

Supplementary Information for Whole Genome Sequencing to Characterise Breast Cancer Response to Aromatase Inhibitors.

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A. Supplementary Materials and Methods

Whole-genome Sequencing and Alignment

We followed the procedure described by Mardis *et al.*¹ for library construction and sequencing. Illumina 2x75 or 2x100bp lanes were aligned individually to NCBI Build 36 of the human reference sequence using BWA 0.5.5 and samtools r544. Alignments were merged into a single BAM file and marked for duplicates using Picard 1.17. Only non-duplicate reads were used for all downstream analyses.

Exome-capture sequencing Library Construction

Genomic DNA samples (3ug) were constructed into Illumina libraries according to the manufacturer's protocol (Illumina Inc, San Diego, CA) with the following modifications: 1) DNA was fragmented using Covaris S2 DNA Sonicator (Covaris, Inc. Woburn, MA). Fragment sizes ranged between 100 and 500bp. 2) Illumina adapter-ligated DNA was amplified in a single 50µl PCR for five cycles. 3) Solid Phase Reversible Immobilization (SPRI) bead cleanup was used to purify the PCR and select for 300-500bp fragments.

Exome Capture Hybridization and Sequencing

Sequencing libraries were hybridized using Roche NimbleGen SeqCap EZ Human Exome Library v2.0 kits according to the manufacturer's protocol². Illumina library quantification was completed using the KAPA SYBR FAST qPCR Kit (KAPA Biosystems, Woburn, MA).

Exome Alignment, De-duplication, and BAM File Generation

Illumina reads were mapped to the Ensembl release 45 version of Human NCBI Build 36 using BWA³ v0.5.7 with soft trimming (-q 5). For each sample, individual lane alignments in BAM format were merged together using SAMtools⁴ r544. Duplicates were marked in the merged BAM files by the MarkDuplicates class of Picard⁵ v1.17. Reads with mapping quality of zero, or that were marked as duplicates by Picard, were excluded from further analysis.

SNV and Small Indel Detection

Candidate point mutations were predicted using SomaticSniper, previously referred to as glfSomatic^{1,6}. Putative SNVs with somatic score ≥ 40 and average mapping quality ≥ 40 were considered high-confidence (HC); all others were deemed low-confidence (LC). Small indels were predicted using a combination of GATK⁷ IndelGenotyper, Pindel⁸, and a modified version of SAMtools⁴. Both SNVs and indels were annotated using gene structure and conservation information, and classified by tier as previously described⁹. Briefly, tier 1 mutations alter protein coding sequences, tier 2 mutations map to conserved and/or regulatory sequences, tier 3 mutations occur in unique noncoding sequences, and tier 4 mutations map to repetitive regions. High confidence tier 2 and tier 3 mutations, and all tier 1 mutations (regardless of confidence) were selected for validation (see below).

Copy Number Variation (CNV) Analysis

Genome-wide copy number estimates were generated on three independent platforms: array CGH, high-density SNP array, and whole genome sequencing. Array CGH data were produced using Agilent 244K arrays for all cases except BRC26, BRC38, BRC34, BRC39, BRC48, and BRC52. High-density SNP array data were produced using Illumina 1M arrays (BRC2-BRC47) and iScan arrays (BRC48-52) and were collated into a single set based on probe positions. CGH and SNP array data were processed using the CBS and CGHcall algorithms, yielding two call sets in identical format. Calls with probability scores of less than 0.5 were removed prior to subsequent analysis.

Copy number calls from whole-genome sequencing data were generated using the cnvHMM algorithm (cnvHMM, K. Chen et al, <http://genome.wustl.edu/software/cnvhmm>). First, cnvHMM divided the genome into non-overlapping windows 10kbp in size. For each window, the raw copy number was estimated as the number of reads confidently mapped (mapping quality > 35) divided by the median such value across all windows in the genome, then multiplied by two (to reflect diploid genomes). A Hidden Markov Model (HMM) was then used to perform the segmentation. Each state in the HMM corresponds to a discrete copy number value. The emission probability was modeled as a single Gaussian probability density function. A standard Viterbi algorithm was used to estimate the HMM parameters and determined the segmentation. We derived copy number altered regions (CNARs) by comparing the segmentation of the tumour genome versus that of the normal genome. A log likelihood ratio (LLR) score was computed for each CNAR to quantify the possibility of being a true CNAR from being the null (copy-number neutral) hypothesis. Calls with LLR score smaller than 20 were dropped from further consideration.

Copy number calls from CGH array, high-density SNP array, and WGS were intersected into a single set that included only calls confidently and consistently (identical gain or loss status) supported by at least two platforms.

Structural Variation (SV) Analysis

Structural variants (SVs) were predicted by BreakDancer¹⁰ with TIGRA_SV assembly¹¹, SquareDancer (K. Chen et al, in preparation), and Pindel⁸. Copy number differences with regions of SV were determined by BreakDancer¹⁰. Putative SVs from BreakDancer were chosen for localized, *de novo* assembly if they (1) had at least 2 supporting discordant read pairs in the tumour, but none in the normal, (2) were supported by a copy number change of >0.5 in the SV region, (3) affected a coding exon, or (4) had one or more breakpoints in any part of a known cancer gene. SV regions were defined as +/- 500bp from the predicted breakpoints.

The depth-weighted average contig length was used as a quality measure of the assembly:

$$q = \frac{\sum_{i=0}^{M-1} d_i l_i}{\sum_{i=0}^{M-1} d_i},$$

where l_i and d_i are the length and the average depth of contig i respectively, and M is the total number of contigs in the TIGRA assembly. Short contigs (< 30 bp) that are assembled from the homopolymer reads are excluded in the calculation. We found this statistic properly summarizes both the size and the coverage and therefore is more informative to measure the assembly quality than the N50 size. Based on our manual examination of the alignment results, we found that the high quality assemblies that contain valid sequence frequently have $q > 100$ bp.

Once assembled, contigs were aligned to their respective local reference sequences (SV region +/- 700 bp; NCBI Build 36) using `cross_match v1.080721` with the parameters “`-bandwidth 20 -minmatch 20 -minscore 25 -penalty -10 -discrep_lists -tags -gap_init -10 -gap_ext -1`”. Contigs whose alignments had >2 segments or were significantly different from the reference (one segment with substitution >0.006 or indel rate of >0.002; or two segments with substitution rate >0.005, indel rate of >0.001, or >5 inserted/deleted bases) were removed. Assembled SVs with contig score ≥ 50 , and whose alignments supported a variant of type and size consistent with the original BD prediction, were selected for validation.

A complementary in house algorithm, SquareDancer, was used to identify candidate SVs by utilizing soft-clipping information from the BWA aligner. Large deletions and moderately-sized insertions were also predicted using a modified

version of the Pindel⁸ tool. Pindel calls with read support in the tumour but not the normal, as well as calls supported by copy number evidence from cnvHMM (copy number > 0.5) were selected for validation. Candidate SVs from BreakDancer, SquareDancer, and Pindel SV regions from different methods that overlapped >75% (allowing a buffer of +/- 50 bp) were merged into a single event.

Capture-based Experimental Validation

Nimblegen custom sequence capture arrays were designed for validation of SNVs, indels, and SVs by targeted enrichment and deep Illumina sequencing. For SNVs and small indels, we targeted ~200 bp regions centered on the variant of interest. For structural variants, we tiled 200 bp targets across the predicted breakpoint, including a minimum buffer of 200 bp in each direction. Thus, for insertions a single region is requested, but for translocations, deletions, inversions etc, we requested two regions, one for each breakpoint. Since BreakDancer reports regions of ambiguity around the breakpoints, we buffered 200 bp upstream and downstream of these regions and requested probes for the entire region. To accommodate SVs flanked by duplicate sequences, we accepted probes if they had five or fewer unique matches in the genome.

A single custom array was designed for each of the 46 cases. Tumour and normal samples were captured and sequenced independently as previously described [1]. Validation lanes were aligned to the reference sequence and BAM files created in the same manner as described above.

Validation Data Analysis

To validate predicted SNVs and small (<3bp) indels, we used VarScan 2 (Koboldt *et al*, submitted) with the following parameters: `--min-coverage 30 --min-var-freq 0.08 --p-value 0.10 --somatic-p-value 0.01 --validation 1`. To validate low-frequency (2-8%) SNVs, we re-ran VarScan with adjusted parameters: `--min-coverage 100 --min-var-freq 0.02 --p-value 0.10 --somatic-p-value 0.01 --validation 1`. In validation mode, VarScan reads data from tumour and normal samples simultaneously, performing pair-wise comparisons at every position covered in both samples. Each position is classified as Reference (wild-type), Germline, LOH, or Somatic, based upon a comparison of the consensus genotypes and supporting read counts (Fisher's Exact Test). Positions called Somatic are further subjected to our internally-developed false-positive filter which removes sequencing- and alignment-related artifacts using several criteria (read count, mapping quality, average read position, strand representation, homopolymer-like sequence context, mismatch quality sum difference, trimmed read length, Q2 distance).

To validate putative SVs, we re-mapped reads and any unmapped mates that had aligned within 500 bp of predicted breakpoints. For this realignment, we used `cross_match v1.080721` with the parameters: `-discrep_lists -minmatch 10 -maxmatch 10 -minscore 15`. Reads were aligned as fragments, independent of their mates. In addition to the SV-containing contig from TIGRA_SV, we mapped reads against reference sequence contigs defined within +/- 1000 bp of each breakpoint. Alignments were considered valid if they had an alignment score of ≥ 50 , substitution and indel rates below 1%, and < 2 unaligned bases at either end. Reads that mapped to reference (wild-type) sequence within +/- 1000 bp of SV breakpoints with $< 1\%$ substitution or indel, alignment score > 50 , and < 2 unaligned bases at either end were considered reference-supporting reads.

SV breakpoints are defined in the discovery phase and include any ambiguity in positioning the variant due to repetitive sequence. To be considered an SV-supporting read, a read must span the entire breakpoint region and include at least 10 additional bases beyond the region endpoints (e.g. if BreakDancer calls the breakpoint anywhere within nucleotides 200-230 in an SV contig, an SV-supporting read must cover positions 190-240). The normal and tumour bam files are used to get SV-supporting reads from each tissue. A Fisher's Exact Test of the number of variant-supporting reads and total number of reads aligned within 500 bp of SV breakpoints is used to determine significance.

SV calls were classified as somatic, germline, wild-type (no event), or ambiguous based on the supporting evidence from the validation data. For somatic SVs, we required the tumour to have at least 5 SV-supporting reads, and more SV-supporting reads than the normal, with a FET p-value of less than 0.05. We further required < 10 SV-supporting reads in the normal. For germline SVs, we require at least 20 SV-supporting reads in both tumour and normal samples; SVs classified as germline in any patient were removed from the candidate lists of all patients. If no SV-supporting reads are found in tumour or normal, the variant is classified wild-type (no event). Candidate SVs that did not meet criteria for somatic, germline, or wild-type categories were classified as ambiguous.

Manual Review of Homozygous Deletions

Read depths for the 768 validated deletions were calculated in 100 bp windows using the tumour validation BAM. Some 15% of deletions were too small to be surveyed at this window size. For the remaining 85%, read depth was manually reviewed across deletion breakpoints to determine heterozygous or homozygous status. Of these, 26 were determined to be homozygous.

Recurrence Screening

All significantly mutated genes identified in the 46 whole genome sequenced cases were screened for recurrent mutations in an additional cohort of 121 tumour normal pairs in a manner described previously [1,2]. Briefly, using Primer3, universal-tailed PCR primers were designed to amplify all coding exons in all known isoforms. Whole genome amplified tumour DNA was PCR amplified using AmpliTaq Gold PCR Master mix and sequenced using BigDye 3.1 Sequencing Kits loaded on ABI 3730xl capillary sequencers. Data were assembled using Consed and mutations were identified using Polyscan and Polyphred. Additional attempts were made to obtain sequence coverage of genes with < 80% coverage of coding exons. All high confidence putative somatic mutations were validated with additional rounds of PCR amplification and Sanger sequencing that utilized a second independent source of tumour genomic DNA and normal DNA.

Mutation Rate and Spectrum Analysis

Mutation rate and spectrum analyses utilized validated SNVs in tier 1 (coding), tier 2 (conserved/regulatory), and tier 3 (unique noncoding) regions. For the mutation rate calculation, the number of validated SNVs in each tier was compared to the total number of bases in that tier. The number of bases in each tier was determined using our internal annotation database. On NCBI Build 36, there were 43.89 Mbp, 248.21 Mbp, and 1198.99 Mbp in tiers 1, 2, and 3, respectively. The mutation rate (mutations per megabase) was calculated independently for each tier, and then for all three tiers combined to determine the overall mutation rate.

Downstream Analysis of Mutation Significance In Cancer (MuSIC)

We applied our suite of downstream analysis tools, collectively called Mutation Significance In Cancer (MuSiC, ¹²), to validated mutations in the discovery set and recurrence panel. First, the overall background mutation rate (BMR) for several categories of mutations was determined by dividing the number of validated non-synonymous mutations in each category by the number of coding bases sufficiently covered for mutation detection (14x for tumour, 8x for normal) in that category. We used these categories: AT transitions, AT transversions, CpG transitions, CpG transversions, CG (non CpG) transitions and transversions, and a seventh “indel” category, for which we use the entirety of the covered space when comparing indels versus available bases. P-values describing mutational significance were assigned to each gene for each category by comparing the gene’s mutation rate (MR) of that category to the overall BMR in the same category. Significantly mutated genes (SMGs) were identified on the basis of three tests used to sum the p-values from the 7 mutation categories. These tests include a convolution test, which calculates a summarized log statistic of joint binomial

point probability, a likelihood-ratio test, which summarizes p-values using a likelihood ratio-based statistic calculated using the given mutation number, the BMR, the coverage, and the maximum likelihood estimate of the MR, and lastly, a Fisher's combined p-value test, which combines p-values from different mutation categories into a statistic using Fisher's method¹³, and then compares this statistic to a χ^2 distribution to determine significance.

Once SMGs were identified, we used a correlation test to determine co-occurrence (positive correlation) and mutual exclusivity relationships (negative correlation) between mutations in SMGs. These tests are performed pair-wise between each SMG and every other SMG, and p-values are calculated using a controlled permutation method which takes into account the distribution of mutation counts amongst the samples.

The entire list of mutations was also compared to the collected clinical data using a clinical correlation test. A Pearson's correlation is used to compare numerical clinical data to mutation counts, while a Fisher's exact test was used to compare categorical clinical data to mutation counts. Other MuSiC packages identified clusters of mutations in close proximity to one another within a gene, as well as mutated residues previously reported to COSMIC and OMIM databases.

Clinical Correlation Analysis

Mutation frequency of a gene in SET 1 and SET 2 and within each category of a categorical variable was calculated. The Fisher's exact test or Chi-square test whichever proper was used to examine the mutation difference between the two sets and associations between categorical variables and gene mutations. The geometric mean of Ki67 at baseline, surgery and corresponding percentage change were calculated (with the zero values at baseline and surgery replaced by 0.001 and 0.0001 individually). The Wilcoxon rank sum test was applied to compare the Ki67 distribution between mutant and wildtype cases. To address the concern of multiple testing, adjusted p-values based on Benjamini-Hochberg false discovery rate (FDR) and 1000 permutations were obtained for the whole set (SET 1 and 2 combined). To confirm the reproducibility of significant associations despite set division, a leaving half-out cross-validation procedure (1000 times) was adopted where the whole set of 317 samples were randomly split into two sets of equal sample size and association test p-values were calculated from both set to derive the percentage of times an association is significant with both raw p-values $\leq 5\%$.

Gene Interaction Network Analysis

The interaction networks were compiled from Metacore maps (GeneGo, Inc.) significantly intersecting with the mutation list (corrected FDR < 0.05). Mutated genes in multiple network objects were only considered in one object to prevent redundant mutation counts. Network objects were classified into eight functional networks and arranged hierarchically in Cytoscape [10]. SMGs AGTR2, STMN2, MLL3, and SF3B1 were not included in any maps by Metacore, so curated interactions were added with members of the most applicable network. Some interactions between non-mutated nodes were removed for clarity. The number of tumors harboring a node mutation is indicated by node size. SMGs from each network are differentiated in red and by a reference number; other mutated objects are colored black. All 77 tumors were classified by network and SMG mutation status in a concentric display. Each patient is represented by a spoke in the wheel, affected networks for each patient are indicated by the appropriate color, and SMG mutations are shown as black dots in the parent network. The MLL2/3 complex is represented as a single network node with multiple mutated constituent genes. Of these, only MLL3 was considered an SMG in patient classification. (Supplementary Data Files)

PARADIGM integrated pathway analysis of copy number and expression data

Integration of copy number, gene expression, and pathway interaction data was performed using the PARADIGM software¹⁴. Briefly, this procedure infers integrated pathway levels (IPLs) for all *pathway features* including genes, complexes, and processes using pathway interactions and genomic and functional genomic data from a single patient sample. PARADIGM uses a factor graph model based on a pathway database. In this paper, we used, a *SuperPathway*, which is an integration of a network of cellular pathways drawn from the NCI and Reactome database and includes both genes and abstract pathway concepts. The SuperPathway contains interactions for 16,363 features including 5541 proteins. PARADIGM inferred pathway features are preferable over gene expression since PARADIGM integrates knowledge of CNV. Additionally, PARADIGM infers IPLs that are not available by current assays.

We applied PARADIGM to the analysis of the 77 discovery samples and then separately to the 124 validation samples for which both gene expression and copy number data were available. We first asked what genes received significantly high or low activities in the tumour samples relative to normal such that they would be suggested markers of disease. To this end, we formed a background distribution by creating 1000 “simulated patient samples” made up of randomly permuted data tuples. The construction of a simulated sample was made by distributing the data arbitrarily about the SuperPathway. PARADIGM was then rerun using these simulated samples, thus producing a background of inferred activities for each gene. Using this background we could then assess if an inferred level of a gene in a particular sample exceeded c

standard deviations from the average seen in the simulated control samples. If a gene exceeded c in at least 2 samples it was categorized as *modulated*. Sweeping through higher (more stringent) values of c yielded fewer genes. When the number of genes was plotted against this modulation cutoff (Supplementary Figure 7a) it revealed that many genes with appreciable levels of noise are discarded at low cutoffs but a robust set of genes with significant activities were invariant to a range of higher levels. We identified 724 genes as the “elbow” in the curve as that point of diminishing returns where we expect to find the largest number of such modulated genes – raising the cutoff more had little effect on the retained set.

It is important to note that the procedure to identify this set of genes used only the samples in the discovery set. This allowed us to assess the overall reproducibility of the PARADIGM method on the validation set using a straightforward comparison of the modulated genes discovered independently in the validation set.

If the inferences found for the genes using the samples from the discovery set are robust then the set of genes receiving significantly modulated (high- or low-activities relative to normal) should correspond to the same genes identified as modulated in the validation set. Indeed, we found this to be true. By sweeping through modulation cutoffs on both the validation and discovery sets we found that the set of genes identified as the most overlapping between the two were very close to the “elbow” point on the curves identified as the point where the set of reliable genes were identified (Supplementary Figure 7b-c). The overlap of the genes modulated in the discovery set with those modulated in the validation set was 70% which is highly significant (hypergeometric test, $P < 10^{-300}$).

To produce a single PARADIGM result, we next combined the 77-sample discovery and 124-sample validation sets and reran PARADIGM on the combined dataset. We repeated the modulation analysis and found 628 genes (87% overlap with the test set). The inferred pathway activities of the 628 modulated genes across the discovery samples were plotted (Supplementary Figure 7). The genes and samples were ordered using hierarchical agglomerative clustering as coded in the Eisen 2.0 Software Package¹⁵. The gene clusters were then overlapped with the constituent sub-pathways that were used to build the SuperPathway in order to annotate which subnetworks had been selected by modulation and reveal their cohort signatures. The TreeView-formatted dataset is available as a Supplementary Data File.

Differential Pathway Signature Correlation

The pathway activities inferred by PARADIGM can be used analogously to gene expression levels for the purpose of identifying signatures that predict the presence or absence of a particular tumour attribute of interest. Signatures were derived by classifying samples into dichotomous sets based on clinical features or the presence of a mutation. Each mutation dichotomizes the samples into two groups: those with the mutation and all others. The IPL values for all proteins were then fed to Significance Analysis of Microarrays (SAM) to determine the Differential IPLs (DPLs). SAM uses a dichotomization of the samples in a two-way test. The DPL scores are then summarized using Gene Set Enrichment Analysis. The gene sets are drawn from the underlying NCI and Reactome databases as well as Gene Ontology (GO). Cluster-Eisen then clusters the data from SAM. The Gene Set Enrichment Analysis labels are applied to the heatmap rendered by Java Treeview¹⁶.

Comparison of PARADIGM sub-networks to MetaCore Maps

We asked whether the pathways identified by the mutation-directed MetaCore analysis were coincident with the pathways identified by PARADIGM as modulated when viewing the transcription and copy number data of the 77 sample discovery cohort. To do this, we first determined which of the constituent pathways that were used to build PARADIGM's SuperPathway were present among the modulated features. We found 233 such sub-networks among the 3974 modulated features. We performed all pair-wise intersections between these 233 sub-networks and the 104 MetaCore maps using only the proteins present in each sub-network. Proteins were identified by mapping both the SuperPathway sub-networks and MetaCore maps to HUGO gene symbols. We used a stringent p-value cutoff to impose a multiple testing correction due to the $233 \times 104/2$ unique comparisons. The result of this analysis determined that 75 (72%) of the MetaCore maps were also identified as modulated by PARADIGM and represented as one of 87 modulated SuperPathway sub-networks (Supplementary Figure 9). The list of common sub-networks are listed in Supplementary Table 20 and include many expected and important pathways involving regulation of retinoblastoma, mTOR signaling, ATM and ATR signaling, endothelins, HIF1A, RAS signaling, and so on. This finding is highly significant and is reassuring that these two approaches using different data sources converge on the same set of altered pathways.

Pathway-based signatures of response

Differential pathway levels (DPLs) associated with Ki67 response are then computed using the SAM approach that computes a corrected t-statistic for each gene in the pathway. A network of interlinked differentially active genes we refer

to as a PathMark was then identified as those interactions in the SuperPathway connecting two genes with absolute SAM scores better than average (Supplementary Data Files). Because the original inferences were derived from an underlying connected network, it is possible that the observed subnetworks of interconnected markers arise from serendipitous but random associations simply due to PARADIGM's belief propagation framework. We asked whether the observed PathMark is significant. If the interconnection among the genes in the PathMark are indeed associated with response then one would expect that the size of the sub-networks would be larger than networks obtained from random patients in which data tuples were permuted around the SuperPathway. We indeed found that the observed largest connected sub-pathway was significantly larger than expected by chance (Supplementary Figure 10a). We repeated the entire procedure on the validation set and found that the DPLs were very similar (Supplementary Figure 10b)

Associating tumour attributes with pathway signatures

The derivation of PARADIGM inferred activities enables a molecular pathway-based comparison of samples that may help reveal new connections between mutations, clinical outcomes, and cancer subtypes. A dichotomous division of samples into two groups was formed for every categorical variable. A positive class made up of samples that have a particular value of an attribute and a negative class that lack the value of the attribute in question. For continuous-valued variables, such as Ki67 response, positive and negative classes of samples can be defined using a threshold to turn the attribute into a discrete-valued categorical variable. Once a dichotomous variable was established for a tumour attribute we calculated a signature for the dichotomy made from an associated DPL vector as described above again using the SAM software. The DPL signature encapsulates the pathway-informed up- and down-regulation of genes that are characteristic of patients with a particular tumour feature such as the presence of a mutation or Ki67 response. The relationships between these clinical and genomic characteristics could then be assessed by comparing their DPL signatures to one another. The correlation between all pairs of dichotomous variables was then assessed by computing the Pearson correlation between all pairwise clinical- and mutation-derived DPL signatures.

Histone modification genes in luminal breast cancer

An array of coding mutations (a significant fraction of them leading to protein truncations) and structural variations was discovered in methyltransferases (*MLL2*, *MLL3*, *MLL4*, and *MLL5*), demethyltransferases (*KDM6A*, *KDM4A*, *KDM5B*, and *KDM5C*), and acetyltransferase (*MYST1*, *MYST3*, and *MYST4*) (**Supplementary Table 19**). Furthermore, our analysis identified several adenine-thymine (AT)-rich interactive domain-containing protein genes (*ARID1A*, *ARID2*, *ARID3B*, and *ARID4B*) that harbored mutations and large deletions, reinforcing the role of members from the SNF/SWI family in breast

cancer. Inactivating mutations in *MLL2* and *MLL3* were recently reported in 16% of medulloblastoma patients¹⁷ and *ARID1A* was previously found to be highly mutated in ovarian clear cell carcinoma¹⁸. Taken together, over 52% (24 out of 46) of patients exhibited alterations in histone lysine methyltransferase, demethylase, and acetyltransferase pathways. Thus, studies investigating the contribution made by chromatin modifications to the development of luminal breast cancer are warranted.

Frequently mutated non-coding regions

To investigate the potential importance of mutations found in non-coding regions, we applied a sliding window-based approach to detect clusters of mutations in tiers 2-3. We observed *ATR* intronic mutation clusters, as well as six tier 2 mutations within a 1 kb region of *GPR126*, and one tier 2 and four tier 3 mutations within a 2 kb window of *NRG3* (**Supplementary Table 7**). *GPR126* is required for myelination¹⁹ and was not previously linked to breast cancer. On the other hand, *NRG3* germline loss has been shown to lead to congenital breast aplasia in mice and is required for early breast morphogenesis²⁰⁻²².

Complex landscape of copy number alterations and structural variations

Copy number alterations (CNAs) present in the 46 tumour genomes were identified using data from three platforms: array CGH, SNP array, and whole genome sequencing. The 3 results subsequently were intersected to produce a unique set of CNAs supported by at least 2 platforms. Analysis of cumulative log₂ ratios revealed arm-level gains (cumulative log₂ ≥ 5) for 1q, 5p, 8q, 16p, 17q, 20p, and 20q and arm-level losses (cumulative log₂ ≤ -5) for 1p, 8p, 16q, and 17p, consistent with previous reports for luminal breast cancer²³ (**Supplementary Fig. 5**). CMDS²⁴ was used to identify recurrent focal CNAs using the whole-genome data set (**Supplementary Table 10**). This analysis yielded 35 focal regions of amplification, all encompassing 10 or fewer genes. Some of the most common focal amplifications included the cancer-associated genes *ZNF217*, *GAB2*, *BCAS1* (breast carcinoma-amplified sequence 1), and *ELF5*, each amplified in greater than 10% of tumours. CMDS also identified 24 focal deletions, of which 20 harbor fewer than 10 genes.

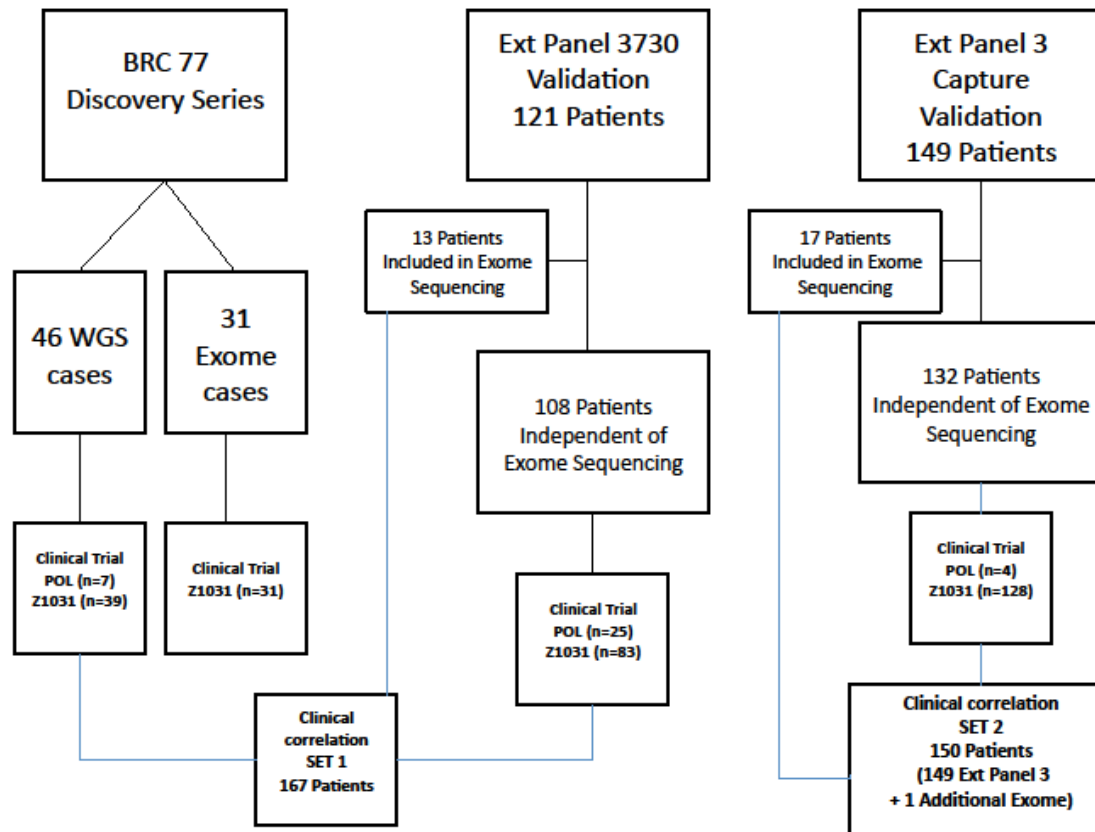
A total of 773 SVs (579 deletions, 189 translocations, and 5 inversions) identified by WGS were validated as somatic in 46 breast cancer genomes by capture validation (**Supplementary Table 11** and Supplementary Information). Paired end reads identified 579 deletions, including 163 events smaller than 1kb that are likely below the resolution of array-based detection.

Among the 7,815 genes affected by SVs, only 534 were previously described in Stephens *et al.*²⁵. Although a large number of genes (1,793) were recurrently affected by SVs, only 74 occurred within deletions smaller than 5 Mbp or in other types of structural alteration (**Supplementary Table 12**). Of note, recurrent SVs occur in widely divergent gene families, including tyrosine protein phosphatases (e.g., *PTPRR*, *PTPRQ*, *PTPN1*, and *PTPN5*), MAP kinases (e.g., *MAP3K1*, *MAP4K2* and *MAP2K4*) (**Fig. 3a**), histone post-translational modification enzymes (e.g., *SETDB1*, *MYST3*, and *MYST4*), and transcription factors (e.g., *ETV3* and *PAX6*).

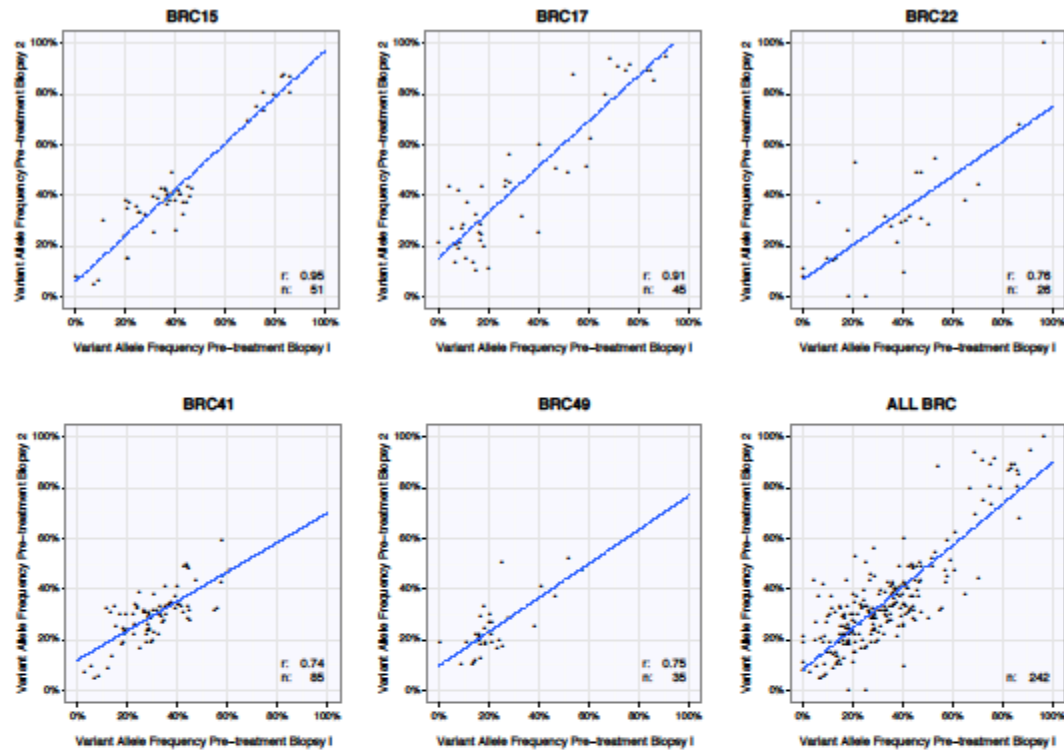
NRG1 encodes a number of isoforms that are ligands of the EGFR family. Gene losses and rearrangements in *NRG1* have been reported^{26,27}, including our earlier observation in a basal breast tumour of a 109,563 bp heterozygous deletion that removed three exons of *NRG1*²⁸. In this series, three *NRG1* deletions were observed with sizes of 555 bp, 3,338,927 bp, and 4,253,849 bp, respectively, further reinforcing the involvement of *NRG1* loss in breast cancer. Among 773 validated SVs, 7 deletions and 7 translocations were predicted to give rise to in-frame fusion proteins. We confirmed the expression of fusion transcripts for 6 of these events using RT-PCR, including ELP3-*NRG1*, *APIP-ABTB2*, *DNAH9-MYOCD*, *CHDH-ULK4*, *NAV2-C11orf49*, and *BCAS3-ATP8B4* (**Supplementary Table 13**). The ELP3-*NRG1* fusion (ENST00000256398-ENST00000405606) (**Fig. 3a**) could encode a protein with the first 522 (of 547) amino acids of ELP3 (elongator complex protein 3) fused to the *NRG1* transmembrane and cytoplasmic domains. The potential fusion protein eliminates all of the *NRG1* extracellular domains including the EGF-like and the Ig-like C2-type ligand-binding domains. Another validated fusion is the *BCAS3-ATP8B4* (ENST00000407086-ENST00000284509) fusion found in patient BRC6, wherein 406 codons of *BCAS3*, including two WD (tryptophan-aspartate) repeats, are fused to *ATP8B4* codons 429 to 1192. *ATP8B4* belongs to the cation transport ATPase (P-type) family. *BCAS3* (breast carcinoma amplified sequence 3) is fused to *BCAS4* in the MCF7 breast cancer cell line²⁹ and chimeric transcripts encoding portions of *BCAS3* and *MET* are overexpressed in esophageal adenocarcinoma³⁰. Further, *BCAS3* overexpression in hormone receptor-positive premenopausal breast cancer has been associated with impaired tamoxifen responses³¹.

B. Supplementary Figures

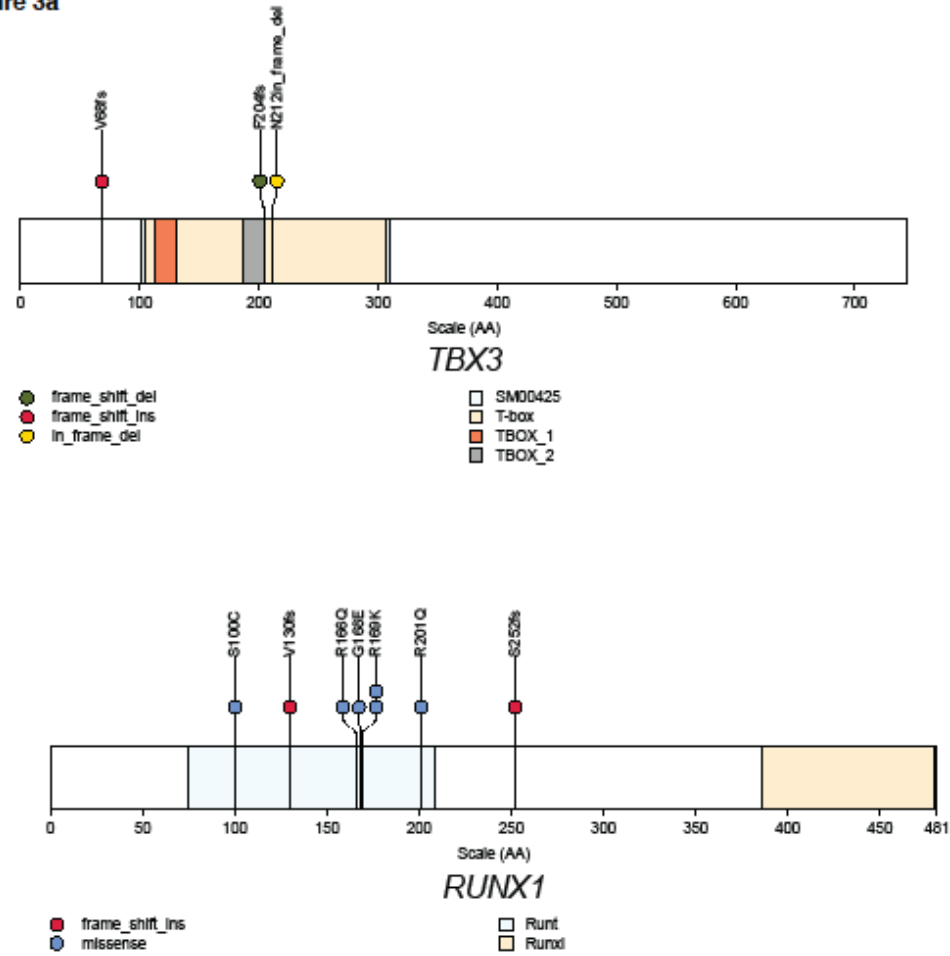
Supplementary Figure 1



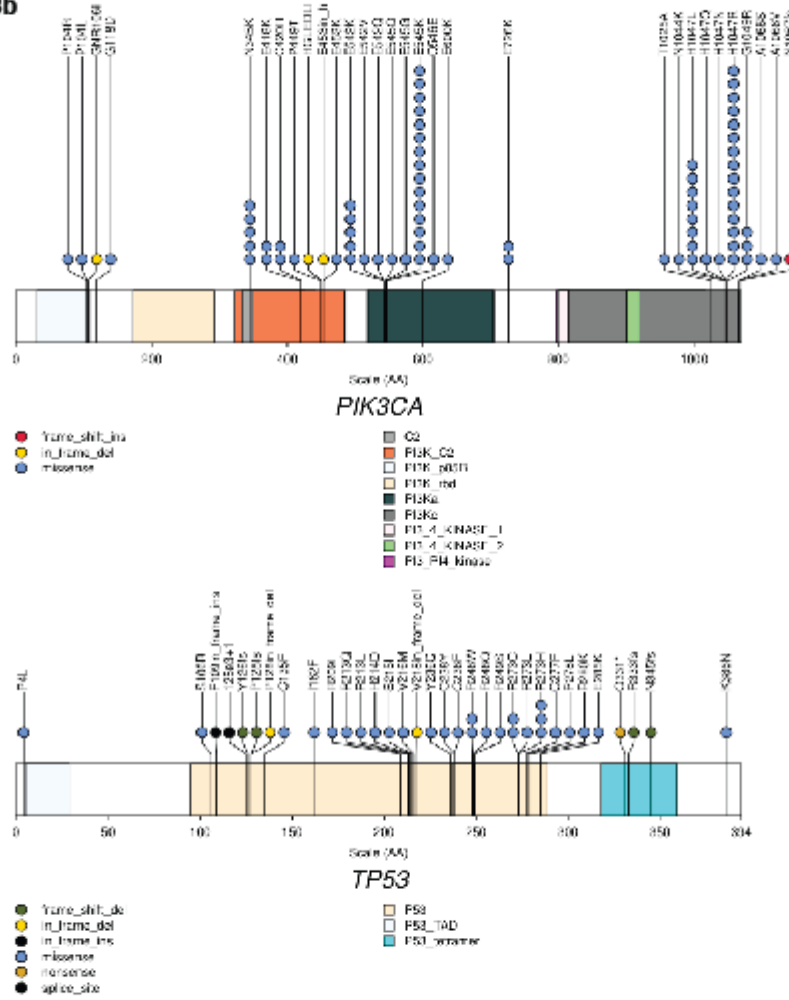
Supplementary Figure 2



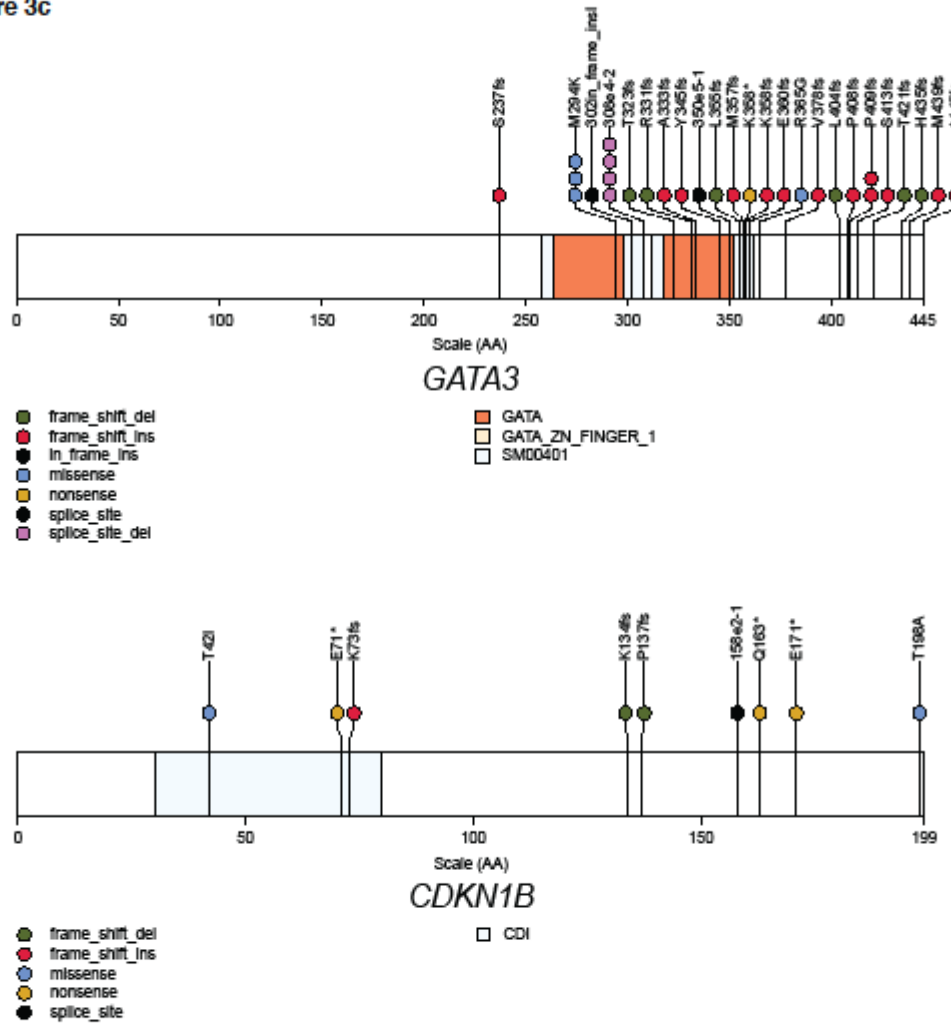
Supplementary Figure 3a



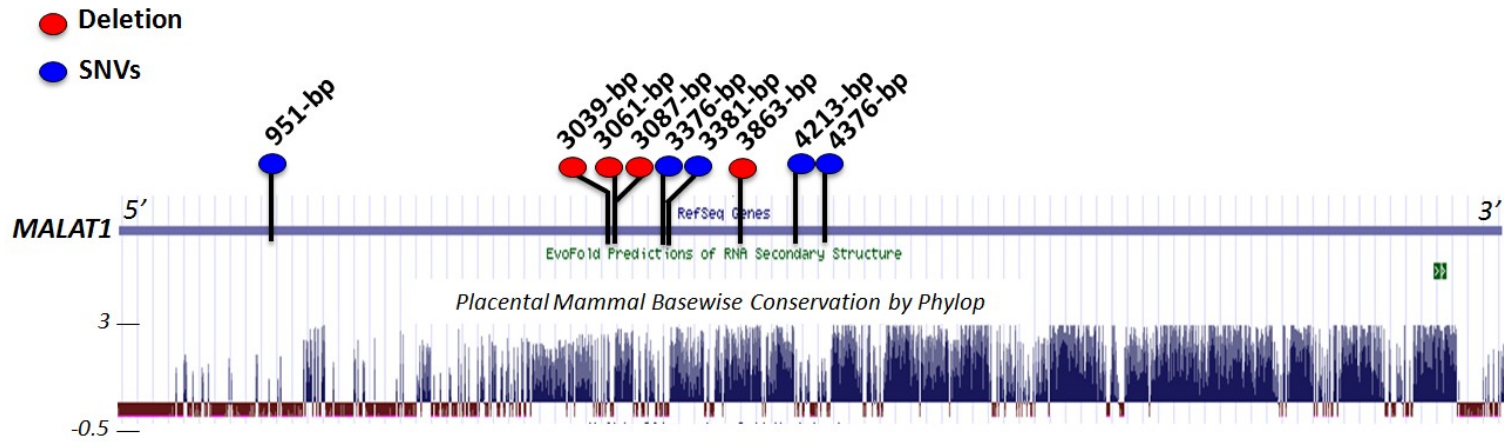
Supplementary Figure 3b



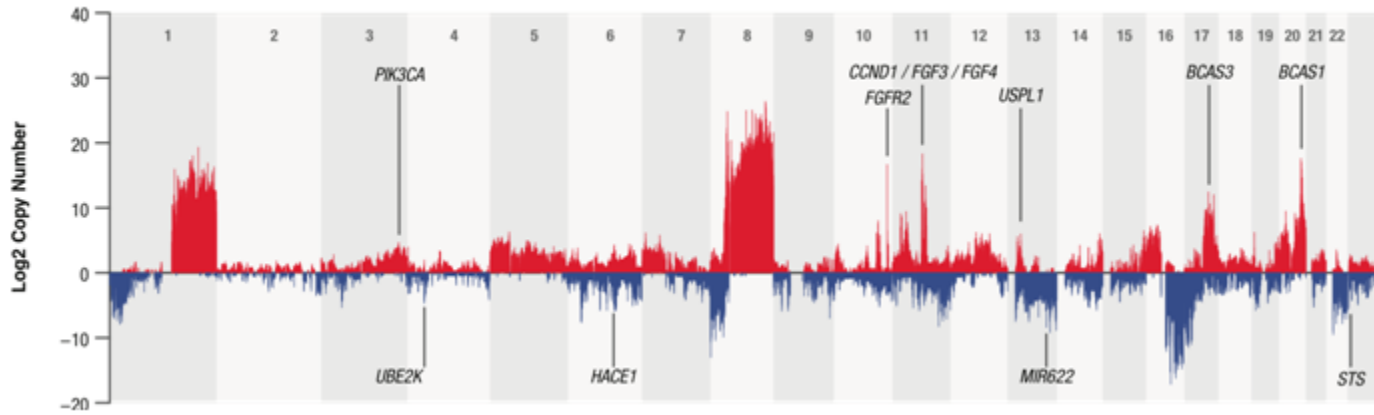
Supplementary Figure 3c



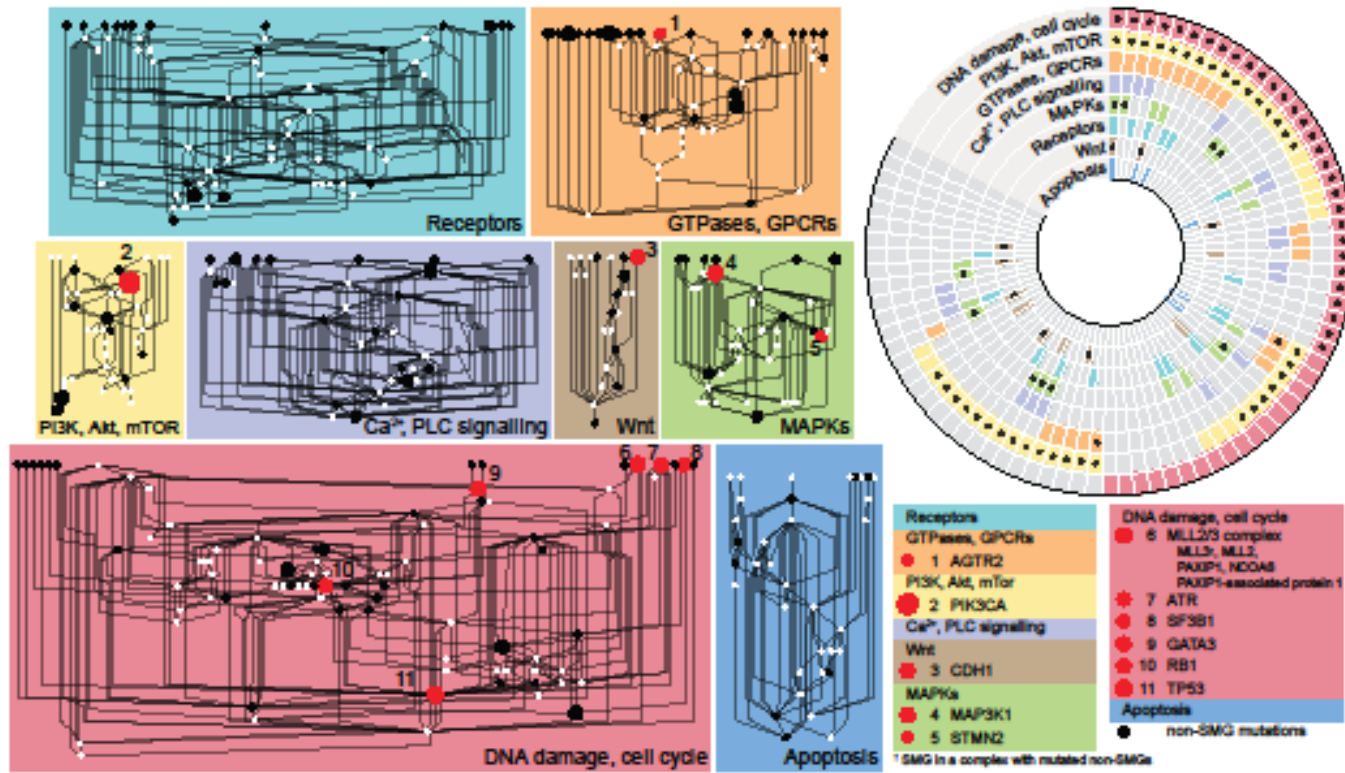
Supplementary Figure 4



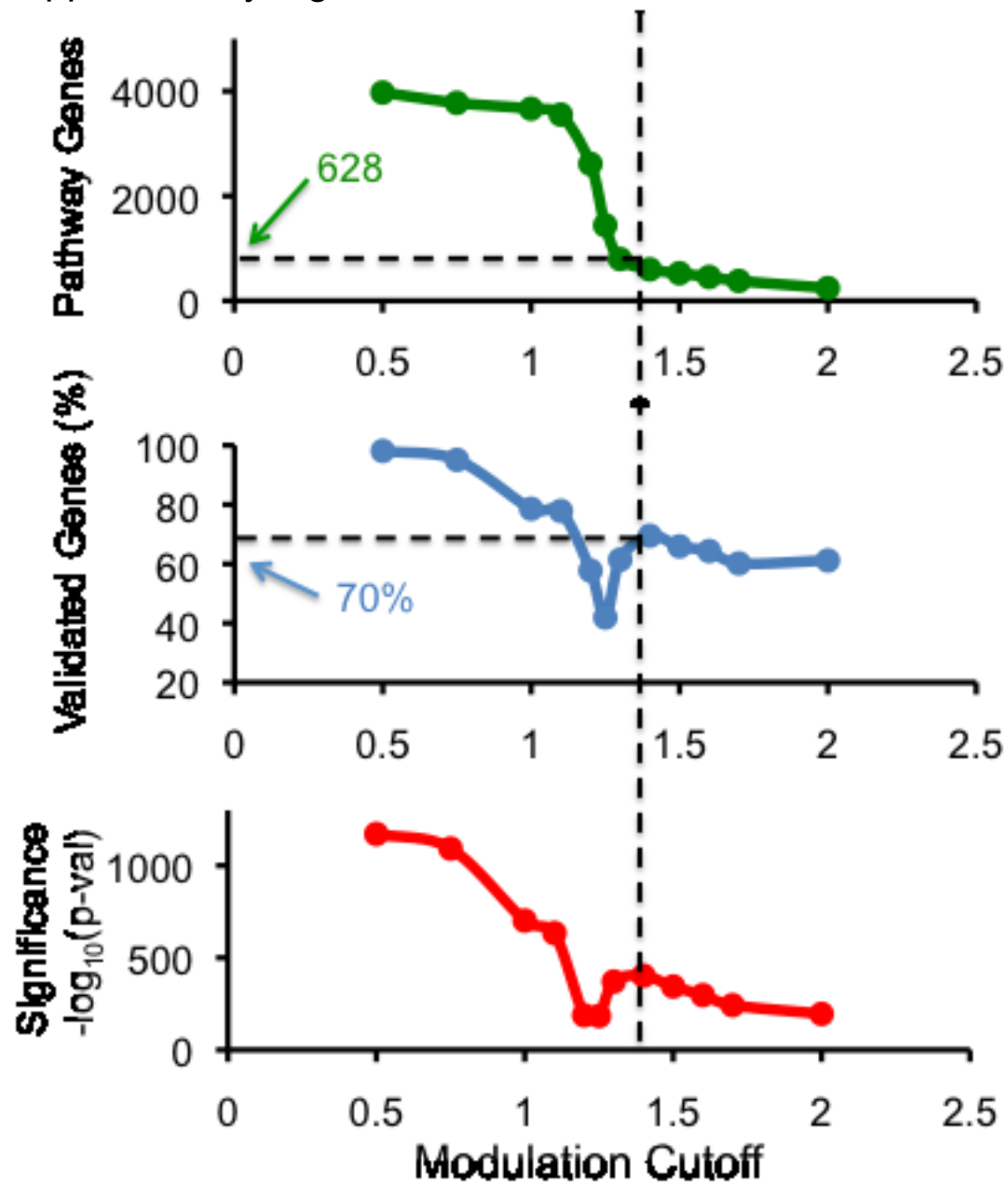
Supplementary Figure 5



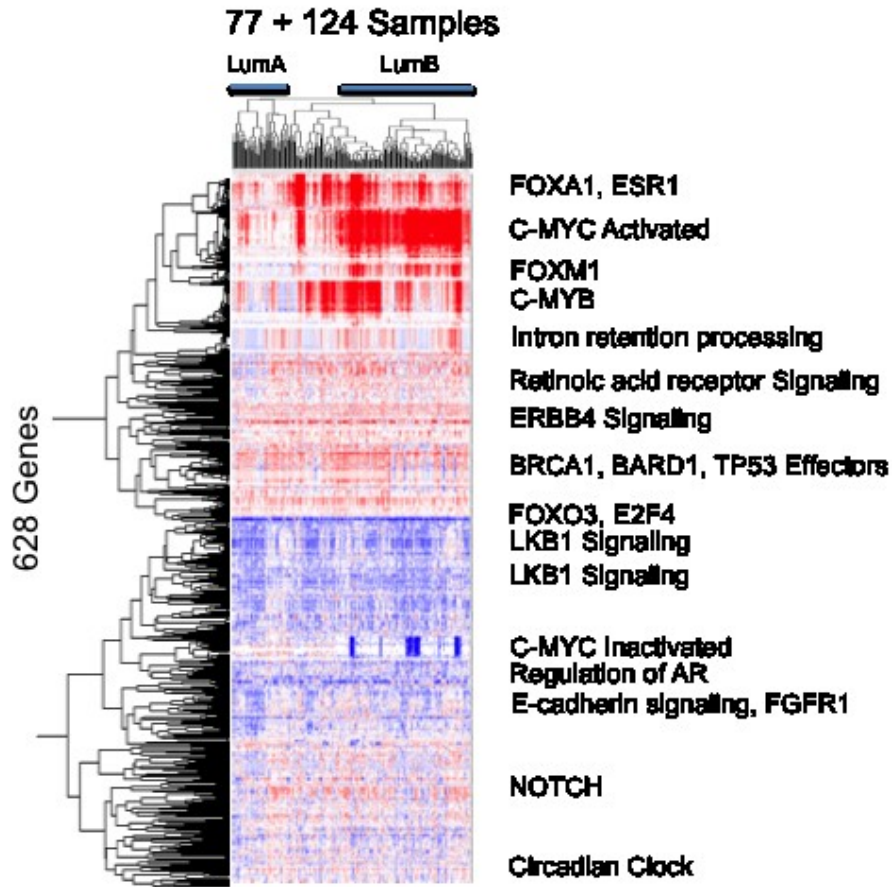
Supplementary Figure 6



Supplementary Figure 7



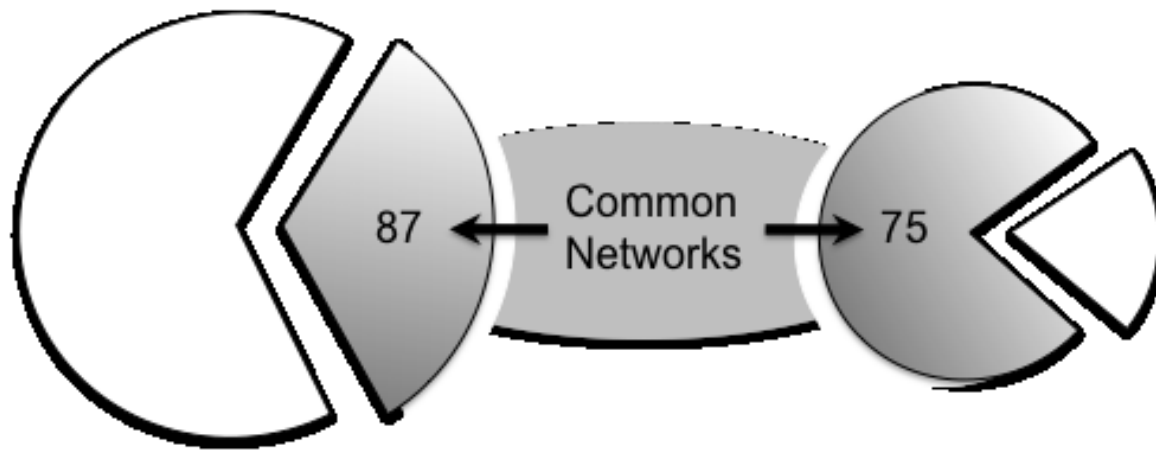
Supplementary Figure 8



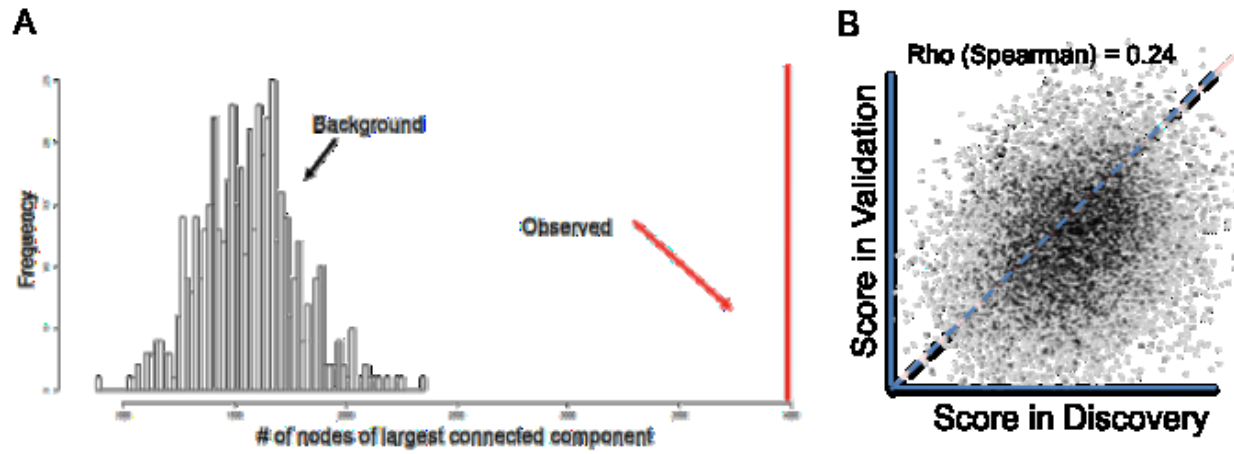
Supplementary Figure 9

233 PARADIGM Subnets

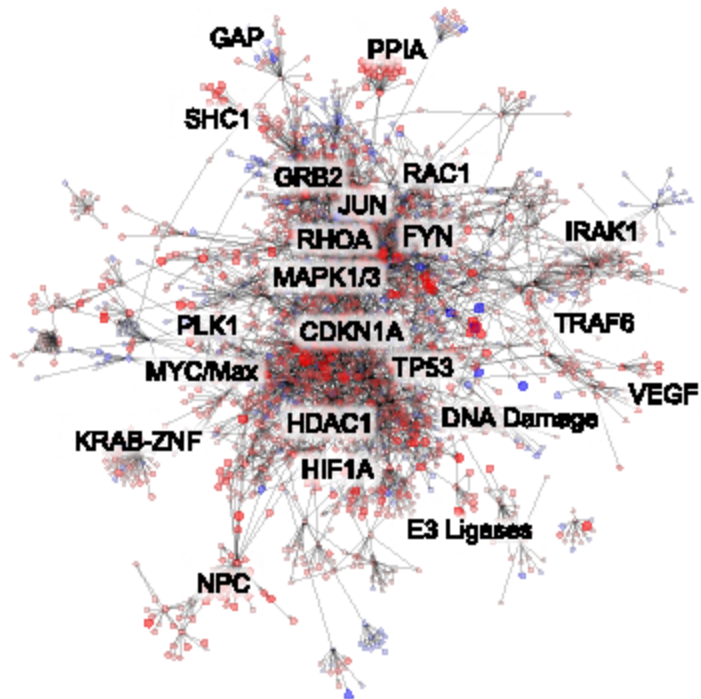
104 MetaCore Maps



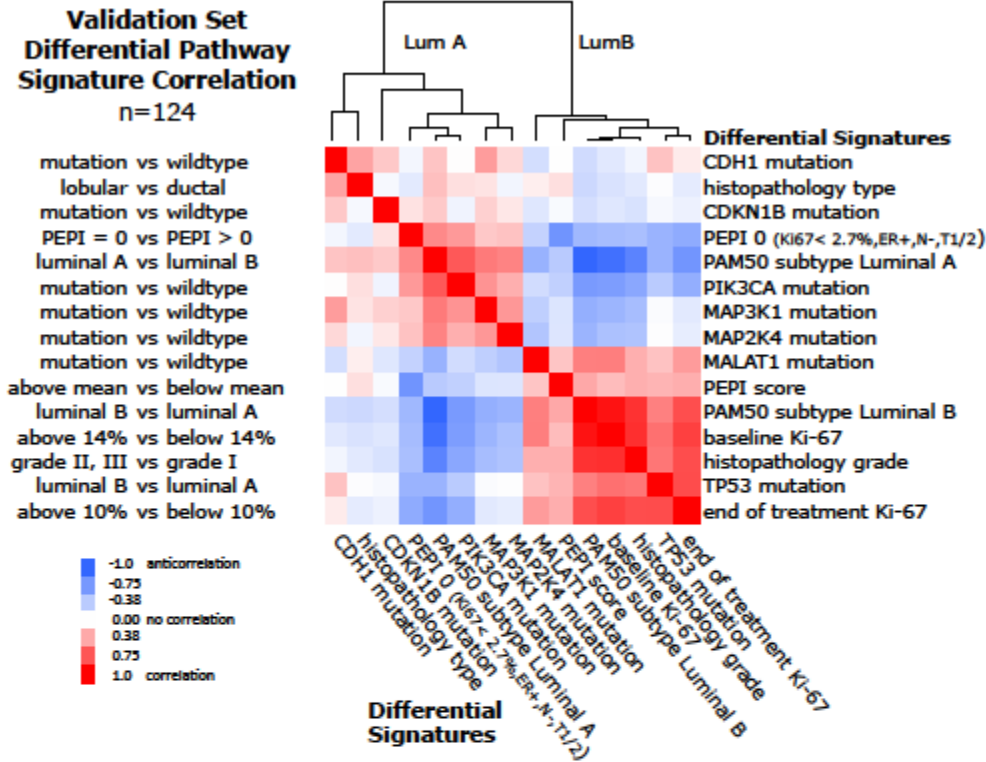
Supplementary Figure 10



Supplementary Figure 11



Supplementary Figure 12



C. Supplementary Figure Legends

Supplementary Figure 1. Experimental design of and sequencing overview of Set1 and Set2

Supplementary Figure 2. Mutational comparison of synchronous core biopsies. Scatter plots display variant allele frequencies from predicted tier 1 somatic mutations identified in genomic DNAs from two independent, synchronous core-biopsies of five pre-treatment luminal breast tumours. For each case the Pearson correlation coefficient values (r) and total number of mutations (N) are shown. Panels 1 to 5 represent the five cases and panel 6 represents the combined data.

