Longitudinal study of recurrent metastatic melanoma cell lines underscores the individuality of cancer biology

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Short title: Recurrent metastases retain specific traits

Abbreviations: aCGH, array comparative genomic hybridization; ANOVA, analysis of variance; CN, copy number; CNA copy number alteration; FDR, false discovery rate; GX, gene expression; MDS, multidimensional scaling; RM ANOVA, repeated measures analysis of variance

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Abstract

Recurrent metastatic melanoma provides a unique opportunity to analyze disease evolution in metastatic cancer. Here, we followed 8 patients with an unusually prolonged history of metastatic melanoma, who developed a total of 26 recurrences over several years. Cell lines derived from each metastasis were analyzed by comparative genomic hybridization and global transcript analysis. We observed that conserved, patient-specific characteristics remain stable in recurrent metastatic melanoma even after years and several recurrences. Differences among individual patients exceeded within-patient lesion variability, both at the DNA copy number ($p<0.001$) and RNA gene expression level ($p<0.001$). Conserved patient-specific traits included expression of several cancer/testis antigens and the c-kit proto-oncogene throughout multiple recurrences. Interestingly, subsequent recurrences of different patients did not display consistent or convergent changes toward a more aggressive disease phenotype. Finally, sequential recurrences of the same patient did not descend progressively from each other, as irreversible mutations, such as homozygous deletions were frequently not inherited from previous metastases. This study suggests that the late evolution of metastatic melanoma, which dramatically turns an indolent disease into a lethal phase, is prone to preserve case-specific traits over multiple recurrences and occurs through a series of random events that do not follow a consistent step-wise process.

Introduction

Cancer progression is usually studied cross-sectionally, comparing lesions obtained from different patients, excised at various stages. By combining these snapshots, the natural history of the disease can be indirectly reconstructed. In contrast, the preferable longitudinal analysis of sequential lesions in the same patients is usually not feasible, especially difficult to perform in rapidly progressing cancers, such as melanoma, and particularly challenging when analyzing disease progression in metastases (Bonsing et al, 1993; Kuukasjarvi et al, 1997; Navin et al, 2011).

However, the limited number of such longitudinal studies leaves several questions open. First, cross-sectional studies do not allow an estimate of the extent in which patient-specific traits remain stable over time. Therefore, it is difficult to assess the stability of such patient-specific traits over time, which is a question of basic importance in personalized cancer therapy (Gupta et al, 2009; Harbst et al, 2010; Navin et al, 2010).

In addition, with cross-sectional analyses it is impossible to test, whether late disease development follows a pattern of sequential somatic microevolution, or subsequent metastases represent individual buddings from a stable set of cancer progenitors creating independently established new metastatic lesions (Sabatino et al, 2008; Wang et al, 2006).

Finally, it is difficult to quantify whether sequential steps are involved in late stage progression, and estimate whether consistent changes are required for the late progression of melanoma from a metastatic phase that progresses slowly, to a rapid evolution in the declining phase of one patient's life.

Studying longitudinally several recurrent melanoma metastases of a rare collection of eight individuals who developed multiple recurrences over a period of years (see Table S1), we sought a better understanding of the above questions. This study is a follow up from a previous longitudinal study

of a single case (Sabatino et al, 2008; Wang et al, 2006) focusing on traits remaining stable and changes repeated consistently among multiple developing recurrent metastases of several melanoma patients. To our best knowledge, these questions have not yet been analyzed by others.

Results

Long term metastatic melanoma is consistent with canonical melanoma genomics

Since the cases with multiple recurrent metastases studied here differ behaviorally from classic metastatic melanoma due to their unusually protracted course, we first evaluated whether the cell lines derived from these unusual cases would differ markedly from typical cases of melanoma as published by others.

Array comparative genomic hybridization (aCGH) confirmed that the chromosomal distribution of copy number (CN) alterations (CNAs) prominently observed here are in line with previous observations (Fig. 1a) (Jonsson et al, 2007; Roschke et al, 2003; Spivey et al, 2012; Thompson et al, 1995). Also, at the individual gene level, most genes were affected by copy number gains and losses in accordance with others' reports (Grafstrom et al, 2005; Jonsson et al, 2007; Okamoto et al, 1999; Pirker et al, 2003; Shi et al, 2012) (Fig. 1b, see full data set in Table S2).

Finally, similar to others' reports, we also found that a correlation between CN and gene expression (GX) data is present, but limited in advanced cancer (Bacolod and Barany, 2010; Sabatino et al, 2008; Spivey et al, 2012). Among 4,340 genes eligible for analysis, 2,766 correlated weakly (Pearson's correlation $R<0.3$, $p<0.05$, false discovery rate (FDR) 0.05) and 272 strongly ($R<0.5$, $p<0.05$, FDR 0.01) in CN and GX (see Figure S1).

Taken together, this dataset was representative of typical characteristics of metastatic melanoma genomics, as reported in the literature (Bacolod and Barany, 2010; Jonsson et al, 2007; Roschke et al, 2003; Sabatino et al, 2008; Spivey et al, 2012; Thompson et al, 1995).

Advanced melanoma retains case-specific fingerprints after years of disease progression

Following a rare case of metastatic melanoma that recurred several times over a decade, we previously observed that in spite of the stochastic and selective forces affecting its genome, stable characteristics prevailed to the point that recurrent lesions derived from this patient clustered away from heterologous randomly collected cases (Sabatino et al, 2008; Wang et al, 2006). This patient-specific stability, if shared by other cases of advanced melanoma, could have fundamental implications for personalized cancer therapy. Thus, in this study, we first analyzed whether the previous observations could be generalized to a larger set of patients.

First we compared CNA and GX patterns on a global genomic scale among cell lines from the eight patients with multiple recurrences. Multidimensional scaling (MDS), a computational method enabling visualization of sample relatedness within large scale genetic data demonstrated that even after years, recurrent metastases of a given patient remained closely related, keeping clear distance from others' metastases (Fig. 2a and 2c). By comparing all metastases in all possible pairs (325 pairs total), we found that MDS distances between subsequent metastases (estimates of sample relatedness) of the same patient were significantly shorter than those between metastases of different patients (Fig. 2b and 2d). This finding held true whether CNA or GX data were compared.

Stable patient-specific traits include genes of relevance to melanoma biology

We next searched for genomic aberrations typically specific to a given patient. We found that stable case-specific CNAs occurred in chromosomes 1, 5, 13, and 19 (Fig. 3a One Way Analysis of variance (ANOVA), $p<0.05$, FDR<0.001, see Table S3 for details). Similarly, 925 genes were found to have stable, patient-specific expression; 61 among them could be categorized functionally as melanoma-related by the Ingenuity Pathway Analysis database (Fig. 3b, One-Way ANOVA, $p<0.05$, FDR<0.05). The latter included several genes with known tumorigenic properties supporting autonomous proliferation (KIT, MYC, CDK2, RBL2), controlling genomic stability (BRCA1), apoptosis and cell survival (TP53BP2, CASP8, TEP1), adhesion and motility (CDH1, ITGA4), invasiveness, matrix remodeling (MMP15, MMP19), angiogenesis (ANGPT1, EGF), modulation of anti-tumor immunity, (large clusters of major histocompatibility complex class I and II transcripts, the latter correlating with CIITA expression) and several melanoma antigens (MAGE-A1, -A4, -A9, -B2, -C2). This observation suggests that genes highly relevant to melanoma progression retain stable patient-specific expression levels over long periods of time (Fig. 3b).

Notably among all possible patient-to-patient comparisons (28 pairwise comparisons involving 8 patients), 37 genes demonstrated patient-specific expression pattern with significant differences among patients and an at least two-fold change in >70% of all pair wise comparisons. These included MAGE-A4, -B2, -C2, BAGE-2, and KIT (see Table S4). To further test these results, we analyzed KIT protein levels by flow cytometry in the investigated cell lines. Our analysis disclosed that although KIT expression is frequently affected by post-transcriptional regulation, KIT protein levels remain consistent throughout multiple recurrences of individual patients, and whenever expressed, correlate well with mRNA data (Fig. S2). Taken together, these observations suggest that genes relevant to melanoma immunology and melanoma cell biology are expressed stably within a given patient, and may, in turn, be responsible for behavioral differences among individual cancers.

Lack of evidence for convergent evolution and consistent changes among patients over time

Next, we asked whether subsequent metastases from different patients progressively converge to reach a terminal, potentially lethal "hyper-aggressive" status. This would imply that on average, early (e.g. first) metastases of individual patients would be more different, more distant from each other than late (e.g. the last) metastases of the same individuals. MDS genomic distances demonstrate that this is not the case (Fig. 4a and 4b), neither at the CN or at the GX level.

To corroborate this finding, we next attempted to identify consistent CN or GX changes that might represent a recurrent theme in the transition from earlier to later metastases in a given patient. However, statistical analysis was unable to identify changes in CN alterations or GX patterns that constitute consistent trends in subsequent recurrences of metastatic melanoma, (Two-Way RM ANOVA $p<0.05$ FDR 0.05). First, an analysis of all recurrent metastases inclusive of patient identity and lesion sequence revealed no consistent changes between subsequent metastases. Next, since patients with large numbers of recurrences dominate the analysis in such a pair wise comparison, we decreased or eliminated differences in per-patient sample sizes. To this end, we first replaced multiple synchronous metastases with a single averaged value for each parameter tested ($p<0.05$ FDR 0.05). Also, in a separate analysis we limited the evaluated cases to 3 randomly selected samples per patient ($p<0.05$ FDR 0.05). No consistent changes were found by either analysis. Next, assuming that the first and last available lesions in a given patient were most distant genetically, we restricted the analysis to these extreme pairs; but again, a pair wise analysis including patient identity failed to identify statistically significant differences ($p<0.05$ FDR 0.05). Finally, hypothesizing that the last, supposedly most advanced, fatal lesion in a given patient might be different from earlier ones, we compared the latter with the former ($p<0.05$ FDR 0.05), again without observing consistent differences. Taken together, no consistent progression patterns could be observed between subsequent metastases, either at the DNA copy

number or RNA gene expression level, regardless of the approach used for sample selection and grouping before statistical analysis.

In line with this observation, comparison of the first metastasis from a given patient with his subsequent ones demonstrated that the latter are not necessarily drifting progressively further from the original one (Fig. 4c and 4d). Rather, the data suggest a stochastic drift among subsequent recurrent metastases.

We also tested whether multiple cycles of phenotype switching between proposed invasive and proliferative phenotypes (Hoek et al, 2008) could explain a seemingly stochastic drifting of recurrent melanoma metastases. We found that this model may provide partial explanation for our observations, as key genes of the two phenotypes were expressed in an alternating fashion, and the two phenotypes seemed to change frequently back and forth through the recurrences of most (e.g. patients B, C, D, F, G), although certainly not all patients (e.g. patients A and E, Fig. S3).

The fate of homozygous deletions does not support cumulative changes in the evolution of melanoma

Since no step-wise evolutionary pattern could be discerned, we next asked whether recurrent metastases from the same patient descend sequentially from one another, i.e. if they acquire new mutations in a cumulative fashion. To this end, we followed the fate of common BRAF, NRAS mutations (Colombino et al, 2012) and homozygous deletions (-/-) in subsequent recurrent metastases. Unfortunately, BRAF and NRAS status turned out to be uninformative in this regard, because as frequently observed in melanoma, all recurrent melanomas analyzed were BRAFV600E mutated and NRAS wild type throughout (not shown). Next we analyzed the fate of homozygous deletions (-/-) that are thought to be irreversible since no known mechanisms for structural restoration of these alterations

have been described. Based on this, we assumed that if subsequent recurrent metastases of the same patient show reversions of homozygous deletions, they cannot sequentially descend from each other.

A total of 33 contiguous homozygous deletions were found affecting the CDKN2A/CDKN2B region, various interferon genes, B2M, major histocompatibility complex genes, etc. Out of these, 25 deletions were eligible for analysis as they emerged in a metastasis for which there was at least a subsequent metastasis to evaluate (Fig. 5b). Out of 25 eligible homozygous deletions, 15 (60%) appeared to be reverted in a given patient's disease history, suggesting that in subsequent metastases of recurrent melanoma, new mutations are not acquired in a cumulative fashion, and hence, recurrent metastases do not descend from each other (Fig. 5b).

Recurrent melanomas show hints of slower growth, but more frequent metastasis formation

In initial MDS analyses, cancer cells from patients with recurrent long term metastatic disease were hardly discernible from those from sporadically excised, melanoma cases (Fig. 2a and 2c). Nevertheless, we identified a set of 177 genes differentially expressed between the two phenotypes, which is a very small number compared to patient-to-patient differences, 8 of which were melanoma-related. Interestingly, these genes hint to slower tumor growth (retained CDKN1A and ANAPC expression), higher sensitivity to immune- or therapy-mediated eradication (higher FAS but lower levels of MGMT expression), and higher pro-metastatic tendency (elevated levels of ALCAM, Fig. S4).

Discussion

This study analyzes a specific time point in the natural history of cancer when advanced disease of an indolent nature turns into an aggressive and lethal stage. We studied the genetic profile of

melanoma cell lines derived from sequentially excised metastases in unusual cases when the metastatic process followed a protracted course. Although the use of cell lines has significant limitations, we observed that early passage cell lines maintain stable genetic traits in vitro that relate to the in vivo phenotype of parental tumors (Spivey et al, 2012). Nevertheless, our samples clearly do not equal whole tumors, and these cases may have represented a special subset of melanoma, as well. First, these recurrent melanomas displayed CDK2NA, PTEN, and BRAF copy number aberrations more frequently than average cases (Hodis et al, 2012; Krauthammer et al, 2012). In addition, all 26 metastases of the analyzed 8 patients carried BRAF V600E, but displayed wild type NRAS. Conservation of BRAF mutation status across metastases is in line with others' observations (Niessner et al, 2013). However, this particular BRAF/NRAS pattern is typical for melanomas arising in intermittently sun-exposed areas (Colombino et al, 2012), affects cell proliferation rate (Liu et al, 2007), prognosis (Long et al, 2011), treatment of choice, and in this latter context, also BRAF copy numbers (Shi et al, 2012).

Keeping these limitations in mind, our data suggest that key elements of the framework of recurrent metastatic melanomas remain stable with time; since such stability was observed in 8 out of 8 patients, it possibly represents the rule rather than the exception. This is a remarkable finding considering that at the same time, our data also support the accepted view of late stage cancer evolution being a highly dynamic process, also shown recently by others (Gerlinger et al, 2012; Shah et al, 2012) using indirect computational inference; however, this study uniquely provides direct evidence by studying serially asynchronous metastases over a long period.

Our findings suggest that individuality is maintained throughout a non-directional drift that does not follow a clearly linear progression, with each metastatic signature stemming de novo from a stable progenitor entity. Moreover, there was no sign of a convergent evolution in advanced late stage melanoma toward the creation of a convergent lethal phenotype, and recurrent metastases did not

seemtobeeachother'sclonaldescendants,oraccumulateincrementalchanges,whichisinlinewith others'recentlypublishedobservations (Colombino et al, 2012).

Ontheotherhand,theobservationthatstableexpressionofcancer/testisantigensandthec-kit proto-oncogeneacrossmultiplerecurrencesofmelanomaimpliesthat, late stage melanoma is capable of displaying stable, case-specific differences directly affecting markers determining vulnerability to novel forms of immunological or small molecule biotherapy (Guo et al, 2011; Tyagi et al, 2005; Tyagi and Mirakhur, 2009).

It remains to be clarified to what extent these observations are attributable to the effects of clonal heterogeneity (Gerlinger et al, 2012; Shah et al, 2012), circulating tumor cells (Maheswaran et al, 2008; Yu et al, 2011) that may remain dormant for years and reset the evolutionary clock upon their reactivation, multiple events of phenotype switching (Eichhoff et al, 2010; Hoek et al, 2008), or persistent cancer stem cells opening multiple alternative ways to cancer evolution with each individual recurrence (La Porta, 2012; Shakhova and Sommer, 2012). Larger and more comprehensive studies involving genome-wide DNA sequencing, epigenetic and proteomic analyses, analyzing patients with averagesurvivaltimes,andresectedwholetumorsinsteadofcelllines,are strongly warranted to clarify these questions and confirm the applicability of our findings to usual cases of advanced melanoma.

Materials and Methods

Patients and samples

Twenty-six recurrent melanoma metastases were surgically isolated from 8 patients experiencing relapse after one or more successful treatment intervention(s) with no signs of residual disease. Recurrent metastases from different tissues appeared in periods spanning 10-148 months with 8-101 months between recurrences (see Table S1 for all data regarding samples, patients, treatments and disease history). Patients received therapy and underwent surgery at the Surgery Branch of the National Cancer Institute, National Institutes of Health, USA, or at the Centro di Riferimento Oncologico (Italian National Cancer Institute) in Aviano, Italy. Patients were treated and samples obtained after signing informed consent, with the approval of each institute's review board, and in accordance with the Declaration of Helsinki Principles. From all lesions, stable cell cultures were established and maintained at the Department of Transfusion Medicine, Clinical Center, National Institutes of Health for at least eight passages. Patients experiencing recurrent metastases were labeled with capital letters; "A", "B", "C", etc., their subsequent metastases as "A/1", "A/2", "B/1", "B/2", etc., while synchronous metastases in a given patient were labeled as "A/1a", "A/1b" etc. All recurrent melanoma metastases analyzed appeared after a single primary tumor. Another 22 melanoma cell lines isolated and maintained as above were expanded from melanoma patients with rapid disease course, for whom only one metastasis was available. As no extended follow up was possible in these cases, the cell lines are considered representative of random time points in the natural course of metastatic melanoma. These cell lines were labeled with Arabic numbers, as "1", "2", "3", etc.

DNA Isolation

Total genomic DNA of cell lines was isolated using the QuickGene DNA whole blood kit S and a QuickGene-810 Nucleic Acid Isolation System (Fujifilm, Tokyo, Japan).

HLA-Typing

To exclude accidental cross-contamination of samples, low resolution HLA-typing was performed at the HLA Laboratory, Laboratory Services Section, Department of Transfusion Medicine, Clinical Center, National Institutes of Health.

BRAF and NRAS genotyping

PCR was performed from 50 ng genomic DNA using the HotStarTaq Master Mix Kit (Qiagen, Valencia, CA) and the following primers: BRAF exon 15 forward: 5'-TCATAATGCTTGCTCTGATAGGA-3' BRAF exon 15 reverse: 5'-GGCCAAAAATTTAATCAGTGGA-3', NRAS exon 2 forward: 5'-ATAGCATTGCATTCCCTGTG-3' NRAS exon 2 reverse: 5'-CACAAAGATCATCCTTTCAGAGA-3'. PCR products were labeled using a Big Dye terminator kit v3.1 (Life Technologies, Carlsbad, CA). Sequencing was performed using a 3730 Genetic Analyzer (Applied Biosystems) and analyzed by Sequencher software (Gene Codes, Ann Arbor, MI).

Array Comparative Genome Hybridization (aCGH)

All aCGH studies were performed using Agilent's oligo aCGH platform. Briefly, 1 µg of genomic DNA per sample was directly labeled with a Genomic DNA Enzymatic Labeling Kit, prepared for hybridization with

help of an Oligo aCGH Hybridization Kit, and hybridized to 105K Human Genome CGH 105A Oligo Microarrays. Arrays were washed with Oligo aCGH Wash Buffers and scanned in a High-Resolution Microarray Scanner (all from Agilent, Santa Clara, CA). Data were deposited in the GEO public database under GSE38187.

RNA Isolation

Total RNA was isolated using Qiagen's RNEasy Mini Kit, following standard protocol.

Gene expression microarray

For expression array studies, the Affymetrix Gene Array System was utilized. Briefly, 250 ng total RNA per sample was amplified using a WT expression kit. Next, cDNA was labeled with help of a GeneChip WT Terminal Label and Control Reactions kit. Samples were then prepared for hybridization using the GeneChip Hyb Wash and Stain Kit and loaded to Human Gene ST 1.0 Arrays. Arrays were washed, PE-labeled on a GeneChip Fluidics Station 450, and loaded into a GeneChip Scanner 3000 7G with autoloader for scanning (all from Affymetrix, Santa Clara, CA). Data were submitted to GEO and made publicly available under accession GSE38187.

