.03	1.8E-01	0	0.02	0.28	/I	2.4E-01	1.04	1.8E-01	1.04	0.78
rs61761201	105238820	C	G	0.06	0.92	0.06	1.8E-01	31.1	0.03	0.05	/I	7.2E-01	1.02	7.2E-01	0.98	0.50
rs10438247	105411781	A	G	0.47	1.03	0.02	1.8E-01	60.62	<0.01	0.48	/I	1.0E-01	1.04	1.3E-01	1.03	0.95
rs10143150	105580134	G	A	0.11	0.95	0.04	1.8E-01	0	<0.01	0.14	/I	1.7E-01	0.94	1.7E-01	0.94	0.82
rs11627214	105315047	T	A	0.04	0.92	0.06	1.8E-01	54.15	<0.01	0.06	/I	3.2E-01	0.94	2.1E-01	0.92	0.72
rs113157419	105592275	G	T	0.12	1.05	0.04	1.8E-01	0	<0.01	0.12	/I	2.1E-01	1.05	2.9E-01	1.04	0.88
rs12588965	105246692	A	T	0.05	1.07	0.05	1.8E-01	9.92	0.04	0.02	/I	1.0E+00	1.00	7.7E-01	0.98	0.78
rs10151729	105469942	T	C	0.11	0.95	0.03	1.8E-01	0	<0.01	0.10	/I	1.5E-01	0.95	9.7E-02	0.94	0.96
rs7149875	104990528	G	T	0.36	0.96	0.03	1.8E-01	22.48	<0.01	0.39	/I	1.3E-01	0.96	1.6E-01	0.96	0.85
rs142838860	105119991	T	C	0.15	1.05	0.04	1.8E-01	52.83	<0.01	0.14	/I	2.9E-01	1.02	4.6E-01	1.03	0.61
rs2841283	105395429	G	A	0.44	0.97	0.02	1.8E-01	43.8	<0.01	0.42	/I	9.2E-02	0.96	1.0E-01	0.96	0.86
rs190347870	105321492	T	G	0.18	1.05	0.04	1.8E-01	23.73	<0.01	0.19	/I	2.1E-01	1.05	2.1E-01	1.05	0.50
rs8004038	105385437	A	G	0.48	1.03	0.02	1.8E-01	12.19	<0.01	0.49	/I	1.1E-01	1.04	1.4E-01	1.03	0.86
rs2304759	105344182	T	C	0.08	0.94	0.05	1.8E-01	57.37	<0.01	0.11	/I	1.2E-01	0.93	1.6E-01	0.94	0.77
rs76147286	105164934	T	C	0.15	1.04	0.03	1.8E-01	0	0.15	0.19	/I	5.7E-01	1.02	9.3E-01	1.00	0.89
rs12880651	105060029	C	T	0.38	0.97	0.03	1.8E-01	0	<0.01	0.43	/I	1.9E-01	0.97	2.2E-01	0.97	0.88
rs7160272	105682527	T	C	0.28	1.03	0.02	1.8E-01	0	<0.01	0.32	G*/I	2.0E-01	1.03	2.2E-01	1.03	0.94
rs8022211	105138662	C	G	0.43	1.04	0.03	1.8E-01	0	0.02	0.44	/I	3.2E-01	1.03	3.1E-01	1.03	0.86
rs117997087	105644788	A	G	0.02	1.12	0.09	1.8E-01	0	<0.01	0.03	/I	9.0E-02	1.16	1.1E-01	1.15	0.87
rs4380004	104977254	C	T	0.20	0.96	0.03	1.8E-01	74.71	<0.01	0.17	/I	1.1E-01	0.95	1.3E-01	0.95	0.87
rs79003030	105415422	A	G	0.29	1.04	0.03	1.8E-01	0	<0.01	0.29	/I	1.9E-02	1.08	3.2E-02	1.07	0.56
rs11851852	105168428	T	C	0.08	1.05	0.04	1.8E-01	50.42	0.14	0.12	G/G	8.7E-01	0.99	6.2E-01	0.98	1.00
rs111716346	105596716	G	A	0.02	1.13	0.09	1.8E-01	0	0.01	0.02	/I	2.8E-01	1.11	3.4E-01	1.09	0.81
rs75478023	105683386	C	T	0.07	1.07	0.05	1.8E-01	0	<0.01	0.10	/I	2.3E-01	1.06	3.0E-01	1.05	0.69
rs116001927	105320956	G	A	0.37	1.03	0.02	1.8E-01	0	0.04	0.32	/I	8.3E-02	1.04	1.2E-01	1.04	0.89
rs4983530	105167807	T	C	0.03	1.12	0.09	1.8E-01	16.42	0.01	0.01	/I	8.0E-01	1.02	5.2E-01	1.06	0.48
rs80112741	104907641	T	C	0.02	1.11	0.08	1.8E-01	0	<0.01	0.01	/I	1.5E-01	1.12	1.7E-01	1.12	0.72
rs12889428	105538526	T	C	0.30	1.03	0.02	1.9E-01	3.74	<0.01	0.28	/I	2.1E-01	1.03	1.2E-01	1.04	0.93
rs10134757	105295911	G	A	0.28	1.04	0.03	1.9E-01	73.86	<0.01	0.25	/I	6.2E-02	1.05	1.0E-01	1.05	0.71
rs146093414	105183615	T	C	0.02	0.85	0.12	1.9E-01	0	<0.01	0.02	/I	2.8E-01	0.88	1.7E-01	0.85	0.55
rs4983561	105333539	G	A	0.35	1.03	0.02	1.9E-01	0	0.05	0.32	G/G	6.9E-02	1.04	1.2E-01	1.03	1.00
rs72715968	105186178	T	A	0.20	0.96	0.03	1.9E-01	0	0.11	0.20	/I	1.0E-01	0.95	8.0E-01	1.01	0.89
rs72715966	105186163	T	C	0.20	0.96	0.03	1.9E-01	0	0.11	0.20	/I	1.0E-01	0.95	8.0E-01	1.01	0.89
rs61995990	105338536	A	G	0.46	1.03	0.02	1.9E-01	0	0.05	0.45	/I	5.3E-02	1.04	6.2E-02	1.04	0.93
rs2582568	105458521	C	T	0.18	1.04	0.03	1.9E-01	0	<0.01	0.17	/I	2.4E-01	1.03	1.6E-01	1.04	0.98
rs12890464	105303312	T	C	0.20	0.96	0.03	1.9E-01	73.34	0.01	0.17	/I	1.3E-01	0.95	2.2E-01	0.96	0.75
rs41310934	105344603	T	C	0.43	1.03	0.02	1.9E-01	0	0.04	0.39	/I	3.5E-02	1.05	4.6E-02	1.04	0.98
rs61421370	105406372	T	C	0.48	1.03	0.02	1.9E-01	24.66	<0.01	0.48	/I	1.1E-01	1.04	1.2E-01	1.03	0.95
rs34178085	104744830	G	A	0.42	1.03	0.03	1.9E-01	0	<0.01	0.42	/I	1.9E-01	1.03	2.1E-01	1.03	0.84
rs8009473	105301841	A	G	0.20	0.96	0.03	1.9E-01	74.19	0.01	0.17	/I	1.4E-01	0.96	2.4E-01	0.96	0.75
rs2841225	105335710	G	A	0.35	1.03	0.02	1.9E-01	0	0.05	0.32	/I	7.0E-02	1.04	1.2E-01	1.03	1.00
rs2841216	105322519	G	A	0.37	1.03	0.02	1.9E-01	0	0.05	0.34	/I	6.2E-02	1.04	1.3E-01	1.03	0.94
rs41307094	105236377	A	G	0.01	0.88	0.10	1.9E-01	0	0.06	0.03	/I	3.6E-01	0.91	2.4E-01	0.89	0.77
rs78551665	105346203	A	G	0.04	1.09	0.06	1.9E-01	0	<0.01	0.05	/I	2.3E-01	1.08	2.5E-01	1.07	0.73
rs11845484	105378311	A	G	0.29	1.03	0.02	1.9E-01	57.12	0.01	0.26	/I	7.3E-02	1.04	7.1E-02	1.05	0.95
rs75458767	105150467	A	G	0.04	1.09	0.06	1.9E-01	0	<0.01	0.03	/I	2.5E-02	1.16	6.4E-02	1.13	0.59
rs7157579	104988350	G	A	0.36	0.97	0.03	1.9E-01	24.71	<0.01	0.39	/I	1.5E-01	0.96	1.6E-01	0.96	0.85
rs8010024	105302190	T	G	0.20	0.96	0.03	1.9E-01	74.3	0.01	0.17	/I	1.4E-01	0.96	2.4E-01	0.96	0.75
rs7157046	105464163	T	C	0.19	1.04	0.03	1.9E-01	0	<0.01	0.18	/I</					

rs72709734	105695931	A	G	0.11	1.06	0.05	2.0E-01	5.9	<0.01	0.09	/I	2.3E-01	1.06	3.7E-01	1.04	0.49
rs7156936	105171812	G	A	0.23	0.96	0.03	2.0E-01	0	0.09	0.22	/I	1.3E-01	0.96	8.7E-01	1.00	0.91
rs141136095	105119621	T	C	0.02	1.12	0.09	2.0E-01	0	<0.01	0.01	/I	4.1E-01	1.08	5.3E-01	1.06	0.81
rs80252681	105055897	A	G	0.09	1.05	0.04	2.0E-01	54.82	<0.01	0.09	/I	1.7E-01	1.06	1.8E-01	1.06	0.90
rs73363341	105132462	A	G	0.12	1.05	0.04	2.0E-01	24.11	<0.01	0.09	/I	5.1E-01	1.03	1.9E-01	1.05	0.82
rs41317300	105344761	T	C	0.43	1.03	0.02	2.0E-01	1.79	0.04	0.39	/I	3.8E-02	1.04	5.0E-02	1.04	0.98
rs7155932	105476065	C	T	0.18	1.04	0.03	2.0E-01	0	<0.01	0.17	/I	2.4E-01	1.03	1.7E-01	1.04	0.98
rs61996025	105399975	G	C	0.49	1.03	0.02	2.0E-01	59.69	<0.01	0.49	/I	1.5E-01	1.03	1.8E-01	1.03	0.92
rs74089043	105102323	C	G	0.33	1.04	0.03	2.0E-01	53.85	0.03	0.37	/I	4.5E-01	1.02	6.6E-01	1.01	0.82
rs11160825	105410411	T	C	0.47	1.03	0.02	2.0E-01	58.51	<0.01	0.48	/I	1.3E-01	1.03	1.6E-01	1.03	0.97
rs8014544	105693791	G	C	0.28	1.03	0.03	2.0E-01	0	<0.01	0.32	/I	2.3E-01	1.03	2.5E-01	1.03	0.89
rs4344668	105496739	T	G	0.19	1.03	0.03	2.0E-01	0	<0.01	0.18	/I	2.4E-01	1.03	1.6E-01	1.04	0.98
rs10151872	105080703	G	A	0.23	0.97	0.03	2.0E-01	0	<0.01	0.26	/I	1.9E-01	0.97	2.6E-01	0.97	0.93
rs2841278	105391748	G	C	0.47	0.97	0.02	2.0E-01	62.99	<0.01	0.49	/I	1.4E-01	0.97	1.7E-01	0.97	0.97
rs2819469	105394859	A	G	0.47	0.97	0.02	2.0E-01	61.06	<0.01	0.50	/I	1.4E-01	0.97	1.7E-01	0.97	0.97
rs73359083	105134186	A	G	0.11	1.05	0.04	2.0E-01	13.21	<0.01	0.08	/I	5.0E-01	1.03	1.7E-01	1.06	0.82
rs920499	105366499	T	C	0.29	1.03	0.02	2.0E-01	62.07	0.01	0.26	G*/I	7.8E-02	1.04	7.6E-02	1.04	0.96
rs11160834	105563262	A	T	0.12	1.05	0.04	2.0E-01	0	<0.01	0.13	/I	2.5E-01	1.04	1.8E-01	1.05	0.89
rs12895274	105546711	T	G	0.33	1.03	0.02	2.0E-01	57.83	<0.01	0.31	/I	2.2E-01	1.03	1.3E-01	1.04	0.91
rs4474629	105580774	A	T	0.12	1.05	0.04	2.0E-01	0	<0.01	0.13	/I	2.5E-01	1.04	1.8E-01	1.05	0.91
rs10141053	105409907	C	T	0.48	1.03	0.02	2.0E-01	17.84	<0.01	0.48	/I	1.1E-01	1.03	1.3E-01	1.03	0.94
rs2819424	105410775	G	A	0.46	1.03	0.02	2.0E-01	63.18	<0.01	0.48	/I	1.3E-01	1.03	1.7E-01	1.03	0.96
rs79697519	105582014	T	C	0.02	1.15	0.11	2.0E-01	0	0.01	0.03	/I	1.2E-01	1.18	9.6E-02	1.19	0.57
rs2841281	105394669	T	C	0.47	0.97	0.02	2.0E-01	60.98	<0.01	0.50	/I	1.4E-01	0.97	1.7E-01	0.97	0.97
rs10151692	105080510	G	A	0.23	0.97	0.03	2.0E-01	0	<0.01	0.26	/I	1.9E-01	0.97	2.6E-01	0.97	0.93
rs28664663	105538994	A	G	0.30	1.03	0.02	2.0E-01	13.37	<0.01	0.28	/I	2.2E-01	1.03	1.2E-01	1.04	0.94
rs4265748	105530334	A	G	0.29	1.03	0.02	2.0E-01	0	<0.01	0.27	/I	2.1E-01	1.03	1.1E-01	1.04	0.95
rs12894037	105369235	T	A	0.29	1.03	0.02	2.0E-01	60.8	0.01	0.26	/I	7.9E-02	1.04	7.7E-02	1.04	0.95
rs4622449	104830620	T	C	0.22	0.96	0.03	2.0E-01	0	<0.01	0.25	/I	2.8E-01	0.97	2.6E-01	0.96	0.84
rs148113337	105712829	T	C	0.02	1.14	0.10	2.0E-01	0	<0.01	0.02	/I	2.5E-01	1.13	2.7E-01	1.12	0.60
rs28427389	105337803	T	C	0.40	1.03	0.02	2.0E-01	0	0.04	0.39	/I	6.1E-02	1.04	1.0E-01	1.04	0.97
rs117084961	105190942	G	A	0.02	0.85	0.13	2.0E-01	0	0.01	0.02	/I	6.1E-01	0.94	4.1E-01	0.90	0.50
rs56190325	105436904	A	G	0.02	0.88	0.10	2.0E-01	4.78	<0.01	0.02	/I	1.9E-01	0.88	2.2E-01	0.88	0.56
rs12436986	105412554	G	T	0.34	1.03	0.03	2.0E-01	0	<0.01	0.31	/I	9.0E-02	1.05	1.3E-01	1.04	0.66
rs11845745	105483996	G	A	0.19	1.03	0.03	2.0E-01	0	<0.01	0.17	/I	2.3E-01	1.03	1.5E-01	1.04	0.96
rs11628851	105482065	G	A	0.18	1.04	0.03	2.1E-01	0	<0.01	0.17	/I	2.5E-01	1.03	1.7E-01	1.04	0.98
rs7159216	105585608	A	G	0.11	0.95	0.04	2.1E-01	0	<0.01	0.14	G*/I	2.0E-01	0.95	1.9E-01	0.95	0.86
rs56152263	105103809	A	G	0.34	1.04	0.03	2.1E-01	52.39	0.04	0.39	/I	4.4E-01	1.02	6.6E-01	1.01	0.82
rs4983595	105005216	T	C	0.23	1.04	0.03	2.1E-01	6.71	<0.01	0.20	/I	2.2E-01	1.04	2.7E-01	1.04	0.70
rs909236	105606156	T	C	0.23	1.04	0.03	2.1E-01	0	<0.01	0.25	/I	2.5E-01	1.03	1.8E-01	1.04	0.87
rs1134959	105056105	G	C	0.09	1.05	0.04	2.1E-01	59.8	<0.01	0.09	/I	1.7E-01	1.05	1.9E-01	1.05	0.90
rs11850949	105408827	C	A	0.49	1.03	0.02	2.1E-01	27.6	<0.01	0.48	/I	1.2E-01	1.03	1.7E-01	1.03	0.88
rs71423803	105469755	T	C	0.11	0.96	0.03	2.1E-01	0	<0.01	0.10	/I	1.8E-01	0.95	1.2E-01	0.95	0.98
rs8020981	105136781	A	G	0.03	1.08	0.06	2.1E-01	0	<0.01	0.04	/I/G	3.4E-01	1.06	2.7E-01	1.07	0.90
rs58946503	104836058	T	C	0.30	0.96	0.03	2.1E-01	0	<0.01	0.32	/I	2.5E-01	0.97	2.6E-01	0.97	0.85
rs184023841	105321399	T	G	0.09	1.07	0.05	2.1E-01	0	<0.01	0.08	/I	1.9E-01	1.07	1.6E-01	1.07	0.48
rs7158820	105467700	G	A	0.18	1.03	0.03	2.1E-01	0	<0.01	0.17	/I	2.5E-01	1.03	1.7E-01	1.04	0.99
rs2494751	105262961	A	G	0.07	0.95	0.04	2.1E-01	0	0.07	0.08	/I/G	1.0E+00	1.00	6.6E-01	1.02	0.93
rs77541926	104945518	G	C	0.06	1.06	0.05	2.1E-01	31.11	0.01	0.02	/I	1.7E-01	1.07	1.8E-01	1.07	0.83
rs72707603	105594257	G	T	0.12	1.05	0.04	2.1E-01	4.82	<0.01	0.12	/I	2.4E-01	1.04	3.2E-01	1.04	0.89
rs7148837	105000753	G	T	0.28	0.97	0.03	2.1E-01	0	<0.01	0.26	G*/I	1.9E-01	0.96	1.3E-01	0.96	0.87
rs10149533	105308529	A	G	0.29	1.04	0.03	2.1E-01	70.7	<0.01	0.25	/I	6.7E-02	1.05	1.0E-01	1.05	0.75
rs10130338	105310163	A	G	0.29	1.04	0.03	2.1E-01	71.75	<0.01	0.25	/I	6.7E-02	1.05	1.0E-01	1.05	0.75
rs112720520	105313876	G	T	0.02	1.14	0.10	2.1E-01	0	0.01	0.04	/I	2.3E-01	1.13	2.2E-01	1.14	0.56
rs9324079	105424173	C	A	0.04	0.90	0.08	2.1E-01	31.85	0.01	0.02	/I	1.8E-01	0.89	1.4E-01	0.88	0.68
rs6420941	105498785	A	G	0.19	1.03	0.03	2.1E-01	0	<0.01	0.18	/I	2.5E-01	1.03	1.7E-01	1.04	0.98
rs2735810	105592259	G	A	0.23	1.04	0.03	2.1E-01	0	<0.01	0.31	/I	2.5E-01	1.04	2.8E-01	1.04	0.67
rs35459099	105306816	A	C	0.28	1.04	0.03	2.1E-01	73.41	<0.01	0.25	/I	6.7E-02	1.05	9.9E-02	1.05	0.74
rs2735800	105605643	A	G	0.23	1.04	0.03	2.1E-01	0	<0.01	0.25	/I	2.5E-01	1.03	1.9E-01	1.04	0.87
rs4264330	105306468	T	C	0.28	1.04	0.03	2.1E-01	73.43	<0.01	0.25	/I	6.7E-02	1.05	1.0E-01	1.05	0.74
rs10146073	104976398	C	T	0.21	0.96	0.03	2.1E-01	74.27	<0.01	0.17	/I	1.2E-01	0.95	1.4E-01	0.96	0.87
rs4354858	105499073	C	T	0.19	1.03	0.03	2.1E-01	0	<0.01	0.18	/I	2.5E-01	1.03	1.7E-01	1.04	0.98
rs894039	105461067	T	C	0.18	1.03	0.03	2.1E-01	0	<0.01	0.17	G*/I	2.6E-01	1.03	1.8E-01	1.04	0.99
rs61995988	105338458	T	C	0.44	1.03	0.02	2.1E-01	35.54	0.04	0.41	/I	5.0E-02	1.04	6.0E-02	1.04	0.98
rs6576065	105465841	A	G	0.18	1.03	0.03	2.1E-01	0	<0.01	0.17	/I	2.6E-01	1.03	1.7E-01	1.04	0.99
rs117932691	105285212	G	C	0.03	0.89	0.09	2.1E-01	32.54	<0.01	0.05	/I	4.4E-01	0.93	3.2E-01	0.91	0.52
rs6576066	105466027	G	A	0.18	1.03	0.03	2.1E-01	0	<0.01	0.17	/I	2.6E-01	1.03	1.7E-01	1.04	0.99
rs2841230	105338721	G	A	0.36	1.03	0.02	2.1E-01	0	0.05	0.35	/I	8.2E-02	1.04	1.3E-01	1.03	0.94
rs4264331	105306664	A	C	0.28	1.04	0.03	2.1E-01	73.44	<0.01	0.25	/I	6.7E-02	1.05	1.0E-01	1.05	0.74
rs1128866	105185567	G	A	0.20	0.96	0.03	2.1E-01	0	0.11	0.20	/I	1.2E-01	0.96	7.5E-01	1.01	0.89
rs10131315	105477349	C	G	0.18	1.03	0.03	2.1E-01	0	<0.01	0.17	/I	2.6E-01	1.03	1.8E-01	1.04	0.99
rs10134371	105424190	T	A	0.04	0.90	0.08	2.1E-01	33.2	0.01	0.02	/I	1.8E-01	0.89	1.5E-01	0.89	0.67
rs10134910	105110674	G	A	0.46	1.03	0.03	2.1E-01	2.13	0.05	0.49	/I	3.5E-01	1.02	6.0E-01	1.01	0.84
rs10147047	105110538	C	T	0.46	1.03	0.03	2.1E-01	2.13	0.05	0.49	/I	3.5E-01	1.02	6.0E-01	1.01	0.84
rs2582557	105348051	G	A	0.36	1.03	0.02	2.1E-01	0	0.04	0.32	/I	7.4E-02	1.04	1.2E-01	1.03</	

rs7146872	105671418	C	G	0.29	1.03	0.02	2.2E-01	0	<0.01	0.32	/I	2.4E-01	1.03	2.6E-01	1.03	0.92
rs7150561	105345035	A	C	0.43	1.03	0.02	2.2E-01	8.76	0.04	0.39	/I	4.3E-02	1.04	5.5E-02	1.04	0.98
rs7143466	105343593	G	A	0.41	1.03	0.02	2.2E-01	11	0.05	0.36	/I	6.0E-02	1.04	8.2E-02	1.04	0.98
rs4075086	105479490	C	T	0.18	1.03	0.03	2.2E-01	0	<0.01	0.17	/I	2.7E-01	1.03	1.8E-01	1.04	0.98
rs61995995	105344293	T	C	0.43	1.03	0.02	2.2E-01	8.36	0.04	0.39	/I	4.3E-02	1.04	5.6E-02	1.04	0.98
rs7145273	105081374	A	C	0.23	0.97	0.03	2.2E-01	0	<0.01	0.26	/I	2.0E-01	0.97	2.8E-01	0.97	0.93
rs2582567	105459924	G	A	0.18	1.03	0.03	2.2E-01	0	<0.01	0.17	/I	2.7E-01	1.03	1.8E-01	1.04	0.99
rs2304757	105344347	G	C	0.43	1.03	0.02	2.2E-01	8.12	0.04	0.39	/I	4.3E-02	1.04	5.6E-02	1.04	0.98
rs2841280	105393556	C	G	0.47	0.97	0.02	2.2E-01	62.88	<0.01	0.49	/I	1.5E-01	0.97	1.9E-01	0.97	0.97
rs11160829	105481927	T	C	0.18	1.03	0.03	2.2E-01	0	<0.01	0.17	/I	2.7E-01	1.03	1.8E-01	1.04	0.98
rs111298327	105338889	T	C	0.01	0.86	0.12	2.2E-01	0	<0.01	0.02	/I	2.6E-01	0.87	2.4E-01	0.87	0.68
rs59766306	105149067	C	A	0.03	1.10	0.08	2.2E-01	0	0.04	0.02	/I	3.9E-01	1.07	5.3E-01	1.05	0.56
rs10138409	105132771	C	T	0.15	1.05	0.04	2.2E-01	0	<0.01	0.15	/I	5.5E-01	1.02	5.5E-01	1.02	0.73
rs8020062	105538299	T	C	0.29	1.03	0.02	2.2E-01	10.9	<0.01	0.27	/I	2.4E-01	1.03	1.4E-01	1.04	0.94
rs11160830	105481988	G	A	0.18	1.03	0.03	2.2E-01	0	<0.01	0.17	/I	2.7E-01	1.03	1.8E-01	1.04	0.98
rs58541277	105056247	C	T	0.24	1.04	0.03	2.2E-01	0	0.03	0.26	/I	2.2E-01	1.04	2.0E-01	1.04	0.86
rs111327615	105163427	T	C	0.15	1.04	0.03	2.2E-01	0	0.15	0.19	/I	6.4E-01	1.01	8.5E-01	0.99	0.88
rs7157491	104995563	G	A	0.29	0.97	0.03	2.2E-01	0	<0.01	0.28	/I	1.9E-01	0.96	1.3E-01	0.96	0.86
rs12889498	105302536	A	G	0.20	0.96	0.03	2.2E-01	77.06	0.01	0.17	/I	1.6E-01	0.96	2.6E-01	0.97	0.75
rs34499888	105411153	A	G	0.45	1.03	0.02	2.2E-01	18.2	<0.01	0.46	/I	1.3E-01	1.03	1.5E-01	1.03	0.90
rs4309336	105482373	T	A	0.18	1.03	0.03	2.2E-01	0	<0.01	0.17	/I	2.7E-01	1.03	1.9E-01	1.04	0.98
rs28534935	105583264	C	T	0.12	0.95	0.04	2.2E-01	0	<0.01	0.14	/I	2.1E-01	0.95	2.2E-01	0.95	0.85
rs12147593	105100625	A	G	0.05	1.07	0.06	2.2E-01	0	<0.01	0.02	/I	6.2E-01	1.03	1.0E-01	1.10	0.78
rs12889174	105302400	A	G	0.20	0.96	0.03	2.2E-01	77.06	0.01	0.17	/I	1.6E-01	0.96	2.6E-01	0.97	0.75
rs7153053	105150273	T	C	0.42	1.03	0.03	2.2E-01	20.4	<0.01	0.43	/I	7.9E-01	1.01	7.3E-01	1.01	0.67
rs2119394	105341100	A	T	0.36	1.03	0.02	2.2E-01	0	0.04	0.34	/I	9.2E-02	1.04	1.5E-01	1.03	0.99
rs57566178	105507382	T	C	0.11	0.96	0.03	2.2E-01	0	<0.01	0.10	/I	1.9E-01	0.96	1.3E-01	0.95	0.96
rs111800069	104886682	G	T	0.04	1.10	0.08	2.2E-01	0	<0.01	0.05	/I	2.3E-01	1.09	1.7E-01	1.11	0.51
rs8010782	105672250	T	C	0.29	1.03	0.02	2.2E-01	0	<0.01	0.32	/I	2.5E-01	1.03	2.8E-01	1.03	0.92
rs142502252	105691007	T	C	0.02	0.87	0.11	2.3E-01	56.5	0.01	0.02	/I	2.4E-01	0.88	2.0E-01	0.86	0.68
rs12881514	105570467	G	T	0.12	1.04	0.04	2.3E-01	0	<0.01	0.13	/I	2.9E-01	1.04	2.0E-01	1.05	0.90
rs10147051	105110551	C	T	0.14	1.05	0.04	2.3E-01	40.87	<0.01	0.14	/I	2.4E-01	1.04	3.2E-01	1.04	0.84
rs10146871	105110417	C	T	0.14	1.05	0.04	2.3E-01	40.82	<0.01	0.14	/I	2.4E-01	1.04	3.2E-01	1.04	0.84
rs8011377	105475270	T	C	0.18	1.03	0.03	2.3E-01	0	<0.01	0.17	/I	2.8E-01	1.03	1.9E-01	1.04	0.98
rs76459533	105191310	G	A	0.01	0.85	0.14	2.3E-01	0	<0.01	0.02	/I	6.0E-01	0.93	4.2E-01	0.90	0.50
rs7158362	105276036	G	A	0.16	0.96	0.03	2.3E-01	0	0.09	0.16	/I	8.4E-01	0.99	9.1E-01	1.00	0.65
rs59950617	105145853	G	C	0.06	1.06	0.05	2.3E-01	37.12	0.01	0.06	/I	1.2E-01	1.07	2.0E-01	1.06	0.90
rs4359377	105500152	A	G	0.34	1.03	0.02	2.3E-01	0	<0.01	0.33	/I	1.9E-01	1.03	9.3E-02	1.04	0.99
rs8005029	105686852	A	G	0.28	1.03	0.02	2.3E-01	0	<0.01	0.32	/I	2.5E-01	1.03	2.7E-01	1.03	0.94
rs8008979	105486931	A	G	0.11	0.96	0.03	2.3E-01	0	<0.01	0.11	/I	2.0E-01	0.96	1.3E-01	0.95	0.95
rs72702027	105414629	A	G	0.47	1.03	0.02	2.3E-01	60.93	<0.01	0.49	/I	1.6E-01	1.03	2.0E-01	1.03	0.94
rs4983389	105323685	A	G	0.44	1.03	0.02	2.3E-01	41.24	0.05	0.41	/I	5.5E-02	1.04	6.7E-02	1.04	0.96
rs4334222	105163142	G	A	0.44	1.03	0.02	2.3E-01	21.2	0.13	0.42	/I	2.2E-01	0.97	4.2E-01	0.98	0.88
rs4247031	105181851	T	C	0.47	0.97	0.02	2.3E-01	0	0.07	0.46	/I	6.1E-01	1.01	8.3E-01	1.00	0.92
rs71421302	105291928	C	T	0.08	0.94	0.05	2.3E-01	45.19	<0.01	0.04	/I	4.3E-01	0.96	1.4E-01	0.92	0.48
rs3809464	105533699	C	G	0.29	1.03	0.02	2.3E-01	0	<0.01	0.27	/I	2.3E-01	1.03	1.2E-01	1.04	0.94
rs8022294	105469626	A	G	0.18	1.03	0.03	2.3E-01	0	<0.01	0.17	/I	2.9E-01	1.03	2.0E-01	1.04	0.99
rs3803322	105518336	T	G	0.06	0.95	0.05	2.3E-01	51.5	<0.01	0.06	G*/I	2.6E-01	0.95	2.4E-01	0.95	0.91
rs8270	105675701	A	C	0.28	1.03	0.02	2.3E-01	0	<0.01	0.32	G*/I	2.5E-01	1.03	2.8E-01	1.03	0.94
rs56118449	105342846	T	A	0.44	1.03	0.02	2.3E-01	32.75	0.04	0.41	/I	5.5E-02	1.04	6.8E-02	1.04	0.98
rs116996185	105164285	A	G	0.04	1.07	0.06	2.3E-01	0	0.03	0.05	/I	7.7E-01	1.02	4.2E-01	1.13	0.63
rs56168451	105580883	A	G	0.11	0.95	0.04	2.3E-01	0	<0.01	0.14	/I	2.2E-01	0.95	2.1E-01	0.95	0.85
rs12889014	105171258	T	C	0.21	0.97	0.03	2.3E-01	0	0.08	0.21	/I	1.2E-01	0.96	8.1E-01	1.01	0.89
rs7158032	104995838	G	A	0.29	0.97	0.03	2.3E-01	0	<0.01	0.26	/I	2.0E-01	0.96	1.3E-01	0.96	0.86
rs11160824	105371729	A	G	0.43	1.03	0.03	2.3E-01	51.6	0.02	0.36	/I	9.5E-02	1.04	9.1E-02	1.04	0.72
rs2582514	105413204	T	G	0.49	1.03	0.02	2.3E-01	63.05	<0.01	0.48	/I	1.8E-01	1.03	2.2E-01	1.03	0.85
rs59411735	104832933	T	A	0.21	0.96	0.03	2.3E-01	0	<0.01	0.23	/I	3.2E-01	0.97	2.9E-01	0.97	0.84
rs56191719	105580541	C	T	0.11	0.95	0.04	2.3E-01	0	<0.01	0.14	/I	2.2E-01	0.95	2.1E-01	0.95	0.84
rs59481248	104834504	G	C	0.21	0.96	0.03	2.3E-01	0	<0.01	0.23	/I	3.3E-01	0.97	2.9E-01	0.97	0.84
rs9806113	105694857	G	A	0.09	0.94	0.05	2.3E-01	69.98	<0.01	0.13	/I	1.9E-01	0.94	2.0E-01	0.94	0.59
rs12232105	105506249	G	A	0.11	0.96	0.03	2.3E-01	0	<0.01	0.10	/I	2.1E-01	0.96	1.4E-01	0.95	0.96
rs74088728	104946356	A	G	0.06	1.06	0.05	2.3E-01	29.44	0.01	0.02	/I	2.1E-01	1.06	2.2E-01	1.06	0.84
rs60562761	105521340	G	A	0.30	1.03	0.02	2.4E-01	0	<0.01	0.26	/I	2.7E-01	1.03	1.5E-01	1.04	0.85
rs2582533	105398787	C	G	0.46	1.03	0.02	2.4E-01	63.83	<0.01	0.48	/I	1.5E-01	1.03	2.0E-01	1.03	0.97
rs10873553	105462570	G	C	0.18	1.03	0.03	2.4E-01	0	<0.01	0.17	/I	2.9E-01	1.03	2.0E-01	1.04	0.99
rs111771947	104953954	G	A	0.06	1.06	0.05	2.4E-01	30.73	<0.01	0.02	/I	2.0E-01	1.06	2.2E-01	1.06	0.87
rs7157567	105522201	T	C	0.29	1.03	0.02	2.4E-01	0	<0.01	0.28	/I	2.5E-01	1.03	1.4E-01	1.04	0.94
rs4304960	105581048	G	A	0.12	1.04	0.04	2.4E-01	0	<0.01	0.13	/I	3.0E-01	1.04	2.2E-01	1.04	0.90
rs61998902	105186323	G	A	0.12	1.04	0.03	2.4E-01	0	<0.01	0.11	/I	7.2E-01	0.99	2.8E-01	0.96	0.89
rs28373763	104942807	G	A	0.20	1.03	0.03	2.4E-01	0	<0.01	0.26	/I	3.1E-01	1.03	2.6E-01	1.03	0.97
rs12880486	105084774	T	C	0.23	0.97	0.03	2.4E-01	0	<0.01	0.27	/I	2.2E-01	0.97	3.0E-01	0.97	0.94
rs4983509	105097438	C	T	0.16	1.04	0.04	2.4E-01	50.29	0.01	0.16	/I	2.1E-01	1.05	3.0E-01	1.04	0.79
rs7159235	105673692	C	A	0.29	1.03	0.02	2.4E-01	0	<0.01	0.32	/I	2.6E-01	1.03	2.9E-01	1.03	0.93
rs4146327	105636674	A	G	0.10	0.95	0.04	2.4E-01	16.37	<0.01	0.11	/I	3.4E-01	0.96	3.4E-01	0.96	0.83
rs11848564	105413790	A	G	0.48	1.03	0.02	2.4E-01	19.53	<0.01	0.47	/					