Supplementary Figure 3. *CDKN1B*, *GATA3*, *PIK3CA*, and *TP53* mutations observed in 317 cases and *RUNX1* and *MALAT1* mutations observed in 209 luminal breast tumours. Somatic status of all mutations was obtained by Sanger sequencing of PCR products or Illumina sequencing of targeted capture products. The locations of conserved protein domains are highlighted. Each nonsynonymous substitution, splice site mutation, or indel is designated with a circle at the representative protein position with color to indicate translational effects of the mutation.

Supplementary Figure 4. Conservation of *MALAT1*. The UCSC schematic shows conserved RNA secondary structures predicted by EvoFold (green rectangle) and basepair conservation across 46 species determined by PhyloP. *MALAT1* mutations are displayed relative to the transcript (red – deletion; blue – SNV). Only the SNV at position 951 resides in the region of lower conservation at the 5' end of *MALAT1*. The only predicted secondary structure is located towards the 3' end of *MALAT1* and does not overlap the predicted mutations.

Supplementary Figure 5. Cumulative log₂ copy number plot of 46 whole genome sequenced BRC samples. Labeled peaks reflect selected regions of recurrent and focal CN change identified by CMDS along with broad peaks identified by analysis of recurrence.

Supplementary Figure 6. Key cancer pathway components altered in luminal breast tumours. Eight interaction networks from canonical maps are significantly over-represented by mutations in 77 luminal breast tumours (46 WGS and 31 exome cases). Maps were grouped by function and arranged to reflect overall hierarchy of signaling through protein-protein interactions. Mutated genes are represented in black and sized to reflect the number of tumors containing each mutation. SMGs are shown as red nodes with reference numbers indicated in the key. White nodes are non-mutated network objects. In the concentric circle diagram, tumors are arranged as radial spokes and categorized by their mutation status in each network (concentric ring color) and SMG mutation status (black dots). Tumor classification by pathway analysis shows many tumors unaffected by a given SMG often harbor other mutations in the same network. For full annotation, see Supplementary Information for Gene Interaction Network Analysis.

Supplementary Figure 7. Genes with significant pathway-informed modulation (either more active or more inactive in tumours compared to normal) correspond to those genes rediscovered in the validation set. The inferred activity of every gene in every sample was compared to a set of 100 randomly simulated controls. Those genes with levels larger than a *modulation cutoff* of at least c standard deviations (x -axis) were retained. Various values of c were swept through to define a different set of retained pathway genes (y -axis; upper plot). The proportion of these retained genes were compared to those retained in the validation set using an identical but independent modulation filter (y -axis; middle plot). The significance of this overlap in $-\log_{10}(\text{p-value})$ were also calculated (y -axis; lower plot). A maximum significance was identified to the right of the significance representing bias due to large compared sets, which identified a network containing 628 genes with a 70% validation rate.

Supplementary Figure 8. PARADIGM inferences for all 628 significantly modulated genes (rows) across both the 77 discovery and 126 validation samples (columns). Subnetwork enrichment analysis of the gene clusters revealed several coordinated subnetworks which are listed on the right. Genes inferred to have activities higher in tumour compared to normal are shown in red while those inferred to be less active are shown in blue. The first sample division defined a set of luminal A enriched samples (left hand side) and luminal B enriched samples (right hand side).

Supplementary Figure 9. Comparison of mutation-derived MetaCore Maps to transcriptionally-derived PARADIGM networks reveals high pathway concordance. 233 PARADIGM sub-networks were represented among the 3974 significantly modulated features (742 modulated genes) as identified using expression and copy number data on the 77 sample discovery set. MetaCore analysis produced 104 “maps” of interconnected genes using the significantly mutated genes identified on the discovery set. We overlapped every MetaCore map with every PARADIGM sub-network and determined if each overlap was significant at a significance level of 0.05 using a Bonferroni multiple testing correction for the 12,116 unique pair-wise comparisons. Of the 104 maps, 75 (72%) were found to have a significant overlap ($P < 4.1 \times 10^{-6}$) with one of 87 modulated PARADIGM sub-networks.

Supplementary Figure 10. Significance and reproducibility of pathway-based signatures of response. The size of the pathway determined to be correlated with Ki67 response was computed (red line) and compared to 1000 random networks derived from permuted samples (histogram). B. The differential inferred activity for each gene was determined and plotted for both the discovery set (x-axis) and validation set (y-axis) and an overall Pearson correlation of 0.24 was calculated.

Supplementary Figure 11. PARADIGM-based AI response network and associations in luminal breast tumours pathway signature for Ki67 response. Pathway features including genes (circles), complexes (hexagons), biological processes (rectangles), and gene families (triangles) from the largest connected component with inferred activities either positively correlated (red) or anti-correlated (blue) to Ki67 response and connected to other correlated features from the SuperPathway are shown. For display purposes the “hubs” (genes with 10 or more connections) along with their neighbors are kept; hubs with 35 or more connections labeled. Cytoscape sessions are available as Supplementary Data Files.

Supplementary Figure 12. PARADIGM-based AI response network and associations in luminal breast tumours pathway signatures reveal connections between mutations and clinical outcomes.

PARADIGM-based pathway signatures were derived for tumour feature dichotomies including mutation driven gene signatures (mutant vs. non-mutant), histopathology type (lobular vs. ductal), preoperative endocrine prognostic index (PEPI) score (PEPI=0 favorable vs. PEPI>0 unfavorable), PAM50 Luminal A subtype (LumA vs. LumB) and the reverse (LumB vs. LumA), histopathology grade (grades II&III vs. I), baseline Ki67 levels ($\geq 14\%$ vs. $< 14\%$), and end-of-treatment Ki67 levels ($\geq 10\%$ vs. $< 10\%$) and overall PEPI score (higher than mean unfavorable vs. lower than mean favorable). Pearson correlations were computed between all pair-wise signatures; positive correlations, red; negative correlations, blue; column features ordered identically as rows. Correlation analysis on the 124 validation samples.

D. Supplementary Tables

Case	Sample	Lanes	Input Bases	Haploid Coverage	Unfiltered Heterozygous SNP Concordance (%)	Filtered Heterozygous SNP Concordance (%)
BRC3	Normal	40	113.855 Gb	27.654	98.89	97.83
BRC3	Tumour	40	113.728 Gb	34.202	97.58	96.03
BRC4	Normal	50	91.347 Gb	24.481	97.26	95.88
BRC4	Tumour	55	105.433 Gb	32.882	98.55	97.44
BRC5	Normal	64	124.555 Gb	29.759	99.09	98.01
BRC5	Tumour	64	170.612 Gb	44.664	97.52	96.59
BRC6	Normal	45	113.223 Gb	34.455	99.28	98.47
BRC6	Tumour	45	160.630 Gb	45.979	98.66	97.53
BRC7	Normal	59	176.983 Gb	33.354	99.65	99.14
BRC7	Tumour	42	125.322 Gb	26.752	99.1	98.27
BRC8	Normal	16	102.461 Gb	29.933	99.1	98.48
BRC8	Tumour	18	103.710 Gb	31.113	97.42	96.54
BRC9	Normal	16	95.327 Gb	29.074	99.4	98.76
BRC9	Tumour	16	103.341 Gb	31.49	98.53	97.5
BRC10	Normal	56	100.000 Gb	27.403	98.81	97.17
BRC10	Tumour	48	104.251 Gb	30.312	97.23	95.39
BRC11	Normal	37	110.503 Gb	30.75	99.19	98.33
BRC11	Tumour	44	126.853 Gb	35.185	99.33	98.58
BRC12	Normal	72	129.696 Gb	33.183	99.34	98.54
BRC12	Tumour	38	113.354 Gb	28.787	97.14	95.11
BRC13	Normal	40	112.862 Gb	31.875	99.58	99.04
BRC13	Tumour	59	156.556 Gb	32.54	97.94	97.2
BRC14	Normal	40	135.748 Gb	42.171	99.41	98.81
BRC14	Tumour	40	113.264 Gb	35.53	98.7	97.61
BRC15	Normal	40	113.779 Gb	32.192	99.17	98.51
BRC15	Tumour	40	113.818 Gb	34.344	98.4	97.65
BRC16	Normal	40	126.585 Gb	38.705	99.56	98.53
BRC16	Tumour	40	123.170 Gb	38.879	98.78	97.87
BRC17	Normal	16	90.679 Gb	26.96	99.34	98.66
BRC17	Tumour	20	112.146 Gb	30.216	98.56	97.68
BRC18	Normal	19	96.719 Gb	27.576	99.38	98.76
BRC18	Tumour	20	116.843 Gb	32.811	99.09	98.35
BRC19	Normal	17	98.004 Gb	27.243	99.27	98.54

BRC19	Tumour	23	128.223 Gb	35.419	99.56	99.02
BRC20	Normal	16	93.769 Gb	26.164	99.39	98.78
BRC20	Tumour	17	103.117 Gb	30.433	97.33	96.07
BRC21	Normal	16	90.725 Gb	25.735	99.17	98.44
BRC21	Tumour	28	155.572 Gb	35.29	99.42	98.86
BRC22	Normal	16	106.655 Gb	29.184	99.29	98.63
BRC22	Tumour	20	127.673 Gb	34.984	98.74	97.88
BRC23	Normal	16	111.177 Gb	29.477	99.16	98.46
BRC23	Tumour	18	122.696 Gb	32.74	98.79	97.93
BRC24	Normal	24	100.587 Gb	26.112	98.75	97.85
BRC24	Tumour	29	131.223 Gb	36.18	99.22	98.57
BRC25	Normal	16	94.215 Gb	27.196	99.39	98.74
BRC25	Tumour	20	116.712 Gb	31.701	99.48	98.91
BRC26	Normal	16	99.524 Gb	26.355	99.18	98.45
BRC26	Tumour	32	175.125 Gb	34.999	99.48	98.98
BRC28	Normal	16	106.529 Gb	27.418	98.83	98.02
BRC28	Tumour	22	138.806 Gb	34.375	99.09	98.49
BRC29	Normal	20	120.610 Gb	29.703	98.78	98.04
BRC29	Tumour	29	167.494 Gb	38.662	97.05	95.87
BRC30	Normal	16	101.750 Gb	28.733	98.35	97.44
BRC30	Tumour	20	132.754 Gb	37.25	99.32	98.68
BRC31	Normal	16	103.046 Gb	29.327	99.32	98.65
BRC31	Tumour	20	146.877 Gb	40.286	98.88	98.13
BRC32	Normal	20	125.735 Gb	34.362	99.68	99.25
BRC32	Tumour	20	128.777 Gb	34.976	99.16	98.56
BRC33	Normal	18	103.760 Gb	28.728	99.57	99.09
BRC33	Tumour	20	132.134 Gb	36.413	99.53	99.05
BRC34	Normal	16	115.028 Gb	31.264	99.16	98.41
BRC34	Tumour	16	114.572 Gb	30.441	98.61	97.63
BRC35	Normal	16	105.900 Gb	28.958	99.16	98.49
BRC35	Tumour	16	108.696 Gb	29.735	96.86	95.37
BRC36	Normal	16	119.231 Gb	32.438	99.23	98.68
BRC36	Tumour	20	141.290 Gb	38.158	98.52	97.6
BRC37	Normal	24	137.748 Gb	37.437	99.33	98.7
BRC37	Tumour	28	144.163 Gb	40.271	98.35	97.53
BRC38	Normal	32	168.143 Gb	42.928	99.58	99.05
BRC38	Tumour	40	199.366 Gb	50.334	99.39	98.79

BRC39	Normal	16	103.249 Gb	29.161	99.43	98.87
BRC39	Tumour	24	151.752 Gb	43.961	98.47	97.55
BRC40	Normal	16	108.881 Gb	30.057	98.93	98.15
BRC40	Tumour	20	120.819 Gb	32.949	99.21	98.59
BRC41	Normal	19	114.686 Gb	31.018	99.12	98.43
BRC41	Tumour	20	137.862 Gb	36.65	98.18	97.24
BRC42	Normal	23	122.689 Gb	26.625	99.34	98.76
BRC42	Tumour	19	136.862 Gb	34.45	98.23	97.28
BRC44	Normal	16	106.921 Gb	29.112	99.28	98.62
BRC44	Tumour	20	143.478 Gb	35.93	98.11	97.03
BRC47	Normal	16	104.567 Gb	29.59	98.85	98.02
BRC47	Tumour	25	116.135 Gb	34.032	99.49	98.97
BRC48	Normal	16	100.958 Gb	29.088	99.42	98.42
BRC48	Tumour	29	165.553 Gb	46.01	99.5	98.98
BRC49	Normal	24	131.319 Gb	35.482	99.77	99.35
BRC49	Tumour	28	115.531 Gb	33.225	99.15	98.46
BRC50	Normal	19	102.160 Gb	29.445	99.73	99.32
BRC50	Tumour	26	132.305 Gb	33.422	99.38	98.8
BRC51	Normal	8	126.242 Gb	29.994	99.35	98.63
BRC51	Tumour	24	181.792 Gb	46.961	99.4	98.71
BRC52	Normal	24	123.108 Gb	36.444	99.46	99.23
BRC52	Tumour	32	238.236 Gb	61.952	99.69	99.29

Supplementary Table 1: Whole genome sequence coverage

Haploid and diploid coverage estimates are given for 46 whole-genome sequenced cases. “Lanes” indicates number of Illumina lanes generated. “Gbp” indicates total gigabases of sequence generated. Haploid coverage is calculated as the amount of non-redundant mapped read bases divided by the haploid size of the human genome. Diploid coverage is estimated from the fraction of heterozygous SNPs from high-density SNP array data that were present in SAMtools raw (unfiltered) or filtered SNP calls.

Case	Sample	Target	1x(%)	10x(%)	20x(%)
BRC3	Normal	4296026	90.816	83.312	80.538
BRC3	Tumour	4296026	91.069	83.16	80.429
BRC4	Normal	5729952	91.979	82.806	79.715
BRC4	Tumour	5729952	91.394	83.2	79.716
BRC5	Normal	5697397	84.553	71.43	63.569
BRC5	Tumour	5697397	91.612	79.89	75.664
BRC6	Normal	5038908	88.222	80.959	78.407
BRC6	Tumour	5038908	92.828	83.058	80.276
BRC7	Normal	4036434	90.132	82.78	80.488
BRC7	Tumour	4036434	93.298	83.93	81.251
BRC8	Normal	4216306	89.123	81.178	78.696
BRC8	Tumour	4216306	91.639	82.775	79.895
BRC9	Normal	4379816	89.848	75.278	68.876
BRC9	Tumour	4379816	91.059	82.792	79.954
BRC10	Normal	3663451	93.908	87.696	85.175
BRC10	Tumour	3663451	91.794	85.246	82.657
BRC11	Normal	6037709	90.815	83.712	80.966
BRC11	Tumour	6022942	92.025	85.153	82.597
BRC12	Normal	3850997	92.143	85.96	83.506
BRC12	Tumour	3850997	91.306	84.356	81.896
BRC13	Normal	5022349	91.304	86.102	84.056
BRC13	Tumour	5022349	92.467	75.627	66.953
BRC14	Normal	6381814	93.064	86.863	84.672
BRC14	Tumour	6381814	93.276	87.242	84.711
BRC15	Normal	5046488	92.476	86.203	83.644
BRC15	Tumour	5046488	92.287	85.794	83.315
BRC16	Normal	6422110	92.624	86.018	83.675
BRC16	Tumour	6422110	87.581	77.336	70.64
BRC17	Normal	6232240	90.037	82.329	79.509
BRC17	Tumour	6232240	92.053	83.299	80.361
BRC18	Normal	5999444	92.528	85.702	83.454

BRC18	Tumour	5999444	92.375	84.863	82.077
BRC19	Normal	4256081	91.081	84.037	81.664
BRC19	Tumour	4256081	91.209	83.702	81.197
BRC20	Normal	4858565	90.936	81.97	78.034
BRC20	Tumour	4858565	90.421	82.582	79.557
BRC21	Normal	6344075	90.122	83.336	80.619
BRC21	Tumour	5145893	90.937	83.334	80.68
BRC22	Normal	4752350	88.763	81.515	78.879
BRC22	Tumour	4761232	83.21	72.477	67.259
BRC23	Normal	4963580	88.125	80.198	77.767
BRC23	Tumour	4963580	93.454	81.716	78.253
BRC24	Normal	5096509	88.323	80.666	77.803
BRC24	Tumour	5096509	90.297	82.798	80.081
BRC25	Normal	4342531	90.356	82.805	80.066
BRC25	Tumour	4342531	90.411	83.697	81.351
BRC26	Normal	4702025	91.029	83.505	80.959
BRC26	Tumour	4702025	91.287	83.552	80.691
BRC28	Normal	4379160	89.979	82.8	80.408
BRC28	Tumour	4379160	91.191	82.916	80.275
BRC29	Normal	5386071	92.338	83.786	81.317
BRC29	Tumour	5386071	86.806	77.002	72.534
BRC30	Normal	4951916	89.302	81.928	79.388
BRC30	Tumour	4951916	89.606	82.164	79.567
BRC31	Normal	6344075	89.679	82.884	80.008
BRC31	Tumour	6344075	92.884	84.378	81.601
BRC32	Normal	4534390	89.468	82.02	79.408
BRC32	Tumour	4534390	89.118	81.407	78.875
BRC33	Normal	4656953	90.135	82.647	79.959
BRC33	Tumour	4656953	92.265	83.024	80.6
BRC34	Normal	4054381	90.888	83.835	81.412
BRC34	Tumour	4054381	90.484	83.599	81.425
BRC35	Normal	4863230	92.004	80.816	77.318
BRC35	Tumour	4863230	90.506	83.583	81.38
BRC36	Normal	4560991	90.254	83.96	81.76

BRC36	Tumour	4560991	90.349	84.174	81.831
BRC37	Normal	4636616	88.7	81.736	79.454
BRC37	Tumour	4636616	90.284	82.896	80.27
BRC38	Normal	5127236	89.583	81.763	78.9
BRC38	Tumour	5127236	89.134	81.518	79.078
BRC39	Normal	7402685	92.373	85.7	83.089
BRC39	Tumour	7402685	90.948	85.824	83.343
BRC40	Normal	3919953	92.089	83.167	80.815
BRC40	Tumour	3919953	91.058	83.404	80.956
BRC41	Normal	5439494	90.95	83.862	81.256
BRC41	Tumour	5439494	90.763	83.868	81.456
BRC42	Normal	4475298	90.378	80.731	78.215
BRC42	Tumour	4475298	91.613	84.205	81.911
BRC44	Normal	5963404	91.948	82.419	79.777
BRC44	Tumour	5963404	91.359	83.696	80.969
BRC47	Normal	5086131	89.742	80.9	78.668
BRC47	Tumour	5086131	90.275	83.372	80.808
BRC48	Normal	4762691	90.351	78.096	73.969
BRC48	Tumour	4762691	89.735	81.861	79.181
BRC49	Normal	5681102	91.988	84.124	81.429
BRC49	Tumour	5681102	91.551	83.666	80.873
BRC50	Normal	5657533	91.976	85.871	83.685
BRC50	Tumour	5657533	92.35	85.047	82.053
BRC51	Normal	6652050	90.422	79.543	75.371
BRC51	Tumour	6652050	90.516	82.503	79.033
BRC52	Normal	5759032	89.889	77.925	73.133
BRC52	Tumour	5759032	90.716	82.695	79.957

Supplementary Table 2: Custom capture sequence coverage

Custom capture validation coverage of putative somatic mutations is reported for the 46 cases in which such data were generated. Shown are the fraction of bases targeted that were covered >1x, >10x, and >20x in each sample.

Case	Tier1	Tier2	Tier3	SV
BRC3	29	185	656	2
BRC4	22	164	810	13
BRC5	46	194	1,024	27
BRC6	18	148	825	30
BRC7	57	332	1,519	4
BRC8	28	152	767	0
BRC9	24	119	590	6
BRC10	12	81	374	11
BRC11	84	605	3,370	25
BRC12	14	70	372	20
BRC13	73	348	1,810	12
BRC14	16	129	582	7
BRC15	34	300	1,639	6
BRC16	55	360	2,025	178
BRC17	19	115	529	16
BRC18	122	798	3,805	1
BRC19	15	77	456	0
BRC20	38	297	1,453	25
BRC21	24	161	812	15
BRC22	27	126	587	14
BRC23	19	90	488	2
BRC24	26	112	558	1
BRC25	0	9	35	1
BRC26	22	215	1,065	9
BRC28	15	95	435	0
BRC29	47	329	1,464	6
BRC30	27	224	1,184	12
BRC31	124	799	3,939	14
BRC32	43	158	764	8
BRC33	24	70	420	1
BRC34	9	100	377	0
BRC35	44	294	1,598	19
BRC36	28	137	806	9
BRC37	21	190	864	10

BRC38	35	177	881	12
BRC39	293	1,773	9,550	3
BRC40	22	137	632	0
BRC41	97	646	3,225	101
BRC42	22	107	721	13
BRC44	81	591	3,136	62
BRC47	74	397	2,081	24
BRC48	12	52	240	0
BRC49	26	131	604	22
BRC50	149	867	4,138	9
BRC51	81	458	2,205	19
BRC52	14	98	541	5

Supplementary Table 3: Validated somatic mutations

Validated somatic SNVs in tiers 1, 2, and 3 are shown for the 46 cases having both whole genome sequence data and custom capture validation.

Study	Tumour Type	Cases	Tier 1 SNVs	Mutation Rate
Ley et al, 2008	Acute myeloid leukemia (M1)	1	8	0.18
Mardis et al, 2009	Acute myeloid leukemia (M1)	1	10	0.23
Chapman et al, 2011	Multiple myeloma	23	34	0.77
Shah et al, 2009*	Lobular breast cancer	1	32	0.73
Ding et al, 2010	Basal-like breast cancer	1	43	0.98
Ellis et al, 2011	Luminal breast cancer	46	45.9	1.05
Totoki et al, 2011	Hepatocellular carcinoma	1	81	1.85
Pleasant et al, 2009**	Malignant melanoma	1	292	6.65
Pleasant et al, 2009**	Small-cell lung cancer	1	134	3.05
Lee et al, 2010	Non-small-cell lung cancer	1	392	8.93

* Mutation rate reflects only non-synonymous SNVs

** Cancer cell line, not primary tumour

Supplementary Table 4: Mutation rates across cancer types

This table compares somatic mutation rates across cancer types. Average number of somatic mutations per megabase of coding sequence (tier 1) is compared to published whole-genome sequencing studies of liquid and solid tumours. Only validated tier 1 SNVs in 46 cases were used in calculations; for two studies, only numbers of nonsynonymous SNVs were readily available. For studies with multiple cases, the average values are shown.

Hugo_Symbol	Chromosome	Start_position	End_position	Variant_Classification	Variant_Type	Reference_Allele	Variant_Allele	Tumour_Sample	Transcript	Annotation
ATAD3A	1	1451715	1451715	Silent	SNP	C	T	CSB21	NM_018188.2	p.S474
LOC728661	1	1587306	1587306	Silent	SNP	C	T	BRC7	XM_001717735.1	p.V489
MORN1	1	2279898	2279898	Missense	SNP	T	A	BRC28	NM_024848.1	p.T288S
ACTRT2	1	2928204	2928204	Missense	SNP	C	T	CSB8	NM_080431.4	p.R32W
KIAA0562	1	3741348	3741348	Splice_Site	SNP	C	A	CSB24	NM_014704.2	e10+1
KIAA0562	1	3755186	3755186	Missense	SNP	C	G	BRC39	NM_014704.2	p.E45Q
HES2	1	6401892	6401892	Silent	SNP	C	A	CSB14	NM_019089.4	p.A79
DNAJC11	1	6618818	6618818	Missense	SNP	C	T	CSB34	NM_018198.3	p.V534I
PER3	1	7770837	7770837	Missense	SNP	T	C	CSB29	NM_016831.1	p.F179S
ENO1	1	8847944	8847944	Missense	SNP	G	C	BRC11	NM_001428.2	p.I284M
ENO1	1	8848959	8848959	Silent	SNP	G	A	BRC41	NM_001428.2	p.G211
UBE4B	1	10161293	10161293	Missense	SNP	C	T	CSB7	NM_001105562.1	p.S1177F
PEX14	1	10612240	10612240	Missense	SNP	C	A	BRC47	NM_004565.2	p.P248Q
FRAP1	1	11129401	11129401	Missense	SNP	C	G	BRC39	NM_004958.3	p.M1535I
PTCHD2	1	11519166	11519166	Missense	SNP	G	A	CSB9	NM_020780.1	p.A1339T
VPS13D	1	12260042	12260042	Missense	SNP	G	C	CSB1	NM_015378.2	p.L1270F
DHRS3	1	12561420	12561420	Missense	SNP	A	G	CSB12	NM_004753.4	p.L204P
AADACL3	1	12708546	12708546	Missense	SNP	T	C	BRC14	NM_001103170.1	p.L350P
PRAMEF18	1	13347456	13347456	Missense	SNP	G	T	CSB22	NM_001099850.1	p.D420E
KIAA1026	1	15300735	15300735	Missense	SNP	C	T	CSB15	NM_201628.2	p.R553W
EFHD2	1	15609339	15609339	Missense	SNP	G	C	CSB1	NM_024329.4	p.K95N
SPEN	1	16108509	16108509	Nonsense	SNP	G	T	CSB7	NM_015001.2	p.E330*
SPEN	1	16128033	16128033	Missense	SNP	A	G	CSB9	NM_015001.2	p.D904G

SPEN	1	16129139	16129139	Nonsense	SNP	G	T	BRC47	NM_015001.2	p.E1273*
SPEN	1	16133350	16133350	Silent	SNP	G	C	BRC47	NM_015001.2	p.V2676
ARHGEF19 ENSG0000018654 3	1	16405149	16405149	Nonsense	SNP	C	A	BRC5	NM_153213.3	p.E439*
PADI6	1	16832421	16832421	Missense	SNP	G	T	CSB12	ENST00000362058	p.A11D
UBR4	1	17594191	17594191	Splice_Site	SNP	G	A	BRC6	ENST00000358481	e13+1
UBR4	1	19314711	19314711	Missense	SNP	G	A	CSB31	NM_020765.2	p.R3611C
UBR4	1	19345000	19345000	Missense	SNP	C	A	CSB24	NM_020765.2	p.G2607W
KIAA0090	1	19418728	19418728	Silent	SNP	T	A	CSB25	NM_015047.1	p.R908
EIF4G3	1	21006493	21006493	Missense	SNP	G	T	BRC26	NM_003760.3	p.P1555H
EIF4G3	1	21085280	21085280	Splice_Site	SNP	C	A	BRC21	NM_003760.3	e12+1
EPHA8	1	22775857	22775857	Silent	SNP	G	T	BRC29	NM_020526.1	p.R240
EPHB2	1	22983964	22983964	Missense	SNP	T	A	BRC16	NM_004442.6	p.F207I
LUZP1	1	23291091	23291091	Missense	SNP	G	A	BRC7	NM_033631.1	p.R751W
HTR1D	1	23393159	23393159	Silent	SNP	G	A	BRC50	NM_000864.4	p.V47
HNRNPR	1	23517576	23517576	Missense	SNP	T	C	BRC47	NM_001102398.1	p.E338G
LDLRAP1	1	25764282	25764282	Nonsense	SNP	C	A	CSB28	NM_015627.2	p.S260*
LDLRAP1	1	25765939	25765939	Missense	SNP	C	G	BRC24	NM_015627.2	p.R266G
AIM1L	1	26536429	26536429	Missense Frame Shift Ins	SNP	G	A	CSB3	NM_001039775.2	p.R180W
ARID1A	1	26967041	26967041		INS		0 T	CSB8	NM_006015.4	p.Y1054fs
ARID1A	1	26972065	26972065	Missense	SNP	G	A	BRC11	NM_006015.4	p.A1239T
ARID1A	1	26978941	26978941	Nonsense	SNP	C	T	BRC18	NM_006015.4	p.R1989*
ARID1A	1	26979538	26979538	Nonsense	SNP	C	T	CSB23	NM_006015.4	p.Q2188*
EYA3	1	28234758	28234758	Missense	SNP	G	A	CSB1	NM_001990.2	p.S82L
DNAJC8	1	28428047	28428047	Silent	SNP	G	A	BRC50	NM_014280.2	p.S51
PHACTR4	1	28688279	28688279	Missense	SNP	C	G	BRC39	NM_023923.1	p.Q601E
RCC1	1	28734379	28734379	Silent	SNP	G	A	CSB1	NM_001048194.1	p.L218
PTPRU	1	29478622	29478622	Missense	SNP	C	G	CSB1	NM_005704.3	p.S544C
PTPRU	1	29509880	29509880	Splice_Site	SNP	G	C	CSB10	NM_005704.3	e20+1
PEF1	1	31869024	31869024	Missense	SNP	G	A	BRC15	NM_012392.2	p.S211F
KPNA6	1	32392775	32392775	Splice_Site	SNP	G	C	BRC50	NM_012316.4	e2-1
KPNA6	1	32392899	32392899	Missense	SNP	G	A	BRC50	NM_012316.4	p.R43Q
EIF3I	1	32466924	32466924	Missense	SNP	T	A	CSB10	NM_003757.2	p.S217T
FAM167B	1	32485734	32485734	Missense	SNP	C	T	BRC16	NM_032648.2	p.S42L
SYNC	1	32934109	32934109	Silent	SNP	G	A	CSB1	ENST00000409190	p.L59

KIAA1522	1	33008802	33008802	Missense	SNP	C	T	BRC39	NM_020888.2	p.R479W
S100BPB	1	33091299	33091299	Missense	SNP	C	G	BRC47	NM_022753.1	p.Q353E
RNF19B	1	33186511	33186511	Silent	SNP	G	A	BRC11	NM_153341.1	p.I104
PHC2	1	33592689	33592693	Frame Shift Del	DEL	CGTCT		0 CSB2	NM_198040.3	p.E484fs
CSMD2	1	33810747	33810747	Missense	SNP	C	T	BRC39	NM_052896.3	p.E2572K
GJB4	1	34999629	34999629	Missense	SNP	G	A	BRC22	NM_153212.1	p.V63I
ZMYM6	1	35226008	35226008	Missense	SNP	C	T	BRC39	NM_007167.3	p.E1088K
ZMYM1	1	35351259	35351259	Missense	SNP	A	T	BRC23	NM_024772.3	p.Q414L
SFPQ	1	35427248	35427248	Missense	SNP	C	G	CSB1	NM_005066.2	p.R547T
KIAA0319L	1	35717168	35717168	Missense	SNP	G	A	CSB30	NM_024874.3	p.S300L
NCDN	1	35799309	35799309	Missense	SNP	G	A	BRC8	NM_001014839.1	p.E324K
GNL2	1	37828989	37828989	Missense	SNP	C	G	CSB1	NM_013285.2	p.E97Q
CDCA8	1	37946612	37946612	Missense	SNP	G	A	CSB15	NM_018101.2	p.R277Q
MACF1	1	39322506	39322506	Missense	SNP	G	A	BRC51	NM_012090.3	p.S10N
MACF1	1	39620367	39620367	Missense	SNP	T	A	CSB13	NM_033044.3	p.S3042T
MACF1	1	39698993	39698993	Missense	SNP	G	C	CSB1	NM_033044.3	p.D5598H
EDN2	1	41722365	41722365	Missense	SNP	C	G	CSB16	NM_001956.3	p.W54S
C1orf84	1	43661054	43661054	Frame Shift Del	DEL	C		0 BRC8	ENST00000406439	p.Y651fs
PTPRF	1	43836104	43836104	Missense	SNP	G	A	CSB10	NM_002840.3	p.V638I
PTPRF	1	43837045	43837045	Nonsense	SNP	G	A	BRC31	NM_002840.3	p.W729*
PTPRF	1	43837148	43837148	Missense	SNP	G	T	BRC31	NM_002840.3	p.D764Y
JMJD2A	1	43929104	43929104	Missense	SNP	T	C	BRC5	NM_014663.2	p.V680A
ATP6V0B	1	44214636	44214636	Silent	SNP	C	T	BRC13	NM_004047.1	p.V92
ATP6V0B	1	44214856	44214856	Missense	SNP	T	A	BRC29	NM_004047.1	p.F96I
C1orf228	1	44936444	44936444	Missense	SNP	C	T	BRC39	ENST00000357508	p.A133V
SNORD38A	1	45016103	45016103	RNA	SNP	C	T	BRC18	NR_001456.1	NULL
PTCH2	1	45064581	45064581	Silent	SNP	C	G	BRC39	NM_003738.3	p.L1014
GPBP1L1	1	45892822	45892822	Missense	SNP	G	C	CSB28	NM_021639.4	p.Q153E
TAL1	1	47458412	47458412	Missense	SNP	C	T	BRC37	NM_003189.2	p.R188Q
SPATA6	1	48691373	48691373	Silent	SNP	G	T	CSB21	NM_019073.1	p.V23
FAF1	1	50822971	50822971	Missense	SNP	G	A	CSB1	NM_007051.2	p.S314L
OSBPL9	1	52022832	52022832	Missense	SNP	G	C	CSB15	NM_148909.3	p.A617P
NRD1	1	52029222	52029222	Missense	SNP	C	G	BRC39	NM_002525.1	p.E1065Q
PRPF38A	1	52643956	52643956	Silent	SNP	T	C	CSB28	NM_032864.3	p.D49

ZYG11B	1	53009576	53009576	Nonsense	SNP	C	T	CSB30	NM_024646.2	p.R165*
ZYG11A	1	53125268	53125268	Nonsense	SNP	C	T	CSB1	XM_001133615.1	p.Q687*
TMEM48	1	54066378	54066378	Missense	SNP	G	C	BRC39	NM_018087.3	p.Q113E
ENSG00000212670	1	54342901	54342901	Missense	SNP	C	T	BRC50	ENST00000391366	p.S58L
ENSG00000212670	1	54343117	54343117	Missense	SNP	T	C	BRC16	ENST00000391366	p.L130S
C1orf175	1	54924629	54924629	Silent	SNP	C	T	BRC39	NM_001039464.2	p.I877
PARS2	1	54997200	54997200	Silent	SNP	G	A	CSB31	NM_152268.2	p.L75
USP24	1	55372652	55372652	Missense	SNP	A	T	CSB3	NM_015306.1	p.V915E
C1orf168	1	56982417	56982417	Missense	SNP	C	G	BRC39	NM_001004303.4	p.E500Q
C8B	1	57187831	57187831	Silent	SNP	T	C	BRC29	NM_000066.2	p.K283
OMA1	1	58744375	58744375	Missense	SNP	G	A	CSB1	NM_145243.3	p.S437F
JUN	1	59020997	59020997	Missense	SNP	C	T	CSB1	NM_002228.3	p.E112K
JUN	1	59021055	59021055	Silent	SNP	C	T	BRC39	NM_002228.3	p.P92
JUN	1	59021223	59021223	Missense	SNP	C	G	BRC39	NM_002228.3	p.Q36H
FGGY	1	59846152	59846152	Missense	SNP	G	C	CSB1	NM_018291.1	p.Q219H
CYP2J2	1	60149961	60149961	Silent	SNP	G	A	CSB8	NM_000775.2	p.F197
DOCK7	1	62731037	62731037	Missense	SNP	T	C	CSB31	NM_033407.2	p.I1732V
IL23R	1	67406362	67406362	Splice_Site	SNP	G	C	CSB1	NM_144701.2	e1-1
LRRC40	1	70417260	70417260	Silent	SNP	C	T	CSB1	NM_017768.3	p.L222
SFRS11	1	70482996	70482996	Missense	SNP	C	G	CSB31	NM_004768.2	p.S281C
FPGT	1	74443109	74443109	Missense	SNP	G	A	CSB1	NM_003838.2	p.D264N
C1orf173	1	74810913	74810913	Silent	SNP	G	A	CSB1	NM_001002912.3	p.F1023
NEXN	1	78171747	78171747	Missense	SNP	G	A	CSB2	NM_144573.3	p.G416R
IFI44L	1	78875403	78875403	Missense	SNP	C	G	CSB1	NM_006820.2	p.I286M
TTLL7	1	84149543	84149543	Missense	SNP	G	A	CSB1	NM_024686.4	p.S560L
SYDE2	1	85407357	85407357	Missense	SNP	C	A	CSB2	NM_032184.1	p.K937N
SYDE2	1	85421434	85421434	Silent	SNP	C	T	BRC42	NM_032184.1	p.L493
SH3GLB1	1	86972912	86972912	Del	DEL	C		0 CSB26	NM_016009.3	p.R204fs
CCBL2	1	89221334	89221334	Missense	SNP	T	C	BRC23	NM_019610.1	p.Y255C
GBP1	1	89294451	89294451	Missense	SNP	C	T	CSB34	NM_002053.2	p.A402T
LRRC8D	1	90171639	90171639	Missense	SNP	G	T	BRC16	NM_018103.1	p.D142Y
ZNF644	1	91177652	91177652	Nonsense	SNP	G	C	CSB33	NM_201269.2	p.S616*
HFM1	1	91561250	91561250	Missense	SNP	C	T	BRC20	NM_001017975.3	p.R841Q

CDC7	1	91739955	91739955	Missense	SNP	G	A	BRC18	NM_003503.1	p.E32K
GFI1	1	92714312	92714312	Missense	SNP	G	C	BRC7	NM_005263.1	p.F377L
CCDC18	1	93474459	93474459	Missense	SNP	G	A	BRC18	NM_206886.2	p.E961K
CCDC18	1	93477902	93477902	Missense	SNP	G	C	CSB1	NM_206886.2	p.E1066Q
DNTTIP2	1	94115426	94115426	Missense	SNP	T	C	CSB15	NM_014597.3	p.D218G
ABCA4	1	94234293	94234293	Missense	SNP	G	A	BRC39	NM_000350.2	p.P2259L
ABCA4	1	94298714	94298714	Silent	SNP	C	A	BRC42	NM_000350.2	p.S709
DPYD	1	97688211	97688211	Missense	SNP	G	A	BRC39	NM_000110.3	p.P633S
CCDC76	1	100386082	100386082	Missense	SNP	G	A	BRC39	NM_019083.1	p.E288K
S1PR1	1	101477779	101477779	Silent	SNP	C	A	BRC35	NM_001400.4	p.I217
LOC100129138	1	104417624	104417624	RNA	SNP	G	A	BRC22	XR_036957.1	NULL
PRMT6	1	107401027	107401027	Missense	SNP	T	C	CSB34	ENST00000370078	p.V56A
NTNG1	1	107774894	107774894	Splice_Site	SNP	G	A	BRC39	ENST00000370068	e5-1
VAV3	1	108093174	108093174	Missense	SNP	C	G	CSB1	NM_006113.1	p.E481Q
NBPF4	1	108570881	108570881	Silent	SNP	C	T	CSB2	ENST00000370038	p.P606
ATXN7L2	1	109831223	109831223	Nonsense	SNP	C	T	CSB1	NM_153340.4	p.Q124*
AMIGO1	1	109851628	109851628	Missense	SNP	G	A	CSB8	NM_020703.2	p.S477L
AMIGO1	1	109851696	109851696	Missense	SNP	G	C	BRC41	NM_020703.2	p.N454K
RBM15	1	110685517	110685517	Missense	SNP	C	A	CSB1	NM_022768.4	p.S656Y
HBXIP	1	110751860	110751860	Missense	SNP	C	T	CSB22	NM_006402.2	p.R51Q
KCNA2	1	110948683	110948683	Missense	SNP	C	A	BRC21	NM_004974.2	p.R82L
TMEM77	1	111464792	111464792	Missense	SNP	A	C	BRC28	NM_178454.4	p.F129C
WNT2B	1	112859117	112859117	Missense	SNP	G	A	CSB14	NM_024494.3	p.R94H
LRIG2	1	113458886	113458886	Nonsense	SNP	G	T	BRC11	NM_014813.1	p.E799*
PTPN22	1	114196217	114196217	Missense	SNP	C	G	CSB1	NM_015967.3	p.L261F
C1orf178	1	114225250	114225250	Nonsense	SNP	G	A	CSB28	ENST00000393320	p.R55*
DENND2C	1	114966182	114966182	Missense	SNP	G	A	BRC47	ENST00000369539	p.R362W
LOC401131	1	142051337	142051337	RNA	SNP	C	T	CSB7	XR_017704.1	NULL
LOC727820	1	142534670	142534670	RNA	SNP	A	G	CSB24	XR_041980.1	NULL
NBPF8	1	144035013	144035013	Missense	SNP	A	T	CSB24	ENST00000369330	p.I301F
PRKAB2	1	145106134	145106134	Silent	SNP	G	A	BRC35	NM_005399.3	p.L53
ENSG00000199879	1	146202453	146202453	RNA	SNP	C	T	BRC18	ENST00000363009	NULL
HIST2H2AC	1	148125193	148125193	Silent	SNP	C	G	CSB19	NM_003517.2	p.A15
OTUD7B	1	148188702	148188702	Missense	SNP	G	A	CSB1	NM_020205.2	p.H298Y

C1orf51	1	148525918	148525918	Missense	SNP	G	A	CSB1	NM_144697.2	p.M362I
ADAMTSL4	1	148793198	148793198	Missense	SNP	A	C	BRC29	NM_019032.4	p.E369D
ADAMTSL4	1	148796364	148796364	Missense	SNP	C	G	CSB25	NM_019032.4	p.T659R
CTSK	1	149045894	149045894	Silent	SNP	G	C	CSB1	NM_000396.2	p.L4
BNIP1	1	149276692	149276692	Missense	SNP	G	C	BRC18	NM_138278.2	p.E23Q
THEM5	1	150090198	150090198	Missense	SNP	G	A	BRC32	NM_182578.2	p.S140L
TCHH	1	150353084	150353084	Silent	SNP	G	A	BRC19	NM_007113.2	p.L33
RPTN	1	150395664	150395664	Missense	SNP	C	T	BRC32	ENST00000316073	p.D179N
FLG	1	150547627	150547627	Missense	SNP	T	A	CSB29	NM_002016.1	p.D2120V
FLG	1	150548655	150548655	Silent	SNP	G	A	CSB14	NM_002016.1	p.S1777
FLG2	1	150590405	150590405	Missense	SNP	C	A	CSB22	NM_001014342.2	p.G2161C
FLG2	1	150596266	150596266	Missense	SNP	C	G	BRC39	NM_001014342.2	p.R207T
LCE1C	1	151044335	151044335	Missense	SNP	G	A	CSB1	NM_178351.3	p.R82C
PGLYRP4	1	151584452	151584452	Missense	SNP	G	A	CSB1	NM_020393.2	p.S57F
DENND4B	1	152176602	152176602	Missense	SNP	G	A	BRC31	NM_014856.2	p.R740C
CRTC2	1	152187259	152187259	Silent	SNP	G	A	BRC29	NM_181715.1	p.L678
CRTC2	1	152188220	152188220	Missense	SNP	C	T	BRC44	NM_181715.1	p.G557R
CREB3L4	1	152208130	152208130	Missense	SNP	C	T	BRC16	NM_130898.2	p.S92F
TPM3	1	152411204	152411204	Missense	SNP	G	T	BRC41	ENST00000368545	p.S137R
SHE	1	152740602	152740602	Silent	SNP	C	A	CSB19	NM_001010846.1	p.A175
KCNN3	1	153011131	153011131	Silent	SNP	G	C	CSB1	NM_002249.4	p.L464
PBXIP1	1	153184713	153184713	Silent	SNP	G	A	BRC31	NM_020524.2	p.F687
PYGO2	1	153197900	153197900	Silent	SNP	C	G	BRC41	NM_138300.3	p.L400
GBA	1	153473853	153473853	Missense	SNP	C	T	BRC8	NM_000157.2	p.R301H
C1orf2	1	153490547	153490547	Silent	SNP	G	C	BRC18	NM_006589.2	p.L115
ASH1L	1	153675245	153675245	Silent	SNP	G	A	CSB16	NM_018489.2	p.C1775
SYT11	1	154117657	154117657	Missense	SNP	G	A	BRC31	NM_152280.3	p.A344T
UBQLN4	1	154280567	154280567	Missense	SNP	C	G	CSB1	NM_020131.3	p.E324D
MEF2D	1	154713464	154713464	Silent	SNP	G	T	BRC18	NM_005920.2	p.I273
SH2D2A	1	155043683	155043683	Missense	SNP	C	T	BRC47	NM_003975.2	p.A361T
INSRR	1	155078688	155078688	Splice_Site	SNP	C	G	CSB1	NM_014215.1	e19-1
INSRR	1	155082153	155082153	Missense	SNP	C	A	BRC13	NM_014215.1	p.D686Y
INSRR	1	155083100	155083100	Missense	SNP	C	G	BRC50	NM_014215.1	p.E549Q
NTRK1	1	155111420	155111420	Silent	SNP	C	T	CSB1	NM_002529.1	p.I450
ETV3L	1	155334357	155334357	Silent	SNP	C	T	BRC39	NM_001004341.1	p.L178

FCRL4	1	155825684	155825684	Nonsense	SNP	C	A	CSB7	NM_031282.1	p.G81*	
FCRL2	1	155984998	155984998	Missense	SNP	C	G	CSB24	NM_138738.2	p.Q223H	
FCRL1	1	156036476	156036476	Missense	SNP	G	A	BRC26	NM_052938.3	p.L343F	
LOC649203	1	156103939	156103939	Missense	SNP	A	T	BRC35	XM_001725511.1	p.K160N	
CD1D	1	156418068	156418068	Silent	SNP	A	C	CSB2	NM_001766.3	p.I87	
CD1E	1	156592937	156592937	Missense	SNP	G	C	CSB1	NM_001042584.1	p.D276H	
SPTA1	1	156885048	156885048	Missense	SNP	C	G	CSB5	NM_003126.2	p.E1197Q	
SPTA1	1	156914151	156914151	Missense	SNP	G	A	BRC50	NM_003126.2	p.H304Y	
OR6K6	1	156991268	156991268	Silent	SNP	T	C	BRC11	NM_001005184.1	p.Y13	
OR6N1	1	157002998	157002998	Silent	SNP	G	A	CSB24	NM_001005185.1	p.L33	
MNDA	1	157080469	157080469	Missense	SNP	C	G	BRC16	NM_002432.1	p.A168G	
OR10J1	1	157676265	157676265	Silent	SNP	C	T	CSB6	NM_012351.1	p.F31	
KCNJ10	1	158277964	158277964	Missense	SNP	C	G	BRC7	NM_002241.3	p.S328T	
IGSF8	1	158331315	158331315	Missense	SNP	A	C	BRC11	NM_052868.2	p.L137R	
ATP1A2	1	158372668	158372668	Missense	SNP	C	A	CSB3	NM_000702.3	p.A816D	
NCSTN	1	158593111	158593111	Silent	SNP	C	T	BRC39	NM_015331.2	p.V579	
CD84	1	158787439	158787439	Silent	SNP	T	C	BRC16	NM_003874.2	p.S257	
NIT1	1	159355666	159355666	Missense	SNP	G	C	BRC18	NM_005600.1	p.E73Q	
NR1I3	1	159469743	159469743	Missense	SNP	G	A	BRC48	NM_001077482.1	p.S83L	
DDR2	1	161009903	161009903	Missense	SNP	G	T	CSB22	NM_001014796.1	p.E583D	
LMX1A	1	163449606	163449606	Missense	SNP	C	G	BRC5	NM_177398.1	p.G189R	
RXRG	1	163637140	163637140	Missense	SNP	G	A	BRC31	NM_006917.1	p.P459L	
FAM78B	1	164306265	164306265	Missense	SNP	C	T	BRC32	NM_001017961.2	p.R208Q	
ILDR2	1	165171240	165171240	Missense	SNP	G	C	CSB25	NM_199351.1	p.P268A	
MAEL	1	165252131	165252131	Silent	SNP	T	C	CSB9	NM_032858.1	p.V298	
ADCY10	1	166065273	166065273	Silent	SNP	C	A	BRC21	NM_018417.3	p.L1202	
BLZF1	1	167612580	167612580	Silent	SNP	C	T	BRC30	NM_003666.2	p.L69	
BLZF1	1	167618062	167618062	Silent	SNP	A	C	BRC23	NM_003666.2	p.G312	
F5	1	167786540	167786557	In Frame Del	DEL	GAGAAG GTC ACTCCAT GA		0	CSB31	NM_000130.4	p.HGVTF544 8in Frame del
C1orf112	1	168041825	168041825	Missense	SNP	C	T	BRC51	NM_018186.2	p.H179Y	
LOC646804	1	169319434	169319434	Missense	SNP	C	A	CSB27	XM_929761.1	p.P60T	
BAT2D1	1	169771979	169771979	Missense	SNP	C	T	CSB1	ENST00000392080	p.S742F	
BAT2D1	1	169793633	169793633	Missense	SNP	C	A	BRC44	ENST00000392080	p.P1918T	

C1orf9	1	170806444	170806444	Missense	SNP	A	T	BRC42	NM_016227.3	p.I492L
C1orf9	1	170825149	170825149	Missense	SNP	C	T	BRC48	NM_016227.3	p.S913L
C1orf9	1	170825670	170825670	Silent	SNP	C	T	CSB1	NM_016227.3	p.L1087
KLHL20	1	171989049	171989049	Silent	SNP	C	T	CSB1	NM_014458.3	p.I277
TNN	1	173364412	173364412	Silent	SNP	C	T	CSB33	NM_022093.1	p.A1079
TNR	1	173600998	173600998	Silent	SNP	G	A	BRC41	NM_003285.2	p.T786
PAPPA2	1	175005505	175005505	Missense	SNP	G	A	CSB16	NM_020318.2	p.R1488H
ASTN1	1	175268400	175268400	Missense	SNP	G	C	CSB1	NM_004319.1	p.S227C
ASTN1	1	175268533	175268533	Missense	SNP	G	A	CSB3	NM_004319.1	p.R183C
FAM5B	1	175493127	175493127	Missense	SNP	C	T	BRC29	NM_021165.2	p.A218V
RASAL2	1	176677383	176677383	Missense	SNP	G	A	CSB10	NM_170692.2	p.R284H
RASAL2	1	176694250	176694250	Missense	SNP	G	A	BRC39	NM_170692.2	p.R1056K
TDRD5	1	177871622	177871622	Silent	SNP	C	T	CSB1	NM_173533.2	p.L499
CEP350	1	178250157	178250157	Missense	SNP	C	T	BRC11	NM_014810.4	p.S648F
CEP350	1	178256179	178256179	Missense	SNP	G	C	CSB1	NM_014810.4	p.D882H
IER5	1	179324712	179324712	Silent	SNP	G	A	BRC18	NM_016545.4	p.K17
CACNA1E	1	179816366	179816366	Missense	SNP	G	C	CSB1	NM_000721.2	p.G261A
CACNA1E	1	180011958	180011958	Silent	SNP	C	T	CSB3	NM_000721.2	p.R1746
ZNF648	1	180292762	180292762	Missense	SNP	G	C	BRC41	NM_001009992.1	p.P336R
DHX9	1	181117312	181117312	Missense	SNP	G	A	BRC39	NM_001357.3	p.E941K
DHX9	1	181122878	181122878	Frame Shift Ins	INS		0 A	CSB20	NM_001357.3	p.Y1167fs
LAMC1	1	181376261	181376261	Missense	SNP	G	A	CSB15	NM_002293.3	p.G1525R
LAMC2	1	181479081	181479081	Missense	SNP	G	A	BRC39	NM_005562.2	p.D1169N
EDEM3	1	182943947	182943947	Missense	SNP	G	A	CSB16	NM_025191.3	p.P624L
IVNS1ABP	1	183535829	183535829	Missense	SNP	G	C	BRC18	NM_006469.4	p.Q476E
IVNS1ABP	1	183536856	183536856	Missense	SNP	G	A	CSB13	NM_006469.4	p.P331S
HMCN1	1	184387095	184387095	Missense	SNP	C	T	CSB1	NM_031935.2	p.R4917C
PLA2G4A	1	185213476	185213476	Silent	SNP	G	A	BRC50	NM_024420.2	p.E631
RGS1	1	190814911	190814911	Nonsense	SNP	C	T	CSB9	NM_002922.3	p.R156*
KCNT2	1	194562469	194562469	Splice_Site	SNP	C	T	BRC9	NM_198503.2	e19+1
CFH	1	194915529	194915529	Missense	SNP	C	T	CSB7	NM_000186.3	p.P258L
CFHR5	1	195213401	195213401	Missense	SNP	G	A	BRC47	ENST00000367414	p.R19Q
ASPM	1	195327742	195327742	Missense	SNP	G	A	CSB16	NM_018136.4	p.A3121V
ASPM	1	195336587	195336587	Missense	SNP	G	A	CSB1	NM_018136.4	p.S2806L

ASPM	1	195378966	195378967	Frame Shift Del	DEL	TA	0	CSB1	NM_018136.4	p.D346fs
CRB1	1	195670722	195670722	Missense	SNP	G	A	CSB1	NM_201253.1	p.E1036K
NEK7	1	196498385	196498385	Missense	SNP	C	G	BRC13	NM_133494.2	p.L86V
PTPRC	1	196935355	196935355	Missense	SNP	C	T	BRC47	NM_002838.3	p.A111V
KIF14	1	198800999	198800999	Missense	SNP	A	G	CSB14	NM_014875.2	p.S1298P
PPP1R12B	1	200676456	200676456	Splice_Site	SNP	G	A	BRC35	NM_032105.2	e11-1
SYT2	1	200838284	200838284	Missense	SNP	C	T	BRC17	NM_177402.1	p.V160I
JARID1B	1	200965597	200965597	Missense	SNP	C	T	BRC13	NM_006618.3	p.R1453K
JARID1B	1	201044110	201044110	Missense	SNP	G	T	BRC11	ENST00000235790	p.R119S
CHI3L1	1	201416316	201416316	Missense	SNP	G	C	CSB1	NM_001276.2	p.L267V
CHIT1	1	201461560	201461560	Silent	SNP	A	T	BRC41	NM_003465.2	p.A39
OPTC	1	201735500	201735500	Missense	SNP	G	C	BRC18	NM_014359.3	p.E210D
REN	1	202391978	202391978	Missense	SNP	G	A	BRC31	NM_000537.3	p.S304F
PLEKHA6	1	202503271	202503271	Nonsense	SNP	T	A	CSB29	NM_014935.2	p.K79*
CNTN2	1	203295366	203295366	Missense	SNP	C	T	CSB10	NM_005076.2	p.R244W
TMCC2	1	203492159	203492159	Missense	SNP	G	A	BRC11	ENST00000367159	p.E7K
TMCC2	1	203507603	203507603	Missense	SNP	G	C	CSB1	NM_014858.2	p.E620Q
DYRK3	1	204888754	204888754	Missense	SNP	C	G	BRC50	NM_003582.1	p.L530V
C1orf116	1	205267472	205267472	Missense	SNP	C	G	CSB32	NM_023938.1	p.R32P
CR1	1	205766766	205766766	Frame Shift Del	DEL	G	0	BRC16	NM_000651.3	p.D312fs
PLXNA2	1	206300653	206300653	Splice_Site	SNP	C	T	CSB22	NM_025179.3	e12+1
PLXNA2	1	206457695	206457695	Missense	SNP	C	T	BRC38	NM_025179.3	p.A66T
TRAF3IP3	1	208012939	208012939	Silent	SNP	G	A	CSB1	NM_025228.1	p.L222
C1orf97	1	209631906	209631906	Missense	SNP	C	G	BRC15	ENST00000367003	p.S58W
SMYD2	1	212558106	212558106	Splice_Site	SNP	G	A	BRC40	NM_020197.2	e4+1
PTPN14	1	212651687	212651687	Missense	SNP	G	A	CSB1	NM_005401.3	p.S158F
CENPF	1	212880170	212880170	Nonsense	SNP	G	A	CSB22	NM_016343.3	p.W622*
KCTD3	1	213826567	213826567	Missense	SNP	G	C	BRC31	NM_016121.3	p.D245H
SPATA17	1	215981967	215981967	Missense	SNP	G	A	BRC39	NM_138796.2	p.M141I
TGFB2	1	216674305	216674305	Silent	SNP	A	C	CSB34	NM_003238.1	p.R216
DUSP10	1	219979492	219979492	Missense	SNP	C	A	BRC26	NM_007207.3	p.C73F
HHIPL2	1	220763608	220763608	Missense	SNP	C	G	BRC50	NM_024746.3	p.K619N
HHIPL2	1	220766967	220766967	Missense	SNP	C	T	BRC8	NM_024746.3	p.R591H
MIA3	1	220868308	220868308	Missense	SNP	G	C	BRC18	NM_198551.2	p.D375H

DISP1	1	221234883	221234883	Missense	SNP	C	A	CSB2	NM_032890.2	p.S308Y
DISP1	1	221242949	221242949	Silent	SNP	G	A	CSB1	NM_032890.2	p.L529
LBR	1	223672336	223672336	Silent	SNP	G	C	BRC51	NM_002296.2	p.V270
LEFTY1	1	224141763	224141763	Missense	SNP	C	A	BRC30	NM_020997.2	p.E232D
MIXL1	1	224480043	224480043	Silent	SNP	G	A	BRC18	NM_031944.1	p.Q202
ITPKB	1	224990644	224990644	Missense	SNP	C	G	BRC29	NM_002221.3	p.G380A
CABC1	1	225240827	225240827	Silent	SNP	C	T	CSB1	NM_020247.4	p.F570
ZNF678	1	225909839	225909839	Missense	SNP	G	T	BRC29	NM_178549.2	p.S422I
OBSCN	1	226560801	226560801	Nonsense	SNP	G	A	CSB1	NM_001098623.1	p.W3922*
OBSCN	1	226573579	226573579	Splice_Site	SNP	G	A	BRC22	NM_001098623.1	e54+1
OBSCN	1	226615000	226615000	Missense	SNP	T	C	BRC21	NM_052843.1	p.V6595A
ABCB10	1	227728343	227728343	Silent	SNP	G	A	BRC7	NM_012089.2	p.F623
URB2	1	227838385	227838385	Missense	SNP	C	T	CSB24	NM_014777.2	p.R468W
LOC100129238	1	228201806	228201806	Missense	SNP	G	C	BRC39	XM_001716016.1	p.E295Q p.105in Frame insS
AGT	1	228912907	228912907	In Frame Ins	INS		0 TGC	BRC40	NM_000029.3	
TTC13	1	229118654	229118654	Silent	SNP	C	T	CSB1	NM_024525.1	p.T667
C1orf124	1	229553931	229553931	Missense	SNP	G	C	CSB1	NM_032018.1	p.E237Q
EGLN1	1	229568776	229568788	Frame Shift Del	DEL	GGCTCT A GAAGAC	0	BRC35	NM_022051.1	p.V425fs
DISC1	1	230228879	230228879	Missense	SNP	C	G	BRC31	NM_018662.1	p.Q795E
GGPS1	1	233572236	233572236	Missense	SNP	A	T	BRC12	NM_001037277.1	p.E143D
LYST	1	233927115	233927115	Silent	SNP	G	A	CSB1	NM_000081.2	p.F3485
LYST	1	234039168	234039168	Nonsense	SNP	T	A	BRC41	NM_000081.2	p.K525*
HEATR1	1	234788383	234788383	Missense	SNP	C	G	CSB1	NM_018072.4	p.E1661Q
RYR2	1	235675412	235675412	Missense	SNP	G	A	BRC8	NM_001035.2	p.R420Q
RYR2	1	235840889	235840889	Missense	SNP	C	T	CSB1	NM_001035.2	p.L1630F
RYR2	1	236021390	236021390	Silent	SNP	A	G	BRC12	NM_001035.2	p.L4505
CHRM3	1	238138255	238138255	Missense	SNP	A	G	CSB14	NM_000740.2	p.E294G
WDR64	1	239890574	239890574	Missense	SNP	G	A	BRC18	ENST00000366552	p.D89N
PLD5	1	240449954	240449954	Missense	SNP	A	C	CSB19	NM_152666.1	p.Y140D
C1orf71	1	244877699	244877699	Missense	SNP	G	A	BRC11	NM_152609.1	p.E525K
ENSG0000020207 9	1	245524842	245524842	RNA	SNP	C	G	BRC39	ENST00000365209	NULL
LOC644852	1	245749914	245749914	RNA	SNP	C	G	BRC39	XR_040316.1	NULL
OR2C3	1	245761483	245761483	Silent	SNP	C	T	BRC13	NM_198074.4	p.A317