Microarray data analysis

Agilent aCGH microarray data were imported into the Partek Genomics Suite software (Partek, St. Louis, Missouri), quantile normalized and pre-processed using a built-in chromosomal segmentation algorithm (Hawthorn et al, 2010). Individual chromosomal segments were defined as continuous regions covered by at least 10 consecutive microarray probes, a significant ($p<0.001$) and considerable (>0.3 copies on average) difference between the CN of the given segment and neighboring segments, accepting an error rate of less than +/- 0.3 copies. Segmented genomes were subjected to Multidimensional Scaling (MDS) to describe inter-sample relationships. Partek's One-Way and Two-Way RM ANOVA analyses were performed on segment CNs to identify CNAs different between individual patients, CNAs consistently changed in consecutive metastases of the same patient, and CNAs between recurrent and random cancer samples. To avoid over-estimation of patient-to-patient differences in CNA studies analyzing a mixed-gender group of patients, X and Y chromosome-related data were excluded from all such analyses. Significant differences were identified with a nominal $p<0.05$ and were corrected with FDR of <0.05. Homozygous deletions (-/-) were identified as segments with CN<0.4 at an error rate of <+/- 0.3 copies.

Affymetrix gene expression data were imported to Partek Genomic Suite, quantile normalized and batch-corrected using Distance-Weighted-Discrimination, as described elsewhere (Benito et al, 2004). MDS, One-Way and Two-Way RM ANOVA analyses were performed as above. CN and GX data were integrated and analyzed with help of Partek Genomic Suite. Genes whose expression levels were found to be affected by CNAs were identified by computing Pearson's correlation between CN and GX values. A Pearson's correlation of R>0.3 with <p0.05 and FDR 0.05 was accepted as proof for CNA-affected gene expression.

Flow cytometry

Cells were harvested non-enzymatically using Cellstripper (Corning, Manassas, VA), and stained with LIVE/DEAD Kit (Life Technologies, Carlsbad, CA), anti-CD117(KIT)-APC (BD Biosciences, San Jose, CA), or isotype controls. Data analysis was performed using a MACSQuant Analyser (Miltenyi Biotec, Germany) and FlowJo (TreeStar).

Conflict of interest

The authors state no conflict of interest.

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Figure legends

Figure 1

Description and basic characterization of the analyzed sample set by integrated copy number and gene expression analysis

Panel a) shows frequency and spatial distribution of autosomal CN aberrations in the analyzed melanoma sample set. Panel b) displays combined distribution analysis of CN gains and losses affecting key melanoma genes, and also their distribution between various, disease-related biological functions, as defined by the Ingenuity Pathway Analysis database. Selected key melanoma genes are labeled with their respective HUGO gene symbols.

Figure 2

Comparison of the relative weights of within- versus between-patient differences in metastatic melanoma

Panel a) displays the whole complexity of DNA copy number data reduced to three dimensions (D1-3) by Multidimensional Scaling (MDS). Metastases are symbolized by spheres. Recurrent metastases belonging to the same patient (A-H) are color-coded; non-recurrent, random metastasis samples, serving as controls, are grey. Panel b) shows distribution of MDS plot distances between individual metastases representing the magnitude of actual genomic differences. Statistical comparisons of MDS

distances (~genomic differences) between recurrent metastases belonging to the same, vs. different patients are shown. P-values given are derived from a standard t-test considering all possible recurrent metastasis pairs from the sample set. Panels c) and d) display similar information on whole genome RNA expression data.

Figure 3

Identification of stable individual traits conserved in recurrent metastases of a given patient through years of ongoing disease history

On panel a), examples are shown for stable conserved copy number traits that remain characteristic for a given case of recurrent melanoma (selected examples in yellow frames). Samples belonging to the same patient are aligned horizontally and color coded (to the left). On panel b), conserved gene expression patterns, characteristic for a given case, remain stable throughout multiple recurrences and are shown using a standardized heatmap (selected examples in yellow frames). Samples are aligned vertically and color coded (top). HUGO gene symbols of selected melanoma-related genes are shown to the right.

Figure 4

Testing evolutional convergence and sequential evolution in recurrent metastatic melanomas on a global scale

Panels a) and b) compare MDS-based distances (estimates of genomic difference) between first and last lesions of different patients experiencing multiple recurrences of melanoma. A standard t-test is applied to test whether late lesions are less different from each other than earlier ones, that is, if there is convergent evolution among individual cases of metastatic melanoma. Panels c) and d) analyze the question if subsequent recurrent recurrences (any n^{th} and $n+1^{th}$ lesion) would be more and more distant (~different) from the first diagnosed metastasis, implying incremental changes and thus sequential evolution of subsequent metastases.

Figure 5

Follow-up analysis of the stability of homozygous deletions in evolving recurrent metastatic melanomas

Panel a) displays a histogram of the calculated DNA copy number values associated with every identified chromosome segment in the analyzed melanoma sample set. A blue circle marks segments accepted as homozygous deletions (-/-) considering the accuracy and statistical fidelity limits set for chromosomal segmentation. Panel b) displays the fate of these completely deleted segments in eight patients (A, B, etc.), experiencing several melanoma recurrences in a sequence (A/1, A/2, B/1, B/2, etc.), some of which are multiple synchronous recurrences (A/2a, A/2b, etc.). Yellow frames indicate selected chromosomal regions that, although completely lost at one time point of disease history (-/- = blue), months or years later re-emerged in a recurrence of the same case of cancer (-/+ = grey or +/+ = red).

Supplementary Material

Supplementary Tables (S1-S4) and Figures (S1-S4) have been submitted.

Figure 1

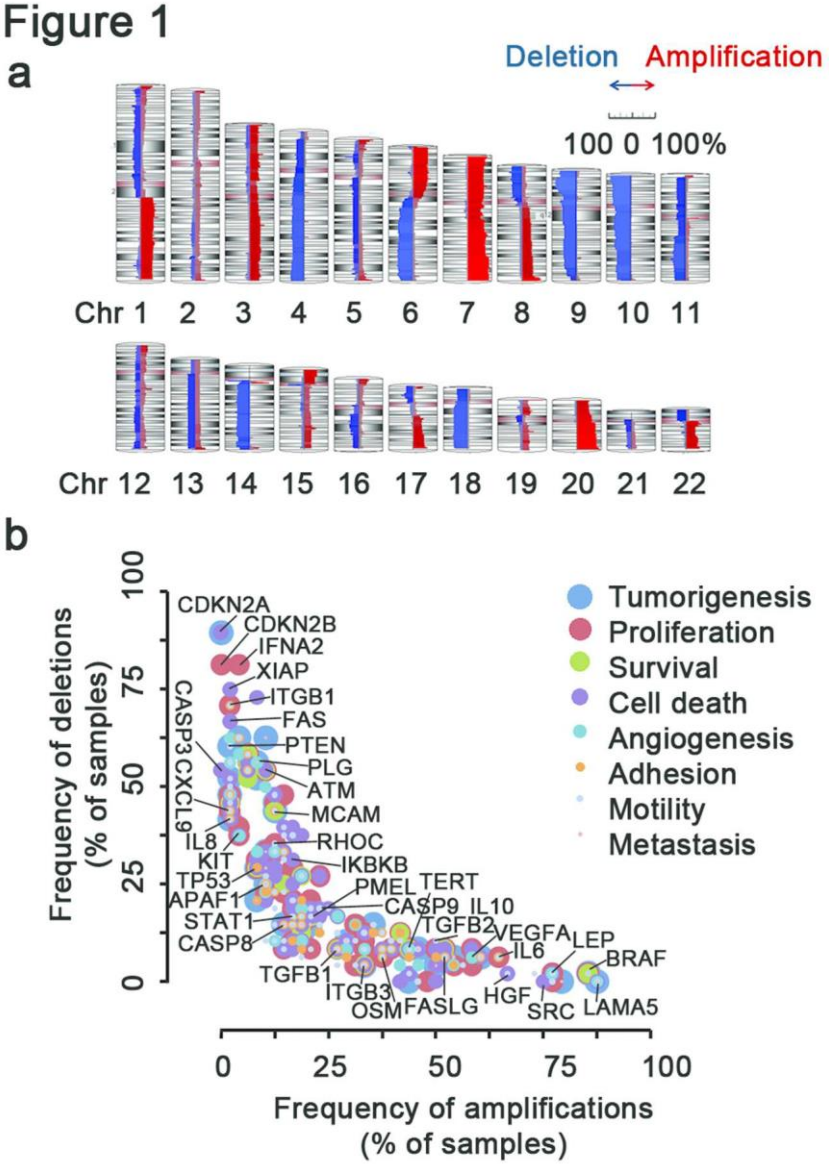

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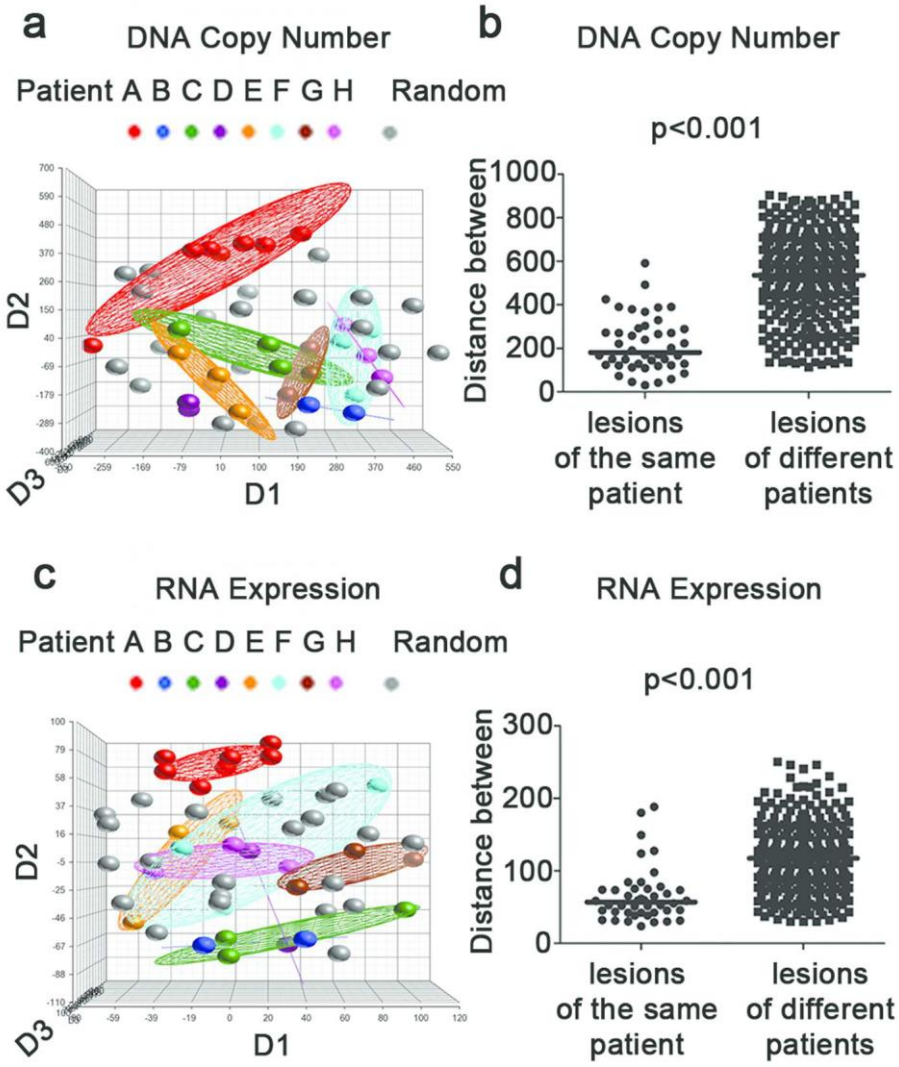
Figure 2



87x114mm (300 x 300 DPI)

Figure 3

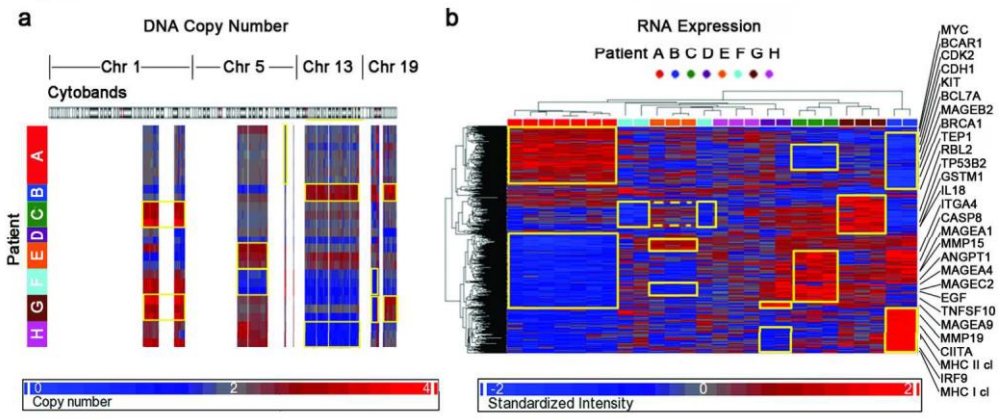


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Figure 4

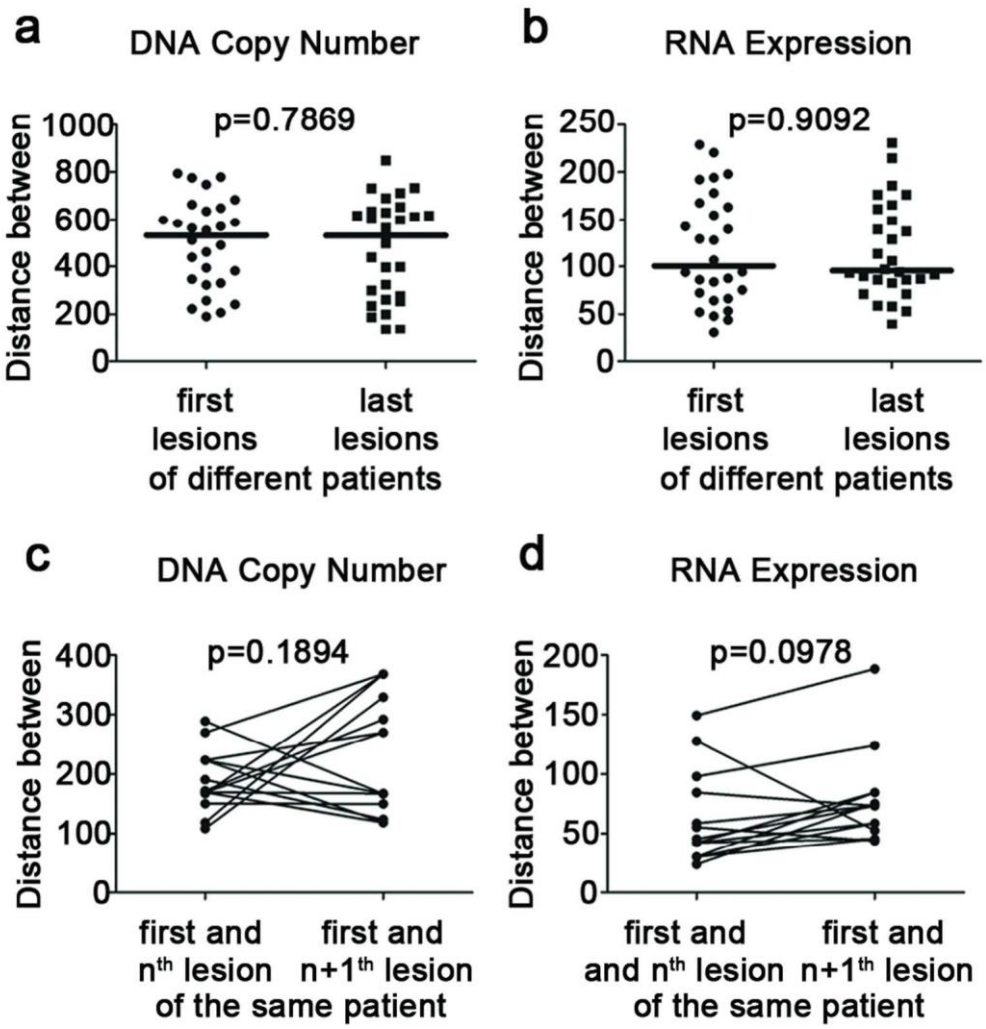

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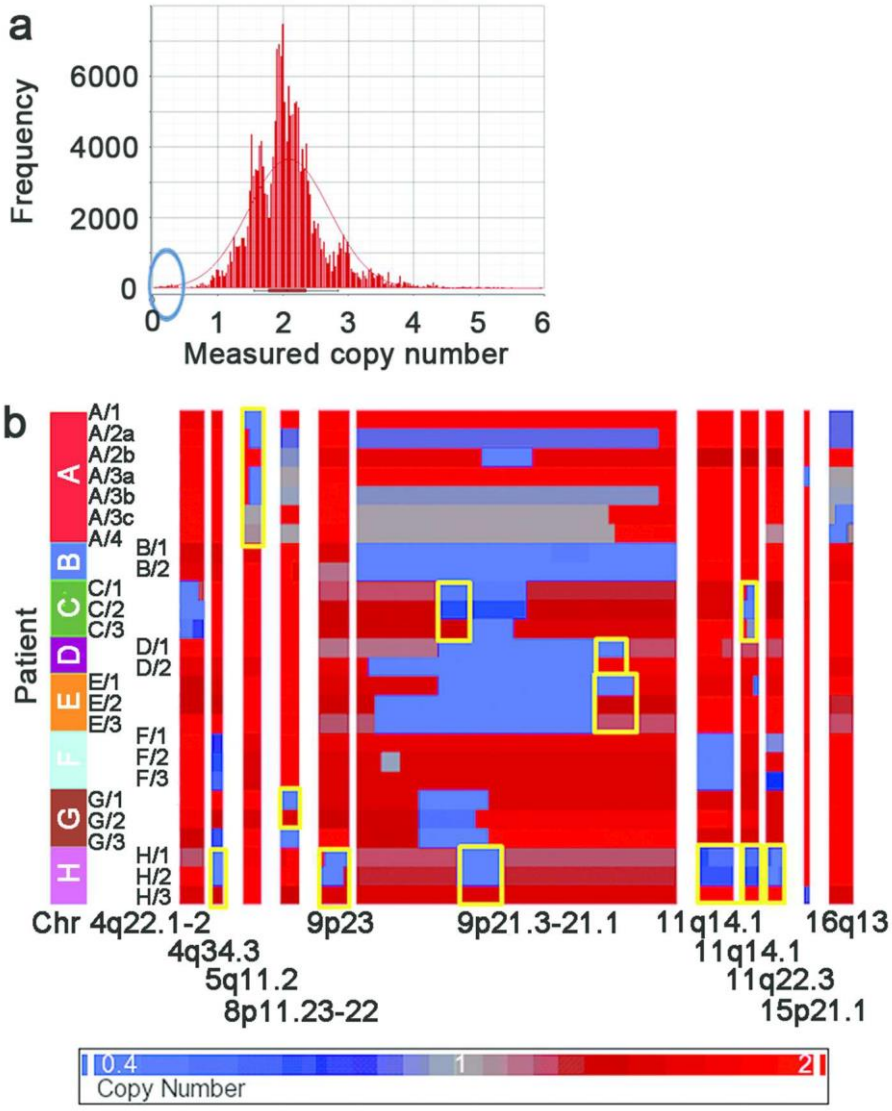
Figure 5