rs7147669	105523817	A	G	0.29	1.03	0.02	2.5E-01	0	<0.01	0.27	/I	2.6E-01	1.03	1.4E-01	1.04	0.94
rs12885313	105562732	G	A	0.37	1.03	0.02	2.5E-01	59.27	<0.01	0.34	/I	2.7E-01	1.03	1.8E-01	1.03	0.84
rs4429223	105482279	G	C	0.18	1.03	0.03	2.5E-01	0	<0.01	0.17	/I	3.1E-01	1.03	2.0E-01	1.04	0.97
rs2247140	105457771	G	A	0.18	1.03	0.03	2.5E-01	0	<0.01	0.16	/I	3.0E-01	1.03	2.1E-01	1.03	0.98
rs3596880	105529530	T	A	0.29	1.03	0.02	2.5E-01	0	<0.01	0.28	/I	2.6E-01	1.03	1.5E-01	1.04	0.95
rs142383191	105616522	T	C	0.02	1.12	0.10	2.5E-01	4.11	<0.01	0.05	/I	1.7E-01	1.14	1.3E-01	1.16	0.55
rs34736195	105485094	A	G	0.12	0.96	0.03	2.5E-01	0	<0.01	0.12	/I	2.3E-01	0.96	1.5E-01	0.95	0.90
rs7159920	105510027	T	G	0.33	1.03	0.02	2.5E-01	0	<0.01	0.32	/I	2.1E-01	1.03	1.0E-01	1.04	0.97
rs4983376	105097587	A	T	0.15	1.04	0.04	2.5E-01	51.51	0.01	0.16	/I	2.2E-01	1.05	3.1E-01	1.04	0.81
rs6576030	104789894	A	G	0.32	0.97	0.03	2.5E-01	0	<0.01	0.26	/I	2.6E-01	0.97	2.6E-01	0.97	0.85
rs28593146	105584431	G	A	0.12	0.96	0.04	2.5E-01	0	<0.01	0.14	/I	2.3E-01	0.95	2.4E-01	0.95	0.85
rs34116292	105520675	T	C	0.29	1.03	0.02	2.5E-01	0	<0.01	0.27	/I	2.6E-01	1.03	1.5E-01	1.04	0.94
rs56270718	105580677	A	G	0.11	0.95	0.04	2.5E-01	0	<0.01	0.14	/I	2.4E-01	0.95	2.3E-01	0.95	0.84
rs143357719	104896897	A	C	0.02	1.11	0.09	2.5E-01	0	<0.01	0.04	/I	2.9E-01	1.11	2.8E-01	1.11	0.70
rs72709736	105695932	G	A	0.11	1.06	0.05	2.5E-01	4.99	<0.01	0.09	/I	2.8E-01	1.05	4.4E-01	1.04	0.49
rs61998907	105187469	A	G	0.46	0.97	0.02	2.5E-01	14.73	0.08	0.47	/I	5.9E-01	1.01	8.4E-01	1.00	0.92
rs45531934	105244651	T	C	0.06	1.05	0.04	2.5E-01	49.96	0.07	0.06	/G	8.3E-01	1.01	8.2E-01	0.99	0.68
rs28499318	105582863	T	C	0.11	0.95	0.04	2.5E-01	0	<0.01	0.14	/I	2.4E-01	0.95	2.3E-01	0.95	0.86
rs34882611	105542298	A	G	0.33	1.03	0.02	2.5E-01	44.06	<0.01	0.31	/I	2.5E-01	1.03	1.5E-01	1.04	0.91
rs8014447	105575854	G	A	0.35	1.03	0.02	2.5E-01	0	<0.01	0.36	/I	2.9E-01	1.03	1.9E-01	1.03	0.86
rs10140600	104840804	A	G	0.23	0.97	0.03	2.5E-01	0	<0.01	0.23	/I	2.9E-01	0.97	2.4E-01	0.97	0.84
rs28560192	105581095	T	C	0.11	0.95	0.04	2.5E-01	0	<0.01	0.14	/I	2.4E-01	0.95	2.3E-01	0.95	0.85
rs9788527	105054260	G	A	0.11	1.05	0.04	2.5E-01	0	<0.01	0.12	/I	4.0E-01	1.03	4.7E-01	1.03	0.81
rs10147635	105303199	G	C	0.32	0.96	0.03	2.5E-01	0	<0.01	0.36	/I	8.6E-02	0.95	2.8E-01	0.96	0.46
rs2582531	105392533	C	A	0.49	0.98	0.02	2.5E-01	51.02	<0.01	0.48	/I	1.5E-01	0.97	1.7E-01	0.97	0.97
rs148480125	105219124	T	C	0.03	0.91	0.09	2.5E-01	0	0.01	0.01	/I	8.6E-01	1.02	7.2E-01	0.97	0.48
rs72705790	105582180	A	G	0.11	0.95	0.04	2.5E-01	0	<0.01	0.14	/I	2.4E-01	0.95	2.3E-01	0.95	0.86
rs78252573	105122187	A	G	0.02	1.11	0.09	2.5E-01	0	<0.01	0.01	/I	5.2E-01	1.06	6.4E-01	1.04	0.81
rs10149501	105581973	G	A	0.11	0.95	0.04	2.5E-01	0	<0.01	0.14	/I	2.4E-01	0.95	2.3E-01	0.95	0.85
rs10145270	105349891	A	G	0.43	1.02	0.02	2.5E-01	0	0.04	0.41	/I	5.3E-02	1.04	6.9E-02	1.04	0.98
rs4636848	104787848	A	C	0.31	0.97	0.03	2.5E-01	0	<0.01	0.26	/I	2.7E-01	0.97	2.6E-01	0.97	0.85
rs72707689	105638217	T	C	0.11	0.95	0.04	2.5E-01	0	<0.01	0.15	/I	3.4E-01	0.96	3.4E-01	0.96	0.86
rs7151529	105581295	A	G	0.11	0.95	0.04	2.5E-01	0	<0.01	0.14	/I	2.4E-01	0.95	2.4E-01	0.95	0.85
rs28674855	104942722	G	A	0.20	1.03	0.03	2.5E-01	0	<0.01	0.26	/I	3.3E-01	1.03	2.7E-01	1.03	0.97
rs11625373	105586439	T	C	0.13	1.04	0.04	2.5E-01	17.28	<0.01	0.12	/I	2.9E-01	1.04	3.9E-01	1.03	0.90
rs144884533	105124210	G	T	0.02	1.11	0.09	2.5E-01	0	<0.01	0.01	/I	5.1E-01	1.06	6.3E-01	1.05	0.82
rs56054225	105190061	A	G	0.20	0.97	0.03	2.5E-01	0	0.11	0.20	/I	1.5E-01	0.96	6.0E-01	1.02	0.86
rs74090132	105423361	C	T	0.04	0.91	0.09	2.5E-01	37.96	0.01	0.02	/I	2.2E-01	0.90	1.8E-01	0.89	0.67
rs2735798	105636719	A	G	0.02	0.87	0.12	2.5E-01	0	0.03	0.04	/I	1.5E-01	0.84	1.6E-01	0.84	0.53
rs2582495	105322534	A	G	0.45	1.02	0.02	2.6E-01	34.92	0.05	0.42	/I	5.5E-02	1.04	8.6E-02	1.04	0.93
rs9672139	105408182	G	T	0.50	1.02	0.02	2.6E-01	51.84	<0.01	0.49	/I	1.5E-01	1.03	1.8E-01	1.03	0.97
rs7146454	105170003	G	T	0.22	0.97	0.03	2.6E-01	0	0.10	0.21	G*/I	1.9E-01	0.96	6.8E-01	1.01	0.91
rs12880814	105054934	G	A	0.11	1.05	0.04	2.6E-01	0	<0.01	0.12	/I	4.1E-01	1.03	4.7E-01	1.03	0.83
rs2816676	105607203	C	T	0.11	1.04	0.04	2.6E-01	0	<0.01	0.08	/I	2.6E-01	1.04	1.9E-01	1.05	0.88
rs10137814	105088609	A	G	0.25	0.97	0.02	2.6E-01	0	<0.01	0.26	/I	1.7E-01	0.97	2.4E-01	0.97	0.86
rs11624335	105590864	A	G	0.13	1.04	0.04	2.6E-01	18.45	<0.01	0.12	G*/I	2.9E-01	1.04	3.9E-01	1.03	0.90
rs61592395	104832713	C	A	0.22	0.96	0.03	2.6E-01	0	<0.01	0.24	/I	3.4E-01	0.97	3.1E-01	0.97	0.84
rs72705796	105590369	T	G	0.13	1.04	0.04	2.6E-01	18.19	<0.01	0.12	G*/I	2.9E-01	1.04	3.9E-01	1.03	0.90
rs12886191	105191400	T	C	0.16	0.97	0.03	2.6E-01	14	0.05	0.10	/I	8.4E-02	0.95	8.1E-01	1.01	0.81
rs2841217	105322529	C	G	0.45	1.02	0.02	2.6E-01	34.48	0.05	0.42	/I	5.5E-02	1.04	8.7E-02	1.04	0.93
rs12431850	105335049	T	C	0.44	1.02	0.02	2.6E-01	47.25	0.05	0.41	/I	6.7E-02	1.04	8.2E-02	1.04	0.97
rs2033932	105447075	T	C	0.18	0.97	0.03	2.6E-01	0	<0.01	0.17	/I	2.2E-01	0.97	1.4E-01	0.96	0.91
rs76814181	105064501	A	G	0.08	1.05	0.04	2.6E-01	52.18	<0.01	0.09	/I	2.2E-01	1.05	2.3E-01	1.05	0.92
rs4633652	105675110	T	C	0.28	1.03	0.02	2.6E-01	0	<0.01	0.32	/I	2.9E-01	1.03	3.1E-01	1.03	0.93
rs10134946	105654606	T	C	0.34	1.03	0.03	2.6E-01	0	<0.01	0.36	G*/I	2.7E-01	1.03	2.9E-01	1.03	0.89
rs183309280	105113375	T	C	0.03	1.10	0.08	2.6E-01	0	<0.01	0.02	/I	3.9E-01	1.08	1.7E-01	1.12	0.54
rs34364862	105559610	T	C	0.19	1.04	0.03	2.6E-01	34.12	<0.01	0.14	/I	3.0E-01	1.03	4.2E-01	1.03	0.69
rs77066495	105486842	A	G	0.10	0.96	0.03	2.6E-01	0	<0.01	0.11	/I	2.2E-01	0.96	1.5E-01	0.95	0.98
rs2841219	105323654	G	C	0.36	1.02	0.02	2.6E-01	0	0.04	0.33	/I	1.1E-01	1.04	1.7E-01	1.03	0.97
rs60172564	105424782	C	T	0.04	0.91	0.08	2.6E-01	26.29	0.01	0.02	/I	2.2E-01	0.90	1.9E-01	0.89	0.67
rs11846022	105675399	C	T	0.29	1.03	0.02	2.6E-01	0	<0.01	0.32	/I	2.9E-01	1.03	3.1E-01	1.03	0.94
rs7152235	105528212	C	T	0.29	1.03	0.02	2.6E-01	0	<0.01	0.27	/I	2.7E-01	1.03	1.5E-01	1.04	0.94
rs75838789	105061132	T	C	0.08	1.05	0.04	2.6E-01	52.65	<0.01	0.09	/I	2.2E-01	1.05	2.3E-01	1.05	0.91
rs10138816	105133187	C	T	0.43	1.03	0.03	2.6E-01	0	0.02	0.44	/I	4.2E-01	1.02	3.7E-01	1.02	0.85
rs2816679	105622056	G	A	0.05	1.07	0.06	2.6E-01	0	<0.01	0.02	/I	3.0E-01	1.06	2.7E-01	1.07	0.81
rs78214055	105593147	T	C	0.13	1.04	0.04	2.6E-01	11.12	<0.01	0.12	/I	3.0E-01	1.04	4.0E-01	1.03	0.89
rs10137728	104998353	T	C	0.28	0.97	0.03	2.6E-01	0	<0.01	0.26	/I	2.3E-01	0.97	1.5E-01	0.96	0.87
rs12586514	105548176	G	A	0.10	1.05	0.04	2.6E-01	0	<0.01	0.12	/I	3.2E-01	1.04	2.4E-01	1.05	0.88
rs3809470	105531945	G	A	0.29	1.03	0.02	2.6E-01	0	<0.01	0.27	G*/I	2.7E-01	1.03	1.5E-01	1.03	0.96
rs73359086	105134689	T	C	0.12	1.05	0.04	2.6E-01	0	<0.01	0.08	/I	6.0E-01	1.02	2.3E-01	1.05	0.82
rs75239420	105066810	C	T	0.08	1.05	0.04	2.6E-01	52.68	<0.01	0.09	/I	2.2E-01	1.05	2.3E-01	1.05	0.92
rs8023080	105543785	T	A	0.07	0.95	0.05	2.6E-01	62.67	<0.01	0.05	/I	3.1E-01	0.95	2.9E-01	0.95	0.88
rs2819419	105406238	C	A	0.46	1.02	0.02	2.6E-01	70.75	<0.01	0.48	G*/I	1.7E-01	1.03	2.2E-01	1.03	0.97
rs4983560	105322471	A	G	0.44	1.02	0.02	2.6E-01	36.26	0.05	0.41	/I	6.6E-02	1.04	8.3E-02	1.04	0.95
rs2091919	105693340	C	A	0.28	1.03	0.03	2.6E-01	0	<0.01	0.32	/I	3.0E-01	1.03	3.2E-01	1.03	0.91
rs7																

rs78109240	105342981	G	C	0.45	1.02	0.02	2.7E-01	41.48	0.04	0.42	/I	6.3E-02	1.04	8.4E-02	1.04	0.96
rs10141968	105113145	G	A	0.14	1.04	0.04	2.7E-01	46	<0.01	0.14	/I	2.9E-01	1.04	3.8E-01	1.03	0.84
rs57982564	104836132	C	G	0.31	0.97	0.03	2.7E-01	0	<0.01	0.32	/I	3.2E-01	0.97	3.3E-01	0.97	0.85
rs4906449	104789323	G	A	0.31	0.97	0.03	2.7E-01	0	<0.01	0.26	/I	2.8E-01	0.97	2.8E-01	0.97	0.85
rs56990841	104836314	G	A	0.31	0.97	0.03	2.7E-01	0	<0.01	0.32	/I	3.2E-01	0.97	3.3E-01	0.97	0.85
rs34995109	105447267	T	C	0.18	0.97	0.03	2.7E-01	0	<0.01	0.17	/I	2.3E-01	0.97	1.5E-01	0.96	0.91
rs4073652	105484781	G	A	0.18	1.03	0.03	2.7E-01	0	<0.01	0.16	/I	3.3E-01	1.03	2.3E-01	1.03	0.98
rs74089037	105099759	A	G	0.02	1.10	0.08	2.7E-01	0	<0.01	0.01	/I	5.1E-01	1.06	6.1E-01	1.04	0.81
rs4983393	105348039	A	G	0.45	1.02	0.02	2.7E-01	0	0.04	0.41	/I	7.0E-02	1.04	8.4E-02	1.04	0.97
rs10135527	105111252	G	A	0.14	1.04	0.04	2.7E-01	45.18	<0.01	0.14	/I	2.9E-01	1.04	3.8E-01	1.03	0.84
rs12436070	105119676	G	A	0.09	1.05	0.05	2.7E-01	38.27	<0.01	0.09	/I	1.6E-01	1.07	2.3E-01	1.06	0.77
rs59570443	104835313	C	T	0.31	0.97	0.03	2.7E-01	0	<0.01	0.32	/I	3.2E-01	0.97	3.3E-01	0.97	0.85
rs10138660	105385241	T	C	0.18	0.96	0.03	2.7E-01	57.79	0.01	0.11	/I	1.3E-01	0.95	6.0E-02	0.94	0.63
rs35769378	105385024	A	G	0.22	1.03	0.03	2.7E-01	55.96	<0.01	0.19	/I	2.1E-01	1.04	1.7E-01	1.04	0.79
rs111485571	105072534	A	G	0.08	1.05	0.04	2.7E-01	53.87	<0.01	0.09	/I	2.3E-01	1.05	2.4E-01	1.05	0.92
rs4983398	105591666	G	A	0.13	1.04	0.04	2.7E-01	8.9	<0.01	0.12	/I	3.2E-01	1.04	4.1E-01	1.03	0.90
rs2819451	105430719	A	G	0.04	0.91	0.08	2.7E-01	5.49	0.01	0.02	/I	2.4E-01	0.91	2.0E-01	0.90	0.68
rs55752802	105315567	G	T	0.09	1.05	0.05	2.7E-01	36.99	<0.01	0.12	/I	3.0E-01	1.05	3.3E-01	1.05	0.58
rs11160805	104866687	T	C	0.22	0.97	0.03	2.7E-01	24.96	<0.01	0.25	/I	2.7E-01	0.97	2.4E-01	0.97	0.90
rs34877077	105189022	T	C	0.20	0.97	0.03	2.7E-01	0	0.11	0.20	/I	1.6E-01	0.96	5.8E-01	1.02	0.86
rs78258865	105073105	T	C	0.08	1.05	0.04	2.8E-01	53.99	<0.01	0.09	/I	2.3E-01	1.05	2.3E-01	1.05	0.92
rs141152411	105109321	A	G	0.02	1.11	0.09	2.8E-01	0	<0.01	0.01	/I	5.3E-01	1.06	6.5E-01	1.04	0.84
rs10133301	105179194	C	T	0.15	0.97	0.03	2.8E-01	0	0.15	0.19	/I	7.0E-01	0.99	7.7E-01	1.01	0.92
rs35886229	105531424	A	C	0.29	1.03	0.02	2.8E-01	0	<0.01	0.27	/I	2.8E-01	1.03	1.6E-01	1.03	0.96
rs59219802	105095548	A	G	0.07	1.06	0.06	2.8E-01	30.53	<0.01	0.02	/I	7.3E-01	1.02	1.4E-01	1.09	0.68
rs2841269	105386149	C	G	0.46	0.98	0.02	2.8E-01	62.15	<0.01	0.49	/I	1.9E-01	1.07	2.4E-01	0.97	0.92
rs61562983	104836134	C	T	0.31	0.97	0.03	2.8E-01	0	<0.01	0.32	/I	3.2E-01	0.97	3.4E-01	0.97	0.85
rs35689208	105447486	T	G	0.18	0.97	0.03	2.8E-01	0	<0.01	0.17	/I	2.4E-01	0.97	1.6E-01	0.96	0.91
rs11624283	105590971	G	A	0.13	1.04	0.04	2.8E-01	8.68	<0.01	0.12	G*/I	3.2E-01	1.04	4.2E-01	1.03	0.90
rs10145528	104997986	A	G	0.29	0.97	0.03	2.8E-01	0	<0.01	0.26	/I	2.4E-01	0.97	1.6E-01	0.96	0.87
rs78590158	105076176	C	T	0.08	1.05	0.04	2.8E-01	54.72	<0.01	0.09	/I	2.3E-01	1.05	2.5E-01	1.05	0.92
rs76810343	105074167	C	T	0.08	1.05	0.04	2.8E-01	54.18	<0.01	0.09	/I	2.3E-01	1.05	2.5E-01	1.05	0.92
rs2238286	105636112	C	T	0.12	0.96	0.04	2.8E-01	14.96	<0.01	0.15	/I	3.9E-01	0.97	3.8E-01	0.97	0.84
rs7150832	105005057	G	A	0.23	1.03	0.03	2.8E-01	20.14	<0.01	0.21	/I	2.9E-01	1.03	3.5E-01	1.03	0.69
rs12147791	105156943	A	G	0.26	1.03	0.03	2.8E-01	0	<0.01	0.31	/I	9.5E-01	1.00	4.1E-01	1.02	0.79
rs4497619	105179043	C	G	0.15	0.97	0.03	2.8E-01	0	0.16	0.19	/I	7.1E-01	0.99	7.6E-01	1.01	0.92
rs3809467	105533338	C	G	0.29	1.03	0.02	2.8E-01	0	<0.01	0.28	/I	2.9E-01	1.03	1.7E-01	1.03	0.95
rs11628893	105590884	C	T	0.13	1.04	0.04	2.8E-01	9.62	<0.01	0.12	G*/I	3.2E-01	1.04	4.2E-01	1.03	0.90
rs115686101	105071338	G	A	0.09	1.04	0.04	2.8E-01	52.47	<0.01	0.11	/I	2.3E-01	1.05	2.5E-01	1.04	0.91
rs12432239	105589032	A	G	0.13	1.04	0.04	2.8E-01	19.59	<0.01	0.12	/I	3.2E-01	1.04	4.3E-01	1.03	0.90
rs79132383	105150850	G	A	0.02	1.10	0.09	2.8E-01	26	0.05	0.02	/I	8.4E-01	1.02	9.9E-01	1.00	0.71
rs77494727	105348018	G	A	0.45	1.02	0.02	2.8E-01	0	<0.01	0.41	/I	7.3E-02	1.04	8.8E-02	1.04	0.97
rs117536281	105494403	G	A	0.03	1.09	0.08	2.8E-01	0	0.02	0.02	/I	4.2E-01	1.06	1.0E-01	1.13	0.59
rs72705798	105590467	C	T	0.13	1.04	0.04	2.8E-01	9.39	<0.01	0.12	G*/I	3.2E-01	1.04	4.2E-01	1.03	0.90
rs4983392	105348021	A	G	0.45	1.02	0.02	2.8E-01	0	0.04	0.41	/I	7.3E-02	1.04	8.8E-02	1.04	0.97
rs75808059	105308832	T	C	0.04	0.93	0.06	2.8E-01	59.36	<0.01	0.06	/I	4.8E-01	0.96	3.2E-01	0.94	0.72
rs4077185	105590273	C	T	0.13	1.04	0.04	2.8E-01	9.27	<0.01	0.12	G*/I	3.2E-01	1.04	4.2E-01	1.03	0.90
rs7160273	105168775	G	A	0.21	0.97	0.03	2.8E-01	0	0.08	0.21	/I	1.5E-01	0.96	7.2E-01	1.01	0.88
rs79322342	104928178	T	G	0.06	1.05	0.04	2.8E-01	0	0.01	0.02	/I	2.2E-01	1.06	2.5E-01	1.05	0.88
rs143072462	105005322	G	A	0.08	0.95	0.05	2.8E-01	0	<0.01	0.08	/I	3.1E-01	0.95	2.6E-01	0.95	0.77
rs3809465	105533687	T	A	0.29	1.03	0.02	2.8E-01	0	<0.01	0.27	/I	2.9E-01	1.03	1.7E-01	1.03	0.96
rs4288933	105534009	A	G	0.29	1.03	0.02	2.8E-01	0	<0.01	0.27	/I	2.9E-01	1.03	1.7E-01	1.03	0.96
rs78030206	105137501	T	C	0.02	1.10	0.09	2.8E-01	0	<0.01	0.01	/I	5.5E-01	1.06	6.7E-01	1.04	0.81
rs149710923	105104810	T	C	0.02	1.11	0.09	2.8E-01	0	<0.01	0.01	/I	5.4E-01	1.06	6.6E-01	1.04	0.84
rs12432500	105584230	T	C	0.12	1.04	0.04	2.8E-01	0	<0.01	0.12	/I	3.1E-01	1.04	4.1E-01	1.03	0.89
rs34753498	105561112	A	G	0.06	0.95	0.05	2.8E-01	81.29	<0.01	0.05	/I	2.8E-01	0.95	2.6E-01	0.94	0.87
rs3759782	105637258	C	T	0.39	1.02	0.02	2.8E-01	40.54	<0.01	0.35	/I	2.3E-01	1.03	2.5E-01	1.03	0.97
rs57746257	105381272	T	C	0.29	1.03	0.02	2.8E-01	63	0.01	0.26	/I	1.2E-01	1.04	1.2E-01	1.04	0.94
rs4077167	105041160	A	G	0.15	1.04	0.04	2.8E-01	23.54	0.01	0.19	/I	3.9E-01	1.03	4.3E-01	1.03	0.76
rs3545162	105472072	G	C	0.10	0.96	0.04	2.8E-01	0	<0.01	0.09	/I	2.4E-01	0.96	1.6E-01	0.95	0.97
rs8014266	105506915	C	G	0.26	1.03	0.02	2.8E-01	0	<0.01	0.26	/I	2.8E-01	1.03	1.6E-01	1.03	0.94
rs9788432	105054709	A	T	0.10	1.04	0.04	2.8E-01	2.05	<0.01	0.12	/I	4.5E-01	1.03	5.1E-01	1.03	0.84
rs7146879	105000466	G	A	0.21	0.97	0.03	2.8E-01	76.67	<0.01	0.21	/I	1.5E-01	0.95	2.2E-01	0.96	0.84
rs12895093	105158044	T	C	0.26	1.03	0.03	2.9E-01	0	<0.01	0.31	/I	9.5E-01	1.00	4.2E-01	1.02	0.79
rs78444311	105077377	C	G	0.08	1.04	0.04	2.9E-01	55.22	<0.01	0.09	/I	2.4E-01	1.05	2.5E-01	1.05	0.92
rs151105261	105303779	T	A	0.28	1.03	0.03	2.9E-01	74.61	<0.01	0.24	/I	1.0E-01	1.05	1.5E-01	1.04	0.74
rs34642994	105188836	A	G	0.20	0.97	0.03	2.9E-01	0	0.11	0.20	/I	1.7E-01	0.96	5.6E-01	1.02	0.87
rs4581644	105540469	G	A	0.30	1.03	0.02	2.9E-01	0	<0.01	0.28	/I	2.8E-01	1.03	1.8E-01	1.03	0.93
rs77355633	105077910	T	C	0.08	1.04	0.04	2.9E-01	55.32	<0.01	0.09	/I	2.4E-01	1.05	2.6E-01	1.05	0.92
rs12147788	105157042	T	C	0.26	1.03	0.03	2.9E-01	0	<0.01	0.31	/I	9.6E-01	1.00	4.2E-01	1.02	0.79
rs12147300	105159027	T	C	0.25	1.03	0.03	2.9E-01	0	<0.01	0.31	/I	9.6E-01	1.00	4.2E-01	1.02	0.79
rs7157172	104998696	A	G	0.29	0.97	0.03	2.9E-01	0	<0.01	0.26	G*/I	2.5E-01	0.97	1.7E-01	0.96	0.87
rs56275808	105543379	G	C	0.32	1.03	0.02	2.9E-01	35.78	<0.01	0.31	/I	2.8E-01	1.03	1.8E-01	1.03	0.92
rs77297817	105613278	C	A	0.14	1.04	0.04	2.9E-01	0	<0.01	0.13	/I	3.2E-01	1.04	4.6E-01	1.03	0.82
rs4075661	105065970	T	C	0.09												