OR2L8	1	246179665	246179665	Missense	SNP	G	A	BRC33	NM_001001963.1	p.E295K
OR2L2	1	246268445	246268445	Missense	SNP	C	G	BRC39	NM_001004686.2	p.L85V
OR2L2	1	246268664	246268664	Missense	SNP	C	T	BRC13	NM_001004686.2	p.H158Y
OR2M2	1	246410114	246410114	Silent	SNP	C	T	BRC11	NM_001004688.1	p.L68
OR2T12	1	246524825	246524825	Missense	SNP	G	T	CSB25	NM_001004692.1	p.R227S
FAM150B	2	273152	273152	Missense	SNP	G	C	CSB24	NM_001002919.2	p.L138V
MYT1L	2	1925842	1925842	Missense	SNP	C	T	BRC49	NM_015025.2	p.D142N
ADI1	2	3496678	3496678	Silent	SNP	G	A	BRC39	NM_018269.2	p.I66
COLEC11	2	3668971	3668971	Nonsense	SNP	C	T	CSB1	NM_024027.3	p.Q131*
CPSF3	2	9490155	9490155	Missense	SNP	G	C	CSB1	NM_016207.2	p.E136Q
TAF1B	2	9909570	9909570	Missense	SNP	C	G	BRC41	ENST00000404869	p.T109R
ATP6V1C2	2	10821976	10821976	Missense	SNP	G	A	BRC51	NM_001039362.1	p.V118M
ROCK2	2	11269351	11269351	Nonsense	SNP	C	A	CSB15	NM_004850.3	p.E704*
KCNS3	2	17976455	17976455	Silent	SNP	C	T	BRC15	NM_002252.3	p.F233
ENSG0000022227 9	2	20238635	20238635	RNA	SNP	G	C	BRC18	ENST00000410347	NULL
APOB	2	21083079	21083079	Missense	SNP	C	G	CSB1	NM_000384.2	p.R3389T
APOB	2	21083771	21083771	Missense	SNP	C	G	CSB1	NM_000384.2	p.L3158F
APOB	2	21091841	21091841	Silent	SNP	G	A	CSB30	NM_000384.2	p.L1138
APOB	2	21099255	21099255	Missense	SNP	C	A	CSB34	NM_000384.2	p.K923N
LOC100129278	2	21218142	21218142	Missense	SNP	A	C	BRC44	XM_001717344.1	p.K1579T
LOC100129278	2	21219314	21219314	Missense	SNP	C	T	BRC31	XM_001717344.1	p.R1970C
ATAD2B	2	23941231	23941231	Missense	SNP	G	T	BRC39	NM_017552.1	p.P419Q
ATAD2B	2	23957034	23957034	Nonsense	SNP	G	A	CSB29	NM_017552.1	p.R294*
C2orf44	2	24115310	24115310	Missense	SNP	C	G	BRC6	NM_025203.1	p.A187P
DNMT3A	2	25322626	25322626	Missense	SNP	C	G	BRC44	NM_022552.3	p.A446P
RAB10	2	26204311	26204311	Missense	SNP	A	G	BRC31	NM_016131.3	p.D169G
HADHB	2	26355537	26355537	Missense	SNP	G	A	BRC51	NM_000183.2	p.E221K
DPYSL5	2	27011051	27011051	Frame Shift Del	DEL	C		0 CSB2	NM_020134.3	p.P298fs
AGBL5	2	27133016	27133016	Nonsense	SNP	A	T	CSB14	NM_021831.2	p.K463*
NRBP1	2	27510053	27510053	Missense	SNP	C	T	CSB14	NM_013392.2	p.R74W
IFT172	2	27530484	27530484	Missense	SNP	G	T	CSB1	NM_015662.1	p.H1194N
SUPT7L	2	27729871	27729871	Silent	SNP	C	T	BRC52	NM_014860.1	p.R410
SUPT7L	2	27737762	27737762	Missense	SNP	C	G	CSB1	ENST00000405491	p.L2F
SLC4A1AP	2	27754145	27754145	Missense	SNP	C	T	BRC50	NM_018158.2	p.A538V

PLB1	2	28605767	28605767	Silent	SNP	C	T	BRC20	NM_153021.3	p.H135
PLB1	2	28682252	28682252	Missense	SNP	C	G	BRC50	NM_153021.3	p.A997G
PLB1	2	28706992	28706992	Missense	SNP	C	A	CSB21	NM_153021.3	p.S1285Y
C2orf71	2	29147607	29147607	Missense	SNP	G	A	BRC47	NM_001029883.1	p.R1009C
C2orf71	2	29150235	29150235	Nonsense	SNP	C	A	BRC39	NM_001029883.1	p.E133*
LBH	2	30310842	30310842	Missense	SNP	G	C	BRC15	NM_030915.3	p.G32R
LCLAT1	2	30644429	30644429	Splice_Site	SNP	G	C	BRC50	NM_182551.1	e5-1
LCLAT1	2	30644486	30644486	Nonsense	SNP	G	T	BRC50	NM_182551.1	p.E228*
BIRC6	2	32494483	32494483	Missense	SNP	T	G	BRC5	NM_016252.3	p.C874G
BIRC6	2	32519971	32519971	Missense	SNP	A	G	BRC42	NM_016252.3	p.D1294G
BIRC6	2	32524103	32524103	Silent	SNP	T	C	BRC12	NM_016252.3	p.Y1449
BIRC6	2	32581365	32581365	Splice_Site	SNP	G	A	BRC15	NM_016252.3	e48-1
BIRC6	2	32591596	32591596	Nonsense	SNP	C	G	BRC51	NM_016252.3	p.S3480*
PRKD3	2	37396937	37396937	Missense	SNP	C	T	BRC38	NM_005813.3	p.E79K
CDC42EP3	2	37727175	37727175	Missense	SNP	A	C	BRC39	NM_006449.3	p.F20L
HNRPLL	2	38654047	38654047	Missense	SNP	G	A	BRC50	NM_138394.1	p.P301S
SFRS7	2	38827373	38827373	Nonsense	SNP	G	C	BRC39	NM_001031684.2	p.S198*
ENSG00000214694	2	39009587	39009587	Missense	SNP	C	G	CSB1	ENST00000409978	p.F37L
SOS1	2	39137352	39137352	Missense	SNP	C	G	BRC47	NM_005633.3	p.D169H
MAP4K3	2	39373428	39373428	Nonsense	SNP	C	A	CSB9	NM_003618.2	p.E421*
EML4	2	42410471	42410471	Missense	SNP	G	T	BRC13	NM_019063.1	p.D856Y
DYNC2LI1	2	43885831	43885831	Missense	SNP	C	T	CSB30	NM_016008.1	p.A312V
ABCG8	2	43952729	43952729	Missense	SNP	T	C	BRC31	NM_022437.2	p.F359L
PRKCE	2	46082106	46082106	Missense	SNP	G	T	CSB13	NM_005400.2	p.D295Y
MSH6	2	47884308	47884308	Nonsense	SNP	A	T	BRC15	NM_000179.2	p.K1140*
FBXO11	2	47919529	47919529	Missense	SNP	C	A	BRC11	NM_025133.1	p.S103I
CHAC2	2	53855101	53855101	Missense	SNP	C	G	CSB1	NM_001008708.2	p.L164V
SPTBN1	2	54729688	54729688	Missense	SNP	G	A	BRC8	NM_003128.2	p.A1687T
EML6	2	54947510	54947510	Missense	SNP	T	C	BRC48	XM_001725001.2	p.L679P
EML6	2	54997408	54997408	Missense	SNP	G	C	CSB1	XM_001725001.2	p.K1169N
CCDC88A	2	55413213	55413213	Missense	SNP	C	T	CSB1	NM_018084.1	p.D950N
SMEK2	2	55679625	55679625	Missense	SNP	C	T	BRC31	NM_020463.1	p.E118K
LOC730134	2	59330525	59330525	Missense	SNP	C	A	BRC18	XM_001132580.1	p.R9M
ENSG00000222030	2	59335877	59335877	Missense	SNP	G	T	BRC50	ENST00000409590	p.D17Y

REL	2	60999236	60999236	Missense	SNP	G	C	BRC50	NM_002908.2	p.D282H
XPO1	2	61573047	61573047	Missense	SNP	A	G	CSB15	NM_003400.3	p.I547T
XPO1	2	61574594	61574594	Missense	SNP	G	A	CSB1	NM_003400.3	p.S395F
FAM161A	2	61922777	61922777	Missense	SNP	G	C	BRC44	NM_032180.2	p.L27V
SLC1A4	2	65091328	65091328	Missense	SNP	G	A	BRC5	NM_003038.1	p.E243K
MEIS1	2	66651934	66651934	Silent	SNP	G	A	BRC39	ENST00000398506	p.V387
WDR92	2	68211936	68211936	Missense	SNP	C	T	BRC18	NM_138458.2	p.V338I
SNRNP27	2	69975784	69975784	Missense	SNP	G	T	CSB6	NM_006857.1	p.R30M
TGFA	2	70546319	70546319	Frame Shift Del	DEL	T		0 BRC33	NM_003236.1	p.H51fs
CLEC4F	2	70896690	70896690	Missense	SNP	C	T	BRC17	NM_173535.2	p.R444H
CD207	2	70914646	70914646	Missense	SNP	C	A	BRC41	NM_015717.2	p.M68I
ZNF638	2	71476824	71476824	Missense	SNP	C	T	CSB1	NM_001014972.1	p.S808F
ZNF638	2	71507981	71507981	Missense	SNP	C	T	CSB9	NM_001014972.1	p.S1825F
DYSF	2	71644722	71644722	Silent	SNP	C	T	BRC10	NM_003494.1	p.V794
DYSF	2	71749410	71749410	Missense	SNP	G	T	BRC3	NM_003494.1	p.V1787F
ALMS1	2	73512878	73512878	Missense	SNP	G	C	BRC39	NM_015120.4	p.L461F
ACTG2	2	73981974	73981974	Missense	SNP	G	A	BRC6	NM_001615.3	p.V10M
DCTN1	2	74451851	74451851	Silent	SNP	C	T	BRC26	ENST00000407639	p.R27
GCS1	2	74542416	74542416	Nonsense	SNP	G	A	CSB1	NM_006302.2	p.Q670*
GCS1	2	74543448	74543448	Missense	SNP	G	C	CSB1	NM_006302.2	p.L326V
TTC31	2	74573777	74573777	Missense	SNP	C	G	BRC39	NM_022492.3	p.P495R
C2orf3	2	75754112	75754112	Missense	SNP	C	G	BRC50	NM_003203.3	p.E619Q
REG3A	2	79239342	79239342	Silent	SNP	G	C	BRC36	NM_002580.1	p.A46
LRRTM1	2	80383498	80383498	Missense	SNP	G	A	BRC44	NM_178839.4	p.R320C
DNHL1	2	84624968	84624968	Missense	SNP	G	C	BRC11	ENST00000237449	p.D255H
TCF7L1	2	85388293	85388293	Silent	SNP	G	A	BRC39	NM_031283.1	p.R425
ELMOD3	2	85458000	85458000	Silent	SNP	G	A	CSB8	NM_032213.1	p.L210
MAT2A	2	85622897	85622897	Missense	SNP	G	C	CSB1	NM_005911.4	p.D220H
RNF103	2	86685495	86685495	Missense	SNP	C	T	BRC5	NM_005667.2	p.G347E
EIF2AK3	2	88656059	88656059	Missense	SNP	G	A	CSB1	NM_004836.4	p.S686F
LOC647597	2	91300398	91300398	Silent	SNP	G	A	CSB24	XM_001715151.1	p.D10
CIAO1	2	96300731	96300731	Missense	SNP	A	T	CSB15	NM_004804.2	p.N312I
uc002swr.2	2	96681436	96681436	Missense	SNP	G	C	BRC35	ENST00000342152	p.Q125H
FER1L5	2	96733680	96733680	Missense	SNP	C	T	BRC26	NM_001077400.1	p.R680C

CNGA3	2	98379872	98379872	Missense	SNP	C	T	BRC50	NM_001298.1	p.R603W
INPP4A	2	98570474	98570474	Missense	SNP	G	A	CSB1	NM_004027.1	p.E930K
C2orf55	2	98804827	98804827	Missense	SNP	C	T	BRC50	NM_207362.2	p.D781N
AFF3	2	99565845	99565845	Missense	SNP	G	C	BRC11	NM_001025108.1	p.I905M
LONRF2	2	100267193	100267193	Nonstop Mutation	SNP	C	G	BRC39	NM_198461.3	p.*755S
LONRF2	2	100269919	100269919	Silent	SNP	G	A	BRC5	NM_198461.3	p.H653
uc002tbb.1	2	101385384	101385384	Silent	SNP	G	A	BRC51	ENST00000376826	p.S97
MAP4K4	2	101870151	101870151	Missense	SNP	C	G	BRC39	NM_004834.3	p.S1038C
IL1R2	2	101992463	101992463	Silent	SNP	C	A	BRC16	NM_004633.3	p.A25
IL1R2	2	101998801	101998801	Silent	SNP	C	T	BRC39	NM_004633.3	p.L123
LOC100131131	2	102104034	102104034	Silent	SNP	C	T	BRC24	XM_001720712.1	p.V15
SLC9A4	2	102488211	102488211	Silent	SNP	G	A	BRC18	NM_001011552.3	p.T349
MFSD9	2	102702069	102702069	Missense	SNP	C	A	BRC42	NM_032718.3	p.A223S
C2orf49	2	105328244	105328244	Missense	SNP	A	T	BRC23	NM_024093.1	p.H228L
LIMS1	2	108655261	108655261	Missense	SNP	A	G	CSB34	NM_004987.3	p.H91R
RANBP2	2	108749170	108749170	Missense	SNP	C	T	CSB1	NM_006267.4	p.P1915S
CCDC138	2	108771758	108771758	Missense	SNP	C	T	CSB1	NM_144978.1	p.S57F
NPHP1	2	110284848	110284848	Nonsense	SNP	C	A	CSB21	NM_000272.3	p.E116*
BUB1	2	111143510	111143510	Silent	SNP	A	C	BRC15	NM_004336.3	p.S186
ACOXL	2	111258783	111258783	Missense	SNP	G	C	CSB1	NM_001105516.2	p.E27Q
TMEM87B	2	112572651	112572651	Missense	SNP	G	T	BRC8	NM_032824.2	p.M427I
TTL	2	112968364	112968364	Missense	SNP	G	C	CSB1	NM_153712.4	p.R137T
LOC100130100	2	113880455	113880455	Missense	SNP	G	C	CSB33	XM_001716615.1	p.V5L
SLC35F5	2	114229521	114229521	Silent	SNP	G	C	BRC44	NM_025181.2	p.L37
CCDC93	2	118432509	118432509	Missense	SNP	C	T	BRC13	NM_019044.3	p.E303K
MARCO	2	119448418	119448418	Missense	SNP	C	T	BRC17	NM_006770.3	p.A167V
PTPN4	2	120434936	120434936	Missense	SNP	G	C	BRC44	NM_002830.2	p.Q739H
CNTNAP5	2	124891639	124891639	Splice_Site	SNP	T	C	BRC35	NM_130773.2	e4+2
CNTNAP5	2	125238172	125238172	Silent	SNP	C	T	CSB2	NM_130773.2	p.D836
LOC339760	2	127374001	127374001	Silent	SNP	G	A	BRC18	XM_295058.1	p.K411
IWS1	2	127979042	127979042	Frame Shift Ins	INS		0 AA	BRC7	NM_017969.2	p.E303fs
MYO7B	2	128055988	128055988	Missense	SNP	G	A	BRC39	NM_001080527.1	p.R378Q
WDR33	2	128194139	128194139	Missense	SNP	G	C	BRC13	NM_018383.1	p.Q644E
SAP130	2	128490583	128490583	Silent	SNP	C	T	CSB13	NM_024545.1	p.P145

LOC653781	2	131106662	131106662	Nonsense	SNP	C	T	CSB1	XM_929706.3	p.Q421*
LOC730032	2	131389155	131389155	Missense	SNP	C	T	BRC40	XM_001132160.2	p.P389L
uc002tsy.2	2	131995028	131995028	Missense	SNP	A	T	BRC14	ENST00000356430	p.Q216L
NAP5	2	133206014	133206014	Missense	SNP	G	A	CSB30	NM_207363.2	p.R1737C
NAP5	2	133257650	133257650	Silent	SNP	G	A	BRC31	NM_207363.2	p.I1068
CCNT2	2	135410980	135410986	Frame Shift Del	DEL	C		0 BRC39	NM_058241.2	p.L114fs
DARS	2	136396834	136396834	Frame Shift Del	DEL	A		0 BRC15	NM_001349.2	p.I268fs
ENSG0000021608 1	2	137018450	137018450	RNA	SNP	G	T	BRC47	ENST00000401262	NULL
THSD7B	2	138046567	138046567	Missense	SNP	G	C	CSB1	NM_001080427.1	p.E1103Q
LRP1B	2	141250216	141250216	Silent	SNP	G	A	BRC17	NM_018557.2	p.D1807
LRP1B	2	141382099	141382099	Missense	SNP	C	A	BRC7	NM_018557.2	p.A1113S
LRP1B	2	141721388	141721388	Missense	SNP	C	G	BRC51	NM_018557.2	p.D157H
ORC4L	2	148426459	148426459	Nonsense	SNP	G	A	BRC39	NM_002552.2	p.Q181*
MBD5	2	148943342	148943342	Missense	SNP	G	C	BRC39	NM_018328.3	p.E454Q
RIF1	2	152028956	152028956	Missense	SNP	C	T	BRC39	NM_018151.3	p.A1559V
NEB	2	152079190	152079190	Splice_Site	SNP	T	C	BRC36	NM_004543.3	e130-2
NEB	2	152222800	152222800	Silent	SNP	G	A	BRC39	NM_004543.3	p.L2042
FMNL2	2	153183775	153183775	Missense	SNP	C	A	CSB3	NM_052905.3	p.P495Q
GALNT13	2	154807660	154807660	Missense	SNP	G	A	CSB34	NM_052917.2	p.D228N
GALNT13	2	154810642	154810642	Missense	SNP	T	A	BRC28	NM_052917.2	p.M253K
KCNJ3	2	155264183	155264183	Missense	SNP	A	G	CSB7	NM_002239.2	p.N217S
ACVR1	2	158325645	158325645	Silent	SNP	C	T	CSB1	NM_001105.4	p.V419
LY75	2	160425623	160425623	Missense	SNP	A	C	BRC48	NM_002349.2	p.N741K
SLC4A10	2	162443929	162443929	Missense	SNP	G	A	BRC38	NM_022058.3	p.A301T
KCNH7	2	163082528	163082528	Missense	SNP	C	T	BRC50	NM_033272.2	p.V284I
SCN3A	2	165656007	165656007	Silent	SNP	C	G	BRC39	NM_006922.1	p.L1634
SCN2A	2	165953677	165953677	Silent	SNP	C	T	CSB1	NM_001040142.1	p.I1705
SCN1A	2	166560783	166560783	Missense	SNP	T	C	CSB1	NM_006920.4	p.I1512V
SCN1A	2	166567243	166567243	Silent	SNP	G	A	BRC39	NM_006920.4	p.L1412
SCN1A	2	166567350	166567350	Missense	SNP	C	T	CSB6	NM_006920.4	p.E1377K
SCN7A	2	166981630	166981630	Missense	SNP	T	C	BRC30	NM_002976.2	p.R1083G
SCN7A	2	167042347	167042347	Missense	SNP	C	T	CSB1	NM_002976.2	p.E36K
XIRP2	2	167818879	167818879	Missense	SNP	A	G	BRC20	NM_001079810.2	p.H423R

LRP2	2	169704034	169704034	Missense	SNP	A	G	BRC23	NM_004525.2	p.L4454P
LRP2	2	169771306	169771306	Silent	SNP	G	A	BRC13	NM_004525.2	p.L2390
LRP2	2	169771369	169771369	Silent	SNP	G	A	CSB2	NM_004525.2	p.D2369
LRP2	2	169774389	169774389	Missense Frame Shift	SNP	C	T	BRC29	NM_004525.2	p.A2097T
PPIG	2	170179438	170179438	Ins	INS		0 T	BRC35	NM_004792.2	p.R170fs
PHOSPHO2	2	170265988	170265988	Missense	SNP	G	C	BRC11	NM_001008489.2	p.K87N
DLX2	2	172673662	172673662	Missense	SNP	G	C	BRC50	NM_004405.3	p.P281R
DLX2	2	172675399	172675399	Silent	SNP	A	C	CSB15	NM_004405.3	p.G38
SP3	2	174528157	174528157	Silent	SNP	C	G	CSB1	NM_003111.3	p.L443
NFE2L2	2	177804156	177804156	Missense	SNP	A	C	CSB21	NM_006164.1	p.I474S
PDE11A	2	178253812	178253812	Missense	SNP	C	T	BRC40	NM_016953.1	p.R804H
TTN	2	179136954	179136954	Missense	SNP	G	A	BRC37	ENST00000375038	p.A23365V
TTN	2	179148663	179148663	Missense	SNP	G	C	BRC39	ENST00000375038	p.S19462C
TTN	2	179151115	179151115	Missense	SNP	C	G	CSB1	ENST00000375038	p.K18772N
TTN	2	179163706	179163706	Missense	SNP	C	G	CSB1	ENST00000375038	p.R16312T
TTN	2	179186199	179186199	Missense	SNP	C	T	BRC50	ENST00000375038	p.E12510K
TTN	2	179191373	179191373	Missense	SNP	C	T	CSB10	ENST00000375038	p.G11668E
TTN	2	179277122	179277122	Missense	SNP	C	T	BRC16	ENST00000375038	p.E8830K
TTN	2	179348472	179348472	Missense	SNP	C	T	CSB1	NM_133379.3	p.D2122N p.A736in
CCDC141	2	179410260	179410260	In Frame Ins	INS		0 AGT	CSB21	NM_173648.2	Frame insDS
CWC22	2	180546203	180546203	Missense	SNP	C	T	BRC50	NM_020943.2	p.A256T
CERKL	2	182121702	182121702	Silent	SNP	G	A	BRC50	NM_201548.1	p.S341
NEUROD1	2	182251123	182251123	Missense	SNP	G	C	CSB1	NM_002500.2	p.S237C
NEUROD1	2	182251241	182251241	Missense	SNP	C	G	BRC47	NM_002500.2	p.E198Q
ZNF804A	2	185509680	185509680	Missense	SNP	C	G	BRC18	NM_194250.1	p.Q438E
FLJ44048	2	186378962	186378962	Missense	SNP	A	T	BRC51	NM_207482.2	p.N260Y
COL3A1	2	189567040	189567040	Missense	SNP	G	C	BRC4	NM_000090.3	p.G394A
COL3A1	2	189580517	189580517	Missense	SNP	G	C	BRC5	NM_000090.3	p.G1101A
MSTN	2	190630276	190630276	Missense	SNP	A	G	CSB15	NM_005259.2	p.Y361H
STAT4	2	191719705	191719705	Missense	SNP	G	C	BRC31	NM_003151.2	p.T51S
DNAH7	2	196459207	196459207	Missense	SNP	C	A	BRC38	NM_018897.2	p.R1814L
HECW2	2	196902591	196902591	Missense	SNP	G	A	BRC9	NM_020760.1	p.A175V
HECW2	2	197006281	197006281	Missense	SNP	G	A	CSB22	NM_020760.1	p.P38S
SF3B1	2	197975079	197975079	Missense	SNP	T	C	CSB13	NM_012433.1	p.K700E

SF3B1	2	197975079	197975079	Missense	SNP	T	C	CSB21	NM_012433.1	p.K700E
SF3B1	2	197975606	197975606	Missense	SNP	T	G	BRC32	NM_012433.1	p.K666Q
HSPD1	2	198071643	198071643	Splice_Site	SNP	C	T	BRC26	NM_002156.4	e1+1
SGOL2	2	201109047	201109047	Silent	SNP	A	T	BRC51	NM_152524.4	p.I108
SGOL2	2	201145298	201145298	Missense	SNP	G	A	BRC31	NM_152524.4	p.E662K
AOX1	2	201215769	201215769	Silent	SNP	G	A	BRC20	NM_001159.3	p.K949
ALS2CR11	2	202174757	202174757	Missense	SNP	C	T	BRC39	NM_152525.4	p.E156K
FZD7	2	202608568	202608568	Missense	SNP	G	A	CSB1	NM_003507.1	p.R318H
ZDBF2	2	206881620	206881620	Missense	SNP	C	G	CSB1	NM_020923.1	p.Q1375E
DYTN	2	207236055	207236055	Missense	SNP	G	C	BRC39	NM_001093730.1	p.Q484E
FZD5	2	208340734	208340734	Silent	SNP	G	A	CSB1	NM_003468.3	p.F325
PIP5K3	2	208898413	208898413	Missense	SNP	C	T	CSB14	NM_015040.3	p.A878V
uc002vdl.1	2	210549219	210549219	Missense	SNP	G	A	BRC34	ENST00000333907	p.V307M
ACADL	2	210791061	210791061	Missense	SNP	C	T	BRC11	NM_001608.3	p.A82T
BARD1	2	215318760	215318760	Missense	SNP	G	T	BRC20	NM_000465.2	p.Q581K
ENSG0000021205 5	2	216451862	216451862	RNA	SNP	G	A	BRC31	ENST00000390766	NULL
VIL1	2	219004846	219004846	Silent	SNP	C	T	CSB19	NM_007127.2	p.F375
CYP27A1	2	219385261	219385261	Silent	SNP	C	G	CSB1	NM_000784.3	p.L173
NHEJ1	2	219730485	219730485	Missense	SNP	G	T	CSB3	NM_024782.2	p.L1151
ABCB6	2	219783252	219783252	Silent	SNP	C	A	CSB19	NM_005689.1	p.V788
DES	2	219996744	219996744	Missense	SNP	A	G	CSB16	NM_001927.3	p.I416V
CHPF	2	220112745	220112745	Missense	SNP	G	T	BRC36	NM_024536.5	p.F644L
STK11IP	2	220184992	220184992	Missense	SNP	G	A	BRC44	ENST00000295641	p.D803N
PAX3	2	222794281	222794281	Missense	SNP	G	A	BRC13	NM_181459.4	p.H288Y
SGPP2	2	223131563	223131563	Missense	SNP	C	T	BRC41	NM_152386.2	p.S301F
COL4A4	2	227632523	227632523	Missense	SNP	C	T	BRC41	NM_000092.4	p.G742E
PID1	2	229835723	229835723	Missense	SNP	T	A	CSB22	NM_017933.1	p.R15W
DNER	2	230164756	230164756	Nonsense Frame Shift	SNP	G	T	CSB13	NM_139072.3	p.C123*
TRIP12	2	230432024	230432024	Del	DEL	G		0 CSB7	NM_004238.1	p.S204fs
SP110	2	230785824	230785824	Missense	SNP	C	T	CSB1	NM_080424.3	p.G160E
SP140	2	230884533	230884533	Missense	SNP	G	C	CSB1	NM_007237.2	p.Q828H
SP140L	2	230974367	230974367	Missense	SNP	A	T	CSB29	NM_138402.4	p.S489C
ITM2C	2	231448739	231448739	Missense	SNP	C	A	BRC41	NM_030926.1	p.P141H
PSMD1	2	231648517	231648517	Missense	SNP	G	C	BRC39	NM_002807.2	p.K310N

ARMC9	2	231835287	231835287	Missense	SNP	G	C	CSB1	NM_025139.3	p.E351Q
NCL	2	232036229	232036229	Missense	SNP	G	A	CSB1	NM_005381.2	p.P21S
DIS3L2	2	232873062	232873062	Silent	SNP	C	T	BRC33	NM_152383.4	p.R576
LOC100131009	2	233017737	233017737	Missense	SNP	T	A	BRC41	XM_001718359.1	p.D15V
COL6A3	2	237914288	237914288	Silent	SNP	C	T	BRC49	NM_004369.3	p.A2670
COL6A3	2	237940159	237940159	Missense	SNP	C	T	BRC3	NM_004369.3	p.E1804K
COL6A3	2	237952567	237952567	Missense	SNP	C	T	CSB7	NM_004369.3	p.V650I
LRRFIP1	2	238336786	238336786	Nonsense	SNP	C	G	BRC51	NM_004735.1	p.S540*
PER2	2	238835669	238835669	Missense	SNP	C	T	CSB1	ENST00000254658	p.E368K
FLJ43879	2	239512258	239512258	RNA	SNP	G	A	BRC50	XR_041560.1	NULL
uc002vym.1	2	240169670	240169670	Missense	SNP	A	G	BRC4	ENST00000358775	p.S174G
GPR35	2	241218733	241218733	Silent	SNP	C	T	CSB1	NM_005301.2	p.L231
KIF1A	2	241325197	241325197	Silent	SNP	G	A	CSB1	NM_004321.4	p.L1220
SNED1	2	241675520	241675520	Nonsense	SNP	A	T	BRC28	NM_001080437.1	p.K1388*
HDLBP	2	241827854	241827854	Missense	SNP	C	T	BRC14	NM_005336.3	p.V816I
HDLBP	2	241836399	241836399	Missense	SNP	C	G	CSB1	NM_005336.3	p.R517T
LRRN1	3	3862773	3862773	Missense	SNP	C	A	CSB23	NM_020873.5	p.T483N
BHLHE40	3	5000350	5000350	Silent	SNP	C	T	CSB23	NM_003670.2	p.P404
EDEM1	3	5204526	5204526	Silent	SNP	C	T	BRC33	NM_014674.2	p.L12
THUMPD3	3	9400954	9400954	Missense	SNP	C	A	CSB12	NM_015453.1	p.R432S
SETD5	3	9490137	9490137	Missense	SNP	C	T	CSB31	NM_001080517.1	p.S1138F
IL17RC	3	9940679	9940679	Missense	SNP	C	G	BRC30	NM_153461.4	p.P317R
LOC100129929	3	11901972	11901972	Silent	SNP	C	G	BRC18	XM_001716291.1	p.L374
SYN2	3	12157170	12157170	Frame Shift Del	DEL	A		CSB14	ENST00000341648	p.V66fs
PPARG	3	12422406	12422406	Silent	SNP	G	A	BRC29	NM_015869.5	p.Q215
RAF1	3	12601636	12601636	Silent	SNP	G	A	BRC41	NM_002880.3	p.I551
NUP210	3	13345319	13345319	Missense	SNP	C	T	CSB1	NM_024923.2	p.G1413E
NUP210	3	13359727	13359727	Missense	SNP	G	C	BRC14	NM_024923.2	p.A971G
NUP210	3	13392828	13392828	Missense	SNP	G	A	CSB28	NM_024923.2	p.T419M
CHCHD4	3	14133020	14133020	Missense	SNP	C	T	CSB15	NM_144636.1	p.D23N
XPC	3	14181947	14181947	Missense	SNP	G	A	CSB26	ENST00000285021	p.S255L
GRIP2	3	14523351	14523351	Missense	SNP	C	G	CSB1	NM_001080423.1	p.W885S
LOC344875	3	15181697	15181697	Missense	SNP	A	G	BRC30	XM_497913.1	p.S925P
CAPN7	3	15240062	15240062	Missense	SNP	A	G	BRC31	NM_014296.2	p.M239V

METTL6	3	15432435	15432439	Frame Shift Del	DEL	TATCA		0	BRC41	NM_152396.2	p.D126fs
COLQ	3	15538086	15538086	Silent	SNP	G	A		BRC50	NM_005677.3	p.F17
SATB1	3	18365903	18365903	Silent	SNP	G	A		CSB12	NM_002971.1	p.P685
SATB1	3	18437347	18437347	Silent	SNP	C	G		CSB20	NM_002971.1	p.P39
EFHB	3	19901034	19901034	Missense	SNP	C	A		BRC16	NM_144715.3	p.D671Y
EFHB	3	19950292	19950292	Missense	SNP	C	T		CSB27	NM_144715.3	p.E75K
KAT2B	3	20117790	20117790	Missense	SNP	A	T		CSB25	NM_003884.4	p.N226I
SGOL1	3	20200523	20200523	Missense	SNP	T	A		BRC17	NM_001012410.1	p.M1L
UBE2E1	3	23905618	23905618	Silent	SNP	G	A		BRC18	NM_003341.3	p.R116
OXSM	3	25808017	25808017	Nonsense	SNP	C	T		CSB1	NM_017897.1	p.Q168*
TRIM71	3	32834598	32834598	Missense	SNP	G	A		CSB10	NM_001039111.1	p.D8N
ARPP-21	3	35810402	35810402	Missense	SNP	G	A		BRC38	NM_016300.1	p.C796Y
DCLK3	3	36754022	36754022	Missense	SNP	G	A		BRC49	NM_033403.1	p.T378I
DCLK3	3	36754254	36754254	Missense	SNP	T	C		BRC18	NM_033403.1	p.K301E
LBA1	3	36849061	36849061	Silent	SNP	G	C		BRC48	NM_014831.1	p.L1745
ITGA9	3	37700429	37700429	Silent	SNP	C	A		CSB22	NM_002207.2	p.S662
OXSRI	3	38207250	38207250	Missense	SNP	T	C		BRC24	NM_005109.2	p.C70R
SLC22A14	3	38322621	38322621	Silent	SNP	C	T		BRC50	NM_004803.3	p.L34
SCN5A	3	38582993	38582993	Missense	SNP	C	T		CSB22	NM_001099404.4	p.V1251M
SCN10A	3	38730576	38730576	Splice_Site	SNP	C	G		BRC50	NM_006514.2	e21-1
SCN10A	3	38773518	38773518	Missense	SNP	G	T		CSB19	NM_006514.2	p.Q363K
SCN11A	3	38911069	38911069	Missense	SNP	C	G		BRC39	NM_014139.2	p.D932H
WDR48	3	39096304	39096304	Splice_Site	INS		T	0	CSB19	NM_020839.2	e11+1
ULK4	3	41914930	41914930	Missense	SNP	G	A		CSB1	NM_017886.2	p.S449L
ULK4	3	41952357	41952365	In Frame Del	DEL	AATCAG GTC		0	BRC41	NM_017886.2	p.DLI104in Frame del
TRAK1	3	42208092	42208092	Silent	SNP	G	A		BRC8	NM_001042646.1	p.E243
CYP8B1	3	42891053	42891053	Missense	SNP	G	T		BRC41	NM_004391.2	p.F420L
TGM4	3	44904184	44904184	Splice_Site	SNP	G	A		BRC30	NM_003241.3	e3-1
TGM4	3	44907221	44907221	Nonsense	SNP	G	A		BRC44	NM_003241.3	p.W141*
NBEAL2	3	47011567	47011567	Missense	SNP	C	G		BRC11	NM_015175.1	p.I446M
SMARCC1	3	47727250	47727253	Frame Shift Del	DEL	TCAT		0	BRC29	NM_003074.3	p.N281fs
MAP4	3	47932951	47932951	Missense	SNP	T	G		BRC32	NM_002375.1	p.N457T
COL7A1	3	48585116	48585116	Missense	SNP	G	T		CSB2	NM_000094.3	p.P2298T

CELSR3	3	48658072	48658072	Silent	SNP	G	A	CSB15	NM_001407.2	p.D2535
CELSR3	3	48684968	48684968	Missense	SNP	C	G	BRC11	ENST00000383733	p.K6N
WDR6	3	49026671	49026671	Silent	SNP	A	G	BRC41	NM_018031.3	p.E869
CCDC71	3	49175841	49175841	Nonsense	SNP	G	A	CSB33	NM_022903.3	p.R269*
AMIGO3	3	49730699	49730699	Silent	SNP	G	A	BRC5	NM_198722.2	p.L402
HYAL2	3	50330824	50330824	Missense	SNP	G	T	CSB12	NM_003773.3	p.H388N
MAPKAPK3	3	50659592	50659592	Missense	SNP	C	T	CSB6	NM_004635.3	p.T317M
IQCF1	3	51912103	51912103	Missense	SNP	C	A	CSB6	NM_152397.1	p.D16Y
BAP1	3	52415946	52415946	Missense	SNP	C	T	BRC13	NM_004656.2	p.E200K
PBRM1	3	52573122	52573122	Missense	SNP	C	T	CSB1	NM_018165.4	p.E1255K
ITIH1	3	52794214	52794214	Missense	SNP	G	A	BRC18	NM_002215.2	p.E508K
DCP1A	3	53313338	53313339	Del	DEL	AT		0 BRC51	NM_018403.4	p.I178fs
CACNA1D	3	53819103	53819103	Nonsense	SNP	C	A	BRC18	NM_000720.2	p.S1997*
WNT5A	3	55488394	55488394	Missense	SNP	C	A	BRC24	NM_003392.3	p.V127L
ERC2	3	56305476	56305476	Nonsense	SNP	G	A	BRC39	NM_015576.1	p.Q229*
C3orf63	3	56655883	56655883	Missense	SNP	T	C	BRC31	NM_015224.1	p.Q245R
DNAH12L	3	57469968	57469968	Missense	SNP	G	C	CSB1	ENST00000311202	p.L161V
FAM116A	3	57624473	57624473	Missense	SNP	G	A	BRC41	NM_152678.2	p.A148V
KCTD6	3	58462296	58462296	Missense	SNP	C	T	CSB20	NM_153331.1	p.T204M
PRICKLE2	3	64059960	64059960	Missense	SNP	G	A	CSB1	NM_198859.3	p.S781F
ADAMTS9	3	64522382	64522382	Missense	SNP	C	T	BRC21	NM_182920.1	p.C1537Y
KBTBD8	3	67132162	67132162	Missense	SNP	C	A	BRC29	NM_032505.1	p.D2E
FAM19A4	3	68864988	68864988	Missense	SNP	G	A	BRC8	NM_001005527.1	p.R140W
CNTN3	3	74493859	74493859	Missense	SNP	C	G	CSB1	NM_020872.1	p.K412N
GBE1	3	81781662	81781662	Missense	SNP	T	G	CSB34	NM_000158.3	p.H177P
CADM2	3	85934032	85934032	Ins	INS		0 A	BRC15	NM_153184.2	p.A72fs
VGLL3	3	87094883	87094883	Nonstop Mutation	SNP	C	A	BRC5	ENST00000383698	p.*321L
PROS1	3	95107425	95107425	Missense	SNP	G	A	BRC39	NM_000313.3	p.S165L
DHFRL1	3	95262629	95262629	Silent	SNP	G	A	BRC18	NM_176815.3	p.I139
OR5H14	3	99351346	99351346	Missense	SNP	C	T	CSB23	NM_001005514.1	p.R143W
OR5H2	3	99485015	99485015	Silent	SNP	T	C	BRC39	NM_001005482.1	p.S198
TBC1D23	3	101525150	101525150	Missense	SNP	C	G	BRC20	NM_018309.2	p.T668S
TOMM70A	3	101588474	101588474	Silent	SNP	G	A	CSB2	NM_014820.3	p.G121

SENP7	3	102533590	102533590	Missense	SNP	T	C	BRC8	NM_020654.1	p.Y876C
SENP7	3	102568045	102568045	Missense	SNP	C	T	BRC39	NM_020654.1	p.E413K
CEP97	3	102958616	102958616	Missense	SNP	A	G	BRC4	NM_024548.2	p.M305V
FAM55C	3	103002781	103002781	Missense Frame Shift	SNP	G	A	CSB1	NM_145037.1	p.E36K
NFKBIZ	3	103054957	103054957	Ins	INS		0 C	CSB25	NM_031419.1	p.H300fs
MYH15	3	109646293	109646293	Missense	SNP	C	T	BRC39	NM_014981.1	p.E867K
MORC1	3	110186308	110186308	Silent	SNP	G	A	CSB25	NM_014429.3	p.L757
PVRL3	3	112335564	112335564	Nonsense	SNP	G	T	CSB13	NM_015480.1	p.E488*
PHLDB2	3	113120618	113120618	Missense	SNP	G	T	CSB15	NM_145753.1	p.G577C
PHLDB2	3	113141027	113141027	Missense	SNP	G	C	BRC51	NM_145753.1	p.D673H
SLC35A5	3	113782416	113782416	Silent	SNP	G	T	BRC31	NM_017945.2	p.L254
WDR52	3	114580871	114580871	Missense	SNP	G	A	CSB1	NM_018338.2	p.S757L
WDR52	3	114598181	114598181	Silent	SNP	G	T	BRC39	NM_018338.2	p.L551
CCDC52	3	114655004	114655004	Missense	SNP	G	T	BRC11	NM_144718.3	p.S714Y
SIDT1	3	114794565	114794565	Missense	SNP	G	A	CSB1	NM_017699.2	p.G342E
KIAA2018	3	114859403	114859403	Silent	SNP	C	A	CSB10	NM_001009899.2	p.T1272
ZDHHC23	3	115157907	115157907	Missense	SNP	C	G	BRC39	NM_173570.3	p.Q302E
ZNF80	3	115438024	115438024	Missense	SNP	C	A	BRC51	NM_007136.2	p.K196N
B4GALT4	3	120425671	120425671	Missense	SNP	C	T	CSB22	NM_003778.3	p.E200K
PLA1A	3	120799511	120799511	Missense	SNP	G	A	BRC37	NM_015900.2	p.V21I
POPDC2	3	120856107	120856107	Missense	SNP	G	C	BRC39	NM_022135.2	p.P179A
C3orf15	3	120908354	120908354	Missense	SNP	T	C	BRC29	NM_033364.3	p.F45L
RABL3	3	121911411	121911411	Silent	SNP	C	T	BRC50	NM_173825.3	p.K58
STXBP5L	3	122609089	122609089	Missense	SNP	G	C	CSB22	NM_014980.2	p.S990T
STXBP5L	3	122614807	122614807	Missense	SNP	C	G	BRC31	NM_014980.2	p.P1045A
POLQ	3	122731297	122731297	Silent	SNP	A	G	BRC32	NM_199420.3	p.Y331
GOLGB1	3	122898170	122898170	Missense	SNP	G	C	CSB8	NM_004487.3	p.S1292C
SLC15A2	3	123133255	123133255	Missense	SNP	C	A	CSB1	NM_021082.2	p.L582M
CASR	3	123463231	123463231	Missense	SNP	G	A	BRC20	NM_000388.3	p.R220Q
CASR	3	123477394	123477394	Missense	SNP	G	A	BRC50	NM_000388.3	p.E475K
CASR	3	123486099	123486099	Missense	SNP	G	A	BRC51	NM_000388.3	p.E870K
PARP14	3	123920080	123920080	Silent	SNP	C	T	CSB1	NM_017554.2	p.I1464
MYLK	3	124953937	124953937	Missense	SNP	C	T	CSB33	NM_053025.3	p.G102R
KALRN	3	125429588	125429588	Silent	SNP	G	A	BRC41	NM_001024660.2	p.V43

KALRN	3	125835457	125835457	Missense	SNP	G	T	CSB22	NM_001024660.2	p.K1844N
HEG1	3	126230761	126230761	Missense	SNP	G	T	CSB6	NM_020733.1	p.A193E
SLC12A8	3	126388841	126388841	Missense	SNP	T	G	CSB22	NM_024628.5	p.Y107S
OSBPL11	3	126761999	126761999	Missense	SNP	C	G	BRC5	NM_022776.4	p.E357Q
SLC41A3	3	127218314	127218314	Silent	SNP	C	T	BRC13	NM_001008485.1	p.K280
TR2IT1	3	127773844	127773844	Missense	SNP	C	T	BRC11	NM_001039783.1	p.R78K
IFT122	3	130716021	130716021	Silent	SNP	C	G	BRC7	NM_052985.2	p.A1080
COL6A6	3	131795839	131795839	Missense	SNP	C	G	CSB1	NM_001102608.1	p.P1499A
ENSG0000022278 3	3	132013453	132013453	RNA	SNP	C	G	BRC41	ENST00000410851	NULL
NPHP3	3	133890184	133890184	Missense	SNP	T	G	BRC44	NM_153240.3	p.K1042T
C3orf36	3	135130121	135130121	Missense	SNP	C	G	BRC39	NM_025041.2	p.E73Q
C3orf36	3	135130328	135130328	Missense	SNP	C	T	BRC39	NM_025041.2	p.E4K
SLCO2A1	3	135150466	135150466	Nonsense	SNP	C	A	BRC39	NM_005630.2	p.E301*
EPHB1	3	136394135	136394135	Missense	SNP	G	A	BRC47	NM_004441.3	p.R637H
STAG1	3	137542985	137542985	Missense	SNP	A	T	CSB9	NM_005862.2	p.V1182E
STAG1	3	137675131	137675131	Missense	SNP	C	G	BRC39	NM_005862.2	p.Q355H
IL20RB	3	138183753	138183753	Missense	SNP	G	A	BRC51	NM_144717.2	p.E93K
COPB2	3	140576117	140576117	Missense	SNP	T	C	BRC5	NM_004766.2	p.K219E
GK5	3	143415113	143415113	Missense	SNP	G	C	BRC18	NM_001039547.1	p.Q88E
XRN1	3	143572091	143572091	Missense	SNP	G	A	CSB9	NM_019001.1	p.R1044C
ATR	3	143659257	143659257	Missense	SNP	G	T	BRC39	NM_001184.3	p.P2512T
ATR	3	143659266	143659266	Missense	SNP	C	G	BRC39	NM_001184.3	p.E2509Q
ATR	3	143659284	143659284	Missense	SNP	C	G	BRC47	NM_001184.3	p.E2503Q
ATR	3	143659286	143659286	Missense	SNP	C	A	BRC16	NM_001184.3	p.G2502V
ATR	3	143670941	143670941	Missense	SNP	C	G	BRC42	NM_001184.3	p.L2160F
ATR	3	143760825	143760825	Missense	SNP	C	G	CSB1	NM_001184.3	p.D564H
SR140	3	144238735	144238735	Missense	SNP	G	T	BRC41	NM_001080415.1	p.A697S
CHST2	3	144323516	144323516	Missense	SNP	C	A	CSB22	NM_004267.3	p.H390N
SLC9A9	3	144696874	144696874	Missense	SNP	C	G	CSB21	NM_173653.2	p.G399A
SLC9A9	3	144780207	144780207	Silent	SNP	G	A	BRC9	NM_173653.2	p.A268
CP	3	150407868	150407868	Silent	SNP	G	C	BRC39	NM_000096.3	p.L336
TM4SF18	3	150525394	150525394	Missense	SNP	C	A	BRC39	NM_138786.2	p.D125Y
EIF2A	3	151772972	151772972	Missense	SNP	C	T	BRC52	NM_032025.3	p.A450V
P2RY14	3	152414773	152414773	Missense	SNP	G	C	CSB16	NM_001081455.1	p.Q8E

MED12L	3	152595218	152595218	Missense	SNP	G	A	CSB22	NM_053002.3	p.G1863D
IGSF10	3	152647942	152647942	Silent	SNP	G	A	BRC51	NM_178822.3	p.G839
IGSF10	3	152648685	152648685	Missense	SNP	C	G	CSB1	NM_178822.3	p.D592H
IGSF10	3	152649485	152649485	Missense	SNP	C	G	BRC44	NM_178822.3	p.G325A
AADACL2	3	152957890	152957890	Missense	SNP	C	G	BRC39	NM_207365.3	p.L320V
AADAC	3	153028618	153028618	Nonsense	SNP	C	T	BRC39	NM_001086.2	p.Q390*
SCHIP1	3	161088383	161088383	Missense	SNP	G	A	BRC31	NM_014575.2	p.D397N
SMC4	3	161613976	161613976	Missense	SNP	T	G	CSB1	NM_001002800.1	p.I334M
SLITRK3	3	166388502	166388502	Silent	SNP	G	A	BRC11	NM_014926.2	p.F937
SLITRK3	3	166390981	166390981	Missense	SNP	T	C	BRC20	NM_014926.2	p.N111S
SLITRK3	3	166391129	166391129	Missense	SNP	C	G	CSB1	NM_014926.2	p.D62H
ZBBX	3	168560400	168560400	Silent	SNP	C	T	BRC44	NM_024687.2	p.K128
GOLIM4	3	169225514	169225514	Missense	SNP	C	T	BRC39	NM_014498.3	p.E563K
PHC3	3	171297724	171297724	Silent	SNP	C	T	BRC39	NM_024947.3	p.L992
ZMAT3	3	180268004	180268004	Silent	SNP	G	A	BRC50	NM_022470.2	p.V77
PIK3CA	3	180399618	180399618	Missense	SNP	C	G	BRC39	NM_006218.2	p.P104R
PIK3CA	3	180399618	180399618	Missense	SNP	C	T	CSB1	NM_006218.2	p.P104L
PIK3CA	3	180399623	180399631	In Frame Del	DEL	GGCAAC CGT		0 CSB19	NM_006218.2	p.GNR106in Frame del
PIK3CA	3	180400172	180400172	Missense	SNP	G	A	BRC9	NM_006218.2	p.G118D
PIK3CA	3	180404247	180404247	Missense	SNP	T	A	BRC52	NM_006218.2	p.N345K
PIK3CA	3	180404247	180404247	Missense	SNP	T	A	CSB26	NM_006218.2	p.N345K
PIK3CA	3	180410674	180410674	Missense	SNP	T	C	CSB15	NM_006218.2	p.C420R
PIK3CA	3	180410761	180410761	Missense	SNP	C	A	BRC36	NM_006218.2	p.P449T
PIK3CA	3	180410773	180410773	Missense	SNP	G	A	BRC13	NM_006218.2	p.E453K
PIK3CA	3	180418776	180418776	Missense	SNP	G	A	BRC5	NM_006218.2	p.E542K
PIK3CA	3	180418776	180418776	Missense	SNP	G	A	BRC47	NM_006218.2	p.E542K
PIK3CA	3	180418777	180418777	Missense	SNP	A	T	CSB3	NM_006218.2	p.E542V
PIK3CA	3	180418785	180418785	Missense	SNP	G	A	BRC3	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense	SNP	G	A	BRC4	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense	SNP	G	A	BRC7	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense	SNP	G	A	BRC28	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense	SNP	G	A	BRC33	NM_006218.2	p.E545K
PIK3CA	3	180418788	180418788	Missense	SNP	C	G	CSB6	NM_006218.2	p.Q546E
PIK3CA	3	180421628	180421628	Missense	SNP	G	A	BRC5	NM_006218.2	p.E726K

PIK3CA	3	180421628	180421628	Missense	SNP	G	A	BRC33	NM_006218.2	p.E726K
PIK3CA	3	180434771	180434771	Missense	SNP	T	A	BRC39	NM_006218.2	p.N1044K
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC9	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC10	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC11	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC13	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC15	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC18	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC20	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC24	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC31	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC37	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC40	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	BRC51	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	CSB13	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	CSB17	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	CSB21	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	CSB24	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	CSB27	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	G	CSB30	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense	SNP	A	T	BRC8	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense	SNP	A	T	BRC50	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense	SNP	A	T	CSB1	NM_006218.2	p.H1047L
PIK3CA	3	180434780	180434780	Missense	SNP	T	A	CSB3	NM_006218.2	p.H1047Q
PIK3CA	3	180434784	180434784	Missense	SNP	G	C	BRC36	NM_006218.2	p.G1049R
PIK3CA	3	180434784	180434784	Missense	SNP	G	C	CSB12	NM_006218.2	p.G1049R
ACTL6A	3	180777360	180777360	Nonsense	SNP	C	T	BRC50	NM_004301.3	p.Q245*
TTC14	3	181806744	181806744	Silent	SNP	C	T	CSB8	NM_133462.2	p.I313
B3GNT5	3	184470770	184470770	Missense	SNP	T	A	CSB22	NM_032047.4	p.S164T
YEATS2	3	184974223	184974223	Missense	SNP	G	A	BRC52	NM_018023.3	p.G772E
PARL	3	185041112	185041112	Silent	SNP	G	C	BRC31	NM_018622.1	p.S256
DVL3	3	185368131	185368131	Missense	SNP	A	G	BRC32	NM_004423.3	p.E423G
ALG3	3	185444076	185444076	Silent	SNP	G	A	BRC35	NM_005787.2	p.P323
ECE2	3	185457976	185457976	Missense	SNP	G	T	BRC18	NM_014693.2	p.S73I
EIF4G1	3	185532012	185532012	Missense	SNP	C	T	CSB1	NM_182917.3	p.S1440F

POLR2H	3	185565627	185565627	Missense	SNP	G	C	CSB22	NM_006232.2	p.R57P
MAGEF1	3	185911428	185911428	Silent	SNP	G	A	CSB16	NM_022149.4	p.A292
LIPH	3	186727969	186727969	Missense	SNP	C	T	BRC50	NM_139248.2	p.D209N
EIF4A2	3	187985078	187985078	Missense	SNP	A	C	BRC41	NM_001967.3	p.D36A
EIF4A2	3	187985160	187985160	Frame Shift Ins	INS		0 TA	CSB9	NM_001967.3	p.I63fs
RFC4	3	187993040	187993040	Missense	SNP	G	A	BRC5	NM_002916.3	p.S203L
MASP1	3	188436984	188436984	Missense	SNP	C	G	BRC11	NM_139125.1	p.E457Q
TP63	3	191094894	191094894	Missense	SNP	C	G	CSB1	NM_003722.1	p.S651C
LOC100130481	3	192010377	192010377	Silent	SNP	C	T	BRC31	XM_001726752.1	p.L234
CCDC50	3	192589997	192589997	Missense	SNP	G	A	BRC11	NM_178335.3	p.M447I
PYDC2	3	192661723	192661723	Silent	SNP	C	T	BRC52	NM_001083308.1	p.F26
HES1	3	195338184	195338184	Missense	SNP	C	G	CSB3	NM_005524.2	p.P104R
ATP13A3	3	195646764	195646764	Missense	SNP	A	C	CSB19	NM_024524.3	p.I513S
TMEM44	3	195819672	195819672	Missense	SNP	C	G	BRC51	ENST00000392432	p.Q245H
LSG1	3	195861015	195861015	Nonsense	SNP	G	T	BRC21	NM_018385.2	p.S240*
PAK2	3	198024075	198024075	Silent	SNP	G	T	BRC50	NM_002577.4	p.V297
FYTTD1	3	198979732	198979732	Frame Shift Ins	INS		0 A	BRC32	NM_032288.1	p.R87fs
LMLN	3	199171572	199171572	Missense	SNP	G	A	CSB1	NM_033029.2	p.R28Q
DGKQ	4	946245	946245	Missense	SNP	G	A	BRC4	NM_001347.2	p.T731M
WHSC1	4	1890127	1890127	Missense	SNP	C	G	CSB1	NM_001042424.2	p.F463L
C4orf15	4	2210238	2210238	Nonsense	SNP	G	A	BRC39	NM_024511.5	p.Q414*
C4orf8	4	2668029	2668029	Missense	SNP	G	A	BRC35	NM_003704.3	p.E849K
ZNF509	4	4355337	4355337	Silent	SNP	C	T	CSB12	NM_145291.3	p.D291
JAKMIP1	4	6078867	6078867	Silent	SNP	G	A	BRC31	NM_001099433.1	p.L829
JAKMIP1	4	6132803	6132803	Silent	SNP	T	C	BRC10	NM_001099433.1	p.S413
JAKMIP1	4	6165462	6165462	Missense	SNP	C	T	BRC5	NM_001099433.1	p.R6Q
MAN2B2	4	6629206	6629206	Missense	SNP	G	A	BRC16	NM_015274.1	p.E47K
FBXL5	4	15247398	15247398	Splice_Site	SNP	C	T	BRC35	NM_012161.2	e5-1
PROM1	4	15617272	15617272	Missense	SNP	C	T	CSB14	NM_006017.1	p.V481I
NCRNA00099	4	21460064	21460064	RNA	SNP	C	T	BRC11	NR_002813.1	NULL
LOC100131836	4	21467470	21467470	Nonsense	SNP	C	T	BRC24	XM_001721969.1	p.Q103*
PPARGC1A	4	23424979	23424979	Missense	SNP	G	T	BRC38	NM_013261.3	p.Q409K
DHX15	4	24138671	24138671	Nonsense	SNP	G	A	BRC41	NM_001358.2	p.Q788*
ZCCHC4	4	24923653	24923653	Missense	SNP	C	G	CSB1	NM_024936.2	p.H42D

KIAA0746	4	25430627	25430627	Missense	SNP	C	T	BRC39	NM_015187.3	p.E442K
PCDH7	4	30332479	30332479	Missense	SNP	G	C	CSB1	NM_032457.2	p.E113Q
ARAP2	4	35888647	35888647	Nonsense	SNP	G	C	BRC31	NM_015230.2	p.S416*
C4orf19	4	37268650	37268650	Missense	SNP	G	T	CSB34	NM_001104629.1	p.G193V
TBC1D1	4	37815254	37815254	Missense	SNP	C	T	CSB1	NM_015173.2	p.S1137L
TLR1	4	38474631	38474631	Silent	SNP	A	G	BRC38	NM_003263.3	p.I739
TLR1	4	38475771	38475771	Silent	SNP	G	A	BRC39	NM_003263.3	p.L359
N4BP2	4	39799735	39799735	Silent	SNP	G	A	CSB5	NM_018177.3	p.Q1203
N4BP2	4	39802190	39802190	Missense	SNP	G	C	BRC39	NM_018177.3	p.E1434Q
CHRNA9	4	40032303	40032303	Missense	SNP	G	A	BRC13	NM_017581.2	p.R21K
SLC30A9	4	41732093	41732093	Silent	SNP	T	C	CSB14	NM_006345.3	p.L219
GUF1	4	44392416	44392416	Silent	SNP	C	T	CSB2	NM_021927.2	p.A581
GABRA2	4	45947260	45947260	Missense	SNP	G	A	CSB8	NM_000807.2	p.T393M
GABRA2	4	46082935	46082935	Missense	SNP	C	T	BRC18	NM_000807.2	p.E34K
SPATA18	4	52632969	52632969	Missense	SNP	G	C	CSB1	NM_145263.2	p.Q216H
PDGFRA	4	54828288	54828288	Missense	SNP	G	A	BRC50	NM_006206.4	p.E279K
PDGFRA	4	54849818	54849818	Missense	SNP	G	A	BRC31	NM_006206.4	p.E924K
KIT	4	55259324	55259324	Missense	SNP	A	T	BRC33	NM_000222.2	p.Q152L
KIT	4	55264732	55264732	Missense	SNP	G	A	BRC39	NM_000222.2	p.R281K
KIT	4	55268031	55268031	Silent	SNP	C	T	BRC13	NM_000222.2	p.F312
CLOCK	4	56011078	56011078	Missense	SNP	T	C	CSB25	NM_004898.2	p.T429A
REST	4	57472170	57472170	Missense	SNP	T	C	CSB7	NM_005612.3	p.S204fs
ENSG0000020568 2	4	61975771	61975771	Del	DEL	T	0	CSB7	NM_005612.3	p.S204fs
SRD5A2L2	4	61975771	61975771	Missense	SNP	C	T	BRC39	ENST00000381217	p.E250K
CENPC1	4	64862995	64862995	Nonsense	SNP	C	A	CSB2	NM_001010874.4	p.E173*
STAP1	4	68038377	68038377	Missense	SNP	A	G	BRC3	NM_001812.2	p.V858A
ENSG0000020742 8	4	68119450	68119450	Silent	SNP	C	T	BRC50	NM_012108.2	p.T58
UGT2B28	4	68552228	68552228	RNA	SNP	T	C	BRC15	ENST00000384697	NULL
SULT1B1	4	70191003	70191003	Nonsense	SNP	C	T	BRC50	NM_053039.1	p.Q399*
C4orf35	4	70655515	70655515	Missense	SNP	G	C	BRC49	NM_014465.3	p.P4A
AMBN	4	71236213	71236213	Missense	SNP	G	C	CSB1	NM_033122.3	p.E290Q
RUFY3	4	71506824	71506824	Missense	SNP	G	A	BRC32	NM_016519.4	p.V378I
NPFRR2	4	71874132	71874132	Missense	SNP	G	C	CSB1	NM_001037442.2	p.K432N
NPFRR2	4	73232095	73232095	Missense	SNP	C	T	CSB26	NM_004885.1	p.A424V

ENSG0000021083 9	4	74111448	74111448	RNA	SNP	G	A	BRC51	ENST00000388104	NULL
ANKRD17	4	74175407	74175407	Missense	SNP	A	C	CSB24	NM_032217.3	p.F2268V
RASSF6	4	74700489	74700489	Missense	SNP	G	C	BRC39	ENST00000335049	p.L31V
CXCL9	4	77146447	77146447	Silent Frame Shift	SNP	G	C	BRC30	NM_002416.1	p.T23
SHROOM3	4	77881026	77881026	Del	DEL	C		0 BRC3	NM_020859.3	p.Q892fs
FRAS1	4	79457558	79457558	Nonsense	SNP	C	G	CSB1	ENST00000380674	p.S611*
BMP2K	4	79991223	79991223	Missense	SNP	A	G	BRC6	NM_198892.3	p.H291R
ARD1B	4	80465815	80465815	Missense	SNP	G	A	BRC48	NM_032693.2	p.H81Y
GK2	4	80546878	80546878	Missense	SNP	C	T	BRC41	NM_033214.2	p.A501T
FGF5	4	81407185	81407185	Silent	SNP	C	T	BRC18	NM_004464.3	p.S61
BMP3	4	82186649	82186649	Silent	SNP	A	G	BRC16	NM_001201.2	p.Q350
RASGEF1B	4	82574856	82574856	Silent	SNP	A	G	CSB16	NM_152545.1	p.G387
FLJ12993	4	83636289	83636289	Missense	SNP	G	C	CSB1	NM_001080506.1	p.L107V
SEC31A	4	83997168	83997168	Missense	SNP	C	A	CSB1	NM_001077207.1	p.Q614H
SEC31A	4	84007436	84007436	Nonsense	SNP	G	A	BRC13	NM_001077207.1	p.R314*
COQ2	4	84407882	84407882	Missense	SNP	A	T	CSB21	NM_015697.6	p.W291R
HPSE	4	84450909	84450909	Missense	SNP	T	C	CSB26	NM_001098540.1	p.M278V
PTPN13	4	87857219	87857219	Missense	SNP	C	T	CSB1	NM_080685.2	p.S437L
SLC10A6	4	87973516	87973516	Nonsense	SNP	G	A	CSB1	NM_197965.2	p.Q155*
AFF1	4	88187315	88187315	Missense	SNP	G	C	BRC39	NM_005935.2	p.E195Q
KLHL8	4	88335706	88335706	Missense	SNP	C	T	BRC11	NM_020803.3	p.D4N
SPARCL1	4	88635246	88635246	Missense	SNP	C	T	BRC51	NM_004684.1	p.D38N
FAM13A	4	89889990	89889990	Silent	SNP	C	T	CSB22	NM_014883.1	p.K678
TIGD2	4	90253232	90253232	Missense	SNP	C	G	BRC18	NM_145715.2	p.F28L
MMRN1	4	91035683	91035683	Missense	SNP	C	G	CSB16	NM_007351.2	p.R180G
GRID2	4	94595842	94595842	Missense	SNP	G	T	CSB6	NM_001510.2	p.D518Y
PDLIM5	4	95717598	95717598	Splice_Site	SNP	G	A	BRC51	ENST00000318007	e5+1
C4orf17	4	100653284	100653284	Missense	SNP	C	T	CSB24	NM_032149.1	p.S8F
LOC285556	4	100789763	100789763	Missense	SNP	G	A	BRC35	XM_373030.1	p.T1722I
LOC285556	4	100793413	100793413	Silent	SNP	G	T	BRC35	XM_373030.1	p.G505
LOC256880	4	101091505	101091505	RNA	SNP	A	T	BRC19	NR_002799.1	NULL
CISD2	4	104009736	104009736	Silent Frame Shift	SNP	G	A	CSB1	NM_001008388.3	p.L18
TBCKL	4	107236187	107236190	Del	DEL	TGCA		0 BRC18	NM_033115.2	p.A761fs