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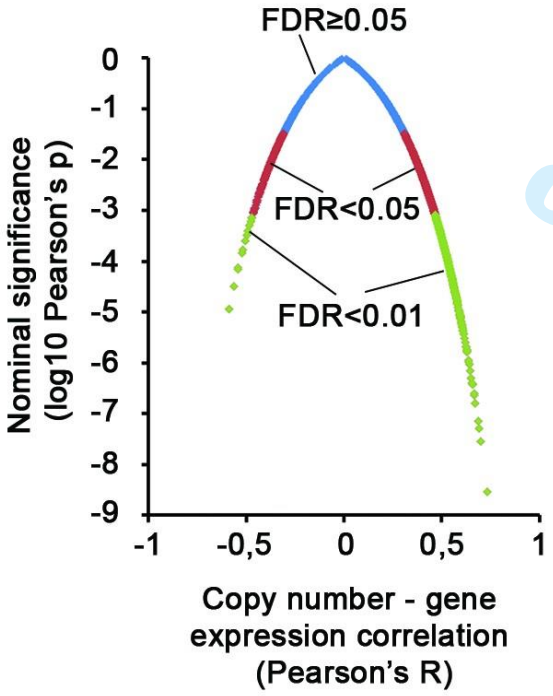

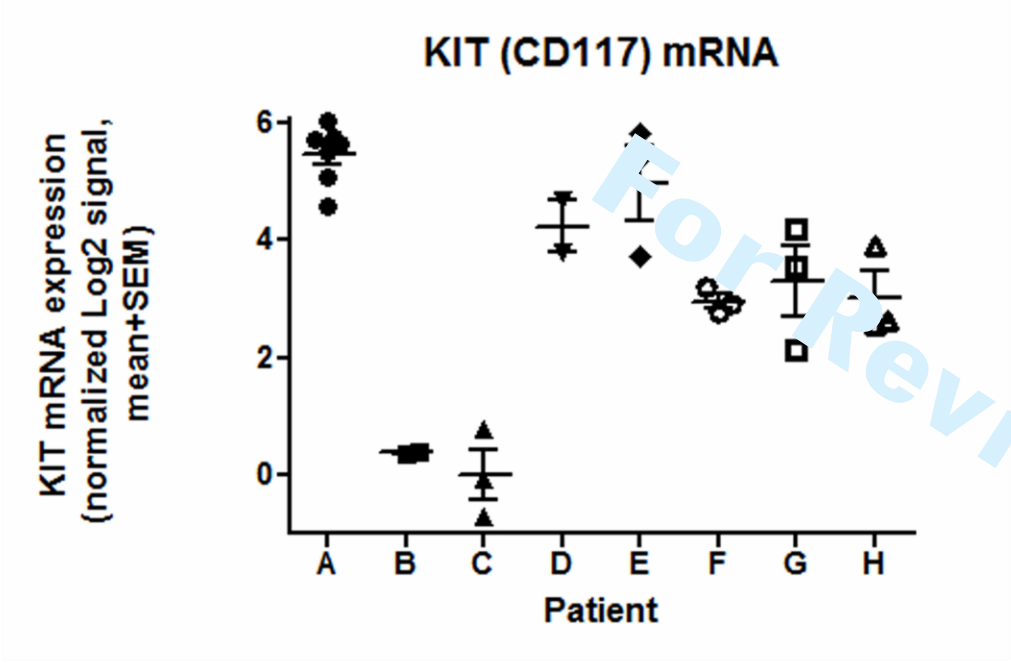

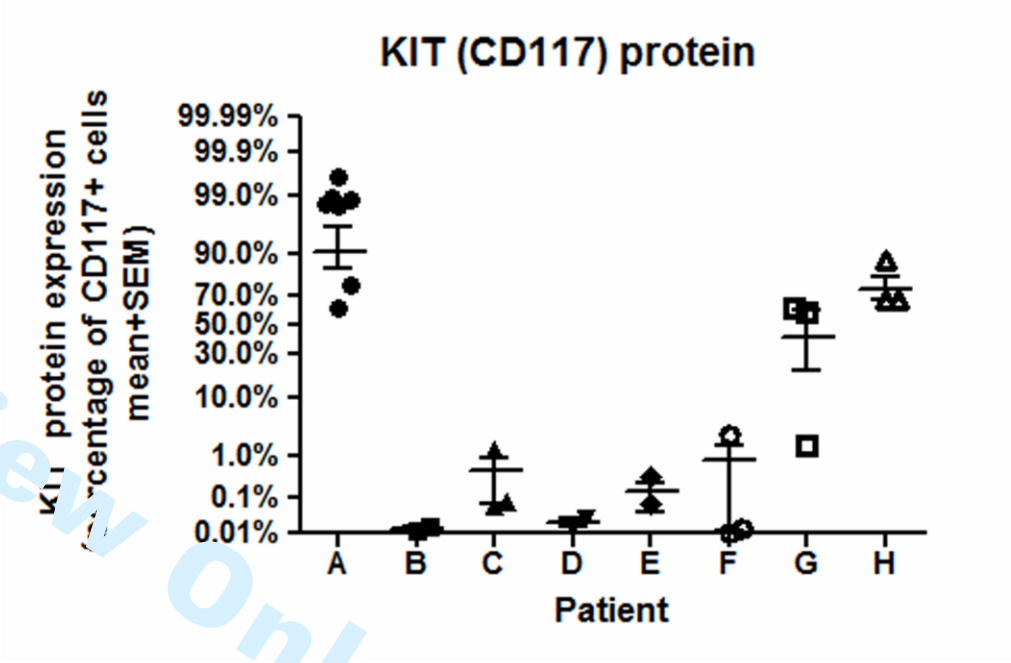

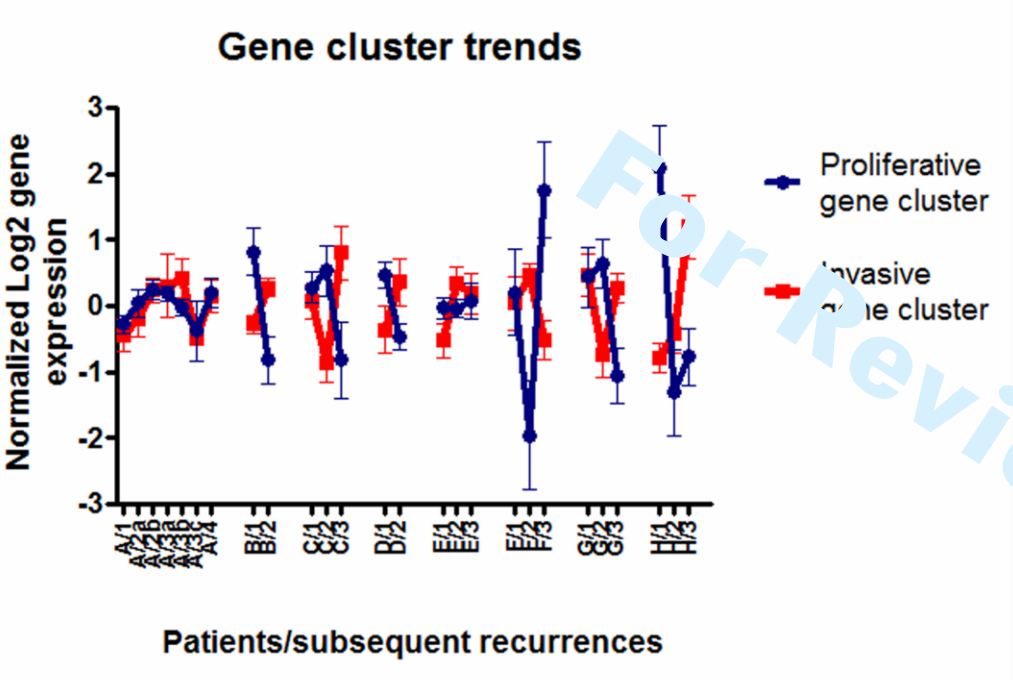

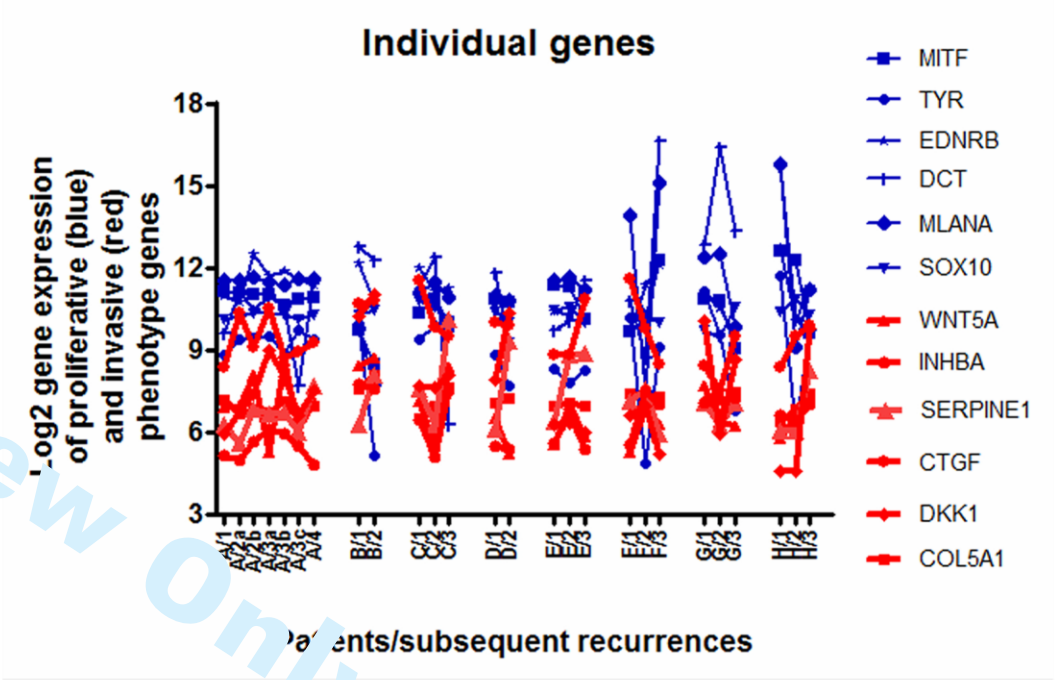

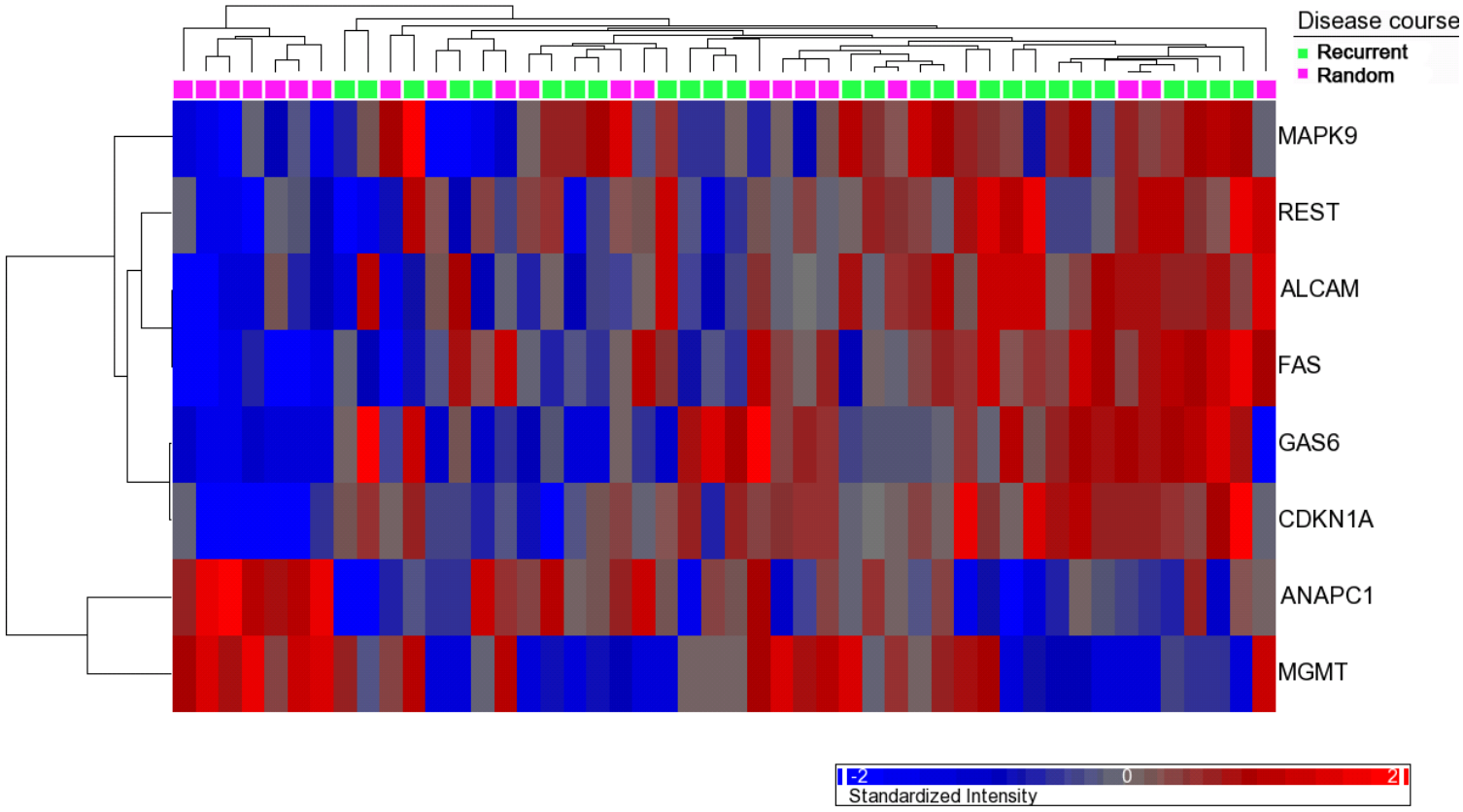
Disease course
Recurrent
Random
MAPK9
REST
ALCAM
FAS
GAS6
CDKN1A
ANAPC1
MGMT
-2
0
2
Standardized Intensity

GEO Microarray ID	Disease course	Patient ID	Lesion ID	Date of Primary	Site of primary	Applied therapy	Date of metastasis	Site of metastasis	Local vs. Distant	Date of death	Gender	Origin
1	Recurrent	A	A/1	12/15/1998	cutaneous, right arm	TIL CELLS/IL2 HD, RADIATION (5000cGy, 3000cGy) DTIC/CDDP	6/21/1989	subcutaneous, soft palate	Distant	8/5/2002	F	Surgery Branch, NIH, Bethesda, USA
2	Recurrent	A	A/2a				6/10/1992	uterine metastasis	Distant	8/5/2002	F	Surgery Branch, NIH, Bethesda, USA
3	Recurrent	A	A/2b				6/10/1992	uterine metastasis	Distant	8/5/2002	F	Surgery Branch, NIH, Bethesda, USA
4	Recurrent	A	A/3a				9/30/2000	subcutaneous, R flank	Distant	8/5/2002	F	Surgery Branch, NIH, Bethesda, USA
5	Recurrent	A	A/3b				9/30/2000	subcutaneous, R flank	Distant	8/5/2002	F	Surgery Branch, NIH, Bethesda, USA
6	Recurrent	A	A/3c				9/30/2000	subcutaneous, R flank	Distant	8/5/2002	F	Surgery Branch, NIH, Bethesda, USA
7	Recurrent	A	A/4				8/28/2001	subcutaneous, R breast	Distant	8/5/2002	F	Surgery Branch, NIH, Bethesda, USA
8	Recurrent	B	B/1	5/28/1985	cutaneous, left foot	SURGERY, DTIC, IL2	9/13/1999	abdominal subcutis	Distant	11/26/2000	F	CRO, Aviano, Italy
9	Recurrent	B	B/2				7/26/2000	cutis of the leg	Local	11/26/2000	F	CRO, Aviano, Italy
10	Recurrent	C	C/1	8/12/1991	cutaneous, right leg	SURGERY, anti-idiotype/IL-2	7/12/1993	in transit cutis/subcutis of the leg	Local	2/1/1995	F	CRO, Aviano, Italy
11	Recurrent	C	C/2				3/23/1994	inguinal lymph nodes	Local	2/1/1995	F	CRO, Aviano, Italy
12	Recurrent	C	C/3				1/17/1995	cutis/subcutis of the arm	Distant	2/1/1995	F	CRO, Aviano, Italy
13	Recurrent	D	D/1	9/28/1990	cutaneous, right arm	SURGERY, DTIC	5/15/1994	axillary lymph nodes	Local	9/3/1998	M	CRO, Aviano, Italy
14	Recurrent	D	D/2				12/23/1997	pancreas	Distant	9/3/1998	M	CRO, Aviano, Italy
15	Recurrent	E	E/1	9/6/1994	cutaneo[illegible] leg	SURGERY, DTIC	8/30/1996	inguinal lymph nodes	Local	6/30/2004	M	CRO, Aviano, Italy
16	Recurrent	E	E/2				6/19/1998	subcutis of the leg	Local	6/30/2004	M	CRO, Aviano, Italy
17	Recurrent	E	E/3				4/20/1999	cutis/subcutis of the leg	Local	6/30/2004	M	CRO, Aviano, Italy
18	Recurrent	F	F/1	10/9/1995	cutaneous, left [illegible]	GP100/MART-1 VACC, TYROS/GP100 VACC,IL2 HD, DTIC/CDDP, CYTOXAN/FLUDARABINE/TIL CELLS/IL2 HD, RADIATION, GAMMA KNIFE	7/7/1999	chest wall (subcutaneous)	Distant	4/25/2004	M	Surgery Branch, NIH, Bethesda, USA
19	Recurrent	F	F/2				6/21/2001	axilla	Distant	4/25/2004	M	Surgery Branch, NIH, Bethesda, USA
20	Recurrent	F	F/3				3/6/2003	thigh (soft tissue - muscle)	Distant	4/25/2004	M	Surgery Branch, NIH, Bethesda, USA
21	Recurrent	G	G/1	8/19/1997	cutaneous, right calf	IF[illegible] MELPHALAN WITH ILP, DTIC/CISPLATIN/VELBAN/IL-[illegible]NA, gpGP100 [illegible]ACC, IL2, CYTOXAN/FLUDARABINE/TIL CELLS/MA[illegible]ACC/IL2 HD, VEMURAFENIB	6/26/2001	pelvis	Distant	Alive	M	Surgery Branch, NIH, Bethesda, USA
22	Recurrent	G	G/2				6/1/2002	thigh/buttock (subcutaneous)	Distant	Alive	M	Surgery Branch, NIH, Bethesda, USA
23	Recurrent	G	G/3				1/14/2003	popliteal fossa	Local	Alive	M	Surgery Branch, NIH, Bethesda, USA
24	Recurrent	H	H/1	12/9/1999	cutaneous, mid back	IFNA/GM-[illegible]GP1[illegible]VACC/ MART-1 VACC /GCSF, CYTOXAN/FL[illegible]R[illegible]NE / TIL CELLS/IL2 HD/MART1 VACC, [illegible]GCSF[illegible]/CDDP	1/21/2002	back (subcutaneous)	Local	10/4/2004	M	Surgery Branch, NIH, Bethesda, USA
25	Recurrent	H	H/2				7/14/2003	shoulder (soft tissue - muscle)	Distant	10/4/2004	M	Surgery Branch, NIH, Bethesda, USA
26	Recurrent	H	H/3				3/31/2004	axilla	Distant	10/4/2004	M	Surgery Branch, NIH, Bethesda, USA
27	Random	1	1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
28	Random	2	2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
29	Random	3	3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
30	Random	4	4	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
31	Random	5	5	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
32	Random	6	6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
33	Random	7	7	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
34	Random	8	8	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
35	Random	9	9	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
36	Random	10	10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
37	Random	11	11	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
38	Random	12	12	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
39	Random	13	13	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
40	Random	14	14	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
41	Random	15	15	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
42	Random	16	16	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
43	Random	17	17	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
44	Random	18	18	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
45	Random	19	19	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
46	Random	20	20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
47	Random	21	21	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA
48	Random	22	22	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Surgery Branch, NIH, Bethesda, USA