rs118034190	104835520	T	G	0.02	0.89	0.12	3.0E-01	0	<0.01	0.02	/I	3.0E-01	0.89	3.0E-01	0.89	0.60
rs67941359	104835757	C	G	0.31	0.97	0.03	3.0E-01	0	<0.01	0.34	/I	3.4E-01	0.97	3.6E-01	0.97	0.85
rs11160804	104792254	A	G	0.32	0.97	0.03	3.0E-01	0	<0.01	0.26	G*/I	3.1E-01	0.97	3.1E-01	0.97	0.85
rs4275790	105162462	C	T	0.44	1.02	0.02	3.0E-01	25.27	0.13	0.42	/I	1.7E-01	0.97	3.4E-01	0.98	0.88
rs2013228	105417774	A	G	0.23	0.97	0.03	3.0E-01	0	0.03	0.21	/I	6.4E-01	0.99	5.2E-01	0.98	0.67
rs8845	105461832	T	C	0.13	0.97	0.03	3.0E-01	0	0.01	0.11	/I	2.2E-01	0.96	1.4E-01	0.96	0.98
rs60319517	104835354	G	A	0.31	0.97	0.03	3.0E-01	0	<0.01	0.33	/I	3.4E-01	0.97	3.6E-01	0.97	0.85
rs4983391	105348013	A	G	0.44	1.02	0.02	3.0E-01	0	0.04	0.41	/I	7.9E-02	1.04	9.5E-02	1.04	0.97
rs73361837	105057049	C	G	0.10	1.04	0.04	3.0E-01	51.87	<0.01	0.09	/I	2.6E-01	1.04	2.8E-01	1.04	0.90
rs56864909	104835184	G	C	0.31	0.97	0.03	3.0E-01	0	<0.01	0.33	/I	3.4E-01	0.97	3.6E-01	0.97	0.85
rs4906464	104906655	C	T	0.18	0.97	0.03	3.0E-01	0	<0.01	0.22	/I	3.7E-01	0.97	3.4E-01	0.97	0.84
rs8015839	105070485	G	A	0.09	1.04	0.04	3.0E-01	50.14	<0.01	0.09	/I	2.5E-01	1.05	2.7E-01	1.04	0.92
rs140517950	105579740	C	T	0.13	1.04	0.04	3.0E-01	0	<0.01	0.12	/I	3.3E-01	1.04	4.4E-01	1.03	0.89
rs142668345	105526773	A	C	0.02	1.12	0.11	3.0E-01	0	0.01	0.02	/I	3.6E-01	1.11	4.6E-01	1.08	0.51
rs8014246	105082460	A	G	0.27	0.97	0.03	3.0E-01	0	<0.01	0.29	/I	3.3E-01	0.97	3.7E-01	0.98	0.85
rs55705411	104972222	A	G	0.09	0.96	0.04	3.0E-01	0	<0.01	0.14	/I	3.2E-01	0.96	3.1E-01	0.96	0.81
rs56138896	105127454	G	A	0.10	1.05	0.05	3.0E-01	33.58	<0.01	0.06	/I	5.3E-01	1.03	1.5E-01	1.07	0.82
rs117150318	105123729	A	G	0.01	1.14	0.13	3.0E-01	0	<0.01	0.02	/I	2.3E-01	1.17	3.1E-01	1.14	0.57
rs55951335	105543248	T	C	0.32	1.03	0.02	3.0E-01	37.92	<0.01	0.31	/I	3.0E-01	1.03	1.9E-01	1.03	0.91
rs11547184	105057340	T	C	0.10	1.04	0.04	3.0E-01	51.49	<0.01	0.09	/I	2.6E-01	1.04	2.8E-01	1.04	0.90
rs2819439	105388298	G	A	0.50	0.98	0.02	3.0E-01	52.26	<0.01	0.50	/I	1.8E-01	0.97	2.2E-01	0.97	0.93
rs113837512	105427578	G	A	0.10	1.05	0.05	3.0E-01	36.89	<0.01	0.09	/I	6.5E-02	1.09	1.1E-01	1.08	0.51
rs77526295	105078043	G	A	0.09	1.04	0.04	3.0E-01	54.07	<0.01	0.09	/I	2.6E-01	1.05	2.7E-01	1.04	0.92
rs77244247	104841476	C	T	0.10	1.05	0.04	3.0E-01	0	<0.01	0.11	/I	3.2E-01	1.04	3.0E-01	1.05	0.81
rs8018405	105096027	G	A	0.15	1.04	0.04	3.0E-01	55.04	<0.01	0.16	/I	2.7E-01	1.04	3.7E-01	1.03	0.76
rs73356774	105149463	T	C	0.02	1.11	0.10	3.0E-01	47.27	0.01	0.04	/I	6.3E-01	1.05	4.8E-01	1.07	0.46
rs7140227	105071735	C	T	0.10	1.04	0.04	3.0E-01	48.85	<0.01	0.09	/I	2.6E-01	1.04	2.8E-01	1.04	0.92
rs56322618	105176682	C	T	0.21	0.97	0.03	3.1E-01	0	0.09	0.21	/I	1.7E-01	0.96	6.4E-01	1.01	0.88
rs78678903	105112772	T	G	0.02	1.10	0.09	3.1E-01	0	<0.01	0.01	/I	5.8E-01	1.05	7.1E-01	1.04	0.83
rs12890937	105585321	T	A	0.07	1.05	0.05	3.1E-01	39.1	<0.01	0.05	/I	2.9E-01	1.05	2.8E-01	1.06	0.80
rs4073459	104794316	A	G	0.32	0.97	0.03	3.1E-01	0	<0.01	0.26	/I	3.2E-01	0.97	3.1E-01	0.97	0.85
rs114055908	105112468	C	T	0.02	1.10	0.09	3.1E-01	0	<0.01	0.01	/I	5.8E-01	1.05	7.1E-01	1.04	0.83
rs7158237	104799390	T	C	0.31	0.97	0.03	3.1E-01	0	<0.01	0.26	/I	3.2E-01	0.97	3.2E-01	0.97	0.85
rs34878850	105537331	C	T	0.29	1.03	0.02	3.1E-01	0	<0.01	0.27	/I	3.2E-01	1.02	3.0E-01	1.03	0.95
rs116303595	105141083	G	A	0.02	1.10	0.09	3.1E-01	0	<0.01	0.01	/I	5.9E-01	1.05	7.2E-01	1.03	0.80
rs4906444	104779904	C	T	0.31	0.97	0.03	3.1E-01	0	<0.01	0.26	/I	3.1E-01	0.97	3.1E-01	0.97	0.85
rs7157265	104995354	G	C	0.20	0.97	0.03	3.1E-01	76.68	<0.01	0.20	/I	1.6E-01	0.96	2.1E-01	0.96	0.85
rs4076041	104794054	G	T	0.31	0.97	0.03	3.1E-01	0	<0.01	0.26	/I	3.2E-01	0.97	3.2E-01	0.97	0.85
rs1003635	105649737	A	G	0.47	1.02	0.02	3.1E-01	0	<0.01	0.48	/I	3.1E-01	1.03	2.8E-01	1.03	0.78
rs138048043	105168421	G	A	0.01	0.86	0.15	3.1E-01	0	<0.01	0.01	/I	6.0E-01	0.93	4.3E-01	0.89	0.46
rs10149967	105630976	C	T	0.12	0.96	0.04	3.1E-01	17.97	<0.01	0.15	/I	4.1E-01	0.97	4.3E-01	0.97	0.85
rs10873545	104799035	A	G	0.32	0.97	0.03	3.1E-01	0	<0.01	0.26	/I	3.2E-01	0.97	3.2E-01	0.97	0.85
rs3784234	105637156	G	A	0.39	1.02	0.02	3.1E-01	39.89	<0.01	0.35	/I	2.6E-01	1.02	2.8E-01	1.02	0.97
rs8014766	104900698	A	G	0.21	0.97	0.03	3.1E-01	0	<0.01	0.27	/I	3.5E-01	0.97	3.0E-01	0.97	0.87
rs12437326	105129825	C	T	0.32	1.03	0.03	3.1E-01	0	0.02	0.35	/I	3.5E-01	1.03	5.4E-01	1.02	0.83
rs4983574	105511929	C	G	0.07	0.96	0.04	3.1E-01	55.44	0.01	0.08	/I	3.8E-01	0.96	3.5E-01	0.96	0.96
rs55928927	105066927	C	T	0.09	1.04	0.04	3.1E-01	43.62	<0.01	0.09	/I	2.7E-01	1.04	2.9E-01	1.04	0.92
rs2248960	105417228	T	C	0.30	1.03	0.03	3.1E-01	0	<0.01	0.28	/I	6.6E-02	1.06	9.4E-02	1.05	0.57
rs4983571	105511309	C	T	0.07	0.96	0.04	3.1E-01	55.42	0.01	0.08	/I	3.8E-01	0.96	3.5E-01	0.96	0.96
rs4900624	104802666	C	T	0.46	0.97	0.03	3.1E-01	5.65	<0.01	0.48	/I	3.6E-01	0.98	3.6E-01	0.98	0.85
rs144161830	105628120	T	A	0.07	1.05	0.05	3.1E-01	0	<0.01	0.13	/I	2.0E-01	1.07	2.2E-01	1.06	0.79
rs71421879	105146920	G	C	0.03	1.09	0.09	3.1E-01	0	<0.01	0.03	/I	4.2E-01	1.07	2.4E-01	1.10	0.54
rs10147802	104995007	C	T	0.21	0.97	0.03	3.1E-01	75.68	<0.01	0.20	/I	1.6E-01	0.96	2.1E-01	0.96	0.84
rs4464021	105541021	C	T	0.30	1.02	0.02	3.1E-01	0	<0.01	0.28	/I	3.1E-01	1.03	2.0E-01	1.03	0.93
rs4983582	104991471	G	A	0.30	0.97	0.03	3.1E-01	0	<0.01	0.29	G*/I	2.8E-01	0.97	2.2E-01	0.97	0.88
rs4983570	105511281	C	T	0.07	0.96	0.04	3.1E-01	55.24	0.01	0.08	/I	3.9E-01	0.96	3.5E-01	0.96	0.96
rs150717954	105109354	A	G	0.02	1.10	0.09	3.1E-01	0	<0.01	0.01	/I	5.9E-01	1.05	7.1E-01	1.03	0.83
rs34674986	105659888	T	C	0.05	0.93	0.07	3.2E-01	56.84	<0.01	0.04	/I	3.6E-01	0.94	3.4E-01	0.94	0.66
rs72709915	105001663	C	T	0.01	0.88	0.13	3.2E-01	0	0.01	0.02	/I	3.0E-01	0.88	2.6E-01	0.87	0.58
rs11621316	105628760	G	A	0.48	1.02	0.02	3.2E-01	67.13	<0.01	0.47	/I	3.0E-01	1.02	3.4E-01	1.02	0.94
rs141742927	105440241	T	C	0.01	1.12	0.11	3.2E-01	45.09	<0.01	0.02	/I	4.8E-01	1.08	5.7E-01	1.06	0.73
rs139431005	105471007	A	G	0.02	0.90	0.10	3.2E-01	0	<0.01	0.02	/I	3.0E-01	0.90	3.6E-01	0.91	0.58
rs2819468	105392729	G	A	0.49	0.98	0.02	3.2E-01	53.39	<0.01	0.48	/I	2.0E-01	0.97	2.3E-01	0.98	0.98
rs733130	105422580	C	T	0.33	1.02	0.02	3.2E-01	10.85	0.02	0.36	/I	2.1E-01	1.03	1.6E-01	1.03	0.91
rs116039120	105103758	C	T	0.02	1.10	0.09	3.2E-01	0	<0.01	0.01	/I	6.0E-01	1.05	7.3E-01	1.03	0.83
rs77954437	105083120	C	T	0.09	1.04	0.04	3.2E-01	54.8	<0.01	0.09	/I	2.7E-01	1.04	2.9E-01	1.04	0.93
rs7144461	104839192	C	T	0.30	0.97	0.03	3.2E-01	0	0.01	0.29	/I	3.3E-01	0.97	3.1E-01	0.97	0.84
rs2816669	105601713	C	A	0.29	0.97	0.03	3.2E-01	60.07	<0.01	0.34	/I	2.9E-01	0.97	3.5E-01	0.97	0.63
rs113266420	105470145	T	C	0.02	0.90	0.11	3.2E-01	76.05	<0.01	0.02	/I	4.6E-01	0.92	4.0E-01	0.92	0.43
rs28703908	105582775	T	C	0.12	0.96	0.04	3.2E-01	0	<0.01	0.14	/I	3.2E-01	0.96	3.1E-01	0.96	0.83
rs12887065	105689846	A	G	0.04	1.06	0.06	3.2E-01	0	0.01	0.04	/I	3.0E-01	1.07	2.3E-01	1.08	0.78
rs4619321	104871866	A	C	0.22	0.97	0.03	3.2E-01	3.09	<0.01	0.25	/I	3.2E-01	0.97	2.9E-01	0.97	0.93
rs12586545	104802311	T	A	0.46	0.97	0.03	3.2E-01	7.15	<0.01	0.49	/I	3.7E-01	0.98	3.7E-01	0.98	0.86
rs60820727	104905351	C	T	0.18	0.97	0.03	3.2E-01	0	<0.01	0.23	/I	3.7E-01	0.97	3.3E-01	0.97	0.84
rs4906461	104890581	T	C	0.22	0.97	0.										

rs4372628	104894761	A	G	0.21	0.97	0.03	3.3E-01	0	<0.01	0.26	/I	3.6E-01	0.97	3.2E-01	0.97	0.86
rs185964341	105321497	T	G	0.07	1.06	0.06	3.3E-01	0	<0.01	0.05	/I	1.4E-01	1.09	1.0E-01	1.10	0.47
rs3784233	105637747	A	G	0.11	0.96	0.04	3.3E-01	0	<0.01	0.14	G*/I	4.4E-01	0.97	4.4E-01	0.97	0.86
rs7152431	104837237	G	A	0.31	0.97	0.03	3.3E-01	0	<0.01	0.32	G*/I	3.8E-01	0.98	4.0E-01	0.98	0.85
rs75411730	104840899	A	G	0.10	1.04	0.04	3.3E-01	0	<0.01	0.11	/I	3.5E-01	1.04	3.3E-01	1.04	0.82
rs10148439	105115162	C	A	0.13	1.04	0.04	3.3E-01	52.96	<0.01	0.14	/I	3.1E-01	1.04	4.2E-01	1.03	0.84
rs12891766	105489912	C	T	0.10	0.97	0.04	3.3E-01	0	<0.01	0.11	/I	3.0E-01	0.96	2.1E-01	0.96	0.97
rs34055148	105184088	C	G	0.46	0.98	0.02	3.3E-01	0	0.07	0.46	/I	4.7E-01	1.02	9.8E-01	1.00	0.93
rs8013434	104948411	A	G	0.06	1.05	0.05	3.3E-01	22.55	0.01	0.02	/I	2.9E-01	1.05	3.0E-01	1.05	0.85
rs4983583	105572539	A	G	0.22	0.97	0.03	3.3E-01	80.44	<0.01	0.19	/I	2.9E-01	0.97	2.3E-01	0.97	0.88
rs10130611	105297968	C	T	0.04	1.08	0.08	3.3E-01	59.7	<0.01	0.05	/I	5.8E-01	1.05	6.3E-01	1.04	0.43
rs34971388	105485091	A	T	0.10	0.96	0.04	3.3E-01	0	<0.01	0.12	/I	2.8E-01	0.96	1.8E-01	0.95	0.85
rs28483417	105487817	T	G	0.14	0.97	0.03	3.3E-01	0	<0.01	0.14	/I	2.6E-01	0.97	1.6E-01	0.96	0.95
rs145490766	105108820	T	C	0.02	1.09	0.09	3.4E-01	0	<0.01	0.01	/I	6.3E-01	1.05	7.5E-01	1.03	0.83
rs7157574	105171847	A	G	0.24	0.97	0.03	3.4E-01	0	0.11	0.22	/I	2.2E-01	0.97	6.7E-01	1.01	0.91
rs45449696	105350178	T	C	0.35	1.03	0.03	3.4E-01	7.64	0.02	0.42	/I	4.6E-01	1.02	3.5E-01	1.03	0.58
rs113733555	105121501	G	A	0.29	1.03	0.03	3.4E-01	40.83	<0.01	0.31	/I	3.5E-01	1.03	6.0E-01	1.02	0.75
rs76611205	105407525	A	G	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.6E-01	1.05	5.5E-01	1.04	0.93
rs77215854	105407327	A	G	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.6E-01	1.05	5.5E-01	1.04	0.93
rs2280797	105623612	C	T	0.48	1.02	0.02	3.4E-01	68.15	<0.01	0.47	/I	3.2E-01	1.02	3.7E-01	1.02	0.95
rs3922890	105156410	A	G	0.26	1.03	0.03	3.4E-01	0	<0.01	0.31	/I	9.8E-01	1.00	8.7E-01	1.02	0.78
rs28653208	104944563	T	C	0.05	1.05	0.05	3.4E-01	26.08	0.01	0.02	/I	2.8E-01	1.06	3.0E-01	1.05	0.84
rs79161962	105404014	A	G	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.6E-01	1.05	5.5E-01	1.04	0.93
rs2841271	105386983	G	A	0.03	1.06	0.06	3.4E-01	16.36	<0.01	0.02	/I	4.7E-01	1.05	5.6E-01	1.04	0.86
rs139646784	105119988	T	G	0.16	1.04	0.04	3.4E-01	7.54	<0.01	0.15	/I	6.1E-01	1.02	7.7E-01	1.01	0.60
rs117884483	105403677	G	A	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.6E-01	1.05	5.5E-01	1.04	0.93
rs7142340	105000311	G	A	0.21	0.97	0.03	3.4E-01	75.91	<0.01	0.20	/I	1.9E-01	0.96	2.6E-01	0.96	0.84
rs111476325	105140384	C	T	0.08	1.04	0.04	3.4E-01	56.75	<0.01	0.09	/I	1.6E-01	1.06	2.8E-01	1.05	0.81
rs12433350	105189056	A	G	0.45	0.98	0.02	3.4E-01	0	0.08	0.47	/I	5.0E-01	1.02	9.1E-01	1.00	0.91
rs12433746	105537476	C	A	0.29	1.02	0.02	3.4E-01	0	<0.01	0.27	G*/I	3.5E-01	1.02	2.1E-01	1.03	0.95
rs12885004	105386657	A	G	0.47	0.98	0.02	3.4E-01	61.75	<0.01	0.48	/I	2.5E-01	0.98	3.1E-01	0.98	0.92
rs12888830	105052509	G	A	0.10	1.04	0.04	3.4E-01	2.69	<0.01	0.12	/I	5.1E-01	1.03	5.6E-01	1.02	0.84
rs117846862	105398698	A	C	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.6E-01	1.05	5.5E-01	1.04	0.93
rs117045355	105479198	A	G	0.03	1.08	0.08	3.4E-01	0	<0.01	0.08	/I	4.6E-01	1.06	3.7E-01	1.07	0.67
rs61745186	105398544	G	A	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.6E-01	1.05	5.5E-01	1.04	0.93
rs4403996	105582524	A	G	0.36	1.02	0.03	3.4E-01	0	<0.01	0.39	G*/I	3.6E-01	1.02	2.3E-01	1.03	0.89
rs4316687	105094058	A	G	0.30	1.03	0.03	3.4E-01	63.55	0.03	0.36	/I	5.4E-01	1.02	7.1E-01	1.01	0.71
rs74316182	105398392	A	G	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.7E-01	1.05	5.5E-01	1.04	0.93
rs2841268	105386039	C	T	0.49	0.98	0.02	3.4E-01	53.3	<0.01	0.49	/I	2.1E-01	0.97	2.4E-01	0.98	0.92
rs78271134	104862876	T	C	0.02	1.09	0.09	3.4E-01	0	0.03	0.01	/I	3.9E-01	1.08	4.1E-01	1.08	0.70
rs36014607	105470963	C	T	0.10	0.97	0.03	3.4E-01	0	<0.01	0.10	/I	3.0E-01	0.97	2.1E-01	0.96	0.99
rs117592050	105395958	A	C	0.03	1.06	0.07	3.4E-01	0	<0.01	0.02	/I	4.7E-01	1.05	5.5E-01	1.04	0.93
rs7158069	104799327	A	C	0.31	0.97	0.03	3.4E-01	0	<0.01	0.26	/I	3.6E-01	0.97	3.6E-01	0.97	0.85
rs71421876	105099639	A	G	0.03	1.08	0.08	3.4E-01	0	<0.01	0.03	/I	4.8E-01	1.06	2.3E-01	1.10	0.53
rs28632777	104936245	T	G	0.07	1.04	0.04	3.4E-01	16.45	0.01	0.02	/I	2.9E-01	1.05	3.0E-01	1.05	0.89
rs80117472	105395446	A	G	0.03	1.06	0.07	3.5E-01	0	<0.01	0.02	/I	4.7E-01	1.05	5.6E-01	1.04	0.93
rs117402111	105093420	A	G	0.06	1.06	0.06	3.5E-01	9.64	<0.01	0.02	/I	8.1E-01	1.01	1.9E-01	1.08	0.68
rs10151777	105535103	G	A	0.29	1.02	0.02	3.5E-01	0	<0.01	0.27	/I	3.6E-01	1.02	2.1E-01	1.03	0.95
rs113756269	105165143	C	G	0.04	0.93	0.08	3.5E-01	32.45	0.02	0.04	/I	9.3E-01	1.01	7.9E-01	0.98	0.51
rs7145271	104788591	T	C	0.30	0.97	0.03	3.5E-01	0	<0.01	0.26	/I	3.5E-01	0.97	3.4E-01	0.97	0.84
rs4586355	104968898	T	C	0.22	0.97	0.03	3.5E-01	72.96	<0.01	0.21	/I	2.2E-01	0.96	2.2E-01	0.96	0.78
rs2819438	105385352	C	A	0.14	1.03	0.03	3.5E-01	0	<0.01	0.11	/I	2.3E-01	1.04	1.4E-01	1.05	0.75
rs35156277	105510475	C	T	0.07	0.96	0.04	3.5E-01	52.37	0.01	0.08	/I	4.2E-01	0.97	3.8E-01	0.96	0.96
rs143397232	105393772	T	C	0.03	1.06	0.07	3.5E-01	0	<0.01	0.02	/I	4.7E-01	1.05	5.6E-01	1.04	0.93
rs140706020	105394614	T	C	0.03	1.06	0.07	3.5E-01	0	<0.01	0.02	/I	4.7E-01	1.05	5.6E-01	1.04	0.93
rs11626476	104866481	T	C	0.21	0.97	0.03	3.5E-01	21.83	<0.01	0.25	/I	3.5E-01	0.97	3.3E-01	0.97	0.85
rs10149868	105691041	C	T	0.29	1.02	0.02	3.5E-01	0	<0.01	0.32	/I	3.8E-01	1.02	4.1E-01	1.02	0.91
rs72712098	105020043	A	G	0.02	1.10	0.10	3.5E-01	0	<0.01	0.03	/I	5.3E-01	1.07	4.5E-01	1.08	0.57
rs142543394	105394414	G	C	0.03	1.06	0.07	3.5E-01	0	<0.01	0.02	/I	4.8E-01	1.05	5.6E-01	1.04	0.93
rs4457938	105539859	C	T	0.27	1.02	0.03	3.5E-01	0	<0.01	0.25	/I	3.6E-01	1.02	2.3E-01	1.03	0.93
rs75991636	105128104	G	T	0.36	1.03	0.03	3.5E-01	0	<0.01	0.41	/I	3.4E-01	1.03	5.7E-01	1.02	0.86
rs28684681	104937554	G	A	0.06	1.04	0.04	3.5E-01	10.73	0.01	0.02	G*/G	2.9E-01	1.05	3.0E-01	1.05	0.92
rs72706020	104823320	G	C	0.09	1.04	0.04	3.5E-01	0	<0.01	0.08	/I	4.1E-01	1.03	4.6E-01	1.03	0.89
rs28795480	104930164	C	G	0.06	1.04	0.04	3.5E-01	2.36	0.01	0.02	/I	2.8E-01	1.05	3.0E-01	1.05	0.90
rs28797843	104929954	A	C	0.06	1.04	0.04	3.5E-01	2.37	0.01	0.02	/I	2.8E-01	1.05	3.0E-01	1.05	0.90
rs76667491	105393736	C	G	0.03	1.06	0.07	3.5E-01	0	<0.01	0.02	/I	4.8E-01	1.05	5.7E-01	1.04	0.93
rs113893478	105276644	T	C	0.03	0.94	0.07	3.5E-01	55.74	<0.01	0.04	/I	9.8E-01	1.00	6.7E-01	0.97	0.63
rs12892530	105454955	T	C	0.04	0.95	0.06	3.5E-01	0	<0.01	0.05	/I	4.4E-01	0.96	4.1E-01	0.95	0.89
rs4900621	104790177	A	G	0.30	0.97	0.03	3.5E-01	0	<0.01	0.25	/I	3.6E-01	0.97	3.6E-01	0.97	0.85
rs10145420	105069485	C	T	0.14	0.97	0.03	3.5E-01	0	0.01	0.17	/I	3.9E-01	0.97	5.0E-01	0.98	0.91
rs150825172	105391822	A	G	0.03	1.06	0.07	3.6E-01	0.14	<0.01	0.02	/I	4.8E-01	1.05	5.7E-01	1.04	0.93
rs145887049	105567947	A	G	0.03	0.92	0.09	3.6E-01	75.48	<0.01	0.03	/I	3.3E-01	0.92	2.9E-01	0.91	0.69
rs12589990	104851006	G	T	0.38	1.02	0.02	3.6E-01	0	<0.01	0.44	/I	4.1E-01	1.02	3.5E-01	1.02	0.79
rs1128880	105185666	T	G	0.46	0.98	0.02	3.6E-01	0	0.08	0.47	G*/I	4.5E-01	1.02	9.8E-01	1.00	0.94
rs6576051	105045922	G	A	0.26	1.02	0.0										

rs7150242	104969887	C	A	0.24	0.97	0.03	3.7E-01	77.25	<0.01	0.22	/I	2.8E-01	0.97	2.5E-01	0.97	0.77
rs2239284	105630489	T	C	0.48	1.02	0.02	3.7E-01	73.44	<0.01	0.48	/I	3.5E-01	1.02	4.1E-01	1.02	0.93
rs10146459	105186333	A	G	0.46	0.98	0.02	3.7E-01	0	0.08	0.47	/I	4.2E-01	1.02	9.6E-01	1.00	0.94
rs192105564	104948342	G	A	0.05	1.05	0.05	3.7E-01	27.02	0.01	0.02	/I	3.1E-01	1.05	3.3E-01	1.05	0.85
rs79379044	104946143	A	G	0.06	1.05	0.05	3.7E-01	33.62	0.01	0.02	/I	3.2E-01	1.05	3.3E-01	1.05	0.86
rs28828521	104930536	T	C	0.06	1.04	0.04	3.7E-01	6.35	0.01	0.02	/I	3.0E-01	1.05	3.1E-01	1.05	0.89
rs4983375	105092769	T	A	0.48	1.03	0.03	3.7E-01	0	0.02	0.49	/I	5.6E-01	1.02	6.7E-01	1.01	0.59
rs117935415	105609692	A	G	0.03	0.93	0.08	3.7E-01	0	0.03	0.02	/I	3.4E-01	0.93	3.7E-01	0.93	0.53
rs58218156	105498601	C	A	0.10	0.97	0.03	3.7E-01	0	<0.01	0.11	/I	3.3E-01	0.97	2.3E-01	0.96	0.98
rs73361863	105062002	G	A	0.10	1.04	0.04	3.7E-01	50.58	<0.01	0.09	/I	3.2E-01	1.04	3.4E-01	1.04	0.91
rs8016851	104786726	T	A	0.30	0.97	0.03	3.7E-01	0	<0.01	0.25	/I	3.7E-01	0.98	3.7E-01	0.97	0.85
rs28873160	104932812	T	G	0.06	1.04	0.04	3.7E-01	10.14	0.01	0.02	/I	3.0E-01	1.05	3.1E-01	1.05	0.91
rs12891330	105468701	T	C	0.13	0.97	0.03	3.7E-01	0	<0.01	0.12	/I	2.9E-01	0.97	1.8E-01	0.96	0.98
rs11625738	105084994	A	C	0.14	0.97	0.03	3.7E-01	0	0.02	0.18	G*/I	3.8E-01	0.97	5.0E-01	0.98	0.93
rs77453682	105695364	T	C	0.05	1.06	0.06	3.7E-01	0	<0.01	0.05	/I	3.6E-01	1.06	2.9E-01	1.07	0.59
rs60129832	104838761	A	G	0.23	0.97	0.03	3.7E-01	0	<0.01	0.24	/I	4.6E-01	0.98	4.4E-01	0.98	0.82
rs4307891	105019955	A	G	0.07	1.04	0.05	3.7E-01	57.79	<0.01	0.06	/I	2.9E-01	1.05	2.5E-01	1.05	0.82
rs12896116	104983370	T	C	0.18	0.97	0.03	3.7E-01	0	<0.01	0.14	/I	3.7E-01	0.97	3.0E-01	0.97	0.83
rs60808852	104838569	G	A	0.31	0.97	0.03	3.7E-01	0	<0.01	0.32	/I	4.2E-01	0.98	4.4E-01	0.98	0.84
rs8021437	104838124	A	T	0.31	0.97	0.03	3.7E-01	0	<0.01	0.32	/I	4.2E-01	0.98	4.4E-01	0.98	0.84
rs4267251	105588928	G	A	0.12	1.03	0.04	3.7E-01	0	<0.01	0.12	/I	4.6E-01	1.03	3.5E-01	1.03	0.92
rs10135029	105117810	A	G	0.26	1.03	0.03	3.7E-01	39.46	0.02	0.30	/I	5.4E-01	1.02	7.5E-01	1.01	0.78
rs7148206	104894901	T	C	0.20	0.97	0.03	3.7E-01	0	<0.01	0.25	/I	3.8E-01	0.97	3.4E-01	0.97	0.85
rs11626849	104750087	C	T	0.39	1.03	0.03	3.7E-01	0	<0.01	0.42	/I	3.5E-01	1.03	4.1E-01	1.02	0.70
rs10133292	105457161	C	T	0.13	0.97	0.03	3.7E-01	0	<0.01	0.12	/I	3.0E-01	0.97	1.9E-01	0.96	0.98
rs59804769	105122710	C	T	0.11	1.04	0.04	3.7E-01	35.56	<0.01	0.10	/I	3.1E-01	1.04	4.4E-01	1.03	0.79
rs8020667	104838191	T	G	0.31	0.97	0.03	3.7E-01	0	<0.01	0.32	/I	4.3E-01	0.98	4.5E-01	0.98	0.84
rs10431753	104762684	T	G	0.16	0.97	0.04	3.8E-01	0	<0.01	0.19	/I	4.0E-01	0.97	4.0E-01	0.97	0.78
rs10136937	105078153	T	C	0.15	0.97	0.03	3.8E-01	0	0.02	0.17	G*/I	3.9E-01	0.97	5.2E-01	0.98	0.93
rs4340263	105078251	T	C	0.15	0.97	0.03	3.8E-01	0	0.02	0.17	G*/I	3.9E-01	0.97	5.2E-01	0.98	0.93
rs7155652	105057102	G	A	0.34	0.98	0.03	3.8E-01	0	0.01	0.39	/I	3.5E-01	0.97	3.6E-01	0.98	0.85
rs4983532	105178098	C	G	0.44	0.98	0.02	3.8E-01	0	0.09	0.49	/I	4.0E-01	1.02	9.7E-01	1.00	0.90
rs8020729	104838403	T	C	0.31	0.97	0.03	3.8E-01	0	<0.01	0.32	/I	4.2E-01	0.98	4.5E-01	0.98	0.84
rs56870907	104756421	C	G	0.15	1.03	0.04	3.8E-01	0	<0.01	0.12	/I	3.7E-01	1.04	4.2E-01	1.03	0.60
rs181382168	105549957	A	C	0.08	0.95	0.06	3.8E-01	19.21	<0.01	0.06	/I	5.4E-01	0.96	4.5E-01	0.96	0.48
rs8011909	105524142	C	T	0.29	1.02	0.02	3.8E-01	0	<0.01	0.29	/I	4.1E-01	1.02	4.5E-01	1.03	0.92
rs28399812	104937659	A	G	0.06	1.04	0.04	3.8E-01	10.49	0.01	0.02	/I	3.1E-01	1.05	3.2E-01	1.04	0.92
rs79483088	104937598	C	T	0.06	1.04	0.04	3.8E-01	10.49	0.01	0.02	/I	3.1E-01	1.05	3.2E-01	1.04	0.92
rs7142224	105066885	C	T	0.14	0.97	0.03	3.8E-01	0	0.01	0.17	/I	4.1E-01	0.97	5.3E-01	0.98	0.91
rs10137730	104834457	T	C	0.09	1.04	0.04	3.8E-01	0	<0.01	0.08	/I	4.3E-01	1.03	4.9E-01	1.03	0.90
rs8020156	104838158	G	A	0.31	0.97	0.03	3.8E-01	0	<0.01	0.32	/I	4.3E-01	0.98	4.5E-01	0.98	0.84
rs76817967	105060361	T	C	0.10	1.03	0.04	3.8E-01	49.38	<0.01	0.09	/I	3.3E-01	1.04	3.5E-01	1.04	0.91
rs4243748	104805674	G	A	0.44	0.98	0.03	3.8E-01	0	<0.01	0.39	/I	4.6E-01	0.98	4.7E-01	0.98	0.83
rs56283836	104834132	A	G	0.09	1.04	0.04	3.8E-01	0	<0.01	0.08	/I	4.3E-01	1.03	4.9E-01	1.03	0.90
rs12431388	105139302	A	G	0.08	1.04	0.04	3.8E-01	48.33	<0.01	0.09	/I	1.8E-01	1.06	3.1E-01	1.05	0.81
rs3001424	105386765	G	A	0.49	0.98	0.02	3.8E-01	51.89	<0.01	0.49	/I	2.4E-01	0.97	3.0E-01	0.98	0.93
rs11621759	104984573	C	T	0.21	0.97	0.03	3.8E-01	77.08	<0.01	0.18	G*/I	2.6E-01	0.97	3.0E-01	0.97	0.88
rs57898178	104817201	G	C	0.09	1.03	0.04	3.8E-01	0	<0.01	0.08	/I	4.5E-01	1.03	4.9E-01	1.03	0.90
rs112819612	104759170	G	C	0.03	1.06	0.07	3.8E-01	0	<0.01	0.02	/I	4.6E-01	1.05	4.6E-01	1.05	0.76
rs4983531	105178089	C	T	0.44	0.98	0.02	3.8E-01	0	0.09	0.48	/I	3.8E-01	1.02	9.6E-01	1.00	0.89
rs28483031	104841554	T	C	0.28	0.97	0.03	3.8E-01	0	0.02	0.25	/I	4.1E-01	0.98	3.8E-01	0.97	0.76
rs34011356	105497500	A	G	0.11	0.97	0.03	3.8E-01	0	<0.01	0.11	/I	3.4E-01	0.97	2.4E-01	0.96	0.98
rs35246301	105052640	G	A	0.10	1.04	0.04	3.8E-01	0	<0.01	0.12	/I	5.6E-01	1.02	6.2E-01	1.02	0.83
rs35153311	105458555	C	T	0.13	0.97	0.03	3.8E-01	0	0.01	0.12	/I	3.0E-01	0.97	1.9E-01	0.96	0.98
rs4983506	105092479	C	T	0.11	0.97	0.03	3.8E-01	0	<0.01	0.15	G/G	2.0E-01	0.96	2.9E-01	0.97	1.00
rs74781693	105013006	A	G	0.13	1.03	0.04	3.8E-01	65.04	<0.01	0.14	/I	4.5E-01	1.03	5.9E-01	1.02	0.78
rs138690995	105498597	C	A	0.10	0.97	0.03	3.8E-01	0	<0.01	0.11	/I	3.4E-01	0.97	2.4E-01	0.96	0.98
rs10151804	105469903	A	G	0.10	0.97	0.03	3.8E-01	0	<0.01	0.10	/I	3.4E-01	0.97	2.4E-01	0.96	0.99
rs79723170	104934067	A	G	0.06	1.04	0.04	3.8E-01	8.97	0.01	0.02	/I	3.1E-01	1.05	3.3E-01	1.04	0.91
rs8007382	104780989	T	C	0.30	0.98	0.03	3.8E-01	0	<0.01	0.25	/I	3.8E-01	0.98	3.8E-01	0.98	0.85
rs34536859	105497910	A	G	0.11	0.97	0.03	3.8E-01	0	<0.01	0.11	/I	3.4E-01	0.97	2.4E-01	0.96	0.98
rs12884743	105052256	A	G	0.10	1.04	0.04	3.8E-01	0	<0.01	0.12	/I	5.6E-01	1.02	6.2E-01	1.02	0.84
rs4994393	105149693	T	C	0.11	1.04	0.05	3.8E-01	46.93	<0.01	0.11	/I	9.4E-01	1.00	9.3E-01	1.00	0.53
rs10129754	105075608	T	A	0.15	0.97	0.03	3.8E-01	0	0.02	0.17	/I	4.0E-01	0.97	5.3E-01	0.98	0.92
rs116763141	105120360	C	A	0.02	1.08	0.09	3.8E-01	0	<0.01	0.01	/I	6.7E-01	1.04	8.1E-01	1.02	0.80
rs7147154	105081712	A	T	0.14	0.97	0.03	3.8E-01	0	0.02	0.17	/I	4.1E-01	0.97	5.3E-01	0.98	0.93
rs78379306	105278345	C	A	0.16	1.03	0.04	3.8E-01	0	0.08	0.16	/I	9.4E-01	1.00	8.2E-01	0.99	0.53
rs190063165	105310454	G	C	0.04	1.06	0.07	3.8E-01	26.25	<0.01	0.02	/I	7.8E-01	1.02	7.8E-01	1.02	0.63
rs10135463	105110944	A	G	0.11	1.04	0.04	3.8E-01	41.64	<0.01	0.13	/I	3.0E-01	1.04	3.7E-01	1.04	0.86
rs10873550	105127721	C	T	0.37	1.02	0.03	3.9E-01	0	0.01	0.41	/I	3.9E-01	1.02	6.3E-01	1.01	0.86
rs10133538	104815368	A	G	0.09	1.03	0.04	3.9E-01	0	<0.01	0.08	/I	4.5E-01	1.03	5.0E-01	1.03	0.90
rs4360859	105620688	A	G	0.11	0.97	0.04	3.9E-01	0	<0.01	0.14	/I	4.9E-01	0.97	5.0E-01	0.97	0.86
rs72705793	105585135	G	A	0.13	1.03	0.04	3.9E-01	0	<0.01	0.12	/I	4.2E-01	1.03	5.4E-01	1.02	0.88
rs57108735	105391474	T	G	0.03	1.06	0.07	3.9E-01	0.83	<0.01	0.02	/I	5.2E-01	1.04	6.1E-01	1.03	0.93
rs4075358	105125821	A	G	0.37	1.02	0.03	3.9E-01	0	0.01	0.41	/I					