AGXT2L1	4	109900906	109900906	Missense	SNP	G	A	BRC39	NM_031279.2	p.S21L
ELOVL6	4	111192269	111192269	Missense	SNP	C	G	BRC52	NM_024090.1	p.D158H
NEUROG2	4	113655576	113655576	Missense	SNP	G	A	CSB19	NM_024019.2	p.R169C
LOC91431	4	113703880	113703880	Splice_Site	SNP	C	G	CSB1	NM_001099776.1	e6-1
C4orf21	4	113760747	113760747	Missense	SNP	C	T	BRC50	NM_018392.3	p.E71K
LARP7	4	113791145	113791145	Missense	SNP	G	T	BRC10	NM_015454.1	p.K458N
ANK2	4	114497225	114497225	Missense	SNP	C	T	CSB15	NM_001148.1	p.P2668S
CEP170L	4	119694622	119694622	Silent	SNP	T	C	CSB19	ENST00000336415	p.A267
PDE5A	4	120646506	120646506	Frame Shift Del	DEL	C		0 CSB3	NM_001083.3	p.R740fs
PDE5A	4	120693241	120693241	Splice_Site	SNP	C	G	CSB33	NM_001083.3	e9-1
ENSG0000022300 6	4	122201939	122201939	RNA	SNP	C	G	BRC39	ENST00000411074	NULL
QRFR	4	122470038	122470038	Missense	SNP	C	T	CSB1	NM_198179.2	p.D393N
TRPC3	4	123073144	123073144	Missense	SNP	G	A	BRC14	NM_003305.1	p.A167V
KIAA1109	4	123367372	123367372	Missense	SNP	G	A	CSB1	NM_015312.2	p.E952K
KIAA1109	4	123458847	123458847	Missense	SNP	G	C	BRC41	NM_015312.2	p.R3589P
ANKRD50	4	125811049	125811049	Missense	SNP	C	T	CSB1	NM_020337.1	p.D945N
ANKRD50	4	125811642	125811642	Missense	SNP	T	C	BRC7	NM_020337.1	p.D747G
FAT4	4	126609182	126609182	Missense	SNP	C	A	BRC11	NM_024582.4	p.P3954T
PLK4	4	129035685	129035685	Missense	SNP	G	A	BRC50	NM_014264.3	p.G897D
LARP2	4	129319058	129319058	Silent	SNP	G	A	CSB31	NM_018078.2	p.Q569
PCDH10	4	134291482	134291482	Missense	SNP	A	T	BRC15	NM_032961.1	p.N246I
PCDH10	4	134295520	134295520	Splice_Site	SNP	A	G	BRC32	NM_032961.1	e3-2
ELF2	4	140199956	140199956	Silent	SNP	T	C	BRC41	NM_201999.2	p.Q459
NARG1	4	140501161	140501161	Missense	SNP	G	A	CSB1	NM_057175.3	p.E490K
SMARCA5	4	144679490	144679490	Silent	SNP	A	G	BRC49	NM_003601.2	p.V573
EDNRA	4	148626626	148626626	Missense	SNP	C	T	BRC31	NM_001957.2	p.P115S
ARHGAP10	4	149163946	149163946	Missense	SNP	C	G	CSB3	NM_024605.3	p.S600W
LRBA	4	151577382	151577382	Missense	SNP	G	A	CSB24	NM_006726.2	p.H2300Y
LRBA	4	151875896	151875896	Silent	SNP	C	T	BRC31	NM_006726.2	p.Q1906
FAM160A1	4	152718448	152718448	Nonsense	SNP	C	T	CSB1	XM_001718535.1	p.Q167*
FAM160A1	4	152796923	152796923	Missense	SNP	C	G	CSB1	XM_001718535.1	p.Q907E
DCHS2	4	155377576	155377576	Missense	SNP	C	T	CSB20	NM_017639.1	p.E2105K
DCHS2	4	155473737	155473737	Missense	SNP	C	T	CSB22	NM_017639.1	p.V526I
NPY2R	4	156355248	156355248	Missense	SNP	C	T	BRC44	NM_000910.2	p.S236L

MAP9	4	156513810	156513810	Missense	SNP	C	T	BRC50	NM_001039580.1	p.E137K
ACCN5	4	156972510	156972510	Missense	SNP	G	A	BRC7	NM_017419.2	p.L415F
GLRB	4	158277215	158277215	Missense	SNP	G	C	BRC31	NM_000824.3	p.E148Q
C4orf46	4	159810333	159810333	Missense	SNP	G	C	BRC3	NM_001008393.2	p.S75C
ETFDH	4	159836150	159836150	Missense	SNP	G	A	BRC18	NM_004453.2	p.E246K
FSTL5	4	162526429	162526429	Missense	SNP	C	G	BRC50	NM_020116.1	p.D822H
FSTL5	4	162595712	162595712	Missense	SNP	C	T	BRC38	NM_020116.1	p.G579R
FSTL5	4	162900082	162900082	Missense	SNP	C	T	BRC34	NM_020116.1	p.V220I
KLHL2	4	166458466	166458466	Missense	SNP	G	A	CSB24	NM_007246.2	p.G550R
NEK1	4	170595986	170595986	Splice_Site	SNP	C	G	BRC50	NM_012224.1	e25-1
CLCN3	4	170855303	170855303	Missense	SNP	C	G	BRC39	NM_173872.2	p.S469C
FBXO8	4	175417476	175417476	Silent	SNP	C	T	BRC16	NM_012180.2	p.L135
ODZ3	4	183910115	183910115	Silent	SNP	G	C	BRC15	NM_001080477.1	p.P1266
STOX2	4	185168140	185168140	Silent	SNP	C	T	BRC31	NM_020225.1	p.D385
SNX25	4	186497612	186497612	Missense	SNP	G	T	CSB15	NM_031953.2	p.W503L
SORBS2	4	186782453	186782453	Missense	SNP	G	A	BRC47	NM_021069.1	p.T371M
TLR3	4	187240510	187240510	Missense	SNP	C	A	BRC51	NM_003265.2	p.L226I
FAT1	4	187778113	187778113	Silent	SNP	G	A	CSB13	NM_005245.3	p.N2207
FAT1	4	187794769	187794769	Missense	SNP	C	A	CSB16	NM_005245.3	p.K1312N
ZFP42	4	189161460	189161460	Missense	SNP	G	A	BRC9	NM_174900.3	p.A169T
PLEKHG4B	5	214960	214960	Silent	SNP	C	G	CSB31	NM_052909.3	p.V494
PLEKHG4B	5	216038	216038	Missense	SNP	C	T	CSB9	NM_052909.3	p.R595W
AHRR	5	475903	475903	Silent	SNP	C	T	CSB1	NM_020731.3	p.F171
SLC9A3	5	535669	535669	Silent	SNP	G	A	BRC18	NM_004174.2	p.I450
TPPP	5	730968	730968	Missense	SNP	C	G	CSB15	NM_007030.2	p.E70Q
ZDHHC11B	5	819884	819884	Missense	SNP	C	G	CSB7	XM_926053.1	p.G51R
SLC12A7	5	1110642	1110642	Silent	SNP	C	T	CSB19	NM_006598.2	p.K990
TERT	5	1346454	1346454	Missense	SNP	T	C	CSB30	NM_198253.2	p.D516G
KIAA0947	5	5542291	5542291	Missense	SNP	G	A	BRC17	NM_015325.1	p.V2217M
SRD5A1	5	6709275	6709275	Missense	SNP	G	T	BRC3	NM_001047.2	p.G182V
FASTKD3	5	7920914	7920914	Nonsense	SNP	T	A	CSB25	NM_024091.2	p.K95*
SEMA5A	5	9103557	9103557	Missense	SNP	G	T	BRC26	NM_003966.2	p.A953E
CTNND2	5	11170644	11170644	Missense	SNP	C	G	BRC39	NM_001332.2	p.R732T
DNAH5	5	13806628	13806628	Missense	SNP	G	C	CSB1	NM_001369.2	p.S3529C
DNAH5	5	13936091	13936091	Missense	SNP	C	A	BRC51	NM_001369.2	p.Q1032H

DNAH5	5	13939228	13939228	Missense	SNP	A	G	BRC32	NM_001369.2	p.V863A
TRIO	5	14524537	14524537	Missense	SNP	G	C	BRC50	NM_007118.2	p.E1958D
MARCH11	5	16120720	16120720	Missense	SNP	C	T	CSB29	NM_001102562.1	p.V357I
ENSG00000201715	5	17398838	17398838	RNA	SNP	C	T	BRC38	ENST00000364845	NULL
LOC340096	5	17544872	17544872	Silent	SNP	C	T	BRC32	XM_293943.2	p.A47
CDH18	5	19757273	19757273	Missense	SNP	C	T	BRC44	NM_004934.2	p.A195T
CDH12	5	21800879	21800879	Missense	SNP	C	T	BRC39	NM_004061.3	p.E494K p.K174in
PRDM9	5	23558177	23558179	In Frame Del	DEL	GAA	0	BRC32	NM_020227.2	Frame del
CDH10	5	24629183	24629183	Missense	SNP	C	G	CSB1	NM_006727.2	p.W58C
CDH9	5	26917203	26917203	Silent	SNP	G	A	BRC37	NM_016279.3	p.N723
LOC391774	5	31089723	31089723	RNA	SNP	G	A	BRC31	XR_017200.1	NULL
CDH6	5	31353717	31353717	Missense	SNP	C	T	BRC51	NM_004932.2	p.A604V
RNASEN	5	31562340	31562340	Missense	SNP	G	A	BRC39	NM_013235.1	p.H153Y
PDZD2	5	32125603	32125603	Missense	SNP	G	A	BRC39	NM_178140.2	p.E2098K
PDZD2	5	32136781	32136781	Silent	SNP	A	C	BRC41	ENST00000397559	p.R23
PDZD2	5	32136808	32136808	Missense	SNP	G	C	BRC36	ENST00000397559	p.G32R
RXFP3	5	33973710	33973710	Missense	SNP	G	A	CSB12	NM_016568.2	p.A370T
PRLR	5	35101895	35101895	Missense	SNP	C	T	BRC39	NM_000949.4	p.E308K
SLC1A3	5	36722003	36722003	Missense	SNP	C	A	BRC33	NM_004172.4	p.L502M
C5orf42	5	37174642	37174642	Missense	SNP	A	G	CSB27	NM_023073.2	p.I1754T
WDR70	5	37758745	37758745	Missense	SNP	C	T	BRC15	NM_018034.2	p.R517W
RICTOR	5	39026846	39026846	Missense	SNP	C	G	CSB1	NM_152756.3	p.R182T
FYB	5	39170828	39170828	Missense	SNP	C	T	CSB1	NM_001465.3	p.D521N
FYB	5	39237816	39237816	Missense	SNP	C	T	BRC44	NM_001465.3	p.G335E
C9	5	39347135	39347135	Silent	SNP	T	C	BRC5	NM_001737.3	p.K324
CARD6	5	40895926	40895926	Missense	SNP	G	A	BRC49	ENST00000381677	p.R304H
HEATR7B2	5	41102979	41102979	Missense	SNP	C	G	CSB1	NM_173489.4	p.M63I
PLCXD3	5	41418351	41418351	Missense	SNP	G	T	BRC51	NM_001005473.2	p.P49Q
NNT	5	43692560	43692560	Missense	SNP	A	C	BRC42	NM_012343.3	p.N781T
EMB	5	49734966	49734966	Missense	SNP	A	T	BRC39	NM_198449.2	p.L227H
PARP8	5	50147095	50147095	Missense	SNP	G	A	BRC39	NM_024615.2	p.E550K
LOC642366	5	50710182	50710182	RNA	SNP	C	T	BRC50	XR_041353.1	NULL
SNX18	5	53850050	53850050	Silent	SNP	C	T	BRC32	NM_052870.1	p.L171
PPAP2A	5	54757495	54757495	Missense	SNP	C	G	CSB22	NM_176895.2	p.D228H

MAP3K1	5	56196978	56196978	Missense	SNP	C	G	BRC8	NM_005921.1	p.R364G
MAP3K1	5	56197437	56197437	Ins	INS		0 A	BRC18	NM_005921.1	p.H393fs
MAP3K1	5	56197437	56197437	Frame Shift	INS		0 TA	CSB14	NM_005921.1	p.H393fs
MAP3K1	5	56197439	56197439	Ins	INS			CSB14	NM_005921.1	p.H393Q
MAP3K1	5	56197551	56197552	Missense	SNP	C	G	CSB14	NM_005921.1	p.H393Q
MAP3K1	5	56197551	56197552	Frame Shift	DEL	TC		0 BRC23	NM_005921.1	p.S431fs
MAP3K1	5	56213653	56213653	Del	DEL	C	T	CSB1	NM_005921.1	p.Q957*
MAP3K1	5	56213820	56213820	Nonsense	SNP	C	T	CSB1	NM_005921.1	p.Q957*
MAP3K1	5	56213820	56213820	Frame Shift	INS		0 A	CSB26	NM_005921.1	p.R1012fs
MAP3K1	5	56213935	56213935	Ins	INS		0 A	CSB26	NM_005921.1	p.R1012fs
MAP3K1	5	56213935	56213935	Frame Shift	DEL	C		0 CSB27	NM_005921.1	p.L1052fs
MAP3K1	5	56215247	56215247	Del	DEL	C		0 CSB27	NM_005921.1	p.L1052fs
MAP3K1	5	56215247	56215247	Ins	INS		0 A	BRC8	NM_005921.1	p.M1269fs
MAP3K1	5	56216279	56216281	In Frame Del	DEL	AAG		0 CSB1	NM_005921.1	p.E1286in Frame del
MAP3K1	5	56217564	56217564	Nonsense	SNP	C	A	BRC33	NM_005921.1	p.S1344* p.V1346in Frame del
MAP3K1	5	56217565	56217567	In Frame Del	DEL	AGT		0 CSB17	NM_005921.1	p.Q1494*
MAP3K1	5	56225205	56225205	Nonsense	SNP	C	T	BRC18	NM_005921.1	p.Q1494*
MIER3	5	56255030	56255030	Silent	SNP	G	T	BRC38	NM_152622.3	p.P444
PLK2	5	57788168	57788169	Frame Shift	SNP	G	T	BRC38	NM_152622.3	p.P444
PLK2	5	57788168	57788169	Del	DEL	CT		0 BRC35	NM_006622.2	p.R387fs
GAPT	5	57826341	57826341	Missense	SNP	C	T	BRC11	NM_152687.2	p.S74L
ERCC8	5	60276518	60276518	Silent	SNP	C	T	CSB1	NM_000082.3	p.R25
IPO11	5	61868289	61868289	Missense	SNP	T	A	CSB7	ENST00000409296	p.L738Q
HTR1A	5	63292432	63292432	Missense	SNP	C	T	BRC15	NM_000524.2	p.E291K
HTR1A	5	63292913	63292913	Silent	SNP	G	A	BRC7	NM_000524.2	p.I130
RGS7BP	5	63839334	63839334	Missense	SNP	A	G	BRC22	NM_001029875.1	p.E69G
ADAMTS6	5	64592195	64592195	Silent	SNP	G	A	BRC50	NM_197941.2	p.S606
MAST4	5	66468196	66468196	Silent	SNP	G	A	BRC12	NM_015183.1	p.Q625 p.KPDL567in Frame del
PIK3R1	5	67626860	67626871	In Frame Del	DEL	TTAAAC CAGACC		0 BRC44	NM_181523.2	p.N581S p.E118in Frame del
BDP1	5	70826934	70826934	Missense	SNP	A	G	BRC26	NM_018429.2	p.N581S p.E118in Frame del
FCHO2	5	72322299	72322301	In Frame Del	DEL	AAG		0 CSB19	NM_138782.1	p.D666N
LOC100131794	5	74412203	74412203	Missense	SNP	C	T	BRC21	XM_001722188.1	p.D666N
SV2C	5	75463423	75463423	Missense	SNP	A	G	BRC52	NM_014979.1	p.N31S
SV2C	5	75656968	75656968	Missense	SNP	A	G	CSB9	NM_014979.1	p.N675S
PDE8B	5	76657213	76657213	Missense	SNP	C	T	CSB1	NM_003719.1	p.P165S

TBCA	5	77039918	77039918	Missense	SNP	C	G	CSB1	NM_004607.2	p.E22Q
AP3B1	5	77547721	77547721	Missense	SNP	C	G	BRC50	NM_003664.3	p.V234L
DMGDH	5	78336875	78336875	Missense	SNP	C	T	CSB1	NM_013391.2	p.E788K
BHMT2	5	78412319	78412319	Missense	SNP	A	C	BRC29	NM_017614.3	p.K104N
CMYA5	5	79062875	79062875	Missense	SNP	C	G	BRC11	NM_153610.3	p.S844C
CMYA5	5	79070743	79070743	Missense	SNP	G	T	BRC12	NM_153610.3	p.A3467S
THBS4	5	79408479	79408479	Silent	SNP	C	T	CSB1	NM_003248.3	p.V646
ACOT12	5	80667477	80667477	Splice_Site	SNP	C	G	BRC31	NM_130767.2	e12-1
ATP6AP1L	5	81649731	81649731	Missense	SNP	C	A	BRC41	NM_001017971.1	p.D177E
ERAP2	5	96241472	96241472	Missense	SNP	C	G	BRC39	NM_022350.1	p.I109M
FLJ43080	5	110030895	110030895	Missense	SNP	G	T	BRC35	XM_001719018.2	p.P18T
SLC25A46	5	110102757	110102757	Missense	SNP	G	C	CSB7	NM_138773.1	p.G13A
APC	5	112185506	112185506	Missense	SNP	G	A	BRC39	NM_000038.4	p.E443K
CCDC112	5	114633392	114633392	Silent	SNP	A	G	BRC15	NM_001040440.2	p.D445
CCDC112	5	114635209	114635209	Nonsense	SNP	C	T	BRC51	NM_001040440.2	p.W311*
TMED7	5	114980039	114980039	Missense	SNP	C	T	BRC50	NM_181836.4	p.M147I
LVRN	5	115326839	115326839	Missense Frame Shift	SNP	C	T	BRC39	NM_173800.4	p.S209L
DMXL1	5	118513201	118513201	Ins	INS		0 TC	CSB16	NM_005509.4	p.I1261fs
SNCAIP	5	121804316	121804316	Missense	SNP	G	A	CSB20	NM_005460.2	p.A464T
CEP120	5	122736339	122736339	Missense	SNP	C	G	BRC50	NM_153223.2	p.K795N
MEGF10	5	126799012	126799012	Missense	SNP	G	A	BRC39	NM_032446.2	p.G679E
FBN2	5	127664420	127664420	Missense	SNP	C	G	CSB21	NM_001999.3	p.E2052Q
FBN2	5	127728257	127728257	Missense	SNP	C	T	BRC23	NM_001999.3	p.R788H
RAPGEF6	5	130862144	130862144	Missense	SNP	G	A	CSB2	NM_016340.4	p.P437L
ACSL6	5	131340282	131340282	Silent	SNP	C	A	BRC30	NM_001009185.1	p.G316
RAD50	5	131943654	131943654	Missense	SNP	G	T	CSB1	NM_005732.2	p.L251F
RAD50	5	132004337	132004337	Missense	SNP	T	A	BRC4	NM_005732.2	p.D1231E
AFF4	5	132260547	132260547	Missense	SNP	C	G	BRC50	NM_014423.3	p.Q558H
ZCCHC10	5	132370394	132370394	Silent	SNP	C	T	BRC13	NM_017665.1	p.K53
PHF15	5	133924351	133924351	Silent	SNP	C	T	CSB21	NM_015288.4	p.D163
SEC24A	5	134038792	134038792	Silent	SNP	C	G	CSB1	NM_021982.1	p.L379
SEC24A	5	134084656	134084656	Missense	SNP	T	C	CSB21	NM_021982.1	p.Y1014H
LOC153328	5	135216377	135216377	Missense	SNP	G	A	BRC13	NM_145282.4	p.R130Q
LOC153328	5	135235293	135235293	Silent	SNP	G	A	CSB15	NM_145282.4	p.A222

ETF1	5	137877275	137877275	Missense	SNP	G	A	CSB1	NM_004730.2	p.S141L
SLC23A1	5	138735714	138735714	Silent	SNP	C	A	BRC18	NM_152685.4	p.L563
DNAJC18	5	138789852	138789852	Missense	SNP	C	T	BRC50	NM_152686.2	p.R156Q
CD14	5	139991639	139991639	Silent	SNP	G	T	BRC29	NM_000591.2	p.R372
PCDHA1	5	140147957	140147957	Missense	SNP	C	T	CSB19	NM_018900.2	p.T633M
PCDHA3	5	140162833	140162833	Missense	SNP	C	T	CSB1	NM_018906.2	p.R623C p.E187in Frame del
PCDHA5	5	140182097	140182099	In Frame Del	DEL	GAA		0 CSB28	NM_018908.2	
PCDHA5	5	140182631	140182631	Missense	SNP	C	G	CSB1	NM_018908.2	p.P363A
PCDHA5	5	140183325	140183325	Missense	SNP	G	A	BRC49	NM_018908.2	p.R594H
PCDHA8	5	140202820	140202820	Missense	SNP	C	T	CSB22	NM_018911.2	p.A577V
PCDHA9	5	140208397	140208397	Missense	SNP	G	A	CSB14	NM_031857.3	p.V45M
PCDHA9	5	140209913	140209913	Missense	SNP	C	T	CSB28	NM_031857.3	p.T550M
PCDHB1	5	140411741	140411741	Missense	SNP	C	A	BRC35	NM_013340.2	p.Q168K
PCDHB1	5	140413401	140413401	Missense	SNP	G	C	BRC50	NM_013340.2	p.R721T
PCDHB16	5	140543210	140543210	Missense	SNP	A	T	CSB34	NM_020957.1	p.T298S
PCDHGA2	5	140700397	140700397	Missense	SNP	G	A	BRC42	NM_018915.2	p.A559T
PCDHGA4	5	140715176	140715176	Silent	SNP	C	T	CSB31	NM_018917.2	p.F75
PCDHGA6	5	140735544	140735544	Silent	SNP	C	T	CSB30	NM_018919.2	p.D570
PCDHGA7	5	140743107	140743107	Missense	SNP	C	T	BRC51	NM_018920.2	p.P153S
PCDHGC3	5	140837831	140837831	Missense	SNP	C	G	CSB3	NM_002588.2	p.S655W
DIAPH1	5	140946896	140946896	Missense	SNP	G	A	CSB1	NM_005219.2	p.S66F
HDAC3	5	140985480	140985480	Missense	SNP	G	T	CSB1	NM_003883.3	p.H339N
PCDH12	5	141315208	141315208	Missense	SNP	A	G	BRC8	NM_016580.2	p.V798A
PCDH12	5	141315495	141315495	Silent	SNP	C	G	BRC39	NM_016580.2	p.L702
PCDH12	5	141316192	141316192	Missense	SNP	C	T	CSB15	NM_016580.2	p.R470Q
KCTD16	5	143833704	143833704	Missense	SNP	G	A	BRC6	NM_020768.3	p.R374K
KCTD16	5	143833731	143833731	Missense	SNP	A	C	CSB22	NM_020768.3	p.K383T
RBM27	5	145589610	145589610	Missense	SNP	G	A	CSB21	ENST00000265271	p.R178H
TCERG1	5	145842436	145842436	Missense	SNP	C	G	CSB1	NM_006706.1	p.L659V
ENSG0000022327 0	5	146016436	146016436	RNA	SNP	G	T	BRC47	ENST00000411338	NULL
LOC153469	5	146955213	146955213	Missense	SNP	C	T	BRC3	XM_001724056.1	p.R86C
SCGB3A2	5	147238586	147238586	Silent	SNP	G	A	CSB1	NM_054023.3	p.L9
FBXO38	5	147775778	147775778	Silent	SNP	C	A	CSB1	NM_205836.3	p.P453
FLJ41603	5	148983800	148983800	Missense	SNP	C	G	CSB1	NM_001001669.2	p.F456L

PDE6A	5	149304114	149304114	Missense	SNP	C	T	BRC18	NM_000440.2	p.A106T
CSF1R	5	149417278	149417278	Missense	SNP	C	G	BRC13	NM_005211.3	p.D735H
CAMK2A	5	149649345	149649345	Missense	SNP	A	G	BRC33	NM_015981.3	p.Y13H
TCOF1	5	149739395	149739395	Silent	SNP	G	A	BRC20	NM_001008656.3	p.S922
TNIP1	5	150409623	150409623	Silent	SNP	C	T	BRC47	NM_006058.3	p.P267
CCDC69	5	150544141	150544141	Missense	SNP	C	T	CSB1	NM_015621.2	p.E224K
FAT2	5	150865463	150865463	Silent	SNP	G	A	BRC11	NM_001447.2	p.L4302
FAT2	5	150865737	150865737	Nonsense	SNP	G	C	BRC5	NM_001447.2	p.S4211*
LARP1	5	154165686	154165686	Nonsense	SNP	C	T	BRC31	NM_033551.3	p.Q867*
CNOT8	5	154223121	154223121	Silent	SNP	C	T	BRC7	NM_004779.4	p.I30
CNOT8	5	154230469	154230469	Missense	SNP	T	C	BRC31	NM_004779.4	p.F123L
FAM71B	5	156522587	156522587	Missense	SNP	C	T	BRC50	NM_130899.2	p.E423K
EBF1	5	158067597	158067597	Missense	SNP	G	A	BRC35	NM_024007.3	p.T571I
HMMR	5	162833754	162833754	Missense	SNP	G	C	BRC47	NM_012484.1	p.E339Q
ODZ2	5	167550031	167550031	Missense	SNP	C	T	BRC32	ENST00000388903	p.T894M
SLIT3	5	168176979	168176979	Nonsense	SNP	G	A	CSB22	NM_003062.2	p.R233*
LOC728095	5	168372862	168372862	RNA	SNP	C	T	BRC22	XR_040697.1	NULL
uc003mag.2	5	169223919	169223919	Missense	SNP	G	A	CSB14	ENST00000377365	p.P515L
uc003mag.2	5	169242207	169242207	Missense	SNP	G	C	BRC39	ENST00000377365	p.S425W
LCP2	5	169620719	169620719	Missense Frame Shift	SNP	C	A	CSB2	NM_005565.3	p.K309N
RANBP17	5	170542787	170542787	Ins	INS		0 A	CSB22	NM_022897.2	p.L629fs
RANBP17	5	170600671	170600671	Silent	SNP	T	C	BRC18	NM_022897.2	p.L853
DUSP1	5	172129202	172129202	Missense	SNP	C	T	BRC50	NM_004417.2	p.E239K
BNIP1	5	172523474	172523474	Missense	SNP	C	G	BRC31	NM_013979.2	p.L254V
PCDH24	5	175955269	175955269	Missense	SNP	C	T	CSB9	NM_017675.3	p.T1308M
HK3	5	176241618	176241618	Missense	SNP	G	C	BRC11	NM_002115.2	p.L724V
NSD1	5	176571787	176571787	Missense	SNP	G	A	CSB1	NM_022455.4	p.E1261K
RGS14	5	176728353	176728353	Missense	SNP	G	C	CSB12	NM_006480.4	p.E293D
DOK3	5	176864698	176864698	Missense	SNP	G	A	BRC39	NM_024872.1	p.S187L
HNRNPAB	5	177570185	177570185	Missense	SNP	G	C	BRC13	NM_031266.3	p.K318N
GRM6	5	178342800	178342800	Missense	SNP	G	A	CSB22	NM_000843.3	p.A718V
CNOT6	5	179927585	179927585	Missense	SNP	C	T	CSB34	NM_015455.3	p.R335W
BTNL9	5	180409739	180409739	Missense	SNP	G	A	CSB1	NM_152547.4	p.G167E
TRIM41	5	180583964	180583964	Missense	SNP	T	A	CSB16	NM_033549.3	p.M120K

RIPK1	6	3051066	3051066	Missense	SNP	C	T	BRC31	NM_003804.3	p.S453L
F13A1	6	6211938	6211942	Del Frame Shift	DEL	CCTGT	0	BRC41	NM_000129.3	p.D140fs
RREB1	6	7156887	7156887	Del	DEL	T	0	CSB23	NM_001003699.2	p.C219fs
RREB1	6	7156926	7156926	Nonsense	SNP	C	G	BRC47	NM_001003699.2	p.S231*
SSR1	6	7248841	7248841	Missense	SNP	G	A	CSB1	NM_003144.3	p.S74F
CAGE1	6	7301341	7301341	Silent	SNP	G	T	BRC50	ENST00000379918	p.L746
DSP	6	7528796	7528796	Missense	SNP	C	T	BRC39	NM_004415.1	p.S2101L
TXNDC5	6	7833983	7833983	Missense	SNP	G	A	CSB16	NM_030810.1	p.T306M
GCNT6	6	10742884	10742884	Silent	SNP	C	T	BRC39	XM_927529.1	p.F314
NHLRC1	6	18230765	18230765	Missense	SNP	C	G	BRC11	NM_198586.2	p.E18Q
NRSN1	6	24249354	24249354	Missense	SNP	G	A	BRC39	ENST00000378475	p.R138Q
LOC100129474	6	25840270	25840270	Missense	SNP	C	T	BRC40	XM_001717559.1	p.A132V
HIST1H1E	6	26265164	26265164	Silent	SNP	G	A	BRC18	NM_005321.2	p.A189
HIST1H2BD	6	26266387	26266387	Missense	SNP	C	A	BRC41	NM_021063.2	p.P4H
HIST1H2BE	6	26292287	26292287	Missense	SNP	C	G	CSB8	NM_003523.2	p.I95M
HIST1H2BF	6	26307970	26307970	Missense	SNP	G	A	CSB1	NM_003522.3	p.D69N
HIST1H2BG	6	26324779	26324779	Missense	SNP	C	G	BRC39	NM_003518.3	p.K24N
HIST1H1D	6	26342993	26342993	Missense	SNP	C	A	CSB29	NM_005320.2	p.A50S
LOC100132361	6	26430313	26430313	Silent	SNP	C	T	BRC34	XM_001717606.1	p.S54
BTN3A1	6	26514140	26514140	Missense	SNP	C	T	CSB1	NM_007048.1	p.S37F
POM121L2	6	27385344	27385344	Missense	SNP	G	T	CSB29	ENST00000377451	p.T798K
ZNF184	6	27528701	27528701	Missense	SNP	T	C	BRC3	NM_007149.2	p.K206E
HIST1H2AI	6	27884174	27884174	Missense	SNP	G	A	CSB23	NM_003509.2	p.A70T
OR2B6	6	28033691	28033691	Missense	SNP	G	A	BRC30	NM_012367.1	p.E232K
NKAPL	6	28335372	28335372	Missense	SNP	G	A	CSB31	NM_001007531.1	p.A82T
OR10C1	6	29516587	29516587	Silent	SNP	G	T	BRC29	NM_013941.2	p.L272
PPP1R10	6	30679372	30679372	Silent	SNP	C	T	BRC9	NM_002714.2	p.G541
DDR1	6	30974660	30974660	Missense	SNP	C	T	BRC20	NM_013994.4	p.A829V
DPCR1	6	31027816	31027816	Missense	SNP	G	A	BRC24	NM_080870.2	p.G41E
LOC729792	6	31105298	31105298	Missense	SNP	G	A	BRC39	XM_001131329.1	p.E1119K
CCHCR1	6	31224237	31224237	Nonsense	SNP	C	A	BRC39	NM_001105564.1	p.E502*
CCHCR1	6	31226507	31226507	Nonsense	SNP	G	A	BRC9	NM_001105564.1	p.R359*
POU5F1	6	31240988	31240988	Missense	SNP	C	T	BRC36	NM_002701.4	p.E238K
AIF1	6	31691982	31691982	Missense	SNP	C	T	BRC39	ENST00000376051	p.H39Y

BAT4	6	31739678	31739678	Missense	SNP	T	G	BRC51	NM_033177.2	p.E186A
VARS	6	31855820	31855820	Silent	SNP	G	A	BRC35	NM_006295.2	p.Y1005
EGFL8	6	32241962	32241962	Missense	SNP	C	G	CSB1	NM_030652.2	p.F14L
PSMB8	6	32920125	32920125	Missense	SNP	G	A	CSB9	NM_004159.4	p.S15F
BRD2	6	33053911	33053911	Missense	SNP	C	G	BRC31	NM_005104.1	p.L537V
COL11A2	6	33264187	33264187	Missense	SNP	G	A	BRC18	NM_080680.2	p.A179V
RGL2	6	33372200	33372200	Missense	SNP	G	A	CSB1	NM_004761.2	p.H147Y
TAPBP	6	33380284	33380284	Silent	SNP	C	T	BRC4	NM_003190.3	p.L326
ITPR3	6	33740721	33740721	Silent	SNP	C	G	CSB1	NM_002224.2	p.L415
HMGA1	6	34316646	34316646	Silent	SNP	C	T	CSB19	NM_145899.3	p.P37
TAF11	6	34963619	34963619	Missense	SNP	C	G	BRC7	NM_005643.2	p.D32H
TCP11	6	35194234	35194234	Silent	SNP	G	C	CSB1	NM_001093728.1	p.L447
SCUBE3	6	35320404	35320404	Splice_Site	SNP	G	C	CSB5	NM_152753.2	e18-1
SRPK1	6	35946136	35946136	Silent	SNP	G	T	CSB10	NM_003137.3	p.G297
LOC100131043	6	36831425	36831425	Missense	SNP	G	C	BRC51	XM_001725057.1	p.R149G
PPIL1	6	36931614	36931614	Missense	SNP	G	A	BRC22	NM_016059.4	p.R152C
DNAH8	6	38878968	38878968	Missense	SNP	C	A	CSB3	NM_001371.2	p.H762Q
DNAH8	6	38918574	38918574	Missense	SNP	A	G	CSB6	NM_001371.2	p.T1371A
GLP1R	6	39148739	39148739	Silent	SNP	G	A	BRC52	NM_002062.3	p.Q211
DAAM2	6	39936772	39936772	Splice_Site	SNP	G	T	CSB27	NM_015345.2	e2+1
USP49	6	41881700	41881700	Missense	SNP	C	T	CSB13	NM_018561.3	p.G334S
TRERF1	6	42332502	42332502	Missense	SNP	C	T	CSB1	NM_033502.2	p.G841E
C6orf153	6	43104932	43104932	Missense	SNP	G	C	BRC39	NM_033112.2	p.L256F
CUL7	6	43113599	43113599	Silent	SNP	C	T	CSB1	NM_014780.3	p.L1634
CUL7	6	43128103	43128103	Silent	SNP	A	G	BRC32	NM_014780.3	p.P134
PTK7	6	43220217	43220217	Missense	SNP	G	T	CSB28	NM_002821.3	p.A768S
CUL9	6	43274517	43274517	Missense	SNP	T	G	BRC5	NM_015089.2	p.L999R
CUL9	6	43289624	43289624	Missense	SNP	G	C	CSB2	NM_015089.2	p.C1895S
ZNF318	6	43431363	43431363	Missense	SNP	T	A	BRC5	NM_014345.2	p.M563L
CAPN11	6	44249089	44249089	Silent	SNP	T	C	BRC47	NM_007058.3	p.G236
CAPN11	6	44255679	44255679	Nonsense	SNP	C	T	CSB1	NM_007058.3	p.Q444*
SLC29A1	6	44308564	44308564	Missense	SNP	C	T	BRC9	NM_001078174.1	p.R368W
SPATS1	6	44452082	44452082	Missense	SNP	C	G	BRC39	NM_145026.2	p.F256L
TDRD6	6	46769663	46769663	Missense	SNP	G	C	CSB2	NM_001010870.1	p.E1947Q
GPR115	6	47790293	47790293	Silent	SNP	G	T	CSB6	NM_153838.3	p.L451

GPR115	6	47792529	47792529	Missense	SNP	T	C	CSB2	NM_153838.3	p.I654T
OPN5	6	47871047	47871047	Missense	SNP	C	T	BRC31	NM_181744.1	p.S182L
RPS17P5	6	50933069	50933069	Missense	SNP	G	A	CSB1	ENST00000331146	p.S89L
PKHD1	6	51879039	51879039	Silent	SNP	G	A	CSB10	NM_138694.3	p.C2247
PAQR8	6	52376495	52376495	Silent	SNP	C	T	CSB1	NM_133367.4	p.F175
GSTA5	6	52806987	52806987	Missense	SNP	G	C	BRC41	NM_153699.1	p.L109V
FBXO9	6	53053741	53053741	Missense	SNP	G	T	BRC29	ENST00000244426	p.D152Y
DST	6	56465038	56465038	Silent	SNP	T	C	BRC21	NM_183380.1	p.Q460A
DST	6	56490044	56490044	Missense	SNP	A	T	BRC37	NM_183380.1	p.L3793M
DST	6	56589710	56589710	Missense	SNP	C	T	BRC39	NM_001723.1	p.E2172K
DST	6	56591259	56591259	Missense	SNP	G	T	CSB1	NM_001723.1	p.N1844K
DST	6	56623892	56623892	Missense	SNP	C	T	BRC50	NM_183380.1	p.E231K
BEND6	6	56987941	56987941	Missense	SNP	C	T	BRC32	NM_152731.2	p.A117V
LOC100132588	6	58378242	58378242	Missense	SNP	C	G	BRC47	XM_001714205.1	p.R106T
COL19A1	6	70694520	70694520	Splice_Site	SNP	A	G	CSB19	NM_001858.4	e4-2
COL9A1	6	71020950	71020950	Nonsense	SNP	C	A	BRC5	NM_001851.4	p.E557*
FAM135A	6	71247323	71247323	Splice_Site	SNP	A	C	BRC20	NM_001105531.1	e6-2
C6orf57	6	71333369	71333369	Missense	SNP	C	G	CSB24	NM_145267.2	p.T2S
SMAP1	6	71521403	71521403	Splice_Site	SNP	G	C	CSB33	NM_001044305.1	e3-1
RIMS1	6	73100037	73100037	Missense	SNP	A	C	BRC42	NM_014989.3	p.K1382Q
COL12A1	6	75855574	75855574	Missense	SNP	G	A	BRC39	NM_004370.5	p.S2993F
COL12A1	6	75880167	75880167	Missense	SNP	T	G	BRC13	NM_004370.5	p.N2571H
TMEM30A	6	76022712	76022712	Missense	SNP	A	T	BRC6	NM_018247.1	p.F304L
ELOVL4	6	80688233	80688233	Splice_Site	SNP	C	G	BRC39	NM_022726.3	e4-1
ME1	6	84112734	84112734	Missense	SNP	C	G	CSB1	NM_002395.3	p.L159F
KIAA1009	6	84952925	84952925	Silent	SNP	T	C	BRC15	NM_014895.2	p.L415
LOC643926	6	87198690	87198690	Nonsense	SNP	A	T	BRC34	XM_927187.1	p.K3*
CGA	6	87854608	87854608	Missense	SNP	G	C	CSB1	NM_000735.2	p.I10M
ZNF292	6	88022203	88022203	Missense	SNP	C	T	BRC32	NM_015021.1	p.R713C
ZNF292	6	88027946	88027946	Nonsense	SNP	C	G	BRC47	NM_015021.1	p.S2627*
MDN1	6	90416487	90416487	Missense	SNP	T	A	CSB21	NM_014611.1	p.M5395L
EPHA7	6	94009970	94009970	Missense	SNP	C	G	BRC20	NM_004440.3	p.M964I
KIAA0776	6	97102828	97102828	Missense	SNP	A	G	BRC26	NM_015323.4	p.I490M
FBXL4	6	99428959	99428959	Missense	SNP	G	C	CSB1	NM_012160.3	p.F594L
SFRS18	6	99965552	99965579	Frame Shift	DEL	ATTCCCC	0	CSB34	NM_015491.1	p.E93fs

						Del	AT TCTATTT AAG ATTTAGG CA					
SIM1	6	101003156	101003156	Silent	SNP	G	A	CSB20	NM_005068.2		p.A221	
HACE1	6	105387699	105387699	Missense	SNP	C	T	BRC39	NM_020771.3		p.D149N	
PRDM1	6	106660148	106660148	Missense	SNP	G	A	BRC18	NM_001198.3		p.G438R	
PRDM1	6	106660498	106660498	Silent	SNP	G	A	BRC18	NM_001198.3		p.L554	
BEND3	6	107496832	107496832	Silent	SNP	G	A	BRC11	NM_001080450.1		p.F752	
BEND3	6	107496938	107496938	Missense	SNP	G	A	BRC11	NM_001080450.1		p.S717F	
CDC40	6	110640983	110640983	Missense	SNP	G	A	BRC30	NM_015891.2		p.G290D	
TRAF3IP2	6	112019923	112019923	Silent	SNP	C	T	BRC13	NM_147200.1		p.L29	
TSPYL1	6	116707110	116707110	Missense	SNP	C	T	CSB1	NM_003309.2		p.E193K	
ZUFSP	6	117094935	117094935	Silent	SNP	A	T	BRC3	NM_145062.1		p.G38	
GPRC6A	6	117234474	117234474	Missense	SNP	C	A	BRC41	NM_148963.2		p.A363S	
C6orf204	6	118909715	118909715	Missense	SNP	G	C	BRC39	NM_001042475.1		p.I555M	
MAN1A1	6	119556652	119556652	Missense	SNP	C	G	BRC39	NM_005907.2		p.D439H	
MAN1A1	6	119711492	119711492	Silent	SNP	G	A	CSB1	NM_005907.2		p.I146	
C6orf170	6	121494537	121494537	Missense	SNP	A	G	BRC33	NM_152730.4		p.I945T	
KIAA0408	6	127810509	127810509	Silent	SNP	G	T	BRC11	NM_014702.3		p.I216	
LAMA2	6	129712147	129712147	Missense	SNP	C	G	CSB1	NM_000426.3		p.S1483C	
EPB41L2	6	131253263	131253263	Missense	SNP	G	C	BRC18	NM_001431.1		p.F508L	
MED23	6	131956964	131956964	Missense	SNP	T	C	CSB34	NM_004830.2		p.Y1067C	
MED23	6	131972919	131972919	Missense	SNP	A	G	CSB20	NM_004830.2		p.F346S	
TAAR1	6	133008478	133008478	Missense	SNP	C	G	CSB1	NM_138327.1		p.D120H	
SLC2A12	6	134369725	134369725	Silent	SNP	G	A	BRC39	NM_145176.2		p.I495	
SLC2A12	6	134392467	134392467	Silent	SNP	C	T	CSB5	NM_145176.2		p.G63	
MAP7	6	136728718	136728718	Missense	SNP	C	T	BRC15	NM_003980.3		p.R374K	
MAP3K5	6	137005362	137005362	Silent	SNP	G	A	BRC22	NM_005923.3		p.V609	
GPR126	6	142774215	142774215	Missense	SNP	C	A	BRC11	NM_198569.2		p.H839N	
HIVEP2	6	143116672	143116672	Silent	SNP	G	A	BRC47	NM_006734.3		p.F2202	
HIVEP2	6	143123249	143123249	Missense	SNP	C	A	BRC41	NM_006734.3		p.V1957F	
HIVEP2	6	143135403	143135412	Missense Frame Shift Del	DEL	GCCCAC AGGA		0 BRC14	NM_006734.3		p.P720fs	
PEX3	6	143841907	143841907	Missense	SNP	C	T	BRC18	NM_003630.2		p.P274S	
FAM164B	6	144261507	144261507	Missense	SNP	G	A	CSB34	XM_928657.2		p.A159T	

STX11	6	144550103	144550103	Missense	SNP	C	T	BRC17	NM_003764.3	p.R216C
GRM1	6	146392952	146392952	Silent	SNP	G	A	CSB1	NM_000838.3	p.L202
MAP3K7IP2	6	149742141	149742141	Missense	SNP	T	C	BRC35	NM_015093.3	p.I466T
SYNE1	6	152574344	152574344	Missense	SNP	C	G	BRC13	NM_182961.2	p.E7523Q
SYNE1	6	152692997	152692997	Missense	SNP	A	G	BRC5	NM_182961.2	p.L4839P
SYNE1	6	152750043	152750043	Missense	SNP	C	T	BRC18	NM_182961.2	p.E2782K
SYNE1	6	152754153	152754153	Missense	SNP	G	T	BRC14	NM_182961.2	p.S2652R
SYNE1	6	152791155	152791155	Missense	SNP	C	G	BRC24	NM_182961.2	p.K1618N
SYNE1	6	152851280	152851280	Missense	SNP	C	G	BRC11	NM_182961.2	p.E331Q
FBXO5	6	153337916	153337916	Missense	SNP	G	A	CSB1	NM_012177.1	p.P213S
LOC729436	6	155324026	155324026	Nonsense	SNP	C	G	BRC9	XM_001133246.1	p.S101*
TULP4	6	158655230	158655230	Missense	SNP	G	T	BRC16	NM_020245.1	p.R65L p.RS168in Frame del
SYTL3	6	159049392	159049397	In Frame Del	DEL	GCAGCC	0	CSB2	NM_001009991.2	
FNDC1	6	159538515	159538515	Silent	SNP	G	A	BRC4	NM_032532.2	p.T58
IGF2R	6	160370658	160370658	Missense	SNP	G	A	BRC38	NM_000876.2	p.C288Y
MAP3K4	6	161450922	161450922	Missense	SNP	A	G	BRC14	NM_005922.2	p.H1461R
PDE10A	6	165672811	165672811	Silent	SNP	T	A	CSB6	NM_006661.1	p.I698
TLL2	6	167674941	167674941	Silent	SNP	C	G	BRC31	NM_031949.4	p.L521
TCTE3	6	169886137	169886137	Missense	SNP	C	G	BRC39	NM_174910.1	p.K93N
DLL1	6	170439325	170439325	Silent	SNP	G	A	CSB15	NM_005618.3	p.F199
FAM120B	6	170468721	170468721	Silent	SNP	C	G	BRC39	NM_032448.1	p.L106
C7orf20	7	892250	892250	Missense	SNP	C	T	CSB20	NM_015949.2	p.R63W
INTS1	7	1492834	1492834	Missense	SNP	G	A	CSB22	NM_001080453.2	p.R1107W
uc003slc.1	7	1699783	1699783	Missense	SNP	C	T	BRC11	ENST00000382528	p.R92Q
C7orf27	7	2549426	2549426	Silent	SNP	C	T	BRC47	NM_152743.2	p.L287
TNRC18	7	5315430	5315430	Silent	SNP	G	C	BRC31	NM_001080495.2	p.L1547
COL28A1	7	7364908	7364908	Nonsense	SNP	G	A	BRC39	NM_001037763.2	p.R1087*
COL28A1	7	7379637	7379637	Missense	SNP	C	T	CSB14	NM_001037763.2	p.V809M
COL28A1	7	7459623	7459623	Silent	SNP	G	A	CSB16	NM_001037763.2	p.P471
MIOS	7	7579155	7579155	Missense	SNP	C	T	CSB13	NM_019005.3	p.T175I
GLCC11	7	8092591	8092591	Silent	SNP	C	T	CSB1	NM_138426.2	p.G514
ETV1	7	13906928	13906928	Missense	SNP	C	T	CSB29	ENST00000405358	p.R405H
ANKMY2	7	16633306	16633306	Missense	SNP	T	C	BRC19	NM_020319.1	p.H52R
BZW2	7	16710795	16710795	Missense	SNP	G	C	CSB22	NM_014038.1	p.E403Q

HDAC9	7	18635583	18635583	Silent	SNP	T	C	CSB1	NM_178425.1	p.D250
MACC1	7	20166046	20166046	Nonsense	SNP	G	A	CSB1	NM_182762.3	p.Q155*
ITGB8	7	20385315	20385315	Missense	SNP	G	A	BRC3	NM_002214.2	p.V169I
ABCB5	7	20651923	20651923	Missense	SNP	G	C	CSB31	ENST00000404938	p.S233T
DNAH11	7	21549515	21549515	Missense	SNP	G	A	CSB1	ENST00000328843	p.E43K
DNAH11	7	21607002	21607002	Missense	SNP	G	A	CSB1	ENST00000328843	p.D1062N
DNAH11	7	21741813	21741813	Missense	SNP	C	T	CSB1	ENST00000328843	p.R2498C
DNAH11	7	21900928	21900928	Missense	SNP	C	A	BRC33	ENST00000328843	p.Q4312K
KLHL7	7	23129984	23129984	Missense	SNP	C	T	BRC47	NM_001031710.2	p.L62F
KLHL7	7	23146938	23146938	Silent	SNP	A	G	CSB22	NM_001031710.2	p.L156
KIAA0087	7	26542937	26542937	Missense	SNP	G	A	BRC31	ENST00000242109	p.T126I
uc003syb.1	7	26645308	26645308	Missense Frame Shift	SNP	C	G	BRC52	ENST00000409974	p.A7G
HOXA2	7	27107604	27107604	Del	DEL	G		0 BRC31	NM_006735.3	p.L133fs
EVX1	7	27252565	27252565	Missense	SNP	G	C	BRC7	NM_001989.3	p.R407T
CREB5	7	28730371	28730371	Missense	SNP	G	A	CSB9	NM_182898.1	p.R200Q
CREB5	7	28730475	28730475	Splice_Site	SNP	G	T	BRC10	NM_182898.1	e7+1
CPVL	7	29098777	29098777	Missense	SNP	G	A	BRC21	NM_019029.2	p.R177W
CPVL	7	29098829	29098829	Missense	SNP	G	T	CSB1	NM_019029.2	p.F159L
C7orf16	7	31701700	31701700	Missense	SNP	G	A	CSB10	NM_006658.1	p.D59N
KBTBD2	7	32875867	32875867	Missense	SNP	G	A	CSB1	NM_015483.2	p.S496L
KBTBD2	7	32876299	32876299	Nonsense	SNP	C	T	BRC3	NM_015483.2	p.W352*
NT5C3	7	33023699	33023699	Silent	SNP	A	G	BRC42	NM_001002010.1	p.H195
EEPD1	7	36303312	36303312	Missense	SNP	G	T	BRC41	NM_030636.2	p.V501F
ANLN	7	36412386	36412386	Missense	SNP	C	G	BRC39	NM_018685.2	p.L187V
TXNDC3	7	37856842	37856842	Missense	SNP	G	A	BRC13	NM_016616.3	p.E60K
TXNDC3	7	37873946	37873946	Missense	SNP	G	A	BRC29	NM_016616.3	p.E247K
INHBA	7	41706374	41706374	Missense	SNP	C	T	BRC5	NM_002192.2	p.A42T
GLI3	7	42054731	42054731	Missense	SNP	G	A	CSB1	NM_000168.5	p.S188F
URG4	7	43883996	43883996	Missense	SNP	G	A	CSB21	NM_001077663.1	p.R531W
GCK	7	44153777	44153777	Missense	SNP	T	A	CSB8	NM_033507.3	p.Q288L
NPC1L1	7	44545366	44545366	Silent	SNP	G	A	CSB9	NM_013389.1	p.A385
NPC1L1	7	44546100	44546100	Missense	SNP	G	A	CSB19	NM_013389.1	p.R141C
DDX56	7	44579789	44579789	Missense	SNP	A	C	BRC29	NM_019082.2	p.L47R
LOC100128364	7	45084616	45084616	Missense	SNP	C	T	BRC26	XM_001725500.1	p.R429H

PKD1L1	7	47891927	47891927	Silent	SNP	C	T	CSB25	NM_138295.2	p.G1029
LOC100130988	7	50146259	50146259	Missense	SNP	A	T	BRC44	XM_001713888.1	p.D256V
COBL	7	51060527	51060527	Nonsense Frame Shift	SNP	G	A	BRC8	NM_015198.3	p.R1181*
ECOP	7	55527564	55527564	Del	DEL	C		0 CSB7	NM_030796.3	p.G78fs
ZNF713	7	55974212	55974212	Missense	SNP	G	C	BRC13	NM_182633.1	p.Q104H
uc003tsb.2	7	56151330	56151330	Missense	SNP	G	T	CSB31	ENST00000329309	p.L58M
LOC730382	7	56722486	56722486	Silent	SNP	C	G	BRC50	XM_001714509.2	p.V48
ENSG0000019923 1	7	62273806	62273806	RNA	SNP	C	T	BRC31	ENST00000362361	NULL
AUTS2	7	69866264	69866264	Splice_Site	SNP	G	T	BRC29	NM_015570.1	e7+1
BAZ1B	7	72494539	72494539	Missense	SNP	C	G	CSB1	NM_032408.2	p.D1459H
CLIP2	7	73428320	73428320	Silent	SNP	G	T	CSB31	NM_003388.4	p.S551
GTF2I	7	73811070	73811070	Missense	SNP	C	G	CSB2	NM_032999.3	p.S988C
WBSCR16	7	74124456	74124456	Missense	SNP	T	C	CSB13	NM_030798.3	p.K130E
HIP1	7	75059629	75059629	Silent	SNP	C	T	BRC21	NM_005338.4	p.P108
ENSG0000021657 5	7	75200876	75200876	Missense	SNP	G	C	BRC32	ENST00000404944	p.S42C
STYXL1	7	75472637	75472637	Missense	SNP	A	G	CSB27	NM_016086.2	p.Y159H
FGL2	7	76664200	76664200	Missense	SNP	C	T	BRC33	NM_006682.2	p.A218T
MAGI2	7	77627524	77627524	Missense	SNP	C	G	CSB1	NM_012301.3	p.E867Q
LOC100131944	7	78644251	78644251	Missense	SNP	C	G	BRC47	XM_001723309.1	p.Q31E
PCLO	7	82289861	82289861	Missense	SNP	G	A	BRC5	NM_033026.2	p.H4893Y
SEMA3E	7	82872737	82872737	Silent	SNP	C	T	BRC11	NM_012431.1	p.K321
SEMA3E	7	83115716	83115716	Missense	SNP	C	G	CSB1	NM_012431.1	p.D27H
ABCB1	7	87016707	87016707	Missense	SNP	C	T	BRC31	NM_000927.3	p.A540T
ENSG0000021151 8	7	88107799	88107799	RNA	DEL	A		0 BRC21	ENST00000390184	NULL
PFTK1	7	90451424	90451424	Missense	SNP	A	C	BRC47	NM_012395.2	p.M307L
AKAP9	7	91574587	91574587	Missense	SNP	G	C	CSB1	NM_005751.4	p.E3821Q
FAM133B	7	92044419	92044419	Silent	SNP	C	T	BRC13	NM_152789.1	p.K133
SAMD9	7	92570331	92570331	Nonsense	SNP	G	A	BRC39	NM_017654.2	p.Q1006*
SAMD9	7	92570978	92570978	Missense	SNP	T	C	CSB15	NM_017654.2	p.E790G
SAMD9	7	92571945	92571945	Missense	SNP	C	G	CSB5	NM_017654.2	p.V468L
FLJ42280	7	95950220	95950220	RNA	SNP	C	A	BRC7	XR_040255.1	NULL
DLX5	7	96489575	96489575	Missense	SNP	T	G	BRC39	NM_005221.5	p.K133T
ACN9	7	96585091	96585091	Silent	SNP	G	A	BRC13	NM_020186.2	p.R40

TMEM130	7	98295746	98295746	Silent	SNP	G	A	CSB19	NM_152913.1	p.F181
PTCD1	7	98859412	98859412	Missense	SNP	C	A	CSB15	NM_015545.2	p.K614N
ZKSCAN1	7	99459082	99459082	Missense	SNP	C	T	CSB24	NM_003439.1	p.S6L
PVRIG	7	99656572	99656572	Missense	SNP	C	A	BRC29	NM_024070.3	p.A248D
EPO	7	100158238	100158238	Missense	SNP	G	A	BRC12	NM_000799.2	p.V88I
EPHB4	7	100248680	100248680	Missense	SNP	C	T	BRC20	NM_004444.4	p.V615I
MUC17	7	100465370	100465370	Missense	SNP	C	T	CSB1	NM_001040105.1	p.S1318F
MUC17	7	100466732	100466732	Missense	SNP	C	T	BRC42	NM_001040105.1	p.T1772I
MUC17	7	100473204	100473204	Silent	SNP	C	T	BRC39	NM_001040105.1	p.I3929
PLOD3	7	100640376	100640376	Nonsense	SNP	C	A	BRC30	NM_001084.4	p.E524*
PRKRIP1	7	101825105	101825105	Missense	SNP	G	A	CSB1	NM_024653.3	p.E54K
LRWD1	7	101897026	101897026	Missense	SNP	C	T	CSB22	NM_152892.1	p.T410M
DNAJC2	7	102769460	102769460	Missense	SNP	G	A	CSB14	NM_014377.1	p.P81L
RELN	7	102925795	102925795	Missense	SNP	T	G	BRC17	NM_005045.3	p.Q2936H
RELN	7	102930701	102930701	Silent	SNP	T	G	BRC29	NM_005045.3	p.G2829
RELN	7	102993990	102993990	Missense	SNP	G	C	BRC41	NM_005045.3	p.A1618G
MLL5	7	104535463	104535463	Missense	SNP	T	C	BRC9	NM_018682.3	p.M1108T
SRPK2	7	104588290	104588290	Missense	SNP	C	A	BRC8	NM_182692.1	p.C174F
PIK3CG	7	106295294	106295294	Nonsense	SNP	C	T	CSB28	NM_002649.2	p.R18*
LAMB1	7	107357276	107357276	Missense	SNP	A	G	CSB21	NM_002291.2	p.I1521T
LAMB4	7	107497506	107497506	Missense	SNP	C	T	BRC39	NM_007356.2	p.E729K
NRCAM	7	107607959	107607959	Missense	SNP	T	C	CSB22	NM_001037132.1	p.N932S
DOCK4	7	111155611	111155611	Silent	SNP	G	A	BRC51	NM_014705.3	p.P1952
DOCK4	7	111174722	111174722	Missense	SNP	G	C	CSB31	NM_014705.3	p.P1468R
C7orf60	7	112366922	112366922	Silent	SNP	C	G	BRC24	NM_152556.2	p.V40
MET	7	116127162	116127162	Missense	SNP	C	T	BRC20	NM_000245.2	p.T263M
CAPZA2	7	116333610	116333610	Nonsense	SNP	C	T	CSB1	NM_006136.2	p.Q162*
CTTNBP2	7	117204908	117204908	Missense	SNP	C	G	BRC39	NM_033427.2	p.E891Q
PTPRZ1	7	121437752	121437752	Silent	SNP	G	C	CSB6	NM_002851.2	p.T472
CADPS2	7	121878761	121878761	Missense	SNP	C	A	BRC31	NM_017954.2	p.D731Y
SLC13A1	7	122574556	122574556	Silent	SNP	C	G	BRC39	NM_022444.3	p.V235
PAX4	7	127038484	127038484	Frame Shift Del	DEL	G		0 BRC6	NM_006193.2	p.P301fs
SND1	7	127132144	127132144	Missense	SNP	G	A	BRC37	NM_014390.2	p.E286K
IMPDH1	7	127828371	127828371	Silent	SNP	C	T	BRC51	NM_000883.3	p.L146

METTL2B	7	127906591	127906591	Missense	SNP	T	A	CSB23	NM_018396.2	p.F116I
FAM71F1	7	128157269	128157269	Missense	SNP	T	C	BRC29	NM_032599.2	p.W311R
CALU	7	128181684	128181684	Silent	SNP	C	T	BRC31	NM_001219.1	p.L118
CCDC136	7	128245110	128245110	Silent	SNP	G	A	CSB27	NM_022742.3	p.S1142
KCP	7	128334397	128334397	Missense	SNP	C	T	BRC19	ENST00000257704	p.R159H
CPA4	7	129732917	129732917	Missense	SNP	G	A	BRC23	NM_016352.3	p.R171Q
CPA5	7	129789554	129789554	Missense	SNP	G	A	CSB20	NM_080385.1	p.D192N
CPA5	7	129794513	129794513	Silent	SNP	G	A	BRC7	NM_080385.1	p.P301
PLXNA4	7	131468405	131468405	Missense	SNP	G	C	CSB1	NM_020911.1	p.F1844L
PLXNA4	7	131842825	131842825	Missense	SNP	C	T	BRC18	NM_020911.1	p.D390N
PLXNA4	7	131843852	131843852	Silent	SNP	G	A	BRC22	NM_020911.1	p.P47
CHRM2	7	136350455	136350455	Silent	SNP	C	T	BRC16	NM_000739.2	p.A101
CHRM2	7	136350481	136350481	Missense	SNP	C	T	BRC39	NM_000739.2	p.S110L
TTC26	7	138470079	138470079	Splice_Site	SNP	G	A	CSB19	NM_024926.1	e2+1
KLRG2	7	138788937	138788937	Missense	SNP	C	T	CSB19	NM_198508.2	p.G389D
BRAF	7	140099603	140099603	Missense	SNP	T	C	BRC15	NM_004333.4	p.K601E
BRAF	7	140181072	140181072	Missense	SNP	C	A	CSB2	NM_004333.4	p.G104W
LOC100131199	7	140817035	140817035	Nonsense	SNP	G	T	BRC37	XM_001714428.1	p.E190*
PRSS1	7	142170855	142170855	Silent	SNP	C	T	BRC37	ENST00000311737	p.F87
PRSS1	7	142171043	142171043	Missense	SNP	C	G	BRC37	ENST00000311737	p.S150C
EPHB6	7	142274838	142274838	Missense	SNP	T	A	CSB2	NM_004445.3	p.V532E
TRPV5	7	142332792	142332792	Missense	SNP	C	T	BRC15	NM_019841.4	p.R359H
OR6V1	7	142460240	142460240	Silent	SNP	C	A	BRC41	NM_001001667.1	p.P227
CASP2	7	142712173	142712173	Missense	SNP	G	C	CSB1	NM_032982.2	p.D416H
FAM131B	7	142764612	142764612	Missense	SNP	C	T	CSB1	NM_001031690.2	p.E137K
TAS2R41	7	142885386	142885386	Missense	SNP	G	T	CSB15	NM_176883.2	p.C100F
ENSG0000022214 9	7	148453866	148453866	RNA	SNP	G	C	BRC50	ENST00000410217	NULL
ZNF783	7	148611865	148611865	RNA	SNP	C	G	BRC7	NM_001004302.2	NULL
SSPO	7	149153945	149153945	Missense	SNP	T	A	BRC41	ENST00000326295	p.W133R
GIMAP4	7	149900852	149900852	Missense	SNP	G	T	BRC16	NM_018326.2	p.R254L
GIMAP1	7	150048548	150048548	Missense	SNP	C	T	BRC8	NM_130759.2	p.R175C
ASB10	7	150509324	150509324	Missense	SNP	C	T	BRC31	NM_080871.1	p.E247K
ABCF2	7	150549678	150549678	Silent	SNP	G	A	BRC33	NM_005692.3	p.L280
WDR86	7	150723909	150723909	Silent	SNP	G	A	CSB20	NM_198285.2	p.P204