HUGO Gene Symbol	% of samples with deletions	% samples with amplifications	Entrez Gene Name	Location	Type(s)	Drug(s)	Tumorigenesis	Proliferation, Cell Cycle	Survival	Cell death, Apoptosis	Angiogenesis	Adhesion, Binding, Attachment, Detachment	Movement, Migration, Invasion	Metastasis
CDKN2A	90	0	cyclin-dependent kinase inhibitor 2A (me	Nucleus	transcription regulator		+	-	-	+	-	-	-	-
CDKN2B	81	0	cyclin-dependent kinase inhibitor 2B (p1	Nucleus	transcription regulator		-	+	-	-	-	-	-	-
IFNA2	81	4	interferon, alpha 2	Extracellular Space	cytokine		-	+	-	-	-	-	-	-
XIAP	75	2	X-linked inhibitor of apoptosis	Cytoplasm	other		-	-	-	+	-	-	-	-
SAT1	73	8	spermidine/spermine N1-acetyltransfera	Cytoplasm	enzyme		-	-	-	+	-	-	-	-
ITGB1	71	2	integrin, beta 1 (fibronectin receptor, be	Plasma Membrane	transmembrane receptor		-	+	-	-	-	+	+	-
FAS	67	2	Fas (TNF receptor superfamily, member	Plasma Membrane	transmembrane receptor		-	-	-	+	-	-	-	-
PLAU	63	2	plasminogen activator, urokinase	Extracellular Space	peptidase		-	-	-	-	+	-	-	-
CXCL12	63	4	chemokine (C-X-C motif) ligand 12	Extracellular Space	cytokine		-	-	-	-	-	+	+	-
RET	63	4	ret proto-oncogene	Plasma Membrane	kinase	sunitinib	+	-	-	-	-	-	-	-
CD274	63	10	CD274 molecule	Plasma Membrane	other		+	-	-	-	-	-	-	+
PTEN	60	2	phosphatase and tensin homolog	Cytoplasm	phosphatase		+	-	-	-	-	-	+	-
MAPK8	58	4	mitogen-activated protein kinase 8	Cytoplasm	kinase	aplidine	-	-	-	-	+	-	-	-
FLNA	58	6	filamin A, alpha	Cytoplasm	other		-	-	+	-	-	-	+	-
L1CAM	58	6	L1 cell adhesion molecule	Plasma Membrane	other		-	-	-	-	-	+	+	-
POU3F2	58	6	POU class 3 homeobox 2	Nucleus	transcription regulator		-	+	-	-	-	-	-	-
SMPD2	58	6	sphingomyelin phosphodiesterase 2, neu	Cytoplasm	enzyme		-	-	-	-	-	+	-	-
DNMBP	56	2	dynamin binding protein	Cytoplasm	other		-	-	-	-	-	-	+	-
FGF8	56	2	fibroblast growth factor 8 (androgen-indu	Extracellular Space	growth factor		-	-	-	-	+	-	-	-
MGMT	56	6	O-6-methylguanine-DNA methyltransfera	Nucleus	enzyme	O6-benzylg	-	-	+	-	-	-	-	-
PMAIP1	56	6	phorbol-12-myristate-13-acetate-ind	Cytoplasm	other		-	-	-	+	-	-	-	-
SMAD4	56	6	SMAD family member 4	Nucleus	transcription regulator		-	+	-	-	-	-	-	-
PLG	56	8	plasminogen	Extracellular Space	peptidase	tenecteplа	+	-	-	-	+	-	-	+
CASP3	54	0	caspase 3, apoptosis-re	Cytoplasm	peptidase	IDN-6556	-	-	-	+	-	-	-	-
BCL2	54	6	B-cell CLL/lymphoma 2		other	oblimersen	-	-	+	+	-	-	-	-
CDH2	54	6	cadherin 2, type 1, N-cadherin (neuro	Plasma Membrane	other		-	-	-	-	-	+	-	-
SMAD7	54	6	SMAD family member 7	Nucleus	transcription regulator		-	-	-	-	-	-	+	-
ATM	54	10	ataxia telangiectasia mutated		kinase		-	+	+	+	-	-	-	-
CTSL1	52	2	cathepsin L1	Cytoplasm	peptidase		+	-	-	-	-	-	+	-
GADD45G	52	2	growth arrest and DNA-damage-inducibl	Nucleus	other		-	-	-	+	-	-	-	-
S1PR3	52	2	sphingosine-1-phosphate receptor 3	Plasma Membrane	G-prote	ceptor	fingolimod	-	-	-	-	-	+	-
BAG1	52	6	BCL2-associated athanogene	Cytoplasm	other		-	-	+	-	-	-	-	-
AKIRIN2	52	8	akirin 2	Nucleus	oth		+	-	-	-	-	-	-	-
LTBP2	50	2	latent transforming growth factor beta bi	Extracellular Space	other		-	-	-	-	-	-	+	-
CRYAB	50	10	crystallin, alpha B	Nucleus	other		-	-	-	-	+	-	-	-
IL18	50	10	interleukin 18 (interferon-gamma-inducin	Extracellular Space	cytokine		-	-	-	-	+	-	-	-
BMP4	48	2	bone morphogenetic protein 4	Extracellular Space	growth factor		-	-	-	-	-	-	+	-
FGF2	48	2	fibroblast growth factor 2 (basic)	Extracellular Space	growth factor	26644	+	-	-	+	-	-	-	-
IL2	48	2	interleukin 2	Extracellular Space	cytokine		-	-	-	-	+	-	-	-
PRKACG	48	2	protein kinase, cAMP-dependent, catalyt	Cytoplasm	kinase		-	+	-	-	-	-	-	-
SPP1	48	2	secreted phosphoprotein 1	Extracellular Space	cytokine		+	-	-	+	-	+	+	-
TNC	48	2	tenascin C	Extracellular Space	other		+	-	-	-	-	-	-	-
BIRC2	48	13	baculoviral IAP repeat containing 2	Cytoplasm	other		-	-	-	+	-	-	-	-
CASP4	48	13	caspase 4, apoptosis-related cysteine pe	Cytoplasm	peptidase		-	-	-	+	-	-	-	-
ZBTB16	48	13	zinc finger and BTB domain containing 16	Nucleus	transcription regulator		-	-	-	-	-	-	+	-
TFE3	48	15	transcription factor binding to IGHM enh	Nucleus	transcription regulator		-	-	-	-	-	-	-	-
AIMP1	46	2	aminoacyl tRNA synthetase complex-inte	Extracellular Space	cytokine		-	-	+	-	-	-	-	-
ARHGAP5	46	2	Rho GTPase activating protein 5	Cytoplasm	enzyme		-	-	-	-	-	-	+	-
GSN	46	2	gelsolin	Extracellular Space	other		-	-	-	-	-	-	+	-
GZMB	46	2	granzyme B (granzyme 2, cytotoxic T-lym	Cytoplasm	peptidase		-	-	-	+	-	-	-	-
RAPGEF2	46	2	Rap guanine nucleotide exchange factor (	Cytoplasm	other		-	+	-	+	-	-	-	-
NOX4	46	13	NADPH oxidase 4	Cytoplasm	enzyme		+	+	-	-	-	-	-	-
CXCL1	44	2	chemokine (C-X-C motif) ligand 1 (melan	Extracellular Space	cytokine		-	+	-	-	-	-	-	-
CXCL9	44	2	chemokine (C-X-C motif) ligand 9	Extracellular Space	cytokine		-	-	-	-	-	+	+	-
HSPA5	44	2	heat shock 70kDa protein 5 (glucose-reg	Cytoplasm	other		-	-	-	+	-	-	-	-
MCAM	44	13	melanoma cell adhesion molecule	Plasma Membrane	other		+	-	+	-	-	+	+	-
IL8	42	2	interleukin 8	Extracellular Space	cytokine		+	-	-	-	-	-	+	-
MMP14	42	2	matrix metallopeptidase 14 (membrane-i	Extracellular Space	peptidase		-	-	-	-	-	-	+	-
STATH	42	2	statherin	Nucleus	other		-	-	-	-	-	+	-	-
SPTAN1	40	4	spectrin, alpha, non-erythrocytic 1 (alpha	Plasma Membrane	other		-	+	-	-	-	-	-	-
CTSB	40	15	cathepsin B	Cytoplasm	peptidase		-	-	-	+	-	-	+	-
PBK	40	17	PDZ binding kinase	Cytoplasm	kinase		-	-	-	+	-	-	-	-
KDR	38	4	kinase insert domain receptor (a type III r	Plasma Membrane	kinase	AEE 788, s	-	-	-	-	+	-	-	-
KIT	38	4	v-kit Hardy-Zuckerman 4 feline sarcoma v	Plasma Membrane	kinase	dasatinib,	-	+	-	-	-	-	-	-
REST	38	4	RE1-silencing transcription factor	Nucleus	transcription regulator		-	-	-	+	-	-	-	-
NRG1	38	15	neuregulin 1	Extracellular Space	growth factor		-	-	-	-	-	-	+	-
PACS2	38	17	phosphofurin acidic cluster sorting protei	Cytoplasm	other		-	-	-	+	-	-	-	-
PTK2B	38	17	PTK2B protein tyrosine kinase 2 beta	Cytoplasm	kinase		-	-	-	-	-	-	+	-
TNFRSF10B	38	19	tumor necrosis factor receptor superfam	Plasma Membrane	transmembrane receptor	tigatuzuma	-	-	-	+	-	-	-	-
TNFRSF10C	38	19	tumor necrosis factor receptor superfam	Plasma Membrane	transmembrane receptor		-	-	-	+	-	-	-	-
TNFRSF10D	38	19	tumor necrosis factor receptor superfam	Plasma Membrane	transmembrane receptor		-	-	-	+	-	-	-	-
RHOC	35	13	ras homolog gene family, member C	Plasma Membrane	enzyme		-	-	-	-	-	-	+	-
TRIM33	35	13	tripartite motif containing 33	Nucleus	transcription regulator		-	+	-	-	-	-	-	-
HTATIP2	33	8	HIV-1 Tat interactive protein 2, 30kDa	Nucleus	transcription regulator		-	-	-	-	+	-	-	-
CSRP3	33	10	cysteine and glycine-rich protein 3 (cardia	Nucleus	other		+	-	-	-	-	-	-	+
TEAD1	33	10	TEA domain family member 1 (SV40 trans	Nucleus	transcription regulator		-	+	-	+	-	-	-	-
CYLD	33	13	cylindromatosis (turban tumor syndrome	Nucleus	transcription regulator		-	+	-	-	-	-	-	-
MMP2	33	13	matrix metallopeptidase 2 (gelatinase A,	Extracellular Space	peptidase		-	-	-	-	+	-	+	-
NOL3	33	13	nucleolar protein 3 (apoptosis repressor	Nucleus	other		-	-	-	+	-	-	-	-
CDH1	33	15	cadherin 1, type 1, E-cadherin (epithelial	Plasma Membrane	other		-	-	-	+	-	+	+	-
CAT	31	8	catalase	Cytoplasm	enzyme		-	+	-	-	-	-	-	-
WT1	31	8	Wilms tumor 1	Nucleus	transcription regulator		-	-	-	+	-	-	-	-
NGF	31	15	nerve growth factor (beta polypeptide)	Extracellular Space	growth factor		-	-	-	-	-	-	+	-
IKBKB	31	17	inhibitor of kappa light polypeptide gene	Cytoplasm	kinase		-	-	-	+	-	-	-	-
CD44	29	8	CD44 molecule (Indian blood group)	Plasma Membrane	other		-	+	-	-	-	+	-	-

HUGO Gene Symbol	% of samples with deletions	% samples with amplifications	Entrez Gene Name	Location	Type(s)	Drug(s)	Tumorigenesis	Proliferation, Cell Cycle	Survival	Cell death, Apoptosis	Angiogenesis	Adhesion, Binding, Attachment, Detachment	Movement, Migration, Invasion	Metastasis
TP53	29	8	tumor protein p53	Nucleus	transcription regulator		+	-	+	+	-	-	-	-
F3	29	10	coagulation factor III (thromboplastin, tis	Plasma Membrane	transmembrane receptor		+	-	-	-	-	-	-	+
XAF1	29	10	XIAP associated factor 1	Nucleus	other		-	-	-	+	-	-	-	-
JUN	29	13	jun proto-oncogene	Nucleus	transcription regulator		-	-	-	+	-	-	-	-
ARRB1	29	17	arrestin, beta 1	Cytoplasm	other		-	+	-	-	-	-	-	-
VCAM1	27	10	vascular cell adhesion molecule 1	Plasma Membrane	other		-	-	-	-	-	-	+	-
GADD45A	27	13	growth arrest and DNA-damage-inducibl	Nucleus	other		-	-	-	+	-	-	-	-
JAK1	27	13	Janus kinase 1	Cytoplasm	kinase		-	+	-	-	-	-	-	-
CCND1	27	15	cyclin D1	Nucleus	other		-	+	-	-	-	-	-	-
CAPN1	27	19	calpain 1, (mu/I) large subunit	Cytoplasm	peptidase		-	-	-	-	-	-	+	-
FLT1	27	19	fms-related tyrosine kinase 1 (vascular en	Plasma Membrane	kinase	sunitinib,	-	-	-	-	+	-	-	-
HDAC1	27	19	histone deacetylase 1	Nucleus	transcription regulator	tributyrin,	-	-	-	+	-	-	-	-
RBBP4	27	19	retinoblastoma binding protein 4	Nucleus	enzyme		-	-	+	-	-	-	-	-
DCT	27	23	dopachrome tautomerase (dopachrome	Cytoplasm	enzyme		-	-	-	+	-	-	-	-
ING1	27	23	inhibitor of growth family, member 1	Nucleus	transcription regulator		-	+	-	-	-	-	-	-
APAF1	25	10	apoptotic peptidase activating factor 1	Cytoplasm	other		-	-	-	+	-	-	-	-
ITGA1	25	10	integrin, alpha 1	Plasma Membrane	other		-	-	-	-	+	-	-	-
ITGA2	25	10	integrin, alpha 2 (CD49B, alpha 2 subunit	Plasma Membrane	other		+	-	-	-	-	+	+	+
BANP	25	13	BTG3 associated nuclear protein	Nucleus	other		-	+	-	-	-	-	-	-
RPS6KA1	25	15	ribosomal protein S6 kinase, 90kDa, poly	Cytoplasm	kinase		-	-	+	-	-	-	-	-
YBX1	25	17	Y box binding protein 1	Nucleus	transcription regulator		-	-	-	+	-	-	-	-
MAPK7	23	10	mitogen-activated protein ki	Cytoplasm	kinase		-	-	-	-	+	-	-	-
VCAN	23	10	versican	Extracellular Space	other		-	+	-	-	-	+	-	-
BCAR1	23	13	breast cancer anti-estro	Plasma Membrane	other		-	-	-	-	-	-	+	-
EFNA5	23	13	ephrin-A5	Membrane	kinase		-	-	-	-	-	+	-	-
CSF2	23	15	colony stimulating factor 2 (granulocy	Extra ular Space	cytokine		-	+	-	-	-	-	-	-
WASF2	23	15	WAS protein family, member 2	Cyt n	other		-	-	-	-	-	-	+	-
F2R	21	8	coagulation factor II (thrombin) receptor	Me	G-protein coupled receptor	chrysalin,	-	-	-	-	-	+	-	-
F2R	21	8	coagulation factor II (thrombin) receptor	Plasma M ane	G-protein c pled receptor	chrysalin,	+	-	-	-	-	-	-	+
PAWR	21	10	PRKC, apoptosis, WT1, regulator	Nucleus	transcript ator		-	-	-	+	-	-	-	-
CSNK1A1	21	17	casein kinase 1, alpha 1	Cytoplasm	kinase		-	+	-	+	-	-	-	-
SPARC	21	17	secreted protein, acidic, cysteine-rich (os	Extracellular Space	other		-	-	-	-	-	-	+	-
SCARB1	21	19	scavenger receptor class B, member 1	Plasma Membrane	tra er		-	-	-	-	-	+	-	-
CASC1	21	21	cancer susceptibility candidate 1	Cytoplasm	other		-	+	-	-	-	-	-	-
RAPGEF3	19	13	Rap guanine nucleotide exchange factor (	Nucleus	other		-	-	-	-	-	-	+	-
ATF1	19	17	activating transcription factor 1	Nucleus	transcription regul		-	-	-	+	-	-	-	-
EGR1	19	17	early growth response 1	Nucleus	transcription regulat		-	+	-	+	-	-	-	-
PHLDA1	19	17	pleckstrin homology-like domain, family	Cytoplasm	other		-	-	-	+	-	-	-	-
IFNG	19	19	interferon, gamma	Extracellular Space	cytokine		-	+	-	+	+	-	-	-
HSPB8	19	21	heat shock 22kDa protein 8	Cytoplasm	kinase		-	-	-	+	-	-	-	-
PXN	19	21	paxillin	Cytoplasm	other		-	-	-	-	-	-	+	-
CASP9	19	23	caspase 9, apoptosis-related cysteine pe	Cytoplasm	peptidase		-	-	-	+	-	-	-	-
DIABLO	19	23	diablo, IAP-binding mitochondrial protein	Cytoplasm	other		-	-	-	+	-	-	-	-
PEBP1	19	23	phosphatidylethanolamine binding prote	Cytoplasm	other		-	-	-	+	-	-	-	-
PEBP1	19	23	phosphatidylethanolamine binding prote	Cytoplasm	other		-	-	-	-	-	-	+	-
RAP1GAP	19	23	RAP1 GTPase activating protein	Cytoplasm	other		-	-	-	-	-	-	+	-
CDKN1B	19	25	cyclin-dependent kinase inhibitor 1B (p2	Nucleus	other		-	-	-	+	-	-	+	-
MX1	17	17	myxovirus (influenza virus) resistance 1, i	Nucleus	enzyme		-	-	-	-	-	-	+	-
STAT1	17	17	signal transducer and activator of transc	Nucleus	transcription regulator		+	-	-	-	-	-	-	-
ITGA5	17	19	integrin, alpha 5 (fibronectin receptor, al	Plasma Membrane	other		-	-	-	-	-	+	+	-
COL4A3	17	21	collagen, type IV, alpha 3 (Goodpasture a	Extracellular Space	other	collagenas	-	+	-	-	-	-	+	-
GSTM1	17	21	glutathione S-transferase mu 1	Cytoplasm	enzyme		+	+	-	+	-	-	-	-
PMEL	17	21	premelanosome protein	Plasma Membrane	enzyme		-	+	-	-	-	-	-	-
BCL2L10	17	23	BCL2-like 10 (apoptosis facilitator)	Cytoplasm	other		-	-	-	-	-	-	-	-
PAX3	17	23	paired box 3	Nucleus	transcription regulator		-	-	-	+	-	-	-	-
B4GALNT1	17	27	beta-1,4-N-acetyl-galactosaminyl transfe	Cytoplasm	enzyme		-	-	-	-	+	-	-	-
DDIT3	17	27	DNA-damage-inducible transcript 3	Nucleus	transcription regulator		-	-	-	-	-	-	-	-
CTBP1	15	13	C-terminal binding protein 1	Nucleus	enzyme		-	-	-	-	-	-	+	-
CASP8	15	15	caspase 8, apoptosis-related cysteine pe	Nucleus	peptidase		-	-	-	+	-	-	-	-
CFLAR	15	15	CASP8 and FADD-like apoptosis regulator	Cytoplasm	other		-	-	-	+	-	-	-	-
FN1	15	15	fibronectin 1	Plasma Membrane	enzyme		+	-	-	-	-	+	+	+
ITGA4	15	17	integrin, alpha 4 (antigen CD49D, alpha 4	Plasma Membrane	other	natalizuma	-	-	-	-	-	+	+	-
PLCL1	15	17	phospholipase C-like 1	Cytoplasm	enzyme		-	-	-	-	-	-	+	-
ATF2	15	19	activating transcription factor 2	Nucleus	transcription regulator		+	+	+	+	-	-	-	+
ITGA6	15	19	integrin, alpha 6	Plasma Membrane	other		-	-	-	-	-	+	-	-
ITGAV	15	19	integrin, alpha V (vitronectin receptor, al	Plasma Membrane	other	abciximab	+	-	+	+	-	+	+	+
COL18A1	15	21	collagen, type XVIII, alpha 1	Extracellular Space	other	collagenas	+	-	-	-	-	-	-	+
SHC4	15	23	SHC (Src homology 2 domain containing)	Cytoplasm	other		-	-	-	-	-	-	+	-
LTBR	15	31	lymphotoxin beta receptor (TNFR superf	Plasma Membrane	transmembrane receptor		-	-	-	-	+	-	-	-
PPARG	15	31	peroxisome proliferator-activated recept	Nucleus	ligand-dependent nuclear receptor	pioglitazon	-	+	-	-	-	-	-	-
RAF1	15	31	v-raf-1 murine leukemia viral oncogene h	Cytoplasm	kinase	sorafenib	-	+	-	-	-	-	-	-
VWF	15	31	von Willebrand factor	Extracellular Space	other		-	-	-	-	-	+	-	-
WNT5A	15	35	wingless-type MMTV integration site fam	Extracellular Space	cytokine		+	-	-	-	-	-	+	-
DPP4	13	19	dipeptidyl-peptidase 4	Plasma Membrane	peptidase	saxagliptin	+	-	+	-	-	-	-	-
THBS1	13	23	thrombospondin 1	Extracellular Space	other		-	-	-	-	-	+	-	-
ADAM10	13	27	ADAM metallopeptidase domain 10	Plasma Membrane	peptidase		-	-	-	-	-	-	+	-
FLNB	13	33	filamin B, beta	Cytoplasm	other		-	-	-	+	-	-	-	-
SKI	13	33	v-ski sarcoma viral oncogene homolog (av	Nucleus	transcription regulator		-	+	-	-	-	-	+	-
LTF	13	35	lactotransferrin	Extracellular Space	peptidase		-	-	-	-	-	+	-	-
ITPR1	13	38	inositol 1,4,5-triphosphate receptor, type	Cytoplasm	ion channel		-	-	-	-	-	-	+	-
RPSA	13	38	ribosomal protein SA	Cytoplasm	translation regulator		-	-	-	-	-	+	+	-
GAS6	13	42	growth arrest-specific 6	Extracellular Space	growth factor		-	+	+	-	-	-	-	-
ITGA9	13	42	integrin, alpha 9	Plasma Membrane	other		-	-	-	-	-	+	-	-
VTN	10	10	vitronectin	Extracellular Space	other		-	-	-	-	-	-	+	-
CCR7	10	13	chemokine (C-C motif) receptor 7	Plasma Membrane	G-protein coupled receptor		-	-	-	-	-	-	+	-