rs75364586	105396269	T	C	0.03	1.06	0.07	3.9E-01	0	<0.01	0.02	/I	5.1E-01	1.05	5.9E-01	1.04	0.91
rs2396457	105417766	A	G	0.06	0.95	0.06	3.9E-01	52.11	<0.01	0.06	/I	3.2E-01	0.95	2.3E-01	0.94	0.70
rs4304959	104875537	G	T	0.22	0.98	0.03	3.9E-01	6.13	<0.01	0.25	/I	3.9E-01	0.98	3.5E-01	0.97	0.92
rs10873543	104799002	C	T	0.31	0.98	0.03	3.9E-01	0	<0.01	0.26	/I	4.0E-01	0.98	4.0E-01	0.98	0.85
rs2816663	105596731	A	G	0.35	1.02	0.03	3.9E-01	0	<0.01	0.36	/I	4.2E-01	1.02	2.7E-01	1.03	0.87
rs10137691	105079467	C	T	0.15	0.97	0.03	3.9E-01	0	0.02	0.17	G*/I	4.1E-01	0.97	5.4E-01	0.98	0.93
rs4288925	105585347	A	G	0.08	1.04	0.04	4.0E-01	0	<0.01	0.09	G*/I	4.6E-01	1.03	3.9E-01	1.04	0.91
rs7149759	105086306	T	C	0.08	1.04	0.04	4.0E-01	57.04	<0.01	0.09	/I	3.4E-01	1.04	3.6E-01	1.04	0.93
rs10135130	105079171	C	T	0.15	0.97	0.03	4.0E-01	0	0.02	0.17	G*/I	4.1E-01	0.97	5.4E-01	0.98	0.93
rs78565684	104949744	C	T	0.06	1.04	0.05	4.0E-01	31.62	0.01	0.02	/I	3.5E-01	1.05	3.6E-01	1.05	0.86
rs6576035	104861468	A	G	0.02	1.08	0.09	4.0E-01	0	0.03	0.01	/I	4.6E-01	1.07	4.8E-01	1.07	0.69
rs11628117	104795151	A	G	0.30	0.98	0.03	4.0E-01	0	<0.01	0.25	/I	4.0E-01	0.98	4.0E-01	0.98	0.85
rs8016394	104982879	T	C	0.21	0.97	0.03	4.0E-01	74.42	<0.01	0.18	/I	2.8E-01	0.97	3.1E-01	0.97	0.87
rs7158841	105128025	C	G	0.37	1.02	0.03	4.0E-01	0	0.01	0.41	/I	4.0E-01	1.02	6.5E-01	1.01	0.86
rs8018619	104977500	A	T	0.43	1.02	0.03	4.0E-01	43.36	<0.01	0.41	/I	5.3E-01	1.02	4.3E-01	1.02	0.65
rs116954970	105147901	G	A	0.02	0.92	0.10	4.0E-01	7.5	0.06	0.04	/I	4.4E-01	0.93	4.1E-01	0.92	0.51
rs74605003	104931304	A	G	0.06	1.04	0.04	4.0E-01	9.65	0.01	0.02	/I	3.2E-01	1.04	3.4E-01	1.04	0.91
rs12879330	105060024	G	A	0.27	0.98	0.03	4.0E-01	44.34	<0.01	0.34	/I	4.6E-01	0.98	5.0E-01	0.98	0.85
rs4983567	104983536	T	C	0.21	0.97	0.03	4.0E-01	76.94	<0.01	0.18	/I	2.8E-01	0.97	3.1E-01	0.97	0.88
rs10220575	105641485	C	T	0.11	0.97	0.04	4.0E-01	0	<0.01	0.14	G*/I	5.4E-01	0.98	5.3E-01	0.98	0.86
rs11624098	104746900	T	C	0.23	1.03	0.03	4.0E-01	0	<0.01	0.28	/I	4.0E-01	1.03	4.4E-01	1.02	0.70
rs8005538	105097284	A	T	0.30	1.02	0.03	4.0E-01	61.59	0.03	0.36	/I	6.5E-01	1.01	8.5E-01	1.01	0.78
rs11160806	104876720	C	A	0.22	0.98	0.03	4.0E-01	0	<0.01	0.25	/I	4.0E-01	0.98	3.6E-01	0.98	0.92
rs4243745	104776139	A	G	0.31	0.98	0.03	4.0E-01	0	<0.01	0.26	/I	4.0E-01	0.98	4.0E-01	0.98	0.84
rs144323040	105417396	G	C	0.04	1.05	0.06	4.0E-01	0	<0.01	0.04	/I	5.4E-01	1.04	6.5E-01	1.03	0.82
rs71423804	105480067	A	G	0.05	0.96	0.05	4.0E-01	16.11	<0.01	0.06	/I	5.2E-01	0.97	4.8E-01	0.96	0.90
rs56043710	104877500	G	A	0.22	0.98	0.03	4.0E-01	4.21	<0.01	0.25	/I	4.0E-01	0.98	3.7E-01	0.98	0.91
rs117545408	105006134	G	A	0.06	1.05	0.06	4.0E-01	14.25	<0.01	0.04	/I	6.8E-01	1.03	2.6E-01	1.07	0.54
rs3825765	105532812	G	A	0.27	1.02	0.02	4.0E-01	0	<0.01	0.25	/I	4.1E-01	1.02	2.7E-01	1.03	0.94
rs12436101	105119532	A	G	0.08	1.04	0.05	4.0E-01	50.81	<0.01	0.09	/I	2.2E-01	1.06	3.1E-01	1.05	0.79
rs10150848	105500760	A	T	0.24	1.02	0.02	4.0E-01	0	<0.01	0.24	G/G	3.7E-01	1.02	2.5E-01	1.03	0.99
rs184625231	104841704	G	A	0.04	0.95	0.07	4.1E-01	0	<0.01	0.01	/I	4.5E-01	0.95	4.1E-01	0.95	0.69
rs4983511	105100021	T	C	0.14	1.03	0.04	4.1E-01	48.39	0.01	0.16	G*/I	3.6E-01	1.03	5.0E-01	1.03	0.86
rs4074077	105126354	C	A	0.37	1.02	0.03	4.1E-01	0	0.71	0.41	G*/I	4.2E-01	1.02	6.7E-01	1.01	0.87
rs73363386	105470192	G	A	0.09	0.97	0.04	4.1E-01	0	<0.01	0.08	/I	3.5E-01	0.96	2.5E-01	0.96	0.92
rs7147439	105523663	A	G	0.27	1.02	0.02	4.1E-01	0	<0.01	0.25	/I	4.0E-01	1.02	2.6E-01	1.03	0.93
rs28669700	104753219	G	A	0.40	1.02	0.03	4.1E-01	0	<0.01	0.42	/I	3.8E-01	1.03	4.4E-01	1.02	0.66
rs4900619	104782751	G	A	0.31	0.98	0.03	4.1E-01	0	<0.01	0.26	/I	4.1E-01	0.98	4.1E-01	0.98	0.85
rs7142008	105678266	A	G	0.29	1.02	0.02	4.1E-01	0	<0.01	0.32	/I	4.5E-01	1.02	4.8E-01	1.02	0.94
rs7153225	104779130	A	T	0.31	0.98	0.03	4.1E-01	0	<0.01	0.26	/I	4.1E-01	0.98	4.1E-01	0.98	0.85
rs4265747	104841309	C	T	0.23	1.02	0.03	4.1E-01	0	<0.01	0.24	/I	4.8E-01	1.02	5.0E-01	1.02	0.79
rs76902772	104917787	A	G	0.07	1.04	0.04	4.1E-01	0	0.01	0.03	/I	3.7E-01	1.04	3.9E-01	1.04	0.83
rs7153433	104837477	A	G	0.31	0.98	0.03	4.1E-01	0	<0.01	0.31	/I	4.6E-01	0.98	4.8E-01	0.98	0.84
rs10151705	105108984	C	A	0.11	1.03	0.04	4.1E-01	42.41	<0.01	0.13	/I	3.2E-01	1.04	3.9E-01	1.04	0.86
rs4993268	104751196	T	C	0.35	1.03	0.03	4.1E-01	0	<0.01	0.40	/I	3.9E-01	1.03	4.6E-01	1.02	0.62
rs61998875	105000267	A	G	0.47	1.02	0.03	4.1E-01	60.89	<0.01	0.49	/I	5.7E-01	1.02	4.0E-01	1.02	0.80
rs10873546	104799171	C	T	0.31	0.98	0.03	4.1E-01	0	<0.01	0.26	/I	4.2E-01	0.98	4.2E-01	0.98	0.85
rs34726969	105510511	C	A	0.07	0.97	0.04	4.1E-01	53.8	0.01	0.08	/I	4.9E-01	0.97	4.5E-01	0.97	0.95
rs2242634	105615026	G	A	0.36	1.02	0.02	4.1E-01	50.71	<0.01	0.32	/I	3.5E-01	1.02	4.1E-01	1.02	0.97
rs10135061	104798035	G	A	0.31	0.98	0.03	4.1E-01	0	<0.01	0.26	/I	4.2E-01	0.98	4.2E-01	0.98	0.85
rs7155540	105019692	T	A	0.07	1.04	0.05	4.1E-01	50.14	<0.01	0.08	/I	3.5E-01	1.05	3.3E-01	1.05	0.83
rs4900623	104798088	C	T	0.31	0.98	0.03	4.1E-01	0	<0.01	0.25	/I	4.2E-01	0.98	4.1E-01	0.98	0.85
rs4993270	104751157	T	C	0.34	1.03	0.03	4.1E-01	0	<0.01	0.40	/I	3.9E-01	1.03	4.6E-01	1.02	0.61
rs9671797	104985279	G	A	0.21	0.98	0.03	4.1E-01	76.84	<0.01	0.18	/I	2.9E-01	0.97	3.2E-01	0.97	0.87
rs111464799	105087833	A	G	0.08	1.03	0.04	4.1E-01	55.77	<0.01	0.08	/I	3.5E-01	1.04	3.7E-01	1.04	0.92
rs1057744	105617042	T	C	0.47	1.02	0.02	4.1E-01	68.06	<0.01	0.46	G*/I	3.9E-01	1.02	4.4E-01	1.02	0.95
rs12883736	104890738	A	T	0.21	0.98	0.03	4.1E-01	0	<0.01	0.25	/I	4.3E-01	0.98	3.9E-01	0.98	0.87
rs7161689	105184463	C	T	0.44	0.98	0.02	4.1E-01	0	0.08	0.49	/I	3.3E-01	1.02	8.8E-01	1.00	0.91
rs7156003	104891972	T	C	0.21	0.98	0.03	4.1E-01	0	<0.01	0.25	/I	4.3E-01	0.98	3.9E-01	0.98	0.87
rs10148829	104795489	G	A	0.31	0.98	0.03	4.1E-01	0	<0.01	0.25	/I	4.2E-01	0.98	4.2E-01	0.98	0.85
rs36036939	104900295	G	T	0.23	0.98	0.03	4.1E-01	0	<0.01	0.27	/I	4.7E-01	0.98	4.1E-01	0.98	0.84
rs10144325	105515219	G	A	0.07	1.05	0.06	4.1E-01	0	<0.01	0.02	/I	3.5E-01	1.06	3.3E-01	1.06	0.52
rs117924517	104881560	C	T	0.22	0.98	0.03	4.1E-01	0	<0.01	0.25	/I	4.2E-01	0.98	3.8E-01	0.98	0.92
rs139953068	104881544	C	T	0.22	0.98	0.03	4.1E-01	0	<0.01	0.25	/I	4.2E-01	0.98	3.8E-01	0.98	0.92
rs11160826	105412260	C	G	0.07	0.96	0.05	4.1E-01	64.76	<0.01	0.08	/I	3.8E-01	0.96	2.9E-01	0.95	0.67
rs3087836	105676048	C	G	0.29	1.02	0.02	4.1E-01	0	<0.01	0.32	/I	4.5E-01	1.02	4.8E-01	1.02	0.94
rs2819417	105397850	G	C	0.03	1.05	0.06	4.1E-01	12.81	<0.01	0.02	/I	5.5E-01	1.04	6.4E-01	1.03	0.90
rs12887459	104891255	T	C	0.21	0.98	0.03	4.2E-01	0	<0.01	0.25	/I	4.4E-01	0.98	3.9E-01	0.98	0.87
rs6576031	104799236	A	T	0.30	0.98	0.03	4.2E-01	0	<0.01	0.25	/I	4.2E-01	0.98	4.2E-01	0.98	0.85
rs143412532	105387063	A	G	0.03	1.05	0.07	4.2E-01	3.89	<0.01	0.02	/I	5.6E-01	1.04	6.6E-01	1.03	0.88
rs118026124	104908761	A	G	0.06	0.96	0.05	4.2E-01	12.59	<0.01	0.10	/I	5.3E-01	0.97	4.4E-01	0.96	0.79
rs11622102	104750123	G	A	0.39	1.02	0.03	4.2E-01	0	<0.01	0.42	/I	3.9E-01	1.02	4.6E-01	1.02	0.70
rs61995998	105344872	T	C	0.47	1.02	0.02	4.2E-01	20.19	0.02	0.48	/I	6.7E-02	1.04	2.2E-01	1.03	0.83
rs4077166	105040916	C	A	0.07	1.04	0.05	4.2E-01	0	<0.01	0.06	/I	6.1E-01	1.03	6.3E-01	1.03	0.71
rs4077165	105040896	T	C	0.07	1.04	0.05	4.2E-									

rs78014542	105406235	C	A	0.02	0.94	0.08	4.3E-01	0	<0.01	0.02	/I	6.2E-01	0.96	5.2E-01	0.95	0.72
rs6576056	105137291	A	G	0.35	1.02	0.03	4.3E-01	61.12	0.02	0.35	/I	8.9E-01	1.00	6.8E-01	1.01	0.82
rs2735807	105594861	C	T	0.12	1.03	0.04	4.4E-01	0	<0.01	0.13	/I	5.4E-01	1.02	4.2E-01	1.03	0.91
rs186804688	105440931	T	C	0.01	0.90	0.13	4.4E-01	0	<0.01	0.01	/I	2.6E-01	0.86	2.7E-01	0.87	0.52
rs2894635	105417225	G	C	0.31	1.02	0.03	4.4E-01	0	<0.01	0.29	/I	1.0E-01	1.05	1.4E-01	1.05	0.57
rs2819463	105451772	T	C	0.03	1.07	0.09	4.4E-01	0	<0.01	0.05	/I	5.2E-01	1.06	5.1E-01	1.06	0.65
rs28545079	104753154	A	G	0.40	1.02	0.03	4.4E-01	0	<0.01	0.42	/I	4.0E-01	1.02	4.7E-01	1.02	0.65
rs57420438	105653210	G	A	0.39	1.02	0.03	4.4E-01	17.19	<0.01	0.39	/I	3.7E-01	1.02	4.3E-01	1.02	0.76
rs9972231	105615648	T	C	0.13	0.97	0.04	4.4E-01	0	<0.01	0.16	/I	5.2E-01	0.98	4.9E-01	0.97	0.86
rs55764224	105134136	A	T	0.35	1.02	0.03	4.4E-01	60.72	0.02	0.35	/I	9.0E-01	1.00	6.8E-01	1.01	0.82
rs35769770	104938865	C	G	0.06	1.03	0.04	4.4E-01	11.08	0.01	0.02	/I	3.6E-01	1.04	3.8E-01	1.04	0.91
rs118138381	105551156	T	C	0.03	1.06	0.07	4.4E-01	20.75	<0.01	0.02	/I	5.4E-01	1.04	6.5E-01	1.03	0.77
rs140083307	105626330	G	C	0.03	1.07	0.09	4.4E-01	46.02	<0.01	0.03	/I	4.4E-01	1.07	4.6E-01	1.07	0.60
rs2816660	105595651	C	T	0.12	1.03	0.04	4.4E-01	0	<0.01	0.12	/I	5.4E-01	1.02	4.2E-01	1.03	0.92
rs150521726	104970972	A	G	0.02	1.08	0.10	4.4E-01	0	<0.01	0.02	/I	5.9E-01	1.05	5.7E-01	1.06	0.69
rs117194149	105441049	A	G	0.03	1.06	0.07	4.4E-01	3.23	<0.01	0.03	/I	5.3E-01	1.05	6.3E-01	1.03	0.87
rs10138227	105259706	T	C	0.14	1.02	0.03	4.4E-01	0	<0.01	0.15	/I	1.1E-01	1.05	1.5E-01	1.05	0.76
rs113127653	105386180	T	C	0.03	1.05	0.07	4.4E-01	11.08	<0.01	0.02	/I	5.8E-01	1.04	6.9E-01	1.03	0.88
rs11625865	105644421	A	G	0.39	1.02	0.02	4.4E-01	47.99	<0.01	0.36	G*/I	3.8E-01	1.02	4.0E-01	1.02	0.99
rs7154928	104751889	G	A	0.39	1.02	0.03	4.4E-01	0	<0.01	0.42	/I	4.1E-01	1.02	4.8E-01	1.02	0.67
rs7155082	104751911	A	C	0.39	1.02	0.03	4.4E-01	0	<0.01	0.42	/I	4.1E-01	1.02	4.8E-01	1.02	0.67
rs141319327	104903390	C	G	0.02	1.08	0.11	4.4E-01	0	<0.01	0.04	/I	5.1E-01	1.07	5.3E-01	1.07	0.66
rs10137134	104751918	T	C	0.39	1.02	0.03	4.4E-01	0	<0.01	0.42	/I	4.1E-01	1.02	4.8E-01	1.02	0.67
rs117761136	104965751	A	G	0.02	0.91	0.12	4.4E-01	4.25	<0.01	0.05	/I	4.2E-01	0.91	5.1E-01	0.92	0.47
rs55713209	105107075	A	C	0.12	1.03	0.04	4.4E-01	43.81	<0.01	0.12	/I	3.5E-01	1.04	4.2E-01	1.03	0.85
rs28619327	104753286	C	T	0.40	1.02	0.03	4.4E-01	0	<0.01	0.42	/I	4.1E-01	1.02	4.8E-01	1.02	0.66
rs28652801	104750871	A	G	0.39	1.02	0.03	4.4E-01	0	<0.01	0.42	/I	4.1E-01	1.02	4.8E-01	1.02	0.69
rs2494740	105247881	T	A	0.29	1.02	0.02	4.4E-01	0	<0.01	0.26	I/G	9.5E-01	1.00	7.9E-01	1.01	0.62
rs72713869	105130931	A	G	0.08	1.04	0.05	4.4E-01	52.4	<0.01	0.09	/I	2.1E-01	1.06	3.3E-01	1.05	0.79
rs4983588	104994807	A	T	0.21	0.98	0.03	4.4E-01	76.27	<0.01	0.20	/I	2.5E-01	0.96	3.1E-01	0.97	0.85
rs4374099	104875686	T	C	0.22	0.98	0.03	4.4E-01	0.74	<0.01	0.25	/I	4.5E-01	0.98	4.1E-01	0.98	0.92
rs7159100	104995655	C	T	0.21	0.98	0.03	4.4E-01	75.51	<0.01	0.20	/I	2.5E-01	0.96	3.1E-01	0.97	0.85
rs150641823	105144096	A	C	0.01	0.90	0.13	4.5E-01	39.01	<0.01	0.02	/I	6.5E-01	0.94	4.9E-01	0.91	0.49
rs4993267	104751237	T	C	0.39	1.02	0.03	4.5E-01	0	<0.01	0.42	/I	4.2E-01	1.02	4.8E-01	1.02	0.68
rs12436200	104772534	G	A	0.30	0.98	0.03	4.5E-01	0	<0.01	0.25	/I	4.4E-01	0.98	4.5E-01	0.98	0.84
rs11160840	105661997	C	A	0.30	1.02	0.03	4.5E-01	0	<0.01	0.31	/I	5.0E-01	1.02	4.8E-01	1.02	0.83
rs188283218	105356533	G	A	0.08	1.04	0.05	4.5E-01	0	<0.01	0.02	/I	7.2E-01	1.02	3.9E-01	1.05	0.52
rs2919624	105386726	G	C	0.49	0.98	0.02	4.5E-01	53.86	<0.01	0.49	/I	2.9E-01	0.98	3.3E-01	0.98	0.93
rs74091119	105161674	G	C	0.18	1.02	0.03	4.5E-01	0	0.12	0.19	/I	6.9E-01	0.99	8.8E-01	1.00	0.80
rs4391998	105536162	C	T	0.27	1.02	0.02	4.5E-01	0	<0.01	0.25	/I	4.4E-01	1.02	2.9E-01	1.03	0.95
rs4983377	105137311	G	C	0.08	1.04	0.05	4.5E-01	50.32	<0.01	0.09	/I	2.0E-01	1.06	3.4E-01	1.04	0.79
rs2006918	105672535	G	A	0.30	1.02	0.02	4.5E-01	0	<0.01	0.34	/I	4.9E-01	1.02	5.2E-01	1.02	0.92
rs76741286	105599773	G	C	0.02	1.07	0.09	4.5E-01	28.16	<0.01	0.02	/I	2.8E-01	1.10	2.3E-01	1.12	0.50
rs8020454	105685865	C	T	0.30	1.02	0.02	4.5E-01	0	<0.01	0.32	G*/I	4.9E-01	1.02	5.2E-01	1.02	0.95
rs6576027	104781231	C	A	0.31	0.98	0.03	4.5E-01	0	<0.01	0.26	/I	4.4E-01	0.98	4.4E-01	0.98	0.84
rs3742943	105608564	T	C	0.13	0.97	0.04	4.5E-01	0	<0.01	0.16	/I	5.3E-01	0.98	5.0E-01	0.97	0.85
rs74976219	105108735	C	T	0.32	1.02	0.03	4.5E-01	48.02	0.03	0.38	/I	6.3E-01	1.01	8.8E-01	1.00	0.84
rs56101862	105101749	T	C	0.03	0.94	0.08	4.5E-01	22.75	<0.01	0.04	/I	3.4E-01	0.93	2.1E-01	0.90	0.62
rs12436313	105509242	G	A	0.22	1.02	0.03	4.5E-01	0	<0.01	0.20	/I	4.3E-01	1.02	2.8E-01	1.03	0.97
rs7155678	104751499	C	T	0.39	1.02	0.03	4.5E-01	0	<0.01	0.42	/I	4.2E-01	1.02	4.9E-01	1.02	0.68
rs12588430	104752472	T	C	0.39	1.02	0.03	4.5E-01	0	<0.01	0.42	/I	4.2E-01	1.02	4.9E-01	1.02	0.67
rs71423826	105659114	T	C	0.11	0.97	0.04	4.5E-01	20.34	<0.01	0.11	/I	6.2E-01	0.98	5.8E-01	0.98	0.68
rs4983627	105025757	G	C	0.15	0.98	0.03	4.5E-01	1.33	<0.01	0.16	/I	4.8E-01	0.98	3.4E-01	0.97	0.89
rs8012933	105026262	A	G	0.15	0.98	0.03	4.5E-01	6.88	<0.01	0.16	/I	4.8E-01	0.98	3.4E-01	0.97	0.89
rs2816675	105605350	C	T	0.11	1.03	0.04	4.5E-01	0	<0.01	0.10	/I	4.7E-01	1.03	3.7E-01	1.03	0.90
rs4310788	104885264	C	G	0.22	0.98	0.03	4.5E-01	0	<0.01	0.25	/I	4.6E-01	0.98	4.2E-01	0.98	0.92
rs4072285	105161275	A	G	0.18	1.02	0.03	4.5E-01	0	0.12	0.19	/I	7.1E-01	0.99	8.7E-01	1.00	0.80
rs12591007	104752373	C	T	0.39	1.02	0.03	4.5E-01	0	<0.01	0.42	/I	4.2E-01	1.02	4.9E-01	1.02	0.67
rs2735806	105595101	G	A	0.09	1.03	0.04	4.5E-01	0	<0.01	0.09	/I	5.3E-01	1.03	4.5E-01	1.03	0.90
rs8008808	104781153	C	T	0.31	0.98	0.03	4.6E-01	0	<0.01	0.26	/I	4.5E-01	0.98	4.5E-01	0.98	0.85
rs9806114	105694903	C	G	0.08	0.96	0.05	4.6E-01	70.85	<0.01	0.12	/I	4.0E-01	0.96	4.0E-01	0.96	0.61
rs4993269	104751195	G	T	0.35	1.02	0.03	4.6E-01	0	<0.01	0.40	/I	4.4E-01	1.02	5.1E-01	1.02	0.62
rs72713881	105134917	C	T	0.08	1.03	0.05	4.6E-01	50.34	<0.01	0.09	/I	2.1E-01	1.06	3.5E-01	1.04	0.79
rs4993272	104751143	G	A	0.39	1.02	0.03	4.6E-01	0	<0.01	0.42	/I	4.3E-01	1.02	4.9E-01	1.02	0.68
rs8007138	105131102	C	A	0.33	1.02	0.03	4.6E-01	0	0.02	0.37	/I	5.1E-01	1.02	7.9E-01	1.01	0.85
rs9671466	105135634	G	A	0.34	1.02	0.03	4.6E-01	65.67	0.02	0.34	/I	9.7E-01	1.00	7.3E-01	1.01	0.81
rs8021799	104773336	C	T	0.30	0.98	0.03	4.6E-01	0	<0.01	0.25	/I	4.5E-01	0.98	4.6E-01	0.98	0.84
rs3784228	105679644	G	C	0.30	1.02	0.02	4.6E-01	0	<0.01	0.32	/I	5.0E-01	1.02	5.3E-01	1.02	0.94
rs186056825	105015063	G	A	0.14	1.03	0.04	4.6E-01	70.9	<0.01	0.12	/I	6.7E-01	1.02	8.0E-01	1.01	0.82
rs34860972	105467240	G	T	0.12	0.98	0.03	4.6E-01	0	<0.01	0.11	/I	3.6E-01	0.97	2.4E-01	0.96	0.99
rs7144934	105279202	A	G	0.13	0.97	0.04	4.6E-01	68.02	<0.01	0.09	/I	2.6E-01	0.96	5.5E-01	0.98	0.58
rs145238396	105403611	C	T	0.03	1.05	0.07	4.6E-01	45.83	<0.01	0.02	/I	6.2E-01	1.03	7.2E-01	1.03	0.91
rs73352317	105314669	A	C	0.05	1.04	0.06	4.6E-01	0	<0.01	0.03	/I	9.0E-01	1.01	9.2E-01	1.01	0.72
rs12895547	105460359	T	C	0.12	0.98	0.03	4.6E-01	0	<0.01	0.11	I/G	3.6E-01	0.97	2.5E-01	0.96	1.00
rs79764956	105402085	A	G	0.03	1.05	0										