MLL3	7	151480834	151480834	Nonsense Frame Shift	SNP	G	A	BRC6	NM_170606.2	p.R4139*
MLL3	7	151487020	151487023	Del Frame Shift	DEL	CTTC	0	CSB27	NM_170606.2	p.G3843fs
MLL3	7	151508119	151508123	Del Frame Shift	DEL	AGAAT	0	BRC3	NM_170606.2	p.I2391fs
MLL3	7	151550670	151550670	Ins	INS		0	T BRC21	NM_170606.2	p.T1118fs
MLL3	7	151552526	151552526	Missense	SNP	C	T	CSB28	NM_170606.2	p.D1029N
FLJ42291	7	152738587	152738587	RNA	SNP	G	T	BRC51	XR_040032.1	NULL
LOC100130228	7	153052662	153052662	Missense	SNP	C	T	BRC39	XM_001721136.1	p.S26L
DPP6	7	154308212	154308212	Silent	SNP	G	A	BRC39	ENST00000377770	p.P12
PAXIP1	7	154369027	154369027	Missense	SNP	G	C	CSB9	NM_007349.3	p.Q1059E
PAXIP1	7	154398605	154398605	Missense	SNP	C	T	CSB26	NM_007349.3	p.E270K
PTPRN2	7	157677785	157677785	Missense	SNP	C	T	CSB14	NM_002847.3	p.A182T
FAM62B	7	158224519	158224519	Silent	SNP	G	A	BRC16	NM_020728.2	p.H768
WDR60	7	158415953	158415953	Missense	SNP	C	G	BRC47	NM_018051.4	p.I844M
WDR60	7	158427503	158427503	Missense	SNP	G	A	BRC32	NM_018051.4	p.V969M
DLGAP2	8	1603946	1603946	Missense	SNP	C	T	BRC5	NM_004745.3	p.P539S
ARHGEF10	8	1812297	1812297	Missense	SNP	A	G	BRC11	NM_014629.2	p.H278R
MFHAS1	8	8786122	8786122	Silent	SNP	C	T	BRC50	NM_004225.2	p.Q619
RP1L1	8	10504177	10504177	Missense	SNP	C	T	BRC29	NM_178857.5	p.R1614Q
DLC1	8	13401710	13401710	Missense	SNP	A	T	BRC20	NM_182643.3	p.L81H
DLC1	8	13401920	13401920	Missense	SNP	T	A	BRC47	NM_182643.3	p.E11V
TUSC3	8	15524981	15524981	Missense	SNP	G	A	CSB1	NM_006765.2	p.E54K
EFHA2	8	16983590	16983590	Missense	SNP	G	A	BRC50	NM_181723.1	p.E222K
PCM1	8	17841860	17841860	Silent	SNP	G	A	BRC18	ENST00000325126	p.R271
PCM1	8	17854914	17854914	Silent Frame Shift	SNP	A	G	BRC15	NM_006197.3	p.K409
LPL	8	19861171	19861172	Del	DEL	TG	0	BRC11	NM_000237.2	p.L380fs
STC1	8	23764908	23764908	Missense	SNP	A	G	BRC50	NM_003155.2	p.S115P
NEFL	8	24869868	24869868	Missense	SNP	A	G	BRC41	ENST00000221169	p.S27P
KCTD9	8	25359683	25359683	Missense	SNP	C	T	CSB34	NM_017634.2	p.V17M
EBF2	8	25946585	25946585	Nonsense	SNP	G	A	BRC15	NM_022659.2	p.R162*
BNIP3L	8	26321686	26321686	Missense	SNP	G	A	BRC50	NM_004331.2	p.R163H
LOC100130267	8	26362105	26362105	Missense	SNP	A	C	BRC11	XM_001723339.1	p.R18S
SCARA3	8	27572424	27572424	Missense	SNP	G	C	CSB21	NM_016240.2	p.G273A
SCARA5	8	27820596	27820596	Missense	SNP	G	A	BRC22	NM_173833.4	p.R362C

C8orf41	8	33486943	33486943	Missense	SNP	G	C	CSB1	NM_001102401.1	p.L233V
UNC5D	8	35703352	35703352	Missense	SNP	A	G	BRC51	NM_080872.2	p.K477E
KCNU1	8	36761175	36761175	Missense	SNP	C	T	BRC47	NM_001031836.2	p.S30F
RAB11FIP1	8	37854056	37854056	Missense	SNP	A	T	CSB9	NM_001002814.1	p.N181K
ADAM9	8	39067988	39067988	Missense	SNP	G	A	CSB30	NM_003816.1	p.R755Q
ADAM2	8	39726063	39726063	Missense	SNP	G	C	BRC11	NM_001464.3	p.Q647E
ADAM2	8	39813854	39813854	Silent	SNP	C	T	CSB8	NM_001464.3	p.P30
IDO2	8	39955779	39955779	Missense	SNP	C	T	CSB7	NM_194294.2	p.R91W
LOC100129400	8	41641896	41641896	Silent	SNP	G	T	BRC33	XM_001724708.1	p.L133
DKK4	8	42350894	42350894	Missense	SNP	G	C	BRC31	NM_014420.2	p.Q186E
SLC20A2	8	42413901	42413901	Missense	SNP	C	T	CSB22	NM_006749.3	p.R429H
HOOK3	8	42940805	42940805	Missense	SNP	G	A	BRC36	NM_032410.3	p.R271H
HGSNAT	8	43173702	43173702	Missense	SNP	C	G	BRC39	NM_152419.2	p.L581V
POTEA	8	43267031	43267031	Missense	SNP	C	T	CSB1	NM_001005365.1	p.L83F
PXDNL	8	52532730	52532730	Missense	SNP	C	A	BRC6	NM_144651.4	p.G288V
ST18	8	53289319	53289319	Missense	SNP	C	G	BRC6	NM_014682.2	p.E18Q
RB1CC1	8	53731514	53731514	Missense	SNP	C	T	BRC39	NM_014781.1	p.R1143K
RB1CC1	8	53732391	53732391	Missense	SNP	C	G	BRC29	NM_014781.1	p.V851L
RB1CC1	8	53743173	53743173	Silent	SNP	G	A	BRC41	NM_014781.1	p.S378
LYN	8	57073516	57073516	Missense	SNP	G	A	BRC44	NM_002350.1	p.A370T
SDCBP	8	59653206	59653206	Missense	SNP	G	A	BRC16	NM_001007067.1	p.G155R
SDCBP	8	59654817	59654817	Silent	SNP	C	G	CSB1	NM_001007067.1	p.S220
CHD7	8	61875512	61875512	Silent	SNP	C	T	CSB34	NM_017780.2	p.S750
CHD7	8	61897163	61897163	Silent	SNP	G	A	BRC18	NM_017780.2	p.K954
CHD7	8	61940408	61940408	Missense	SNP	G	A	CSB1	NM_017780.2	p.G2786R
MYBL1	8	67654945	67654945	Missense	SNP	C	T	BRC31	NM_001080416.2	p.E360K
SGK3	8	67910567	67910567	Missense	SNP	C	T	BRC44	NM_001033578.1	p.R181W
COPS5	8	68131378	68131378	Missense	SNP	C	G	BRC5	NM_006837.2	p.D197H
CSPP1	8	68238552	68238552	Missense	SNP	C	T	CSB22	NM_001077204.1	p.P922L
SULF1	8	70661203	70661203	Missense	SNP	G	A	CSB2	NM_015170.1	p.R157Q
XKR9	8	71809147	71809147	Silent	SNP	A	G	BRC49	NM_001011720.1	p.K352
TRPA1	8	73097809	73097809	Silent	SNP	A	G	CSB19	NM_007332.2	p.D1082
CRISPLD1	8	76087255	76087255	Missense	SNP	A	T	BRC16	NM_031461.4	p.E97D
ZFHX4	8	77779962	77779962	Missense	SNP	G	A	BRC32	NM_024721.3	p.G362S
FAM164A	8	79761292	79761292	Silent	SNP	G	A	BRC50	NM_016010.2	p.R82

STMN2	8	80711613	80711613	Frame Shift Del	DEL	A		0	CSB14	NM_007029.2	p.E14fs
STMN2	8	80711634	80711634	Missense	SNP	T	C		BRC51	NM_007029.2	p.I21T
HEY1	8	80840453	80840453	Missense	SNP	G	C		BRC47	NM_001040708.1	p.S151C
NBN	8	91064211	91064211	Missense	SNP	T	C		CSB16	NM_002485.4	p.K29R
DECR1	8	91126283	91126283	Missense	SNP	A	G		BRC38	NM_001359.1	p.T257A
LRRC69	8	92282051	92282051	Missense	SNP	C	T		BRC32	ENST00000343709	p.A107V
TMEM67	8	94863061	94863061	Splice_Site	SNP	G	A		BRC13	NM_153704.1	e10-1
INTS8	8	95946940	95946940	Nonsense	SNP	G	T		CSB1	NM_017864.2	p.E703* p.E973in Frame del
INTS8	8	95961563	95961563	In Frame Del	DEL	AGA		0	CSB3	NM_017864.2	
CCNE2	8	95966898	95966898	Missense	SNP	T	C		BRC33	NM_057749.1	p.D222G
PTDSS1	8	97365517	97365517	Silent	SNP	G	A		CSB19	NM_014754.1	p.P92
PGCP	8	97866601	97866601	Silent	SNP	G	A		CSB22	NM_016134.2	p.L100
MATN2	8	99111979	99111983	Frame Shift Del	DEL	GATGA		0	BRC39	NM_002380.3	p.E825fs
C8orf47	8	99170572	99170572	Missense	SNP	G	C		BRC39	NM_173549.1	p.D51H
C8orf47	8	99174719	99174719	Missense	SNP	C	A		CSB20	NM_173549.1	p.D369E
NIPAL2	8	99293833	99293833	Missense	SNP	G	T		BRC19	NM_024759.1	p.L211M
PABPC1	8	101788101	101788101	Missense	SNP	T	C		BRC22	NM_002568.3	p.N519S
GRHL2	8	102640125	102640125	Missense	SNP	C	T		CSB1	NM_024915.3	p.S196L
FZD6	8	104406806	104406806	Silent	SNP	C	T		BRC5	NM_003506.2	p.L432
TMEM74	8	109865816	109865816	Missense	SNP	G	A		CSB9	NM_153015.1	p.R230C
PKHD1L1	8	110571415	110571415	Silent	SNP	T	C		CSB22	NM_177531.4	p.D3313
GOLSYN	8	110657322	110657322	Silent	SNP	G	A		BRC18	NM_001099744.1	p.L327
CSMD3	8	113763973	113763973	Nonsense	SNP	G	A		BRC39	NM_198123.2	p.Q851*
TRPS1	8	116496381	116496381	Missense	SNP	G	T		BRC26	NM_014112.2	p.N977K
TRPS1	8	116701262	116701262	Missense	SNP	G	A		CSB20	NM_014112.2	p.P80S
HAS2AS	8	122725856	122725856	RNA	SNP	C	T		BRC52	NR_002835.1	NULL
ATAD2	8	124419208	124419208	Silent	SNP	T	C		CSB20	NM_014109.3	p.P963
KLHL38	8	124734097	124734097	Missense	SNP	G	A		CSB24	NM_001081675.2	p.T84I
FER1L6	8	125176447	125176447	Missense	SNP	C	G		BRC41	NM_001039112.2	p.P1561R
ZNF572	8	126059038	126059038	Missense	SNP	C	A		BRC39	NM_152412.2	p.F449L
KIAA0196	8	126140936	126140936	Missense	SNP	G	C		CSB1	NM_014846.3	p.L518V
KCNQ3	8	133267554	133267554	Missense	SNP	T	C		BRC19	NM_004519.2	p.Y148C
TMEM71	8	133795602	133795602	Nonsense	SNP	G	C		BRC50	NM_144649.1	p.S246*

TG	8	133963394	133963394	Missense	SNP	C	A	CSB2	NM_003235.4	p.T248K
ZFATAS	8	135679858	135679858	RNA	SNP	G	C	BRC18	NR_002438.1	NULL
KHDRBS3	8	136688401	136688401	Missense	SNP	A	T	BRC32	NM_006558.1	p.T277S
FAM135B	8	139234390	139234390	Missense	SNP	T	C	BRC22	NM_015912.3	p.I504V
COL22A1	8	139737362	139737362	Missense	SNP	G	C	BRC11	NM_152888.1	p.S1098C
TRAPPC9	8	141505920	141505920	Missense	SNP	C	G	BRC9	NM_031466.4	p.A386P
DENND3	8	142231005	142231005	Nonsense	SNP	C	T	BRC18	NM_014957.2	p.Q241*
LY6K	8	143780022	143780022	Missense	SNP	G	A	BRC10	NM_017527.2	p.E94K
TOP1MT	8	144482989	144482989	Missense	SNP	G	A	CSB28	NM_052963.1	p.A89V
MAPK15	8	144874916	144874916	Missense	SNP	G	C	CSB20	NM_139021.2	p.D279H
SCRIB	8	144957978	144957978	Missense	SNP	G	T	BRC18	NM_182706.3	p.P1081T
PUF60	8	144972604	144972604	Missense	SNP	C	T	BRC21	NM_078480.1	p.R146H
NRBP2	8	144992872	144992872	Missense	SNP	C	T	BRC38	NM_178564.2	p.A27T
PLEC1	8	145065644	145065644	Missense	SNP	T	C	CSB24	NM_201380.2	p.I3582V
PLEC1	8	145080804	145080804	Missense	SNP	T	A	CSB3	NM_201380.2	p.Y480F
PLEC1	8	145080997	145080997	Missense	SNP	C	T	CSB15	NM_201380.2	p.R442H
LOC392275	8	145177308	145177308	Missense	SNP	G	T	BRC47	XM_001714032.1	p.V313L
CYC1	8	145222865	145222865	Missense	SNP	C	T	CSB5	NM_001916.3	p.P91S
SLC39A4	8	145611471	145611471	Silent	SNP	G	A	CSB1	NM_130849.2	p.F205
SLC39A4	8	145612910	145612910	Silent	SNP	C	T	CSB14	NM_130849.2	p.P24
KIFC2	8	145663508	145663508	Missense	SNP	C	T	BRC51	NM_145754.2	p.R149W
MFSD3	8	145707298	145707298	Silent	SNP	C	T	CSB1	NM_138431.1	p.L394
ZNF251	8	145949966	145949966	Missense	SNP	C	G	BRC11	NM_138367.1	p.E62Q
SMARCA2	9	2113881	2113881	Missense	SNP	C	T	CSB22	NM_003070.3	p.R1309C
RFX3	9	3247062	3247062	Silent	SNP	C	T	BRC13	NM_134428.2	p.L581
SLC1A1	9	4551493	4551493	Missense	SNP	C	T	CSB25	NM_004170.4	p.R93C
PDCD1LG2	9	5539492	5539492	Silent	SNP	C	G	BRC51	NM_025239.3	p.L173
ERMP1	9	5795058	5795058	Missense	SNP	G	A	CSB14	NM_024896.2	p.A628V
GLDC	9	6578669	6578669	Missense	SNP	C	G	CSB1	NM_000170.2	p.M538I
PTPRD	9	8508269	8508269	Silent	SNP	C	A	CSB21	NM_002839.1	p.A374
PTPRD	9	8511518	8511518	Silent	SNP	G	T	BRC18	NM_002839.1	p.I240
PTPRD	9	8723783	8723783	Missense	SNP	C	T	CSB1	NM_002839.1	p.E21K
TYRP1	9	12688602	12688602	Missense	SNP	G	A	BRC11	NM_000550.2	p.R287Q
MPDZ	9	13116716	13116716	Missense	SNP	A	G	BRC15	NM_003829.3	p.I1507T
MPDZ	9	13212308	13212308	Missense	SNP	G	A	BRC50	NM_003829.3	p.S224L

NFIB	9	14140237	14140237	Missense	SNP	T	C	BRC30	NM_005596.2	p.N238S
ZDHHC21	9	14680384	14680384	Splice_Site	SNP	C	G	BRC11	NM_178566.3	e1-1
FREM1	9	14802998	14802998	Nonsense	SNP	G	C	CSB1	NM_144966.4	p.S902*
TTC39B	9	15179623	15179623	Silent	SNP	G	A	CSB12	NM_152574.1	p.L328
SNAPC3	9	15437146	15437146	Silent	SNP	C	G	BRC51	NM_001039697.1	p.L212
PSIP1	9	15459328	15459328	Missense	SNP	G	A	CSB31	NM_033222.1	p.S347L
C9orf93	9	15656202	15656202	Silent	SNP	G	A	CSB28	NM_173550.2	p.K319
ADAMTSL1	9	18767806	18767806	Silent	SNP	C	T	CSB20	NM_001040272.4	p.S1193
IFNA1	9	21431033	21431033	Missense	SNP	C	T	BRC44	NM_024013.1	p.S176F
MTAP	9	21849395	21849395	Missense	SNP	G	C	CSB1	NM_002451.3	p.E262Q
ENSG00000222693	9	25079077	25079077	RNA	SNP	C	T	BRC30	ENST00000410761	NULL
PLAA	9	26895515	26895515	Silent	SNP	C	T	BRC16	NM_001031689.2	p.L794
TAF1L	9	32621395	32621395	Nonsense	SNP	G	A	BRC52	NM_153809.2	p.R1395*
TAF1L	9	32621994	32621994	Missense	SNP	C	A	BRC3	NM_153809.2	p.G1195V
DNAJA1	9	33016607	33016607	Missense	SNP	G	A	BRC39	NM_001539.2	p.G42E
B4GALT1	9	33106008	33106008	Missense	SNP	C	A	CSB7	NM_001497.3	p.D314Y
GALT	9	34639008	34639008	Missense	SNP	C	G	BRC51	NM_000155.2	p.I278M
STOML2	9	35090607	35090607	Silent	SNP	G	A	BRC41	NM_013442.1	p.S307
UNC13B	9	35390417	35390417	Missense	SNP	T	G	BRC44	NM_006377.3	p.F1405C
FAM166B	9	35552658	35552658	Missense	SNP	A	C	CSB27	NM_001099951.1	p.F178V
TLN1	9	35702914	35702914	Missense	SNP	T	A	BRC16	NM_006289.3	p.D1160V
NPR2	9	35792255	35792255	Missense	SNP	G	A	BRC36	NM_003995.3	p.R562Q
RECK	9	36111586	36111586	Silent	SNP	C	T	BRC44	NM_021111.2	p.H865
RNF38	9	36346321	36346321	Missense	SNP	G	C	CSB1	NM_022781.4	p.F296L
ZBTB5	9	37431928	37431928	Silent	SNP	G	C	CSB1	NM_014872.2	p.P207
FRMPD1	9	37697533	37697533	Silent	SNP	T	A	BRC41	NM_014907.1	p.S74
PRKACG	9	70818516	70818516	Missense	SNP	C	T	BRC23	NM_002732.3	p.V105I
TMEM2	9	73522697	73522697	Missense	SNP	C	T	BRC38	NM_013390.1	p.V796I
GDA	9	74032733	74032733	Missense	SNP	G	A	BRC13	NM_004293.3	p.E293K
ALDH1A1	9	74721661	74721661	Missense	SNP	G	A	BRC51	NM_000689.3	p.P344S
PCSK5	9	77900755	77900755	Missense	SNP	G	A	CSB20	NM_006200.3	p.G342R
PCSK5	9	77993865	77993865	Missense	SNP	G	A	BRC18	NM_006200.3	p.G806S
PRUNE2	9	78510036	78510036	Missense	SNP	G	A	BRC7	ENST00000376718	p.S1966F
PRUNE2	9	78514569	78514569	Missense Frame Shift Del	DEL	T		0 CSB29	ENST00000376718	p.N455fs

PRUNE2	9	78515666	78515666	Silent	SNP	G	A	BRC16	ENST00000376718	p.D89
PRUNE2	9	78655327	78655327	Silent	SNP	C	T	BRC13	ENST00000376713	p.T72
VPS13A	9	79006133	79006133	Silent	SNP	T	C	BRC16	NM_033305.1	p.V59
VPS13A	9	79123107	79123107	Del	DEL	G		0 CSB34	NM_033305.1	p.W1698fs
VPS13A	9	79126436	79126436	Silent	SNP	C	T	BRC13	NM_033305.1	p.F1928
VPS13A	9	79156119	79156119	Silent	SNP	G	A	BRC36	NM_033305.1	p.P2452
ENSG0000020456 2	9	83722507	83722507	Missense	SNP	C	T	CSB29	ENST00000376459	p.S127F
FAM75B	9	83865976	83865976	Missense	SNP	G	A	BRC4	NM_001098807.1	p.P90L
KIF27	9	85708147	85708147	Missense	SNP	G	C	BRC32	NM_017576.1	p.A369G
C9orf79	9	89690389	89690389	Silent	SNP	G	T	BRC17	NM_178828.4	p.P389
C9orf79	9	89692916	89692916	Missense	SNP	C	A	BRC49	NM_178828.4	p.H1232N
LOC645961	9	89935654	89935654	RNA	SNP	G	C	CSB1	XR_040572.1	NULL
NXNL2	9	90340449	90340449	Missense	SNP	C	T	BRC44	NM_145283.1	p.P94S
LOC340515	9	92384781	92384781	RNA	SNP	C	T	BRC6	XR_041526.1	NULL
FAM120A	9	95366400	95366400	Silent	SNP	G	A	CSB1	NM_014612.3	p.S1038
ZNF169	9	96103293	96103293	Silent	SNP	C	T	CSB12	NM_194320.2	p.C544
C9orf3	9	96758027	96758027	Missense	SNP	G	A	CSB25	NM_032823.3	p.R495Q
MIRN23B	9	96887356	96887356	RNA	SNP	C	T	CSB12	ENST00000384832	NULL
HABP4	9	98292117	98292117	Silent	SNP	G	A	CSB7	NM_014282.2	p.P406
FAM22G	9	98739364	98739364	Missense	SNP	C	T	CSB1	NM_001045477.1	p.H394Y
FAM22G	9	98740069	98740069	Nonsense	SNP	G	T	CSB1	NM_001045477.1	p.E469*
KIAA1529	9	99127289	99127289	Missense	SNP	G	A	CSB10	ENST00000395220	p.R668K
NCBP1	9	99465094	99465094	Missense	SNP	G	A	BRC44	NM_002486.4	p.E581K
GALNT12	9	100628870	100628870	Missense	SNP	G	A	BRC26	NM_024642.3	p.R186H
COL15A1	9	100787774	100787774	Silent	SNP	C	T	BRC47	NM_001855.3	p.F69
INVS	9	102055237	102055237	Missense	SNP	G	A	BRC39	NM_014425.2	p.E488K
GRIN3A	9	103472603	103472603	Missense	SNP	G	A	BRC37	NM_133445.2	p.R638W
GRIN3A	9	103539621	103539621	Silent	SNP	G	A	CSB1	NM_133445.2	p.I154
SMC2	9	105916847	105916847	Silent	SNP	G	C	CSB1	NM_001042550.1	p.L529
OR13C8	9	106371919	106371919	Missense	SNP	C	G	CSB1	NM_001004483.1	p.S217C
OR13C9	9	106419955	106419955	Missense	SNP	T	G	BRC41	NM_001001956.1	p.M118L
TMEM38B	9	107550217	107550217	Missense	SNP	C	G	BRC11	NM_018112.1	p.F195L
ZNF462	9	108727182	108727182	Missense	SNP	G	A	BRC39	NM_021224.4	p.E390K
PALM2	9	111744850	111744850	Missense	SNP	C	G	BRC39	NM_053016.1	p.S189C

SVEP1	9	112189536	112189536	Missense	SNP	C	G	BRC50	NM_153366.3	p.E3304Q
SVEP1	9	112273507	112273507	Missense	SNP	G	C	BRC21	NM_153366.3	p.P986A
FKBP15	9	114988395	114988395	Silent	SNP	G	T	CSB10	NM_015258.1	p.R485
C9orf43	9	115225529	115225529	Missense	SNP	G	A	BRC50	NM_152786.1	p.E196K
KIF12	9	115895429	115895429	Silent	SNP	C	T	CSB15	NM_138424.1	p.L361
TNC	9	116828730	116828730	Missense	SNP	G	T	CSB2	NM_002160.2	p.H2079N
DIPAS	9	118199210	118199210	RNA	SNP	G	C	BRC39	XR_041635.1	NULL
TLR4	9	119516123	119516123	Silent	SNP	C	A	BRC44	NM_138554.3	p.T632
LOC389787	9	119885252	119885252	Missense	SNP	T	A	CSB25	XM_001725747.1	p.H43L
C5	9	122755936	122755936	Silent	SNP	A	G	BRC13	NM_001735.2	p.I1598
TLL11	9	123791343	123791343	Missense	SNP	G	C	BRC39	NM_194252.1	p.F497L
OR1N1	9	124328545	124328545	Missense	SNP	C	G	CSB1	NM_012363.1	p.L283F
OR1L4	9	124526164	124526164	Missense	SNP	G	C	BRC39	NM_001005235.1	p.Q25H
RC3H2	9	124667603	124667603	Missense	SNP	T	C	CSB25	NM_001100588.1	p.N494D
ZBTB6	9	124713114	124713114	Silent	SNP	G	A	CSB34	NM_006626.4	p.P353
RABGAP1	9	124905222	124905222	Missense	SNP	A	G	CSB29	NM_012197.3	p.N968S
NR6A1	9	126356467	126356467	Missense	SNP	G	A	BRC13	NM_033334.3	p.R116C
HSPA5	9	127041310	127041310	Missense	SNP	C	T	CSB1	NM_005347.3	p.E243K
C9orf117	9	129515162	129515162	Del	DEL	G		0 BRC38	NM_001012502.2	p.Q450fs
TTC16	9	129522183	129522183	Silent	SNP	A	G	BRC51	NM_144965.1	p.Q144
FPGS	9	129609381	129609381	Missense	SNP	G	C	CSB1	NM_004957.1	p.E192Q
AK1	9	129675155	129675155	Missense	SNP	A	C	CSB22	NM_000476.2	p.L5R
ODF2	9	130296676	130296676	Missense	SNP	G	A	CSB1	NM_002540.3	p.E583K
CCBL1	9	130638145	130638145	Silent	SNP	G	A	BRC31	NM_004059.1	p.T239
FNBP1	9	131702132	131702132	Silent	SNP	G	A	CSB21	NM_015033.2	p.D540
HMCN2	9	132264807	132264807	Missense	SNP	G	A	BRC50	ENST00000277491	p.E740K
ABL1	9	132719390	132719390	Silent	SNP	C	T	BRC50	NM_007313.3	p.F85
FIBCD1	9	132769401	132769401	Silent	SNP	G	C	CSB1	NM_032843.1	p.L419
LAMC3	9	132906928	132906928	Missense	SNP	G	A	BRC16	NM_006059.3	p.G456D
RAPGEF1	9	133491571	133491571	Missense	SNP	G	T	BRC3	NM_198679.2	p.P422T
SETX	9	134134869	134134869	Missense	SNP	C	T	CSB8	NM_015046.5	p.R2414Q
TSC1	9	134761659	134761659	Silent	SNP	T	C	CSB20	NM_000368.3	p.R1093
CEL	9	134929708	134929708	Missense	SNP	T	A	CSB27	NM_001807.3	p.F58I
ADAMTS13	9	135281234	135281234	Missense	SNP	G	A	BRC11	NM_139025.3	p.E212K

COL5A1	9	136740445	136740445	Missense	SNP	C	G	BRC12	ENST00000371814	p.Q119E
EHMT1	9	139830231	139830231	Silent	SNP	C	G	BRC39	NM_024757.1	p.L1059
CACNA1B	9	139931555	139931555	Missense	SNP	C	T	CSB22	NM_000718.2	p.P273S
ZMYND11	10	284307	284307	Missense	SNP	C	T	BRC5	NM_006624.3	p.S380F
LARP5	10	872396	872396	Missense	SNP	G	T	BRC35	NM_015155.1	p.Q233K
GTPBP4	10	1048488	1048488	Missense	SNP	G	C	CSB1	NM_012341.2	p.E476D
LOC100129894	10	1324961	1324961	Silent	SNP	G	A	BRC9	XM_001718251.1	p.S35
LOC728209	10	2240023	2240023	Missense	SNP	C	G	BRC18	XM_001126868.1	p.I10M
AKR1CL2	10	4873992	4873992	Silent	SNP	G	C	BRC44	NM_001040177.1	p.L232
NET1	10	5488190	5488190	Silent	SNP	G	C	CSB1	NM_001047160.1	p.V446
PFKFB3	10	6285280	6285280	Silent	SNP	G	A	CSB31	NM_004566.1	p.V17
PRKCQ	10	6523947	6523947	Missense	SNP	C	T	CSB1	NM_006257.2	p.E584K
SFMBT2	10	7449734	7449734	Missense	SNP	G	A	CSB29	NM_001029880.1	p.R107C
ITIH5	10	7662007	7662007	Missense	SNP	T	C	CSB15	NM_030569.1	p.R379G
ATP5C1	10	7884806	7884806	Missense	SNP	C	G	BRC5	NM_001001973.1	p.I291M
TAF3	10	8096665	8096665	Missense	SNP	G	A	CSB16	NM_031923.2	p.C912Y
GATA3	10	8146064	8146064	Missense	SNP	T	A	BRC18	NM_001002295.1	p.M294K p.302in Frame insl
GATA3	10	8146086	8146087	In Frame Ins	INS		0 ATT	CSB29	NM_001002295.1	
GATA3	10	8151439	8151440	Splice_Site	DEL	CA		0 CSB7	NM_001002295.1	e4-2
GATA3	10	8151439	8151440	Splice_Site Frame Shift	DEL	CA		0 BRC21	NM_001002295.1	e4-2
GATA3	10	8151512	8151513	Ins	INS		0 T	CSB29	NM_001002295.1	p.A333fs
GATA3	10	8155707	8155707	Splice_Site Frame Shift	SNP	G		C CSB22	NM_001002295.1	e5-1
GATA3	10	8155724	8155724	Ins Frame Shift	INS		0 TATGA	BRC32	NM_001002295.1	p.K358fs
GATA3	10	8155880	8155880	Ins	INS		0 T	BRC6	NM_001002295.1	p.P409fs
C10orf31	10	11398884	11398884	RNA Frame Shift	SNP	G		A BRC39	XR_041927.1	NULL
UPF2	10	12049411	12049411	Del	DEL	G		0 CSB26	NM_015542.2	p.R668fs
SEC61A2	10	12239021	12239021	Silent	SNP	C	A	BRC39	NM_018144.1	p.L242
SEC61A2	10	12243116	12243116	Missense	SNP	C	T	BRC18	NM_018144.1	p.S386L
MCM10	10	13262500	13262500	Missense	SNP	C	A	CSB2	NM_182751.3	p.L274M
PHYH	10	13376527	13376527	Silent	SNP	C	T	CSB1	NM_006214.1	p.S107
FAM171A1	10	15295260	15295260	Missense	SNP	C	G	CSB1	NM_001010924.1	p.R778P
LOC729195	10	19538360	19538360	Silent	SNP	C	T	BRC50	XM_001129637.2	p.L552
MLLT10	10	22062023	22062026	Splice_Site	DEL	GTAA		0 BRC33	NM_004641.1	e18+1

BMI1	10	22656983	22656983	Missense	SNP	G	A	BRC31	NM_005180.5	p.D139N
MYO3A	10	26486445	26486445	Silent	SNP	A	T	BRC16	NM_017433.4	p.I998
ANKRD26	10	27395472	27395472	Missense	SNP	C	A	BRC35	NM_014915.2	p.A407S
MASTL	10	27494387	27494387	Missense	SNP	A	G	BRC33	NM_032844.2	p.T242A
LOC220906	10	28853515	28853515	Missense	SNP	G	A	BRC31	XM_001716412.1	p.H226Y
WAC	10	28937273	28937273	Nonsense	SNP	C	T	BRC18	NM_016628.3	p.Q358*
NRP1	10	33521353	33521353	Splice_Site	SNP	C	G	CSB1	NM_003873.2	e13-1
PARD3	10	34666222	34666222	Silent	SNP	G	A	BRC20	NM_019619.2	p.S852
CUL2	10	35383400	35383400	Missense	SNP	C	G	BRC44	NM_003591.2	p.D131H
ANKRD30A	10	37473954	37473954	Silent	SNP	A	G	CSB16	NM_052997.2	p.K417
ANKRD30A	10	37476373	37476376	Frame Shift Del	DEL	ATAA		0 BRC5	NM_052997.2	p.N454fs
ZNF33A	10	38368420	38368420	Nonsense	SNP	C	T	BRC29	ENST00000265892	p.Q68*
CSGALNACT2	10	42991421	42991421	Missense	SNP	C	A	CSB15	NM_018590.3	p.S424Y
OR13A1	10	45119126	45119126	Missense	SNP	C	G	BRC50	NM_001004297.2	p.G251R
LOC100128244	10	45524271	45524271	Silent	SNP	C	G	CSB8	XM_001717633.1	p.L72
RBP3	10	48007873	48007873	Missense	SNP	G	T	BRC35	NM_002900.2	p.P1004H
GDF2	10	48034239	48034239	Missense	SNP	T	G	CSB15	NM_016204.1	p.K212T
WDFY4	10	49621123	49621123	Silent	SNP	C	G	CSB1	ENST00000325239	p.L661
WDFY4	10	49695367	49695367	Silent	SNP	C	T	BRC39	ENST00000374161	p.L332
LRRC18	10	49792151	49792151	Missense	SNP	C	T	CSB22	NM_001006939.3	p.R19K
C10orf53	10	50571899	50571899	Silent	SNP	G	A	BRC50	NM_182554.1	p.V57
FAM21A	10	51499357	51499357	Missense	SNP	G	C	BRC11	NM_001005751.1	p.R57S
A1CF	10	52243741	52243741	Missense	SNP	C	G	CSB1	NM_138932.2	p.G410A
PRKG1	10	53718720	53718720	Missense	SNP	G	C	BRC17	NM_006258.1	p.G619A
PCDH15	10	55251808	55251808	Nonsense	SNP	G	T	BRC39	NM_033056.1	p.S1895* p.F47in
TMEM26	10	62882705	62882707	In Frame Del	DEL	GAA		0 BRC49	NM_178505.6	Frame del
ZNF365	10	63829297	63829297	Nonsense	SNP	C	T	BRC33	NM_014951.2	p.R323*
LRRTM3	10	68356885	68356885	Missense	SNP	C	T	CSB1	NM_178011.3	p.R69C
DNA2	10	69876061	69876061	Missense	SNP	C	T	BRC16	NM_001080449.1	p.R438K
CCAR1	10	70152281	70152281	Missense	SNP	G	A	BRC50	NM_018237.2	p.G5E
SUPV3L1	10	70628872	70628872	Missense	SNP	A	G	CSB30	NM_003171.3	p.K404R
HKDC1	10	70662838	70662838	Silent	SNP	G	A	BRC39	NM_025130.3	p.K146
NEUROG3	10	71002534	71002534	Missense	SNP	C	T	CSB14	NM_020999.2	p.R91H
H2AFY2	10	71521552	71521552	Missense	SNP	G	A	BRC32	NM_018649.2	p.V105I

CDH23	10	73131959	73131959	Missense	SNP	G	A	CSB14	NM_022124.4	p.V858I
SPOCK2	10	73500172	73500172	Silent	SNP	C	T	BRC31	NM_014767.1	p.V126
CBARA1	10	73963518	73963518	Missense	SNP	C	G	CSB1	NM_006077.2	p.D177H
NUDT13	10	74544165	74544165	Silent	SNP	A	G	BRC12	NM_015901.4	p.K12
PPP3CB	10	74904686	74904686	Missense	SNP	C	G	BRC13	NM_021132.1	p.E174Q
NDST2	10	75237147	75237147	Splice_Site	SNP	C	T	BRC41	NM_003635.3	e1+1
MYST4	10	76273215	76273215	Silent	SNP	C	T	BRC20	NM_012330.2	p.V198
MYST4	10	76450952	76450952	Missense	SNP	C	T	BRC44	NM_012330.2	p.S975F
SFTPD	10	81687695	81687695	Frame Shift Del	DEL	C		0 CSB1	NM_003019.4	p.E341fs
LRIT2	10	85972109	85972109	Silent	SNP	C	A	CSB14	NM_001017924.2	p.S400
RGR	10	86002636	86002636	Silent	SNP	C	T	CSB1	NM_002921.1	p.F138
GRID1	10	87352163	87352163	Silent	SNP	C	T	CSB20	NM_017551.2	p.A959
LDB3	10	88429238	88429238	Silent	SNP	G	A	BRC41	NM_007078.1	p.L76
ENSG00000200176	10	88639342	88639342	RNA	SNP	A	T	BRC36	ENST00000363306	NULL
MMRN2	10	88693424	88693424	Missense	SNP	G	A	BRC51	NM_024756.2	p.P366L
C10orf59	10	90112372	90112372	Missense	SNP	A	C	CSB2	NM_001031709.1	p.I206S
ACTA2	10	90685101	90685101	Silent	SNP	G	T	BRC38	NM_001613.1	p.I331
IFIT1L	10	91133239	91133239	Silent	SNP	C	T	CSB34	NM_001010987.1	p.H63
KIF20B	10	91487981	91487981	Missense	SNP	C	G	BRC39	NM_016195.2	p.L1095V
KIF20B	10	91518106	91518106	Missense	SNP	C	T	CSB1	NM_016195.2	p.S1650F
RPP30	10	92624615	92624615	Missense	SNP	C	T	BRC39	NM_001104546.1	p.S31L
IDE	10	94257869	94257869	Missense	SNP	G	T	BRC32	NM_004969.2	p.D378E
LGI1	10	95546890	95546890	Missense	SNP	C	G	BRC13	NM_005097.2	p.F338L
NOC3L	10	96102650	96102650	Missense	SNP	G	A	BRC39	NM_022451.9	p.S284F
CYP2C19	10	96592682	96592682	Nonsense	SNP	G	T	BRC39	NM_000769.1	p.E354*
C10orf129	10	96957047	96957047	Missense	SNP	G	A	BRC39	NM_207321.2	p.E11K
SORBS1	10	97164576	97164576	Missense	SNP	C	T	BRC15	NM_001034954.1	p.V159I
ZNF518	10	97908210	97908210	Missense	SNP	C	G	CSB1	ENST00000371192	p.S714C
TM9SF3	10	98315135	98315135	Missense	SNP	C	T	CSB1	NM_020123.3	p.D113N
SLIT1	10	98752583	98752583	Missense	SNP	G	C	CSB2	NM_003061.2	p.P1341R
SLIT1	10	98768370	98768370	Missense	SNP	T	G	CSB2	NM_003061.2	p.T978P
LOC100128300	10	99619241	99619241	Silent	SNP	C	G	BRC47	XM_001725350.1	p.L87
CRTAC1	10	99673094	99673094	Missense	SNP	C	A	CSB1	NM_018058.4	p.D159Y
ABCC2	10	101546989	101546989	Missense	SNP	C	T	CSB29	NM_000392.3	p.R260W

DNMBP	10	101705356	101705356	Missense	SNP	G	A	CSB6	NM_015221.2	p.S622F
SEC31B	10	102238694	102238694	Missense	SNP	C	G	BRC18	NM_015490.3	p.E1067Q
C10orf2	10	102740682	102740682	Silent	SNP	G	C	CSB1	NM_021830.3	p.V553
LZTS2	10	102752562	102752562	Missense	SNP	G	A	CSB1	NM_032429.1	p.E93K
NPM3	10	103532621	103532621	Missense	SNP	C	T	BRC50	NM_006993.2	p.E57K
GBF1	10	104101078	104101078	Missense	SNP	C	T	BRC50	NM_004193.1	p.T124M
PSD	10	104153711	104153711	Missense	SNP	C	T	BRC38	NM_002779.3	p.E908K
PSD	10	104161898	104161898	Missense	SNP	G	C	CSB1	NM_002779.3	p.L609V
PSD	10	104166750	104166750	Silent	SNP	G	A	CSB10	NM_002779.3	p.G12
CYP17A1	10	104582846	104582846	Missense	SNP	G	A	CSB1	NM_000102.3	p.S288L
AS3MT	10	104619917	104619917	Frame Shift Del	DEL	C		0 BRC31	NM_020682.3	p.R44fs
PDCD11	10	105159489	105159489	Missense	SNP	C	T	BRC39	NM_014976.1	p.T305M
NEURL	10	105321490	105321490	Missense	SNP	C	A	BRC41	NM_004210.4	p.F190L
SLK	10	105748961	105748961	Missense	SNP	A	G	BRC36	NM_014720.2	p.M228V
SORCS3	10	106966794	106966794	Silent	SNP	G	A	BRC50	NM_014978.1	p.A886
LOC100128304	10	109664761	109664761	Silent	SNP	G	A	BRC9	XM_001718321.1	p.P135
SMC3	10	112350187	112350187	Missense	SNP	G	A	CSB1	NM_005445.3	p.E810K
GPAM	10	113927780	113927780	Missense	SNP	G	A	BRC29	NM_020918.4	p.P84L
CASP7	10	115441768	115441768	Missense	SNP	G	C	CSB9	NM_033338.3	p.K16N
C10orf81	10	115527282	115527282	Missense	SNP	G	C	BRC11	ENST00000369310	p.D431H
FAM160B1	10	116611047	116611047	Missense	SNP	G	A	CSB1	NM_020940.1	p.R719K
PNLIPRP1	10	118341311	118341311	Missense	SNP	G	A	CSB12	NM_006229.2	p.D30N
PNLIPRP1	10	118344276	118344276	Missense	SNP	G	C	CSB1	NM_006229.2	p.W125C
PNLIPRP2	10	118394572	118394572	Missense	SNP	G	A	BRC32	ENST00000298771	p.V461I
VAX1	10	118881785	118881785	Silent	SNP	C	T	BRC39	NM_199131.1	p.K162
PDZD8	10	119033303	119033303	Silent	SNP	G	A	BRC18	NM_173791.3	p.N977
EIF3A	10	120800083	120800083	Missense	SNP	T	C	CSB16	NM_003750.2	p.T805A
SFXN4	10	120915047	120915047	Missense	SNP	C	T	CSB1	NM_213649.1	p.E35K
INPP5F	10	121500656	121500656	Missense	SNP	C	T	BRC47	NM_014937.2	p.S59L
TACC2	10	124003532	124003532	Missense	SNP	G	A	BRC28	NM_206862.2	p.E2940K
HTRA1	10	124256240	124256240	Missense	SNP	G	A	BRC47	NM_002775.4	p.R274Q
DMBT1	10	124349596	124349596	Missense	SNP	C	G	BRC39	NM_007329.2	p.P1103A
HMX3	10	124886608	124886608	Missense	SNP	A	C	BRC41	NM_001105574.1	p.T149P
BUB3	10	124907318	124907318	Missense	SNP	G	A	CSB1	NM_004725.2	p.D117N

GPR26	10	125416420	125416420	Silent	SNP	C	T	BRC41	NM_153442.3	p.F169
OAT	10	126087299	126087299	Splice_Site	SNP	C	T	CSB16	NM_000274.2	e2+1
METTL10	10	126444060	126444060	Missense	SNP	C	G	BRC41	NM_212554.2	p.K169N
ZRANB1	10	126652898	126652898	Silent	SNP	T	C	BRC28	NM_017580.2	p.Y456
LOC728065	10	128575298	128575298	Silent	SNP	C	T	BRC20	XM_001126459.1	p.G2
C10orf141	10	128863607	128863607	Missense	SNP	C	T	BRC36	NM_001039762.2	p.R348Q
LOC387720	10	129423948	129423948	RNA	SNP	C	T	BRC11	XR_039803.1	NULL
MKI67	10	129797414	129797414	Missense	SNP	C	T	BRC31	NM_002417.1	p.E894K
DPYSL4	10	133854282	133854282	Silent	SNP	C	T	CSB34	NM_006426.2	p.D27
LRRC27	10	134019312	134019312	Missense	SNP	G	C	BRC31	NM_030626.1	p.E368Q
INPP5A	10	134445424	134445424	Missense	SNP	G	T	CSB22	NM_005539.3	p.V410F
KNDC1	10	134865315	134865315	Missense	SNP	G	A	BRC16	NM_152643.6	p.G1104R
						GGGTCA				
						AC				
				Frame Shift		AACTCTG				
ATHL1	11	283193	283208	Del	DEL	T	0	BRC31	NM_025092.4	p.V258fs
PHRF1	11	598188	598188	Missense	SNP	C	A	BRC35	NM_020901.2	p.A911D
MUPCDH	11	611194	611194	Silent	SNP	C	T	CSB1	NM_021924.3	p.L225
DEAF1	11	674921	674921	Missense	SNP	C	T	CSB19	NM_021008.2	p.A283T
TSPAN4	11	852658	852658	Missense	SNP	A	G	BRC38	NM_001025234.1	p.I58V
MUC5B	11	1219076	1219076	Missense	SNP	G	A	BRC16	NM_002458.1	p.E1467K
TOLLIP	11	1268038	1268038	Missense	SNP	C	A	CSB21	NM_019009.2	p.D121Y
ENSG0000020575 1	11	1954030	1954030	Missense	SNP	C	T	BRC31	ENST00000381512	p.S212F
KCNQ1	11	2549182	2549182	Missense	SNP	G	C	BRC17	NM_000218.2	p.G219A
ZNF195	11	3337560	3337560	Missense	SNP	G	C	BRC7	NM_007152.1	p.I346M
ART1	11	3637426	3637426	Missense	SNP	C	G	CSB1	NM_004314.2	p.S34C
OR52M1	11	4523188	4523188	Missense	SNP	C	G	CSB2	NM_001004137.1	p.F64L
OR51F2	11	4799316	4799316	Missense	SNP	C	G	BRC48	NM_001004753.1	p.S42C
OR51G2	11	4893168	4893168	Missense	SNP	G	T	BRC35	NM_001005238.1	p.A101D
OR51B5	11	5320515	5320515	Silent	SNP	G	A	CSB1	NM_001005567.1	p.L272
OR51B5	11	5320762	5320762	Missense	SNP	G	T	CSB3	NM_001005567.1	p.T190N
OR51B5	11	5321053	5321053	Missense	SNP	G	A	CSB1	NM_001005567.1	p.A93V
OR51J1	11	5381061	5381061	Missense	SNP	A	T	BRC41	ENST00000332043	p.Y220F
OR52H1	11	5522945	5522945	Missense	SNP	C	G	BRC50	NM_001005289.1	p.D129H
TRIM6-TRIM34	11	5610071	5610071	Silent	SNP	G	T	BRC29	NM_001003819.2	p.G332

ENSG0000018090											
9	11	6130340	6130340	Missense	SNP	G	C	BRC51	ENST00000316506	p.L19V	
CNGA4	11	6217952	6217952	Missense	SNP	G	A	CSB1	NM_001037329.2	p.D118N	
APBB1	11	6381136	6381136	Silent	SNP	A	T	CSB2	NM_001164.2	p.A343	
DCHS1	11	6604610	6604610	Missense	SNP	T	G	BRC44	NM_003737.2	p.E2079A	
DCHS1	11	6610077	6610077	Missense	SNP	T	A	CSB31	NM_003737.2	p.E1081V	
OR10A2	11	6847815	6847815	Missense	SNP	C	T	CSB22	NM_001004460.1	p.A85V	
NLRP10	11	7938805	7938805	Silent	SNP	G	T	BRC48	NM_176821.3	p.V310	
IPO7	11	9406722	9406722	Missense	SNP	C	A	CSB1	NM_006391.2	p.F465L	
IPO7	11	9407822	9407822	Silent	SNP	C	T	BRC39	NM_006391.2	p.I539	
DKK3	11	11976903	11976903	Splice_Site	SNP	C	T	CSB1	NM_001018057.1	e3-1	
INSC	11	15090598	15090598	Missense	SNP	C	T	CSB1	NM_001031853.3	p.R3W	
USH1C	11	17504557	17504557	Missense	SNP	C	T	BRC31	NM_153676.3	p.R196Q	
OTOG	11	17613309	17613309	Silent	SNP	C	T	BRC47	XM_291816.1	p.C2576	
MRGPRX1	11	18912064	18912064	Missense	SNP	G	C	BRC39	NM_147199.3	p.Q282E	
NAV2	11	19912087	19912087	Missense	SNP	G	C	CSB16	NM_182964.1	p.G597A	
LOC100130160	11	21262093	21262093	Missense	SNP	G	A	BRC41	XM_001722925.1	p.G66D	
GAS2	11	22704457	22704457	Missense	SNP	C	G	CSB1	NM_005256.1	p.S104W	
ANO3	11	26638525	26638525	Silent	SNP	A	G	BRC44	NM_031418.2	p.Q968	
LGR4	11	27346281	27346281	Silent	SNP	C	T	BRC47	NM_018490.2	p.L855	
BDNF	11	27636695	27636695	Missense	SNP	C	T	BRC36	NM_170734.1	p.R13K	
DCDC1	11	31306361	31306361	Nonsense	SNP	G	A	CSB1	NM_181807.2	p.Q15*	
ELP4	11	31610340	31610340	Missense	SNP	A	G	BRC8	NM_019040.3	p.K247E	
WT1	11	32394663	32394663	Splice_Site	SNP	C	G	CSB24	NM_024426.3	e5-1	
TCP11L1	11	33035358	33035358	Splice_Site	SNP	G	A	BRC47	NM_018393.1	e3+1	
CAPRN1	11	34067526	34067526	Missense	SNP	G	C	CSB1	NM_005898.4	p.E414Q	
SLC1A2	11	35259055	35259055	Silent	SNP	G	C	CSB1	NM_004171.3	p.L452	
RAG1	11	36552994	36552994	Missense	SNP	T	A	CSB22	NM_000448.2	p.W522R	
ACCS	11	44056034	44056034	Missense	SNP	G	A	BRC13	NM_032592.1	p.E240K	
ACCS	11	44056049	44056049	Splice_Site	SNP	G	T	BRC29	NM_032592.1	e7+1	
ALX4	11	44253635	44253635	Missense	SNP	C	T	BRC3	NM_021926.2	p.D206N	
CHRM4	11	46363259	46363259	Silent	SNP	G	A	BRC41	NM_000741.2	p.I475	
MYBPC3	11	47327911	47327911	Missense	SNP	C	T	CSB15	NM_000256.3	p.R215H	
CUGBP1	11	47460824	47460824	Missense	SNP	G	A	CSB8	NM_001025596.1	p.A229V	
LOC120824	11	48953777	48953777	Missense	SNP	G	C	BRC26	XM_062300.1	p.P403R	

OR4C46	11	51371900	51371900	Missense	SNP	C	G	BRC24	NM_001004703.1	p.L15V
ENSG00000181943	11	55015876	55015876	Silent	SNP	C	T	BRC39	ENST00000314657	p.V194
OR4C15	11	55079295	55079295	Missense	SNP	C	G	BRC21	NM_001001920.1	p.R313G
SPRYD5	11	55415305	55415305	Missense	SNP	G	T	BRC37	NM_032681.3	p.C168F
OR5I1	11	55459862	55459865	Del	DEL	ATTA	0	BRC44	NM_006637.1	p.I196fs
OR7E5P	11	55503838	55503838	Silent	SNP	C	T	BRC44	ENST00000399170	p.L65
OR5F1	11	55518216	55518216	Silent	SNP	C	T	BRC39	NM_003697.1	p.L154
OR8I2	11	55617390	55617390	Missense	SNP	G	A	BRC16	NM_001003750.1	p.V11I
OR8H2	11	55629521	55629521	Missense	SNP	G	A	BRC7	NM_001005200.1	p.A143T
OR8J3	11	55661114	55661114	Silent	SNP	G	A	CSB1	NM_001004064.1	p.F219
OR5R1	11	55941805	55941805	Silent	SNP	G	A	BRC12	NM_001004744.1	p.T160
TNKS1BP1	11	56826514	56826514	Missense	SNP	T	G	BRC15	NM_033396.2	p.I1560L
SLC43A3	11	56939136	56939136	Missense	SNP	C	G	CSB1	NM_014096.2	p.Q263H
OR5B2	11	57946504	57946504	Missense	SNP	G	T	CSB22	NM_001005566.1	p.D269E
ENSG00000204989	11	59016177	59016177	Missense	SNP	G	T	CSB21	ENST00000378245	p.Q124H
PATL1	11	59180639	59180639	Missense	SNP	G	A	BRC35	NM_152716.2	p.P68L
VWCE	11	60789076	60789076	Silent	SNP	G	A	CSB1	NM_152718.2	p.Y689
SYT7	11	61042759	61042759	Silent	SNP	G	A	BRC26	NM_004200.2	p.S376
SYT7	11	61080243	61080243	Missense	SNP	C	T	BRC44	NM_004200.2	p.R15H
DAGLA	11	61244257	61244257	Silent	SNP	C	T	BRC5	NM_006133.1	p.L18
ENSG00000200898	11	61462019	61462019	RNA	SNP	A	C	BRC17	ENST00000364028	NULL
INCENP	11	61654580	61654580	Silent	SNP	G	A	CSB1	NM_001040694.1	p.A335
AHNAK	11	62043662	62043662	Missense	SNP	G	T	BRC16	NM_001620.1	p.P4935T
AHNAK	11	62048414	62048414	Missense	SNP	G	A	CSB1	NM_001620.1	p.R3351C
AHNAK	11	62050577	62050577	Missense	SNP	G	C	CSB1	NM_001620.1	p.Q2630E
INTS5	11	62171900	62171900	Missense	SNP	C	T	BRC50	NM_030628.1	p.G743E
INTS5	11	62172303	62172303	Missense	SNP	C	G	BRC50	NM_030628.1	p.D609H
INTS5	11	62177220	62177220	Silent	SNP	G	A	BRC31	NM_030628.1	p.L26
C11orf48	11	62187302	62187302	Missense	SNP	C	G	BRC31	NM_024099.3	p.R248T
SLC22A10	11	62828250	62828250	Missense	SNP	C	G	BRC18	NM_001039752.3	p.I460M
FLRT1	11	63640684	63640684	Silent	SNP	C	T	BRC7	NM_013280.4	p.I123
NUDT22	11	63750902	63750902	Missense	SNP	C	G	BRC39	NM_032344.1	p.L68V
SLC22A12	11	64115780	64115780	Missense	SNP	C	T	CSB1	NM_144585.2	p.A59V

C11orf85	11	64464659	64464659	Missense	SNP	C	T		BRC31	NM_001037225.1	p.R170K
SAC3D1	11	64568690	64568690	Missense	SNP	G	A		BRC41	NM_013299.3	p.S331N
NCRNA00084	11	64962411	64962414	RNA	DEL	TATT		0	BRC44	NR_002802.1	NULL
MALAT1	11	65024869	65024872	RNA	DEL	TTTA		0	BRC31	NR_002819.2	NULL
MALAT1	11	65024891	65024893	RNA	DEL	GGG		0	BRC4	NR_002819.2	NULL
MALAT1	11	65025671	65025673	RNA	DEL	AGA		0	BRC5	NR_002819.2	NULL
MALAT1	11	65026021	65026021	RNA	SNP	A	C		BRC51	NR_002819.2	NULL
LTBP3	11	65076065	65076065	Missense	SNP	C	G		BRC47	NM_021070.1	p.E495D
PCNXL3	11	65159415	65159415	Missense	SNP	C	T		BRC19	NM_032223.2	p.R1702C
						GCGGCG					
						CA					
						TGCAGC					
						AG					p.LERLLHAP
						CCGCTC					66in Frame
FIBP	11	65412045	65412068	In Frame Del	DEL	GA		0	CSB28	NM_198897.4	del
SF3B2	11	65583861	65583861	Silent	SNP	C	T		BRC37	NM_006842.2	p.H478
SLC29A2	11	65891855	65891855	Silent	SNP	G	T		BRC13	NM_001532.2	p.L204
RBM14	11	66149377	66149377	Missense	SNP	C	T		BRC29	NM_006328.3	p.S485F
PC	11	66373006	66373006	Silent	SNP	C	T		CSB21	NM_000920.3	p.K1159
LRFN4	11	66381948	66381948	Silent	SNP	C	T		CSB31	NM_024036.4	p.L53
LRFN4	11	66382262	66382262	Silent	SNP	C	T		CSB31	NM_024036.4	p.L157
LRFN4	11	66383712	66383712	Silent	SNP	C	T		CSB31	NM_024036.4	p.L460
SSH3	11	66828902	66828902	Missense	SNP	G	C		BRC39	NM_017857.2	p.E63Q
				Nonstop							
SSH3	11	66835933	66835933	Mutation	SNP	G	C		BRC31	NM_017857.2	p.*660S
RAD9A	11	66919782	66919782	Silent	SNP	C	T		CSB1	NM_004584.2	p.L157
RAD9A	11	66920319	66920319	Silent	SNP	C	T		CSB1	NM_004584.2	p.I248
C11orf72	11	67128782	67128782	Missense	SNP	A	C		CSB2	ENST00000333139	p.I112R
FADD	11	69730112	69730112	Missense	SNP	A	T		CSB26	NM_003824.3	p.N171I
SHANK2	11	70011077	70011077	Nonsense	SNP	G	C		CSB1	NM_012309.1	p.S395*
SHANK2	11	70014128	70014128	Missense	SNP	G	A		CSB22	NM_012309.1	p.R223C
SHANK2	11	70507681	70507681	Nonsense	SNP	G	A		BRC39	ENST00000338508	p.Q85*
INPPL1	11	71625968	71625968	Missense	SNP	C	T		CSB1	NM_001567.3	p.S1011F
ARAP1	11	72084492	72084492	Silent	SNP	C	T		CSB16	NM_001040118.2	p.T1113
RELT	11	72783369	72783369	Missense	SNP	C	T		BRC39	NM_032871.3	p.P330S
				Frame Shift							
XRRA1	11	74316096	74316097	Del	DEL	AA		0	CSB19	NM_182969.1	p.F162fs
PRKRIR	11	75740620	75740620	Missense	SNP	G	C		CSB1	NM_004705.2	p.L408V

C11orf30	11	75840639	75840639	Missense	SNP	A	G	CSB7	NM_020193.3	p.K54E
ACER3	11	76347670	76347670	Splice_Site	SNP	G	A	BRC44	NM_018367.5	e3-1
MYO7A	11	76546996	76546996	Missense	SNP	G	A	BRC18	NM_000260.3	p.R292Q
KCTD21	11	77562864	77562864	Missense	SNP	C	T	CSB1	NM_001029859.1	p.E129K
GAB2	11	77610397	77610397	Missense	SNP	C	G	BRC44	NM_080491.2	p.D579H
ODZ4	11	78058842	78058842	Nonsense	SNP	G	A	BRC47	NM_001098816.2	p.R1404*
ODZ4	11	78292128	78292128	Silent	SNP	C	T	BRC8	ENST00000278550	p.A194
PRCP	11	82227202	82227202	Missense	SNP	G	C	CSB1	NM_199418.2	p.H404Q
DLG2	11	84543283	84543283	Missense	SNP	G	C	BRC39	ENST00000376104	p.Q83E
SYTL2	11	85113138	85113138	Missense	SNP	T	G	CSB16	NM_206927.3	p.K670N
CCDC83	11	85301348	85301358	Frame Shift Del	DEL	TGCTACA TTCC		0 BRC41	NM_173556.3	p.L269fs
PRSS23	11	86196541	86196541	Missense	SNP	C	G	BRC44	NM_007173.4	p.H70D
TMEM135	11	86460290	86460290	Missense	SNP	T	C	CSB3	NM_022918.2	p.I116T
TYR	11	88551015	88551015	Silent	SNP	C	T	BRC36	NM_000372.4	p.S82
FAT3	11	91725470	91725470	Missense	SNP	G	T	BRC44	NM_001008781.2	p.A182S
KIAA1731	11	93102306	93102306	Missense	SNP	C	T	BRC39	ENST00000344196	p.S634L
MRE11A	11	93802760	93802760	Missense	SNP	G	C	CSB1	NM_005591.3	p.Q679E
ENSG0000020114 9	11	94896900	94896900	RNA	SNP	G	A	BRC20	ENST00000364279	NULL
CCDC82	11	95756837	95756837	Missense Nonstop	SNP	C	G	BRC50	NM_024725.3	p.Q241H
YAP1	11	101605881	101605881	Mutation	SNP	G	C	CSB1	NM_006106.1	p.*455Y
MMP20	11	101992936	101992936	Missense	SNP	C	T	BRC50	NM_004771.3	p.G64E
MMP10	11	102148852	102148852	Missense	SNP	C	T	BRC47	NM_002425.1	p.D388N
DYNC2H1	11	102490090	102490090	Missense	SNP	A	T	BRC20	NM_001080463.1	p.S139C
DYNC2H1	11	102490166	102490166	Missense	SNP	A	G	BRC30	NM_001080463.1	p.D164G
DYNC2H1	11	102560955	102560955	Missense	SNP	C	G	BRC30	NM_001080463.1	p.L2200V
CASP1	11	104410366	104410366	Missense	SNP	C	G	CSB1	NM_033292.3	p.G18A
GRIA4	11	105128987	105128987	Missense	SNP	G	C	CSB1	NM_000829.3	p.L106F
GRIA4	11	105300447	105300447	Missense	SNP	A	T	BRC7	NM_000829.3	p.Q530L
KIAA1826	11	105385516	105385516	Missense	SNP	C	G	BRC13	NM_032424.1	p.E332Q
CUL5	11	107454155	107454155	Missense	SNP	G	C	BRC11	NM_003478.3	p.E386Q
ENSG0000020016 8	11	110416119	110416119	RNA	SNP	G	A	BRC44	ENST00000363298	NULL
C11orf53	11	110661915	110661915	Missense	SNP	C	T	CSB7	NM_198498.1	p.H213Y
TTC12	11	112699930	112699930	Missense	SNP	C	A	BRC41	NM_017868.3	p.A76E

USP28	11	113180909	113180909	Nonsense	SNP	G	A	BRC18	NM_020886.2	p.R824*
HTR3B	11	113308944	113308944	Silent	SNP	T	C	BRC21	NM_006028.3	p.S205
SIDT2	11	116569110	116569110	Missense	SNP	G	A	BRC18	NM_001040455.1	p.D713N
CEP164	11	116786792	116786792	Nonsense	SNP	G	T	BRC8	NM_014956.4	p.E1379*
DSCAML1	11	116879942	116879942	Silent	SNP	G	A	BRC30	NM_020693.2	p.S789
TMPRSS4	11	117487746	117487746	Missense	SNP	A	G	BRC47	NM_019894.1	p.I222V
UBE4A	11	117751124	117751124	Nonsense	SNP	G	T	CSB8	NM_004788.2	p.E481*
MLL	11	117881697	117881697	Missense	SNP	T	C	CSB34	NM_005933.2	p.S3291P
PHLDB1	11	118004149	118004149	Missense	SNP	G	A	BRC20	NM_015157.1	p.R467Q
HYOU1	11	118423921	118423921	Missense	SNP	C	T	CSB1	NM_006389.1	p.E820K
DPAGT1	11	118474397	118474397	Silent	SNP	C	T	CSB24	NM_001382.3	p.R218
CBL	11	118653723	118653723	Missense	SNP	T	G	BRC7	NM_005188.2	p.L352V
PVRL1	11	119014083	119014083	Missense	SNP	G	T	CSB6	NM_203285.4	p.L438M
LOC729173	11	119545045	119545045	Missense	SNP	G	A	BRC32	XM_001129552.2	p.D28N
POU2F3	11	119622394	119622394	Missense	SNP	G	A	BRC39	NM_014352.2	p.D19N
TECTA	11	120489057	120489057	Missense	SNP	G	A	BRC9	NM_005422.2	p.E185K
HSPA8	11	122436176	122436176	Missense	SNP	T	C	CSB23	NM_006597.3	p.N141S
OR10G8	11	123406199	123406199	Silent	SNP	C	T	BRC13	NM_001004464.1	p.I220
OR8G2	11	123601404	123601404	Missense	SNP	G	C	CSB1	NM_001007249.1	p.G266A
SIAE	11	124014971	124014971	Missense	SNP	T	A	BRC51	NM_170601.3	p.L323F
ROBO3	11	124253748	124253748	Missense	SNP	A	G	BRC32	NM_022370.2	p.S1127G
ROBO4	11	124261843	124261843	Missense	SNP	C	A	BRC39	NM_019055.5	p.D841Y
HEPACAM	11	124297507	124297507	Missense	SNP	A	T	CSB2	NM_152722.4	p.I312N
KIRREL3	11	125820155	125820155	Missense	SNP	C	A	BRC51	NM_032531.2	p.G394V
KIRREL3	11	125838410	125838410	Silent	SNP	G	A	CSB31	NM_032531.2	p.T198
KCNJ5	11	128291753	128291753	Missense	SNP	G	C	BRC31	NM_000890.3	p.G393R
LOC100131487	11	128312226	128312226	Missense	SNP	A	G	BRC49	XM_001726592.1	p.M10V
LOC399978	11	130221984	130221984	RNA	SNP	C	A	BRC39	XR_041554.1	NULL
LOC646522	11	133159485	133159485	RNA	SNP	A	G	BRC40	XR_040074.1	NULL
LOC646522	11	133185512	133185512	RNA	SNP	C	T	BRC24	XR_040074.1	NULL
NCAPD3	11	133532202	133532202	Splice_Site	SNP	T	C	BRC44	NM_015261.2	e32-2
GLB1L3	11	133689442	133689442	Missense	SNP	C	G	BRC39	NM_001080407.2	p.S600C
ADIPOR2	12	1765374	1765374	Missense	SNP	C	T	BRC5	NM_024551.2	p.H346Y
DCP1B	12	1945052	1945052	Missense	SNP	T	C	BRC47	NM_152640.3	p.N152S
FGF23	12	4350048	4350048	Missense	SNP	G	A	CSB9	NM_020638.2	p.R160W