HUGO Gene Symbol	% of samples with deletions	% samples with amplifications	Entrez Gene Name	Location	Type(s)	Drug(s)	Tumorigenesis	Proliferation, Cell Cycle	Survival	Cell death, Apoptosis	Angiogenesis	Adhesion, Binding, Attachment, Detachment	Movement, Migration, Invasion	Metastasis
ERBB2	10	13	v-erb-b2 erythroblastic leukemia viral on	Plasma Membrane	kinase	trastuzum	-	-	-	-	+	-	-	-
CXCR4	10	15	chemokine (C-X-C motif) receptor 4	Plasma Membrane	G-protein coupled receptor	plerixafor	-	-	-	-	-	-	+	-
ICOS	10	17	inducible T-cell co-stimulator	Plasma Membrane	other		-	-	-	-	-	+	-	-
IL1A	10	17	interleukin 1, alpha	Extracellular Space	cytokine	IL-1 trap	-	+	-	+	-	-	-	-
IL1B	10	17	interleukin 1, beta	Extracellular Space	cytokine	IL-1 trap, c	-	+	-	-	-	-	-	-
IL1RN	10	17	interleukin 1 receptor antagonist	Extracellular Space	cytokine		+	+	-	-	-	-	-	-
KIDINS220	10	19	kinase D-interacting substrate, 220kDa	Nucleus	transcription regulator		-	+	-	+	-	-	-	-
RRM2	10	19	ribonucleotide reductase M2	Nucleus	enzyme	gemcitabi	-	-	-	-	+	-	-	-
CNN1	10	29	calponin 1, basic, smooth muscle	Cytoplasm	other		+	-	-	-	-	-	+	+
EPOR	10	29	erythropoietin receptor	Plasma Membrane	transmembrane receptor	darbepoet	-	-	-	+	-	-	-	-
IGF1R	10	29	insulin-like growth factor 1 receptor	Plasma Membrane	transmembrane receptor	OSI-906, c	-	-	-	+	-	-	-	-
CSPG4	10	31	chondroitin sulfate proteoglycan 4	Plasma Membrane	other		-	-	-	-	-	-	+	-
PRKACA	10	33	protein kinase, cAMP-dependent, catalyt	Cytoplasm	kinase		-	+	-	-	-	-	-	-
RHOA	10	40	ras homolog gene family, member A	Cytoplasm	enzyme		-	-	-	-	-	-	+	-
ENPP2	10	42	ectonucleotide pyrophosphatase/phosph	Plasma Membrane	enzyme		-	-	-	-	-	-	+	-
TGFB2	10	50	transforming growth factor, beta 2	Extracellular Space	growth factor	AP-12009	-	-	-	-	-	-	+	-
STAT3	8	15	signal transducer and activator of transcr	Nucleus	transcription regulator		-	+	-	+	-	-	+	-
PLK1	8	17	polo-like kinase 1	Nucleus	kinase	BI 2536	-	-	-	+	-	-	-	-
POMC	8	19	proopiomelanocortin	Extracellular Space	other		-	-	-	-	-	+	-	-
MAPK3	8	21	mitogen-activated protein kinase 3	Cytoplasm	kinase		-	+	-	-	-	-	-	-
RND3	8	21	Rho family GTPase 3	Cytoplasm	enzyme		-	-	-	-	-	-	+	-
AXL	8	27	AXL receptor tyrosine kinase	Plasma Membrane	kinase		-	+	+	-	-	-	-	-
DNASE1	8	27	deoxyribonuclease I	Extracellular Space	enzyme		-	-	-	+	-	-	-	-
MAP2K1	8	27	mitogen-activated prote se kinase 1	Cytoplasm	kinase	PD 032590	-	-	-	+	-	-	-	-
MIA	8	27	melanoma inhibitory activity	ellular Space	other		-	+	-	+	-	-	+	-
TGFB1	8	27	transforming growth factor, beta 1	Extra ular Space	growth factor		-	+	-	-	-	+	+	-
AKT1S1	8	29	AKT1 substrate 1 (proline-rich)	Cyt m	other		-	-	-	+	-	-	-	-
BAX	8	29	BCL2-associated X protein	asm	other		-	-	-	+	-	-	-	-
BBC3	8	29	BCL2 binding component 3	Cytoplasm	other		-	-	-	+	-	-	-	-
MAPK9	8	29	mitogen-activated protein kinase 9	Cytoplasm	kinase		-	-	-	-	+	-	-	-
PPP1R15A	8	29	protein phosphatase 1, regulatory (inhibi	Cytoplasm	other		-	-	-	+	-	-	-	-
SDCBP	8	33	syndecan binding protein (syntenin)	Plasma Membrane	enzyme		-	-	-	-	-	-	+	-
TP73	8	33	tumor protein p73	Nucleus	tra ic gulator		-	-	-	-	+	-	-	-
TYK2	8	33	tyrosine kinase 2	Plasma Membrane	kinase		-	+	-	-	-	-	-	-
MMP16	8	38	matrix metallopeptidase 16 (membrane-i	Extracellular Space	peptidase		-	-	-	-	-	-	+	-
MUC4	8	38	mucin 4, cell surface associated	Extracellular Space	growth factor		-	-	-	+	-	+	-	-
CHRD	8	40	chordin	Extracellular Space	other		-	-	-	-	-	-	+	-
HMOX1	8	40	heme oxygenase (decycling) 1	Cytoplasm	enzyme	esopo	-	+	-	-	-	-	-	-
KNG1	8	40	kininogen 1	Extracellular Space	other		-	-	-	-	-	+	-	-
MFI2	8	40	antigen p97 (melanoma associated) ident	Plasma Membrane	other		-	-	-	-	-	-	+	-
TNFSF10	8	40	tumor necrosis factor (ligand) superfami	Extracellular Space	cytokine		-	-	-	+	-	-	-	-
MYC	8	44	v-myc myelocytomatosis viral oncogene h	Nucleus	transcription regulator		+	+	-	+	+	-	-	-
NOV	8	44	nephroblastoma overexpressed gene	Extracellular Space	growth factor		-	-	-	-	-	-	+	-
TERT	8	44	telomerase reverse transcriptase	Nucleus	enzyme	GRN163L	+	+	+	+	-	-	-	-
PRNP	8	46	prion protein	Plasma Membrane	other		-	-	-	-	-	-	+	-
SIRPA	8	46	signal-regulatory protein alpha	Plasma Membrane	phosphatase		-	-	-	-	-	-	+	-
SMOX	8	46	spermine oxidase	Cytoplasm	enzyme		-	-	-	+	-	-	-	-
WISP1	8	46	WNT1 inducible signaling pathway protei	Extracellular Space	other		+	-	-	-	-	-	-	+
TASP1	8	50	taspase, threonine aspartase, 1	Nucleus	peptidase		-	+	-	+	-	-	-	-
IL10	8	52	interleukin 10	Extracellular Space	cytokine		-	+	+	-	-	-	-	-
IL24	8	52	interleukin 24	Extracellular Space	cytokine		-	-	-	+	-	-	-	-
CDKN1A	8	58	cyclin-dependent kinase inhibitor 1A (p2	Nucleus	other		-	+	-	+	-	-	-	-
MAPK14	8	58	mitogen-activated protein kinase 14	Cytoplasm	kinase	SCIO-469,	-	+	-	-	-	-	-	-
CHST10	6	19	carbohydrate sulfotransferase 10	Cytoplasm	enzyme		-	-	-	-	-	-	+	-
MAP4K4	6	19	mitogen-activated protein kinase kinase k	Cytoplasm	kinase		-	-	-	-	-	-	+	-
SLC4A1	6	29	solute carrier family 4, anion exchanger,	Plasma Membrane	transporter		-	-	-	-	-	+	-	-
ALCAM	6	38	activated leukocyte cell adhesion molecul	Plasma Membrane	other		-	-	-	-	-	+	-	-
CD47	6	38	CD47 molecule	Plasma Membrane	other		-	-	-	-	-	+	+	-
OSM	6	38	oncostatin M	Extracellular Space	cytokine		-	+	-	-	-	-	-	-
PTK2	6	44	PTK2 protein tyrosine kinase 2	Cytoplasm	kinase		-	-	-	-	-	+	-	-
MGAT1	6	50	mannosyl (alpha-1,3-)-glycoprotein beta-	Cytoplasm	enzyme		-	-	-	-	-	+	-	-
FASLG	6	52	Fas ligand (TNF superfamily, member 6)	Extracellular Space	cytokine		-	-	-	+	-	-	+	-
GCLC	6	52	glutamate-cysteine ligase, catalytic subun	Cytoplasm	enzyme		-	-	+	-	-	-	-	-
SELP	6	52	selectin P (granule membrane protein 14	Plasma Membrane	other		-	-	-	-	-	+	-	-
KISS1	6	54	KiSS-1 metastasis-suppressor	Cytoplasm	other		+	-	-	-	-	-	-	+
VEGFA	6	58	vascular endothelial growth factor A	Extracellular Space	growth factor	bevacizum	+	-	-	-	+	-	-	-
DEK	6	60	DEK oncogene	Nucleus	transcription regulator		-	-	-	+	-	-	-	-
EDN1	6	60	endothelin 1	Extracellular Space	other		-	-	-	-	-	-	+	-
LTA	6	60	lymphotoxin alpha (TNF superfamily, me	Extracellular Space	cytokine		+	-	-	-	-	-	-	+
THBD	6	60	thrombomodulin	Plasma Membrane	transmembrane receptor		-	-	-	-	-	+	-	-
TNF	6	60	tumor necrosis factor	Extracellular Space	cytokine	adalimum	-	-	-	+	-	-	-	-
IL6	6	65	interleukin 6 (interferon, beta 2)	Extracellular Space	cytokine	tocilizumat	-	+	-	-	-	+	-	-
PTP4A3	6	65	protein tyrosine phosphatase type IVA, m	Plasma Membrane	phosphatase		-	+	-	-	-	+	+	-
LSP1	4	27	lymphocyte-specific protein 1	Cytoplasm	other		-	-	-	-	-	-	+	-
BRSK2	4	31	BR serine/threonine kinase 2	unknown	kinase		-	+	-	-	-	-	-	-
CD151	4	31	CD151 molecule (Raph blood group)	Plasma Membrane	other		-	-	-	-	-	-	+	-
DNAJA3	4	33	DnaJ (Hsp40) homolog, subfamily A, mem	Cytoplasm	other		-	+	-	-	-	-	-	-
HOXB7	4	33	homeobox B7	Nucleus	transcription regulator		-	+	-	-	-	-	-	-
ITGA3	4	33	integrin, alpha 3 (antigen CD49C, alpha 3	Plasma Membrane	other		-	-	-	-	-	+	-	-
ITGB3	4	33	integrin, beta 3 (platelet glycoprotein IIIa	Plasma Membrane	transmembrane receptor	TP 9201, E	+	-	+	+	-	+	+	+
AGTR1	4	42	angiotensin II receptor, type 1	Plasma Membrane	G-protein coupled receptor	amlodipin	-	-	-	-	+	-	-	-
IL12A	4	46	interleukin 12A (natural killer cell stimula	Extracellular Space	cytokine		-	-	-	-	+	-	-	-
BIK	4	50	BCL2-interacting killer (apoptosis-inducin	Cytoplasm	other		-	-	-	+	-	-	-	-
TXNIP	4	50	thioredoxin interacting protein	Cytoplasm	other		+	-	-	-	-	-	-	+
MCL1	4	52	myeloid cell leukemia sequence 1 (BCL2-r	Cytoplasm	transporter		-	-	-	+	-	-	-	-

HUGO Gene Symbol	% of samples with deletions	% samples with amplifications	Entrez Gene Name	Location	Type(s)	Drug(s)	Tumorigenesis	Proliferation, Cell Cycle	Survival	Cell death, Apoptosis	Angiogenesis	Adhesion, Binding, Attachment, Detachment	Movement, Migration, Invasion	Metastasis
ADAM15	4	54	ADAM metallopeptidase domain 15	Plasma Membrane	peptidase		-	-	-	-	-	+	-	-
DDR2	4	54	discoidin domain receptor tyrosine kinase	Plasma Membrane	kinase		-	+	-	-	-	-	-	-
EFNA1	4	54	ephrin-A1	Plasma Membrane	other		-	-	-	-	+	-	-	-
CD36	4	56	CD36 molecule (thrombospondin recepto	Plasma Membrane	transmembrane receptor		-	-	-	-	-	-	+	-
CCND3	4	58	cyclin D3	Nucleus	other		-	+	-	-	-	-	-	-
PRKCA	2	44	protein kinase C, alpha	Cytoplasm	kinase	L-threo-saf	-	-	-	-	-	-	+	-
SPHK1	2	44	sphingosine kinase 1	Cytoplasm	kinase		-	-	-	+	-	-	+	-
HGF	2	67	hepatocyte growth factor (hepapoietin A	Extracellular Space	growth factor		-	-	-	+	-	-	-	-
HGF	2	67	hepatocyte growth factor (hepapoietin A	Extracellular Space	growth factor		-	-	-	-	-	-	+	-
NRCAM	2	73	neuronal cell adhesion molecule	Plasma Membrane	other		-	-	-	-	-	-	+	-
EPO	2	77	erythropoietin	Extracellular Space	cytokine		-	-	-	+	-	-	+	-
LEP	2	77	leptin	Extracellular Space	growth factor		-	+	-	-	-	-	-	-
SERPINE1	2	77	serpin peptidase inhibitor, clade E (nexin	Extracellular Space	other	drotrecogi	-	-	-	-	+	-	-	-
BRAF	2	85	v-raf murine sarcoma viral oncogene hom	Cytoplasm	enzyme	sorafenib	-	+	+	-	-	-	+	-
NOS3	2	85	nitric oxide synthase 3 (endothelial cell)	Cytoplasm	enzyme	GW 27362	+	-	-	-	-	-	-	+
PKMYT1	0	42	protein kinase, membrane associated tyr	Cytoplasm	kinase		-	-	-	+	-	-	-	-
BIRC5	0	44	baculoviral IAP repeat containing 5	Cytoplasm	other		+	-	-	-	-	-	-	-
TIMP2	0	46	TIMP metallopeptidase inhibitor 2	Extracellular Space	other		-	-	-	-	-	-	+	-
FASN	0	48	fatty acid synthase	Cytoplasm	enzyme		-	+	-	-	-	-	-	-
HGS	0	48	hepatocyte growth factor-regulated tyros	Cytoplasm	other		-	+	-	-	-	-	-	-
P4HB	0	50	prolyl 4-hydroxylase, beta pol	Cytoplasm	enzyme		-	-	-	+	-	-	-	-
SRC	0	75	v-src sarcoma (Schmidt-Rup	Cytoplasm	kinase	dasatinib,	-	-	-	+	-	-	-	-
CD40	0	77	CD40 molecule, TNF recep	Plasma Membrane	transmembrane receptor	SGN-40 (ar	-	+	-	-	-	-	-	-
MMP9	0	77	matrix metallopeptidas	Extracellular Space	peptidase		-	-	-	-	-	-	+	-
CSE1L	0	79	CSE1 chromosome segrega on 1-like		transporter		+	-	-	-	-	-	-	+
BIRC7	0	88	baculoviral IAP repeat containing 7	Cytop	other		-	-	-	+	-	-	-	-
LAMA5	0	88	laminin, alpha 5	Extr	other		+	-	-	+	+	-	+	+