rs117751669	105395374	A	G	0.03	1.05	0.07	4.7E-01	47.39	<0.01	0.02	/I	6.3E-01	1.03	7.3E-01	1.02	0.91
rs9788596	105350930	A	G	0.04	1.04	0.06	4.7E-01	0	<0.01	0.05	/I	6.7E-01	1.02	6.6E-01	1.02	0.90
rs4906458	104883184	T	A	0.22	0.98	0.03	4.7E-01	0	<0.01	0.25	G*/I	4.7E-01	0.98	4.3E-01	0.98	0.92
rs12101275	105057586	G	C	0.27	0.98	0.03	4.7E-01	49.83	<0.01	0.34	/I	5.3E-01	0.98	5.7E-01	0.98	0.85
rs4906459	104883763	T	C	0.22	0.98	0.03	4.7E-01	0	<0.01	0.25	G*/I	4.7E-01	0.98	4.3E-01	0.98	0.92
rs55792168	105122109	G	A	0.36	1.02	0.03	4.7E-01	0	0.01	0.40	/I	4.8E-01	1.02	7.5E-01	1.01	0.85
rs2289454	105457780	G	T	0.12	0.98	0.03	4.7E-01	0	<0.01	0.11	/I	3.7E-01	0.97	2.5E-01	0.96	1.00
rs3825761	105638931	C	T	0.39	1.02	0.02	4.7E-01	47.31	<0.01	0.36	/I	4.0E-01	1.02	4.3E-01	1.02	0.99
rs12101279	105057469	A	G	0.27	0.98	0.03	4.7E-01	49.93	<0.01	0.34	/I	5.3E-01	0.98	5.7E-01	0.98	0.85
rs55849896	105559489	C	G	0.18	0.98	0.03	4.7E-01	85.03	<0.01	0.14	/I	4.6E-01	0.98	3.3E-01	0.97	0.81
rs7155060	105086888	G	A	0.13	0.98	0.03	4.7E-01	0	0.01	0.16	/I	4.4E-01	0.98	5.4E-01	0.98	0.92
rs141397123	105690030	A	G	0.02	1.07	0.10	4.7E-01	13.09	<0.01	0.01	/I	4.8E-01	1.07	5.2E-01	1.06	0.63
rs10142703	105107865	A	C	0.11	1.03	0.04	4.7E-01	40.26	<0.01	0.13	/I	3.5E-01	1.04	4.5E-01	1.03	0.87
rs3002448	105262042	C	G	0.04	0.95	0.07	4.7E-01	45.88	<0.01	0.06	/I	9.2E-02	0.89	2.3E-01	0.92	0.52
rs8017525	105065452	G	A	0.13	0.98	0.03	4.7E-01	0	0.01	0.16	/I	4.9E-01	0.98	6.2E-01	0.98	0.91
rs6576032	104827897	C	T	0.40	0.98	0.03	4.7E-01	0	0.01	0.42	/I	4.8E-01	0.98	4.7E-01	0.98	0.85
rs12436984	104901662	T	G	0.22	0.98	0.03	4.7E-01	0	<0.01	0.28	/I	5.3E-01	0.98	4.5E-01	0.98	0.87
rs4078242	105148536	T	C	0.30	1.02	0.03	4.7E-01	0	0.03	0.34	/I	6.7E-01	1.01	8.4E-01	1.01	0.63
rs73352311	105311570	A	G	0.05	1.04	0.06	4.7E-01	0	<0.01	0.03	/I	9.3E-01	1.01	9.5E-01	1.00	0.71
rs4341690	105017531	C	T	0.10	1.03	0.04	4.7E-01	57.8	<0.01	0.09	/I	5.1E-01	1.03	6.2E-01	1.02	0.87
rs12436635	105132647	T	C	0.08	1.03	0.05	4.7E-01	53.4	<0.01	0.09	/I	2.2E-01	1.06	3.6E-01	1.04	0.79
rs35916062	105541197	A	G	0.20	0.98	0.03	4.7E-01	53.34	<0.01	0.16	/I	4.3E-01	0.98	3.1E-01	0.97	0.89
rs74246318	104928020	C	T	0.28	0.98	0.02	4.8E-01	0	<0.01	0.32	/I	5.9E-01	0.99	5.1E-01	0.98	0.93
rs61997128	104900881	C	G	0.04	0.95	0.08	4.8E-01	0	<0.01	0.02	/I	4.9E-01	0.95	5.0E-01	0.95	0.61
rs12892790	104883585	T	A	0.22	0.98	0.03	4.8E-01	0	<0.01	0.25	/I	4.8E-01	0.98	4.4E-01	0.98	0.92
rs12101271	105057529	G	A	0.27	0.98	0.03	4.8E-01	50.62	<0.01	0.34	/I	5.4E-01	0.98	5.4E-01	0.98	0.85
rs2238287	105618670	C	T	0.34	1.02	0.02	4.8E-01	45.26	<0.01	0.31	/I	3.9E-01	1.02	4.1E-01	1.02	0.94
rs116117446	104903000	T	G	0.04	0.95	0.08	4.8E-01	0	<0.01	0.02	/I	4.9E-01	0.95	5.0E-01	0.95	0.62
rs2816661	105596010	A	C	0.12	1.03	0.04	4.8E-01	0	<0.01	0.12	/I	5.8E-01	1.02	4.6E-01	1.03	0.92
rs149735065	105384560	T	C	0.02	1.05	0.07	4.8E-01	21.43	<0.01	0.02	/I	6.7E-01	1.03	7.6E-01	1.02	0.86
rs4906445	104780294	C	T	0.31	0.98	0.03	4.8E-01	0	<0.01	0.26	G*/I	4.7E-01	0.98	4.8E-01	0.98	0.85
rs12434065	104988896	C	G	0.16	1.03	0.04	4.8E-01	0	<0.01	0.21	/I	5.2E-01	1.02	5.4E-01	1.02	0.83
rs11844119	105640486	G	A	0.39	1.02	0.02	4.8E-01	47.51	<0.01	0.35	/I	4.1E-01	1.02	4.4E-01	1.02	0.99
rs12433715	104899549	C	A	0.23	0.98	0.03	4.8E-01	0	<0.01	0.26	/I	5.4E-01	0.98	4.7E-01	0.98	0.84
rs10141511	105298022	T	C	0.07	1.04	0.05	4.8E-01	0	<0.01	0.12	/I	3.8E-01	1.05	4.8E-01	1.04	0.61
rs2816673	105605199	C	T	0.11	1.03	0.04	4.8E-01	0	<0.01	0.10	/I	4.9E-01	1.03	3.9E-01	1.03	0.90
rs73352310	105311527	T	C	0.05	1.04	0.06	4.8E-01	0	<0.01	0.03	/I	9.4E-01	1.00	9.5E-01	1.00	0.71
rs113127878	105034783	T	C	0.06	1.04	0.05	4.8E-01	53.62	0.01	0.06	/I	3.5E-01	1.05	3.2E-01	1.05	0.83
rs7154167	104751430	T	C	0.39	1.02	0.03	4.8E-01	0	<0.01	0.42	/I	4.5E-01	1.02	5.2E-01	1.02	0.68
rs3825763	105642639	G	A	0.39	1.01	0.02	4.8E-01	47.82	<0.01	0.36	/I	4.1E-01	1.02	4.4E-01	1.02	0.99
rs182264948	105351066	A	C	0.03	1.06	0.08	4.8E-01	0	<0.01	0.05	/I	6.4E-01	1.04	7.1E-01	1.03	0.57
rs2006925	105672497	T	C	0.30	1.02	0.02	4.8E-01	0	<0.01	0.32	/I	5.3E-01	1.02	5.6E-01	1.01	0.93
rs10139182	104996272	A	C	0.21	0.98	0.03	4.8E-01	76.14	<0.01	0.20	/I	2.9E-01	0.97	3.4E-01	0.97	0.85
rs117678142	105625424	T	C	0.11	0.97	0.04	4.8E-01	0	<0.01	0.14	/I	6.2E-01	0.98	6.2E-01	0.98	0.87
rs7151473	105668531	C	T	0.30	1.02	0.02	4.8E-01	0	<0.01	0.32	/I	5.3E-01	1.02	5.6E-01	1.01	0.93
rs3784227	105679928	C	T	0.30	1.02	0.02	4.9E-01	0	<0.01	0.32	/I	5.2E-01	1.02	5.5E-01	1.01	0.94
rs7142130	105671232	A	C	0.30	1.02	0.02	4.9E-01	0	<0.01	0.32	/I	5.3E-01	1.02	5.6E-01	1.01	0.93
rs116922905	105386543	C	G	0.03	1.05	0.07	4.9E-01	5.2	<0.01	0.02	/I	6.3E-01	1.03	7.3E-01	1.02	0.89
rs117677402	105386533	G	T	0.03	1.05	0.07	4.9E-01	5.15	<0.01	0.02	/I	6.3E-01	1.03	7.3E-01	1.02	0.89
rs2816674	105605252	C	T	0.11	1.03	0.04	4.9E-01	0	<0.01	0.10	/I	5.0E-01	1.03	4.0E-01	1.03	0.90
rs117033424	104799865	T	C	0.02	1.07	0.10	4.9E-01	13.09	<0.01	0.03	/I	3.8E-01	1.09	4.2E-01	1.08	0.60
rs8010223	105712091	C	T	0.01	1.08	0.11	4.9E-01	27.64	<0.01	0.01	/I	7.0E-01	1.04	5.6E-01	1.07	0.81
rs11622864	104921616	T	C	0.21	0.98	0.03	4.9E-01	0	<0.01	0.29	G/G	5.5E-01	0.99	4.8E-01	0.98	1.00
rs112009092	105315087	T	C	0.05	1.04	0.05	4.9E-01	0	<0.01	0.04	/I	9.8E-01	1.00	9.9E-01	1.00	0.75
rs28716932	104942132	G	A	0.23	1.02	0.03	4.9E-01	0	<0.01	0.27	/I	5.6E-01	1.02	4.8E-01	1.02	0.92
rs4519286	104888368	T	C	0.22	0.98	0.03	4.9E-01	0	<0.01	0.23	/I	5.0E-01	0.98	4.6E-01	0.98	0.83
rs7151532	105669310	G	C	0.30	1.02	0.02	4.9E-01	0	<0.01	0.32	/I	5.3E-01	1.02	5.7E-01	1.01	0.93
rs34369401	105150580	T	C	0.15	0.97	0.04	4.9E-01	0	0.05	0.14	/I	3.4E-01	0.97	8.1E-01	1.01	0.66
rs76848025	104944374	A	G	0.05	1.04	0.05	4.9E-01	25.07	0.01	0.02	/I	4.1E-01	1.04	4.3E-01	1.04	0.85
rs117999220	105064067	C	T	0.01	0.92	0.12	4.9E-01	35.6	<0.01	0.01	/I	6.7E-01	0.95	5.7E-01	0.94	0.70
rs113614574	104943299	T	C	0.05	1.04	0.05	4.9E-01	24.72	0.01	0.02	/I	4.1E-01	1.04	4.3E-01	1.04	0.85
rs11627935	105092303	T	C	0.49	1.02	0.03	4.9E-01	0	<0.01	0.49	/I	3.4E-01	1.03	2.7E-01	1.03	0.53
rs2841218	105323581	C	G	0.04	1.04	0.06	4.9E-01	33.31	<0.01	0.05	/I	5.9E-01	1.03	7.2E-01	1.02	0.89
rs4326984	105162054	C	T	0.48	1.02	0.02	4.9E-01	0	<0.01	0.49	/I	1.9E-01	0.97	5.5E-01	0.99	0.87
rs11160842	105674225	G	A	0.30	1.02	0.02	4.9E-01	0	<0.01	0.32	/I	5.3E-01	1.02	5.7E-01	1.01	0.93
rs7153223	104749048	C	T	0.39	1.02	0.03	4.9E-01	0	<0.01	0.43	/I	4.5E-01	1.02	5.2E-01	1.02	0.71
rs2241865	105459140	C	A	0.12	0.98	0.03	4.9E-01	0	<0.01	0.11	G/G	3.9E-01	0.97	2.7E-01	0.97	1.00
rs80032152	104943862	T	C	0.05	1.04	0.05	4.9E-01	24.52	0.01	0.02	/I	4.1E-01	1.04	4.3E-01	1.04	0.86
rs57918775	105695493	T	C	0.36	0.98	0.03	4.9E-01	38.47	<0.01	0.32	/I	4.6E-01	0.98	6.5E-01	0.99	0.70
rs35736913	105680474	T	C	0.09	0.97	0.05	4.9E-01	0	0.02	0.09	/I	5.4E-01	0.97	6.5E-01	0.98	0.73
rs4471603	104899788	T	C	0.23	0.98	0.03	4.9E-01	0	<0.01	0.27	/I	5.6E-01	0.98	4.9E-01	0.98	0.85
rs10129716	105300536	C	T	0.05	0.95	0.07	5.0E-01	0	<0.01	0.02	/I	5.6E-01	0.96	3.5E-01	0.94	0.47
rs4983512	105102261	A	G	0.12	1.03	0.04	5.0E-01	52.38	<0.01	0.15	/I	3.3E-01	1.04	4.4E-01	1.03	0.86
rs8010249	105495550	G	T	0.20	1.02	0.03	5.0E-01	0	<0.01	0.22	/I	5.7E-01	1.02	3.8E-01	1.03	0.69
rs4371093	105135861	C	A	0.07	1.03	0.05</										

rs77825258	105387609	C	T	0.03	1.05	0.07	5.1E-01	0	<0.01	0.02	/I	6.5E-01	1.03	7.6E-01	1.02	0.90
rs8010342	105672066	C	A	0.30	1.02	0.02	5.1E-01	0	<0.01	0.32	/I	5.5E-01	1.01	6.0E-01	1.01	0.92
rs184571245	105356532	G	T	0.09	0.97	0.05	5.1E-01	60.73	<0.01	0.16	/I	2.5E-01	0.94	3.2E-01	0.95	0.49
rs7157285	105669360	A	T	0.30	1.02	0.02	5.1E-01	0	<0.01	0.32	/I	5.5E-01	1.01	5.9E-01	1.01	0.93
rs4906460	104883844	C	T	0.22	0.98	0.03	5.1E-01	0	<0.01	0.25	/I	5.1E-01	0.98	4.7E-01	0.98	0.92
rs4906457	104883143	C	G	0.22	0.98	0.03	5.1E-01	0	<0.01	0.25	/I	5.1E-01	0.98	4.7E-01	0.98	0.92
rs77384212	105428491	C	T	0.03	1.04	0.06	5.1E-01	0	<0.01	0.02	/I	8.2E-01	1.02	1.0E+00	1.00	0.84
rs8005486	105686570	C	T	0.29	1.02	0.02	5.1E-01	0	<0.01	0.32	/I	5.5E-01	1.01	5.8E-01	1.01	0.94
rs34413418	104987822	T	C	0.35	0.98	0.03	5.1E-01	0	<0.01	0.41	/I	3.9E-01	0.98	5.7E-01	0.98	0.68
rs12883636	105692697	C	G	0.29	1.02	0.02	5.1E-01	0	<0.01	0.32	/I	5.7E-01	1.01	6.0E-01	1.01	0.93
rs8007360	105130941	A	G	0.33	1.02	0.03	5.1E-01	0	0.02	0.37	/I	5.6E-01	1.02	8.5E-01	1.01	0.86
rs74603289	105401180	T	C	0.02	1.06	0.09	5.1E-01	36.92	<0.01	0.01	/I	4.4E-01	1.07	5.1E-01	1.06	0.66
rs187776716	105128241	A	G	0.02	0.93	0.11	5.1E-01	34.26	<0.01	0.02	/I	8.8E-01	0.98	6.4E-01	0.95	0.54
rs4424849	105508666	G	A	0.26	1.02	0.02	5.1E-01	0	<0.01	0.25	/I	4.1E-01	1.02	2.3E-01	1.03	1.00
rs2841263	105374626	T	C	0.08	1.02	0.04	5.1E-01	21.1	<0.01	0.08	/I	8.4E-01	1.01	9.5E-01	1.00	0.98
rs77732021	105149150	A	C	0.05	0.95	0.07	5.1E-01	67.59	<0.01	0.04	/I	3.8E-01	0.94	8.2E-01	0.98	0.48
rs74088594	104841866	G	A	0.09	1.03	0.04	5.1E-01	0	<0.01	0.08	/I	5.9E-01	1.02	6.6E-01	1.02	0.77
rs4993271	104751156	A	G	0.34	1.02	0.03	5.1E-01	0	<0.01	0.40	/I	4.9E-01	1.02	5.7E-01	1.02	0.61
rs60806965	105423663	C	T	0.03	1.05	0.07	5.1E-01	9.85	<0.01	0.02	/I	5.6E-01	1.04	6.9E-01	1.03	0.85
rs74090133	105423666	C	A	0.03	1.05	0.07	5.1E-01	9.84	<0.01	0.02	/I	5.6E-01	1.04	6.9E-01	1.03	0.85
rs61995971	105288348	A	G	0.07	0.97	0.05	5.1E-01	61.23	<0.01	0.08	/I	7.3E-01	1.02	9.6E-01	1.00	0.53
rs78090212	104860797	A	G	0.07	1.04	0.06	5.1E-01	0	<0.01	0.07	/I	5.3E-01	1.04	4.0E-01	1.05	0.61
rs191711895	105291932	C	T	0.07	0.96	0.06	5.1E-01	45.64	<0.01	0.05	/I	7.3E-01	0.98	4.2E-01	0.95	0.49
rs2010787	105690092	T	C	0.29	1.02	0.02	5.1E-01	0	<0.01	0.32	G*/I	5.5E-01	1.01	5.8E-01	1.01	0.95
rs1882848	105644151	C	T	0.39	1.01	0.02	5.2E-01	48.04	<0.01	0.36	/I	4.5E-01	1.02	4.7E-01	1.02	1.00
rs145296877	105455602	C	T	0.02	1.06	0.10	5.2E-01	0	<0.01	0.02	/I	4.7E-01	1.07	5.5E-01	1.06	0.76
rs11621385	105687199	C	T	0.29	1.02	0.02	5.2E-01	0	<0.01	0.32	/I	5.6E-01	1.01	5.9E-01	1.01	0.94
rs146095558	105121639	A	T	0.04	1.05	0.07	5.2E-01	54.88	<0.01	0.02	/I	7.6E-01	1.02	8.0E-01	1.02	0.64
rs182868140	105351246	C	T	0.11	0.97	0.04	5.2E-01	13.42	<0.01	0.15	/I	5.4E-01	0.97	7.8E-01	0.99	0.54
rs4983508	105093301	C	T	0.12	1.03	0.04	5.2E-01	52.36	<0.01	0.15	/I	3.6E-01	1.04	4.6E-01	1.03	0.68
rs12434207	105128105	G	T	0.08	1.03	0.05	5.2E-01	52.72	<0.01	0.09	/I	2.6E-01	1.05	3.6E-01	1.04	0.79
rs2819440	105417894	G	C	0.24	1.02	0.03	5.2E-01	34.93	0.02	0.23	/I	3.4E-01	1.03	2.6E-01	1.04	0.64
rs10139596	105643619	A	G	0.39	1.01	0.02	5.2E-01	50.1	<0.01	0.36	/I	4.5E-01	1.02	4.8E-01	1.02	1.00
rs72703898	105535253	A	G	0.02	1.06	0.08	5.2E-01	0	<0.01	0.04	/I	7.7E-01	1.03	7.8E-01	1.02	0.84
rs2582517	105313442	G	A	0.08	1.03	0.04	5.2E-01	0	<0.01	0.07	/I	9.9E-01	1.00	9.1E-01	1.00	0.78
rs45515697	105457282	A	G	0.13	0.98	0.03	5.2E-01	0	<0.01	0.12	/I	4.3E-01	0.98	2.9E-01	0.97	0.99
rs10129642	105103694	A	G	0.12	1.03	0.04	5.2E-01	52.89	<0.01	0.15	/I	3.6E-01	1.04	4.7E-01	1.03	0.86
rs10400759	105687536	G	A	0.29	1.02	0.02	5.2E-01	0	<0.01	0.32	/I	5.6E-01	1.01	5.9E-01	1.01	0.94
rs4983590	105646179	A	G	0.39	1.01	0.02	5.2E-01	51.37	<0.01	0.36	G*/G	4.5E-01	1.02	4.8E-01	1.02	0.99
rs2242636	105614032	G	C	0.36	1.01	0.02	5.2E-01	56.13	<0.01	0.32	/I	4.3E-01	1.02	5.0E-01	1.01	0.97
rs73363318	105091286	G	C	0.11	1.02	0.04	5.2E-01	71.91	<0.01	0.09	/I	4.9E-01	1.03	5.6E-01	1.02	0.81
rs17620990	105687771	C	T	0.29	1.02	0.02	5.3E-01	0	<0.01	0.32	/I	5.7E-01	1.01	6.0E-01	1.01	0.94
rs10140111	105644282	G	C	0.39	1.01	0.02	5.3E-01	49.48	<0.01	0.36	/I	4.5E-01	1.02	4.8E-01	1.02	1.00
rs117743574	105391469	C	G	0.03	1.04	0.07	5.3E-01	51.94	<0.01	0.02	/I	7.0E-01	1.03	8.0E-01	1.02	0.91
rs10139451	104752022	G	A	0.39	1.02	0.03	5.3E-01	0	<0.01	0.42	/I	4.9E-01	1.02	5.6E-01	1.02	0.67
rs10139455	104752043	G	A	0.39	1.02	0.03	5.3E-01	0	<0.01	0.42	/I	4.9E-01	1.02	5.6E-01	1.02	0.67
rs4983513	105102555	C	T	0.13	1.02	0.04	5.3E-01	52.89	<0.01	0.15	/I	3.7E-01	1.04	4.7E-01	1.03	0.85
rs75100193	105472994	A	T	0.03	1.04	0.06	5.3E-01	30.7	<0.01	0.02	/I	6.5E-01	1.03	7.5E-01	1.02	0.94
rs28458861	104753148	A	G	0.37	1.02	0.03	5.3E-01	0	<0.01	0.42	/I	5.0E-01	1.02	5.7E-01	1.02	0.61
rs11626524	104762402	C	T	0.14	0.98	0.04	5.3E-01	0	<0.01	0.15	/I	5.7E-01	0.98	5.8E-01	0.98	0.78
rs144769838	105385516	T	G	0.03	1.04	0.07	5.3E-01	0	<0.01	0.02	/I	7.2E-01	1.02	8.2E-01	1.02	0.89
rs3784241	105622960	T	G	0.11	0.97	0.04	5.3E-01	0	<0.01	0.14	/I	6.7E-01	0.98	6.8E-01	0.98	0.87
rs10138846	105618886	G	C	0.11	0.97	0.04	5.3E-01	0	<0.01	0.14	/I	6.7E-01	0.98	6.8E-01	0.98	0.87
rs34058091	105042927	G	T	0.10	1.03	0.04	5.3E-01	24.41	<0.01	0.12	/I	7.5E-01	1.01	8.0E-01	1.01	0.88
rs60794775	105066923	C	T	0.10	1.02	0.04	5.4E-01	49.32	<0.01	0.11	/I	4.6E-01	1.03	5.0E-01	1.03	0.89
rs76280735	105499854	G	C	0.12	1.03	0.04	5.4E-01	0.75	<0.01	0.11	/I	4.4E-01	1.03	3.8E-01	1.04	0.51
rs4146328	105636587	A	G	0.40	1.01	0.02	5.4E-01	46.79	<0.01	0.35	/I	5.5E-01	1.01	5.8E-01	1.01	0.85
rs14592	105717265	T	C	0.06	0.96	0.06	5.4E-01	0	0.01	0.09	G*/I	5.9E-01	0.97	6.0E-01	0.97	0.61
rs2091920	105693309	G	C	0.29	1.02	0.02	5.4E-01	0	<0.01	0.32	/I	6.0E-01	1.01	6.3E-01	1.01	0.91
rs146795886	105484119	T	G	0.03	1.04	0.06	5.4E-01	31.91	<0.01	0.02	/I	6.6E-01	1.03	7.6E-01	1.02	0.94
rs28502730	104926595	T	C	0.07	1.03	0.04	5.4E-01	28.31	<0.01	0.02	/I	4.6E-01	1.03	4.8E-01	1.03	0.88
rs74976966	105671033	A	C	0.02	1.06	0.10	5.4E-01	0.28	<0.01	0.01	/I	5.5E-01	1.06	5.9E-01	1.05	0.64
rs7143644	105107537	A	G	0.07	1.03	0.05	5.4E-01	0	<0.01	0.04	/I	9.7E-01	1.00	3.0E-01	1.06	0.73
rs56307141	105131197	C	A	0.33	1.02	0.03	5.4E-01	0	0.02	0.37	/I	6.0E-01	1.01	8.9E-01	1.00	0.85
rs56401486	105278921	A	G	0.41	0.98	0.03	5.4E-01	0	0.06	0.41	/I	6.4E-01	1.01	8.0E-01	0.99	0.52
rs3784226	105681602	T	C	0.05	0.96	0.06	5.4E-01	0	<0.01	0.04	/I	6.6E-01	0.97	6.1E-01	0.97	0.63
rs4073645	105105769	T	C	0.11	1.02	0.04	5.4E-01	37.75	<0.01	0.13	G*/I	4.1E-01	1.03	5.0E-01	1.03	0.87
rs78262814	105612885	A	G	0.12	0.98	0.04	5.4E-01	0	<0.01	0.15	/I	6.6E-01	0.98	6.5E-01	0.98	0.85
rs10149229	105609335	G	A	0.36	1.01	0.02	5.4E-01	49.03	<0.01	0.32	/I	4.6E-01	1.02	5.3E-01	1.01	0.94
rs12589619	105046728	C	T	0.12	1.02	0.04	5.5E-01	3.65	<0.01	0.12	/I	7.8E-01	1.01	8.4E-01	1.01	0.88
rs28525465	104753146	G	A	0.37	1.02	0.03	5.5E-01	0	<0.01	0.42	/I	5.2E-01	1.02	5.9E-01	1.02	0.61
rs10138987	105084021	T	A	0.13	0.98	0.03	5.5E-01	0	<0.01	0.16	/I	5.1E-01	0.98	6.2E-01	0.98	0.92
rs2072674	105623512	C	T	0.37	1.01	0.02	5.5E-01	57.3	<0.01	0.34	/I	4.6E-01	1.02	5.1E-01	1.01	0.99
rs59917589	105490983	A	G	0.03	1.04	0.06	5.5E-01	34.31	<0.01	0.02	/I	6.7E-01	1.03	7.7E-01	1.02	0.93
rs74921260	1054823															

rs10873549	105126319	C	T	0.08	1.03	0.05	5.7E-01	52.18	<0.01	0.09	/I	3.2E-01	1.05	4.3E-01	1.04	0.80
rs59373922	105416784	G	A	0.08	1.03	0.05	5.7E-01	0	0.02	0.09	/I	7.0E-01	1.02	6.9E-01	1.02	0.64
rs4270105	105048542	T	C	0.10	1.02	0.04	5.7E-01	22	<0.01	0.12	/I	7.9E-01	1.01	8.5E-01	1.01	0.87
rs4983404	105015189	A	G	0.16	1.02	0.03	5.7E-01	0	<0.01	0.12	/I	5.6E-01	1.02	6.0E-01	1.02	0.75
rs11620834	105677983	G	C	0.02	1.06	0.10	5.7E-01	0	<0.01	0.02	/I	5.9E-01	1.05	6.6E-01	1.04	0.67
rs73350401	105302637	T	C	0.05	1.03	0.06	5.7E-01	0	<0.01	0.03	/I	9.3E-01	0.99	9.3E-01	0.99	0.69
rs10873555	105648608	C	T	0.39	1.01	0.02	5.7E-01	58.71	<0.01	0.36	/I	5.0E-01	1.01	5.3E-01	1.01	0.96
rs2582559	105347248	G	C	0.08	1.02	0.04	5.7E-01	41.39	<0.01	0.08	/I	8.5E-01	1.01	9.4E-01	1.00	0.97
rs73350365	105281754	G	A	0.05	1.03	0.06	5.7E-01	0	<0.01	0.03	/I	9.1E-01	0.99	9.2E-01	0.99	0.66
rs61998865	104995783	T	C	0.49	1.01	0.03	5.7E-01	52.49	<0.01	0.48	/I	7.4E-01	1.01	5.1E-01	1.02	0.84
rs185665842	105331497	T	C	0.04	1.03	0.06	5.7E-01	20.89	<0.01	0.05	/I	7.4E-01	1.02	7.4E-01	1.01	0.77
rs2003181	105642016	T	C	0.39	1.01	0.02	5.7E-01	52.85	<0.01	0.36	/I	5.0E-01	1.01	5.3E-01	1.01	0.99
rs7140257	104963012	T	C	0.06	1.03	0.05	5.7E-01	27.58	<0.01	0.02	/I	5.2E-01	1.03	5.4E-01	1.03	0.85
rs79705661	104905717	C	T	0.05	1.03	0.06	5.7E-01	37.23	<0.01	0.08	/I	6.0E-01	1.03	6.6E-01	1.03	0.72
rs10873554	105648606	A	G	0.39	1.01	0.02	5.7E-01	58.79	<0.01	0.36	/I	5.1E-01	1.01	5.4E-01	1.01	0.96
rs35064464	104985530	G	A	0.38	0.98	0.03	5.7E-01	18.47	<0.01	0.39	/I	4.9E-01	0.98	6.8E-01	0.99	0.72
rs4994394	105149647	A	G	0.18	1.02	0.04	5.7E-01	0	<0.01	0.16	/I	4.7E-01	1.03	5.9E-01	1.02	0.51
rs58784542	104951222	T	C	0.06	1.03	0.05	5.7E-01	23.61	<0.01	0.02	/I	5.2E-01	1.03	5.4E-01	1.03	0.85
rs183140846	105117133	A	G	0.01	0.93	0.13	5.7E-01	4.75	<0.01	0.02	/I	8.0E-01	0.97	6.4E-01	0.94	0.57
rs61998869	104999302	A	C	0.48	1.01	0.03	5.7E-01	54.07	<0.01	0.48	/I	7.3E-01	1.01	5.1E-01	1.02	0.83
rs75442513	105040821	G	A	0.19	1.02	0.03	5.8E-01	36.69	<0.01	0.19	/I	6.8E-01	1.01	6.4E-01	1.01	0.76
rs4983536	105183236	C	T	0.44	0.99	0.02	5.8E-01	14.96	0.08	0.44	/I	2.9E-01	1.03	8.1E-01	1.01	0.87
rs59432264	104995291	A	G	0.49	1.01	0.03	5.8E-01	52.45	<0.01	0.48	/I	7.4E-01	1.01	5.2E-01	1.02	0.84
rs56076302	104966947	A	T	0.49	1.01	0.03	5.8E-01	52.28	<0.01	0.48	/I	7.4E-01	1.01	5.2E-01	1.02	0.85
rs11160839	105648963	A	T	0.39	1.01	0.02	5.8E-01	58.13	<0.01	0.36	/I	5.1E-01	1.01	5.4E-01	1.01	0.96
rs79206914	105323424	A	C	0.41	1.01	0.02	5.8E-01	0	0.04	0.39	/I	2.5E-01	1.03	3.9E-01	1.02	0.91
rs58867885	105309645	G	A	0.08	1.02	0.04	5.8E-01	4.8	<0.01	0.07	/I	9.4E-01	1.00	8.5E-01	0.99	0.77
rs112768215	105302750	C	T	0.05	1.03	0.06	5.8E-01	0	<0.01	0.03	/I	9.2E-01	0.99	9.2E-01	0.99	0.69
rs192661426	105579870	T	C	0.04	1.04	0.07	5.8E-01	0	<0.01	0.04	/I	7.1E-01	1.03	8.6E-01	1.01	0.69
rs143189615	104871416	A	G	0.01	0.94	0.12	5.8E-01	0	<0.01	0.01	/I	6.5E-01	0.95	6.1E-01	0.94	0.64
rs11850848	105415608	C	G	0.23	1.02	0.03	5.8E-01	32.19	<0.01	0.24	/I	2.5E-01	1.04	3.9E-01	1.03	0.56
rs2293806	105617891	T	C	0.11	0.98	0.04	5.8E-01	0	<0.01	0.14	G*/I	7.2E-01	0.99	7.3E-01	0.99	0.87
rs4072256	104809949	G	T	0.12	1.02	0.03	5.8E-01	0	<0.01	0.11	/I	6.9E-01	1.01	7.2E-01	1.01	0.87
rs61997100	104767248	G	A	0.14	1.02	0.04	5.8E-01	0	<0.01	0.15	/I	5.7E-01	1.02	5.6E-01	1.02	0.72
rs78669334	104953864	G	C	0.06	1.03	0.05	5.8E-01	23.77	<0.01	0.02	/I	5.2E-01	1.03	5.5E-01	1.03	0.85
rs3809461	105058498	G	A	0.14	0.98	0.03	5.8E-01	0	<0.01	0.18	/I	6.2E-01	0.98	7.5E-01	0.99	0.91
rs76429488	105026578	T	C	0.06	1.03	0.05	5.8E-01	52.53	0.01	0.06	/I	4.5E-01	1.04	4.0E-01	1.04	0.83
rs4283166	104888387	T	C	0.19	0.98	0.03	5.8E-01	2.25	<0.01	0.21	/I	6.2E-01	0.98	5.7E-01	0.98	0.82
rs10131020	104744191	A	G	0.10	0.98	0.05	5.8E-01	0	<0.01	0.12	/I	5.9E-01	0.98	6.0E-01	0.98	0.70
rs113987641	105467965	C	G	0.15	0.98	0.04	5.8E-01	21.91	<0.01	0.12	/I	9.1E-01	1.00	8.4E-01	1.01	0.57
rs55972700	104819663	C	T	0.41	0.99	0.03	5.8E-01	0	<0.01	0.42	/I	5.9E-01	0.99	5.8E-01	0.99	0.85
rs2582494	105378056	A	G	0.08	1.02	0.04	5.8E-01	0	<0.01	0.08	/I	9.0E-01	1.00	8.9E-01	0.99	0.99
rs61998867	104997397	T	C	0.06	1.03	0.06	5.9E-01	0	<0.01	0.04	/I	7.8E-01	1.02	4.1E-01	1.05	0.58
rs4380006	105377950	T	A	0.08	1.02	0.04	5.9E-01	0	<0.01	0.08	/I	9.0E-01	1.00	8.9E-01	0.99	0.99
rs2582493	105378121	T	C	0.08	1.02	0.04	5.9E-01	0	<0.01	0.08	/I	9.0E-01	1.00	8.9E-01	0.99	0.99
rs2582522	105379716	C	A	0.08	1.02	0.04	5.9E-01	0	<0.01	0.08	/I	9.0E-01	1.00	8.9E-01	0.99	0.99
rs112356118	105066109	C	G	0.03	1.05	0.08	5.9E-01	0	0.08	0.05	/I	4.9E-01	1.06	6.0E-01	1.04	0.67
rs2841249	105368733	A	G	0.08	1.02	0.04	5.9E-01	0	<0.01	0.08	G/G	9.0E-01	1.00	8.9E-01	0.99	1.00
rs79623988	105301130	T	C	0.05	1.03	0.06	5.9E-01	0	<0.01	0.03	/I	9.0E-01	0.99	9.0E-01	0.99	0.69
rs57362922	105366351	C	T	0.08	1.02	0.04	5.9E-01	0	<0.01	0.08	/I	9.0E-01	1.00	8.9E-01	0.99	0.99
rs11160838	105648901	C	T	0.39	1.01	0.02	5.9E-01	58.69	<0.01	0.36	/I	5.2E-01	1.01	5.9E-01	1.01	0.96
rs28728425	105002331	C	A	0.16	0.98	0.04	5.9E-01	14.47	<0.01	0.14	/I	5.4E-01	0.98	6.2E-01	0.98	0.66
rs144144778	105187519	G	A	0.06	1.03	0.06	5.9E-01	0.93	<0.01	0.04	/I	8.8E-01	1.01	4.8E-01	1.04	0.50
rs12433394	105129218	T	C	0.08	1.02	0.05	6.0E-01	55.81	<0.01	0.09	/I	3.4E-01	1.04	4.6E-01	1.03	0.80
rs55664235	105330148	G	C	0.42	1.01	0.02	6.0E-01	0	<0.01	0.43	/I	3.4E-01	1.02	4.2E-01	1.02	0.82
rs12891835	105026600	G	A	0.17	0.98	0.03	6.0E-01	0.68	<0.01	0.16	/I	5.9E-01	0.98	4.4E-01	0.98	0.90
rs4983431	105035446	T	C	0.16	0.98	0.03	6.0E-01	0	<0.01	0.18	/I	6.1E-01	0.98	4.5E-01	0.98	0.90
rs4633639	105508577	G	A	0.26	1.01	0.02	6.0E-01	0	<0.01	0.25	G/G	4.8E-01	1.02	2.8E-01	1.03	1.00
rs4983410	105026076	G	A	0.17	0.98	0.03	6.0E-01	0.99	<0.01	0.16	/I	5.9E-01	0.98	4.4E-01	0.98	0.90
rs4983577	105554626	G	C	0.22	0.98	0.03	6.0E-01	79.23	<0.01	0.18	/I	5.4E-01	0.98	4.3E-01	0.98	0.90
rs67294498	105513297	C	T	0.03	0.96	0.08	6.0E-01	0	<0.01	0.02	/I	5.9E-01	0.96	6.0E-01	0.96	0.73
rs12890617	105508998	T	G	0.27	1.01	0.02	6.0E-01	0	<0.01	0.25	/I	4.8E-01	1.02	2.8E-01	1.03	1.00
rs11160833	105557054	G	C	0.23	0.99	0.03	6.0E-01	80.72	<0.01	0.19	/I	5.5E-01	0.98	4.3E-01	0.98	0.89
rs7157637	105036239	A	G	0.16	0.98	0.03	6.0E-01	0	<0.01	0.18	/I	6.1E-01	0.98	4.5E-01	0.98	0.91
rs3809455	105173831	T	G	0.06	0.97	0.05	6.0E-01	58.41	0.02	0.04	/I	3.7E-01	1.05	7.5E-01	1.02	0.59
rs12892858	105220558	G	A	0.12	0.98	0.03	6.0E-01	0	0.03	0.06	/I	3.0E-02	0.93	6.3E-01	1.02	0.94
rs11625862	105644382	A	G	0.40	1.01	0.02	6.0E-01	54.03	<0.01	0.36	/I	5.3E-01	1.01	5.6E-01	1.01	0.97
rs28435446	105128979	T	C	0.08	1.02	0.05	6.0E-01	55.42	<0.01	0.09	/I	3.5E-01	1.04	4.6E-01	1.03	0.80
rs75232889	105310876	T	C	0.03	0.96	0.08	6.0E-01	0	<0.01	0.04	/I	6.3E-01	0.96	5.4E-01	0.95	0.45
rs118005222	105722913	A	G	0.02	1.05	0.10	6.0E-01	0	<0.01	0.05	/I	5.9E-01	1.06	7.0E-01	1.04	0.53
rs35165446	105223853	C	T	0.12	0.98	0.03	6.0E-01	0	0.03	0.06	/I	3.0E-02	0.93	6.3E-01	1.02	0.94
rs4359373	105499859	C	G	0.14	1.02	0.04	6.0E-01	0	<0.01	0.14	/I	6.9E-01	1.02	5.7E-01	1.02	0.51
rs72700197	105357771	T	C	0.04	1.03	0.06	6.0E-01	0	<0.01	0.05	/I	7.6E-01	1.02	8.8E-01	1.01	0.95
rs113605200	105276100	G	A	0.13	1.02	0.03	6.1E-01	0	0.01	0.14	/I	1.7E-01	1.05	2.1E-01	1.04	0.74
rs34283552	105558360	G														