FGF6	12	4424816	4424816	Missense	SNP	G	C	BRC7	NM_020996.1	p.S61C	
KCNA1	12	4891482	4891482	Missense	SNP	C	T	CSB13	NM_000217.2	p.T226M	
NTF3	12	5474132	5474132	Missense	SNP	C	T	BRC24	NM_001102654.1	p.S177L	
ANO2	12	5578918	5578918	Missense	SNP	C	T	BRC51	NM_020373.2	p.M743I	
NCAPD2	12	6507214	6507214	Missense	SNP	C	G	BRC39	NM_014865.3	p.S973C	
CHD4	12	6567358	6567358	Missense	SNP	G	A	BRC32	NM_001273.2	p.R1162W	
CHD4	12	6567743	6567743	Missense	SNP	G	T	CSB1	NM_001273.2	p.N1149K	
CD4	12	6795510	6795510	Missense	SNP	A	G	CSB30	NM_000616.3	p.Y212C	
PHB2	12	6947853	6947853	Silent	SNP	C	T	BRC39	NM_007273.1	p.L153	
CD163L1	12	7417227	7417227	Missense	SNP	C	T	BRC52	NM_174941.4	p.R1229Q	
SLC2A14	12	7872580	7872580	Missense	SNP	C	G	BRC50	NM_153449.2	p.E244D	
ZNF705A	12	8221060	8221060	Missense	SNP	C	A	CSB1	NM_001004328.2	p.Q173K	
M6PR	12	8986307	8986307	Missense	SNP	A	T	BRC24	NM_002355.2	p.F228Y	
C12orf33	12	9101523	9101523	RNA	SNP	C	T	BRC7	XR_041988.1	NULL	
A2M	12	9116519	9116519	Silent	SNP	G	C	CSB1	NM_000014.4	p.L1324	
CLEC7A	12	10173939	10173939	Missense	SNP	G	A	BRC39	NM_197947.4	p.H4Y	
KLRC2	12	10479670	10479670	Nonsense	SNP	G	T	BRC31	NM_002260.3	p.C61*	
CSDA	12	10753880	10753880	Missense	SNP	C	A	CSB2	NM_003651.1	p.R225L	
TAS2R8	12	10849947	10849947	Silent	SNP	C	T	BRC50	NM_023918.1	p.L300	
TAS2R14	12	10983040	10983040	Missense	SNP	C	G	CSB16	NM_023922.1	p.V12L	
PRB1	12	11397916	11397916	Nonsense	SNP	G	A	CSB7	ENST00000381832	p.Q253*	
DUSP16	12	12521828	12521828	Missense	SNP	G	C	BRC44	NM_030640.1	p.L402V	
CDKN1B	12	12762252	12762252	Ins	INS		0	G	BRC20	NM_004064.3	p.K73fs
CDKN1B	12	12763037	12763037	Nonsense	SNP	C	T	BRC18	NM_004064.3	p.Q163*	
DDX47	12	12865928	12865928	Splice_Site	SNP	G	A	CSB24	NM_016355.3	e4+1	
GPRC5A	12	12952642	12952642	Missense	SNP	G	A	CSB15	NM_003979.3	p.M64I	
WBP11	12	14835428	14835428	Missense	SNP	C	A	BRC31	NM_016312.2	p.K319N	
						AGTTGCA					
						T					
				Frame Shift		TTAGGTT					
LOC729025	12	16302041	16302056	Del	DEL			0	CSB25	XM_001129090.1	p.M200fs
PIK3C2G	12	18638746	18638746	Missense	SNP	G	C	CSB1	ENST00000266497	p.E1314Q	
PLCZ1	12	18739278	18739278	Missense	SNP	C	T	BRC16	NM_033123.2	p.A432T	
PDE3A	12	20691080	20691080	Missense	SNP	G	T	CSB2	NM_000921.3	p.A832S	
GYS2	12	21602509	21602509	Silent	SNP	C	T	BRC20	NM_021957.3	p.Q438	

GYS2	12	21603857	21603857	Missense	SNP	T	A	CSB16	NM_021957.3	p.L408F
ABCC9	12	21908676	21908676	Missense	SNP	A	G	CSB1	NM_005691.2	p.V734A
ABCC9	12	21970173	21970173	Missense	SNP	C	T	BRC47	NM_005691.2	p.E126K
CASC1	12	25239236	25239236	Missense	SNP	T	C	BRC15	NM_001082972.1	p.T10A
KRAS	12	25289551	25289551	Missense	SNP	C	T	CSB1	NM_033360.3	p.G12D
SSPN	12	26274973	26274973	Silent	SNP	C	T	CSB2	NM_005086.1	p.A143
TMTC1	12	29561698	29561698	Missense	SNP	C	T	CSB1	NM_175861.2	p.E592K
TMTC1	12	29580469	29580469	Missense	SNP	G	C	BRC52	NM_175861.2	p.I467M
TMTC1	12	29601123	29601123	Missense	SNP	T	C	CSB28	NM_175861.2	p.Y429C
C12orf35	12	32029657	32029657	Missense	SNP	G	A	CSB9	NM_018169.2	p.G1501S
DNM1L	12	32764902	32764902	Missense	SNP	G	A	CSB1	NM_012062.3	p.D260N
LRRK2	12	38973667	38973667	Missense	SNP	G	A	CSB1	NM_198578.3	p.E915K
LRRK2	12	38989280	38989280	Missense	SNP	A	G	CSB19	NM_198578.3	p.K1432R
PDZRN4	12	40252517	40252517	Missense	SNP	C	T	BRC48	NM_013377.3	p.R299C
ZCRB1	12	40993986	40993986	Missense	SNP	C	G	CSB1	NM_033114.3	p.E135Q
PRICKLE1	12	41144790	41144790	Missense	SNP	C	T	CSB19	NM_153026.1	p.R438Q
ADAMTS20	12	42119987	42119987	Missense Frame Shift	SNP	C	T	BRC13	NM_025003.3	p.E815K
ARID2	12	44530397	44530398	Del	DEL	TC		0 BRC15	NM_152641.2	p.S742fs
AMIGO2	12	45758946	45758946	Missense	SNP	C	T	CSB7	NM_181847.1	p.G36D
COL2A1	12	46660629	46660629	Missense	SNP	C	A	BRC38	NM_001844.4	p.G867V
COL2A1	12	46661874	46661874	Silent	SNP	C	T	CSB1	NM_001844.4	p.L787
PFKM	12	46825644	46825644	Silent	SNP	G	A	BRC40	NM_000289.4	p.L743
H1FNT	12	47009605	47009605	Silent	SNP	C	T	CSB22	NM_181788.1	p.Y88
C12orf54	12	47170884	47170884	Missense Frame Shift	SNP	G	A	CSB1	NM_152319.2	p.R64Q
MLL2	12	47711616	47711616	Del	DEL	G		0 BRC32	NM_003482.3	p.P4380fs
MLL2	12	47713099	47713099	Nonsense	SNP	G	A	CSB7	NM_003482.3	p.Q3886*
MLL2	12	47733011	47733011	Nonsense	SNP	G	A	BRC19	NM_003482.3	p.Q356*
ENSG0000020258 2	12	48557808	48557808	Missense	SNP	G	A	BRC4	ENST00000365712	p.H387Y
LARP4	12	49110619	49110619	Nonsense	SNP	C	T	BRC15	NM_199188.3	p.R139*
DIP2B	12	49320891	49320891	Missense	SNP	G	A	CSB29	NM_173602.2	p.R97Q
DIP2B	12	49411439	49411439	Missense	SNP	C	G	BRC40	NM_173602.2	p.S1221C
LETMD1	12	49728417	49728417	Missense	SNP	C	G	CSB1	NM_015416.1	p.S4C
LETMD1	12	49732243	49732243	Missense	SNP	G	A	CSB31	NM_015416.1	p.E126K

SLC4A8	12	50169989	50169989	Missense	SNP	C	T	BRC44	NM_001039960.1	p.T896M
C12orf44	12	50753789	50753789	Silent	SNP	C	T	CSB1	NM_001098673.1	p.L30
KRT79	12	51514065	51514065	Missense	SNP	G	A	CSB10	NM_175834.2	p.R83W
TENC1	12	51740935	51740944	Frame Shift Del	DEL	GGGGCC ACTC		0 CSB3	NM_015319.2	p.G1003fs
CSAD	12	51852437	51852437	Missense	SNP	G	C	BRC39	NM_015989.4	p.L102V
MFSD5	12	51933814	51933814	Nonsense Frame Shift	SNP	C	T	BRC39	NM_032889.3	p.Q310*
PCBP2	12	52148868	52148869	Del Frame Shift	DEL	CA		0 BRC52	NM_005016.2	p.T294fs
MAP3K12	12	52167053	52167054	Del	DEL	AG		0 BRC38	NM_006301.2	p.P97fs
HOXC10	12	52669329	52669329	Missense	SNP	T	A	CSB1	NM_017409.3	p.F287L
HOXC5	12	52697090	52697090	RNA	SNP	G	C	BRC41	NR_003084.2	NULL
LOC644222	12	52843019	52843019	Missense	SNP	G	C	BRC39	XM_932052.1	p.E5Q
CBX5	12	52926248	52926248	Missense	SNP	G	A	BRC31	NM_012117.1	p.R115W
PDE1B	12	53255265	53255265	Missense	SNP	G	C	CSB22	NM_000924.2	p.R394P
KIAA0748	12	53642797	53642797	Silent	SNP	C	T	CSB10	NM_001098815.1	p.S384
PHC1B	12	54094358	54094358	Nonsense	SNP	G	A	CSB15	ENST00000326184	p.Q144*
SLC39A5	12	54915617	54915617	Missense	SNP	G	A	BRC50	NM_173596.1	p.E270K
COQ10A	12	54949534	54949534	Silent	SNP	C	G	BRC41	NM_144576.1	p.L166
STAT2	12	55036219	55036219	Silent	SNP	C	T	BRC50	NM_005419.2	p.L83
LRP1	12	55856065	55856065	Missense	SNP	C	G	BRC39	NM_002332.2	p.I1300M
LRP1	12	55884741	55884741	Silent	SNP	C	T	BRC50	NM_002332.2	p.I3712
R3HDM2	12	55963942	55963942	Missense	SNP	G	C	CSB1	NM_014925.3	p.S15C
R3HDM2	12	55978219	55978219	Splice_Site	SNP	C	G	BRC18	ENST00000403821	e5-1
INHBE	12	56135863	56135863	Missense	SNP	A	T	BRC14	NM_031479.3	p.I93F
ARHGAP9	12	56157634	56157634	Missense	SNP	G	T	CSB22	NM_032496.1	p.P211T
OS9	12	56400181	56400181	Missense	SNP	G	A	BRC51	NM_006812.1	p.V545I
MON2	12	61181707	61181707	Missense	SNP	G	C	BRC50	NM_015026.2	p.E251Q
MON2	12	61240912	61240912	Missense	SNP	G	C	BRC39	NM_015026.2	p.D1262H
DPY19L2	12	62240636	62240636	Missense	SNP	C	T	CSB33	NM_173812.4	p.V734I
TBK1	12	63146963	63146963	Missense	SNP	A	G	CSB23	NM_013254.2	p.H125R
TBK1	12	63181396	63181396	Missense	SNP	G	T	CSB15	NM_013254.2	p.D720Y
KIAA0984	12	63516598	63516598	Missense	SNP	C	T	BRC40	XM_037557.1	p.A382V
WIF1	12	63748879	63748879	Missense	SNP	A	G	BRC8	NM_007191.3	p.M157T
MSRB3	12	64049047	64049047	Missense	SNP	C	T	BRC39	NM_198080.1	p.S96L

HMGA2	12	64595174	64595174	Silent	SNP	C	T	CSB1	NM_003484.4	p.H106
IRAK3	12	64925266	64925266	Missense	SNP	G	A	BRC31	NM_007199.1	p.R424Q
DYRK2	12	66337629	66337629	Silent	SNP	C	G	BRC39	NM_006482.3	p.L225
ENSG00000206650	12	67307332	67307332	RNA	SNP	G	A	BRC39	ENST00000383923	NULL
NAV3	12	76884180	76884180	Missense	SNP	G	C	CSB1	NM_014903.4	p.R152T
PPP1R12A	12	78723581	78723581	Missense	SNP	G	C	BRC32	NM_002480.1	p.A641G
PPP1R12A	12	78726489	78726489	Splice_Site	INS		T	CSB22	NM_002480.1	e11-1
PPP1R12A	12	78750381	78750381	Missense	SNP	C	T	BRC13	NM_002480.1	p.R170Q
ACSS3	12	80061105	80061105	Nonsense	SNP	C	G	CSB1	NM_024560.2	p.S290*
SLC6A15	12	83791129	83791129	Missense	SNP	C	G	BRC41	NM_182767.5	p.R326T
LRRIQ1	12	83973765	83973765	Nonsense Frame Shift	SNP	G	T	CSB2	NM_001079910.1	p.E355*
GALNT4	12	88442277	88442277	Del	DEL	G		CSB33	NM_003774.3	p.R61fs
ATP2B1	12	88542195	88542195	Nonsense	SNP	G	A	BRC38	NM_001682.1	p.Q414*
LOC643153	12	88628064	88628064	Silent	SNP	C	T	BRC50	XM_931367.1	p.A5
C12orf63	12	95609088	95609088	Missense	SNP	C	A	CSB1	NM_198520.2	p.Q470K
LOC121456	12	97373685	97373685	RNA	SNP	C	T	BRC7	XR_016411.1	NULL
APAF1	12	97566680	97566680	Missense	SNP	C	G	BRC39	NM_181861.2	p.S95C
ANKS1B	12	98724371	98724371	Missense	SNP	T	C	BRC3	NM_152788.2	p.N204S
UHRF1BP1L	12	98976764	98976764	Missense	SNP	G	C	CSB7	NM_015054.1	p.L808V
GAS2L3	12	99541525	99541525	Missense	SNP	C	A	BRC39	NM_174942.1	p.Q271K
UTP20	12	100208661	100208661	Missense	SNP	G	A	BRC13	NM_014503.2	p.R252Q
UTP20	12	100274943	100274943	Silent	SNP	C	G	BRC39	NM_014503.2	p.L1881
GNPTAB	12	100679106	100679106	Missense	SNP	G	T	BRC28	NM_024312.3	p.S1022Y
IGF1	12	101337437	101337437	Missense	SNP	C	T	CSB16	NM_000618.3	p.D128N
STAB2	12	102655583	102655583	Silent	SNP	G	A	BRC51	NM_017564.9	p.Q1864
NT5DC3	12	102732916	102732916	Missense	SNP	C	T	BRC29	NM_001031701.2	p.V108M
ENSG00000214198	12	102833546	102833546	Missense	SNP	G	C	BRC41	ENST00000388789	p.P77R
TXNRD1	12	103229281	103229281	Silent	SNP	C	T	BRC41	ENST00000354940	p.I16
TXNRD1	12	103236856	103236856	Nonsense	SNP	C	T	CSB24	ENST00000354940	p.Q106*
SLC41A2	12	103827630	103827630	Nonsense	SNP	A	C	BRC16	NM_032148.3	p.L116*
NUAK1	12	105004681	105004681	Silent	SNP	G	A	BRC39	NM_014840.2	p.F158
LOC341378	12	105090077	105090077	Nonsense	SNP	C	A	BRC33	XM_001715424.1	p.S264*
RFX4	12	105633435	105633435	Missense	SNP	G	T	BRC41	NM_213594.3	p.R374L

CRY1	12	105917540	105917540	Nonsense	SNP	C	T	CSB22	NM_004075.3	p.W352*
CORO1C	12	107619135	107619135	Missense	SNP	G	C	BRC7	NM_014325.2	p.S30C
DAO	12	107817315	107817315	Missense	SNP	C	T	BRC31	NM_001917.4	p.R283W
ACACB	12	108128972	108128972	Silent	SNP	C	T	BRC13	NM_001093.3	p.F996
ACACB	12	108182762	108182762	Silent	SNP	G	A	CSB1	NM_001093.3	p.A2197
GIT2	12	108883513	108883513	Missense	SNP	C	T	BRC30	NM_057169.1	p.V314I
ANKRD13A	12	108959592	108959592	Silent	SNP	C	T	CSB15	NM_033121.1	p.P541
ANAPC7	12	109305095	109305095	Missense	SNP	C	T	CSB1	NM_016238.1	p.E291K
MYL2	12	109835500	109835500	Missense	SNP	C	T	CSB1	NM_000432.3	p.E96K
PTPN11	12	111372593	111372593	Missense	SNP	G	A	BRC50	NM_002834.3	p.E76K
TBX3	12	113596584	113596584	Silent	SNP	G	A	BRC7	NM_016569.3	p.F513 p.N212in
TBX3	12	113603087	113603089	In Frame Del Frame Shift	DEL	TGT		0 BRC24	NM_016569.3	Frame del
TBX3	12	113603113	113603113	Del Frame Shift	DEL	A		0 CSB30	NM_016569.3	p.F204fs
TBX3	12	113605185	113605185	Ins	INS		0 A	CSB34	NM_016569.3	p.V68fs
MED13L	12	114928073	114928073	Missense	SNP	T	A	CSB19	NM_015335.3	p.D818V
MED13L	12	114931040	114931040	Missense	SNP	T	A	BRC44	NM_015335.3	p.S521C
RFC5	12	116947079	116947079	Missense	SNP	C	G	BRC11	NM_007370.1	p.I154M
LOC100128895	12	116962573	116962573	Nonsense	SNP	C	T	BRC44	XM_001723671.1	p.Q47*
TAOK3	12	117094815	117094815	Missense Nonstop	SNP	C	T	CSB1	NM_016281.3	p.E577K
HSPB8	12	118116045	118116045	Mutation	SNP	G	C	CSB1	NM_014365.2	p.*197S
CCDC60	12	118427440	118427440	Missense	SNP	G	A	BRC31	NM_178499.3	p.E278K
GATC	12	119379319	119379319	Silent	SNP	A	G	BRC16	NM_176818.1	p.L104
HPD	12	120778895	120778895	Missense	SNP	G	A	BRC13	NM_002150.2	p.S73L
LRRC43	12	121253933	121253933	Missense	SNP	C	A	CSB14	NM_001098519.1	p.F654L
KNTC1	12	121638247	121638247	Missense	SNP	C	T	CSB1	NM_014708.4	p.S1256F
KNTC1	12	121664200	121664200	Missense	SNP	G	T	CSB2	NM_014708.4	p.C1939F
GPR81	12	121780333	121780333	Silent	SNP	G	A	BRC11	NM_032554.3	p.I169
DNAH10	12	122916539	122916539	Missense	SNP	A	G	CSB19	ENST00000409039	p.Y2260C
TMEM132B	12	124400421	124400421	Missense	SNP	C	T	BRC36	NM_052907.2	p.R175W
TMEM132D	12	128125372	128125372	Silent	SNP	G	A	BRC39	NM_133448.2	p.V767
PIWIL1	12	129406054	129406054	Silent	SNP	C	T	BRC10	NM_004764.3	p.N431
PIWIL1	12	129413557	129413557	Missense	SNP	G	T	BRC16	NM_004764.3	p.V704L
RIMBP2	12	129487351	129487351	Missense	SNP	C	T	BRC39	NM_015347.4	p.E682K

GPR133	12	130064736	130064736	Silent	SNP	C	T	BRC22	NM_198827.3	p.F457
GPR133	12	130156313	130156313	Missense	SNP	C	A	BRC5	NM_198827.3	p.L613M
PUS1	12	130992448	130992448	Silent	SNP	C	T	BRC31	NM_025215.1	p.A401
NOC4L	12	131199392	131199392	Silent	SNP	C	T	CSB1	NM_024078.1	p.L300
POLE	12	131719371	131719371	Frame Shift Del	DEL	C		0 BRC17	NM_006231.2	p.A2030fs
POLE	12	131724707	131724707	Missense	SNP	C	G	CSB1	NM_006231.2	p.D1882H
GOLGA3	12	131882652	131882652	Silent	SNP	G	A	CSB27	NM_005895.3	p.I776
GOLGA3	12	131888527	131888527	Nonsense	SNP	C	A	CSB10	NM_005895.3	p.E567*
ZNF140	12	132192590	132192590	Missense	SNP	G	C	BRC42	NM_003440.2	p.E218D
MPHOSPH8	13	19138645	19138645	Missense	SNP	G	C	BRC39	NM_017520.2	p.Q700H
C13orf3	13	20640454	20640454	Missense	SNP	G	C	CSB5	NM_145061.4	p.S139C
SGCG	13	22792834	22792834	Missense	SNP	G	A	BRC9	NM_000231.2	p.A213T
PCOTH	13	23364043	23364043	Silent	SNP	G	A	CSB8	NM_001014442.2	p.T99
SPATA13	13	23766929	23766929	Missense	SNP	C	G	BRC18	NM_153023.1	p.L420V
ATP12A	13	24161466	24161466	Missense	SNP	G	C	CSB28	NM_001676.4	p.A167P
CENPJ	13	24378378	24378378	Missense	SNP	T	A	CSB25	NM_018451.3	p.I600F
CENPJ	13	24385012	24385012	Missense	SNP	G	C	CSB1	NM_018451.3	p.S51C
MTMR6	13	24725956	24725956	Missense	SNP	G	A	CSB1	NM_004685.3	p.S431L
ATP8A2	13	25015503	25015503	Missense	SNP	T	C	BRC20	NM_016529.4	p.I285T
RNF6	13	25691769	25691769	Silent	SNP	C	A	BRC18	NM_005977.3	p.S6
PAN3	13	27738983	27738983	Missense	SNP	G	A	BRC18	NM_175854.5	p.D315N
FRY	13	31619488	31619488	Nonsense	SNP	C	T	CSB1	NM_023037.2	p.R417*
FRY	13	31716220	31716220	Silent	SNP	C	G	BRC39	NM_023037.2	p.L2243
FRY	13	31739473	31739473	Missense	SNP	C	T	BRC13	NM_023037.2	p.H2705Y
FRY	13	31761860	31761860	Missense	SNP	G	A	BRC39	NM_023037.2	p.E2854K
BRCA2	13	31791245	31791245	Silent	SNP	A	G	BRC39	NM_000059.3	p.E33
BRCA2	13	31809274	31809275	Frame Shift Ins	INS		0 TTTT	CSB2	NM_000059.3	p.L929fs
KL	13	32532897	32532897	Missense	SNP	G	A	BRC39	NM_004795.3	p.D561N
SPG20	13	35807391	35807391	Missense	SNP	C	T	BRC38	NM_015087.1	p.E193K
TRPC4	13	37146390	37146390	Missense	SNP	G	A	BRC21	NM_016179.1	p.S450F
TRPC4	13	37164459	37164459	Missense	SNP	G	C	BRC30	NM_016179.1	p.P304R
FREM2	13	38159912	38159912	Missense	SNP	G	T	BRC39	NM_207361.4	p.R144L
FREM2	13	38161045	38161045	Missense	SNP	G	A	CSB1	NM_207361.4	p.D522N
AKAP11	13	41771561	41771561	Missense	SNP	C	G	BRC16	NM_016248.2	p.H227D

TSC22D1	13	43908640	43908640	Missense	SNP	C	T	BRC31	NM_006022.2	p.S42N
SLC25A30	13	44876501	44876501	Silent	SNP	G	A	CSB24	NM_001010875.2	p.V118
LCP1	13	45614517	45614517	Silent	SNP	C	T	CSB1	NM_002298.4	p.A471
ITM2B	13	47728346	47728346	Nonsense	SNP	C	A	BRC49	NM_021999.4	p.Y93*
RB1	13	47814760	47814760	Nonsense	SNP	G	T	BRC41	NM_000321.2	p.E97*
RB1	13	47853581	47853581	Splice_Site	SNP	G	C	BRC20	NM_000321.2	e17+1
RB1	13	47931858	47931858	Missense	SNP	T	G	BRC47	NM_000321.2	p.L665R
RB1	13	47931965	47931965	Missense	SNP	G	A	BRC51	NM_000321.2	p.D701N
SETDB2	13	48955642	48955642	Missense	SNP	C	T	BRC39	NM_031915.1	p.S487L
TRIM13	13	49485223	49485223	Missense	SNP	C	G	BRC47	NM_001007278.1	p.F385L
WDFY2	13	51199900	51199900	Silent	SNP	C	T	BRC11	NM_052950.3	p.L191
NEK3	13	51605836	51605836	Missense	SNP	C	T	BRC47	ENST00000258597	p.E477K
VPS36	13	51887991	51887991	Missense	SNP	G	C	CSB30	NM_016075.2	p.P379R
PCDH17	13	57106729	57106729	Missense	SNP	C	T	CSB2	NM_001040429.2	p.S683L
DIAPH3	13	59311559	59311559	Missense	SNP	T	A	BRC21	NM_001042517.1	p.N9211
KLHL1	13	69173840	69173840	Missense	SNP	G	A	BRC47	NM_020866.2	p.P748S
COMMD6	13	75009920	75009920	Missense	SNP	G	A	CSB8	NM_203497.2	p.P8L
MYCBP2	13	76549332	76549332	Silent	SNP	C	T	BRC39	NM_015057.3	p.R3854
MYCBP2	13	76613014	76613014	Missense	SNP	C	T	BRC8	NM_015057.3	p.V2419I
MYCBP2	13	76733476	76733476	Missense	SNP	G	C	CSB1	NM_015057.3	p.I523M
EDNRB	13	77390669	77390669	Missense	SNP	G	A	BRC37	NM_000115.2	p.A14V
SLITRK1	13	83352847	83352847	Missense	SNP	C	T	CSB2	NM_052910.1	p.R266Q
MBNL2	13	96784568	96784568	Missense	SNP	C	A	CSB2	NM_144778.2	p.P71H
SLC15A1	13	98156450	98156450	Missense	SNP	C	A	CSB1	NM_005073.3	p.G403V
ENSG0000020179 3	13	98656140	98656140	RNA	SNP	C	G	BRC18	ENST00000364923	NULL
PHGDHL1	13	98694791	98694791	Missense	SNP	G	C	BRC8	ENST00000403766	p.V101L
FGF14	13	101851922	101851922	Silent	SNP	C	A	BRC44	NM_175929.3	p.S36
KDELC1	13	102241696	102241696	Missense	SNP	A	T	BRC30	NM_024089.2	p.I253N
ERCC5	13	102302591	102302591	Missense	SNP	C	A	BRC32	NM_000123.2	p.R71S
ERCC5	13	102325815	102325815	Missense	SNP	T	C	CSB6	NM_000123.2	p.M1041T
LIG4	13	107660261	107660261	Missense	SNP	C	G	CSB27	NM_001098268.1	p.E453Q
COL4A2	13	109875101	109875101	Missense	SNP	G	A	BRC3	NM_001846.2	p.G67D
COL4A2	13	109936036	109936036	Nonsense	SNP	C	G	BRC7	NM_001846.2	p.S1020*
TUBGCP3	13	112250010	112250010	Missense	SNP	G	A	BRC50	NM_006322.4	p.R365W

MCF2L	13	112779373	112779373	Missense	SNP	G	A	BRC9	NM_024979.1	p.V501M
PROZ	13	112860990	112860990	Silent	SNP	C	T	CSB1	NM_003891.1	p.V5
CUL4A	13	112957089	112957089	Missense	SNP	G	A	BRC16	NM_001008895.1	p.E612K
ATP4B	13	113355734	113355734	Silent	SNP	C	T	BRC5	NM_000705.2	p.P86
FLJ39632	14	18960115	18960115	RNA	INS		0 GCGG	BRC32	XR_015133.1	NULL
uc001vwc.2	14	19072291	19072291	Silent	SNP	T	C	CSB22	ENST00000356930	p.Q377
OR4M1	14	19319250	19319250	Missense	SNP	G	A	BRC39	NM_001005500.1	p.C310Y
OR4N2	14	19365723	19365723	Silent	SNP	C	A	CSB21	NM_001004723.1	p.I92
OR4K17	14	19655948	19655948	Silent	SNP	C	A	CSB23	NM_001004715.1	p.L181
OR4K17	14	19656106	19656106	Missense	SNP	G	T	CSB29	NM_001004715.1	p.S234I
KLHL33	14	19967960	19967960	Missense	SNP	G	A	CSB14	XM_001716896.1	p.R525C
OR5AU1	14	20693500	20693500	Silent	SNP	G	A	CSB9	NM_001004731.1	p.A175
SUPT16H	14	20910016	20910017	Frame Shift Del	DEL	CA		0 BRC42	NM_007192.3	p.D63fs
TOX4	14	21026668	21026668	Missense	SNP	C	G	BRC47	NM_014828.2	p.S133C
MYH7	14	22968302	22968302	Silent	SNP	G	A	BRC18	NM_000257.2	p.V411
CPNE6	14	23614323	23614323	Missense	SNP	G	C	CSB1	NM_006032.2	p.E259Q
NRL	14	23620599	23620599	Missense	SNP	C	T	BRC39	NM_006177.3	p.D134N
RNF31	14	23694268	23694268	Silent	SNP	C	T	BRC51	NM_017999.4	p.T731
TM9SF1	14	23731819	23731819	Missense	SNP	T	C	BRC10	NM_006405.1	p.D281G
CIDEB	14	23845096	23845096	Missense	SNP	T	C	BRC33	NM_014430.2	p.N142D
KIAA1305	14	23948443	23948443	Missense	SNP	C	T	BRC17	NM_025081.2	p.P535S
LOC100129469	14	23957384	23957384	Missense	SNP	G	A	BRC36	XM_001720680.1	p.R66Q
GZMH	14	24146302	24146302	Missense	SNP	G	T	CSB12	NM_033423.3	p.L164M
GZMB	14	24173212	24173212	Missense	SNP	C	G	CSB1	ENST00000382542	p.E33Q
NOVA1	14	26011390	26011390	Silent	SNP	G	A	BRC44	NM_002515.2	p.P165
NOVA1	14	26134557	26134557	Frame Shift Ins	INS		0 T	CSB31	NM_002515.2	p.A61fs
PRKD1	14	29116350	29116350	Missense	SNP	G	A	BRC49	NM_002742.2	p.H862Y
SCFD1	14	30239207	30239207	Missense	SNP	C	A	BRC38	NM_016106.2	p.P468T
ARHGAP5	14	31630585	31630585	Missense	SNP	C	T	BRC39	NM_001030055.1	p.S320L
ARHGAP5	14	31630809	31630815	Frame Shift Del	DEL	ATTAATG		0 CSB19	NM_001030055.1	p.N396fs
ARHGAP5	14	31632225	31632225	Nonsense	SNP	C	T	CSB7	NM_001030055.1	p.R867*
NPAS3	14	32594951	32594951	Missense	SNP	A	G	CSB6	ENST00000356141	p.N47S
PSMA6	14	34847912	34847912	Missense	SNP	G	C	BRC31	NM_002791.1	p.K71N

MBIP	14	35853793	35853793	Missense	SNP	C	T	BRC39	NM_016586.1	p.G110E	
FOXA1	14	37131440	37131440	Silent	SNP	G	A	BRC39	NM_004496.2	p.G100	
MIA2	14	38786791	38786791	Missense	SNP	C	A	BRC41	NM_054024.3	p.P421H	
LRFN5	14	41425896	41425896	Silent	SNP	G	A	BRC39	NM_152447.3	p.L106	
FSCB	14	44043674	44043674	Missense	SNP	A	T	CSB28	NM_032135.3	p.V756E	
FANCM	14	44715350	44715350	Nonsense	SNP	A	T	CSB22	NM_020937.2	p.K1215*	
L2HGDH	14	49805644	49805644	Missense	SNP	C	T	BRC50	NM_024884.2	p.G298E	
ATP5S	14	49849496	49849496	Missense	SNP	G	C	BRC40	NM_001003803.1	p.C3S	
NIN	14	50293477	50293477	Nonsense	SNP	G	A	BRC44	NM_020921.3	p.Q1341*	
PYGL	14	50457045	50457045	Silent	SNP	G	A	CSB31	NM_002863.3	p.A273	
DDHD1	14	52599544	52599544	Missense	SNP	C	T	CSB8	NM_030637.1	p.D545N	
C14orf101	14	56158061	56158061	Missense	SNP	C	G	BRC41	NM_017799.3	p.S429C	
C14orf37	14	57675163	57675163	Missense	SNP	C	T	CSB1	NM_001001872.2	p.E223K	
ARID4A	14	57864716	57864716	Silent	SNP	T	G	BRC28	NM_002892.3	p.S197	
KIAA0586	14	58076572	58076572	Missense	SNP	T	C	CSB23	NM_014749.3	p.I1411T	
C14orf135	14	59654803	59654803	Missense	SNP	G	A	BRC41	NM_022495.5	p.G294S	
SLC38A6	14	60579642	60579642	Missense	SNP	C	G	CSB3	NM_153811.1	p.P217A	
HIF1A	14	61277454	61277454	Missense	SNP	G	C	CSB1	NM_001530.3	p.D630H	
SYT16	14	61532692	61532692	Missense	SNP	G	A	BRC11	NM_031914.2	p.E68K	
LOC100130953	14	61614111	61614111	Missense	SNP	A	T	BRC4	XM_001718078.1	p.L117Q	
SYNE2	14	63561694	63561694	Missense	SNP	G	C	BRC18	NM_182914.4	p.L2018F	
MTHFD1	14	63937303	63937303	Silent	SNP	G	A	CSB1	NM_005956.3	p.L27	
SPTB	14	64285804	64285808	Frame Shift Del	DEL	TCTCT		0	CSB2	NM_001024858.4	p.K2319fs
SPTB	14	64329798	64329798	Missense	SNP	C	T	CSB28	NM_001024858.4	p.R779Q	
SMOC1	14	69489919	69489919	Missense	SNP	C	T	CSB20	NM_001034852.1	p.R99W	
ADAM21	14	69994792	69994792	Missense	SNP	G	T	BRC6	NM_003813.2	p.V275F	
PCNX	14	70514203	70514203	Missense	SNP	G	A	BRC13	NM_014982.2	p.E466K	
WDR21A	14	72492943	72492943	Missense	SNP	G	A	BRC50	NM_015604.2	p.E426K	
PAPLN	14	72797186	72797186	Missense	SNP	G	T	BRC40	NM_173462.3	p.D641Y	
COQ6	14	73494639	73494639	Missense	SNP	G	A	BRC47	NM_182476.1	p.R173H	
TMEM90A	14	73946120	73946120	Silent	SNP	C	T	BRC21	NM_001105579.1	p.E27	
FCF1	14	74251380	74251380	Missense	SNP	G	A	CSB7	NM_015962.4	p.A42T	
MLH3	14	74568533	74568533	Missense	SNP	C	G	BRC50	NM_001040108.1	p.R1273T	
NEK9	14	74653696	74653696	Silent	SNP	G	A	CSB33	NM_033116.4	p.C239	

TLL5	14	75281599	75281599	Missense	SNP	G	A	BRC38	NM_015072.3	p.R470Q
TLL5	14	75418806	75418806	Missense	SNP	C	G	BRC9	NM_015072.3	p.P1183R
ANGEL1	14	76342649	76342649	Missense	SNP	C	G	BRC47	NM_015305.3	p.D415H
TMEM63C	14	76785394	76785394	Silent	SNP	C	A	BRC51	NM_020431.2	p.L626
ISM2	14	77020550	77020550	Missense	SNP	C	T	BRC13	NM_199296.3	p.E166K
ADCK1	14	77469367	77469367	Silent	SNP	C	T	CSB2	NM_020421.1	p.F484
EML5	14	88276526	88276526	Missense	SNP	C	G	CSB1	NM_183387.1	p.W223C
TRIP11	14	91547873	91547873	Missense	SNP	C	T	BRC18	NM_004239.2	p.M402I
CPSF2	14	91679217	91679217	Silent	SNP	C	T	CSB1	NM_017437.1	p.S322
SLC24A4	14	91985213	91985213	Missense	SNP	G	C	CSB1	NM_153646.2	p.K243N
CHGA	14	92467727	92467727	Silent	SNP	C	G	BRC11	NM_001275.3	p.P245
PRIMA1	14	93273363	93273363	Silent	SNP	G	A	CSB1	NM_178013.3	p.I112
SERPINA5	14	94126375	94126375	Silent	SNP	G	A	BRC17	NM_000624.4	p.R288
DICER1	14	94632740	94632740	Missense	SNP	C	G	CSB1	NM_030621.3	p.E1424Q
DICER1	14	94644495	94644495	Silent	SNP	G	C	CSB1	NM_030621.3	p.L785
EVL	14	99673671	99673671	Missense	SNP	C	G	BRC36	NM_016337.2	p.A323G
MIRN136	14	100420863	100420863	RNA	SNP	C	G	BRC28	ENST00000385207	NULL
MIRN329-2	14	100563226	100563226	RNA	SNP	C	T	BRC31	ENST00000385029	NULL
DYNC1H1	14	101522296	101522296	Frame Shift Ins	INS		0 AC	CSB15	NM_001376.4	p.M662fs
DYNC1H1	14	101551314	101551314	Frame Shift Del	DEL	C		0 BRC30	NM_001376.4	p.L2379fs
TECPR2	14	101912826	101912827	Frame Shift Del	DEL	AG		0 BRC26	NM_014844.2	p.E6fs
AKT1	14	104314098	104314098	Missense	SNP	C	A	CSB25	NM_001014431.1	p.C77F
KIAA0284	14	104422838	104422838	Missense	SNP	G	C	CSB1	NM_015005.1	p.D550H
PLD4	14	104465191	104465191	Missense	SNP	C	G	CSB1	NM_138790.2	p.S76C
AHNAK2	14	104479844	104479844	Missense	SNP	G	A	BRC29	NM_138420.2	p.A4330V
OR4N4	15	19884670	19884670	Missense	SNP	C	G	BRC41	NM_001005241.1	p.I278M
CYFIP1	15	20541623	20541623	Silent	SNP	G	A	BRC38	NM_014608.1	p.L934
WHAMML1	15	20751724	20751724	Missense	SNP	G	A	BRC24	ENST00000400153	p.A80V
SNORD116-1	15	22847781	22847781	RNA	SNP	C	G	BRC31	NR_003316.1	NULL
SNORD115-40	15	23039865	23039865	RNA	SNP	G	A	BRC39	NR_003355.1	NULL
ATP10A	15	23488026	23488026	Missense	SNP	C	T	CSB34	NM_024490.3	p.G1032R
GABRB3	15	24376565	24376565	Missense	SNP	C	T	BRC40	NM_000814.4	p.A226T
GABRB3	15	24417757	24417757	Missense	SNP	C	A	BRC7	NM_000814.4	p.M86I

OCA2	15	25946757	25946757	Missense	SNP	C	T	BRC50	NM_000275.2	p.E124K
HERC2	15	26147083	26147083	Missense	SNP	G	C	BRC50	NM_004667.4	p.I1780M
HERC2	15	26193172	26193172	Silent	SNP	G	A	BRC39	NM_004667.4	p.L220
APBA2	15	27133389	27133389	Missense	SNP	C	T	BRC47	NM_005503.1	p.R4W
APBA2	15	27181267	27181267	Silent	SNP	C	T	CSB16	NM_005503.1	p.F504
TJP1	15	27783709	27783709	Missense	SNP	T	C	CSB16	ENST00000400011	p.M1645V
LOC727909	15	28633304	28633304	Ins	INS		0 A	BRC40	XM_001126407.2	p.N23fs
RYR3	15	31934374	31934374	Missense	SNP	T	C	BRC44	NM_001036.3	p.I4659T
LOC441722	15	33172571	33172571	Missense	SNP	C	T	CSB1	XM_497450.1	p.R200C
MEIS2	15	35163285	35163285	Missense	SNP	C	G	CSB21	NM_170675.2	p.G245R
TMCO5A	15	36016383	36016383	Missense	SNP	G	A	BRC47	NM_152453.2	p.E62K
LOC728288	15	36152652	36152652	Missense	SNP	A	C	BRC15	XM_001128351.2	p.D138A
SPRED1	15	36430589	36430589	Missense	SNP	G	A	BRC44	NM_152594.2	p.R256H
THBS1	15	37672585	37672585	Missense	SNP	G	C	BRC39	NM_003246.2	p.E954Q
PLCB2	15	38376104	38376105	Del	DEL	CA		0 BRC42	NM_004573.2	p.E504fs
SPINT1	15	38932978	38932978	Splice_Site	SNP	G	C	CSB1	NM_181642.1	e3-1
VPS18	15	38982187	38982187	Missense	SNP	G	T	CSB14	NM_020857.2	p.A760S
VPS18	15	38982314	38982314	Missense	SNP	A	G	CSB33	NM_020857.2	p.K802R
LTK	15	39587637	39587637	Missense	SNP	A	T	CSB7	NM_002344.1	p.W391R
SPTBN5	15	39959762	39959762	Missense	SNP	C	A	BRC15	NM_016642.2	p.G900V
STARD9	15	40769177	40769177	Missense	SNP	G	C	BRC39	XM_001129482.2	p.E2318D
CDAN1	15	40815557	40815557	Missense	SNP	G	A	BRC31	NM_138477.2	p.S194F
TTBK2	15	40856624	40856624	Missense	SNP	C	T	BRC39	NM_173500.3	p.D436N
CCNDBP1	15	41271039	41271039	Missense	SNP	T	A	BRC18	NM_012142.2	p.L245H
ZSCAN29	15	41445748	41445748	Missense	SNP	C	G	CSB1	NM_152455.3	p.E358D
STRC	15	41682827	41682827	Missense	SNP	C	G	BRC18	NM_153700.2	p.E1484Q
STRC	15	41697394	41697394	Missense	SNP	C	T	CSB9	NM_153700.2	p.A173T
CKMT1A	15	41778483	41778483	Silent	SNP	C	T	CSB22	NM_001015001.1	p.V386
SPG11	15	42645461	42645461	Silent	SNP	G	A	BRC11	NM_025137.3	p.L2294
SPG11	15	42652292	42652292	Missense	SNP	T	A	CSB5	NM_025137.3	p.N2075I
TRIM69	15	42839242	42839242	Missense	SNP	G	C	BRC39	NM_182985.3	p.E281Q
C15orf43	15	43036449	43036449	Missense	SNP	C	T	BRC50	NM_152448.1	p.S43L
DUOX1	15	43230616	43230616	Silent	SNP	C	G	CSB1	NM_017434.3	p.P964
SEMA6D	15	45842554	45842554	Silent	SNP	C	T	CSB15	NM_153618.1	p.F236

MYEF2	15	46231756	46231756	Missense	SNP	G	A	BRC50	NM_016132.3	p.P369S
SLC12A1	15	46347150	46347150	Missense	SNP	C	T	BRC8	NM_000338.2	p.A752V
ATP8B4	15	47939961	47939961	Missense	SNP	G	A	BRC16	NM_024837.2	p.R1101C
HDC	15	48322481	48322481	Silent	SNP	G	T	BRC11	NM_002112.2	p.L419
TRPM7	15	48693209	48693209	Missense	SNP	G	A	BRC39	NM_017672.3	p.P586L
DMXL2	15	49560165	49560165	Nonsense	SNP	G	A	BRC16	NM_015263.2	p.R2144*
DMXL2	15	49615729	49615729	Missense	SNP	C	G	BRC39	NM_015263.2	p.R747P
DMXL2	15	49617942	49617942	Splice_Site	SNP	C	A	CSB17	NM_015263.2	e10-1
SCG3	15	49768753	49768753	Missense	SNP	G	A	BRC47	NM_013243.2	p.V196I
LEO1	15	50045990	50045990	Missense	SNP	G	A	BRC11	NM_138792.2	p.S21F
MYO5A	15	50396679	50396679	Missense	SNP	C	T	BRC50	NM_000259.3	p.R1731H
MYO5A	15	50487553	50487553	Missense	SNP	C	G	BRC29	NM_000259.3	p.R278P
WDR72	15	51695332	51695332	Missense	SNP	G	T	CSB15	NM_182758.2	p.A788D
PYGO1	15	53626179	53626179	Silent	SNP	G	A	BRC13	NM_015617.1	p.P198
PRTG	15	53703990	53703990	Missense	SNP	A	T	CSB28	NM_173814.4	p.S979T
NEDD4	15	53995017	53995017	Missense	SNP	G	C	CSB1	NM_198400.2	p.I435M
NEDD4	15	53995887	53995887	Silent	SNP	G	T	BRC20	NM_198400.2	p.A145
SLTM	15	56993187	56993187	Missense	SNP	C	A	BRC41	NM_024755.1	p.D106Y
MYO1E	15	57297432	57297432	Missense	SNP	C	T	BRC41	NM_004998.2	p.D353N
NARG2	15	58527595	58527595	Nonsense	SNP	C	A	CSB9	NM_024611.1	p.E721*
TLN2	15	60919776	60919776	Missense	SNP	C	A	BRC18	NM_015059.2	p.L2515M
CA12	15	61425855	61425855	Silent	SNP	G	A	BRC50	NM_001218.3	p.L71
HERC1	15	61774116	61774116	Missense	SNP	G	C	BRC39	NM_003922.3	p.Q1718E
PPIB	15	62236038	62236038	Missense Frame Shift	SNP	G	A	BRC37	NM_000942.4	p.T156I
ZNF609	15	62757545	62757546	Del	DEL	CC		0 BRC41	NM_015042.1	p.P1194fs
PDCD7	15	63212436	63212436	Missense	SNP	C	T	BRC28	NM_005707.1	p.R246Q
TIPIN	15	64416361	64416361	Missense	SNP	C	T	CSB1	NM_017858.2	p.E299K
ITGA11	15	66410490	66410490	Nonsense	SNP	G	C	CSB1	NM_001004439.1	p.S595*
UACA	15	68744130	68744130	Silent	SNP	C	T	BRC18	NM_018003.1	p.G1346
NR2E3	15	69891744	69891744	Missense	SNP	G	A	BRC47	ENST00000326995	p.D196N
MYO9A	15	70039308	70039308	Missense	SNP	G	A	CSB8	NM_006901.2	p.H724Y
HEXA	15	70428638	70428638	Silent	SNP	C	T	BRC31	NM_000520.4	p.L274
CCDC33	15	72359442	72359442	Nonsense	SNP	C	G	CSB1	NM_025055.3	p.S282* p.ED246in
SEMA7A	15	72496030	72496035	In Frame Del	DEL	TCCTCT		0 BRC32	NM_003612.1	Frame del

POLR3K	16	41638	41638	Missense	SNP	T	G	BRC35	NM_016310.2	p.N40T
AXIN1	16	336251	336251	Missense	SNP	C	T	CSB1	NM_003502.2	p.R259K
FBXL16	16	685716	685716	Missense	SNP	G	C	CSB27	NM_153350.2	p.T281R
SOX8	16	975292	975292	Missense	SNP	G	A	CSB9	NM_014587.3	p.A416T
CACNA1H	16	1195139	1195139	Missense	SNP	G	C	CSB1	NM_021098.1	p.E826Q
UNKL	16	1404051	1404051	Silent	SNP	C	T	CSB33	NM_001037125.1	p.L28
CRAMP1L	16	1646329	1646329	Missense	SNP	G	A	CSB1	NM_020825.3	p.E320K
E4F1	16	2218477	2218477	Silent	SNP	G	A	CSB1	NM_004424.3	p.P87
E4F1	16	2223903	2223903	Nonsense	SNP	C	G	BRC11	NM_004424.3	p.S429*
RNPS1	16	2254277	2254277	Nonsense	SNP	G	C	BRC39	NM_006711.2	p.S43*
CCNF	16	2443483	2443483	Silent	SNP	C	T	CSB1	NM_001761.2	p.L553
TBC1D24	16	2486633	2486633	Silent	SNP	C	T	BRC18	NM_020705.1	p.C161
PRSS27	16	2702693	2702693	Missense	SNP	G	A	BRC51	NM_031948.3	p.H268Y
SRRM2	16	2752102	2752102	Missense	SNP	A	T	BRC41	NM_016333.3	p.R524S
SRRM2	16	2756708	2756708	Nonsense	SNP	C	T	BRC47	NM_016333.3	p.R2060*
THOC6	16	3017201	3017201	Silent	SNP	C	T	CSB6	NM_024339.1	p.L243
IL32	16	3059298	3059298	Missense	SNP	C	T	BRC9	NM_001012631.1	p.R170W
MEFV	16	3233200	3233200	Missense	SNP	C	T	BRC50	NM_000243.2	p.G763E
MEFV	16	3239584	3239584	Nonsense	SNP	G	A	BRC51	NM_000243.2	p.Q370*
ZNF174	16	3392273	3392273	Missense	SNP	G	A	CSB27	NM_003450.2	p.V90M
BTBD12	16	3587858	3587858	Missense	SNP	G	A	CSB12	NM_032444.2	p.A436V
CREBBP	16	3719616	3719616	Silent	SNP	C	T	CSB1	NM_004380.1	p.K1811
GLIS2	16	4322446	4322446	Missense	SNP	C	A	BRC29	NM_032575.2	p.P55Q
NMRAL1	16	4456284	4456284	Missense	SNP	C	G	CSB1	NM_020677.2	p.G134R
ZNF500	16	4742911	4742911	Missense	SNP	G	A	CSB29	NM_021646.1	p.P304S
N-PAC	16	4801782	4801782	Missense	SNP	C	G	BRC31	NM_032569.3	p.K435N
PPL	16	4874376	4874376	Silent	SNP	C	T	CSB10	NM_002705.4	p.L1427
SEC14L5	16	4990903	4990903	Missense	SNP	C	A	CSB5	NM_014692.1	p.T369K
SEC14L5	16	5004916	5004916	Missense	SNP	G	A	CSB3	NM_014692.1	p.A679T
NAGPA	16	5021832	5021832	Silent	SNP	C	T	BRC13	NM_016256.2	p.L199
A2BP1	16	7508291	7508291	Missense	SNP	A	G	BRC4	NM_145891.1	p.T77A
A2BP1	16	7569799	7569799	Missense	SNP	C	T	CSB12	NM_145891.1	p.P117L
GRIN2A	16	9766019	9766019	Missense	SNP	G	T	CSB26	NM_000833.3	p.N961K
TXNDC11	16	11680639	11680639	Silent	SNP	G	A	BRC4	NM_015914.5	p.T930
SNX29	16	12526190	12526190	Missense	SNP	C	T	CSB24	NM_001080530.2	p.P385L

NOMO1	16	14853887	14853887	Missense	SNP	G	C	CSB1	NM_014287.3	p.E228Q
KIAA0430	16	15605614	15605614	Missense	SNP	T	C	BRC9	NM_014647.2	p.E1442G
MYH11	16	15722333	15722341	In Frame Del	DEL	CT		0 CSB1	NM_001040114.1	p.ELE1557in Frame del
ABCC1	16	16142611	16142611	Missense	SNP	G	T	BRC44	NM_004996.3	p.S1523I p.I403in Frame del
NOMO3	16	16257503	16257505	In Frame Del	DEL	ATT		0 BRC33	NM_001004067.2	Frame del
SMG1	16	18736175	18736175	Missense	SNP	G	A	CSB1	NM_015092.4	p.S3338L
SMG1	16	18751782	18751782	Missense	SNP	G	C	BRC39	NM_015092.4	p.H2925D
SMG1	16	18757499	18757499	Missense	SNP	G	C	CSB2	NM_015092.4	p.S2320C
CP110	16	19460870	19460870	Missense	SNP	C	T	BRC39	NM_014711.4	p.S737L
ACSM2A	16	20390453	20390453	Missense	SNP	T	A	CSB26	NM_001010845.2	p.L279I
ACSM1	16	20543035	20543035	Missense	SNP	C	A	BRC5	NM_052956.2	p.V511L
ACSM3	16	20688995	20688995	Missense	SNP	G	A	CSB24	NM_005622.3	p.M46I
DNAH3	16	20863462	20863462	Missense	SNP	G	C	CSB1	NM_017539.1	p.L3790V
DNAH3	16	21025336	21025336	Frame Shift Del	DEL	G		0 CSB3	NM_017539.1	p.L754fs
CRYM	16	21197061	21197061	Missense	SNP	G	T	CSB28	NM_001888.1	p.P5T
POLR3E	16	22250994	22250994	Missense	SNP	A	T	CSB9	NM_018119.2	p.D686V
PALB2	16	23526814	23526814	Silent	SNP	C	A	BRC16	NM_024675.3	p.L1074
PRKCB	16	24109971	24109971	Missense	SNP	C	G	BRC18	NM_002738.6	p.I594M
HS3ST4	16	26054572	26054572	Silent	SNP	G	A	BRC39	ENST00000331351	p.V29I
GTF3C1	16	27380209	27380209	Missense	SNP	G	A	BRC6	NM_001520.3	p.P2098L
GTF3C1	16	27401904	27401904	Missense	SNP	C	A	BRC6	NM_001520.3	p.D1349Y
ATP2A1	16	28819492	28819492	Silent	SNP	G	A	CSB1	NM_173201.3	p.G618
SPN	16	29582665	29582665	Missense	SNP	C	T	BRC23	NM_001030288.1	p.P39S
C16orf53	16	29736084	29736084	Missense	SNP	G	A	BRC48	NM_024516.3	p.D179N
MVP	16	29763406	29763406	Missense	SNP	G	A	BRC7	NM_005115.3	p.A576T
SEZ6L2	16	29814606	29814606	Silent	SNP	G	C	CSB27	NM_201575.1	p.T196
FAM57B	16	29945473	29945473	Silent	SNP	G	C	CSB1	NM_031478.4	p.L134
MAPK3	16	30037236	30037236	Missense	SNP	C	T	CSB25	NM_002746.1	p.A160T
CD2BP2	16	30273455	30273455	Nonsense	SNP	C	A	CSB1	NM_006110.2	p.E17* p.E119in Frame del
ZNF785	16	30502243	30502245	In Frame Del	DEL	CTC		0 BRC19	NM_152458.5	Frame del
SRCAP	16	30642754	30642754	Missense	SNP	C	T	BRC47	NM_006662.2	p.S1503L
ZNF629	16	30701433	30701433	Missense	SNP	C	A	CSB31	NM_001080417.1	p.V573L
ZNF629	16	30702709	30702709	Silent	SNP	C	T	CSB1	NM_001080417.1	p.E147

SETD1A	16	30888464	30888464	Missense	SNP	G	A	CSB1	NM_014712.1	p.R990Q
STX1B	16	30912008	30912008	Missense	SNP	C	T	BRC12	NM_052874.3	p.E244K
MYST1	16	31049401	31049401	Missense	SNP	G	A	BRC39	NM_182958.1	p.R377Q
LOC100129315	16	31567479	31567479	Missense	SNP	C	T	BRC18	XM_001717900.1	p.P117S
LOC401847	16	33477678	33477678	Silent	SNP	C	T	BRC47	XM_001718104.1	p.D105
ABCC11	16	46821886	46821886	Missense	SNP	C	T	BRC10	NM_032583.3	p.A67T
PAPD5	16	48814781	48814781	Missense	SNP	G	A	CSB1	NM_001040284.1	p.E231K
NOD2	16	49299280	49299280	Missense	SNP	T	G	BRC5	NM_022162.1	p.L185R
NOD2	16	49303213	49303213	Silent	SNP	C	T	CSB31	NM_022162.1	p.F630
RBL2	16	52030535	52030535	Missense	SNP	G	C	BRC44	NM_005611.3	p.R116T
IRX5	16	53524223	53524223	Missense	SNP	G	A	CSB6	NM_005853.5	p.E188K
SLC6A2	16	54276593	54276593	Missense	SNP	C	T	BRC31	NM_001043.2	p.H228Y
SLC6A2	16	54290968	54290968	Silent	SNP	A	T	BRC24	NM_001043.2	p.G497
CES1	16	54404393	54404393	Nonsense	SNP	G	A	BRC50	NM_001025195.1	p.Q337*
GNAO1	16	54920078	54920078	Missense	SNP	G	A	CSB3	NM_020988.2	p.R113Q
NUP93	16	55339700	55339700	Missense	SNP	G	A	BRC34	NM_014669.3	p.E14K
GPR56	16	56247979	56247979	Missense	SNP	A	T	CSB2	NM_005682.1	p.E372D
CCDC135	16	56298906	56298906	Missense	SNP	G	A	BRC22	NM_032269.5	p.G298S
KATNB1	16	56344635	56344635	Missense	SNP	G	A	CSB14	NM_005886.2	p.R334Q
CDH5	16	64980836	64980836	Missense	SNP	G	C	BRC44	NM_001795.3	p.D231H
CBFB	16	65658114	65658114	Missense	SNP	A	G	CSB26	NM_022845.2	p.N104S
CBFB	16	65673635	65673635	Nonsense	SNP	C	T	CSB27	NM_022845.2	p.Q140*
E2F4	16	65784245	65784245	Missense	SNP	G	T	CSB34	NM_001950.3	p.E72D
PLEKHG4	16	65876556	65876556	Missense	SNP	C	A	BRC47	NM_015432.1	p.A711D p.S272in Frame del
CTCF	16	66203385	66203387	In Frame Del	DEL	GCA		0 BRC24	NM_006565.2	
CTCF	16	66203447	66203447	Missense	SNP	A	G	BRC36	NM_006565.2	p.R292G
NUTF2	16	66462218	66462218	Silent	SNP	C	T	BRC37	NM_005796.1	p.P95
ENSG0000022152 6	16	66469091	66469091	RNA	SNP	A	G	CSB25	ENST00000408599	NULL
EDC4	16	66472773	66472773	Missense	SNP	C	T	BRC7	NM_014329.3	p.S914F
ZFP90	16	67155905	67155905	Missense	SNP	G	C	BRC11	NM_133458.2	p.E572Q
CDH3	16	67283143	67283143	Silent	SNP	C	T	BRC7	NM_001793.4	p.S605
CDH1	16	67393289	67393289	Frame Shift Del	DEL	C		0 CSB14	NM_004360.3	p.H128fs
CDH1	16	67399852	67399852	Missense	SNP	G	A	BRC39	NM_004360.3	p.E138K

						GATCCT G						
						AGCTCC						
CDH1	16	67403177	67403190	Frame Shift Del	DEL	C		0	CSB31	NM_004360.3		p.D308fs
CDH1	16	67403226	67403230	Frame Shift Del	DEL	GAGTC		0	CSB12	NM_004360.3		p.G324fs
CDH1	16	67403668	67403668	Splice_Site Frame Shift	SNP	G	A		BRC38	NM_004360.3		e8+1
CDH1	16	67407118	67407118	Del	DEL	C		0	CSB30	NM_004360.3		p.Y508fs
CDH1	16	67410696	67410696	Nonsense	SNP	G	A		CSB1	NM_004360.3		p.W526*
						ATCCGG						
						A						p.NPDTGA53
						CACTGG						6in Frame
CDH1	16	67410725	67410739	In Frame Del	DEL	TG		0	CSB28	NM_004360.3		delT
CIRH1A	16	67751845	67751845	Silent	SNP	C	T		BRC18	NM_032830.2		p.V510
VPS4A	16	67910808	67910808	Missense Frame Shift	SNP	C	T		BRC4	NM_013245.2		p.R161W
AARS	16	68850558	68850559	Del	DEL	TG		0	CSB9	NM_001605.2		p.T606fs
ST3GAL2	16	68973144	68973144	Silent	SNP	G	A		BRC5	NM_006927.3		p.I334
HYDIN	16	69401406	69401406	Silent	SNP	C	T		CSB1	NM_032821.2		p.T4887
TAT	16	70167695	70167695	Missense	SNP	G	A		CSB1	NM_000353.2		p.S42F
PKD1L3	16	70575538	70575538	Silent	SNP	G	A		BRC33	ENST00000335106		p.S288
LOC440386	16	72958334	72958334	RNA	SNP	G	C		BRC50	XR_040492.1		NULL
												p.Q192in
NPIPL2	16	72982901	72982903	In Frame Del	DEL	CAA		0	CSB30	ENST00000355290		Frame del
WDR59	16	73515363	73515363	Missense	SNP	G	A		BRC18	NM_030581.3		p.L231F
SDR42E1	16	80590218	80590218	Silent	SNP	C	T		BRC39	NM_145168.2		p.*394
NECAB2	16	82569609	82569609	Missense	SNP	G	C		BRC39	NM_019065.2		p.E96Q
LOC100132344	16	83187209	83187209	Missense	SNP	G	C		BRC11	XM_001726866.1		p.E98Q
FAM92B	16	83690316	83690316	Silent	SNP	G	A		CSB1	NM_198491.1		p.L297
ACSF3	16	87694670	87694670	Missense	SNP	G	A		BRC13	NM_174917.1		p.R27K
ANKRD11	16	87874800	87874800	Nonsense	SNP	G	C		BRC44	NM_013275.4		p.S1884*
ANKRD11	16	87874972	87874972	Missense	SNP	G	A		CSB15	NM_013275.4		p.P1827S
TUBB3	16	88528816	88528816	Silent	SNP	C	T		BRC39	NM_006086.2		p.I152
VPS53	17	477238	477238	Silent	SNP	C	T		BRC50	NM_018289.1		p.E271
SLC43A2	17	1440976	1440976	Missense	SNP	C	A		BRC49	NM_152346.1		p.M316I
SLC43A2	17	1441441	1441441	Missense	SNP	G	A		BRC35	NM_152346.1		p.T268M
LOC727910	17	1557955	1557955	Silent	SNP	C	T		BRC18	XM_001126126.2		p.G396
LOC727910	17	1558057	1558057	Missense	SNP	C	T		BRC18	XM_001126126.2		p.M362I