Chromosome	cytoband	Start	Stop	Nominal p-value	FDR	ength (bps)	Total Amplifications	Amplification Average Copy Number	Samples with Amplification	Total Deletions	Deletion Average Copy Number	Samples with Deletion	Total Aberrations	Total Unchanged
1	1q24.2	167549043	167571390	5,87E-05	0,000866875	22348	26	3,27985	10 11 12 15 16 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45 47	2	1,64918	8 14	28	20
1	1q24.2	167571390	167606344	5,87E-05	0,000866875	34955	26	3,19567	10 11 12 15 16 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45 47	2	1,64918	8 14	28	20
1	1q24.2	167606344	167618519	5,87E-05	0,000866875	12176	26	2,94368	10 11 12 15 16 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45 47	2	1,64918	8 14	28	20
1	1q24.2 - 1q25.2	167618519	178375347	6,13E-05	0,000894545	10756829	25	2,95053	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45 47	3	1,58223	8 14 16	28	20
1	1q25.3	178624120	179822871	5,54E-05	0,000830233	1198752	25	2,94731	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45 47	3	1,58223	8 14 16	28	20
1	1q25.3 - 1q31.1	180126375	184543632	5,20E-05	0,000799827	4417258	25	2,94731	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45 47	3	1,58223	8 14 16	28	20
1	1q31.1	184543632	185412170	5,20E-05	0,000799827	868539	24	2,97255	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 34 35 36 39 40 42 43 45 47	3	1,58223	8 14 16	27	21
1	1q31.1	185412170	185582619	5,20E-05	0,000799827	170450	23	2,99504	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 34 35 36 39 42 43 45 47	3	1,58223	8 14 16	26	22
1	1q31.1 - 1q31.2	185582619	190567298	5,20E-05	0,000799827	4984680	23	2,99504	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 34 35 36 39 42 43 45 47	3	1,58223	8 14 16	26	22
1	1q31.2	190567298	191078486	5,20E-05	0,000799827	511189	24	2,97428	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 34 35 36 39 40 42 43 45 47	3	1,58223	8 14 16	27	21
1	1q31.2	191372033	191691062	5,46E-05	0,00082484	319030	24	2,97428	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 34 35 36 39 40 42 43 45 47	3	1,53425	8 14 16	27	21
1	1q31.2 - 1q31.3	191691062	194822570	5,46E-05	0,00082484	3131509	23	2,99504	10 11 12 15 18 19 20 21 22 23 24 25 26 27 29 34 35 36 39 42 43 45 47	3	1,53425	8 14 16	26	22
1	1q41 - 1q42.13	221829600	226558551	1,98E-07	6,82E-05	4728952	23	2,93637	10 11 12 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45	8	1,46627	8 13 14 15 16 31 41 47	31	17
1	1q42.13	226719912	226732899	1,32E-07	6,82E-05	12988	23	3,03017	10 11 12 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45	8	1,46627	8 13 14 15 16 31 41 47	31	17
1	1q42.13 - 1q42.2	226732899	228988418	1,32E-07	6,82E-05	2255520	23	2,92551	10 11 12 18 19 20 21 22 23 24 25 26 27 29 32 34 35 36 39 40 42 43 45	8	1,46627	8 13 14 15 16 31 41 47	31	17
1	1q42.2	228988418	229892270	2,14E-06	0,000171693	903853	22	2,95193	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45	8	1,46627	8 13 14 15 16 31 41 47	30	18
1	1q42.2	229892270	229915153	5,54E-05	0,000830233	22884	22	2,95193	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45	10	1,37709	5 7 8 13 14 15 16 31 41 47	32	16
1	1q42.2	229915153	229934501	7,35E-06	0,000190706	19349	22	2,95193	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45	13	1,26599	1 2 5 6 7 8 13 14 15 16 31 41 47	35	13
1	1q42.2	229934501	230279270	3,66E-07	9,70E-05	344770	22	2,95193	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45	14	1,24733	1 2 4 5 6 7 8 13 14 15 16 31 41 47	36	12
1	1q42.2	230279270	231411430	2,33E-05	0,000428846	1132161	23	2,93936	6 10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45	8	1,46627	8 13 14 15 16 31 41 47	31	17
1	1q42.2 - 1q42.3	231411430	234073195	1,68E-06	0,000171693	2661766	22	2,95193	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45	8	1,46627	8 13 14 15 16 31 41 47	30	18
1	1q42.3 - 1q43	234073195	234788348	1,68E-06	0,000171693	715154	23	2,97486	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45 47	7	1,49333	8 13 14 15 16 31 41	30	18
1	1q43	234788348	234847183	1,68E-06	0,000171693	58836	23	3,05131	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45 47	7	1,49333	8 13 14 15 16 31 41	30	18
1	1q43	234847183	235073018	1,68E-06	0,000171693	225836	23	3,05131	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,53438	8 13 14 15 16 31	29	19
1	1q43	235073018	235210904	1,68E-06	0,000171693	137887	23	2,98229	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,53438	8 13 14 15 16 31	29	19
1	1q43	235210904	235284808	1,58E-06	0,000171693	73905	23	2,98229	10 11 12 18 19 20 21 22 23 24 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,49116	8 13 14 15 16 31	29	19
1	1q43	235569369	236124544	1,96E-06	0,000171693	555176	22	3,01138	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,49116	8 13 14 15 16 31	28	20
1	1q43	236124544	236320923	1,96E-06	0,000171693	196380	22	3,09862	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,49116	8 13 14 15 16 31	28	20
1	1q43	236320923	236819468	1,96E-06	0,000171693	498546	22	3,09862	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,49116	8 13 14 15 16 31	28	20
1	1q43	236819468	238243880	1,96E-06	0,000171693	1424413	22	3,00733	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,49116	8 13 14 15 16 31	28	20
1	1q43	238243880	238530190	7,92E-06	0,000191764	286311	22	3,00733	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,36752	8 13 14 15 16 31	28	20
1	1q43	238530190	239281160	7,92E-06	0,000191764	750971	22	3,00539	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,36752	8 13 14 15 16 31	28	20
1	1q43	239281160	239425690	7,92E-06	0,000191764	144531	22	3,00539	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,36752	8 13 14 15 16 31	28	20
1	1q43	239425690	239527732	7,92E-06	0,000191764	102043	22	3,00539	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,36752	8 13 14 15 16 31	28	20
1	1q43	239527732	239860403	1,94E-06	0,000171693	332672	22	3,00539	10 11 12 18 19 20 21 22 23 26 27 29 32 34 35 36 39 40 42 43 45 47	6	1,49281	8 13 14 15 16 31	28	20
4	4q21.1	78147832	78304252	6,00E-05	0,000878529	156421	1	2,34065	18	22	1,4876	8 9 14 15 16 24 25 26 27 28 29 30 31 32 33 34 36 40 43 44 45 48	23	25
4	4q22.1	93833262	93920215	6,13E-08	6,82E-05	86954	1	2,34065	18	25	1,35728	8 9 10 11 12 14 15 16 23 24 26 27 28 29 30 31 32 33 34 36 40 43 44 46 48	26	22
4	4q22.1 - 4q22.2	93920215	94026249	6,13E-08	6,82E-05	106035	1	2,34065	18	25	1,32744	8 9 10 11 12 14 15 16 23 24 26 27 28 29 30 31 32 33 34 36 40 43 44 46 48	26	22
4	4q22.2	94026249	94043491	9,17E-07	0,000171693	17243	1	2,34065	18	25	1,34016	8 9 10 11 12 14 15 16 23 24 26 27 28 29 30 31 32 33 34 36 40 43 44 46 48	26	22
5	5q14.3	82857645	83303986	4,23E-06	0,000173307	446342	5	2,46604	15 16 24 25 26	11	1,59211	8 14 18 19 20 31 32 34 36 40 43	16	32
5	5q14.3	83303986	83355082	2,87E-05	0,0005135	51097	6	2,44179	1 15 16 24 25 26	11	1,59211	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q14.3	83355082	84566238	2,87E-05	0,0005135	1211157	6	2,44179	1 15 16 24 25 26	11	1,56198	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q14.3	84566238	84798044	5,44E-05	0,00082484	231807	6	2,53179	1 15 16 24 25 26	11	1,56198	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q14.3	84798044	85417863	7,79E-06	0,000191764	619820	6	2,63201	1 15 16 24 25 26	11	1,56198	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q14.3	85417863	90208286	7,79E-06	0,000191764	4790424	6	2,63201	1 15 16 24 25 26	11	1,58157	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q14.3 - 5q15	90508445	93558039	1,15E-05	0,000248423	3049595	6	2,63201	1 15 16 24 25 26	11	1,58157	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q15 - 5q21.1	93930505	100522215	8,26E-06	0,000198199	6591711	6	2,63201	1 15 16 24 25 26	11	1,58698	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q21.1 - 5q21.2	101581405	104344033	8,29E-06	0,000198199	2762629	6	2,63201	1 15 16 24 25 26	11	1,58698	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q21.2 - 5q21.3	104344033	105350570	7,07E-05	0,000995102	1006538	6	2,52363	1 15 16 24 25 26	11	1,58698	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q21.3 - 5q23.1	105350570	120081981	3,23E-05	0,000553553	14731412	6	2,43638	1 15 16 24 25 26	11	1,58698	8 14 18 19 20 31 32 34 36 40 43	17	31
5	5q23.1	120081981	121320288	3,23E-05	0,000553553	1238308	7	2,46382	1 15 16 24 25 26 36	10	1,5855	8 14 18 19 20 31 32 34 40 43	17	31
5	5q23.1 - 5q23.2	121320288	122787427	3,23E-05	0,000553553	1467140	7	2,46382	1 15 16 24 25 26 36	11	1,55067	8 14 18 19 20 31 32 34 40 43 47	18	30
5	5q23.2	122787427	123282827	3,23E-05	0,000553553	495401	7	2,46382	1 15 16 24 25 26 36	10	1,5855	8 14 18 19 20 31 32 34 40 43	17	31
5	5q23.2 - 5q31.1	123282827	131089080	3,23E-05	0,000553553	7806254	7	2,46382	1 15 16 24 25 26 36	11	1,5486	8 14 18 19 20 31 32 34 40 43 47	18	30
5	5q31.1	131089080	133534214	3,23E-05	0,000553553	2445135	7	2,46382	1 15 16 24 25 26 36	11	1,56401	8 14 18 19 20 31 32 34 40 43 47	18	30
5	5q31.1	133534214	133739648	3,23E-05	0,000553553	205435	8	2,58256	1 15 16 24 25 26 36 38	11	1,56401	8 14 18 19 20 31 32 34 40 43 47	19	29
5	5q31.1	133739648	133939701	3,23E-05	0,000553553	200054	7	2,46382	1 15 16 24 25 26 36	11	1,56401	8 14 18 19 20 31 32 34 40 43 47	18	30
5	5q31.1	134414015	134454265	1,58E-06	0,000171693	40251	8	2,53538	1 15 16 17 24 25 26 36	11	1,56401	8 14 18 19 20 31 32 34 40 43 47	19	29
5	5q31.1	134454265	134509512	1,58E-06	0,000171693	55248	8	2,53538	1 15 16 17 24 25 26 36	10	1,60245	8 14 18 19 20 31 32 34 40 43	18	30
5	5q31.1	134509512	134679639	1,77E-06	0,000171693	170128	8	2,57818	1 15 16 17 24 25 26 36	10	1,60245	8 14 18 19 20 31 32 34 40 43	18	30
5	5q34	165107405	165204424	1,87E-06	0,000171693	97020	10	2,62545	1 15 16 18 19 20 24 25 26 36	7	1,61451	8 14 31 32 34 38 43	17	31
5	5q34	165669205	165820375	4,84E-05	0,000768626	151171	9	2,80761	15 16 18 19 20 24 25 26 36	12	1,47745	1 2 5 6 7 8 14 31 32 34 38 43	21	27
5	5q34	165820375	166781934	4,84E-05	0,000768626	961560	9	2,80761	15 16 18 19 20 24 25 26 36	13	1,46032	1 2 5 6 7 8 14 31 32 34 38 43 45	22	26
5	5q35.3	180492584	180644840	4,56E-05	0,000742503	152257	12	2,54506	1 15 18 19 20 22 23 24 25 26 36 40	8	1,56569	8 11 14 31 32 38 39 42	20	28
6	6p21.32	32577065	32840913	8,83E-05	0,000928715	263851	27	4,21953	5 10 11 12 13 14 16 17 18 19 20 21 22 23 26 30 34 35 36 37 38 39 42 43 46 47 48	10	1,35788	7 15 24 27 28 29 31 32 40 44	37	11
6	6p21.32	32640915	32666562	7,78E-06	0,000191764	19650	29	4,11846	3 5 10 11 12 13 14 16 17 18 19 20 21 22 23 26 30 34 35 36 37 38 39 42 43 44 46 47 48	8	1,3595	15 24 27 28 29 31 32 40	37	11
6	6p21.32	32666562	32696414	7,78E-06	0,000191764	29853	31	4,0377	3 5 10 11 12 13 14 16 17 18 19 20 21 22 23 26 28 29 30 34 35 36 37 38 39 42 43 44 46 47	5	1,34149	15 24 27 32 40	36	12
6	6p21.32	32696414	32725906	3,53E-06	0,000171693	29493	31	3,53076	3 5 10 11 12 13 14 16 17 18 19 20 21 22 23 26 28 29 30 32 34 35 36 38 39 42 43 44 46 47	4	1,43095	15 24 27 40	35	13
6	6p21.32	32725906	32755558	3,53E-06	0,000171693	29653	31	3,53076	3 5 10 11 12 13 14 16 17 18 19 20 21 22 23 26 28 29 30 32 34 35 36 38 39 42 43 44 46 47	4	1,57238	15 24 27 40	35	13
6	6q13	74610279	75233066	7,24E-06	0,000189168	622788	8	2,67869	3 10 11 12 14 16 29 44	21	1,40449	8 9 15 18 19 20 21 22 23 26 27 33 34 35 36 38 41 43 46 47 48	29	19
6	6q13	75233066	75797327	7,24E-06	0,000189168	564262	8	2,67869	3 10 11 12 14 16 29 44	21	1,38404	8 9 15 18 19 20 21 22 23 26 27 33 34 35 36 38 41 43 46 47 48	29	19
6	6q13 - 6q14.1	75797327	77256850	7,24E-06	0,000189168	1459524	8	2,67869	3 10 11 12 14 16 29 44	21	1,40342	8 9 15 18 19 20 21 22 23 26 27 33 34 35 36 38 41 43 46 47 48	29	19
7	7q11.21	65353359	65748424	4,69E-06	0,000173307	395066	27	2,84903	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47 48	4	1,59535	7 22 32 36	31	17
7	7q11.21	65748424	65951441	4,69E-06	0,000173307	203018	27	2,89589	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47 48	4	1,59535	7 22 32 36	31	17
7	7q11.21 - 7q11.22	65951441	69116350	4,69E-06	0,000173307	3164910	26	2,89398	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	4	1,59535	7 22 32 36	30	18
7	7q11.22	69116350	69402857	4,69E-06	0,000173307	286508	26	2,89398	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	5	1,57018	7 22 27 32 36	31	17
7	7q11.22	69402857	69556543	4,69E-06	0,000173307	153687	25	2,90611	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 33 34 38 39 40 43 46 47	7	1,53979	7 22 27 28 31 32 36	32	16
7	7q11.22	69556543	69621487	1,33E-05	0,000268788	64945	25	2,87885	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 33 34 38 39 40 43 46 47	7	1,53979	7 22 27 28 31 32 36	32	16
7	7q11.22	69621487	69850553	1,33E-05	0,000268788	229067	26	2,8742	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	4	1,59535	7 22 32 36	30	18
7	7q11.22	69850553	70379093	4,89E-06	0,000173307	528541	26	2,89293	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	4	1,59535	7 22 32 36	30	18
7	7q11.22	70409236	70666575	5,25E-07	0,000122604	257340	23	2,8658	3 8 9 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	6	1,47201	7 11 12 22 32 36	29	19
7	7q11.22	70666575	70991064	5,16E-06	0,000173307	324490	26	2,89472	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	4	1,59535	7 22 32 36	30	18
7	7q11.22	70991064	71038531	3,68E-06	0,000171693	47468	26	2,89472	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	3	1,61214	7 32 36	29	19
7	7q11.22	71038531	71054109	6,62E-06	0,000181226	15579	26	2,91802	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	3	1,61214	7 32 36	29	19
7	7q11.22	71054109	71067232	4,41E-06	0,000173307	13124	26	2,93175	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	3	1,61214	7 32 36	29	19
7	7q11.22	71067232	71462207	3,02E-05	0,000537041	394975	26	2,97903	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	3	1,61214	7 32 36	29	19
7	7q11.22	71462207	71520322	4,40E-05	0,000722357	58116	26	2,97903	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47	3	1,61214	7 32 36	29	19
7	7q11.22 - 7q11.23	71520322	72012969	4,40E-05	0,000722357	492648	27	2,96085	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 46 47 48	3	1,61214	7 32 36	30	18
7	7q11.23	72012969	72641094	4,40E-05	0,000722357	628126	29	2,94972	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 45 46 47 48	3	1,61214	7 32 36	32	16
7	7q11.23	72641094	75080051	4,40E-05	0,000722357	2438958	29	2,96583	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 45 46 47 48	3	1,61214	7 32 36	32	16
7	7q11.23	75080051	75272618	4,40E-05	0,000722357	192568	29	3,04167	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 45 46 47 48	3	1,61214	7 32 36	32	16
7	7q11.23	75272618	75330849	4,40E-05	0,000722357	58232	29	2,9713	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 45 46 47 48	3	1,61214	7 32 36	32	16
7	7q11.23	75330849	75415470	4,40E-05	0,000722357	84622	30	2,96207	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 42 43 44 45 46 47 48	3	1,61214	7 32 36	33	15
7	7q11.23	75787126	75800988	7,12E-05	0,000995102	13863	29	3,12583	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 45 46 47 48	3	1,61214	7 32 36	32	16
7	7q11.23	75800988	75979950	7,12E-05	0,000995102	178963	28	2,92745	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 45 47 48	3	1,61214	7 32 36	31	17
7	7q11.23	75979950	76040010	7,12E-05	0,000995102	60061	28	2,91089	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 45 47 48	3	1,61214	7 32 36	31	17
7	7q11.23	76040010	76174461	7,12E-05	0,000995102	134452	27	2,92707	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 44 47 48	3	1,61214	7 32 36	30	18
7	7q11.23	76174461	76451814	7,12E-05	0,000995102	277354	26	2,94979	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 47 48	3	1,61214	7 32 36	29	19
7	7q11.23	76451814	77053177	7,12E-05	0,000995102	601364	26	2,94979	3 8 9 10 11 12 13 14 16 17 18 19 20 24 25 26 29 31 33 34 38 39 40 43 47 48	2	1,60752	7 36	28	20
8	8p11.23	39274410	39328101	1,99E-07	6,82E-05	56692	12	2,79492	9 10 11 14 18 19 20 34 36 38 39 43	16	1,32682	2 3 4 5 6 7 22 24 26 27 31 32 33 40 46 48	28	20