rs28497781	104940181	C	G	0.06	1.02	0.04	6.1E-01	13.47	0.01	0.02	/I	5.2E-01	1.03	5.3E-01	1.03	0.88
rs10139080	104988732	C	G	0.48	1.01	0.03	6.1E-01	49.91	<0.01	0.47	/I	7.2E-01	1.01	5.8E-01	1.01	0.86
rs34448993	105680769	C	A	0.34	1.01	0.02	6.1E-01	0	<0.01	0.38	/I	7.0E-01	1.01	7.2E-01	1.01	0.85
rs2816639	105607205	C	T	0.11	1.02	0.04	6.1E-01	0	<0.01	0.09	/I	6.3E-01	1.02	5.1E-01	1.02	0.89
rs2841250	105368868	A	G	0.08	1.02	0.04	6.1E-01	0	<0.01	0.08	/I	9.4E-01	1.00	8.6E-01	0.99	1.00
rs11850227	105375295	A	G	0.08	1.02	0.04	6.1E-01	0	<0.01	0.08	/I	9.3E-01	1.00	8.6E-01	0.99	0.99
rs2735802	105597476	G	A	0.12	1.02	0.03	6.2E-01	0	<0.01	0.12	/I	7.3E-01	1.01	5.9E-01	1.02	0.92
rs74089858	105629046	C	T	0.13	0.98	0.04	6.2E-01	65.1	<0.01	0.10	/I	5.3E-01	0.97	6.1E-01	0.98	0.69
rs73350395	105299174	A	G	0.05	1.03	0.06	6.2E-01	0	<0.01	0.03	/I	8.7E-01	0.99	8.7E-01	0.99	0.69
rs147014778	104938934	T	G	0.02	1.07	0.13	6.2E-01	0.96	<0.01	0.01	/I	6.5E-01	1.06	5.6E-01	1.08	0.43
rs12878336	105050966	T	C	0.10	1.02	0.04	6.2E-01	10.13	<0.01	0.12	/I	8.3E-01	1.01	8.9E-01	1.01	0.85
rs60332569	105298970	T	C	0.05	1.03	0.06	6.2E-01	0	<0.01	0.03	/I	8.7E-01	0.99	8.7E-01	0.99	0.69
rs57147900	105423476	T	C	0.03	1.03	0.06	6.2E-01	16.98	<0.01	0.03	/I	6.7E-01	1.03	8.0E-01	1.02	0.90
rs58365272	105423450	G	T	0.03	1.03	0.06	6.2E-01	16.97	<0.01	0.03	/I	6.7E-01	1.03	8.0E-01	1.02	0.90
rs12894325	105028944	C	G	0.14	0.98	0.03	6.2E-01	0	<0.01	0.16	/I	6.6E-01	0.99	4.9E-01	0.98	0.89
rs4983432	105035484	C	T	0.31	1.01	0.02	6.2E-01	0	<0.01	0.31	/I	6.8E-01	1.01	7.6E-01	1.01	0.91
rs73350392	105297331	C	G	0.05	1.03	0.06	6.2E-01	0	<0.01	0.03	/I	8.7E-01	0.99	8.7E-01	0.99	0.69
rs73350393	105297741	C	G	0.05	1.03	0.06	6.2E-01	0	<0.01	0.03	/I	8.6E-01	0.99	8.7E-01	0.99	0.69
rs10149727	104986678	A	G	0.48	1.01	0.03	6.2E-01	50.17	<0.01	0.49	/I	7.3E-01	1.01	5.9E-01	1.01	0.86
rs12885343	105201635	G	C	0.12	0.98	0.03	6.2E-01	0	0.03	0.07	/I	3.5E-02	0.93	6.1E-01	1.02	0.96
rs10136831	104749671	C	T	0.41	1.01	0.03	6.2E-01	0	<0.01	0.44	/I	5.8E-01	1.02	6.6E-01	1.01	0.68
rs73363311	105088545	A	C	0.03	1.04	0.08	6.2E-01	31.87	<0.01	0.04	/I	6.2E-01	1.04	6.7E-01	1.03	0.72
rs113769274	105296393	A	C	0.05	1.03	0.06	6.2E-01	0	<0.01	0.03	/I	8.6E-01	0.99	8.7E-01	0.99	0.68
rs79333620	105428714	G	A	0.03	1.03	0.06	6.2E-01	20.5	<0.01	0.03	/I	6.8E-01	1.03	8.0E-01	1.02	0.90
rs55639933	1054123940	A	G	0.08	1.02	0.05	6.2E-01	53.5	<0.01	0.09	/I	3.6E-01	1.04	4.8E-01	1.03	0.80
rs8003900	104747573	A	G	0.39	1.01	0.03	6.2E-01	0	<0.01	0.42	/I	5.8E-01	1.02	6.5E-01	1.01	0.73
rs142521279	105428813	G	A	0.03	1.03	0.06	6.2E-01	20.51	<0.01	0.03	/I	6.8E-01	1.03	8.0E-01	1.02	0.90
rs12879749	105649390	T	G	0.03	0.96	0.08	6.2E-01	55.64	<0.01	0.02	/I	7.1E-01	0.97	7.0E-01	0.97	0.61
rs2816657	105595037	C	A	0.35	1.01	0.03	6.2E-01	0	<0.01	0.38	/I	6.5E-01	1.01	4.6E-01	1.02	0.88
rs77347348	105426645	G	A	0.03	1.03	0.06	6.2E-01	17.73	<0.01	0.03	/I	6.8E-01	1.03	8.0E-01	1.02	0.90
rs2816667	105600995	A	G	0.12	1.02	0.03	6.2E-01	0	<0.01	0.12	/I	7.4E-01	1.01	5.9E-01	1.02	0.91
rs184755905	105616349	G	T	0.14	0.98	0.04	6.2E-01	0	<0.01	0.16	/I	4.8E-01	0.97	6.0E-01	0.98	0.56
rs77677417	105473072	G	T	0.03	1.03	0.06	6.3E-01	34.72	<0.01	0.02	/I	7.5E-01	1.02	8.6E-01	1.01	0.93
rs2894636	105417765	C	A	0.06	0.97	0.05	6.3E-01	48.48	<0.01	0.06	/I	5.3E-01	0.97	4.0E-01	0.95	0.70
rs75836410	105442910	A	G	0.04	1.03	0.06	6.3E-01	0	<0.01	0.04	/I	9.2E-01	1.01	8.9E-01	0.99	0.86
rs4247025	105035098	C	T	0.16	0.98	0.03	6.3E-01	0	<0.01	0.18	/I	6.4E-01	0.99	4.8E-01	0.98	0.90
rs1595949	105374213	C	T	0.08	1.02	0.04	6.3E-01	0	<0.01	0.08	G*/I	9.5E-01	1.00	8.4E-01	0.99	1.00
rs3809460	105058609	C	T	0.14	0.98	0.03	6.3E-01	0	0.01	0.16	/I	6.6E-01	0.99	8.1E-01	0.99	0.92
rs72713847	105105804	T	C	0.07	1.03	0.05	6.3E-01	27.63	<0.01	0.04	/I	9.6E-01	1.00	3.6E-01	1.05	0.71
rs111512781	105433422	C	T	0.03	1.03	0.07	6.3E-01	0.49	<0.01	0.03	/I	7.1E-01	1.02	8.5E-01	1.01	0.89
rs1595950	105374260	C	T	0.08	1.02	0.04	6.3E-01	0	<0.01	0.08	G*/I	9.5E-01	1.00	8.4E-01	0.99	1.00
rs1595948	105374049	G	C	0.08	1.02	0.04	6.3E-01	0	<0.01	0.08	G*/I	9.5E-01	1.00	8.4E-01	0.99	1.00
rs28645503	104940506	A	C	0.06	1.02	0.05	6.3E-01	17.67	0.01	0.02	/I	5.3E-01	1.03	5.5E-01	1.03	0.88
rs11851065	105375579	G	A	0.08	1.02	0.04	6.3E-01	0	<0.01	0.08	/I	9.5E-01	1.00	8.4E-01	0.99	1.00
rs7156604	105376212	G	A	0.08	1.02	0.04	6.3E-01	0	<0.01	0.08	/I	9.5E-01	1.00	8.4E-01	0.99	0.99
rs59862477	105031290	G	A	0.14	0.98	0.03	6.3E-01	0	<0.01	0.16	/I	6.7E-01	0.99	5.0E-01	0.98	0.88
rs2119393	105377099	A	G	0.08	1.02	0.04	6.3E-01	0	<0.01	0.08	/I	9.5E-01	1.00	8.4E-01	0.99	0.99
rs12434042	105679131	A	G	0.10	0.98	0.04	6.3E-01	20.12	<0.01	0.10	/I	7.0E-01	0.98	6.8E-01	0.98	0.86
rs72713855	105120783	G	A	0.29	1.01	0.03	6.3E-01	45.6	0.01	0.32	/I	8.2E-01	1.01	9.4E-01	1.00	0.82
rs12878589	105050924	A	G	0.10	1.02	0.04	6.3E-01	30.01	<0.01	0.12	/I	8.5E-01	1.01	8.9E-01	1.01	0.84
rs4255721	104772276	G	A	0.48	0.99	0.03	6.3E-01	0	<0.01	0.48	/I	6.5E-01	0.99	6.8E-01	0.99	0.84
rs59346268	105166252	T	C	0.10	1.02	0.04	6.3E-01	0	0.04	0.06	/I	5.7E-01	0.98	2.5E-01	0.95	0.91
rs112198348	105427770	A	G	0.04	1.03	0.07	6.3E-01	0	0.04	0.05	/I	6.8E-01	1.03	8.0E-01	1.02	0.74
rs72713854	105120669	T	G	0.29	1.01	0.03	6.3E-01	45.63	0.01	0.32	/I	8.3E-01	1.01	9.4E-01	1.00	0.82
rs4983420	105029230	C	T	0.17	0.99	0.03	6.3E-01	0	<0.01	0.17	/I	6.4E-01	0.99	4.8E-01	0.98	0.90
rs12885092	105291917	G	A	0.07	0.97	0.06	6.3E-01	36.67	<0.01	0.04	/I	7.2E-01	0.98	5.0E-01	0.96	0.51
rs4983545	105214471	C	T	0.12	0.99	0.03	6.3E-01	0	0.03	0.07	/I	3.8E-02	0.93	5.9E-01	1.02	0.95
rs184390485	105400046	G	A	0.10	1.02	0.05	6.3E-01	16.44	<0.01	0.12	/I	5.9E-01	1.03	7.3E-01	1.02	0.54
rs3784225	105681667	G	A	0.40	1.01	0.02	6.4E-01	0	<0.01	0.43	/I	6.5E-01	1.01	6.8E-01	1.01	0.96
rs3784231	105678906	T	A	0.38	1.01	0.02	6.4E-01	0	<0.01	0.40	/I	6.6E-01	1.01	7.0E-01	1.01	0.96
rs60629623	105030588	A	G	0.13	0.98	0.03	6.4E-01	0	<0.01	0.16	/I	6.7E-01	0.99	5.0E-01	0.98	0.89
rs4494478	105028823	C	G	0.17	0.99	0.03	6.4E-01	0	<0.01	0.17	/I	6.4E-01	0.99	4.8E-01	0.98	0.90
rs2072675	105623498	T	C	0.36	1.01	0.02	6.4E-01	59.26	<0.01	0.33	I/G	5.5E-01	1.01	6.0E-01	1.01	1.00
rs12881199	105218422	T	C	0.12	0.99	0.03	6.4E-01	0	0.03	0.07	/I	3.7E-02	0.93	5.9E-01	1.02	0.95
rs4983421	105029266	C	T	0.17	0.99	0.03	6.4E-01	0	<0.01	0.17	/I	6.4E-01	0.99	4.8E-01	0.98	0.90
rs7152988	104895028	C	G	0.21	0.99	0.03	6.4E-01	0	<0.01	0.24	/I	6.4E-01	0.99	6.0E-01	0.98	0.81
rs71421298	104791736	A	C	0.05	0.97	0.07	6.4E-01	0	<0.01	0.05	/I	6.4E-01	0.97	6.3E-01	0.97	0.58
rs34024274	105047280	T	C	0.10	1.02	0.04	6.4E-01	14.49	<0.01	0.12	/I	8.7E-01	1.01	9.3E-01	1.00	0.88
rs61489465	104999497	C	T	0.48	1.01	0.03	6.4E-01	47.49	<0.01	0.49	/I	8.1E-01	1.01	5.6E-01	1.02	0.81
rs72705782	105576363	A	G	0.11	0.98	0.04	6.4E-01	0	<0.01	0.14	/I	5.1E-01	0.97	6.0E-01	0.98	0.80
rs4983383	105200006	A	G	0.07	0.98	0.04	6.4E-01	0	<0.01	0.04	/I	7.1E-02	0.92	7.9E-01	1.01	0.76
rs2841262	105373360	G	T	0.08	1.02	0.04	6.4E-01	0	<0.01	0.08	/I	9.7E-01	1.00	8.3E-01	0.99	1.00
rs3809457	105058810	T	G	0.14	0.98	0.03	6.4E-01	0	0.01	0.16	G*/I	6.7E-01	0.99	8.2E-01	0.99	0.92
rs2819425	105411260	G	A	0.02	1.05	0.10	6.4E-01	0	0.01	0.02	/I	8.5E-01	1.02	9.6E-01	1.01	0.44
rs28407239	105098625	T	C	0.12	1.02	0.04	6									

rs73357552	105013840	T	C	0.19	1.01	0.03	6.5E-01	1.02	<0.01	0.19	/I	6.8E-01	1.01	6.9E-01	1.01	0.91
rs78333034	105549187	T	C	0.06	0.98	0.05	6.5E-01	71.43	<0.01	0.05	/I	7.3E-01	0.98	7.1E-01	0.98	0.86
rs11160818	105189222	G	A	0.14	0.99	0.03	6.5E-01	0	0.13	0.18	/I	8.8E-01	1.00	4.0E-01	1.03	0.94
rs2272591	105611282	G	A	0.36	1.01	0.02	6.5E-01	57.33	<0.01	0.32	/I	5.6E-01	1.01	6.5E-01	1.01	0.95
rs35455320	105205481	G	C	0.12	0.99	0.03	6.5E-01	0	0.03	0.07	/I	4.1E-02	0.94	5.8E-01	1.02	0.94
rs72700175	105346449	T	C	0.03	1.03	0.06	6.5E-01	0	<0.01	0.05	/I	8.2E-01	1.01	9.2E-01	1.01	0.94
rs5009021	105499890	C	G	0.24	1.02	0.03	6.5E-01	0	<0.01	0.25	/I	4.1E-01	1.03	2.8E-01	1.04	0.52
rs10136434	105091348	C	T	0.13	0.99	0.03	6.5E-01	16.3	<0.01	0.14	/I	5.0E-01	0.98	6.1E-01	0.98	0.80
rs7156199	105300107	G	A	0.04	0.97	0.08	6.6E-01	64.84	<0.01	0.05	/I	9.3E-01	1.01	8.3E-01	0.98	0.53
rs45452103	105716377	T	C	0.02	1.05	0.10	6.6E-01	37.12	0.01	0.02	/I	5.2E-01	1.07	5.5E-01	1.06	0.56
rs10132112	105051455	G	C	0.11	1.02	0.04	6.6E-01	0	<0.01	0.12	/I	8.9E-01	1.01	9.6E-01	1.00	0.85
rs71421301	105009213	G	A	0.05	0.97	0.07	6.6E-01	0	<0.01	0.05	/I	8.8E-01	0.99	9.9E-01	1.00	0.48
rs7140668	105036463	C	G	0.17	0.99	0.03	6.6E-01	0	<0.01	0.18	/I	6.7E-01	0.99	5.0E-01	0.98	0.91
rs4983438	105037467	A	T	0.17	0.99	0.03	6.6E-01	0	<0.01	0.18	/I	6.7E-01	0.99	5.0E-01	0.98	0.91
rs72700202	105361424	A	G	0.03	1.03	0.06	6.6E-01	0	<0.01	0.05	/I	8.2E-01	1.01	9.3E-01	1.01	0.94
rs72713804	105032048	C	G	0.13	0.98	0.03	6.6E-01	0	<0.01	0.16	/I	6.9E-01	0.99	5.2E-01	0.98	0.88
rs34407486	105037344	A	G	0.17	0.99	0.03	6.6E-01	0	<0.01	0.18	/I	6.7E-01	0.99	5.0E-01	0.98	0.91
rs72707615	105616558	T	C	0.13	0.98	0.04	6.6E-01	0	<0.01	0.16	/I	7.5E-01	0.99	7.2E-01	0.99	0.86
rs10147203	105091346	G	C	0.26	0.99	0.02	6.6E-01	0	<0.01	0.26	/I	4.5E-01	0.98	6.0E-01	0.99	0.81
rs8012919	105314982	G	A	0.03	1.03	0.06	6.6E-01	0	<0.01	0.05	/I	8.5E-01	1.01	9.7E-01	1.00	0.85
rs148957187	1050320853	T	C	0.48	1.01	0.02	6.6E-01	0	0.06	0.48	/I	3.3E-01	1.02	3.2E-01	1.02	0.77
rs35590716	105195321	A	G	0.12	0.99	0.03	6.6E-01	0	0.03	0.07	/I	4.3E-02	0.93	5.7E-01	1.02	0.95
rs72700187	105348770	G	A	0.03	1.03	0.06	6.6E-01	0	<0.01	0.05	/I	8.3E-01	1.01	9.3E-01	1.01	0.95
rs8015164	105091444	A	G	0.13	0.99	0.03	6.6E-01	17.95	<0.01	0.14	/I	5.1E-01	0.98	6.1E-01	0.98	0.80
rs4983547	105215941	A	G	0.12	0.99	0.03	6.6E-01	0	0.03	0.07	/I	4.0E-02	0.93	5.6E-01	1.02	0.95
rs72729035	104760684	A	G	0.06	0.98	0.05	6.6E-01	0	0.01	0.06	/I	6.9E-01	0.98	6.6E-01	0.98	0.78
rs72700184	105348271	T	C	0.03	1.03	0.06	6.6E-01	0	<0.01	0.05	/I	8.3E-01	1.01	9.3E-01	1.00	0.95
rs189204199	105400222	T	C	0.09	0.98	0.05	6.6E-01	47.04	<0.01	0.09	/I	4.4E-01	0.96	5.3E-01	0.97	0.59
rs71421880	105206172	A	T	0.12	0.99	0.03	6.6E-01	0	0.03	0.06	/I	3.8E-02	0.93	5.6E-01	1.02	0.95
rs4983594	105694870	A	G	0.13	1.02	0.04	6.6E-01	26.46	<0.01	0.12	/I	6.0E-01	1.02	4.9E-01	1.03	0.67
rs12882082	105160979	A	G	0.18	0.99	0.03	6.6E-01	0	0.06	0.21	/I	7.1E-01	0.99	4.7E-01	1.02	0.77
rs77294420	105127012	T	C	0.26	1.01	0.03	6.7E-01	35.65	<0.01	0.31	/I	7.5E-01	1.01	9.5E-01	1.00	0.82
rs4983430	105033619	A	G	0.14	0.99	0.03	6.7E-01	0	<0.01	0.16	/I	7.0E-01	0.99	5.2E-01	0.98	0.88
rs10138223	105088984	T	G	0.27	0.99	0.02	6.7E-01	0	<0.01	0.25	/I	4.4E-01	0.98	5.6E-01	0.99	0.87
rs10431751	104761950	T	C	0.13	0.98	0.04	6.7E-01	0	<0.01	0.14	/I	7.2E-01	0.99	7.2E-01	0.99	0.77
rs73357587	105436831	T	C	0.07	0.98	0.05	6.7E-01	38.52	0.02	0.05	/I	5.8E-01	0.97	4.5E-01	0.96	0.79
rs12434765	104989343	T	C	0.15	1.02	0.04	6.7E-01	0	<0.01	0.21	/I	7.3E-01	1.01	7.4E-01	1.01	0.84
rs4983437	105037425	G	A	0.16	0.99	0.03	6.7E-01	0	<0.01	0.18	G*/I	6.8E-01	0.99	5.1E-01	0.98	0.92
rs78353106	105418638	G	A	0.05	1.02	0.05	6.7E-01	50.44	0.02	0.05	/I	7.0E-01	1.02	8.6E-01	1.01	0.86
rs10138381	105500553	G	A	0.23	1.01	0.02	6.7E-01	0	<0.01	0.24	/I	6.3E-01	1.01	4.6E-01	1.02	0.98
rs7146661	105090555	G	C	0.26	0.99	0.02	6.7E-01	0	<0.01	0.25	/I	4.5E-01	0.98	5.7E-01	0.99	0.86
rs12434169	104989254	A	G	0.15	1.02	0.04	6.7E-01	0	<0.01	0.21	/I	7.3E-01	1.01	7.5E-01	1.01	0.84
rs72700185	105348338	G	C	0.03	1.02	0.06	6.7E-01	0	<0.01	0.05	/I	8.4E-01	1.01	9.5E-01	1.00	0.94
rs117059470	105610361	A	G	0.02	0.95	0.11	6.7E-01	0	<0.01	0.04	/I	5.0E-01	0.93	4.7E-01	0.92	0.68
rs145666787	105321401	A	G	0.33	0.99	0.03	6.7E-01	0	<0.01	0.36	/I	6.7E-01	0.99	7.5E-01	0.99	0.59
rs73350371	105285220	G	A	0.05	1.02	0.06	6.7E-01	0	<0.01	0.03	/I	8.0E-01	0.99	8.1E-01	0.99	0.67
rs76260431	105617550	A	C	0.39	1.01	0.03	6.7E-01	76.67	<0.01	0.41	/I	7.9E-01	1.01	8.2E-01	1.01	0.65
rs67944534	105029728	G	C	0.16	0.99	0.03	6.7E-01	1.96	<0.01	0.17	/I	7.0E-01	0.99	5.4E-01	0.98	0.88
rs4430684	105499978	G	C	0.26	0.99	0.03	6.7E-01	0	<0.01	0.24	/I	9.6E-01	1.00	8.6E-01	1.01	0.50
rs4247024	105027938	C	G	0.32	1.01	0.02	6.7E-01	11.08	<0.01	0.30	/I	7.4E-01	1.01	8.1E-01	1.01	0.91
rs10444691	104988326	A	G	0.15	1.02	0.04	6.7E-01	0	<0.01	0.21	/I	7.3E-01	1.01	7.5E-01	1.01	0.84
rs2582523	105379952	C	T	0.08	1.02	0.04	6.7E-01	0	<0.01	0.08	/I	9.4E-01	1.00	7.3E-01	0.99	0.98
rs56078065	105151982	G	T	0.11	1.02	0.04	6.7E-01	0	0.03	0.06	/I	7.3E-01	0.99	3.3E-01	0.96	0.74
rs6576055	105090000	A	G	0.13	0.99	0.03	6.7E-01	2.4	<0.01	0.14	I/G	5.5E-01	0.99	6.4E-01	0.99	0.86
rs10431752	104762003	T	C	0.13	0.98	0.04	6.7E-01	0	<0.01	0.14	/I	7.2E-01	0.99	7.3E-01	0.99	0.77
rs4983542	105210172	A	G	0.12	0.99	0.03	6.7E-01	0	0.03	0.07	/I	4.2E-02	0.94	5.5E-01	1.02	0.95
rs185871859	105321481	A	G	0.23	1.01	0.03	6.8E-01	0	<0.01	0.28	/I	3.5E-01	1.03	3.4E-01	1.03	0.54
rs112196905	105058879	A	G	0.06	1.02	0.05	6.8E-01	57.58	0.02	0.06	/I	4.9E-01	1.04	4.6E-01	1.04	0.88
rs7705982	105019026	A	G	0.19	1.01	0.03	6.8E-01	0	<0.01	0.19	/I	7.1E-01	1.01	7.2E-01	1.01	0.91
rs1595947	105373951	G	A	0.08	1.02	0.04	6.8E-01	0	<0.01	0.08	G*/I	9.9E-01	1.00	7.8E-01	0.99	1.00
rs4983517	104927329	G	A	0.23	0.99	0.03	6.8E-01	0	<0.01	0.24	/I	8.1E-01	0.99	7.5E-01	0.99	0.88
rs11850889	105202643	A	G	0.12	0.99	0.03	6.8E-01	0	0.03	0.07	/I	4.2E-02	0.94	5.6E-01	1.02	0.96
rs77480445	105435394	T	C	0.03	1.03	0.07	6.8E-01	7.71	<0.01	0.03	/I	7.6E-01	1.02	9.0E-01	1.01	0.90
rs4983500	105045524	G	A	0.12	1.02	0.04	6.8E-01	0	<0.01	0.12	G*/I	9.4E-01	1.00	1.0E+00	1.00	0.90
rs12050087	105346869	A	G	0.03	1.02	0.06	6.8E-01	0	<0.01	0.05	/I	8.5E-01	1.01	9.5E-01	1.00	0.94
rs12896579	105225130	T	C	0.12	0.99	0.03	6.8E-01	0	0.03	0.06	/I	4.1E-02	0.93	5.4E-01	1.02	0.94
rs140423947	105231921	T	C	0.01	1.05	0.12	6.8E-01	0	<0.01	0.01	/I	9.4E-01	0.99	7.5E-01	0.96	0.71
rs35527175	105048421	C	A	0.12	1.02	0.04	6.8E-01	0	<0.01	0.12	/I	9.4E-01	1.00	1.0E+00	1.00	0.88
rs143157819	104917262	G	C	0.02	1.05	0.13	6.8E-01	0.94	<0.01	0.01	/I	7.1E-01	1.05	6.2E-01	1.07	0.43
rs4906438	104771729	T	C	0.48	0.99	0.03	6.8E-01	0	<0.01	0.48	/I	7.0E-01	0.99	7.3E-01	0.99	0.84
rs2841272	105387120	G	A	0.03	1.03	0.06	6.8E-01	2.5	<0.01	0.02	/I	8.7E-01	1.01	9.7E-01	1.00	0.81
rs72700176	105346632	A	G	0.03	1.02	0.06	6.8E-01	0	<0.01	0.05	/I	8.5E-01	1.01	9.6E-01	1.00	0.94
rs4381528	105230815	T	C	0.12	0.99	0.03	6.8E-01	0	0.03	0.06	/I	4.2E-02	0.93	5.3E-01	1.02	0.93
rs34437981	105575272	C	A	0.45	1.01	0.03	6.8E-01	13.37	<0.01	0.49	/I	7.0E-01	1.01	5.1E-01	1.02	0.74
rs5015594	105129278	G	A	0.26	1.01	0.03	6.8E-01	43.8	<0.01	0.31						