RPA1	17	1730671	1730671	Missense	SNP	G	T	BRC24	NM_002945.3	p.V393L
SMG6	17	1918876	1918876	Missense	SNP	T	A	CSB1	NM_017575.4	p.S1261C
SRR	17	2168896	2168896	Nonsense	SNP	C	T	CSB27	NM_021947.1	p.Q108*
KIAA0664	17	2546483	2546483	Missense	SNP	G	A	BRC39	NM_015229.3	p.S723L
SPATA22	17	3319339	3319339	Missense	SNP	G	C	BRC39	NM_032598.3	p.R11G
ITGAE	17	3607904	3607904	Splice_Site	SNP	T	C	BRC39	NM_002208.4	e9-2
ITGAE	17	3611978	3611978	Missense	SNP	G	A	BRC7	NM_002208.4	p.R99W
CYB5D2	17	4007112	4007112	Missense	SNP	C	T	CSB1	NM_144611.3	p.S261F
ALOX15	17	4482978	4482978	Silent	SNP	C	T	BRC20	NM_001140.3	p.V489
CAMTA2	17	4822526	4822526	Missense	SNP	G	A	BRC39	NM_015099.2	p.P588S
KIF1C	17	4844283	4844283	Silent	SNP	G	A	CSB1	NM_006612.4	p.V6
ZNF594	17	5026629	5026629	Silent	SNP	G	A	CSB1	NM_032530.1	p.F549
RABEP1	17	5205301	5205301	Missense	SNP	C	A	BRC18	NM_004703.1	p.F390L
NUP88	17	5239026	5239026	Splice_Site	SNP	C	T	BRC40	NM_002532.3	e9-1
WSCD1	17	5939165	5939165	Silent	SNP	C	T	CSB21	NM_015253.1	p.R249
PHF23	17	7080087	7080087	Missense	SNP	G	C	BRC50	NM_024297.2	p.P295A
GPS2	17	7157429	7157429	Missense	SNP	G	C	CSB1	NM_004489.4	p.Q240E
MPDU1	17	7430114	7430114	Missense	SNP	C	T	CSB24	NM_004870.3	p.P99L
TP53	17	7513676	7513676	Missense	SNP	C	G	BRC44	NM_000546.4	p.K386N
TP53	17	7514669	7514669	Silent	SNP	C	A	BRC44	NM_000546.4	p.G361
TP53	17	7514755	7514755	Frame Shift Del	DEL	G		0 BRC37	NM_000546.4	p.R333fs
TP53	17	7517580	7517580	Nonsense	SNP	G	A	CSB24	NM_000546.4	p.Q331*
TP53	17	7517810	7517810	Missense	SNP	C	T	BRC44	NM_000546.4	p.E285K
TP53	17	7517824	7517824	Missense	SNP	C	T	BRC4	NM_000546.4	p.R280K
TP53	17	7517833	7517833	Missense	SNP	C	A	BRC31	NM_000546.4	p.C277F
TP53	17	7517845	7517845	Missense	SNP	C	A	BRC20	NM_000546.4	p.R273L
TP53	17	7517846	7517846	Missense	SNP	G	A	CSB33	NM_000546.4	p.R273C
TP53	17	7518264	7518264	Missense	SNP	G	A	CSB15	NM_000546.4	p.R248W
TP53	17	7518293	7518293	Missense	SNP	C	T	BRC29	NM_000546.4	p.C238Y
TP53	17	7518928	7518928	Missense	SNP	C	T	BRC51	NM_000546.4	p.V216M
TP53	17	7518934	7518934	Missense	SNP	G	C	BRC47	NM_000546.4	p.H214D
TP53	17	7518936	7518936	Missense	SNP	C	A	BRC13	NM_000546.4	p.R213L
TP53	17	7518948	7518948	Missense	SNP	C	A	BRC44	NM_000546.4	p.R209I
TP53	17	7519251	7519251	Missense	SNP	C	A	BRC16	NM_000546.4	p.C135F

TP53	17	7520036	7520036	Splice_Site	SNP	C	A	CSB9	NM_000546.4	e3+1
TP53	17	7520112	7520112	Silent	SNP	C	T	BRC44	NM_000546.4	p.Q100
						TCTGC				p.RENL672in
DNAH2	17	7601239	7601250	In Frame Del	DEL	GTGAAAA	0	BRC39	NM_020877.2	Frame del
DNAH2	17	7642243	7642243	Missense	SNP	G	T	BRC7	NM_020877.2	p.M2758I
KCNAB3	17	7767150	7767150	Nonsense	SNP	T	A	BRC23	NM_004732.2	p.K404*
ALOXE3	17	7958647	7958647	Missense	SNP	C	T	BRC38	NM_021628.2	p.G187E
RANGRF	17	8133077	8133077	Silent	SNP	C	G	BRC31	NM_016492.3	p.L52
MYH10	17	8336403	8336403	Silent	SNP	C	T	BRC39	NM_005964.1	p.Q1505
CCDC42	17	8585709	8585709	Silent	SNP	G	A	CSB8	NM_144681.1	p.N100
MYH8	17	10259420	10259420	Missense	SNP	G	C	BRC39	NM_002472.2	p.L219V
MYH4	17	10310595	10310595	Nonsense	SNP	C	A	CSB6	NM_017533.2	p.E65*
MYH1	17	10340587	10340587	Missense	SNP	G	C	BRC18	NM_005963.3	p.S1554C
MYH1	17	10349909	10349909	Missense	SNP	G	A	BRC31	NM_005963.3	p.R707C
MYH2	17	10383363	10383363	Missense	SNP	C	T	BRC39	NM_001100112.1	p.V434I
DNAH9	17	11513414	11513414	Silent	SNP	C	G	BRC50	NM_001372.3	p.V977
DNAH9	17	11601667	11601667	Missense	SNP	G	A	CSB1	NM_001372.3	p.E2310K
ZNF18	17	11822340	11822340	Nonsense	SNP	G	A	CSB30	NM_144680.2	p.Q437*
MAP2K4	17	11899036	11899036	Splice_Site	SNP	G	T	BRC3	NM_003010.2	e2+3
MAP2K4	17	11951869	11951869	Missense	SNP	C	T	BRC50	NM_003010.2	p.S184L
LOC100131109	17	14148096	14148096	Nonsense	SNP	G	A	BRC31	XM_001722018.1	p.R128*
TEKT3	17	15175368	15175368	Missense	SNP	C	G	CSB1	NM_031898.2	p.R87T
NCOR1	17	15878884	15878884	Nonsense	SNP	G	C	BRC24	NM_006311.2	p.S2352*
LOC100133337	17	16226471	16226471	Missense	SNP	C	T	CSB1	XM_001722328.1	p.D60N
C17orf39	17	17889210	17889210	Missense	SNP	C	T	BRC19	NM_024052.4	p.L155F
FLII	17	18092760	18092760	Missense	SNP	C	G	BRC19	NM_002018.2	p.R673S
MFAP4	17	19231013	19231013	Silent	SNP	C	G	CSB1	ENST00000395592	p.L4
SLC47A2	17	19546530	19546530	Missense	SNP	G	T	BRC39	NM_152908.1	p.H418N
ULK2	17	19645785	19645785	Silent	SNP	G	A	BRC50	NM_014683.1	p.F446
ULK2	17	19660670	19660670	Silent	SNP	G	A	BRC32	NM_014683.1	p.I360
DHRS7B	17	21027675	21027675	Silent	SNP	C	T	CSB1	NM_015510.3	p.V162
KIAA0100	17	23984207	23984207	Missense	SNP	G	C	CSB1	NM_014680.2	p.L1229V
KIAA0100	17	23984497	23984497	Missense	SNP	G	C	CSB1	NM_014680.2	p.S1172C
KIAA0100	17	23984817	23984817	Silent	SNP	G	C	CSB1	NM_014680.2	p.L1114
TLCD1	17	24076655	24076655	Missense	SNP	G	C	CSB1	NM_138463.2	p.S83C

MYO18A	17	24437631	24437631	Missense	SNP	C	T	BRC41	NM_078471.3	p.A1935T
TAOK1	17	24853832	24853832	Nonsense	SNP	C	T	BRC51	NM_020791.1	p.R435*
SSH2	17	25006708	25006708	Missense	SNP	C	T	CSB1	NM_033389.2	p.R332Q
EFCAB5	17	25320373	25320373	Missense	SNP	C	G	BRC14	NM_198529.1	p.P210R
EFCAB5	17	25404924	25404924	Missense	SNP	G	A	BRC24	NM_198529.1	p.R609H
TMIGD1	17	25680602	25680602	Missense	SNP	G	C	CSB1	NM_206832.1	p.L52V
CPD	17	25793538	25793538	Missense	SNP	G	C	CSB1	NM_001304.3	p.E773Q
ATAD5	17	26244603	26244603	Missense	SNP	G	A	BRC11	NM_024857.3	p.D1536N
LOC646021	17	26359426	26359426	Del	DEL	C		0 BRC22	XM_933339.1	p.I63fs
NF1	17	26586796	26586796	Silent	SNP	G	A	CSB31	NM_001042492.2	p.R1250
NF1	17	26587155	26587155	Missense	SNP	G	C	CSB1	NM_001042492.2	p.D1322H
RHBDL3	17	27672351	27672351	Missense	SNP	C	A	CSB14	NM_138328.2	p.P402H
TMEM98	17	28290641	28290641	Silent	SNP	G	A	BRC32	NM_001033504.1	p.P149
SPACA3	17	28343075	28343075	Silent	SNP	C	G	BRC51	NM_173847.3	p.V2
SLFN5	17	30610003	30610003	Missense	SNP	G	C	CSB1	NM_144975.3	p.E61Q
SLFN5	17	30610110	30610110	Missense	SNP	G	C	CSB1	NM_144975.3	p.L96F
MYO19	17	31931148	31931148	Silent	SNP	G	A	CSB1	NM_025109.1	p.L507
GGNBP2	17	32016481	32016481	Missense	SNP	G	A	CSB1	NM_024835.2	p.E489K
ACACA	17	32552457	32552457	Silent	SNP	G	A	BRC41	NM_198834.1	p.D2069
DDX52	17	33066327	33066327	Missense	SNP	G	C	CSB1	NM_007010.2	p.Q178E
PIP4K2B	17	34187468	34187468	Missense	SNP	C	G	CSB1	NM_003559.4	p.E269Q
CACNB1	17	34596323	34596323	Silent	SNP	G	A	CSB1	NM_000723.3	p.L194
FBXL20	17	34708818	34708818	Nonsense	SNP	G	A	BRC47	NM_032875.1	p.R94*
CRKRS	17	34880670	34880670	Missense	SNP	G	T	BRC29	NM_016507.1	p.M353I
CRKRS	17	34940604	34940604	Missense	SNP	T	A	BRC17	NM_016507.1	p.Y1328N
STARD3	17	35070246	35070246	Missense	SNP	G	A	BRC4	NM_006804.2	p.E299K
ERBB2	17	35134526	35134526	Missense	SNP	G	C	BRC14	NM_004448.1	p.V777L
ZBP2	17	35278185	35278185	Missense	SNP	G	A	CSB7	NM_199321.2	p.V18I
GSDMB	17	35315961	35315961	Nonsense	SNP	T	A	CSB31	NM_001042471.1	p.R260*
GSDMB	17	35322248	35322248	Silent	SNP	A	G	BRC41	NM_001042471.1	p.D88
GSDMB	17	35326965	35326965	Missense	SNP	C	G	CSB1	NM_001042471.1	p.R44T
CCR7	17	35964547	35964547	Silent	SNP	G	A	CSB14	NM_001838.2	p.A370
KRT33A	17	36760508	36760508	Missense	SNP	C	T	CSB2	NM_004138.2	p.R13H
KRT31	17	36806216	36806216	Silent	SNP	G	A	CSB30	NM_002277.2	p.L190

KRT9	17	36977955	36977955	Missense	SNP	C	A	BRC39	NM_000226.3	p.G460V
KRT9	17	36978335	36978335	Missense	SNP	C	T	CSB1	NM_000226.3	p.R374Q
KRT9	17	36981682	36981682	Missense	SNP	G	C	BRC16	NM_000226.3	p.S30C
NT5C3L	17	37237324	37237324	Missense	SNP	G	T	BRC7	NM_052935.3	p.F208L
ACLY	17	37318793	37318793	Silent	SNP	G	A	CSB1	NM_001096.2	p.F197
DNAJC7	17	37393442	37393442	Missense	SNP	C	T	CSB1	NM_003315.1	p.D301N
DHX58	17	37514878	37514878	Missense	SNP	G	A	BRC44	NM_024119.2	p.P205L
GHDC	17	37597843	37597843	Silent	SNP	G	A	BRC18	NM_032484.1	p.L277
STAT3	17	37739249	37739249	Missense	SNP	G	C	BRC39	NM_139276.3	p.I339M
CNTNAP1	17	38097452	38097452	Missense	SNP	C	G	BRC20	NM_003632.2	p.S816C
BRCA1	17	38499341	38499341	Missense	SNP	G	A	BRC39	NM_007294.2	p.S578F
MPP2	17	39315904	39315904	Missense	SNP	C	T	CSB22	NM_005374.3	p.E116K
C17orf53	17	39581354	39581354	Missense	SNP	A	C	CSB21	NM_024032.2	p.K219N
FAM171A2	17	39792520	39792520	Missense	SNP	G	A	CSB15	ENST00000398346	p.T131M
uc002igz.2	17	40099649	40099649	Missense	SNP	G	C	BRC39	ENST00000409122	p.E282Q
DBF4B	17	40142233	40142233	Nonsense	SNP	G	T	CSB1	NM_145663.2	p.E19*
DCAKD	17	40457430	40457430	Missense	SNP	C	T	BRC44	NM_024819.1	p.R198H
NMT1	17	40526636	40526636	Missense	SNP	A	T	BRC31	NM_021079.3	p.E148V
PLEKHM1	17	40901503	40901503	Missense	SNP	T	C	CSB15	NM_014798.1	p.Q388R
ENSG00000221016	17	42550894	42550894	RNA	SNP	T	C	BRC42	ENST00000408089	NULL
LOC653479	17	42923506	42923506	RNA	SNP	G	A	CSB31	XR_017538.2	NULL
KPNB1	17	43091003	43091003	Missense	SNP	C	A	BRC32	NM_002265.4	p.T205N
KPNB1	17	43103074	43103074	Missense	SNP	C	G	BRC39	NM_002265.4	p.S475C
TBX21	17	43177166	43177166	Missense	SNP	A	C	BRC51	NM_013351.1	p.Q348P
SCRN2	17	43272649	43272649	Missense	SNP	G	A	BRC49	NM_138355.1	p.A88V
SP2	17	43349076	43349076	Missense	SNP	C	G	CSB1	NM_003110.5	p.L214V
ATAD4	17	43385295	43385295	Missense	SNP	G	A	BRC44	NM_024320.2	p.S102L
SNX11	17	43545718	43545718	Silent	SNP	G	A	BRC30	NM_013323.2	p.E62
LOC100129841	17	43576510	43576510	Missense	SNP	C	T	BRC31	XM_001726539.1	p.G31R
HOXB3	17	43982824	43982824	Silent	SNP	C	T	BRC8	NM_002146.4	p.A389
SLC35B1	17	45133819	45133819	Nonstop Mutation	SNP	C	A	BRC20	NM_005827.1	p.*323Y
SAMD14	17	45546660	45546660	Missense	SNP	G	C	CSB1	NM_174920.2	p.L306V
WFIKKN2	17	46268398	46268398	Missense	SNP	C	T	BRC7	NM_175575.5	p.A34V
COX11	17	50400933	50400934	Missense	DNP	GG	AA	BRC51	NM_004375.2	p.P25L

NOG	17	52026993	52026993	Missense	SNP	T	A	BRC44	NM_005450.4	p.L137Q
BZRAP1	17	53740939	53740939	Missense	SNP	G	A	BRC49	NM_004758.2	p.R1565C
HSF5	17	53912272	53912272	Silent	SNP	C	T	BRC37	NM_001080439.1	p.S302
TEX14	17	54005579	54005579	Missense	SNP	T	G	CSB24	NM_198393.3	p.N1198T
ENSG00000212195	17	54064142	54064142	RNA	SNP	C	T	BRC50	ENST00000390893	NULL
TEX14	17	54084306	54084306	Missense	SNP	C	G	BRC50	NM_198393.3	p.R19T
RAD51C	17	54125064	54125064	Missense	SNP	C	G	CSB1	NM_058216.2	p.P21A
PRR11	17	54617227	54617227	Silent	SNP	A	G	BRC22	NM_018304.2	p.Q53
RPS6KB1	17	55372983	55372983	Missense	SNP	C	T	BRC44	NM_003161.2	p.S375F
CA4	17	55589603	55589603	Missense	SNP	C	T	CSB15	NM_000717.3	p.S101F
USP32	17	55703559	55703559	Nonsense	SNP	C	A	BRC23	NM_032582.3	p.G213*
BCAS3	17	56448032	56448032	Missense	SNP	C	T	BRC50	NM_001099432.1	p.T542I
TLK2	17	58037247	58037247	Silent	SNP	G	A	CSB29	NM_006852.1	p.V628
MARCH10	17	58167483	58167483	Nonsense	SNP	G	T	BRC50	NM_001100875.1	p.S493*
MARCH10	17	58168259	58168259	Silent	SNP	G	T	CSB17	NM_001100875.1	p.A234
TANC2	17	58786426	58786426	Missense	SNP	G	A	BRC39	NM_025185.3	p.R768Q
GH1	17	59348871	59348871	Missense	SNP	C	G	BRC51	NM_000515.3	p.G146A
ERN1	17	59488930	59488930	Silent	SNP	C	T	BRC13	NM_001433.3	p.L454
PLEKHM1P	17	60227336	60227336	Missense	SNP	G	A	BRC11	ENST00000290422	p.R56C
LRRC37A3	17	60295070	60295070	Missense	SNP	G	C	BRC39	NM_199340.2	p.L1009V
GNA13	17	60483024	60483024	Missense	SNP	C	G	CSB15	NM_006572.4	p.K50N
BPTF	17	63319972	63319972	Missense	SNP	G	C	BRC22	NM_182641.6	p.E694Q
ARSG	17	63876290	63876290	Silent	SNP	C	T	BRC22	NM_014960.3	p.S237
ABCA6	17	64620995	64620995	Silent	SNP	G	A	BRC34	NM_080284.2	p.F668
SOX9	17	67631461	67631461	Missense	SNP	G	A	BRC39	NM_000346.3	p.D290N
SDK2	17	68943204	68943204	Missense	SNP	G	T	CSB9	ENST00000334543	p.S71Y
GPR142	17	69880219	69880219	Missense	SNP	T	A	BRC41	NM_181790.1	p.V425D
CD300LD	17	70087795	70087795	Silent	SNP	G	A	BRC44	ENST00000375352	p.L176
C17orf28	17	70469965	70469965	Silent	SNP	G	A	BRC11	NM_030630.2	p.F190
SLC16A5	17	70601479	70601479	Missense	SNP	G	C	CSB1	NM_004695.2	p.E51D
HN1	17	70656315	70656315	Missense	SNP	C	G	BRC39	NM_001002032.1	p.D35H
NUP85	17	70719746	70719746	Missense	SNP	G	A	BRC6	NM_024844.3	p.V119I
GGA3	17	70750780	70750780	Missense	SNP	G	A	CSB1	NM_138619.2	p.R163C
FBF1	17	71425456	71425456	Silent	SNP	G	T	CSB14	NM_001080542.1	p.I804

CDK3	17	71510206	71510206	Missense	SNP	G	A	CSB19	NM_001258.2	p.R169H
EVPL	17	71516869	71516869	Missense	SNP	G	A	CSB30	NM_001988.2	p.R1338W
EXOC7	17	71598071	71598071	Missense	SNP	G	A	CSB1	ENST00000335146	p.H330Y
MGAT5B	17	72412053	72412053	Missense	SNP	A	G	CSB31	NM_198955.2	p.N226S
MGAT5B	17	72456422	72456422	Silent	SNP	C	T	CSB1	NM_198955.2	p.F771
C17orf99	17	73671799	73671799	Silent	SNP	C	T	BRC11	ENST00000340363	p.F133
DNAH17	17	73936853	73936853	Missense	SNP	C	T	CSB1	ENST00000300671	p.E4112K
DNAH17	17	74078687	74078687	Missense	SNP	C	T	BRC23	ENST00000300671	p.V286M
CBX4	17	75423496	75423496	Silent	SNP	C	T	CSB26	NM_003655.2	p.A180
CCDC40	17	75637124	75637124	Missense	SNP	G	A	BRC21	NM_017950.2	p.G275E
CCDC40	17	75647321	75647321	Nonsense	SNP	C	T	CSB21	NM_017950.2	p.Q463*
CCDC40	17	75674451	75674451	Missense	SNP	G	A	CSB1	NM_017950.2	p.D764N
RNF213	17	75958032	75958032	Silent	SNP	C	T	CSB22	NM_020914.3	p.F2170
AATK	17	76722778	76722778	Silent	SNP	G	A	BRC13	ENST00000326724	p.G58
BAHCC1	17	77044540	77044540	Silent	SNP	C	T	CSB1	NM_001080519.2	p.V2643
FSCN2	17	77110900	77110900	Nonsense	SNP	G	T	BRC51	ENST00000334850	p.E250*
GPS1	17	77605050	77605050	Silent	SNP	G	A	BRC35	NM_212492.4	p.A88
FASN	17	77631650	77631650	Missense	SNP	G	A	BRC41	NM_004104.4	p.A2311V
FASN	17	77635873	77635873	Missense	SNP	C	G	CSB1	NM_004104.4	p.E1525Q
FASN	17	77636946	77636946	Missense	SNP	G	A	CSB1	NM_004104.4	p.R1275C
FASN	17	77646574	77646576	In Frame Del	DEL	AAG		0 BRC5	NM_004104.4	p.F65in Frame del
HEXDC	17	77993726	77993726	Missense	SNP	A	T	CSB28	NM_173620.2	p.E576V
RAB40B	17	78210791	78210791	Missense	SNP	C	T	CSB22	NM_006822.2	p.R99H
LOC100130247	18	1166892	1166892	Missense	SNP	A	C	BRC13	XM_001716684.1	p.V41G
NDC80	18	2598807	2598807	Missense	SNP	G	A	BRC39	NM_006101.2	p.E556K
SMCHD1	18	2728476	2728476	Missense	SNP	G	C	CSB1	NM_015295.2	p.D1120H
SMCHD1	18	2774593	2774593	Frame Shift Ins	INS		0 G	BRC41	NM_015295.2	p.C1899fs
LPIN2	18	2930711	2930711	Splice_Site	SNP	C	G	CSB1	NM_014646.2	e4-1
LAMA1	18	7013307	7013307	Missense	SNP	C	T	BRC3	NM_005559.2	p.G853S
RNMT	18	13742361	13742361	Missense	SNP	G	A	BRC44	NM_003799.1	p.E432K
MC5R	18	13816295	13816295	Missense	SNP	C	A	BRC50	NM_005913.1	p.F177L
MC5R	18	13816372	13816372	Missense	SNP	C	T	BRC18	NM_005913.1	p.S203F
ROCK1	18	16804456	16804456	Nonsense	SNP	G	A	BRC50	NM_005406.2	p.Q891*
MIB1	18	17602599	17602599	Missense	SNP	G	A	CSB13	NM_020774.2	p.R140H

MIB1	18	17649647	17649647	Nonsense	SNP	C	T	BRC39	NM_020774.2	p.R518*
LAMA3	18	19680361	19680361	Silent	SNP	C	T	BRC31	NM_198129.3	p.T1274
LAMA3	18	19777916	19777916	Missense	SNP	G	A	BRC7	NM_198129.3	p.D3065N
OSBPL1A	18	20001294	20001294	Silent	SNP	G	A	CSB21	NM_080597.3	p.A844
ZNF521	18	21059459	21059459	Missense	SNP	C	G	BRC31	NM_015461.2	p.K807N
CHST9	18	22751025	22751025	Silent	SNP	C	T	CSB33	NM_031422.3	p.E176
DSC2	18	26920572	26920572	Missense	SNP	C	T	CSB15	NM_024422.3	p.V303M
RNF125	18	27852975	27852975	Missense	SNP	C	T	CSB1	NM_017831.3	p.R51C
DTNA	18	30652285	30652285	Missense	SNP	C	A	BRC13	NM_001390.1	p.T290K
GALNT1	18	31497738	31497738	Silent	SNP	A	G	CSB22	NM_020474.3	p.R96
RPRD1A	18	31867717	31867717	Missense	SNP	G	C	CSB12	NM_018170.3	p.T78R
SLC14A2	18	41503401	41503401	Silent	SNP	G	C	BRC47	NM_007163.3	p.T723
KIAA1632	18	41694106	41694106	Missense	SNP	C	T	BRC48	NM_020964.2	p.E2324K
LOXHD1	18	42393468	42393468	Missense	SNP	C	G	BRC39	ENST00000398722	p.D775H
LOC647055	18	44185251	44185251	Silent	SNP	G	T	BRC13	XM_001715324.1	p.L42
SMAD4	18	46845889	46845889	Missense	SNP	G	A	CSB29	NM_005359.5	p.G352R
SMAD4	18	46847404	46847404	Missense	SNP	G	T	CSB29	NM_005359.5	p.G386V
TCF4	18	51403581	51403581	Missense	SNP	T	C	CSB22	NM_001083962.1	p.M25V
FLJ45743	18	51886636	51886636	RNA	SNP	C	T	BRC22	XR_041396.1	NULL
ALPK2	18	54353132	54353132	Missense	SNP	T	C	CSB15	NM_052947.3	p.K1756R
ALPK2	18	54355880	54355880	Missense	SNP	G	A	BRC35	NM_052947.3	p.T840M
ALPK2	18	54425599	54425599	Silent	SNP	C	G	CSB1	NM_052947.3	p.G54
MC4R	18	56189883	56189883	Missense	SNP	G	A	BRC5	NM_005912.2	p.A227V
CDH20	18	57317425	57317425	Silent	SNP	C	T	BRC28	NM_031891.2	p.D91
SERPINB4	18	59457402	59457402	Silent	SNP	C	T	CSB10	NM_002974.2	p.Q255
SERPINB10	18	59736198	59736198	Missense	SNP	C	T	BRC29	NM_005024.1	p.S85L
DSEL	18	63332588	63332588	Missense	SNP	G	A	CSB28	NM_032160.2	p.R90C
ADNP2	18	75995063	75995063	Missense	SNP	G	T	BRC29	NM_014913.3	p.G259V
MED16	19	826318	826318	Missense	SNP	G	T	CSB19	NM_005481.2	p.P566H
TCF3	19	1574994	1574994	Missense	SNP	G	C	CSB1	NM_003200.1	p.Q169E
AP3D1	19	2065241	2065241	Silent	SNP	T	C	CSB26	NM_003938.1	p.K828
DOT1L	19	2153725	2153725	Missense	SNP	T	G	BRC15	NM_032482.2	p.F245C
PIAS4	19	3988823	3988823	Missense	SNP	C	T	BRC21	NM_015897.2	p.R495W
TMIGD2	19	4243734	4243734	Silent	SNP	C	T	BRC47	NM_144615.1	p.A237
ARRDC5	19	4842504	4842504	Missense	SNP	C	T	BRC5	NM_001080523.1	p.E195K

PTPRS	19	5225326	5225326	Missense	SNP	C	G	BRC44	NM_002850.3	p.D41H	
SAFB	19	5574391	5574391	Missense	SNP	G	A	CSB10	NM_002967.2	p.E59K	
FUT3	19	5795323	5795323	Silent	SNP	G	A	CSB15	NM_000149.3	p.S176	
CAPS	19	5865629	5865629	Missense	SNP	C	G	BRC10	NM_004058.3	p.R47G	
KHSRP	19	6367776	6367776	Missense	SNP	G	C	BRC18	NM_003685.2	p.H434D	
C3	19	6629299	6629299	Splice_Site	SNP	C	T	BRC22	NM_000064.2	e40-1	
FBN3	19	8080519	8080519	Silent	SNP	G	A	BRC24	NM_032447.3	p.C1484	
MYO1F	19	8519130	8519130	Silent	SNP	C	T	CSB1	NM_012335.2	p.E391	
MYO1F	19	8522678	8522678	Silent	SNP	C	T	CSB2	NM_012335.2	p.S239	
MYO1F	19	8523020	8523020	Missense	SNP	C	T	BRC47	NM_012335.2	p.R178Q	
ZNF558	19	8784238	8784238	Missense	SNP	G	A	BRC44	NM_144693.1	p.T142M	
MUC16	19	8888224	8888224	Missense	SNP	C	T	CSB9	NM_024690.2	p.S12221N	
MUC16	19	8899382	8899382	Missense	SNP	C	A	BRC16	NM_024690.2	p.S12046I	
MUC16	19	8899397	8899397	Nonsense	SNP	C	T	CSB2	NM_024690.2	p.W12041*	
MUC16	19	8917846	8917846	Missense	SNP	C	G	CSB8	NM_024690.2	p.K10200N	
MUC16	19	8919138	8919138	Missense	SNP	C	G	CSB1	NM_024690.2	p.E9770Q	
MUC16	19	8924524	8924524	Silent	SNP	C	G	CSB1	NM_024690.2	p.L7974	
MUC16	19	8949880	8949880	Missense	SNP	G	T	CSB23	NM_024690.2	p.P979T	
OR7G3	19	9098336	9098336	Silent	SNP	G	A	BRC9	NM_001001958.1	p.C97	
OR7D4	19	9185707	9185707	Silent	SNP	C	T	BRC39	NM_001005191.1	p.Q269	
OR7E24	19	9223271	9223271	Silent	SNP	C	T	CSB1	NM_001079935.1	p.L184	
ZNF699	19	9268112	9268112	Missense	SNP	G	C	CSB1	NM_198535.1	p.S323C	
ZNF699	19	9268983	9268983	Missense	SNP	C	G	CSB1	NM_198535.1	p.E153D	
LOC646048	19	9489952	9489952	RNA	SNP	G	A	BRC22	XR_017059.1	NULL	
OLFM2	19	9829471	9829471	Missense	SNP	G	A	BRC22	NM_058164.2	p.R94C	
COL5A3	19	9949097	9949097	Missense	SNP	G	T	CSB22	NM_015719.3	p.L1060M	
PPAN-P2RY11	19	10081697	10081697	Splice_Site	SNP	G	A	BRC20	NM_001040664.1	e7+1	
EIF3G	19	10087476	10087476	Missense	SNP	G	A	CSB1	NM_003755.3	p.R242C	
SLC44A2	19	10606727	10606741	In Frame Del Frame Shift	DEL	GCACTC AT CAAAGAA	0	BRC41	NM_020428.1	p.LIKEA346in Frame del	
ILF3	19	10652083	10652083	Ins	INS		0	A	CSB16	NM_012218.1	p.R307fs
SMARCA4	19	10991353	10991353	Missense	SNP	C	G	CSB1	NM_003072.1	p.I864M	
KANK2	19	11148359	11148359	Missense	SNP	G	C	CSB24	NM_015493.1	p.T552R	
TSPAN16	19	11269877	11269877	Silent	SNP	G	C	BRC18	NM_012466.2	p.L43	

PRKCSH	19	11418086	11418086	Splice_Site	SNP	G	A	CSB20	NM_002743.1	e8-1
LOC730651	19	12180688	12180688	Missense	SNP	G	A	CSB25	XM_001719635.1	p.R396Q
ZNF442	19	12321899	12321899	Silent	SNP	G	A	BRC39	NM_030824.2	p.F500
ZNF490	19	12552865	12552865	Missense	SNP	C	T	BRC20	NM_020714.2	p.A342T
DHPS	19	12647914	12647914	Missense	SNP	C	G	BRC31	NM_001930.2	p.E311Q
HOOK2	19	12743118	12743118	Missense	SNP	C	T	CSB30	NM_013312.1	p.E206K
RNASEH2A	19	12785164	12785164	Missense	SNP	C	A	BRC35	NM_006397.2	p.Q262K
SAMD1	19	14061038	14061038	Missense	SNP	A	T	CSB19	NM_138352.1	p.L258H
CD97	19	14374542	14374542	Silent	SNP	C	G	BRC39	NM_078481.1	p.L439
AKAP8L	19	15352327	15352327	Splice_Site	SNP	C	A	CSB14	NM_014371.2	e13+1
OR10H4	19	15921515	15921515	Missense	SNP	C	T	CSB3	NM_001004465.1	p.A233V
EPS15L1	19	16409659	16409659	Silent	SNP	C	T	CSB1	NM_021235.1	p.L77
NWD1	19	16769601	16769601	Frame Shift Del	DEL	G		0 CSB30	NM_001007525.2	p.A987fs
NWD1	19	16771888	16771888	Silent	SNP	C	T	CSB1	NM_001007525.2	p.L1082
SIN3B	19	16835532	16835532	Missense	SNP	G	T	CSB8	NM_015260.1	p.E468D
CPAMD8	19	16864925	16864925	Missense	SNP	C	G	CSB1	NM_015692.2	p.L1931F
CPAMD8	19	16868119	16868119	Nonsense	SNP	G	T	BRC39	NM_015692.2	p.S1812*
CPAMD8	19	16878920	16878920	Missense	SNP	C	G	BRC39	NM_015692.2	p.R1337T
CPAMD8	19	16893752	16893752	Missense	SNP	T	G	BRC44	NM_015692.2	p.S1245R
UNC13A	19	17612371	17612371	Silent	SNP	G	A	CSB19	NM_001080421.1	p.T1000
UNC13A	19	17619119	17619119	Missense	SNP	C	T	BRC42	NM_001080421.1	p.V755M
MAP1S	19	17697839	17697839	Missense	SNP	G	A	CSB1	NM_018174.4	p.E216K
SLC5A5	19	17860159	17860159	Nonsense	SNP	C	T	CSB22	NM_000453.2	p.R516*
UPF1	19	18826735	18826735	Missense	SNP	C	G	CSB1	NM_002911.3	p.S438C
DDX49	19	18891562	18891562	Silent	SNP	C	T	CSB1	NM_019070.3	p.F4
NCAN	19	19199200	19199200	Missense	SNP	G	A	BRC11	NM_004386.2	p.E591K
NCAN	19	19217140	19217140	Missense	SNP	G	C	CSB1	NM_004386.2	p.E1171Q
GATAD2A	19	19472990	19472990	Missense	SNP	C	A	CSB12	NM_017660.3	p.T279K
ZNF14	19	19685928	19685928	Missense	SNP	C	G	BRC39	NM_021030.2	p.D55H
ZNF506	19	19766575	19766575	Missense	SNP	C	T	CSB1	NM_001099269.2	p.C374Y
ZNF93	19	19906097	19906097	Missense	SNP	A	G	CSB15	NM_031218.2	p.I445V
ZNF826	19	20369320	20369320	Missense	SNP	C	T	BRC31	NM_001039884.2	p.G116E
ZNF431	19	21118269	21118269	Missense	SNP	T	C	BRC50	NM_133473.2	p.Y27H
UQCRFS1	19	34390467	34390467	Missense	SNP	G	A	CSB2	NM_006003.2	p.T218I

C19orf2	19	35197645	35197645	Silent	SNP	A	C	CSB12	NM_003796.2	p.G479
ZNF536	19	35730953	35730953	Missense	SNP	G	C	CSB25	NM_014717.1	p.V863L
ZNF536	19	35731307	35731307	Missense	SNP	C	T	CSB14	NM_014717.1	p.R981W
CHST8	19	38954797	38954797	Silent	SNP	C	T	BRC28	NM_022467.1	p.N88
ZNF599	19	39942169	39942169	Silent	SNP	A	C	BRC50	NM_001007248.2	p.A459
ATP4A	19	40741864	40741864	Missense	SNP	C	T	CSB1	NM_000704.2	p.E376K
SNX26	19	40962594	40962594	Missense	SNP	G	A	BRC42	ENST00000221905	p.C201Y
SNX26	19	40970611	40970611	Missense	SNP	C	T	CSB10	NM_052948.2	p.R941C
POLR2I	19	41296759	41296759	Missense	SNP	C	G	BRC31	NM_006233.4	p.E105Q
CAPNS1	19	41325432	41325432	Missense	SNP	G	C	CSB1	NM_001003962.1	p.E94D
ZNF146	19	41419421	41419421	Nonsense	SNP	C	G	BRC31	NM_001099638.1	p.S80*
ZNF260	19	41697815	41697815	Missense	SNP	C	T	BRC31	NM_001012756.1	p.E56K
ZNF260	19	41697843	41697843	Missense	SNP	C	G	BRC31	NM_001012756.1	p.K46N
ZNF569	19	42597025	42597025	Silent	SNP	C	A	CSB13	NM_152484.2	p.L125
ZNF573	19	42922717	42922717	Missense	SNP	G	A	BRC39	NM_152360.2	p.R114C
SIPA1L3	19	43264517	43264518	Del	DEL	TC	0	CSB15	NM_015073.1	p.S158fs
C19orf15	19	43534843	43534843	Missense	SNP	C	T	BRC13	ENST00000378713	p.R310W
C19orf15	19	43540915	43540915	Missense	SNP	G	C	CSB1	NM_021185.4	p.R97P
RYR1	19	43650111	43650111	Missense	SNP	G	A	CSB34	NM_000540.2	p.R1067H
RYR1	19	43701701	43701701	Silent	SNP	A	T	CSB15	NM_000540.2	p.A3342
LRFN1	19	44497265	44497265	Silent	SNP	C	T	BRC13	NM_020862.1	p.Q184
PLEKHG2	19	44605533	44605533	Missense	SNP	G	A	BRC31	NM_022835.2	p.E625K
PLEKHG2	19	44605746	44605746	Missense	SNP	G	C	CSB1	NM_022835.2	p.G696R
ZNF780B	19	45233102	45233102	Missense	SNP	C	G	BRC11	NM_001005851.1	p.E502Q
ZNF780B	19	45233657	45233657	Missense	SNP	G	A	BRC11	NM_001005851.1	p.H317Y
ZNF780A	19	45273070	45273070	Silent	SNP	G	A	BRC39	NM_001010880.2	p.L339
AKT2	19	45462979	45462979	Missense	SNP	G	A	BRC21	ENST00000358335	p.S11F
PRX	19	45591975	45591975	Missense	SNP	C	T	CSB7	NM_181882.2	p.R1375Q
ADCK4	19	45907857	45907857	Missense	SNP	C	G	BRC7	NM_024876.1	p.G105A
CYP2A7	19	46078225	46078225	Silent	SNP	G	A	BRC51	NM_000764.2	p.H164
AXL	19	46440689	46440689	Silent	SNP	C	T	CSB1	NM_021913.4	p.V458
PSG4	19	48400053	48400053	Silent	SNP	G	A	CSB22	NM_002780.3	p.D85
ZNF223	19	49263211	49263211	Missense	SNP	C	T	CSB2	NM_013361.4	p.R464C
CBLC	19	49977499	49977499	Silent	SNP	C	T	BRC50	NM_012116.1	p.L230

BCAM	19	50014521	50014521	Missense	SNP	G	A	BRC44	NM_005581.1	p.D518N
LOC284352	19	50333632	50333632	Missense	SNP	G	A	BRC31	XM_001723010.1	p.E75K
LOC100132177	19	50433739	50433739	Silent	SNP	C	T	BRC6	XM_001717776.1	p.G135
ERCC2	19	50554005	50554005	Missense Frame Shift	SNP	C	T	CSB6	ENST00000391940	p.A391T
ERCC2	19	50564241	50564246	Del	DEL	TGACCC	0	CSB22	NM_000400.3	p.G36fs
CCDC61	19	51198176	51198176	Silent	SNP	G	A	CSB16	NM_001080402.1	p.V77
SAE1	19	52398792	52398792	Silent	SNP	A	G	CSB34	NM_005500.1	p.P301
ZNF541	19	52739658	52739658	Missense	SNP	G	A	CSB2	ENST00000391901	p.A647V
CCDC114	19	53515389	53515389	Missense	SNP	C	G	BRC31	ENST00000377438	p.E17Q
PLEKHA4	19	54048874	54048874	Silent	SNP	C	T	BRC20	NM_020904.1	p.L401
RUVBL2	19	54206322	54206322	Missense	SNP	C	A	CSB10	NM_006666.1	p.A315D
CGB7	19	54249431	54249431	Missense	SNP	C	A	CSB7	NM_033142.1	p.A143S
TRPM4	19	54395853	54395853	Silent	SNP	C	T	CSB9	NM_017636.2	p.D984
LOC645971	19	54622504	54622504	Silent	SNP	C	T	BRC16	XM_928936.1	p.P7
PRRG2	19	54778691	54778691	Missense	SNP	G	C	CSB1	NM_000951.2	p.E56Q
SCAF1	19	54849850	54849850	Missense	SNP	T	C	CSB19	NM_021228.1	p.S1177P
SIGLEC11	19	55153736	55153736	Missense	SNP	C	T	CSB23	NM_052884.1	p.V435I
MYH14	19	55442162	55442162	Missense	SNP	T	G	CSB34	NM_001077186.1	p.Y434D
POLD1	19	55598563	55598563	Missense	SNP	C	T	BRC16	NM_002691.2	p.A380V
SPIB	19	55623145	55623145	Missense	SNP	G	A	CSB1	NM_003121.3	p.G177R
MYBPC2	19	55646960	55646960	Missense	SNP	C	T	CSB14	NM_004533.3	p.S546L
LRRC4B	19	55714107	55714107	Silent	SNP	C	G	CSB25	NM_001080457.1	p.L225
GPR32	19	55966663	55966663	Missense	SNP	A	C	CSB10	NM_001506.1	p.T332P
ACPT	19	55989536	55989536	Missense	SNP	C	T	BRC38	NM_033068.2	p.T291I
KLK1	19	56015447	56015447	Missense	SNP	G	A	CSB1	NM_002257.2	p.H91Y
KLK7	19	56175499	56175499	Missense	SNP	A	G	BRC35	NM_005046.2	p.I93T
KLK11	19	56218165	56218165	Missense	SNP	A	G	BRC30	NM_144947.1	p.C231R
KLK14	19	56274588	56274588	Silent	SNP	G	A	BRC39	NM_022046.4	p.V148
FLJ40235	19	56459141	56459141	Missense	SNP	G	A	BRC3	NM_173635.1	p.M1I
SIGLEC10	19	56611956	56611956	Missense	SNP	G	A	BRC38	NM_033130.3	p.T161M
SIGLEC12	19	56696660	56696660	Missense Frame Shift	SNP	G	T	BRC37	NM_053003.1	p.S47Y
HAS1	19	56908493	56908494	Del	DEL	CA	0	BRC38	NM_001523.2	p.*579fs
FPR3	19	57019181	57019181	Missense	SNP	G	A	CSB16	NM_002030.3	p.R123H
ZNF350	19	57161001	57161001	Missense	SNP	G	A	CSB1	NM_021632.3	p.H173Y

ZNF615	19	57189795	57189795	Missense	SNP	G	C	BRC18	NM_198480.2	p.Q116E
ZNF83	19	57809128	57809128	Missense	SNP	G	A	BRC47	NM_001105549.1	p.R168C
ZNF347	19	58337017	58337017	Silent	SNP	A	G	CSB25	NM_032584.1	p.Y292
ZNF765	19	58603481	58603481	Silent	SNP	A	G	BRC40	NM_001040185.1	p.T287
ZNF765	19	58603665	58603665	Missense	SNP	C	T	BRC39	NM_001040185.1	p.H349Y
LILRB5	19	59448223	59448223	Silent	SNP	G	C	BRC44	NM_001081442.1	p.A492
LAIR1	19	59564557	59564557	Missense	SNP	C	T	CSB31	NM_002287.3	p.V48M
LENG8	19	59661106	59661106	Missense	SNP	G	C	CSB1	NM_052925.2	p.E639Q
KIR2DL1	19	59989805	59989805	Missense	SNP	G	A	CSB8	ENST00000391730	p.R50H
KIR2DL1	19	59991664	59991664	Silent	SNP	G	A	CSB1	ENST00000391730	p.T186
FCAR	19	60088626	60088626	Missense	SNP	G	A	CSB1	NM_002000.2	p.E80K
NLRP2	19	60200643	60200643	Missense	SNP	C	T	BRC18	NM_017852.2	p.S1009F
TNNI3	19	60357312	60357312	Silent	SNP	G	T	CSB1	NM_000363.4	p.I149
NLRP4	19	61074078	61074078	Missense	SNP	C	T	CSB24	NM_134444.4	p.R810C
NLRP13	19	61101966	61101966	Missense	SNP	C	T	BRC37	NM_176810.2	p.R980H
NLRP5	19	61207176	61207176	Missense	SNP	G	C	BRC42	NM_153447.4	p.E115D
NLRP5	19	61230517	61230517	Missense	SNP	C	A	BRC11	NM_153447.4	p.S350Y
ZNF582	19	61593239	61593239	Missense	SNP	C	G	BRC50	NM_144690.1	p.E59Q
ZNF582	19	61593647	61593647	Silent	SNP	G	A	BRC4	NM_144690.1	p.F15
ZNF583	19	61617595	61617595	Missense	SNP	A	G	BRC3	NM_152478.1	p.K69R
ZNF835	19	61868222	61868222	Nonsense	SNP	C	A	BRC22	NM_001005850.1	p.E75*
ZIM3	19	62338684	62338684	Missense	SNP	G	T	BRC18	NM_052882.1	p.S278Y
AURKC	19	62435830	62435830	Silent	SNP	C	T	CSB26	NM_001015878.1	p.S135
ZNF304	19	62556919	62556919	Silent	SNP	C	T	CSB1	NM_020657.2	p.F16
ZNF547	19	62581167	62581167	Silent	SNP	C	T	BRC42	NM_173631.2	p.S337
ZNF17	19	62623915	62623915	Missense	SNP	G	C	BRC31	NM_006959.2	p.E415Q
ZNF134	19	62824317	62824317	Missense	SNP	G	C	BRC39	NM_003435.3	p.E340Q
ZNF551	19	62891224	62891224	Missense	SNP	G	C	BRC3	NM_138347.3	p.S574T
ZNF417	19	63112294	63112294	Silent	SNP	A	G	BRC16	NM_152475.2	p.S388
ZNF8	19	63489353	63489353	Missense	SNP	G	C	BRC11	NM_021089.2	p.E87Q
ZNF497	19	63560049	63560049	Silent	SNP	G	A	BRC7	NM_198458.1	p.F255
RPS5	19	63591383	63591383	Missense	SNP	T	C	BRC16	NM_001009.3	p.W23R
UBE2M	19	63760301	63760301	Del	DEL	T	0	BRC51	NM_003969.3	p.I49fs
RSPO4	20	896675	896675	Silent	SNP	G	A	BRC8	NM_001029871.2	p.G62

TGM6	20	2323939	2323939	Missense	SNP	A	G	BRC3	NM_198994.2	p.E94G
C20orf141	20	2745597	2745597	Missense	SNP	A	C	BRC34	ENST00000380593	p.E223A
LOC100131194	20	3411548	3411548	Missense	SNP	T	G	BRC7	XM_001724990.1	p.M7R
CDC25B	20	3731771	3731771	Missense	SNP	C	G	BRC32	NM_021873.3	p.T425R
PANK2	20	3817922	3817922	Nonsense	SNP	C	T	CSB1	NM_153638.4	p.R59*
SMOX	20	4111365	4111365	Silent	SNP	C	A	CSB5	NM_175839.1	p.V413
SLC23A2	20	4798569	4798569	Del	DEL	G		CSB5	NM_005116.5	p.I412fs
SLC23A2	20	4802684	4802684	Missense	SNP	C	T	BRC22	NM_005116.5	p.D334N
PROKR2	20	5231294	5231294	Missense	SNP	G	C	CSB1	NM_144773.2	p.L183V
BMP2	20	6707412	6707412	Silent	SNP	G	C	CSB1	NM_001200.2	p.R289
HAO1	20	7834800	7834800	Splice_Site	SNP	C	A	CSB25	NM_017545.2	e4+1
PLCB1	20	8718216	8718216	Silent	SNP	C	T	CSB15	NM_015192.2	p.I1110
PLCB4	20	9388326	9388326	Missense	SNP	G	C	CSB17	NM_000933.2	p.M1027I
ESF1	20	13711699	13711699	Nonsense	SNP	G	A	BRC13	NM_016649.3	p.R30*
MACROD2	20	15791412	15791412	Missense	SNP	T	A	CSB5	NM_080676.1	p.V223D
KIF16B	20	16434487	16434487	Nonsense	SNP	G	A	BRC5	NM_024704.3	p.Q294*
RRBP1	20	17558499	17558499	Silent	SNP	C	T	CSB15	NM_001042576.1	p.E473
C20orf72	20	17904348	17904348	Missense	SNP	G	A	CSB19	NM_052865.2	p.R178Q
CRNKL1	20	19966137	19966137	Missense	SNP	C	T	CSB1	NM_016652.4	p.E737K
LOC643659	20	20004592	20004592	RNA	SNP	C	T	BRC41	XR_041860.1	NULL
LOC200261	20	23054759	23054759	RNA	SNP	G	T	BRC41	XR_041194.1	NULL
LOC100128232	20	24416515	24416515	Missense	SNP	C	T	BRC44	XM_001718796.1	p.A407V
PYGB	20	25200075	25200075	Missense	SNP	C	T	CSB9	NM_002862.3	p.R161C
PYGB	20	25219149	25219149	Silent	SNP	C	A	CSB1	NM_002862.3	p.I620
NANP	20	25545028	25545028	Missense	SNP	C	T	BRC50	NM_152667.2	p.E94K
REM1	20	29533804	29533804	Silent	SNP	C	T	CSB10	NM_014012.4	p.I159
HM13	20	29596496	29596496	Missense	SNP	G	A	BRC18	NM_178581.2	p.E151K
ID1	20	29657128	29657128	Missense	SNP	G	C	BRC44	NM_002165.2	p.E93Q
FOXS1	20	29896325	29896325	Missense	SNP	C	G	CSB1	NM_004118.3	p.E228Q
C20orf114	20	31341356	31341356	Missense	SNP	A	C	BRC29	NM_033197.2	p.K88Q
PXMP4	20	31759335	31759335	Silent	SNP	G	A	BRC39	NM_007238.4	p.L159
NCOA6	20	32794523	32794523	Missense	SNP	C	A	CSB1	NM_014071.2	p.Q1066H
FAM83C	20	33338327	33338327	Missense	SNP	G	A	BRC47	NM_178468.3	p.L557F
GDF5	20	33485860	33485860	Missense	SNP	C	T	BRC7	NM_000557.2	p.G256E

CEP250	20	33544784	33544784	Silent	SNP	C	T	CSB12	NM_007186.1	p.L1002
ERGIC3	20	33606156	33606156	Missense	SNP	G	A	BRC23	ENST00000357394	p.G231R
RBM39	20	33776456	33776456	Missense	SNP	T	C	CSB23	NM_184234.2	p.D151G
C20orf152	20	34023979	34023979	Silent	SNP	C	T	CSB15	NM_080834.1	p.L22
RBL1	20	35108897	35108897	Silent	SNP	G	C	CSB1	NM_002895.2	p.L526
RBL1	20	35129863	35129863	Nonsense	SNP	A	T	CSB3	NM_002895.2	p.L144*
RPRD1B	20	36119361	36119361	Silent	SNP	G	A	BRC39	NM_021215.3	p.K143
KIAA1755	20	36275187	36275187	Nonsense	SNP	G	A	CSB1	NM_001029864.1	p.Q1092*
KIAA1219	20	36629173	36629173	Missense	SNP	A	G	CSB9	NM_020336.2	p.I1280V
FAM83D	20	37004050	37004050	Missense	SNP	T	C	BRC17	NM_030919.2	p.I203T
PTPRT	20	40261295	40261295	Silent	SNP	G	A	CSB1	NM_133170.5	p.F849
SGK2	20	41628498	41628498	Silent	SNP	C	G	BRC14	NM_016276.3	p.L43
IFT52	20	41676020	41676020	Missense	SNP	A	G	CSB34	NM_016004.2	p.Y201C
SERINC3	20	42576036	42576036	Missense	SNP	C	G	CSB1	NM_006811.2	p.K33N
RIMS4	20	42818225	42818225	Silent	SNP	G	C	CSB1	NM_182970.2	p.L258
SEMG1	20	43269739	43269739	Missense	SNP	C	A	BRC41	NM_003007.2	p.H129Q
SLPI	20	43315638	43315638	Missense	SNP	G	C	BRC7	NM_003064.2	p.P79R
MATN4	20	43359974	43359974	Missense	SNP	G	A	CSB15	NM_003833.3	p.P526L
DNTTIP1	20	43867385	43867385	Missense	SNP	C	G	CSB1	NM_052951.2	p.I232M
ZSWIM3	20	43940585	43940585	Missense	SNP	C	G	BRC41	NM_080752.2	p.L661V
C20orf165	20	43948730	43948730	Missense	SNP	G	A	BRC20	NM_080608.3	p.R173W
SULF2	20	45727389	45727389	Missense	SNP	T	C	CSB7	NM_018837.2	p.K653R
PREX1	20	46695970	46695970	Missense	SNP	C	A	CSB34	NM_020820.3	p.G1113V
PREX1	20	46716300	46716300	Missense	SNP	C	T	CSB1	NM_020820.3	p.G556R
ARFGEF2	20	47024770	47024770	Missense	SNP	G	C	BRC18	NM_006420.2	p.E576Q
PTGIS	20	47557966	47557966	Missense	SNP	G	C	BRC39	NM_000961.3	p.I467M
LOC728671	20	47665949	47665949	Missense	SNP	G	A	BRC11	XM_001128100.1	p.A132T
ADNP	20	48941449	48941449	Missense	SNP	T	G	BRC36	NM_015339.2	p.D1070A
MOCS3	20	49009607	49009607	Missense	SNP	G	A	BRC44	NM_014484.3	p.S274N
LOC100128598	20	49054199	49054199	Missense	SNP	C	A	CSB1	XM_001716142.1	p.Q89K
ATP9A	20	49663774	49663774	Missense	SNP	C	T	BRC5	NM_006045.1	p.G807E
SALL4	20	49834607	49834607	Silent	SNP	C	T	BRC18	NM_020436.3	p.A922
C20orf107	20	54544638	54544638	Nonsense	SNP	C	T	BRC16	NM_001013646.2	p.Q85*
CTCF	20	55531569	55531569	Missense	SNP	C	T	CSB1	NM_080618.2	p.E239K
PCK1	20	55573511	55573511	Missense	SNP	T	C	BRC36	NM_002591.3	p.L443P

STX16	20	56677887	56677887	Silent	SNP	C	T	BRC39	NM_001001433.1	p.F176	
PHACTR3	20	57763705	57763705	Silent	SNP	G	A	CSB8	NM_080672.3	p.S144	
COL9A3	20	60923005	60923005	Missense	SNP	G	A	CSB10	NM_001853.3	p.G113R	
DIDO1	20	60983253	60983253	Silent	SNP	G	C	CSB1	NM_033081.3	p.L1500	
DIDO1	20	60993822	60993822	Missense	SNP	A	T	BRC13	NM_033081.3	p.W1103R	
ARFGAP1	20	61379064	61379064	Silent	SNP	C	T	CSB31	NM_175609.2	p.T135	
PRIC285	20	61670553	61670553	Silent	SNP	C	T	BRC12	NM_001037335.2	p.A444	
LOC100128998	20	61945553	61945553	Silent	SNP	G	A	BRC50	XM_001717148.1	p.L80	
MYT1	20	62324942	62324942	Missense	SNP	A	G	CSB13	NM_004535.2	p.I811V	
IGHV1OR15-9	21	9884537	9884537	Silent	SNP	G	A	CSB16	ENST00000302092	p.A15	
HSPA13	21	14675469	14675469	Missense	SNP	C	T	BRC39	NM_006948.4	p.D98N	
NRIP1	21	15258981	15258981	Missense	SNP	C	T	CSB29	NM_003489.3	p.R1135H	
CHODL	21	18554396	18554396	Missense	SNP	C	T	BRC39	NM_024944.2	p.P186S	
PRSS7	21	18677893	18677893	Silent	SNP	G	A	BRC16	NM_002772.2	p.L140	
ENSG0000019793 4	21	26845421	26845421	Missense	SNP	A	G	BRC26	ENST00000357401	p.N91S	
ADAMTS1	21	27132255	27132255	Silent	SNP	C	T	BRC23	NM_006988.3	p.A806	
GRIK1	21	29847819	29847819	Silent	SNP	C	T	BRC10	NM_000830.3	p.T895	
GRIK1	21	29871277	29871277	Missense	SNP	G	C	BRC31	NM_000830.3	p.L670V	
KRTAP6-3	21	30886714	30886714	Missense	SNP	T	C	CSB15	NM_181605.3	p.Y27H	
URB1	21	32641176	32641176	Silent	SNP	G	T	BRC50	ENST00000382751	p.L1276	
C21orf66	21	33064030	33064030	Silent	SNP	C	G	BRC44	NM_016631.3	p.S146	
DNAJC28	21	33783523	33783523	Silent	SNP	C	T	BRC39	NM_001040192.1	p.L16	
RUNX1	21	35174726	35174726	Missense	SNP	C	T	BRC18	NM_001754.2	p.R169K	
RUNX1	21	35174729	35174729	Missense	SNP	C	T	BRC24	NM_001754.2	p.G168E	
RUNX1	21	35174735	35174735	Missense	SNP	C	T	BRC18	NM_001754.2	p.R166Q	
RUNX1	21	35181062	35181062	Missense	SNP	G	C	CSB14	NM_001754.2	p.S100C	
DOPEY2	21	36539901	36539901	Silent	SNP	C	T	CSB1	NM_005128.2	p.L1251	
DOPEY2	21	36539958	36539958	Silent	SNP	C	T	BRC50	NM_005128.2	p.S1270	
TTC3	21	37450973	37450973	Missense	SNP	C	A	CSB34	NM_001001894.1	p.P963T	
BRWD1	21	39558315	39558315	Missense	SNP	G	C	CSB1	NM_018963.1	p.P609R	
DSCAM	21	40662989	40662996	Del	DEL	A		0	CSB8	NM_001389.3	p.D185fs
FAM3B	21	41642430	41642430	Missense	SNP	G	T	BRC50	NM_058186.3	p.S176I	
MX2	21	41701987	41701987	Missense	SNP	C	T	CSB29	NM_002463.1	p.A702V	
PRDM15	21	42147874	42147874	Silent	SNP	G	A	BRC32	NM_022115.1	p.H502	

PRDM15	21	42147934	42147934	Missense	SNP	C	G	BRC50	NM_022115.1	p.W482C
PRDM15	21	42150492	42150492	Silent	SNP	G	T	CSB12	NM_022115.1	p.P415
PDE9A	21	43054048	43054048	Silent	SNP	C	T	CSB20	NM_002606.1	p.A349
PDXK	21	43993306	43993306	Silent	SNP	C	T	BRC36	NM_003681.4	p.Y127
ICOSLG	21	44479636	44479636	Missense	SNP	C	T	BRC36	NM_015259.4	p.C215Y
KRTAP10-8	21	44856472	44856472	Silent	SNP	G	A	CSB30	NM_198695.1	p.T9
ITGB2	21	45133173	45133173	Missense	SNP	G	A	CSB14	NM_000211.3	p.P648L
ADARB1	21	45388995	45388995	Missense	SNP	A	C	BRC41	ENST00000327861	p.R43S
COL18A1	21	45736896	45736896	Missense	SNP	C	T	BRC38	NM_030582.3	p.P906L
FTCD	21	46381672	46381672	Missense	SNP	G	A	BRC47	NM_006657.2	p.A483V
PCNT	21	46676382	46676382	Missense	SNP	G	A	CSB1	NM_006031.5	p.C2859Y
PCNT	21	46685278	46685278	Missense	SNP	T	G	CSB29	NM_006031.5	p.L3159W
CECR2	22	16402248	16402248	Missense	SNP	G	A	BRC24	ENST00000400585	p.G784S
DGCR5	22	17357106	17357106	RNA	SNP	C	T	BRC31	NR_002733.1	NULL
ENSG00000182490	22	17498870	17498870	Missense	SNP	C	T	CSB19	ENST00000383058	p.R274H
DGCR14	22	17512134	17512134	Missense	SNP	G	A	BRC7	NM_022719.2	p.S7L
HIRA	22	17764433	17764433	Silent	SNP	G	A	CSB19	NM_003325.3	p.V177
TBX1	22	18150437	18150437	Silent	SNP	G	A	BRC11	NM_005992.1	p.G337
RANBP1	22	18489894	18489894	Missense	SNP	G	A	BRC31	NM_002882.2	p.R87H
SCARF2	22	19113896	19113896	Missense	SNP	C	T	CSB7	NM_153334.3	p.V451I
CRYBB3	22	23928682	23928682	Silent	SNP	C	T	BRC39	NM_004076.3	p.C39
ADRBK2	22	24448329	24448329	Missense	SNP	G	A	BRC35	NM_005160.3	p.R660H
MYO18B	22	24496083	24496083	Missense	SNP	G	C	CSB1	NM_032608.5	p.E507Q
MYO18B	22	24552461	24552461	Missense	SNP	C	G	CSB1	NM_032608.5	p.I927M
SEZ6L	22	25019073	25019073	Missense	SNP	A	G	CSB20	NM_021115.3	p.I266V
SEZ6L	22	25073798	25073798	Missense	SNP	G	A	CSB22	NM_021115.3	p.G776S
HPS4	22	25196681	25196690	Frame Shift Del	DEL	TCACAGT CCT	0	CSB15	NM_022081.4	p.G198fs
CRYBB1	22	25325542	25325542	Missense	SNP	G	A	BRC35	NM_001887.3	p.P224L
EWSR1	22	28026111	28026111	Splice_Site	SNP	G	C	CSB1	NM_005243.2	e17-1
RFPL1	22	28164879	28164879	Silent	SNP	C	T	CSB1	NM_021026.2	p.L33
ZMAT5	22	28457234	28457234	Missense	SNP	G	T	BRC21	NM_001003692.1	p.P165T
ENSG00000220549	22	29149172	29149172	Silent	SNP	G	A	BRC39	ENST00000402592	p.V45
OSBP2	22	29613526	29613526	Silent	SNP	G	A	BRC11	NM_030758.3	p.A407