Chromosome	cytoband	Start	Stop	Nominal p-value	FDR	length (bps)	Total Amplifications	Amplification Average Copy Number	Samples with Amplification	Total Deletions	Deletion Average Copy Number	Samples with Deletion	Total Aberrations	Total Unchanged
8	8q11.23	53316167	53651879	1,91E-05	0,000354362	335713	18	2,9898	8 9 10 11 13 14 15 16 17 18 19 25 34 38 40 42 43 47	4	1,61834	31 32 33 36	22	26
9	9p24.3	153160	479698	1,13E-05	0,000247263	326539	5	2,50387	24 25 27 39 40	31	1,36055	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 45	36	12
9	9p24.3	479698	968532	1,13E-05	0,000247263	488835	5	2,50387	24 25 27 39 40	30	1,37273	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 48	35	13
9	9p24.3	968532	1142263	1,13E-05	0,000247263	173732	5	2,50387	24 25 27 39 40	30	1,33807	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 48	35	13
9	9p24.3	1142263	1215225	1,13E-05	0,000247263	72963	5	2,50387	24 25 27 39 40	30	1,37104	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 48	35	13
9	9p24.3	1215225	1518403	1,13E-05	0,000247263	303179	5	2,50387	24 25 27 39 40	30	1,35589	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 48	35	13
9	9p24.3	1518403	1743078	1,13E-05	0,000247263	224676	5	2,50387	24 25 27 39 40	31	1,35962	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 46	36	12
9	9p24.3	1743078	2196519	1,13E-05	0,000247263	453442	6	2,62511	24 25 27 39 40 45	31	1,35962	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 46	37	11
9	9p24.3 - 9p24.2	2196519	3070871	1,13E-05	0,000247263	874353	5	2,50387	24 25 27 39 40	31	1,35962	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 46	36	12
9	9p24.2	3070871	3853784	1,13E-05	0,000247263	782914	5	2,50387	24 25 27 39 40	32	1,3451	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 45	37	11
9	9p24.2	4092276	4181841	1,55E-05	0,000294498	89566	5	2,50387	24 25 27 39 40	32	1,3451	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 45	37	11
9	9p24.2 - 9p24.1	4181841	4744597	1,55E-05	0,000294498	562757	5	2,73575	24 25 27 39 40	32	1,3451	3 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 28 29 31 32 34 35 36 37 38 41 43 44 45	37	11
9	9p21.3	21836522	21849188	4,80E-05	0,000768333	12667	1	2,78151	27	42	0,850882	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 28 29 30 31 32 33 34 3	43	5
9	9p21.3	21849188	21863450	4,80E-05	0,000768333	14263	1	2,78151	27	43	0,838348	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 28 29 30 31 32 33 34 3	44	4
9	9p21.3	21863450	21883255	4,80E-05	0,000768333	19806	1	2,78151	27	43	0,812508	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 28 29 30 31 32 33 34 3	44	4
9	9p21.3	21998815	22012740	5,84E-05	0,000866875	13926	0	?		39	0,764042	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 27 28 29 30 31 32 34 36 37 3	39	9
9	9p21.3	22012740	22051651	4,88E-05	0,000768626	38912	0	?		38	0,811066	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 27 28 29 31 32 34 36 37 38 4	38	10
9	9p21.3	22169618	22259388	4,56E-05	0,000742503	89771	0	?		38	0,976016	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 27 28 29 31 32 34 36 37 38 4	38	10
9	9p21.3	22259388	22344256	2,48E-06	0,000171693	84869	1	2,87494	27	36	1,09553	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	22344256	22677460	1,81E-06	0,000171693	333205	1	2,87494	27	36	1,0909	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	22677460	23194640	2,87E-06	0,000171693	517181	1	2,87494	27	36	1,09811	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	23194640	23250421	8,79E-06	0,000208715	55782	1	2,87494	27	36	1,11642	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	23250421	23665151	1,10E-05	0,000247263	414731	1	2,87494	27	36	1,09286	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	23665151	23883374	1,42E-05	0,000280107	218224	1	2,87494	27	36	1,0976	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	23883374	23996963	1,10E-05	0,000247263	113590	1	2,87494	27	36	1,09263	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	23996963	24048126	7,49E-06	0,000190706	51164	1	2,87494	27	36	1,08777	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	24048126	24184595	7,49E-06	0,000190706	136470	1	2,87494	27	36	1,12264	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.3	24184595	24774630	5,67E-06	0,000173307	590036	1	2,87494	27	36	1,11825	2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 4	37	11
9	9p21.2 - 9p21.1	28040629	28130875	2,23E-07	6,82E-05	90247	1	2,87494	27	31	1,30837	3 8 9 10 11 12 13 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 43 44 45 46	32	16
9	9p21.1	28130875	28192442	2,23E-07	6,82E-05	61568	1	2,87494	27	31	1,31233	3 8 9 10 11 12 13 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 43 44 45 46	32	16
9	9p21.1	28192442	28297300	2,23E-07	6,82E-05	104859	0	?		31	1,31233	3 8 9 10 11 12 13 15 16 17 18 19 20 21 24 25 26 28 29 31 32 36 37 38 40 41 43 44 45 46	31	17
10	10q21.2	64047641	64294703	6,92E-05	0,000991895	247063	1	2,30166	32	33	1,39961	8 9 10 11 12 13 15 16 17 18 19 20 21 22 23 26 27 28 29 30 31 33 35 36 37 38 40 41 43 45	34	14
11	11p15.5 - 11p15.4	2323434	2855107	1,98E-07	6,82E-05	531674	12	2,42297	8 13 16 22 26 28 32 36 37 42 44 46	6	1,32845	10 11 12 27 34 48	18	30
11	11p15.4	2855107	2916660	1,98E-07	6,82E-05	61554	12	2,42297	8 13 16 22 26 28 32 36 37 42 44 46	7	1,37316	10 11 12 27 31 34 48	19	29
11	11p15.4	3505200	3630287	1,65E-05	0,000310809	125088	7	2,40668	8 16 28 32 36 37 46	12	1,39051	10 11 12 15 19 20 21 27 29 31 34 48	19	29
11	11p15.4	3630287	3641926	1,65E-05	0,000310809	11640	6	2,38774	8 16 28 32 36 37	14	1,40671	10 11 12 15 19 20 21 27 29 31 34 35 43 48	20	28
11	11p15.4	3641926	3802858	9,32E-06	0,000218911	160933	6	2,38774	8 16 28 32 36 37	15	1,40886	10 11 12 15 19 20 21 23 27 29 31 34 35 43 48	21	27
11	11p11.2	44225644	44618276	6,21E-05	0,000902609	392633	5	2,39534	8 15 16 28 36	13	1,55533	10 11 19 20 21 23 31 33 34 35 43 46 48	18	30
11	11q11	55104986	55178839	4,05E-05	0,000689392	73854	25	3,66138	8 9 10 11 12 13 14 15 16 17 19 21 34 36 37 38 39 40 42 43 44 45 46 47 48	5	1,52876	3 23 28 30 31	30	18
12	12q14.1	56329906	56427879	1,02E-06	0,000171693	97974	15	2,98972	1 8 10 11 12 14 16 22 24 25 32 40 41 45 46	8	1,59079	15 18 19 20 29 36 43 44	23	25
12	12q14.1	56427879	56430465	2,96E-07	8,40E-05	2587	16	2,9548	1 8 10 11 12 14 15 16 22 24 25 32 40 41 45 46	7	1,5905	18 19 20 29 36 43 44	23	25
12	12q14.1	56430465	56464185	3,54E-06	0,000171693	33721	22	3,07054	1 7 8 10 11 12 13 14 15 16 22 24 25 32 35 37 40 41 42 44 45 46	6	1,58907	18 19 20 29 36 43	28	20
12	12q21.32	86954790	87025075	6,44E-06	0,000177634	70285	3	2,34497	14 24 25 ———	13	1,48239	1 15 16 17 18 19 20 29 32 36 43 44 48	16	32
12	12q21.32	87025075	87038759	6,44E-06	0,000177634	13685	3	2,34497	14 24 25	12	1,48897	1 15 16 17 18 19 20 29 36 43 44 48	15	33
12	12q21.32	87038759	87142222	6,44E-06	0,000177634	103464	4	2,3579	14 24 25 40	12	1,50889	1 15 16 17 18 19 20 29 36 43 44 48	16	32
12	12q21.32 - 12q21.33	87142222	88895228	7,15E-05	0,000996822	1753007	5	2,39313	1 14 24 25 40	11	1,49259	15 16 17 18 19 20 29 36 43 44 48	16	32
12	12q23.1	96468826	97289459	7,75E-08	6,82E-05	820634	6	2,46641	14 22 24 25 40 41	12	1,50989	15 16 17 18 19 20 29 32 36 43 44 48	18	30
12	12q23.1	97289459	97345781	4,95E-07	0,000122604	56323	6	2,46641	14 22 24 25 40 41	12	1,47465	15 16 17 18 19 20 29 32 36 43 44 48	18	30
12	12q23.1	97549134	97809034	1,95E-07	6,82E-05	259901	5	2,49637	14 24 25 40 41	12	1,51932	15 16 17 18 19 20 29 32 36 43 44 48	17	31
12	12q24.21	113572551	114831260	1,96E-06	0,000171693	1258710	9	2,53983	8 14 24 25 31 40 41 44 46	9	1,53257	15 16 17 18 19 20 29 36 43	18	30
12	12q24.32	124525018	124566571	1,08E-05	0,000247263	41554	7	2,61564	14 25 31 40 41 44 46	11	1,54437	1 15 16 17 18 19 20 29 32 36 43	18	30
12	12q24.32	124566571	124748151	1,08E-05	0,000247263	181581	7	2,61564	14 25 31 40 41 44 46	12	1,54041	1 15 16 17 18 19 20 29 32 36 43 48	19	29
13	13q12.11 - 13q12.12	19112579	23161851	2,11E-06	0,000171693	4049273	8	2,63501	8 9 16 29 30 31 43 48	13	1,45228	14 18 19 20 21 23 24 25 26 28 35 36 40	21	27
13	13q12.12	23577319	24328729	2,09E-06	0,000171693	751411	8	2,63501	8 9 16 29 30 31 43 48	13	1,4555	14 18 19 20 21 23 24 25 26 28 35 36 40	21	27
13	13q12.12	24328729	24348103	2,09E-06	0,000171693	19375	7	2,61713	8 9 16 29 30 31 43	13	1,4555	14 18 19 20 21 23 24 25 26 28 35 36 40	20	28
13	13q12.12 - 13q12.13	24348103	24410790	2,09E-06	0,000171693	62688	7	2,61713	8 9 16 29 30 31 43	14	1,43655	14 18 19 20 21 23 24 25 26 28 34 35 36 40	21	27
13	13q12.13	24410790	24641266	2,09E-06	0,000171693	230477	8	2,61625	8 9 16 28 29 30 31 43 48	13	1,44847	14 18 19 20 21 23 24 25 26 34 35 36 40	21	27
13	13q12.13	24641266	24642791	2,09E-06	0,000171693	1526	9	2,62652	8 9 16 28 29 30 31 43 48	13	1,44847	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q12.13	24642791	26555431	2,09E-06	0,000171693	1912641	9	2,62652	8 9 16 28 29 30 31 43 48	13	1,48624	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q12.13 - 13q12.2	26555431	26733305	4,48E-06	0,000173307	177875	8	2,66168	8 9 28 29 30 31 43 48	13	1,48624	14 18 19 20 21 23 24 25 26 34 35 36 40	21	27
13	13q12.2 - 13q12.3	26733305	28491360	2,40E-06	0,000171693	1758056	9	2,63031	8 9 16 28 29 30 31 43 48	13	1,48824	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q12.3	28491360	29118508	2,40E-06	0,000171693	627149	9	2,54473	8 9 16 28 29 30 31 43 48	13	1,48824	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q12.3 - 13q13.1	29118508	31280839	2,40E-06	0,000171693	2162332	9	2,63103	8 9 16 28 29 30 31 43 48	13	1,48624	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q13.1	31280839	31519948	4,43E-06	0,000173307	239110	9	2,63103	8 9 16 28 29 30 31 43 48	13	1,4139	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q13.1	31519948	32819586	2,50E-06	0,000171693	1299639	9	2,63103	8 9 16 28 29 30 31 43 48	13	1,48725	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q13.1 - 13q13.2	32819586	33107573	2,50E-06	0,000171693	287988	9	2,3368	8 9 16 28 29 30 31 43 48	13	1,48725	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q13.2	33107573	34312359	2,50E-06	0,000171693	1204787	9	2,63321	8 9 16 28 29 30 31 43 48	13	1,48725	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q13.2	34312359	34495929	2,50E-06	0,000171693	183571	9	2,63321	8 9 16 28 29 30 31 43 48	14	1,4752	14 18 19 20 21 23 24 25 26 34 35 36 40 47	23	25
13	13q13.3	34848979	39159500	3,43E-06	0,000171693	4310522	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,48725	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q14.11	39578982	42674972	3,40E-06	0,000171693	3095991	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,48725	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q14.11	42922543	43283290	1,80E-05	0,000334731	360748	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,42831	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q14.11	43283290	43713363	3,61E-06	0,000171693	430074	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,48914	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q14.11 - 13q14.12	43984660	44717921	3,68E-06	0,000171693	733262	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,49077	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q14.12	44717921	44770079	4,99E-05	0,000782884	52159	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,45432	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q14.12 - 13q14.3	44939200	51474098	3,18E-06	0,000171693	6474899	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,49349	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q14.3 - 13q21.1	51474098	52330178	3,18E-06	0,000171693	856081	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,49349	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q21.1	52330178	52389636	3,18E-06	0,000171693	59459	9	2,63752	8 9 16 28 29 30 31 43 48	13	1,47458	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q21.1	52389636	53086788	3,18E-06	0,000171693	697153	9	2,60744	8 9 16 28 29 30 31 43 48	13	1,47458	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q21.1	53745801	53891133	7,22E-06	0,000189168	145333	9	2,58688	8 9 16 28 29 30 31 43 48	14	1,47053	14 18 19 20 21 23 24 25 26 34 35 36 40 41	23	25
13	13q21.1	53891133	56628243	7,22E-06	0,000189168	2737111	9	2,58688	8 9 16 28 29 30 31 43 48	13	1,47458	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q21.1	56628243	57120994	7,22E-06	0,000189168	492752	8	2,5778	8 9 16 28 29 30 43 48	14	1,48239	14 18 19 20 21 23 24 25 26 31 34 35 36 40	22	26
13	13q21.1 - 13q21.2	57120994	60040881	7,22E-06	0,000189168	2919888	9	2,56891	8 9 16 28 29 30 31 43 48	13	1,47458	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q21.31	61737974	63617064	6,34E-06	0,000177634	1879091	9	2,56891	8 9 16 28 29 30 31 43 48	13	1,47458	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q21.31 - 13q21.32	63617064	64302477	6,34E-06	0,000177634	685414	10	2,5736	8 9 16 28 29 30 31 34 43 48	12	1,45736	14 18 19 20 21 23 24 25 26 35 36 40	22	26
13	13q21.32	64302477	65574384	6,34E-06	0,000177634	1271908	9	2,56891	8 9 16 28 29 30 31 43 48	13	1,47279	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q21.32	65574384	65820302	6,34E-06	0,000177634	245919	10	2,57771	8 9 16 28 29 30 31 39 43 48	13	1,47279	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q21.32	65820302	66003338	6,34E-06	0,000177634	183037	10	2,57771	8 9 16 28 29 30 31 39 43 48	14	1,44605	14 18 19 20 21 23 24 25 26 27 34 35 36 40	24	24
13	13q21.32 - 13q21.33	66003338	71135456	6,34E-06	0,000177634	5132099	10	2,57771	8 9 16 28 29 30 31 39 43 48	13	1,47279	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q21.33	71135436	71385958	6,34E-06	0,000177634	250523	10	2,64006	8 9 16 28 29 30 31 39 43 48	13	1,47279	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q21.33 - 13q22.3	71385958	77797354	6,34E-06	0,000177634	6411397	10	2,64006	8 9 16 28 29 30 31 39 43 48	13	1,48912	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q22.3 - 13q31.1	77797354	78079319	6,14E-06	0,000177634	281966	10	2,7347	8 9 16 28 29 30 31 39 43 48	13	1,48912	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q31.1	78079319	79581335	3,27E-06	0,000171693	1502017	10	2,6541	8 9 16 28 29 30 31 39 43 48	13	1,48912	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q31.1	79581335	79946511	1,41E-05	0,000278255	365177	10	2,6541	8 9 16 28 29 30 31 39 43 48	13	1,45423	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q31.1	79946511	80889482	3,29E-06	0,000171693	942972	10	2,6541	8 9 16 28 29 30 31 39 43 48	13	1,48802	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q31.1	80889482	82549081	3,29E-06	0,000171693	1660500	10	2,6541	8 9 16 28 29 30 31 39 43 48	13	1,47177	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q31.1	82549081	85049685	3,29E-06	0,000171693	2499705	11	2,64114	8 9 16 27 28 29 30 31 39 43 48	13	1,47177	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q31.1	85358247	85731664	3,83E-06	0,000171693	373418	10	2,65875	8 9 16 27 28 29 30 31 39 43 48	13	1,47177	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q31.1	85731664	85872092	5,25E-05	0,000802197	140428	10	2,65875	8 9 16 27 28 29 30 31 39 43 48	14	1,47204	10 14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q31.1	85872092	86413704	5,25E-05	0,000802197	536613	11	2,64597	8 9 16 27 28 29 30 31 39 43 48	14	1,47204	10 14 18 19 20 21 23 24 25 26 34 35 36 40	25	23
13	13q31.1 - 13q31.2	86413704	88486215	3,89E-06	0,000171693	2072512	11	2,64597	8 9 16 27 28 29 30 31 39 43 48	13	1,47177	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24