rs2072673	105624693	C	T	0.36	1.01	0.02	7.0E-01	60.08	<0.01	0.33	G/G	6.0E-01	1.01	6.6E-01	1.01	1.00
rs72713845	105101349	A	G	0.12	1.02	0.04	7.0E-01	48.4	<0.01	0.15	/I	5.1E-01	1.03	6.3E-01	1.02	0.85
rs117462741	105693397	A	G	0.02	0.96	0.10	7.0E-01	55.17	<0.01	0.05	/I	7.4E-01	0.97	6.6E-01	0.96	0.61
rs118083700	105347688	A	G	0.03	1.02	0.06	7.0E-01	0	<0.01	0.05	/I	8.9E-01	1.01	9.8E-01	1.00	0.91
rs3784236	105630032	A	G	0.37	1.01	0.02	7.0E-01	62.08	<0.01	0.32	/I	6.1E-01	1.01	6.6E-01	1.01	0.98
rs12887774	105219918	T	C	0.12	0.99	0.03	7.1E-01	0	0.03	0.08	/I	3.9E-02	0.93	6.0E-01	1.02	0.94
rs35956117	105217856	T	C	0.12	0.99	0.03	7.1E-01	0	0.03	0.07	/I	4.7E-02	0.94	5.2E-01	1.02	0.95
rs7145744	105147288	A	G	0.23	1.01	0.03	7.1E-01	3.03	0.01	0.28	/I	8.4E-01	1.01	9.6E-01	1.00	0.74
rs141058392	105319317	G	C	0.03	1.02	0.06	7.1E-01	0	<0.01	0.05	/I	8.8E-01	1.01	1.0E+00	1.00	0.89
rs79806511	105608784	A	G	0.02	1.04	0.11	7.1E-01	0.38	<0.01	0.02	/I	6.6E-01	1.05	4.9E-01	1.08	0.49
rs72700189	105351579	A	G	0.03	1.02	0.06	7.1E-01	0	<0.01	0.05	/I	8.8E-01	1.01	9.8E-01	1.00	0.95
rs57804458	105432402	T	C	0.03	1.02	0.07	7.1E-01	2.23	<0.01	0.03	/I	7.9E-01	1.02	9.2E-01	1.01	0.90
rs2841256	105371555	T	A	0.08	1.01	0.04	7.1E-01	26.59	<0.01	0.08	/I	9.8E-01	1.00	7.6E-01	0.99	0.96
rs7144557	105352536	T	C	0.03	1.02	0.06	7.1E-01	0	<0.01	0.05	/I	8.8E-01	1.01	9.9E-01	1.00	0.95
rs78455163	105318467	A	C	0.03	1.02	0.06	7.1E-01	0	<0.01	0.05	/I	8.8E-01	1.01	1.0E+00	1.00	0.89
rs4983600	105011617	C	T	0.30	1.01	0.02	7.1E-01	13.92	<0.01	0.29	/I	8.0E-01	1.01	8.6E-01	1.00	0.98
rs190093980	105334361	G	T	0.02	1.05	0.12	7.1E-01	48.86	<0.01	0.01	/I	3.3E-01	1.13	5.0E-01	1.09	0.45
rs9671900	104985592	T	G	0.48	1.01	0.03	7.1E-01	46.59	<0.01	0.49	/I	8.3E-01	1.01	6.9E-01	1.01	0.86
rs57999984	105161289	G	A	0.10	1.01	0.04	7.1E-01	14.1	0.03	0.06	/I	5.9E-01	0.98	2.6E-01	0.95	0.87
rs6576040	104918925	G	A	0.06	1.02	0.04	7.1E-01	28.92	0.01	0.02	/I	6.2E-01	1.02	6.4E-01	1.02	0.89
rs79529286	105035930	A	G	0.04	0.97	0.08	7.1E-01	17.94	0.01	0.06	/I	6.4E-01	0.97	5.5E-01	0.96	0.61
rs4074138	104989969	A	G	0.48	1.01	0.03	7.1E-01	51.97	<0.01	0.48	/I	8.3E-01	1.01	6.8E-01	1.01	0.86
rs4983566	104982013	T	C	0.16	1.01	0.04	7.1E-01	0	<0.01	0.21	G*/I	7.6E-01	1.01	7.7E-01	1.01	0.87
rs80114387	105037508	A	G	0.15	0.99	0.03	7.1E-01	0	<0.01	0.17	/I	7.3E-01	0.99	5.6E-01	0.98	0.89
rs12890038	105091513	A	G	0.09	1.02	0.04	7.1E-01	71.25	<0.01	0.08	/I	6.0E-01	1.02	6.5E-01	1.02	0.81
rs139591407	105317693	G	T	0.03	1.02	0.06	7.1E-01	0	<0.01	0.05	/I	8.8E-01	1.01	1.0E+00	1.00	0.88
rs72700192	105355185	T	G	0.03	1.02	0.06	7.1E-01	0	<0.01	0.05	/I	8.8E-01	1.01	9.9E-01	1.00	0.94
rs2841234	105347296	A	G	0.03	1.02	0.06	7.1E-01	0	<0.01	0.05	/I	8.9E-01	1.01	9.9E-01	1.00	0.95
rs73357588	105439000	C	G	0.07	0.98	0.05	7.1E-01	40.88	0.02	0.05	/I	6.2E-01	0.97	4.8E-01	0.96	0.77
rs28691880	104918369	C	A	0.06	1.02	0.04	7.2E-01	28.92	0.01	0.02	/I	6.2E-01	1.02	6.4E-01	1.02	0.89
rs73359815	105017747	A	C	0.19	1.01	0.03	7.2E-01	0	<0.01	0.19	/I	7.4E-01	1.01	7.5E-01	1.01	0.91
rs7142996	104918348	A	G	0.06	1.02	0.04	7.2E-01	28.91	0.01	0.02	/I	6.2E-01	1.02	6.4E-01	1.02	0.89
rs4435188	104977157	T	C	0.15	1.01	0.04	7.2E-01	1.62	<0.01	0.21	/I	7.5E-01	1.01	7.7E-01	1.01	0.85
rs9743984	105014982	C	A	0.16	0.99	0.03	7.2E-01	0	<0.01	0.18	/I	8.0E-01	0.99	8.0E-01	0.99	0.84
rs73359816	105018839	T	C	0.19	1.01	0.03	7.2E-01	0	<0.01	0.19	/I	7.5E-01	1.01	7.6E-01	1.01	0.91
rs36016599	105155316	A	C	0.09	0.98	0.04	7.2E-01	4.01	0.02	0.05	/I	3.0E-01	0.96	1.0E+00	0.93	0.80
rs59862747	104999880	G	T	0.49	1.01	0.03	7.2E-01	55.67	<0.01	0.48	/I	9.0E-01	1.00	6.5E-01	1.01	0.85
rs8010930	104919105	A	C	0.06	1.02	0.04	7.2E-01	28.5	0.01	0.02	I/G	6.2E-01	1.02	6.4E-01	1.02	0.89
rs7143077	105278420	G	A	0.02	1.03	0.09	7.2E-01	0	<0.01	0.02	/I	7.3E-01	1.03	7.7E-01	1.03	0.62
rs4983537	105183641	T	C	0.21	0.99	0.03	7.2E-01	4.53	0.05	0.23	/I	3.7E-01	0.97	3.4E-01	1.03	0.84
rs28489547	105499982	A	G	0.11	1.01	0.04	7.2E-01	0	<0.01	0.08	/I	9.3E-01	1.00	9.5E-01	1.00	0.75
rs7147000	105007815	G	A	0.30	1.01	0.02	7.2E-01	0	<0.01	0.29	G/G	8.0E-01	1.01	8.7E-01	1.00	1.00
rs41314519	105344823	A	G	0.03	1.02	0.06	7.2E-01	0	<0.01	0.05	/I	9.1E-01	1.01	9.7E-01	1.00	0.92
rs117798473	104935197	G	A	0.04	0.98	0.06	7.2E-01	31.82	<0.01	0.06	/I	7.0E-01	0.98	6.4E-01	0.97	0.77
rs10150180	104783439	A	G	0.44	1.01	0.03	7.2E-01	0	<0.01	0.41	/I	7.7E-01	1.01	7.1E-01	1.01	0.84
rs143579787	105316744	A	G	0.03	1.02	0.06	7.2E-01	0	<0.01	0.02	/I	8.1E-01	0.98	6.6E-01	0.97	0.84
rs142924470	105121616	A	G	0.30	1.01	0.03	7.2E-01	9.06	0.01	0.31	/I	7.3E-01	1.01	9.5E-01	1.00	0.76
rs10137444	104977498	A	G	0.16	1.01	0.04	7.2E-01	1.03	<0.01	0.21	/I	7.6E-01	1.01	7.8E-01	1.01	0.85
rs8011976	104854680	T	C	0.36	1.01	0.02	7.2E-01	0	<0.01	0.39	/I	7.6E-01	1.01	7.6E-01	1.01	0.95
rs72700170	105345608	A	G	0.03	1.02	0.06	7.2E-01	0	<0.01	0.05	/I	9.1E-01	1.01	9.7E-01	1.00	0.92
rs4983446	105039447	C	T	0.17	0.99	0.03	7.3E-01	0	<0.01	0.18	/I	7.2E-01	0.99	5.5E-01	0.98	0.91
rs118031558	104776471	T	C	0.03	0.97	0.08	7.3E-01	8.41	<0.01	0.01	/I	7.9E-01	0.98	8.0E-01	0.98	0.74
rs56047035	105187662	A	G	0.48	1.01	0.03	7.3E-01	0	<0.01	0.48	/I	9.8E-01	1.00	4.3E-01	1.02	0.55
rs2819446	105426369	G	A	0.06	0.98	0.05	7.3E-01	56.27	0.02	0.05	/I	6.4E-01	0.98	5.1E-01	0.97	0.80
rs9743695	105014881	C	T	0.31	1.01	0.02	7.3E-01	11.39	<0.01	0.29	/I	8.1E-01	1.01	8.8E-01	1.00	0.96
rs113977819	105279332	A	G	0.04	0.98	0.07	7.3E-01	0	<0.01	0.02	/I	3.0E-01	0.93	2.9E-01	0.93	0.67
rs34004095	105364047	C	T	0.04	1.02	0.06	7.3E-01	0	<0.01	0.05	/I	8.7E-01	1.01	9.7E-01	1.00	0.87
rs74436077	104752109	A	G	0.01	1.04	0.11	7.3E-01	0	<0.01	0.05	/I	7.3E-01	1.04	7.7E-01	1.03	0.69
rs73359818	105019167	G	A	0.20	1.01	0.03	7.3E-01	17.91	<0.01	0.20	/I	7.7E-01	1.01	7.7E-01	1.01	0.90
rs74090129	105419234	C	T	0.05	1.02	0.05	7.3E-01	50.42	0.02	0.05	/I	7.6E-01	1.02	9.2E-01	1.01	0.86
rs10147927	105092103	G	C	0.14	1.01	0.04	7.3E-01	59.98	<0.01	0.12	/I	4.9E-01	1.03	5.1E-01	1.03	0.56
rs6576039	104918437	T	C	0.06	1.02	0.04	7.3E-01	34.02	0.01	0.02	/I	6.4E-01	1.02	6.6E-01	1.02	0.87
rs113325667	105196076	G	C	0.06	1.02	0.06	7.3E-01	0	<0.01	0.05	/I	5.8E-01	0.97	9.7E-01	1.00	0.54
rs138389157	105414372	G	C	0.04	0.98	0.06	7.3E-01	0	<0.01	0.02	/I	5.1E-01	0.96	3.6E-01	0.95	0.88
rs2582504	105416823	A	G	0.06	1.02	0.05	7.4E-01	42.99	<0.01	0.05	/I	9.1E-01	1.01	8.5E-01	1.01	0.75
rs11845888	104921032	A	G	0.06	1.01	0.04	7.4E-01	32.84	0.01	0.02	/I	6.5E-01	1.02	6.7E-01	1.02	0.87
rs28666641	104917921	C	T	0.06	1.01	0.04	7.4E-01	34.17	0.01	0.02	/I	6.4E-01	1.02	6.6E-01	1.02	0.87
rs34207932	105224459	C	T	0.02	1.03	0.10	7.4E-01	74.74	0.01	0.02	/I	6.1E-01	0.95	4.3E-01	1.08	0.63
rs117530384	105029727	T	C	0.02	0.97	0.09	7.4E-01	36.78	0.02	0.02	/I	9.9E-01	1.00	8.5E-01	0.98	0.69
rs146998654	105375884	T	C	0.03	1.02	0.06	7.4E-01	0	<0.01	0.05	/I	9.0E-01	1.01	9.9E-01	1.00	0.95
rs73352192	104917776	G	T	0.06	1.02	0.04	7.4E-01	28.87	0.01	0.02	/I	6.4E-01	1.02	6.6E-01	1.02	0.88
rs60974569	104999605	A	G	0.49	1.01	0.03	7.4E-01	55.34	<0.01	0.48	/I	9.2E-01	1.00	6.7E-01	1.01	0.85
rs10147900	105092031	T	C	0.14	0.99	0.04	7.4E-01	26.4	<0.01	0.13	/I	2.5E-01	0.95	3.2E-01	0.96	0.54
rs35507185	104849583	T	C	0.29	1.01	0.03	7.4E-01	0	0.01	0.27	/I	8.0E-01	1.01	7.3E-01	1.01	0.61
rs145620270	105444702	G</														

rs11160835	105587644	T	C	0.24	0.99	0.03	7.6E-01	0	<0.01	0.26	G*/I	6.9E-01	0.99	5.8E-01	0.98	0.88
rs8016091	104807712	A	G	0.14	0.99	0.03	7.6E-01	0	<0.01	0.14	G/G	7.0E-01	0.99	6.6E-01	0.99	1.00
rs73350360	105279798	A	G	0.04	0.98	0.06	7.6E-01	0	<0.01	0.03	I/I	3.5E-01	0.94	2.8E-01	0.93	0.72
rs1882845	105631363	T	C	0.37	1.01	0.02	7.6E-01	59.19	<0.01	0.33	I/I	6.7E-01	1.01	7.3E-01	1.01	0.99
rs34050645	105315119	T	C	0.08	0.99	0.05	7.6E-01	0	<0.01	0.05	I/I	3.6E-01	0.96	4.8E-01	0.97	0.69
rs11849605	104924936	G	A	0.05	1.01	0.05	7.6E-01	11.37	<0.01	0.02	I/I	6.5E-01	1.02	6.8E-01	1.02	0.89
rs34919138	105006582	G	C	0.30	1.01	0.02	7.6E-01	0	<0.01	0.29	I/I	8.5E-01	1.00	9.2E-01	1.00	0.97
rs12717694	105046572	C	T	0.12	1.01	0.04	7.7E-01	0	<0.01	0.12	I/I	9.7E-01	1.00	9.1E-01	1.00	0.89
rs7154981	105166274	C	T	0.41	1.01	0.02	7.7E-01	29.95	<0.01	0.39	I/I	1.2E-01	0.96	5.5E-01	0.99	0.92
rs3784238	105629987	A	G	0.37	1.01	0.02	7.7E-01	60.36	<0.01	0.33	I/I	6.7E-01	1.01	7.3E-01	1.01	0.99
rs117121151	105321224	A	G	0.04	1.02	0.07	7.7E-01	66.01	<0.01	0.02	I/I	6.9E-01	1.03	8.2E-01	1.02	0.50
rs4900628	104883986	G	A	0.26	1.01	0.03	7.7E-01	0	<0.01	0.28	I/I	7.7E-01	1.01	8.3E-01	1.01	0.91
rs141569398	105626149	T	C	0.02	0.97	0.10	7.7E-01	27.01	<0.01	0.02	I/I	7.3E-01	0.96	8.6E-01	0.98	0.53
rs116364789	105090931	A	G	0.03	0.97	0.09	7.7E-01	19.85	<0.01	0.04	I/I	9.8E-01	1.00	9.4E-01	0.99	0.64
rs4613001	105499858	G	A	0.16	1.01	0.04	7.7E-01	28.49	<0.01	0.13	I/I	5.7E-01	1.02	5.1E-01	1.03	0.50
rs58456730	105630001	A	G	0.37	1.01	0.02	7.7E-01	61.09	<0.01	0.33	I/I	6.7E-01	1.01	7.3E-01	1.01	0.99
rs66956754	105648000	T	C	0.40	1.01	0.02	7.7E-01	49.63	<0.01	0.38	I/I	7.0E-01	1.01	7.4E-01	1.01	0.95
rs188588418	105218051	A	G	0.04	1.02	0.06	7.7E-01	0	<0.01	0.03	I/I	5.9E-01	0.97	6.4E-01	0.97	0.68
rs2278607	105420215	C	T	0.05	1.02	0.05	7.7E-01	54.1	0.02	0.05	G*/I	8.0E-01	1.01	9.6E-01	1.00	0.87
rs8009494	104885716	A	C	0.26	1.01	0.03	7.7E-01	6.99	<0.01	0.28	I/I	7.8E-01	1.01	8.3E-01	1.01	0.89
rs7156076	104892153	G	A	0.25	1.01	0.03	7.7E-01	0	<0.01	0.28	I/I	7.5E-01	1.01	8.1E-01	1.01	0.86
rs4983581	104991291	A	G	0.15	1.01	0.04	7.7E-01	0	<0.01	0.19	I/I	8.5E-01	1.01	8.8E-01	1.01	0.81
rs2396458	105417768	A	C	0.07	0.98	0.05	7.7E-01	64.99	<0.01	0.06	I/I	7.0E-01	0.98	5.5E-01	0.97	0.72
rs4983605	105015215	G	T	0.11	1.01	0.04	7.7E-01	56.41	<0.01	0.10	I/I	8.8E-01	1.01	9.6E-01	1.00	0.87
rs113499138	105012957	G	A	0.20	1.01	0.03	7.7E-01	35.91	<0.01	0.20	I/I	7.4E-01	1.01	7.4E-01	1.01	0.87
rs73354355	105329462	T	C	0.04	0.98	0.05	7.7E-01	3.18	<0.01	0.03	I/I	4.7E-01	0.96	3.5E-01	0.95	0.96
rs193192486	105356351	A	G	0.08	1.02	0.06	7.7E-01	0	<0.01	0.09	I/I	8.7E-01	1.01	6.4E-01	1.03	0.52
rs74369194	105149628	T	C	0.10	0.99	0.05	7.7E-01	0	<0.01	0.06	I/I	5.8E-01	0.97	2.6E-01	0.95	0.54
rs2816645	105695854	T	C	0.48	1.01	0.03	7.7E-01	5.83	<0.01	0.49	I/I	9.9E-01	1.00	8.9E-01	1.00	0.58
rs59832661	105330360	G	A	0.04	0.98	0.05	7.7E-01	3.72	<0.01	0.03	I/I	4.7E-01	0.96	3.5E-01	0.95	0.96
rs193107475	105286998	G	T	0.03	0.98	0.08	7.8E-01	0	<0.01	0.04	I/I	5.8E-01	0.96	4.8E-01	0.95	0.76
rs183859335	105287004	G	T	0.03	0.98	0.08	7.8E-01	0	<0.01	0.04	I/I	5.8E-01	0.96	4.8E-01	0.95	0.76
rs2841229	105337525	G	A	0.08	1.01	0.04	7.8E-01	58.97	<0.01	0.08	I/I	8.9E-01	0.99	6.8E-01	0.98	0.95
rs7147598	105090350	C	T	0.17	0.99	0.03	7.8E-01	0	<0.01	0.17	I/I	5.7E-01	0.98	7.0E-01	0.99	0.83
rs78110724	105419568	G	A	0.05	1.02	0.06	7.8E-01	58.93	0.02	0.05	I/I	8.2E-01	1.01	9.8E-01	1.00	0.85
rs34836666	104978375	C	G	0.04	0.98	0.09	7.8E-01	0	<0.01	0.04	I/I	7.8E-01	0.98	6.9E-01	0.97	0.45
rs139313255	105337598	A	G	0.02	1.03	0.11	7.8E-01	0	<0.01	0.02	I/I	8.6E-01	1.02	9.4E-01	1.01	0.45
rs35757105	105629049	A	T	0.13	0.99	0.04	7.8E-01	68.42	<0.01	0.11	I/I	7.6E-01	0.99	8.5E-01	0.99	0.71
rs36048730	105013031	A	G	0.14	0.99	0.04	7.8E-01	58.88	<0.01	0.14	I/I	8.3E-01	0.99	6.8E-01	0.99	0.77
rs61577366	104837529	C	T	0.40	0.99	0.03	7.8E-01	0	<0.01	0.40	I/I	7.9E-01	0.99	7.7E-01	0.99	0.85
rs76970682	104754079	A	G	0.14	0.99	0.04	7.8E-01	0	<0.01	0.16	I/I	8.6E-01	0.99	8.0E-01	0.99	0.73
rs4074680	104889344	T	C	0.26	1.01	0.03	7.8E-01	0	<0.01	0.28	I/I	7.7E-01	1.01	8.2E-01	1.01	0.87
rs76346085	104752937	G	A	0.07	0.99	0.05	7.8E-01	0	<0.01	0.06	I/I	8.7E-01	0.99	8.6E-01	0.99	0.80
rs11850450	104749233	T	C	0.12	1.01	0.04	7.8E-01	30.67	<0.01	0.15	I/I	7.1E-01	1.02	7.5E-01	1.01	0.72
rs150949427	105128596	A	C	0.24	1.01	0.03	7.8E-01	40.76	<0.01	0.26	I/I	9.7E-01	1.00	8.6E-01	0.99	0.79
rs28568425	104782761	T	C	0.12	0.99	0.03	7.9E-01	0	<0.01	0.11	I/I	7.7E-01	0.99	7.5E-01	0.99	0.95
rs140558927	104903159	T	C	0.02	0.97	0.10	7.9E-01	0	<0.01	0.01	I/I	5.5E-01	0.94	5.7E-01	0.94	0.48
rs149838113	105621363	A	C	0.02	1.03	0.10	7.9E-01	0	<0.01	0.02	I/I	6.3E-01	1.05	6.8E-01	1.04	0.81
rs4315289	104868223	G	A	0.26	0.99	0.03	7.9E-01	2.29	<0.01	0.28	I/I	7.7E-01	0.99	7.1E-01	0.99	0.87
rs35161378	105342875	C	T	0.04	0.99	0.05	7.9E-01	10.06	<0.01	0.03	I/I	4.8E-01	0.96	3.6E-01	0.95	0.97
rs8007027	105003569	A	G	0.19	0.99	0.03	7.9E-01	0	<0.01	0.18	I/I	7.9E-01	0.99	8.8E-01	1.00	0.78
rs72713838	105091910	C	T	0.10	1.01	0.04	7.9E-01	61.3	<0.01	0.10	I/I	7.8E-01	1.01	8.5E-01	1.01	0.69
rs10135144	105005316	T	C	0.14	0.99	0.04	7.9E-01	0	<0.01	0.13	I/I	8.7E-01	0.99	7.7E-01	0.99	0.75
rs72700152	105335630	A	G	0.03	1.02	0.06	7.9E-01	0	<0.01	0.05	I/I	9.8E-01	1.00	9.0E-01	0.99	0.91
rs9788622	104868852	T	C	0.25	0.99	0.03	7.9E-01	0	<0.01	0.28	I/I	7.7E-01	0.99	7.1E-01	0.99	0.88
rs72713824	105063116	G	C	0.02	0.97	0.10	7.9E-01	52.69	<0.01	0.01	I/I	4.6E-01	0.93	3.6E-01	0.91	0.71
rs8009325	104866482	G	A	0.24	0.99	0.03	7.9E-01	0	<0.01	0.26	I/I	7.7E-01	0.99	7.5E-01	0.99	0.81
rs8007092	105003754	T	C	0.19	0.99	0.03	7.9E-01	0	<0.01	0.18	I/I	7.9E-01	0.99	8.9E-01	1.00	0.78
rs8007108	105003797	G	C	0.19	0.99	0.03	7.9E-01	0	<0.01	0.18	I/I	7.9E-01	0.99	8.9E-01	1.00	0.78
rs4614661	104750712	A	C	0.14	1.01	0.04	7.9E-01	21.36	<0.01	0.16	I/I	7.2E-01	1.01	7.6E-01	1.01	0.78
rs10132768	104753863	C	T	0.41	1.01	0.03	7.9E-01	0	<0.01	0.44	I/I	7.2E-01	1.01	8.2E-01	1.01	0.65
rs6576024	104777091	G	T	0.13	0.99	0.03	7.9E-01	0	<0.01	0.11	I/I	7.8E-01	0.99	7.7E-01	0.99	0.94
rs72718104	105291446	T	C	0.03	0.98	0.08	7.9E-01	0	<0.01	0.04	I/I	5.9E-01	0.96	5.0E-01	0.95	0.77
rs8003959	104777165	C	T	0.13	0.99	0.03	7.9E-01	0	<0.01	0.11	I/I	7.8E-01	0.99	7.7E-01	0.99	0.94
rs4074681	104889349	A	G	0.24	0.99	0.03	7.9E-01	0	<0.01	0.26	I/I	8.3E-01	0.99	7.8E-01	0.99	0.85
rs7150468	105335878	C	T	0.04	0.99	0.05	7.9E-01	13.48	<0.01	0.03	G*/I	4.8E-01	0.96	3.6E-01	0.95	0.97
rs3784230	105679055	G	A	0.39	1.01	0.02	7.9E-01	0	<0.01	0.42	G/G	8.1E-01	1.01	8.5E-01	1.00	1.00
rs72713894	105151165	C	T	0.10	1.01	0.04	7.9E-01	40.55	0.08	0.15	I/I	3.8E-01	0.96	2.4E-01	0.95	0.73
rs4243750	104884293	T	C	0.25	1.01	0.03	7.9E-01	0	<0.01	0.28	I/I	7.9E-01	1.01	8.5E-01	1.01	0.91
rs61071258	105344142	A	G	0.04	0.99	0.05	7.9E-01	7.76	<0.01	0.03	I/I	4.9E-01	0.96	3.6E-01	0.95	0.97
rs188776055	105412152	C	T	0.03	0.98	0.09	7.9E-01	26	<0.01	0.05	I/I	8.0E-01	0.98	7.3E-01	0.97	0.45
rs72706010	104805822	A	G	0.05	0.98	0.06	7.9E-01	25.73	<0.01	0.06	I/I	7.0E-01	0.98	6.6E-01	0.97	0.83
rs118099886	104905956	G	A	0.02	0.97	0.10	7.9E-01	0	<0.01	0.01	I/I	5.6E-01	0.94	5.7E-01	0.94	0.48
rs9671428	104985344	C	T	0.48	1.01	0.03	8.0E-01	50.29	<0.01	0.49	I/I	9.0E-01	1.00	7.6E-01	1.01	0.86
rs147528298	1056263															

rs4995549	104992534	G	A	0.46	1.01	0.03	8.1E-01	55.84	<0.01	0.49	/I	8.8E-01	1.00	8.1E-01	1.01	0.72
rs72704061	104751433	G	A	0.22	0.99	0.03	8.1E-01	0	<0.01	0.25	/I	8.1E-01	0.99	7.4E-01	0.99	0.68
rs74090046	105280434	C	G	0.04	0.99	0.06	8.2E-01	0	<0.01	0.03	/I	3.9E-01	0.95	3.1E-01	0.94	0.72
rs182223240	105321496	T	A	0.06	0.99	0.06	8.2E-01	39.11	<0.01	0.05	/I	7.3E-01	1.02	9.3E-01	0.99	0.46
rs11160807	104886839	T	C	0.25	1.01	0.03	8.2E-01	0	<0.01	0.28	/I	8.1E-01	1.01	8.7E-01	1.00	0.89
rs3935005	104750896	A	G	0.15	1.01	0.04	8.2E-01	36.79	<0.01	0.16	/I	7.6E-01	1.01	8.0E-01	1.01	0.77
rs4983395	104976835	A	G	0.35	1.01	0.03	8.2E-01	70.81	<0.01	0.26	/I	1.0E+00	1.00	8.7E-01	1.00	0.87
rs2239285	105630465	A	G	0.36	1.00	0.02	8.2E-01	60.98	<0.01	0.32	/I	7.3E-01	1.01	7.9E-01	1.01	0.99
rs112069240	105281252	A	G	0.04	0.99	0.06	8.2E-01	0	<0.01	0.03	/I	3.9E-01	0.95	3.1E-01	0.94	0.73
rs10142660	105225620	T	G	0.13	0.99	0.03	8.2E-01	0	0.03	0.08	/I	5.1E-02	0.94	5.8E-01	1.02	0.92
rs28434197	105014973	T	C	0.11	1.01	0.04	8.2E-01	58.14	<0.01	0.09	/I	9.3E-01	1.00	9.7E-01	1.00	0.90
rs6576049	105011827	G	A	0.31	1.01	0.02	8.2E-01	15.38	<0.01	0.29	/I	9.1E-01	1.00	9.8E-01	1.00	0.97
rs117150628	104754978	A	G	0.03	1.01	0.06	8.2E-01	0	<0.01	0.02	/I	8.0E-01	1.02	8.4E-01	1.01	0.86
rs12893121	105010877	C	T	0.31	1.01	0.02	8.2E-01	15.93	<0.01	0.29	/I	9.1E-01	1.00	9.8E-01	1.00	0.97
rs35978178	104988130	G	T	0.48	1.01	0.03	8.2E-01	52.37	<0.01	0.48	/I	9.3E-01	1.00	7.9E-01	1.01	0.85
rs56232771	104839538	C	T	0.40	0.99	0.03	8.2E-01	0	<0.01	0.41	/I	8.3E-01	0.99	8.2E-01	0.99	0.84
rs11628907	104861306	T	A	0.38	1.00	0.02	8.2E-01	0	<0.01	0.40	/I	8.2E-01	1.00	8.2E-01	1.00	0.95
rs190358917	105541309	A	G	0.02	0.97	0.12	8.2E-01	0	<0.01	0.01	/I	9.5E-01	1.01	9.6E-01	0.99	0.45
rs71421895	105416918	C	T	0.04	0.99	0.06	8.2E-01	0	<0.01	0.06	/I	8.6E-01	0.99	8.6E-01	0.99	0.75
rs79719282	105282440	G	A	0.03	0.98	0.07	8.2E-01	0	<0.01	0.04	/I	5.7E-01	0.96	4.5E-01	0.95	0.75
rs111292575	105671090	T	C	0.09	0.99	0.04	8.2E-01	12.24	<0.01	0.10	/I	9.0E-01	0.99	9.7E-01	0.99	0.85
rs61997155	104969888	C	G	0.42	0.99	0.03	8.3E-01	43.96	<0.01	0.48	/I	7.5E-01	0.99	7.9E-01	0.99	0.73
rs147015287	105663437	A	G	0.04	1.02	0.07	8.3E-01	0	0.06	0.05	/I	7.9E-01	1.02	7.8E-01	1.02	0.54
rs58869604	105011925	A	G	0.10	1.01	0.04	8.3E-01	60.53	<0.01	0.09	/I	9.1E-01	1.00	9.6E-01	1.00	0.90
rs11625252	105449106	T	C	0.03	1.02	0.07	8.3E-01	0	<0.01	0.02	/I	8.1E-01	1.02	9.7E-01	1.00	0.67
rs74246316	104796419	T	G	0.09	1.01	0.04	8.3E-01	0	<0.01	0.11	/I	8.2E-01	1.01	8.6E-01	1.01	0.87
rs181484313	105314320	C	T	0.03	1.01	0.07	8.3E-01	0	<0.01	0.04	/I	1.0E+00	1.00	8.7E-01	0.99	0.87
rs2819441	105418275	C	T	0.25	0.99	0.03	8.3E-01	0	<0.01	0.19	/I	7.3E-01	1.01	8.3E-01	1.01	0.58
rs185500193	105685133	A	G	0.03	0.98	0.09	8.3E-01	49.44	<0.01	0.06	/I	8.6E-01	0.99	7.9E-01	0.98	0.63
rs2841214	105318415	C	T	0.07	1.01	0.04	8.3E-01	25.23	<0.01	0.08	/I	6.8E-01	0.98	5.0E-01	0.97	0.87
rs45598737	105244239	T	C	0.09	1.01	0.04	8.3E-01	68.51	0.02	0.08	/G	2.1E-01	0.95	3.3E-01	1.04	0.63
rs10137513	105503676	C	T	0.24	1.01	0.02	8.3E-01	0	<0.01	0.23	/I	8.0E-01	1.01	6.0E-01	1.01	0.96
rs79493001	104916313	G	T	0.05	1.01	0.06	8.3E-01	25.31	<0.01	0.08	/I	8.5E-01	1.01	9.1E-01	1.01	0.76
rs74086909	105012733	T	C	0.20	1.01	0.03	8.3E-01	28.39	<0.01	0.20	/I	8.7E-01	1.00	8.7E-01	1.00	0.91
rs11160811	105055304	G	A	0.38	1.01	0.03	8.4E-01	0	0.02	0.42	/I	7.4E-01	1.01	8.2E-01	1.01	0.74
rs61995960	105247873	A	G	0.02	0.98	0.10	8.4E-01	67.06	<0.01	0.02	/I	5.6E-01	1.06	7.7E-01	1.03	0.63
rs147245048	105129792	A	G	0.25	1.01	0.03	8.4E-01	39.59	<0.01	0.29	/I	9.0E-01	1.00	9.2E-01	1.00	0.80
rs150268207	104899420	C	T	0.04	1.01	0.06	8.4E-01	25.15	<0.01	0.04	/I	6.8E-01	1.03	7.7E-01	1.02	0.79
rs151013711	105418504	T	G	0.04	0.99	0.07	8.4E-01	65.53	0.02	0.04	/I	8.9E-01	0.99	7.3E-01	0.98	0.75
rs60468249	105154870	G	C	0.09	0.99	0.04	8.4E-01	25.19	0.02	0.05	/I	3.9E-01	0.96	1.5E-01	0.94	0.79
rs79142507	104803418	C	G	0.09	1.01	0.04	8.4E-01	0	<0.01	0.11	/I	8.3E-01	1.01	8.3E-01	1.01	0.86
rs150721062	105325831	T	C	0.03	1.01	0.06	8.4E-01	0	<0.01	0.05	/I	9.7E-01	1.00	8.5E-01	0.99	0.89
rs6576034	104855819	C	T	0.34	1.00	0.02	8.4E-01	0	<0.01	0.39	/I	8.8E-01	1.00	8.8E-01	1.00	0.99
rs77775909	104914543	A	C	0.05	1.01	0.06	8.4E-01	25.32	<0.01	0.08	/I	8.6E-01	1.01	9.2E-01	1.01	0.76
rs12100976	105689090	C	T	0.16	0.99	0.03	8.4E-01	4.06	<0.01	0.14	/I	9.0E-01	1.00	9.4E-01	1.00	0.76
rs12147075	105556710	C	T	0.22	0.99	0.03	8.4E-01	79.02	<0.01	0.16	/I	7.9E-01	0.99	6.5E-01	0.99	0.88
rs10144266	105007656	G	A	0.30	1.00	0.02	8.4E-01	0	<0.01	0.29	/I	9.3E-01	1.00	1.0E+00	1.00	0.99
rs12431565	105670991	G	A	0.09	0.99	0.04	8.4E-01	18.12	<0.01	0.09	/I	9.4E-01	1.00	9.0E-01	0.99	0.84
rs8012301	104803220	C	A	0.14	1.01	0.03	8.4E-01	0	<0.01	0.11	/I	9.0E-01	1.00	9.1E-01	1.00	0.95
rs8013126	104863793	T	C	0.36	1.00	0.02	8.4E-01	0	<0.01	0.41	/I	8.7E-01	1.00	8.7E-01	1.00	0.94
rs56187104	105400350	T	C	0.06	1.01	0.06	8.4E-01	0	<0.01	0.03	/I	9.1E-01	1.01	8.3E-01	0.99	0.55
rs28661507	105145372	T	C	0.23	1.01	0.03	8.4E-01	0	0.02	0.27	/I	9.8E-01	1.00	8.3E-01	0.99	0.77
rs10135542	104798366	T	C	0.13	0.99	0.03	8.5E-01	0	<0.01	0.11	/I	8.0E-01	0.99	7.9E-01	0.99	0.98
rs7156695	104855565	C	T	0.34	1.00	0.02	8.5E-01	0	<0.01	0.39	/I	8.9E-01	1.00	8.9E-01	1.00	0.99
rs75756037	104913703	T	C	0.05	1.01	0.06	8.5E-01	25.38	<0.01	0.08	/I	8.6E-01	1.01	9.3E-01	1.01	0.76
rs189474505	105400366	C	G	0.14	1.01	0.04	8.5E-01	66.26	<0.01	0.14	/I	6.2E-01	1.02	7.2E-01	1.02	0.49
rs182614905	105267069	T	C	0.06	1.01	0.05	8.5E-01	61.96	<0.01	0.04	/I	8.3E-01	1.01	9.0E-01	1.01	0.57
rs2816644	105691474	C	T	0.27	0.99	0.03	8.5E-01	58.17	0.02	0.28	/I	8.7E-01	1.00	1.0E+00	1.00	0.70
rs34453164	105012253	A	G	0.11	1.01	0.04	8.5E-01	57.47	<0.01	0.09	/I	9.5E-01	1.00	9.4E-01	1.00	0.91
rs11850969	104855203	T	G	0.35	1.00	0.02	8.5E-01	0	<0.01	0.39	/I	9.0E-01	1.00	9.0E-01	1.00	0.98
rs7151377	105471886	T	C	0.45	1.00	0.02	8.5E-01	0	<0.01	0.43	/I	6.3E-01	1.01	3.9E-01	1.02	0.81
rs12883404	105012423	C	T	0.31	1.00	0.02	8.5E-01	10.71	<0.01	0.29	/I	9.3E-01	1.00	9.9E-01	1.00	0.97
rs76828401	104921964	T	C	0.06	1.01	0.05	8.5E-01	12.66	0.01	0.02	/I	7.4E-01	1.02	7.7E-01	1.01	0.89
rs12894635	104873834	T	C	0.25	1.00	0.03	8.5E-01	0	<0.01	0.28	/I	8.4E-01	0.99	8.4E-01	0.99	0.90
rs8017698	105660766	T	C	0.42	1.01	0.03	8.6E-01	0	<0.01	0.36	/I	8.0E-01	1.01	9.5E-01	1.00	0.62
rs74809562	105434292	C	G	0.03	1.01	0.07	8.6E-01	2.4	<0.01	0.03	/I	9.5E-01	1.00	9.1E-01	0.99	0.88
rs117725127	105286643	A	G	0.03	0.99	0.07	8.6E-01	0	<0.01	0.04	/I	6.7E-01	0.97	5.6E-01	0.96	0.78
rs36050392	105012371	A	G	0.11	1.01	0.04	8.6E-01	55.9	<0.01	0.09	/I	9.5E-01	1.00	9.4E-01	1.00	0.91
rs7144106	104853395	C	T	0.36	1.00	0.02	8.6E-01	0	<0.01	0.39	/I	8.9E-01	1.00	9.0E-01	1.00	0.96
rs4983599	105011436	A	G	0.11	1.01	0.04	8.6E-01	57.14	<0.01	0.09	G*/I	9.6E-01	1.00	9.3E-01	1.00	0.92
rs8013389	104863792	T	G	0.36	1.00	0.02	8.6E-01	0	<0.01	0.41	/I	8.9E-01	1.00	8.9E-01	1.00	0.94
rs28676628	105119073	C	T	0.26	1.01	0.03	8.6E-01	47.89	<0.01	0.31	/I	9.5E-01	1.00	8.5E-01	0.99	0.81
rs11621214	104808984	G	C	0.12	1.01	0.03	8.6E-01	0	<0.01	0.10	/I	9.1E-01	1.00	9.6E-01	1.00	0.95
rs12897418	105242374	A	G	0.12	0.99	0.03	8.6E-01	0	0.03	0.06	/G	5.6E-02	0.94	5.6E-01	1.02	0.90
rs2816670</																

rs111697633	105470037	G	A	0.03	1.01	0.08	8.8E-01	0	0.02	0.05	/I	9.1E-01	1.01	9.8E-01	1.00	0.76
rs11844508	105200350	C	T	0.12	1.00	0.03	8.8E-01	0	0.02	0.07	/I	7.5E-02	0.94	4.2E-01	1.03	0.96
rs8012519	104794811	T	C	0.13	1.00	0.03	8.8E-01	0	<0.01	0.11	G/G	8.4E-01	0.99	8.4E-01	0.99	1.00
rs10143904	105118555	A	G	0.26	1.00	0.03	8.8E-01	47.85	<0.01	0.31	/I	9.7E-01	1.00	8.2E-01	0.99	0.81
rs72704057	104748753	A	G	0.22	1.00	0.03	8.8E-01	0	<0.01	0.25	/I	8.7E-01	0.99	8.0E-01	0.99	0.71
rs190986194	105417732	A	G	0.17	0.99	0.04	8.8E-01	0	0.03	0.14	/I	4.8E-01	1.03	5.1E-01	1.02	0.61
rs8009378	104850573	C	G	0.36	1.00	0.02	8.8E-01	0	<0.01	0.36	/I	8.7E-01	1.00	8.8E-01	1.00	0.85
rs115130814	104791010	A	G	0.13	1.00	0.03	8.8E-01	0	<0.01	0.11	/I	8.3E-01	0.99	8.4E-01	0.99	0.99
rs8023234	104856004	C	T	0.35	1.00	0.02	8.9E-01	0	<0.01	0.39	/I	9.3E-01	1.00	9.3E-01	1.00	0.99
rs149069458	105328017	A	G	0.04	0.99	0.06	8.9E-01	6.07	<0.01	0.04	/I	5.5E-01	0.97	4.1E-01	0.95	0.94
rs10148105	105092087	A	G	0.21	1.01	0.04	8.9E-01	0	<0.01	0.21	/I	5.8E-01	0.98	6.3E-01	0.98	0.57
rs35952476	105013056	A	G	0.13	1.01	0.04	8.9E-01	62.07	<0.01	0.10	/I	9.4E-01	1.00	8.7E-01	0.99	0.82
rs76771769	105118442	A	G	0.26	1.00	0.03	8.9E-01	47.57	<0.01	0.31	/I	9.7E-01	1.00	8.2E-01	0.99	0.81
rs11848499	105626594	A	G	0.37	1.00	0.02	8.9E-01	51.3	<0.01	0.33	/I	7.7E-01	1.01	8.4E-01	1.00	0.98
rs2018404	105695446	T	C	0.17	1.00	0.03	8.9E-01	64.74	<0.01	0.14	G*/I	6.0E-01	1.02	7.3E-01	1.01	0.86
rs12881146	104869315	A	G	0.26	1.00	0.03	8.9E-01	2.9	<0.01	0.28	/I	8.6E-01	1.00	8.1E-01	0.99	0.87
rs72718105	105297219	T	A	0.03	0.99	0.07	8.9E-01	0	<0.01	0.04	/I	7.0E-01	0.97	5.9E-01	0.96	0.81
rs34526701	104752810	G	A	0.22	1.00	0.03	8.9E-01	0	<0.01	0.25	/I	8.9E-01	1.00	8.1E-01	0.99	0.66
rs3001411	105323110	C	T	0.03	1.01	0.06	8.9E-01	0	<0.01	0.05	/I	9.2E-01	0.99	7.9E-01	0.98	0.89
rs6576028	104781769	G	A	0.23	1.00	0.03	8.9E-01	0	<0.01	0.22	/I	9.1E-01	1.00	9.4E-01	1.00	0.89
rs45563833	105353405	A	G	0.04	1.01	0.05	8.9E-01	0	<0.01	0.03	/I	7.9E-01	0.99	6.2E-01	0.97	0.96
rs55997540	105556940	T	C	0.16	1.00	0.03	9.0E-01	62.8	<0.01	0.13	/I	9.8E-01	1.00	8.8E-01	1.00	0.87
rs187869051	105278042	A	G	0.01	0.99	0.12	9.0E-01	66.55	0.01	0.02	/I	6.1E-01	1.06	7.8E-01	1.03	0.69
rs12100742	105091664	C	T	0.03	0.99	0.08	9.0E-01	21.98	<0.01	0.04	/I	9.0E-01	1.01	9.9E-01	1.00	0.59
rs11622572	105690286	G	C	0.06	0.99	0.06	9.0E-01	36.39	<0.01	0.04	/I	1.0E+00	1.00	9.4E-01	1.00	0.63
rs55880426	105134351	G	A	0.23	1.00	0.03	9.0E-01	18.52	0.02	0.27	/I	6.9E-01	0.99	5.7E-01	0.98	0.81
rs8008557	104790133	T	C	0.10	1.01	0.04	9.0E-01	8.75	<0.01	0.12	/I	9.0E-01	1.01	9.4E-01	1.00	0.85
rs7158194	105171694	C	T	0.31	1.00	0.02	9.0E-01	20.14	<0.01	0.34	/I	2.6E-01	0.97	8.8E-01	1.00	0.92
rs76127444	104796640	T	G	0.09	1.01	0.04	9.0E-01	0	<0.01	0.11	/I	8.9E-01	1.01	9.2E-01	1.00	0.87
rs12431709	105695583	T	C	0.08	1.01	0.05	9.0E-01	57.86	<0.01	0.11	/I	9.7E-01	1.00	9.2E-01	1.01	0.60
rs35654509	105545105	G	C	0.21	1.00	0.03	9.0E-01	73.8	<0.01	0.18	/I	9.8E-01	1.00	8.6E-01	0.99	0.87
rs2582532	105392837	C	T	0.03	1.01	0.09	9.1E-01	20.8	0.01	0.02	/I	8.9E-01	1.01	8.2E-01	1.02	0.67
rs145085091	104801233	A	G	0.02	0.99	0.11	9.1E-01	0	<0.01	0.01	/I	8.1E-01	0.97	7.7E-01	0.97	0.56
rs12888736	105186870	C	A	0.05	0.99	0.06	9.1E-01	0	<0.01	0.04	/I	4.1E-01	0.95	6.9E-01	1.03	0.58
rs12885522	105291919	A	G	0.08	1.01	0.06	9.1E-01	32.83	<0.01	0.05	/I	6.9E-01	1.02	9.4E-01	1.00	0.49
rs4983504	104924334	C	T	0.06	1.01	0.05	9.1E-01	33.91	0.01	0.02	/I	8.1E-01	1.01	8.3E-01	1.01	0.86
rs4399485	105591377	A	G	0.25	1.00	0.03	9.1E-01	0	<0.01	0.25	G*/I	8.7E-01	1.00	9.0E-01	1.00	0.91
rs4906456	104875118	C	T	0.26	1.00	0.03	9.1E-01	0	<0.01	0.28	/I	9.2E-01	1.00	9.8E-01	1.00	0.90
rs4900626	104875013	G	A	0.26	1.00	0.03	9.1E-01	0	<0.01	0.28	/I	9.2E-01	1.00	9.8E-01	1.00	0.90
rs139713119	105314351	T	G	0.03	1.01	0.07	9.1E-01	0	<0.01	0.04	/I	9.3E-01	0.99	8.0E-01	0.98	0.89
rs28506007	105581007	A	T	0.23	1.00	0.03	9.1E-01	0	<0.01	0.26	/I	9.7E-01	1.00	9.0E-01	1.00	0.86
rs28450433	105559097	A	G	0.22	1.00	0.03	9.1E-01	76.9	<0.01	0.19	/I	9.0E-01	1.00	7.6E-01	0.99	0.85
rs117085637	105398078	A	G	0.03	0.99	0.07	9.1E-01	0	<0.01	0.02	/I	9.1E-01	0.99	7.2E-01	0.97	0.67
rs28607076	104801758	A	T	0.23	1.00	0.03	9.1E-01	0	<0.01	0.22	/I	9.7E-01	1.00	9.8E-01	1.00	0.92
rs138923544	105119655	G	T	0.20	1.00	0.03	9.1E-01	54.55	<0.01	0.21	/I	9.7E-01	1.00	7.3E-01	0.99	0.69
rs11846175	104882739	C	T	0.25	1.00	0.03	9.1E-01	0	<0.01	0.28	/I	9.2E-01	1.00	9.8E-01	1.00	0.91
rs8015599	104860564	G	A	0.35	1.00	0.02	9.2E-01	0	<0.01	0.39	/I	9.5E-01	1.00	9.6E-01	1.00	1.00
rs12879592	105531342	A	G	0.03	0.99	0.06	9.2E-01	0	<0.01	0.04	/I	9.6E-01	1.00	9.6E-01	1.00	0.85
rs34967457	105013361	C	T	0.11	1.00	0.04	9.2E-01	57.36	<0.01	0.09	/I	9.8E-01	1.00	8.7E-01	0.99	0.91
rs34220962	105013347	A	G	0.11	1.00	0.04	9.2E-01	57.36	<0.01	0.09	/I	9.8E-01	1.00	8.7E-01	0.99	0.91
rs117922515	104884241	A	G	0.04	0.99	0.07	9.2E-01	0	<0.01	0.05	/I	9.4E-01	1.00	9.2E-01	0.99	0.63
rs34785484	105013169	C	T	0.11	1.00	0.04	9.2E-01	57.36	<0.01	0.09	/I	9.8E-01	1.00	8.7E-01	0.99	0.91
rs34677118	105013228	T	C	0.11	1.00	0.04	9.2E-01	57.17	<0.01	0.09	/I	9.8E-01	1.00	8.7E-01	0.99	0.91
rs183417494	105291933	A	G	0.08	0.99	0.06	9.2E-01	0	<0.01	0.07	/I	9.9E-01	1.00	7.8E-01	0.99	0.48
rs11620866	105582926	G	C	0.24	1.00	0.03	9.2E-01	0	<0.01	0.25	/I	1.0E+00	1.00	8.8E-01	1.00	0.86
rs4983604	105015214	G	C	0.11	1.00	0.04	9.2E-01	57.41	<0.01	0.09	/I	9.7E-01	1.00	8.7E-01	0.99	0.90
rs113137338	105390782	G	A	0.02	1.01	0.09	9.2E-01	0	0.02	0.04	/I	8.4E-01	0.98	7.7E-01	0.97	0.68
rs72700128	105313463	G	A	0.03	1.01	0.07	9.2E-01	0	<0.01	0.04	/I	9.2E-01	0.99	7.9E-01	0.98	0.89
rs144916387	105350133	T	C	0.03	0.99	0.07	9.2E-01	44.1	<0.01	0.02	/I	9.0E-01	0.99	7.6E-01	0.98	0.78
rs118009682	105452149	G	A	0.03	1.01	0.09	9.2E-01	0	<0.01	0.02	/I	8.0E-01	1.02	9.2E-01	1.01	0.75
rs8019526	104859419	G	A	0.35	1.00	0.02	9.3E-01	0	<0.01	0.39	G/G	9.6E-01	1.00	9.7E-01	1.00	1.00
rs75489301	105397976	A	G	0.02	0.99	0.09	9.3E-01	35.75	<0.01	0.02	/I	1.0E+00	1.00	9.4E-01	0.99	0.66
rs8020331	104859860	G	A	0.34	1.00	0.02	9.3E-01	0	<0.01	0.38	/I	9.6E-01	1.00	9.6E-01	1.00	1.00
rs113463470	105317273	T	C	0.04	1.00	0.06	9.3E-01	0	<0.01	0.04	/I	4.8E-01	0.96	3.6E-01	0.95	0.86
rs2816671	105603844	T	A	0.12	1.00	0.04	9.3E-01	0	<0.01	0.12	/I	9.2E-01	1.00	9.2E-01	1.00	0.90
rs146999659	105298158	A	C	0.03	0.99	0.07	9.3E-01	0	<0.01	0.04	/I	7.3E-01	0.98	6.2E-01	0.96	0.81
rs10141861	105298166	A	G	0.03	1.01	0.07	9.3E-01	0	<0.01	0.04	/I	7.3E-01	1.02	6.2E-01	1.04	0.81
rs2582530	105391134	G	A	0.02	0.99	0.09	9.3E-01	45.63	0.01	0.02	/I	8.6E-01	0.98	9.1E-01	0.99	0.66
rs34600691	105013854	A	G	0.11	1.00	0.04	9.3E-01	56.52	<0.01	0.09	/I	8.3E-01	0.99	7.3E-01	0.99	0.91
rs59117977	105416087	T	C	0.02	1.01	0.10	9.3E-01	57.57	0.01	0.02	/I	7.9E-01	1.03	8.9E-01	1.01	0.64
rs4332683	104888511	A	G	0.24	1.00	0.03	9.3E-01	15.28	<0.01	0.28	/I	9.3E-01	1.00	1.0E+00	1.00	0.88
rs36051245	105013869	A	G	0.11	1.00	0.04	9.3E-01	56.52	<0.01	0.09	/I	8.3E-01	0.99	7.3E-01	0.99	0.91
rs11850921	104759985	A	G	0.05	1.00	0.05	9.3E-01	0	<0.01	0.04	/I	8.5E-01	1.01	8.9E-01	1.01	0.86
rs7153233	104876076	T	C	0.25	1.00	0.03	9.3E-01	0	<0.01	0.28	/I	9.4E-01	1.00	1.0E+00	1.00	0.90
rs80187653	105379051	T	C													

rs73355745	105368291	A	G	0.04	1.00	0.05	9.5E-01	0	<0.01	0.03	/I	7.7E-01	0.99	6.1E-01	0.97	0.97
rs77928971	104947399	T	C	0.02	1.01	0.10	9.5E-01	0	<0.01	0.04	/I	9.8E-01	1.00	9.9E-01	1.00	0.74
rs73355749	105369645	T	C	0.04	1.00	0.05	9.5E-01	0	<0.01	0.03	/I	7.7E-01	0.99	6.1E-01	0.97	0.97
rs12897807	104856497	T	C	0.35	1.00	0.02	9.5E-01	0	<0.01	0.39	G/G	9.9E-01	1.00	9.9E-01	1.00	1.00
rs188689698	105320712	T	C	0.07	1.00	0.05	9.5E-01	0	<0.01	0.04	/I	3.8E-01	0.95	1.0E+00	1.00	0.52
rs61731617	105360127	A	G	0.04	1.00	0.05	9.5E-01	0	<0.01	0.03	/I	6.7E-01	0.98	5.2E-01	0.97	0.97
rs191797181	105351233	T	C	0.04	1.00	0.07	9.5E-01	51.3	<0.01	0.05	/I	9.8E-01	1.00	8.1E-01	0.98	0.51
rs73355782	105381227	C	T	0.04	1.00	0.05	9.5E-01	0	<0.01	0.03	/I	7.6E-01	0.98	6.0E-01	0.97	0.96
rs8018595	104864798	G	A	0.35	1.00	0.02	9.5E-01	0	<0.01	0.39	/I	9.2E-01	1.00	9.2E-01	1.00	1.00
rs192316673	105400032	G	C	0.03	1.00	0.08	9.5E-01	0	<0.01	0.02	/I	8.7E-01	0.99	7.9E-01	0.98	0.71
rs76774971	105143074	T	C	0.22	1.00	0.03	9.5E-01	14.08	0.02	0.26	/I	8.5E-01	0.99	6.9E-01	0.99	0.79
rs7154471	105086475	T	C	0.06	1.00	0.05	9.5E-01	61.71	0.02	0.05	G*/I	7.4E-01	1.02	7.1E-01	1.02	0.91
rs34793922	105014357	A	C	0.11	1.00	0.04	9.5E-01	57.11	<0.01	0.09	/I	9.5E-01	1.00	8.4E-01	0.99	0.91
rs182064838	105530006	T	G	0.01	1.01	0.12	9.5E-01	48.36	<0.01	0.02	/I	8.8E-01	0.98	8.6E-01	0.98	0.69
rs34686607	105014210	A	C	0.11	1.00	0.04	9.5E-01	57.11	<0.01	0.09	/I	9.4E-01	1.00	8.4E-01	0.99	0.91
rs7148940	104973188	A	T	0.39	1.00	0.03	9.6E-01	39.46	<0.01	0.39	/I	7.9E-01	0.99	9.3E-01	1.00	0.68
rs28699424	104940967	A	G	0.28	1.00	0.02	9.6E-01	0	<0.01	0.29	/I	8.9E-01	1.00	9.9E-01	1.00	0.93
rs10139247	105136852	G	A	0.23	1.00	0.03	9.6E-01	22.31	0.02	0.27	/I	7.5E-01	0.99	6.1E-01	0.98	0.81
rs111260552	105375900	T	C	0.04	1.00	0.05	9.6E-01	0	<0.01	0.03	/I	7.6E-01	0.98	6.0E-01	0.97	0.97
rs12883919	105213904	A	G	0.11	1.00	0.03	9.6E-01	34.16	<0.01	0.08	/I	7.6E-02	0.94	5.9E-01	1.02	0.83
rs113784545	105376104	A	G	0.04	1.00	0.05	9.6E-01	0	<0.01	0.03	/I	7.6E-01	0.98	6.0E-01	0.97	0.97
rs117723806	105385248	A	G	0.02	0.99	0.10	9.6E-01	0	0.01	0.02	/I	7.9E-01	0.97	7.0E-01	0.96	0.66
rs3784240	105623261	A	G	0.08	1.00	0.05	9.6E-01	67.26	<0.01	0.08	G*/I	9.3E-01	1.00	9.1E-01	1.01	0.87
rs11849460	105007585	A	G	0.10	1.00	0.04	9.6E-01	60.58	<0.01	0.09	/I	9.5E-01	1.00	9.5E-01	0.99	0.89
rs11160817	105168414	T	C	0.40	1.00	0.02	9.6E-01	45.28	<0.01	0.39	G*/I	5.5E-02	0.95	3.4E-01	0.98	0.92
rs4247039	105024514	A	G	0.18	1.00	0.03	9.6E-01	0	<0.01	0.19	/I	9.9E-01	1.00	8.2E-01	0.99	0.89
rs72700126	105311723	G	A	0.03	1.00	0.07	9.6E-01	2.37	<0.01	0.04	/I	7.9E-01	0.98	6.8E-01	0.97	0.85
rs8005963	104997159	T	C	0.18	1.00	0.03	9.6E-01	0	<0.01	0.20	/I	9.6E-01	1.00	9.1E-01	1.00	0.78
rs78460270	104752251	A	G	0.22	1.00	0.03	9.6E-01	0	<0.01	0.25	/I	9.5E-01	1.00	8.8E-01	1.00	0.67
rs4983405	105015419	C	T	0.11	1.00	0.04	9.6E-01	56.66	<0.01	0.09	/I	9.4E-01	1.00	8.4E-01	0.99	0.91
rs8018970	104864787	A	G	0.35	1.00	0.02	9.6E-01	0	<0.01	0.39	/I	9.3E-01	1.00	9.3E-01	1.00	1.00
rs112794335	105378989	T	A	0.04	1.00	0.05	9.6E-01	0	<0.01	0.03	/I	7.5E-01	0.98	5.9E-01	0.97	0.97
rs10220709	104761501	T	C	0.05	1.00	0.05	9.6E-01	0	<0.01	0.04	/I	8.8E-01	1.01	9.2E-01	1.01	0.86
rs75111603	105076400	A	G	0.02	1.00	0.10	9.6E-01	39.57	0.04	0.02	/I	7.1E-01	1.04	8.8E-01	1.02	0.72
rs12147310	105552223	T	C	0.06	1.00	0.05	9.6E-01	71.56	<0.01	0.05	/I	9.2E-01	1.01	9.5E-01	1.00	0.89
rs12588041	104864916	G	A	0.41	1.00	0.02	9.6E-01	0	<0.01	0.42	/I	9.9E-01	1.00	9.6E-01	1.00	0.93
rs55906115	105278849	C	T	0.34	1.00	0.03	9.6E-01	17.99	0.07	0.35	/I	4.5E-01	1.02	7.0E-01	1.01	0.49
rs75466941	104937798	T	C	0.05	1.00	0.06	9.7E-01	25.29	<0.01	0.07	/I	9.8E-01	1.00	9.5E-01	1.00	0.77
rs11623953	104795152	C	T	0.13	1.00	0.03	9.7E-01	0	<0.01	0.11	/I	9.1E-01	1.00	9.1E-01	1.00	0.99
rs34344768	105014626	C	T	0.11	1.00	0.04	9.7E-01	56.76	<0.01	0.09	/I	9.3E-01	1.00	8.3E-01	0.99	0.91
rs147377490	105365349	G	A	0.02	1.00	0.12	9.7E-01	0	<0.01	0.02	/I	7.7E-01	1.03	8.9E-01	1.02	0.45
rs3861679	105156180	A	G	0.06	1.00	0.05	9.7E-01	71.88	<0.01	0.05	/I	1.8E-01	1.08	4.1E-01	1.05	0.57
rs140821961	104767375	T	C	0.04	1.00	0.06	9.7E-01	0	<0.01	0.04	/I	9.7E-01	1.00	9.9E-01	1.00	0.90
rs9888596	104778553	G	A	0.22	1.00	0.03	9.7E-01	0	<0.01	0.22	/I	9.8E-01	1.00	9.9E-01	1.00	0.89
rs111798508	105121604	T	A	0.28	1.00	0.03	9.7E-01	0	<0.01	0.33	/I	9.9E-01	1.00	7.1E-01	0.99	0.75
rs4983597	105006170	G	A	0.10	1.00	0.04	9.7E-01	60.45	<0.01	0.09	/I	9.4E-01	1.00	8.2E-01	0.99	0.87
rs73354395	105358629	T	C	0.04	1.00	0.05	9.7E-01	0	<0.01	0.03	/I	6.9E-01	0.98	5.3E-01	0.97	0.96
rs76751100	105283873	G	A	0.09	1.00	0.05	9.7E-01	0	<0.01	0.08	/I	4.2E-01	0.96	9.8E-01	1.00	0.56
rs5027824	105013419	A	G	0.11	1.00	0.04	9.7E-01	56.78	<0.01	0.09	/I	8.7E-01	0.99	7.6E-01	0.99	0.91
rs142219298	105729388	T	C	0.03	1.00	0.08	9.7E-01	6.42	<0.01	0.02	/I	9.2E-01	0.99	8.3E-01	0.98	0.64
rs56134337	105265052	A	G	0.02	1.00	0.12	9.7E-01	0	<0.01	0.01	/I	4.5E-01	1.10	6.2E-01	1.06	0.51
rs11621355	104862327	G	C	0.35	1.00	0.02	9.7E-01	0	<0.01	0.39	/I	9.4E-01	1.00	9.3E-01	1.00	0.98
rs73354005	104922222	C	T	0.06	1.00	0.05	9.7E-01	36.83	0.01	0.02	/I	8.7E-01	1.01	8.9E-01	1.01	0.86
rs112461551	105014970	G	T	0.11	1.00	0.04	9.8E-01	54.47	<0.01	0.09	/I	9.2E-01	1.00	8.2E-01	0.99	0.89
rs35816659	105013791	A	A	0.11	1.00	0.04	9.8E-01	56.82	<0.01	0.09	/I	8.8E-01	0.99	7.7E-01	0.99	0.91
rs8003187	104865071	A	G	0.35	1.00	0.02	9.8E-01	0	<0.01	0.39	G/G	9.4E-01	1.00	9.9E-01	1.00	1.00
rs113728896	105134613	A	G	0.23	1.00	0.03	9.8E-01	22.06	0.02	0.27	/I	7.7E-01	0.99	6.3E-01	0.98	0.81
rs8017378	104864003	T	C	0.34	1.00	0.02	9.8E-01	0	<0.01	0.39	/I	9.4E-01	1.00	9.4E-01	1.00	0.99
rs142270903	104751382	T	C	0.03	1.00	0.07	9.8E-01	0	<0.01	0.03	/I	9.9E-01	1.00	9.5E-01	1.00	0.74
rs4407001	105014063	T	C	0.11	1.00	0.04	9.8E-01	59.03	<0.01	0.09	/I	9.2E-01	1.00	8.1E-01	0.99	0.90
rs1975398	105378226	A	G	0.04	1.00	0.05	9.8E-01	0	<0.01	0.03	/I	7.0E-01	0.98	5.4E-01	0.97	0.97
rs28538818	105015914	G	A	0.11	1.00	0.04	9.8E-01	58.02	<0.01	0.09	/I	9.2E-01	1.00	8.1E-01	0.99	0.90
rs8017224	104863997	T	A	0.34	1.00	0.02	9.8E-01	0	<0.01	0.39	/I	9.5E-01	1.00	9.4E-01	1.00	0.99
rs8003870	104893357	G	C	0.25	1.00	0.03	9.8E-01	0	<0.01	0.28	/I	9.7E-01	1.00	9.7E-01	1.00	0.83
rs61323993	105348334	T	C	0.04	1.00	0.05	9.8E-01	0	<0.01	0.03	/I	7.2E-01	0.98	5.6E-01	0.97	0.98
rs4128849	104992362	T	A	0.20	1.00	0.03	9.8E-01	0	<0.01	0.21	/I	8.6E-01	0.99	8.0E-01	0.99	0.71
rs139798260	105300509	T	C	0.03	1.00	0.07	9.9E-01	0	<0.01	0.03	/I	8.0E-01	0.98	6.9E-01	0.97	0.81
rs182149357	105241607	A	G	0.02	1.00	0.09	9.9E-01	32.48	<0.01	0.01	/I	6.0E-01	0.96	4.9E-01	1.06	0.63
rs56114826	105133054	A	G	0.09	1.00	0.05	9.9E-01	0	0.02	0.08	/I	9.0E-01	0.99	8.9E-01	0.99	0.68
rs112359070	105695324	A	C	0.02	1.00	0.10	9.9E-01	30.97	<0.01	0.01	/I	9.0E-01	1.01	9.4E-01	1.01	0.68
rs34115973	105007529	T	A	0.10	1.00	0.04	9.9E-01	60.35	<0.01	0.09	/I	9.2E-01	1.00	8.1E-01	0.99	0.89
rs187103355	105626346	A	C	0.09	1.00	0.05	9.9E-01	0	<0.01	0.08	/I	8.3E-01	1.01	8.6E-01	1.01	0.53
rs4983607	105015565	C	T	0.11	1.00	0.04	9.9E-01	56.56	<0.01	0.09	/I	8.9E-01	0.99	7.8E-01	0.99	0.91
rs8017207	104863967	G	A	0.35	1.00	0.02	9.9E-01	0	<0.01	0.39	/I	9.5E-01	1.00	9.5E-01	1.00	0.99
rs35164057	105015															