Chromosome	cytoband	Start	Stop	Nominal p-value	FDR	length (bps)	Total Amplifications	Amplification Average Copy Number	Samples with Amplification	Total Deletions	Deletion Average Copy Number	Samples with Deletion	Total Aberrations	Total Unchanged
13	13q31.2 - 13q31.3	88486215	91993239	3,89E-06	0,000171693	3507025	11	2,57447	8 9 16 27 28 29 30 31 39 43 48	13	1,47177	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q31.3 - 13q32.1	91993239	95084294	3,89E-06	0,000171693	3091056	11	2,57447	8 9 16 27 28 29 30 31 39 43 48	13	1,48894	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q32.1	95300442	95412851	3,82E-06	0,000171693	112410	11	2,57447	8 9 16 27 28 29 30 31 39 43 48	13	1,48894	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q32.1 - 13q32.2	95412851	97395958	3,82E-06	0,000171693	1983108	10	2,58076	8 9 16 28 29 30 31 39 43 48	13	1,48894	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q32.2 - 13q32.3	97633255	98506828	3,60E-06	0,000171693	873574	10	2,58076	8 9 16 28 29 30 31 39 43 48	13	1,49079	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q32.3	98506828	99214870	1,67E-06	0,000171693	708043	9	2,59323	8 9 28 29 30 31 39 43 48	13	1,49079	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q32.3	99214870	99412984	1,67E-06	0,000171693	198115	9	2,59323	8 9 28 29 30 31 39 43 48	12	1,50019	14 18 19 20 21 23 24 25 26 34 35 36	21	27
13	13q32.3	99412984	99426056	1,67E-06	0,000171693	13073	9	2,59323	8 9 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q32.3	99426056	99771821	1,67E-06	0,000171693	345766	9	2,59323	8 9 28 29 30 31 39 43 48	14	1,47697	14 18 19 20 21 23 24 25 26 34 35 36 38 40	23	25
13	13q32.3	99771821	100334884	1,67E-06	0,000171693	563064	9	2,59323	8 9 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	22	26
13	13q32.3 - 13q33.1	100334884	102708243	5,64E-06	0,000173307	2373360	10	2,58917	8 9 16 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	23	25
13	13q33.1 - 13q33.3	102708243	107627567	5,64E-06	0,000173307	4919325	11	2,59828	8 9 16 27 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q33.3	107627567	107853324	5,64E-06	0,000173307	225758	11	2,67353	8 9 16 27 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q33.3	108305634	108327674	3,43E-06	0,000171693	22041	11	2,69437	8 9 16 27 28 29 30 31 39 43 48	14	1,4786	14 18 19 20 21 23 24 25 26 33 34 35 36 40	25	23
13	13q33.3	108327674	108695612	3,43E-06	0,000171693	367939	11	2,69437	8 9 16 27 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q33.3 - 13q34	108695612	110583312	3,43E-06	0,000171693	1887701	11	2,72983	8 9 16 27 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	24	24
13	13q34	110583312	111044610	1,51E-05	0,000294498	461299	12	2,69485	2 8 9 16 27 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	25	23
13	13q34	111044610	112522086	3,18E-05	0,000553553	1477477	13	2,66566	2 7 8 9 16 27 28 29 30 31 39 43 48	13	1,48576	14 18 19 20 21 23 24 25 26 34 35 36 40	26	22
13	13q34	112522086	112668506	6,75E-05	0,000971133	146421	13	2,66566	2 7 8 9 16 27 28 29 30 31 39 43 48	13	1,51127	14 18 19 20 21 23 24 25 26 34 35 36 40	26	22
13	13q34	112668506	112718722	6,75E-05	0,000971133	50217	13	2,66566	2 7 8 9 16 27 28 29 30 31 39 43 48	13	1,52668	14 18 19 20 21 23 24 25 26 34 35 36 40	26	22
13	13q34	112718722	113124872	6,75E-05	0,000971133	406151	13	2,66566	2 7 8 9 16 27 28 29 30 31 39 43 48	13	1,52668	14 18 19 20 21 23 24 25 26 34 35 36 40	26	22
14	14q11.2	19244855	19280237	2,45E-05	0,000443684	35383	1	2,33596	48	41	1,06188	1 2 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 20 21 22 23 24 25 26 27 28 29 31 32 33 34 35	42	6
14	14q11.2	19280237	19490547	2,45E-05	0,000443684	210311	1	2,33596	48	41	1,04349	1 2 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 20 21 22 23 24 25 26 27 28 29 31 32 33 34 35	42	6
14	14q11.2	22287328	22518386	1,14E-05	0,000248006	231059	1	2,389	16	20	1,45589	8 9 10 11 12 14 18 20 21 22 23 27 28 29 33 34 35 36 40 43	21	27
14	14q11.2	22518386	22623353	1,29E-05	0,000262536	104968	1	2,389	16	20	1,54472	8 9 10 11 12 14 18 20 21 22 23 27 28 29 33 34 35 36 40 43	21	27
14	14q11.2	22623353	22859317	1,29E-05	0,000262536	235965	1	2,389	16	20	1,54472	8 9 10 11 12 14 18 20 21 22 23 27 28 29 33 34 35 36 40 43	21	27
14	14q11.2	22859317	23130166	1,29E-05	0,000262536	270850	1	2,389	16	20	1,53172	8 9 10 11 12 14 18 20 21 22 23 27 28 29 33 34 35 36 40 43	21	27
14	14q11.2 - 14q12	23130166	23882816	1,29E-05	0,000262536	752651	1	2,389	16	21	1,532	8 9 10 11 12 14 18 20 21 22 23 27 28 29 32 33 34 35 36 40 43	22	26
14	14q12	23882816	24525144	1,29E-05	0,000262536	642329	1	2,389	16	22	1,53404	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43	23	25
14	14q12	24525144	24561043	1,29E-05	0,000262536	35900	1	2,389	16	22	1,53404	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43	23	25
14	14q12	24561043	29122844	1,29E-05	0,000262536	4561802	1	2,389	16	23	1,53369	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43 48	24	24
14	14q12	29122844	29231719	1,29E-05	0,000262536	108876	1	2,389	16	22	1,53404	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43	23	25
14	14q12	29231719	29434301	1,29E-05	0,000262536	202583	1	2,389	16	23	1,51057	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 42 43	24	24
14	14q12 - 14q13.2	29434301	35463933	1,29E-05	0,000262536	6029633	1	2,389	16	22	1,53404	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43	23	25
14	14q13.2 - 14q21.1	35463933	38659696	1,29E-05	0,000262536	3195764	1	2,389	16	23	1,53613	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43 48	24	24
14	14q21.1	38866201	39360684	1,37E-05	0,000272863	494484	1	2,389	16	23	1,5364	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43 48	24	24
14	14q21.1	39360684	39737953	1,37E-05	0,000272863	377270	1	2,389	16	23	1,52186	8 9 10 11 12 14 18 20 21 22 23 27 28 29 31 32 33 34 35 36 40 43 48	24	24
14	14q32.33	104073951	104214391	2,85E-05	0,0005135	140441	8	2,85352	15 16 17 19 24 25 44 46	20	1,39012	1 2 4 5 6 7 8 10 12 22 26 27 28 29 32 35 36 40 42 43	28	20
14	14q32.33	104214391	104312739	1,74E-05	0,000325316	98349	11	2,87255	12 13 15 16 17 19 24 25 26 44 46	17	1,41362	1 2 4 5 6 7 8 10 22 27 28 32 35 36 40 42 43	28	20
14	14q32.33	105104539	105136219	1,37E-05	0,000272863	31681	19	3,07584	9 10 12 13 15 16 17 19 22 24 25 26 33 42 44 45 46 47 48	11	1,32473	1 2 4 5 6 7 27 28 31 32 36	30	18
14	14q32.33	105136219	105304360	5,05E-06	0,000173307	168142	19	3,10195	9 10 12 13 15 16 17 19 22 24 25 26 33 42 44 45 46 47 48	11	1,26034	1 2 4 5 6 7 27 28 31 32 36	30	18
14	14q32.33	105304360	105338567	5,05E-06	0,000173307	34208	17	2,99056	9 10 12 13 15 16 17 19 22 24 25 26 33 42 45 47 48	11	1,26034	1 2 4 5 6 7 27 28 31 32 36	28	20
16	16p13.3	558720	675775	2,02E-05	0,00037379	117056	21	2,67665	9 11 12 13 14 15 16 17 18 20 23 24 25 26 32 34 36 43 44 45 46	5	1,12372	2 4 5 6 7 5	26	22
16	16p13.3	675775	681066	4,10E-05	0,000696355	5292	20	2,6668	9 11 12 13 14 15 16 17 18 20 23 24 26 32 34 36 43 44 45 46	5	1,12372	2 4 5 6 7	25	23
19	19p13.11	19715082	19738293	1,55E-05	0,000294498	23212	10	2,60867	8 9 28 29 32 37 40 42 44 48	7	1,56803	19 20 21 23 31 35 46	17	31
19	19p13.11 - 19p12	19738293	19802995	1,55E-05	0,000294498	64703	8	2,62547	8 9 28 29 32 37 42 48	8	1,58308	19 20 21 23 31 35 44 46	16	32
19	19p12	19802995	19860022	1,55E-05	0,000294498	57028	7	2,60999	8 9 28 29 37 42 48	8	1,58308	19 20 21 23 31 35 44 46	15	33
19	19p12	19860022	19983604	1,55E-05	0,000294498	123583	8	2,5958	8 9 28 29 37 42 43 48	8	1,58308	19 20 21 23 31 35 44 46	16	32
19	19p12	20127978	21344074	3,41E-06	0,000171693	1216097	7	2,54229	8 9 28 29 37 43 48	11	1,54066	19 20 21 22 23 31 34 35 42 44 46	18	30
19	19p12	21344074	22175129	3,41E-06	0,000171693	831056	7	2,54229	8 9 28 29 37 43 48	12	1,52879	19 20 21 22 23 31 34 35 36 42 44 46	19	29
19	19p12	22175129	23070339	3,41E-06	0,000171693	895211	6	2,54992	8 9 28 29 37 48	13	1,47833	19 20 21 22 23 31 34 35 36 42 43 44 46	19	29
19	19p12	23070339	23681699	3,41E-06	0,000171693	611361	6	2,54992	8 9 28 29 37 48	12	1,48501	19 20 21 22 23 31 34 35 42 43 44 46	18	30
19	19p12	23681699	23711544	3,41E-06	0,000171693	29846	6	2,54992	8 9 28 29 37 48	11	1,4821	19 20 21 22 23 31 35 42 43 44 46	17	31
19	19p12 - 19p11	23711544	28338813	3,41E-06	0,000171693	4627270	6	2,54992	8 9 28 29 37 48	11	1,4821	19 20 21 22 23 31 35 42 43 44 46	17	31
19	19p11 - 19q12	28338813	32754721	4,04E-06	0,000173307	4415909	9	2,56661	8 9 21 22 23 29 35 37 48	7	1,51687	19 20 31 42 43 44 46	16	32
19	19q12	32754721	33031788	4,04E-06	0,000173307	277068	9	2,56661	8 9 21 22 23 29 35 37 48	7	1,62931	19 20 31 42 43 44 46	16	32
19	19q13.11 - 19q13.12	40231679	40857477	7,47E-06	0,000190706	625799	13	2,63357	8 9 21 22 23 29 35 37 40 43 45 46 48	4	1,53116	13 15 19 20	17	31
19	19q13.12	40979680	41016382	5,99E-05	0,000878529	36703	15	2,63372	8 9 21 22 23 24 25 29 35 37 40 43 45 46 48	5	1,28313	13 15 19 20 31	20	28
19	19q13.12	41016382	41115596	5,72E-06	0,000173307	99215	13	2,63357	8 9 21 22 23 29 35 37 40 43 45 46 48	5	1,28313	13 15 19 20 31	18	30
19	19q13.12	41115596	41264783	5,72E-06	0,000173307	149188	14	2,62128	8 9 21 22 23 29 32 35 37 40 43 45 46 48	5	1,28313	13 15 19 20 31	19	29
19	19q13.12	41264783	41472929	5,72E-06	0,000173307	208147	14	2,62128	8 9 21 22 23 29 32 35 37 40 43 45 46 48	4	1,56224	13 15 19 20	18	30
19	19q13.12	41472929	42993156	5,72E-06	0,000173307	1520228	11	2,61995	8 9 21 22 23 29 32 35 37 40 43	4	1,56224	13 15 19 20	15	33
19	19q13.12 - 19q13.13	42993156	43107740	5,72E-06	0,000173307	114585	12	2,62385	8 9 21 22 23 29 32 35 37 40 43 48	4	1,56224	13 15 19 20	16	32
19	19q13.13 - 19q13.2	43107740	44707934	5,72E-06	0,000173307	1600195	13	2,61275	8 9 21 22 23 29 32 35 37 40 43 45 48	4	1,56224	13 15 19 20	17	31
19	19q13.2	44707934	44977336	5,72E-06	0,000173307	269403	12	2,62197	8 9 21 22 23 29 32 35 37 40 45 48	5	1,58576	13 15 19 20 43	17	31
19	19q13.2	44977336	47550448	5,72E-06	0,000173307	2573113	13	2,62016	8 9 21 22 23 29 32 35 37 40 43 45 48	4	1,56224	13 15 19 20	17	31
19	19q13.2 - 19q13.31	47779163	47911291	5,78E-06	0,000173874	132129	13	2,62147	8 9 21 22 23 29 32 35 37 40 43 45 48	4	1,56224	13 15 19 20	17	31
19	19q13.31	48425188	49215048	5,47E-06	0,000173307	789861	13	2,62147	8 9 21 22 23 29 32 35 37 40 43 45 48	4	1,56224	13 15 19 20	17	31
19	19q13.31	49215048	49309423	5,47E-06	0,000173307	94376	12	2,6177	8 9 21 22 23 29 32 35 37 40 43 45	4	1,56224	13 15 19 20	16	32
19	19q13.31	49309423	49692017	5,47E-06	0,000173307	382595	11	2,63026	8 9 21 22 23 29 32 35 37 40 43	4	1,56224	13 15 19 20	15	33
19	19q13.31	49692017	49730102	5,47E-06	0,000173307	38086	12	2,63798	8 9 21 22 23 29 32 35 37 40 43 48	4	1,56224	13 15 19 20	16	32
19	19q13.31 - 19q13.32	49730102	51175833	5,47E-06	0,000173307	1445732	13	2,63425	8 9 21 22 23 29 32 35 37 40 43 45 48	4	1,56224	13 15 19 20	17	31
19	19q13.32	51175833	53447663	5,47E-06	0,000173307	2271831	14	2,63914	8 9 21 22 23 29 32 35 37 39 40 43 45 48	4	1,56224	13 15 19 20	18	30
19	19q13.32	53447663	53625403	5,47E-06	0,000173307	177741	15	2,68176	8 9 21 22 23 28 29 32 35 37 39 40 43 45 48	4	1,56224	13 15 19 20	19	29
19	19q13.32 - 19q13.33	53625403	56153019	5,47E-06	0,000173307	2527617	14	2,63914	8 9 21 22 23 29 32 35 37 39 40 43 45 48	4	1,56224	13 15 19 20	18	30
19	19q13.33	56153019	56728846	5,47E-06	0,000173307	575826	13	2,64297	8 9 21 22 23 29 32 35 37 39 40 43 48	4	1,56224	13 15 19 20	17	31
19	19q13.33 - 19q13.41	56728846	59073302	5,47E-06	0,000173307	2344456	12	2,6363	8 9 21 22 23 29 32 35 37 39 40 43	4	1,56224	13 15 19 20	16	32
19	19q13.41 - 19q13.42	59073302	59926385	5,47E-06	0,000173307	853084	13	2,64503	8 9 21 22 23 29 32 35 37 39 40 43 48	4	1,56224	13 15 19 20	17	31
19	19q13.42	59926385	60223566	5,47E-06	0,000173307	297182	13	2,64503	8 9 21 22 23 29 32 35 37 39 40 43 48	5	1,50805	13 15 19 20 33	18	30
19	19q13.42	60223566	60851243	5,47E-06	0,000173307	627678	13	2,64503	8 9 21 22 23 29 32 35 37 39 40 43 48	4	1,56224	13 15 19 20	17	31
19	19q13.42 - 19q13.43	60851243	63745505	5,47E-06	0,000173307	2894263	13	2,61892	8 9 21 22 23 29 32 35 37 39 40 43 48	4	1,56224	13 15 19 20	17	31
20	20p13	378409	599153	2,39E-05	0,000438182	220745	24	3,06386	9 10 11 12 14 15 16 17 18 19 20 24 26 28 29 31 32 33 34 36 43 44 45 48	3	1,16296	6 7 30	27	21
21	21p11.2 - 21q11.2	9896656	13357496	4,70E-05	0,000761937	3460841	4	2,53574	8 9 16 29	14	1,56484	3 13 19 20 27 31 32 33 35 36 38 40 44 46	18	30
21	21q22.3	44395713	44407647	4,17E-05	0,00070451	11935	8	2,49007	8 9 14 23 29 40 43 48	7	1,58853	19 27 32 33 36 44 46	15	33
22	22q12.2	27929293	28036259	4,87E-05	0,000768626	106967	19	2,79507	15 16 18 19 20 24 25 26 28 29 30 31 32 33 34 43 46 47 48	3	1,52495	27 41 44	22	20

HUGO Gene Symbol	Nominal p-value	FDR	Patient specific in % of comparisons	Gene description	RefSeq	Affymetrix TC ID	GO_biological_process
CDH3	2,84E-10	8,20E-06	71	NM_001793 // CDH3 // cadherin 3, type 1, P-cadherin (placental) // 16q22.1 // 10	NM_001793	7996819	NM_001793 // GO:0007155 // cell adhesion // traceable author statement /// NM_0
KIT	1,29E-08	4,65E-05	75	NM_000222 // KIT // v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolo	NM_000222	8095110	NM_000222 // GO:0002318 // myeloid progenitor cell differentiation // inferred f
CYGB	5,29E-07	6,88E-04	71	NM_134268 // CYGB // cytoglobin // 17q25.3 // 114757 /// ENST00000293230 // CYGB	NM_134268	8018754	NM_134268 // GO:0006810 // transport // inferred from electronic annotation ///
NNMT	1,10E-06	1,01E-03	75	NM_006169 // NNMT // nicotinamide N-methyltransferase // 11q23.1 // 4837 /// ENS	NM_006169	7943998	---
NAA11	1,21E-06	1,01E-03	82	NM_032693 // NAA11 // N(alpha)-acetyltransferase 11, NatA catalytic subunit // 4	NM_032693	8101253	NM_032693 // GO:0008152 // metabolic process // inferred from electronic annotat
BAGE2	2,49E-06	1,44E-03	75	NM_182482 // BAGE2 // B melanoma antigen family, member 2 // 21p // 85319 /// NM	NM_182482	8069487	---
TPTE	3,42E-06	1,73E-03	75	NM_199261 // TPTE // transmembrane phosphatase with tensin homology // 21p11 //	NM_199261	8069472	NM_199261 // GO:0006470 // protein amino acid dephosphorylation // inferred from
	1,22E-05	3,58E-03	71	---	---	8045525	---
GNAL	1,46E-05	3,97E-03	71	NM_182978 // GNAL // guanine nucleotide binding protein (G protein), alpha activ	NM_182978	8020164	NM_182978 // GO:0007165 // signal transduction // inferred from electronic annot
TUBA8	1,93E-05	4,56E-03	79	NM_018943 // TUBA8 // tubulin, alpha 8 // 22q11.1 // 51807 /// ENST00000330423 /	NM_018943	8071147	NM_018943 // GO:0007018 // microtubule-based movement // inferred from electroni
MAGEC2	2,12E-05	4,75E-03	75	NM_016249 // MAGEC2 // melanoma antigen family C, 2 // Xq27 // 51438 /// ENST000	NM_016249	8175562	---
TF	2,18E-05	4,80E-03	79	NM_001063 // TF // transferrin // 3q22.1 // 7018 /// ENST00000264998 // TF // tr	NM_001063	8082797	NM_001063 // GO:0006811 // ion transport // inferred from electronic annotation
RNASE1	2,34E-05	5,04E-03	71	NM_198232 // RNASE1 // ribonuclease, RNase A family, 1 (pancreatic) // 14q11.2 /	NM_198232	7977615	---
HORMAD1	2,58E-05	5,11E-03	82	NM_032132 // HORMAD1 // HORMA domain containing 1 // 1q21.3 // 84072 /// ENST000	NM_032132	7919787	NM_032132 // GO:0007067 // mitosis // inferred from electronic annotation /// N
CFI	2,82E-05	5,11E-03	79	NM_000204 // CFI // complement factor I // 4q25 // 3426 /// ENST00000394634 // C	NM_000204	8102328	NM_000204 // GO:0006508 // proteolysis // inferred from electronic annotation /
MAGEB2	3,47E-05	5,59E-03	71	NM_002364 // MAGEB2 // melanoma antigen family B, 2 // Xp21.3 // 4113 /// ENST00	NM_002364	8166611	---
MAGEA4	3,60E-05	5,69E-03	75	NM_[illegible]548 // MAGEA4 // melanoma antigen family A, 4 // Xq28 // 4103 /// NM_00	NM_001011548	8170531	NM_001011548 // GO:0008150 // biological_process // no biological data available
RGS5	5,74E-05	7,47E-03	71	NM_[illegible]617 // RGS5 // regulator of G-protein signaling 5 // 1q23.1 // 8490 /// EN	NM_003617	7921916	NM_003617 // GO:0008277 // regulation of G-protein coupled receptor protein sign
ITGA4	1,11E-04	1,06E-02	75	NM_[illegible] // ITGA4 // integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4	NM_000885	8046695	NM_000885 // GO:0001974 // blood vessel remodeling // inferred from electronic a
TM4SF1	1,13E-04	1,07E-02	75	NM_014220 // TM4SF1 // transmembrane 4 L six family member 1 // 3q21-q25 // 4071	NM_014220	8091411	NM_014220 // GO:0008150 // biological_process // no biological data available /
TDO2	1,24E-04	1,13E-02	75	NM_005651 // TDO2 // tryptophan 2,3-dioxygenase // 4q31-q32 // 6999 /// ENST0000	NM_005651	8097991	NM_005651 // GO:0019441 // tryptophan catabolic process to kynurenine // inferre
SERPINA3	1,45E-04	1,23E-02	82	NM_001085 // SERPINA3 // serpin peptidase inhibitor, clade A (alpha-1 antiprotei	NM_001085	7976496	NM_001085 // GO:0006953 // acute-phase response // inferred from electronic anno
ARHGEF6	1,88E-04	1,46E-02	71	NM_004840 // ARHGEF6 // [illegible]dc42 guanine nucleotide exchange factor (GEF) 6 //	NM_004840	8175393	NM_004840 // GO:0006915 // apoptosis // not recorded /// NM_004840 // GO:000691
DKK3	2,64E-04	1,81E-02	71	NM_015881 // DKK3 // [illegible]kkopf homolog [illegible]enopus laevis) // 11p15.2 // 27122 ///	NM_015881	7946661	NM_015881 // GO:0007275 // multicellular organismal development // inferred from
APCDD1	2,82E-04	1,85E-02	75	NM_153000 // APCDD1 // adenomatosis [illegible]ypo[illegible] coli down-regulated 1 // 18p11.22	NM_153000	8020141	---
LOC100133469	3,14E-04	1,98E-02	71	NR_027457 // LOC100133469 // hypo[illegible]00133469 // --- // 100133469	NR_027457	7977447	---
DSCR8	3,63E-04	2,16E-02	75	NR_026839 // DSCR8 // Down syndr[illegible]al region gene 8 // 21q22.2 // 84677 /	NR_026839	8068570	NR_026839 // GO:0008150 // biological_process // no biological data available /
SLAMF7	4,81E-04	2,55E-02	75	NM_021181 // SLAMF7 // SLAM family m[illegible]ber [illegible]1-q24.1 // 57823 /// ENST000	NM_021181	7906613	NM_021181 // GO:0007155 // cell adhesion // non-traceable author statement ///
VAMP8	8,46E-04	3,49E-02	75	NM_003761 // VAMP8 // vesicle-associated mem[illegible]tei[illegible]8 (endobrevin) // 2p12	NM_003761	8043197	NM_003761 // GO:0006461 // protein complex assembly // inferred from electronic
MGP	8,57E-04	3,51E-02	86	NM_000900 // MGP // matrix Gla protein // 12p1[illegible]12.3 /[illegible]256 /// ENST00000228	NM_000900	7961514	NM_000900 // GO:0001502 // cartilage condensation // traceable author statement
CD200	8,74E-04	3,55E-02	71	NM_001004196 // CD200 // CD200 molecule // 3q12-q13 // [illegible]NM_000944 // CD2	NM_001004196	8081657	---
CD302	8,76E-04	3,55E-02	75	NM_014880 // CD302 // CD302 molecule // 2q24.2 // 9936 // [illegible]59053 // CD	NM_014880	8056102	---
FLRT3	1,10E-03	4,05E-02	75	NM_198391 // FLRT3 // fibronectin leucine rich transmembrane prote[illegible] //	NM_198391	8065071	NM_198391 // GO:0007155 // cell adhesion // inferred from electronic annotation
C1S	1,17E-03	4,16E-02	75	NM_201442 // C1S // complement component 1, s subcomponent // 12p13[illegible]6 // N	NM_201442	7953603	NM_201442 // GO:0006508 // proteolysis // inferred from electronic annotation /
MME	1,26E-03	4,33E-02	79	NM_007288 // MME // membrane metallo-endopeptidase // 3q25.1-q25.2 // 4311 // N	NM_007288	8083494	NM_007288 // GO:0006508 // proteolysis // inferred from electronic annotation /
CYorf15B	1,26E-03	4,33E-02	71	NM_032576 // CYorf15B // chromosome Y open reading frame 15B // Yq11.222 // 8466	NM_032576	8176709	---
SLITRK6	1,40E-03	4,63E-02	75	NM_032229 // SLITRK6 // SLIT and NTRK-like family, member 6 // 13q31.1 // 84189	[illegible]M_032229	7972239	NM_032229 // GO:0007409 // axonogenesis // inferred from electronic annotation