SFI1	22	30301309	30301309	Missense	SNP	C	T	CSB1	NM_001007467.1	p.H339Y	
C22orf30	22	30440362	30440362	Missense	SNP	C	G	BRC39	ENST00000327423	p.E1155Q	
SLC5A1	22	30817669	30817669	Silent	SNP	C	T	BRC29	NM_000343.2	p.S400	
BPIL2	22	31163775	31163775	Missense	SNP	G	A	BRC41	NM_174932.1	p.T240I	
TIMP3	22	31585356	31585356	Missense	SNP	G	A	CSB1	NM_000362.4	p.D210N	
APOL3	22	34886689	34886689	Nonsense	SNP	G	C	CSB1	NM_145640.2	p.S66* p.EEQL1820i	
MYH9	22	35011125	35011136	In Frame Del Frame Shift	DEL	TCCAGC TGCTCC		0	CSB28	NM_002473.4	n Frame del
MYH9	22	35014898	35014907	Del	DEL	CTAGGG CCCC		0	BRC29	NM_002473.4	p.R1528fs
MYH9	22	35025031	35025031	Nonsense	SNP	T	A	CSB30	NM_002473.4	p.K994*	
MYH9	22	35038133	35038133	Missense	SNP	C	G	BRC9	NM_002473.4	p.K545N	
FOXRED2	22	35230224	35230224	Missense	SNP	C	T	BRC11	NM_001102371.1	p.E306K	
CARD10	22	36222449	36222449	Nonsense	SNP	A	T	BRC16	NM_014550.3	p.L671*	
C22orf23	22	36673344	36673344	Missense	SNP	G	A	BRC50	NM_032561.2	p.S80L	
SOX10	22	36703826	36703826	Missense	SNP	G	C	BRC41	NM_006941.3	p.P231A	
PICK1	22	36798953	36798953	Missense	SNP	A	T	BRC17	NM_001039583.1	p.M231L	
KCNJ4	22	37153967	37153967	Silent	SNP	C	T	CSB16	NM_004981.1	p.S39	
						GTAGATT T					
FLJ23865	22	37900224	37900239	Frame Shift Del	DEL	TCCATCT G		0	BRC30	XM_001723522.1	p.Q46fs
CACNA1I	22	38367074	38367074	Missense	SNP	C	A	CSB7	NM_021096.1	p.P333T	
CACNA1I	22	38372696	38372696	Silent	SNP	C	G	BRC38	NM_021096.1	p.V442	
TNRC6B	22	39047107	39047107	Missense	SNP	T	C	BRC44	NM_015088.1	p.L1571P	
SGSM3	22	39131719	39131719	Missense	SNP	G	A	CSB3	NM_015705.4	p.D247N	
PHF5A	22	40193472	40193472	Missense	SNP	G	A	CSB25	NM_032758.3	p.R57C	
XRCC6	22	40389675	40389675	Missense	SNP	G	A	BRC7	NM_001469.3	p.M580I	
SEPT3	22	40718687	40718687	Missense	SNP	G	A	BRC44	NM_145733.5	p.R280Q	
CYP2D6	22	40853579	40853579	Silent	SNP	G	A	BRC51	NM_000106.4	p.R329	
SCUBE1	22	41944329	41944329	Silent	SNP	G	A	BRC13	NM_173050.2	p.I589	
PHF21B	22	43660072	43660072	Silent	SNP	G	C	BRC31	NM_138415.1	p.V425	
SMC1B	22	44173639	44173639	Missense	SNP	C	A	BRC35	NM_148674.3	p.Q371H	
PKDREJ	22	45034150	45034150	Missense	SNP	C	A	BRC51	NM_006071.1	p.G1245V	
LOC100129944	22	48436188	48436188	Silent	SNP	A	G	BRC50	XM_001725094.1	p.T83	
TUBGCP6	22	49001675	49001675	Silent	SNP	G	A	BRC38	NM_020461.3	p.H1080	
NCAPH2	22	49307068	49307068	Missense	SNP	G	A	CSB8	NM_152299.4	p.E345K	

TYMP	22	49312556	49312556	Silent	SNP	G	C	CSB1	NM_001953.1	p.L223
ODF3B	22	49316601	49316601	Missense	SNP	G	T	CSB1	ENST00000405135	p.P117T
CHKB	22	49365090	49365090	Missense	SNP	C	G	BRC39	NM_005198.3	p.K321N
CHKB	22	49365325	49365325	Missense	SNP	C	T	BRC39	NM_005198.3	p.E291K
ENSG0000022307 3	MT	178	178	RNA	SNP	A	G	CSB22	ENST00000411141	NULL
ENSG0000021145 9	MT	711	711	RNA	SNP	G	A	CSB24	ENST00000389680	NULL
ENSG0000021145 9	MT	859	859	RNA	SNP	G	A	CSB6	ENST00000389680	NULL
ENSG0000021145 9	MT	1364	1364	RNA	SNP	G	A	CSB3	ENST00000389680	NULL
ENSG0000021008 2	MT	1696	1696	RNA	SNP	T	C	BRC39	ENST00000387347	NULL
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ENSG0000021008 2	MT	2348	2348	RNA	SNP	T	C	CSB19	ENST00000387347	NULL
ENSG0000021008 2	MT	2911	2911	RNA	SNP	G	A	CSB28	ENST00000387347	NULL
ENSG0000020908 2	MT	3244	3244	RNA	SNP	A	G	CSB12	ENST00000386347	NULL
MT-ND2	MT	5208	5208	Silent	SNP	C	T	CSB15	ENST00000361453	p.S246
MT-ND2	MT	5329	5329	Missense	SNP	C	T	CSB32	ENST00000361453	p.L287F
ENSG0000021014 4	MT	5839	5839	RNA	SNP	G	A	CSB26	ENST00000387409	NULL
MT-CO1	MT	6740	6740	Nonsense	SNP	C	A	BRC18	ENST00000361624	p.S279*
MT-CO1	MT	6751	6751	Silent	SNP	C	T	BRC9	ENST00000361624	p.L283
MT-CO1	MT	7229	7229	Missense	SNP	A	T	BRC39	ENST00000361624	p.D442V
MT-CO3	MT	9362	9362	Missense	SNP	T	C	BRC34	ENST00000362079	p.L52P
MT-CO3	MT	9967	9967	Missense	SNP	G	A	CSB13	ENST00000362079	p.V254I
MT-ND3	MT	10069	10069	Missense	SNP	G	A	BRC35	ENST00000361227	p.A4T
MT-ND3	MT	10369	10369	Missense	SNP	T	C	CSB22	ENST00000361227	p.Y104H
MT-ND4	MT	10523	10523	Missense	SNP	G	A	BRC32	ENST00000361335	p.G18E
MT-ND4	MT	10947	10947	Missense	SNP	A	G	CSB9	ENST00000361381	p.T63A
MT-ND4	MT	11252	11252	Silent	SNP	A	G	CSB22	ENST00000361381	p.L164
MT-ND4	MT	11694	11694	Missense	SNP	G	A	BRC34	ENST00000361381	p.A312T
MT-ND4	MT	11800	11800	Missense	SNP	G	A	BRC24	ENST00000361381	p.G347E
MT-ND4	MT	11819	11819	Silent	SNP	A	G	CSB1	ENST00000361381	p.P353
MT-ND4	MT	11866	11866	Missense	SNP	T	C	BRC51	ENST00000361381	p.L369S

MT-ND4	MT	12016	12016	Missense	SNP	T	C	BRC39	ENST00000361381	p.L419P
MT-ND5	MT	12455	12455	Missense	SNP	G	A	CSB22	ENST00000361567	p.V40I
MT-ND5	MT	12613	12613	Silent	SNP	A	G	CSB22	ENST00000361567	p.V92
MT-ND5	MT	12706	12706	Silent	SNP	T	C	CSB13	ENST00000361567	p.I123
MT-ND5	MT	13800	13800	Missense	SNP	T	C	BRC33	ENST00000361567	p.L488P
MT-ND5	MT	13895	13895	Missense	SNP	T	C	BRC39	ENST00000361567	p.F520L
MT-ND5	MT	13955	13955	Silent	SNP	C	T	CSB28	ENST00000361567	p.L540
MT-CYB	MT	14832	14832	Missense	SNP	G	A	CSB17	ENST00000361789	p.A29T
MT-CYB	MT	15453	15453	Missense	SNP	C	A	CSB22	ENST00000361789	p.L236I
MT-CYB	MT	15675	15675	Missense	SNP	T	C	BRC24	ENST00000361789	p.S310P
MT-CYB	MT	15823	15823	Missense	SNP	T	C	BRC29	ENST00000361789	p.F359S
	NT									
	_1									
	13									
	94									
KIR2DS2	9	135024	135024	Missense	SNP	A	T	CSB25	ENST00000400833	p.Q110L
	NT									
	_1									
	13									
	95									
ENSG0000021288	4	54089	54089	Missense	SNP	T	G	CSB14	ENST00000391570	p.L91R
3										
DHR SX	X	2219556	2219556	Silent	SNP	G	C	CSB7	NM_145177.2	p.V125
GYG2	X	2809191	2809191	Silent	SNP	C	T	CSB22	NM_003918.1	p.I481
ARSD	X	2848740	2848740	Missense	SNP	C	T	BRC32	NM_001669.2	p.R114Q
NLGN4X	X	5957388	5957388	Silent	SNP	G	A	CSB8	NM_020742.2	p.D186
SHROOM2	X	9867242	9867242	Missense	SNP	G	A	CSB31	NM_001649.2	p.E1383K
SHROOM2	X	9874849	9874849	Missense	SNP	T	C	CSB8	NM_001649.2	p.Y1575H
MID1	X	10377466	10377466	Missense	SNP	G	A	CSB22	NM_000381.2	p.T649M
ARHGAP6	X	11070333	11070333	Missense	SNP	T	G	BRC15	NM_013427.2	p.D733A
FRMPD4	X	12537851	12537851	Silent	SNP	G	A	BRC51	NM_014728.2	p.R83
TLR7	X	12814643	12814643	Silent	SNP	A	T	BRC15	NM_016562.3	p.A365
TLR8	X	12849391	12849391	Missense	SNP	G	A	CSB29	NM_138636.3	p.G771R
TCEANC	X	13590865	13590865	Missense	SNP	C	T	BRC51	NM_152634.2	p.S136F
MOSPD2	X	14831031	14831031	Missense	SNP	G	A	CSB16	NM_152581.2	p.M187I
MOSPD2	X	14842565	14842565	Missense	SNP	T	A	CSB20	NM_152581.2	p.F338I
FIGF	X	15283313	15283313	Nonsense	SNP	G	T	BRC30	NM_004469.2	p.S174*
CTPS2	X	16621479	16621479	Missense	SNP	C	G	BRC50	NM_019857.1	p.R164T
RBBP7	X	16780118	16780118	Missense	SNP	C	T	BRC7	NM_002893.3	p.D338N

PPEF1	X	18753835	18753835	Silent	SNP	C	T	BRC50	NM_006240.2	p.L571
PHKA2	X	18829613	18829613	Missense	SNP	G	T	CSB2	NM_000292.2	p.P980T
GPR64	X	18936114	18936114	Missense	SNP	G	A	BRC33	NM_001079858.1	p.L491F
YY2	X	21785547	21785547	Missense	SNP	G	T	BRC14	NM_206923.2	p.V342L
ZNF645	X	22201343	22201343	Missense	SNP	C	T	CSB12	NM_152577.2	p.A105V
DDX53	X	22928263	22928263	Missense	SNP	G	C	BRC26	NM_182699.2	p.K56N
SAT1	X	23711740	23711740	Silent	SNP	T	G	BRC50	NM_002970.1	p.T37
MAGEB6	X	26122753	26122753	Missense	SNP	C	T	BRC4	NM_173523.2	p.S290L
MAGEB4	X	30170819	30170819	Missense	SNP	C	T	BRC49	NM_002367.2	p.R216C
DMD	X	31407037	31407037	Silent	SNP	G	A	CSB1	NM_004006.2	p.L2884
DMD	X	31764847	31764847	Missense	SNP	A	C	BRC41	NM_004006.2	p.I2370R
DMD	X	32292631	32292631	Missense	SNP	C	A	CSB1	NM_004006.2	p.D1715Y
DMD	X	32419363	32419363	Silent	SNP	G	A	CSB22	NM_004006.2	p.T858
FAM47A	X	34060052	34060052	Missense	SNP	C	A	BRC51	NM_203408.2	p.D89Y
TMEM47	X	34567379	34567379	Silent	SNP	G	A	BRC28	NM_031442.3	p.I91
MAGEB16	X	35730507	35730507	In Frame Ins	INS		GAAGA 0 G	BRC41	NM_001099921.1	p.93in Frame insEE
FAM47C	X	36936727	36936727	Missense	SNP	C	T	BRC5	NM_001013736.1	p.S108L
FAM47C	X	36939095	36939095	Silent	SNP	G	A	BRC13	NM_001013736.1	p.L897
SRPX	X	37918375	37918375	Missense	SNP	C	T	CSB1	NM_006307.3	p.D111N
RPGR	X	38029771	38029771	Missense	SNP	T	A	BRC35	NM_001034853.2	p.N1142I
BCOR	X	39798141	39798141	Missense	SNP	C	G	BRC39	NM_017745.1	p.E1606Q
USP9X	X	40910205	40910205	Missense	SNP	G	A	BRC13	NM_001039590.2	p.E708K
USP9X	X	40960563	40960563	Missense	SNP	G	A	CSB1	NM_001039590.2	p.M1933I
USP9X	X	40961443	40961443	Nonsense	SNP	G	T	CSB1	NM_001039590.2	p.E2038*
CASK	X	41354172	41354172	Missense	SNP	C	T	CSB1	NM_003688.2	p.D362N
GPR82	X	41471496	41471496	Silent	SNP	C	T	CSB1	NM_080817.3	p.V91
UTX	X	44826823	44826823	Nonsense	SNP	C	A	BRC29	NM_021140.2	p.S1068*
RGN	X	46836026	46836026	Missense	SNP	C	T	CSB27	NM_004683.4	p.R190C
CFP	X	47371133	47371133	Missense	SNP	G	A	CSB15	NM_002621.1	p.T308I
ZNF81	X	47659282	47659282	Missense	SNP	T	A	BRC41	NM_007137.2	p.I98N
ZNF182	X	47721935	47721935	Missense	SNP	A	T	BRC7	NM_006962.1	p.N165K
ZNF630	X	47802842	47802842	Missense	SNP	G	A	BRC41	NM_001037735.2	p.H521Y
SLC38A5	X	48204048	48204048	Silent	SNP	C	T	CSB10	NM_033518.2	p.P333
TBC1D25	X	48303528	48303528	Missense	SNP	A	C	BRC35	NM_002536.2	p.T430P

LOC100128587	X	48485258	48485258	Silent	SNP	C	T	BRC51	XM_001719769.1	p.P8
GATA1	X	48534575	48534575	Missense	SNP	G	C	CSB1	NM_002049.3	p.E39Q
OTUD5	X	48666245	48666245	Nonsense	SNP	G	T	BRC39	NM_017602.1	p.S436*
MAGIX	X	48909463	48909463	Silent	SNP	C	G	CSB1	NM_024859.1	p.L262
CACNA1F	X	48949105	48949105	Missense	SNP	C	T	BRC20	NM_005183.2	p.R1873H
DGKK	X	50148268	50148268	Missense	SNP	G	A	CSB14	ENST00000376025	p.T672I
XAGE3	X	52912194	52912194	Silent	SNP	C	T	CSB1	NM_130776.1	p.E60
JARID1C	X	53245037	53245037	Missense	SNP	A	G	BRC18	NM_004187.2	p.F697S
HUWE1	X	53620725	53620725	Missense	SNP	C	T	BRC11	NM_031407.4	p.R1915K
PHF8	X	54028108	54028108	Missense	SNP	C	T	BRC19	NM_015107.2	p.D803N
FGD1	X	54511983	54511983	Missense	SNP	C	G	CSB1	NM_004463.2	p.E385Q
MAGED2	X	54852494	54852494	Missense	SNP	C	T	BRC7	NM_014599.4	p.S2F
ALAS2	X	55069011	55069011	Missense	SNP	G	C	CSB1	NM_000032.4	p.Q50E
MAGEH1	X	55496088	55496088	Silent	SNP	C	A	BRC50	NM_014061.3	p.R186
ARHGEF9	X	62842945	62842945	Missense	SNP	C	T	BRC42	NM_015185.2	p.R100Q
MTMR8	X	63405496	63405496	Silent	SNP	G	A	BRC13	NM_017677.2	p.T587
AR	X	66847982	66847982	Missense	SNP	G	C	CSB1	NM_000044.2	p.K633N
EFNB1	X	67977165	67977165	Silent	SNP	C	A	CSB22	NM_004429.4	p.V328
TEX11	X	69815429	69815429	Missense	SNP	T	C	CSB33	NM_001003811.1	p.M413V
GJB1	X	70360736	70360736	Missense	SNP	G	A	CSB13	NM_000166.5	p.V152I
TAF1	X	70591334	70591334	Missense	SNP	C	G	BRC31	NM_004606.3	p.Q1634E
NHSL2	X	71277282	71277282	Silent	SNP	A	G	BRC8	NM_001013627.1	p.Q687
ERCC6L	X	71343555	71343555	Missense	SNP	C	A	BRC39	NM_017669.2	p.R596I
LPAR4	X	77897817	77897817	Nonsense	SNP	C	A	CSB31	NM_005296.2	p.Y265*
P2RY10	X	78103248	78103248	Missense	SNP	C	G	BRC44	NM_014499.2	p.A192G
BRWD3	X	79819343	79819343	Silent	SNP	T	C	CSB2	NM_153252.3	p.G1610
BRWD3	X	79829084	79829084	Missense	SNP	C	A	CSB22	NM_153252.3	p.L1313F
BRWD3	X	79934008	79934008	Splice_Site	SNP	C	T	BRC47	NM_153252.3	e6+1
HDX	X	83610620	83610620	Missense	SNP	C	G	CSB2	NM_144657.3	p.R256T
APOOL	X	84229311	84229311	Missense	SNP	G	A	CSB1	NM_198450.3	p.D260N
ZNF711	X	84412901	84412901	Missense	SNP	A	G	BRC22	NM_021998.4	p.H566R
POF1B	X	84449863	84449863	Missense	SNP	C	G	BRC13	NM_024921.3	p.D325H
TGIF2LX	X	89064225	89064225	Missense	SNP	T	G	BRC38	NM_138960.3	p.L162W
TGIF2LX	X	89064374	89064374	Missense	SNP	G	A	BRC19	NM_138960.3	p.A212T
DIAPH2	X	95880324	95880324	Silent	SNP	G	A	CSB22	NM_006729.4	p.A83

TNMD	X	99741231	99741231	Missense	SNP	G	T	BRC15	NM_022144.2	p.G272V
DRP2	X	100384554	100384554	Silent	SNP	A	T	BRC31	NM_001939.2	p.S327
GLA	X	100545499	100545499	Missense	SNP	C	A	BRC31	NM_000169.2	p.D109Y
GPRASP2	X	101857424	101857424	Missense	SNP	A	T	CSB19	NM_001004051.1	p.D324V
TCEAL4	X	102728686	102728686	Missense	SNP	G	C	CSB1	NM_001006935.1	p.E143Q
IL1RAPL2	X	104885901	104885901	Missense	SNP	G	A	CSB1	NM_017416.1	p.E423K
NRK	X	105070562	105070562	Silent	SNP	G	A	BRC13	ENST00000243300	p.L1281
MORC4	X	106123226	106123226	Silent	SNP	T	C	CSB16	NM_024657.1	p.V66
FRMPD3	X	106730490	106730490	Silent	SNP	C	T	BRC13	XM_042978.1	p.G888
MID2	X	107035513	107035513	Splice_Site	SNP	G	A	BRC35	NM_012216.3	e4+1
CAPN6	X	110378830	110378830	Missense	SNP	C	G	BRC39	NM_014289.2	p.E424Q
TRPC5	X	111082284	111082284	Silent	SNP	T	C	CSB34	NM_012471.2	p.K7
AMOT	X	111921851	111921851	Missense	SNP	T	G	BRC51	NM_133265.1	p.Q188H
LRCH2	X	114306421	114306421	Missense	SNP	C	T	BRC7	NM_020871.3	p.E418K
AGTR2	X	115218111	115218111	Missense	SNP	G	A	BRC7	NM_000686.4	p.V184I
AGTR2	X	115218313	115218313	Missense	SNP	G	A	BRC28	NM_000686.4	p.R251H
KLHL13	X	116919874	116919874	Missense	SNP	G	A	BRC29	NM_033495.2	p.P477L
KLHL13	X	116927862	116927862	Missense	SNP	G	A	BRC39	NM_033495.2	p.R266C
DOCK11	X	117560965	117560965	Missense	SNP	G	C	CSB1	NM_144658.3	p.E90Q
DOCK11	X	117563354	117563354	Missense	SNP	G	C	CSB1	NM_144658.3	p.E145Q
KIAA1210	X	118105771	118105771	Silent	SNP	C	T	BRC31	NM_020721.1	p.G1150
NKRF	X	118608483	118608483	Silent	SNP	C	T	CSB1	NM_017544.2	p.L311
AKAP14	X	118921611	118921611	Missense	SNP	C	T	CSB14	ENST00000371425	p.P88L
GLUD2	X	120009975	120009975	Silent	SNP	C	T	BRC37	NM_012084.3	p.H252
THOC2	X	122668448	122668448	Missense	SNP	G	C	CSB1	NM_001081550.1	p.H55D
STAG2	X	123017718	123017718	Missense	SNP	C	T	BRC35	NM_001042749.1	p.S419L
STAG2	X	123027769	123027769	Silent	SNP	C	A	BRC50	NM_001042749.1	p.I720
SH2D1A	X	123308179	123308179	Silent	SNP	C	T	CSB12	NM_002351.1	p.D2
ODZ1	X	123613457	123613457	Missense	SNP	T	A	CSB9	NM_014253.2	p.T523S
CXorf64	X	125783186	125783186	Missense	SNP	G	A	BRC31	ENST00000371125	p.R295K
ACTRT1	X	127013347	127013347	Silent	SNP	G	A	BRC18	NM_138289.2	p.L174
SMARCA1	X	128469603	128469603	Missense	SNP	G	C	CSB1	NM_003069.3	p.S321C
OCRL	X	128538066	128538066	Silent	SNP	C	T	BRC50	NM_000276.3	p.L657
ELF4	X	129029052	129029052	Silent	SNP	G	T	BRC24	NM_001421.1	p.P439
ZNF280C	X	129198208	129198208	Missense	SNP	C	G	CSB1	NM_017666.3	p.D194H

SLC25A14	X	129326343	129326343	Missense	SNP	G	A	CSB33	NM_003951.2	p.D219N
ENOX2	X	129629187	129629187	Missense	SNP	T	C	BRC13	NM_182314.2	p.Q331R
ENOX2	X	129629202	129629202	Missense	SNP	G	C	BRC39	NM_182314.2	p.S326C
FLJ30058	X	130043427	130043427	Missense	SNP	G	C	CSB22	NM_144967.3	p.G36A
MST4	X	131016383	131016383	Missense	SNP	G	A	CSB19	NM_016542.1	p.R29H
USP26	X	131989404	131989404	Missense	SNP	C	G	BRC48	NM_031907.1	p.E171Q
TFDP3	X	132178893	132178893	Missense	SNP	G	C	CSB1	NM_016521.2	p.S294C
MIRN424	X	133508343	133508343	RNA	SNP	G	T	CSB32	ENST00000362227	NULL
PLAC1	X	133527974	133527974	Silent	SNP	C	T	CSB1	NM_021796.3	p.K135
LOC100128949	X	133983708	133983708	Missense	SNP	G	A	CSB29	XM_001720075.1	p.G108R
LOC650024	X	134175942	134175942	Silent	SNP	G	A	CSB28	XM_001715421.1	p.A139
LOC644717	X	134602695	134602695	Splice_Site	SNP	C	G	BRC12	XR_037249.1	NULL
LOC644717	X	134637410	134637410	RNA	SNP	C	A	CSB1	XR_037249.1	NULL
SAGE1	X	134822228	134822228	Silent	SNP	G	A	BRC41	NM_018666.2	p.K868
GPR112	X	135257364	135257364	Missense	SNP	C	A	BRC50	NM_153834.3	p.S1278Y
GPR112	X	135259247	135259247	Missense	SNP	G	A	BRC39	NM_153834.3	p.E1906K
GPR112	X	135271303	135271303	Missense	SNP	G	A	CSB1	NM_153834.3	p.E2390K
GPR112	X	135307719	135307719	Missense	SNP	C	G	CSB1	NM_153834.3	p.S2733C
MCF2	X	138526283	138526283	Missense	SNP	C	G	BRC39	NM_001099855.1	p.D399H
ATP11C	X	138698131	138698131	Missense	SNP	C	A	CSB33	NM_173694.1	p.C472F
MAGEC3	X	140796895	140796895	Missense	SNP	G	A	BRC7	NM_138702.1	p.E186K
MAGEC3	X	140812728	140812728	Missense	SNP	G	T	CSB22	NM_138702.1	p.E506D
CXorf1	X	144716957	144716957	Missense	SNP	A	G	BRC47	NM_004709.2	p.I24V
AFF2	X	147845835	147845835	Missense	SNP	A	G	CSB15	NM_002025.2	p.K854E
CNGA2	X	150661759	150661759	Missense	SNP	G	A	BRC3	NM_005140.1	p.R193Q
MAGEA4	X	150843498	150843498	Missense	SNP	G	A	BRC4	NM_001011548.1	p.E236K
GABRA3	X	151087367	151087367	Missense	SNP	G	A	BRC26	NM_000808.3	p.R490C
GABRQ	X	151569558	151569558	Missense	SNP	C	T	CSB34	NM_018558.1	p.R254C
GABRQ	X	151571993	151571993	Missense	SNP	G	A	CSB9	NM_018558.1	p.E498K
MAGEA6	X	151620281	151620281	Missense	SNP	C	G	BRC13	NM_005363.2	p.F105L
MAGEA12	X	151650623	151650623	Silent	SNP	G	A	BRC39	NM_005367.4	p.L278
ZNF185	X	151861008	151861008	Missense	SNP	G	A	BRC31	ENST00000318504	p.E34K
ATP2B3	X	152483653	152483653	Missense	SNP	C	A	CSB22	NM_001001344.1	p.D1080E
ABCD1	X	152655896	152655896	Silent	SNP	C	A	BRC20	NM_000033.3	p.I495
HCFC1	X	152875300	152875300	Missense	SNP	C	A	BRC7	NM_005334.2	p.V869F

FLNA	X	153246440	153246440	Missense	SNP	C	T	CSB27	NM_001456.1	p.V591I
PLXNA3	X	153350660	153350660	Missense	SNP	A	T	CSB22	NM_017514.3	p.D1501V
CTAG2	X	153534736	153534736	Missense	SNP	G	A	CSB28	NM_020994.2	p.P83L
MPP1	X	153663230	153663230	Nonsense	SNP	C	A	BRC18	NM_002436.2	p.E330*
BRCC3	X	153953038	153953038	Silent	SNP	C	T	CSB1	NM_024332.1	p.L14
BRCC3	X	154001532	154001532	Missense	SNP	G	T	CSB3	NM_024332.1	p.E288D
SPRY3	X	154657112	154657112	Missense	SNP	C	G	CSB1	NM_005840.1	p.L129V

Supplementary Table 5a: Tier1 somatic mutations

Shown are tier1 coding somatic mutations identified and validated in the 46 whole genome sequenced luminal breast cancer cases and tier1 somatic mutations detected in exome capture sequencing data from 31 tumours. Tier1 mutations that occur exclusively within annotated pseudogenes or transcripts with an incomplete ORF are not shown.

Seq_ID	Patient_ID	Seq_Type
BRC3	15991	WGS
BRC4	804	WGS
BRC5	807	WGS
BRC6	814	WGS
BRC7	828	WGS
BRC8	834	WGS
BRC9	837	WGS
BRC10	16041	WGS
BRC11	15601	WGS
BRC12	15736	WGS
BRC13	16024	WGS
BRC14	15687	WGS
BRC15	16252	WGS
BRC16	15760	WGS
BRC17	16227	WGS
BRC18	16319	WGS
BRC19	16347	WGS
BRC20	16454	WGS
BRC21	15583	WGS
BRC22	15714	WGS
BRC23	16187	WGS
BRC24	16314	WGS
BRC25	16350	WGS
BRC26	16357	WGS
BRC28	16180	WGS
BRC29	16062	WGS
BRC30	16481	WGS
BRC31	15910	WGS

BRC32	16111	WGS
BRC33	15984	WGS
BRC34	16220	WGS
BRC35	15953	WGS
BRC36	15990	WGS
BRC37	15970	WGS
BRC38	16178	WGS
BRC39	16300	WGS
BRC40	15917	WGS
BRC41	15945	WGS
BRC42	16431	WGS
BRC44	15985	WGS
BRC47	16277	WGS
BRC48	16408	WGS
BRC49	16589	WGS
BRC50	16107	WGS
BRC51	820	WGS
BRC52	16918	WGS
CSB1	15544	Exome
CSB2	15574	Exome
CSB3	15901	Exome
CSB5	15952	Exome
CSB6	15976	Exome
CSB7	15980	Exome
CSB8	16007	Exome
CSB9	16043	Exome
CSB10	16074	Exome
CSB12	16148	Exome
CSB13	16170	Exome
CSB14	16171	Exome

CSB15	16202	Exome
CSB16	16216	Exome
CSB17	16237	Exome
CSB19	16315	Exome
CSB20	16326	Exome
CSB21	16364	Exome
CSB22	16376	Exome
CSB23	16398	Exome
CSB24	16727	Exome
CSB25	16754	Exome
CSB26	16786	Exome
CSB27	16837	Exome
CSB28	16846	Exome
CSB29	16912	Exome
CSB30	16947	Exome
CSB31	15462	Exome
CSB32	15858	Exome
CSB33	16566	Exome
CSB34	16847	Exome

Supplementary Table 5b: Sample Key for Whole Genome and Exome Capture Samples

Hugo_Symbol	Chromosome	Start_position	End_position	Variant_Classification	Variant_Type	Reference_Allele	Variant_Allele	Tumor_Sample_Barcode	transcript_name	amino_acid_change
PIK3CA	3	180399623	180399628	In Frame Del	DEL	GGCAAC	0	409	NM_006218.2	p.G106in Frame del
PIK3CA	3	180404243	180404243	Missense Mutation	SNP	T	G	829	NM_006218.2	p.V344G
PIK3CA	3	180404247	180404247	Missense Mutation	SNP	T	A	16069	NM_006218.2	p.N345K
PIK3CA	3	180404247	180404247	Missense Mutation	SNP	T	A	16140	NM_006218.2	p.N345K
PIK3CA	3	180404260	180404260	Missense Mutation	SNP	G	C	808	NM_006218.2	p.D350H
PIK3CA	3	180410671	180410676	In Frame Del	DEL	CACTGT	0	15867	NM_006218.2	p.H419in Frame del
PIK3CA	3	180410674	180410674	Missense Mutation	SNP	T	C	309	NM_006218.2	p.C420R
PIK3CA	3	180410674	180410674	Missense Mutation	SNP	T	C	16442	NM_006218.2	p.C420R
PIK3CA	3	180410920	180410920	Missense Mutation	SNP	C	T	15694	NM_006218.2	p.P471L
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	A	15654	NM_006218.2	p.E542K
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	A	15832	NM_006218.2	p.E542K
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	A	15868	NM_006218.2	p.E542K
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	A	15870	NM_006218.2	p.E542K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	115	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	308	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	15510	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	15547	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	15669	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	15776	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	15797	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	15894	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	16025	NM_006218.2	p.E545K
PIK3CA	3	180418786	180418786	Missense Mutation	SNP	A	C	122	NM_006218.2	p.E545A
PIK3CA	3	180418786	180418786	Missense Mutation	SNP	A	G	15880	NM_006218.2	p.E545G
PIK3CA	3	180418789	180418789	Missense Mutation	SNP	A	G	16402	NM_006218.2	p.Q546R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	112	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	117	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	831	NM_006218.2	p.H1047R

PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15386	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15694	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	15816	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15829	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15977	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15995	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16064	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16099	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16127	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16136	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16411	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	16439	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16450	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16495	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16561	NM_006218.2	p.H1047R
MAP3K1	5	56191315	56191316	Frame Shift Ins	INS	0	C	15894	NM_005921.1	p.V218fs
MAP3K1	5	56191385	56191385	Frame Shift Ins	INDEL	G	TT	15694	NM_005921.1	p.A240fs
MAP3K1	5	56196966	56196966	Frame Shift Del	DEL	T	0	15995	NM_005921.1	p.F360fs
MAP3K1	5	56212767	56212771	Frame Shift Del	DEL	TATAG	0	15510	NM_005921.1	p.I761fs
MAP3K1	5	56212856	56212858	Frame Shift Del	DEL	GGT	0	16561	NM_005921.1	p.R790fs
MAP3K1	5	56213154	56213155	Frame Shift Ins	INS	0	G	15770	NM_005921.1	p.Y790fs
MAP3K1	5	56213522	56213528	Frame Shift Del	INDEL	AAGGATT	TC	15977	NM_005921.1	p.K913fs
MAP3K1	5	56213777	56213778	Frame Shift Ins	INS	0	C	122	NM_005921.1	p.T999fs
MAP3K1	5	56215219	56215219	Nonsense_Mutation	SNP	C	T	15919	NM_005921.1	p.Q1259*
MAP3K1	5	56218969	56218980	In Frame Del	DEL	TTTGCTAATTGA	0	15894	NM_005921.1	p.L1375in Frame del
MAP3K1	5	56225250	56225250	Missense Mutation	SNP	C	T	16392	NM_005921.1	p.R1509C
GATA3	10	8146064	8146064	Missense Mutation	SNP	T	A	115	NM_001002295.1	p.M294K
GATA3	10	8146064	8146064	Missense Mutation	SNP	T	A	808	NM_001002295.1	p.M294K
GATA3	10	8155729	8155729	Nonsense_Mutation	SNP	A	T	16093	NM_001002295.1	p.K358*
GATA3	10	8155867	8155868	Frame Shift Del	DEL	CT	0	15830	NM_001002295.1	p.L404fs
GATA3	10	8155881	8155882	Frame Shift Ins	INS	0	G	15931	NM_001002295.1	p.P408fs
GATA3	10	8155896	8155897	Frame Shift Ins	INS	0	C	16224	NM_001002295.1	p.S413fs
GATA3	10	8155918	8155931	Frame Shift Del	DEL	ACGCCGATGCACCC	0	15968	NM_001002295.1	p.T421fs
GATA3	10	8155961	8155980	Frame Shift Del	DEL	ACCCTCCAGCATGGTCACC	0	818	NM_001002295.1	p.H435fs
GATA3	10	8155973	8155974	Frame Shift Ins	INS	0	AGCAT	15660	NM_001002295.1	p.M439fs

CDKN1B	12	12762165	12762165	Missense Mutation	SNP	C	T	16441	NM_004064.3	p.T42I
CDKN1B	12	12762441	12762441	Frame Shift Del	DEL	A	0	15832	NM_004064.3	p.K134fs
CDKN1B	12	12762450	12762450	Frame Shift Del	DEL	C	0	839	NM_004064.3	p.P137fs
CDKN1B	12	12763025	12763025	Splice Site	SNP	G	C	15832	NM_004064.3	e2-1
TP53	17	7514727	7514727	Missense Mutation	SNP	C	G	15386	NM_000546.4	p.R342P
TP53	17	7517580	7517580	Nonsense_Mutation	SNP	G	A	16392	NM_000546.4	p.Q331*
TP53	17	7517783	7517783	Nonsense_Mutation	SNP	C	A	808	NM_000546.4	p.E294*
TP53	17	7517822	7517822	Missense Mutation	SNP	C	G	409	NM_000546.4	p.D281H
TP53	17	7517831	7517831	Missense Mutation	SNP	G	A	16002	NM_000546.4	p.P278S
TP53	17	7517845	7517845	Missense Mutation	SNP	C	T	16256	NM_000546.4	p.R273H
TP53	17	7517848	7517850	In Frame Del	DEL	ACC	0	307	NM_000546.4	p.V272in Frame del
TP53	17	7518263	7518263	Missense Mutation	SNP	C	T	16091	NM_000546.4	p.R248Q
TP53	17	7518960	7518960	Missense Mutation	SNP	T	A	15445	NM_000546.4	p.Y205F
TP53	17	7518990	7518990	Missense Mutation	SNP	A	G	15868	NM_000546.4	p.I195T
TP53	17	7519000	7519000	Nonsense_Mutation	SNP	G	A	16092	NM_000546.4	p.Q192*
TP53	17	7519204	7519204	Missense Mutation	SNP	G	A	16539	NM_000546.4	p.P151S
TP53	17	7519233	7519233	Missense Mutation	SNP	C	T	122	NM_000546.4	p.C141Y
TP53	17	7519243	7519243	Missense Mutation	SNP	C	G	308	NM_000546.4	p.A138P
TP53	17	7519255	7519255	Missense Mutation	SNP	A	T	104	NM_000546.4	p.F134I
TP53	17	7519259	7519259	Missense Mutation	SNP	C	A	107	NM_000546.4	p.K132N
MAP2K4	17	11925403	11925404	Frame Shift Del	DEL	GA	0	16402	NM_003010.2	p.R75fs
MAP2K4	17	11925416	11925417	Splice Site	DEL	CA	0	16091	NM_003010.2	p.H79fs
MAP2K4	17	11951875	11951875	Missense Mutation	SNP	A	G	16069	NM_003010.2	p.D186G
MAP2K4	17	11951953	11951954	Splice Site	INS	0	T	111	NM_003010.2	e5+2
MAP2K4	17	11973330	11973330	Splice Site	SNP	G	A	409	NM_003010.2	e9+1

Supplementary Table 5c: Tier1 somatic mutations discovered in 3730 sanger sequence data for 108 additional tumor samples

Hugo_Symbol	Chromosome	Start_position	End_position	Variant_Classification	Variant_Type	Reference_Allele	Variant_Allele	Tumor_Sample_Barcode	transcript_name	amino_acid_change
JAK1	1	65072896	65072896	Missense Mutation	SNP	G	C	17327	NM_002227.2	p.F1134L
BIRC6	2	32580395	32580395	Missense Mutation	SNP	C	G	17143	NM_016252.3	p.S3048C
BIRC6	2	32681641	32681641	Nonsense_Mutation	SNP	C	G	16135	NM_016252.3	p.S4686*
ATR	3	143663594	143663594	Missense Mutation	SNP	C	G	17143	NM_001184.3	p.R2357T
ATR	3	143671069	143671069	Missense Mutation	SNP	C	G	17818	NM_001184.3	p.D2118H
ATR	3	143698669	143698669	Missense Mutation	SNP	G	T	16993	NM_001184.3	p.P1872T
ATR	3	143754897	143754897	Silent Mutation	SNP	G	C	17818	NM_001184.3	p.L889
PIK3CA	3	180404247	180404247	Missense Mutation	SNP	T	A	16965	NM_006218.2	p.N345K
PIK3CA	3	180404247	180404247	Missense Mutation	SNP	T	A	17331	NM_006218.2	p.N345K
PIK3CA	3	180404247	180404247	Missense Mutation	SNP	T	A	18155	NM_006218.2	p.N345K
PIK3CA	3	180410668	180410668	Missense Mutation	SNP	G	A	17327	NM_006218.2	p.E418K
PIK3CA	3	180410668	180410668	Missense Mutation	SNP	G	A	17611	NM_006218.2	p.E418K
PIK3CA	3	180410674	180410674	Missense Mutation	SNP	T	C	17612	NM_006218.2	p.C420R
PIK3CA	3	180410761	180410787	In Frame Del	DEL	CCTCATGGATTAGAAGATT TGCTGAAC	0	15921	NM_006218.2	p.H450in_frame_del
PIK3CA	3	180410772	180410774	In Frame Del	DEL	AGA	0	17678	NM_006218.2	p.E453in_frame_del
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	A	16598	NM_006218.2	p.E542K
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	C	17327	NM_006218.2	p.E542Q
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	A	17467	NM_006218.2	p.E542K
PIK3CA	3	180418776	180418776	Missense Mutation	SNP	G	A	17494	NM_006218.2	p.E542K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	15721	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	16135	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	16189	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	16590	NM_006218.2	p.E545K

PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	17138	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	17143	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	17175	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	17384	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	17518	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	C	17611	NM_006218.2	p.E545Q
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	17860	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	18156	NM_006218.2	p.E545K
PIK3CA	3	180418785	180418785	Missense Mutation	SNP	G	A	21009	NM_006218.2	p.E545K
PIK3CA	3	180418786	180418786	Missense Mutation	SNP	A	G	17445	NM_006218.2	p.E545G
PIK3CA	3	180420104	180420104	Missense Mutation	SNP	G	A	16063	NM_006218.2	p.E600K
PIK3CA	3	180434712	180434712	Missense Mutation	SNP	A	G	17612	NM_006218.2	p.T1025A
PIK3CA	3	180434778	180434778	Missense Mutation	SNP	C	A	17835	NM_006218.2	p.H1047N
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	402	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15571	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15750	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15812	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	15906	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16063	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16082	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16185	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16342	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16751	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16757	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16779	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16895	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16956	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16992	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	16998	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	17070	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	17327	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	17328	NM_006218.2	p.H1047R

PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	17407	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	17636	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	17678	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	17688	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	17818	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	T	17835	NM_006218.2	p.H1047L
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	17902	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	17915	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	17946	NM_006218.2	p.H1047R
PIK3CA	3	180434779	180434779	Missense Mutation	SNP	A	G	18183	NM_006218.2	p.H1047R
PIK3CA	3	180434784	180434784	Missense Mutation	SNP	G	C	17384	NM_006218.2	p.G1049R
PIK3CA	3	180434835	180434835	Missense Mutation	SNP	G	T	17518	NM_006218.2	p.A1066S
PIK3CA	3	180434836	180434836	Missense Mutation	SNP	C	T	17518	NM_006218.2	p.A1066V
PIK3CA	3	180434840	180434841	Frame Shift Ins	INS	0	A	16959	NM_006218.2	p.N1067fs
PDGFRA	4	54838417	54838418	Splice_Site	INS	0	T	16825	NM_006206.4	e12+1
KIT	4	55256514	55256514	Silent	SNP	C	T	17774	NM_000222.2	p.R49
MAP3K1	5	56191482	56191483	Frame Shift Del	DEL	AG	0	18183	NM_005921.1	p.R273fs
MAP3K1	5	56196358	56196358	Nonsense_Mutation	SNP	C	G	17612	NM_005921.1	p.S292*
MAP3K1	5	56196461	56196461	Frame Shift Del	DEL	T	0	17646	NM_005921.1	p.F327fs
MAP3K1	5	56196987	56196987	Nonsense_Mutation	SNP	C	T	17818	NM_005921.1	p.Q367*
MAP3K1	5	56197474	56197475	Frame Shift Ins	INS	0	T	18161	NM_005921.1	p.N406fs
MAP3K1	5	56203484	56203500	Frame Shift Del	DEL	TTTTCTATAGCATAAAG	0	17774	NM_005921.1	p.S438fs
MAP3K1	5	56203522	56203522	Frame Shift Del	DEL	C	0	17611	NM_005921.1	p.P444fs
MAP3K1	5	56204524	56204527	Frame Shift Del	DEL	CTTA	0	15906	NM_005921.1	p.T542fs
MAP3K1	5	56206812	56206812	Nonsense_Mutation	SNP	C	G	16063	NM_005921.1	p.S628*
MAP3K1	5	56212323	56212324	Frame Shift Ins	INS	0	T	21009	NM_005921.1	p.L707fs
MAP3K1	5	56213440	56213440	Nonsense_Mutation	SNP	C	T	15921	NM_005921.1	p.Q886*
MAP3K1	5	56213600	56213641	In Frame Del	DEL	CTAGTTCAACAACAACAAAC AACAAACAACAGAGCAA CCAA	0	17586	NM_005921.1	p.S939in_frame_del
MAP3K1	5	56213749	56213750	Frame Shift Del	DEL	TC	0	17612	NM_005921.1	p.S989fs
MAP3K1	5	56213789	56213790	Frame Shift Ins	INS	0	T	17868	NM_005921.1	p.K1003fs
MAP3K1	5	56213845	56213846	Frame Shift Del	DEL	AC	0	16082	NM_005921.1	p.Q1022fs
MAP3K1	5	56213884	56213884	Missense Mutation	SNP	C	T	17327	NM_005921.1	p.P1034S
MAP3K1	5	56215245	56215245	Frame Shift Del	DEL	T	0	17868	NM_005921.1	p.T1267fs

MAP3K1	5	56216254	56216255	Frame Shift Ins	INS	0	A	17733	NM_005921.1	p.Y1276fs
MAP3K1	5	56216311	56216312	Frame Shift Del	DEL	AT	0	17902	NM_005921.1	p.I1295fs
MAP3K1	5	56216341	56216341	Missense Mutation	SNP	A	G	18161	NM_005921.1	p.N1305D
MAP3K1	5	56216343	56216345	In Frame Del	DEL	CAT	0	16082	NM_005921.1	p.I1307in_frame_del
MAP3K1	5	56216383	56216384	Frame Shift Ins	INS	0	A	17352	NM_005921.1	p.Y1319fs
MAP3K1	5	56216394	56216394	Silent	SNP	C	T	17818	NM_005921.1	p.F1322
MAP3K1	5	56217589	56217590	Frame Shift Ins	INS	0	T	17733	NM_005921.1	p.L1352fs
MAP3K1	5	56217626	56217628	In Frame Del	DEL	ATC	0	17611	NM_005921.1	p.I1366in_frame_del
MAP3K1	5	56219034	56219034	Missense Mutation	SNP	C	T	17636	NM_005921.1	p.A1396V
MAP3K1	5	56219091	56219091	Missense Mutation	SNP	T	G	15906	NM_005921.1	p.F1415C
MAP3K1	5	56225135	56225136	Frame Shift Ins	INS	0	C	15750	NM_005921.1	p.S1471fs
MAP3K1	5	56225199	56225199	Nonsense_Mutation	SNP	C	T	18183	NM_005921.1	p.Q1492*
CSF1R	5	149415024	149415024	Missense Mutation	SNP	T	G	17066	NM_005211.3	p.M875L
CSF1R	5	149430277	149430277	Missense Mutation	SNP	C	T	16751	NM_005211.3	p.R378H
CSF1R	5	149439975	149439975	Missense Mutation	SNP	C	T	17881	NM_005211.3	p.R142H
DDR1	6	30972583	30972583	Missense Mutation	SNP	C	T	17733	NM_013994.4	p.R611C
MET	7	116196941	116196941	Missense Mutation	SNP	G	A	17818	NM_000245.2	p.D864N
MET	7	116222969	116222969	Nonsense_Mutation	SNP	G	T	16744	NM_000245.2	p.E1275*
GATA3	10	8140733	8140734	Frame Shift Ins	INS	0	C	17746	NM_001002295.1	p.S237fs
GATA3	10	8151439	8151440	Splice_Site	DEL	CA	0	17383	NM_001002295.1	e4-2
GATA3	10	8151439	8151440	Splice_Site	DEL	CA	0	17733	NM_001002295.1	e4-2
GATA3	10	8151483	8151483	Frame Shift Del	DEL	G	0	16185	NM_001002295.1	p.T323fs
GATA3	10	8151508	8151515	Frame Shift Del	DEL	AGGAATGC	0	16934	NM_001002295.1	p.R331fs
GATA3	10	8151552	8151553	Frame Shift Ins	INS	0	T	21009	NM_001002295.1	p.Y345fs
GATA3	10	8155721	8155721	Frame Shift Del	DEL	T	0	16702	NM_001002295.1	p.L355fs
GATA3	10	8155724	8155725	Frame Shift Ins	INS	0	TA	17467	NM_001002295.1	p.M357fs
GATA3	10	8155733	8155734	Frame Shift Ins	INS	0	G	17278	NM_001002295.1	p.E360fs
GATA3	10	8155750	8155750	Missense Mutation	SNP	A	G	17409	NM_001002295.1	p.R365G
GATA3	10	8155785	8155786	Frame Shift Ins	INS	0	A	17123	NM_001002295.1	p.V378fs
GATA3	10	8155880	8155881	Frame Shift Ins	INS	0	G	16208	NM_001002295.1	p.P409fs
GATA3	10	8155985	8155986	Frame Shift Ins	INS	0	G	16993	NM_001002295.1	p.*445fs
MALAT1	11	65022759	65022759	RNA	SNP	G	T	16965	NR_002819.2	NULL
MALAT1	11	65024847	65024871	RNA	DEL	TGGAACCTTACTTATGGTAA CCTTTT	0	16189	NR_002819.2	NULL
MALAT1	11	65025184	65025184	RNA	SNP	G	C	17066	NR_002819.2	NULL

MALAT1	11	65025189	65025189	RNA	SNP	C	A	16992	NR_002819.2	NULL
MALAT1	11	65026184	65026184	RNA	SNP	C	G	17818	NR_002819.2	NULL
CDKN1B	12	12762251	12762251	Nonsense_Mutation	SNP	G	T	17407	NM_004064.3	p.E71*
CDKN1B	12	12763061	12763061	Nonsense_Mutation	SNP	G	T	17143	NM_004064.3	p.E171*
CDKN1B	12	12763142	12763142	Missense Mutation	SNP	A	G	18183	NM_004064.3	p.T198A
RB1	13	47814767	47814767	Nonsense_Mutation	SNP	G	A	17250	NM_000321.2	p.W99*
RB1	13	47839649	47839649	Nonsense_Mutation	SNP	C	T	16135	NM_000321.2	p.R320*
RB1	13	47948867	47948867	Silent Mutation	SNP	G	A	16993	NM_000321.2	p.Q850
LTK	15	39586746	39586746	Missense Mutation	SNP	C	T	16189	NM_002344.1	p.M460I
LTK	15	39587613	39587613	Missense Mutation	SNP	C	T	16189	NM_002344.1	p.E399K
CDH1	16	67329731	67329731	Frame Shift Del	DEL	C	0	16590	NM_004360.3	p.C28fs
CDH1	16	67329816	67329817	Splice_Site	INS	0	T	16957	NM_004360.3	e2+1
CDH1	16	67393198	67393198	Frame Shift Del	DEL	C	0	18154	NM_004360.3	p.I96fs
CDH1	16	67399915	67399915	Frame Shift Del	DEL	C	0	17738	NM_004360.3	p.P159fs
CDH1	16	67400190	67400191	Frame Shift Del	DEL	AG	0	18156	NM_004360.3	p.R209fs
CDH1	16	67401662	67401663	In Frame Ins	INS	0	CAC	18161	NM_004360.3	p.T251in_frame_ins
CDH1	16	67401704	67401714	Frame Shift Del	DEL	AGGAGGTCTTT	0	17740	NM_004360.3	p.Q264fs
CDH1	16	67403111	67403119	In Frame Del	DEL	GCCACAGAC	0	17208	NM_004360.3	p.T287in_frame_del
CDH1	16	67403556	67403558	Frame Shift Del	DEL	CT	0	18091	NM_004360.3	p.L343fs
CDH1	16	67404720	67404720	Nonsense_Mutation	SNP	A	T	16959	NM_004360.3	p.K381*
CDH1	16	67404846	67404846	Frame Shift Del	DEL	T	0	826	NM_004360.3	p.F423fs
CDH1	16	67407070	67407071	Frame Shift Del	DEL	AG	0	17352	NM_004360.3	p.R492fs
CDH1	16	67410685	67410686	Frame Shift Ins	INS	0	A	17946	NM_004360.3	p.Y523fs
CDH1	16	67413528	67413529	Frame Shift Ins	INS	0	A	17233	NM_004360.3	p.N613fs
CDH1	16	67413556	67413557	Frame Shift Ins	INS	0	AATA	17972	NM_004360.3	p.T622fs
CDH1	16	67414852	67414853	Frame Shift Del	DEL	CT	0	15721	NM_004360.3	p.D662fs
CDH1	16	67414855	67414861	Frame Shift Del	DEL	CAAATC	0	15721	NM_004360.3	p.Y663fs
CDH1	16	67414856	67414856	Frame Shift Del	DEL	A	0	15812	NM_004360.3	p.I665fs
CDH1	16	67414993	67415000	Frame Shift Del	DEL	CATTCTGG	0	17929	NM_004360.3	p.I710fs
CDH1	16	67419577	67419577	Splice_Site	SNP	G	T	17494	NM_004360.3	e14-1
CDH1	16	67419675	67419675	Frame Shift Del	DEL	C	0	17327	NM_004360.3	p.Y755fs
CDH1	16	67421155	67421156	Frame Shift Del	DEL	TT	0	16313	NM_004360.3	p.L798fs
CDH1	16	67421203	67421203	Splice_Site	SNP	T	G	16296	NM_004360.3	e15+2
TP53	17	7514719	7514720	Frame Shift Del	DEL	TC	0	826	NM_000546.4	p.N345fs

TP53	17	7517830	7517830	Missense Mutation	SNP	G	A	16135	NM_000546.4	p.P278L
TP53	17	7517845	7517845	Missense Mutation	SNP	C	T	17157	NM_000546.4	p.R273H
TP53	17	7517845	7517845	Missense Mutation	SNP	C	T	17328	NM_000546.4	p.R273H
TP53	17	7517845	7517845	Missense Mutation	SNP	C	T	17445	NM_000546.4	p.R273H
TP53	17	7517846	7517846	Missense Mutation	SNP	G	A	16040	NM_000546.4	p.R273C
TP53	17	7518259	7518259	Missense Mutation	SNP	C	A	17688	NM_000546.4	p.R249S
TP53	17	7518263	7518263	Missense Mutation	SNP	C	T	17175	NM_000546.4	p.R248Q
TP53	17	7518264	7518264	Missense Mutation	SNP	G	A	17746	NM_000546.4	p.R248W
TP53	17	7518293	7518293	Missense Mutation	SNP	C	A	17774	NM_000546.4	p.C238F
TP53	17	7518299	7518299	Missense Mutation	SNP	T	C	18025	NM_000546.4	p.Y236C
TP53	17	7518920	7518922	In Frame Del	DEL	CAC	0	16982	NM_000546.4	p.V218in_frame_del
TP53	17	7518930	7518930	Missense Mutation	SNP	C	A	17331	NM_000546.4	p.S215I
TP53	17	7518936	7518936	Missense Mutation	SNP	C	T	17278	NM_000546.4	p.R213Q
TP53	17	7519171	7519171	Missense Mutation	SNP	T	A	15616	NM_000546.4	p.I162F
TP53	17	7519252	7519285	Frame Shift Del	DEL	AAAACATCTTGTTGAGGGC AGGGGAGTACTGTAG	0	18091	NM_000546.4	p.Y126fs
TP53	17	7519262	7519272	Frame Shift Del	DEL	GTTGAGGGCAG	0	18182	NM_000546.4	p.P128fs
TP53	17	7519272	7519274	In Frame Del	DEL	GGG	0	17521	NM_000546.4	p.P128in_frame_del
TP53	17	7520087	7520088	In Frame Ins	INS	0	ACC	16744	NM_000546.4	p.108in_frame_insG
TP53	17	7520094	7520094	Missense Mutation	SNP	G	C	17739	NM_000546.4	p.S106R
TP53	17	7520627	7520627	Missense Mutation	SNP	G	A	15866	NM_000546.4	p.P4L
MAP2K4	17	11939623	11939623	Missense Mutation	SNP	C	T	17250	NM_003010.2	p.R134W
MAP2K4	17	11957402	11957405	Frame Shift Del	DEL	AGTA	0	16825	NM_003010.2	p.P272fs
MAP2K4	17	11973180	11973180	Splice_Site	SNP	G	C	15616	NM_003010.2	e9-1
ERBB2	17	35133745	35133759	In Frame Del	DEL	TTGAGGGAAAACACA	0	16757	NM_004448.1	p.L755in_frame_del
RUNX1	21	35128627	35128628	Frame Shift Ins	INS	0	A	17612	NM_001754.2	p.S252fs
RUNX1	21	35153652	35153652	Missense Mutation	SNP	C	T	16590	NM_001754.2	p.R201Q
RUNX1	21	35174726	35174726	Missense Mutation	SNP	C	T	18155	NM_001754.2	p.R169K
RUNX1	21	35174845	35174846	Frame Shift Ins	INS	0	A	16189	NM_001754.2	p.V130fs

Supplementary Table 5d: Tier1 somatic mutations discovered in custom capture Illumina sequence data for 132 additional tumor samples independent of exome sequencing

Gene	SNVs	Indels	P-value FCPT	P-value LRT	P-value CT	FDR FCPT	FDR LRT	FDR CT
MAP3K1	5	8	0	0	0	0	0	0
PIK3CA	44	1	0	0	0	0	0	0
TP53	15	1	0	0	0	0	0	0
GATA3	2	6	3.62E-14	0	1.15E-19	2.34E-10	0	7.41E-16
CDH1	3	5	1.32E-10	5.55E-16	3.07E-15	6.79E-07	2.87E-12	1.59E-11
TBX3	0	3	0.002663729	3.25E-08	2.58E-06	1	0.00012	0.011115
ATR	6	0	0.001511863	1.60E-08	3.73E-06	1	6.87E-05	0.013741
RUNX1	4	0	0.007022425	2.79E-05	6.59E-06	1	0.07198	0.021257
ENSG00000212670	2	0	0.042852637	3.97E-05	2.31E-05	1	0.087265	0.066198
RB1	4	0	0.015087212	8.76E-05	2.76E-05	1	0.125694	0.071238
LDLRAP1	2	0	0.036031591	2.24E-06	4.27E-05	1	0.007215	0.091925
STMN2	1	1	0.048164882	4.79E-05	4.15E-05	1	0.092609	0.091925
MYH9	2	2	0.017345889	8.09E-05	8.96E-05	1	0.122896	0.177917
MLL3	2	3	0.014038346	5.06E-05	0.000103644	1	0.092609	0.191097
CDKN1B	1	1	0.111403112	0.000231951	0.000139355	1	0.211547	0.239811
AGTR2	2	0	0.096022173	1.50E-05	0.000171022	1	0.043064	0.256179
SF3B1	3	0	0.048688866	5.48E-05	0.00017864	1	0.092609	0.256179
CBFB	2	0	0.09098287	0.000158638	0.000170409	1	0.204244	0.256179

Supplementary Table 6: Significantly Mutated Genes.

Shown are the top 18 SMGs based on an FDR cutoff of 0.26. ENSG00000212670 is not annotated by Refseq.

Slicing Window	Tier 1								Tier 2 and 3				Tier 1, 2, and 3											
	Chr	Start	Stop	Total Mutation	Mutated Samples	Tier 1	Gene	Chr	Start	Stop	Total Mutation	Mutated Samples	Tier 2	Tier 3	Gene	Chr	Start	Stop	Total Mutation	Mutated Samples	Tier 1	Tier 2	Tier 3	Gene
1k	3	180434771	180435770	16	16	16	PIK3CA	6	142747899	142748898	6	6	6	0	GPR126	3	180434771	180435770	16	16	16	0	0	PIK3CA
1k	3	180418776	180419775	7	7	7	PIK3CA	10	115501580	115502579	6	5	0	6	C10orf81	3	180418776	180419775	7	7	7	0	0	PIK3CA
1k	17	7518928	7519927	5	5	5	TP53	5	166900648	166901647	4	4	2	2		6	142747899	142748898	6	6	0	6	0	GPR126
1k	17	7517810	7518809	5	5	5	TP53	X	55650388	55651387	3	3	0	3		17	7518928	7519927	5	5	5	0	0	TP53
1k	5	56196978	56197977	3	3	3	MAP3K1	X	42346883	42347882	3	3	1	2		17	7517810	7518809	5	5	5	0	0	TP53
1k	3	143659257	143660256	4	3	4	ATR	X	146598451	146599450	3	3	3	0		10	115501580	115502579	6	5	0	0	6	C10orf81
1k	11	65024869	65025868	3	3	3	MALAT1	X	137599916	137600915	3	3	0	3	FGF13	5	166900648	166901647	4	4	0	2	2	
1k	X	89064225	89065224	2	2	2	TGIF2LX	X	117621913	117622912	3	3	0	3	DOCK11	X	55650388	55651387	3	3	0	0	3	
1k	X	129629187	129630186	2	2	2	ENOX2	9	75995775	75996774	3	3	0	3		X	42346883	42347882	3	3	0	1	2	
1k	X	115218111	115219110	2	2	2	AGTR2	9	73224613	73225612	3	3	0	3		X	146598451	146599450	3	3	0	3	0	
2k	3	180434771	180436770	16	16	16	PIK3CA	6	142747899	142749898	6	6	6	0	GPR126	3	180434771	180436770	16	16	16	0	0	PIK3CA
2k	17	7517810	7519809	10	9	10	TP53	10	84208063	84210062	5	5	1	4	NRG3	17	7517810	7519809	10	9	10	0	0	TP53
2k	3	180418776	180420775	7	7	7	PIK3CA	10	115501580	115503579	6	5	0	6	C10orf81	3	180418776	180420775	7	7	7	0	0	PIK3CA
2k	11	65024869	65026868	4	4	4	MALAT1	X	137599916	137601915	4	4	1	3	FGF13	6	142747899	142749898	6	6	0	6	0	GPR126
2k	5	56196978	56198977	3	3	3	MAP3K1	9	21464508	21466507	4	4	0	4		10	84208063	84210062	5	5	0	1	4	NRG3
2k	3	143659257	143661256	4	3	4	ATR	8	66217115	66219114	4	4	0	4		10	115501580	115503579	6	5	0	0	6	C10orf81
2k	X	89064225	89066224	2	2	2	TGIF2LX	6	124532311	124534310	4	4	1	3	NKAIN2	X	137599916	137601915	4	4	0	1	3	FGF13
2k	X	135257364	135259363	2	2	2	GPR112	6	104414202	104416201	4	4	1	3		9	21464508	21466507	4	4	0	0	4	
2k	X	129629187	129631186	2	2	2	ENOX2	5	63199147	63201146	4	4	0	4		8	66217115	66219114	4	4	0	0	4	
2k	X	115218111	115220110	2	2	2	AGTR2	3	1181390	1183389	4	4	2	2	CNTN6	6	124532311	124534310	4	4	0	1	3	NKAIN2
5k	3	180434771	180439770	16	16	16	PIK3CA	6	142747899	142752898	6	6	6	0	GPR126	3	180434771	180439770	16	16	16	0	0	PIK3CA
5k	3	180418776	180423775	9	7	9	PIK3CA	5	166898863	166903862	6	6	3	3		3	180418776	180423775	9	7	9	0	0	PIK3CA
5k	17	7513676	7518675	8	6	8	TP53	10	84208063	84213062	6	6	1	5	NRG3	6	142747899	142752898	6	6	0	6	0	GPR126
5k	17	7518928	7523927	6	5	6	TP53	6	104411200	104416199	5	5	1	4		5	166898863	166903862	6	6	0	3	3	
5k	11	65024869	65029868	4	4	4	MALAT1	20	4399019	4404018	5	5	1	4		17	7518928	7523927	8	6	6	1	1	TP53
5k	5	56196978	56201977	3	3	3	MAP3K1	10	60058774	60063773	6	5	1	5	BICC1	17	7513676	7518675	8	6	8	0	0	TP53
5k	3	180399618	180404617	3	3	3	PIK3CA	10	115501580	115506579	6	5	0	6	C10orf81	10	84208063	84213062	6	6	0	1	5	NRG3
5k	3	143659257	143664256	4	3	4	ATR	X	76493249	76498248	4	4	2	2		6	104411200	104416199	5	5	0	1	4	
5k	10	8151439	8156438	3	3	3	GATA3	X	30650426	30655425	4	4	0	4	GK	20	4399019	4404018	5	5	0	1	4	
5k	X	89064225	89069224	2	2	2	TGIF2LX	X	28829367	28834366	4	4	0	4	IL1RAPL1	10	60058774	60063773	6	5	0	1	5	BICC1
10k	3	180434771	180444770	16	16	16	PIK3CA	6	142747899	142757898	7	7	6	1	GPR126	3	180434771	180444770	16	16	16	0	0	PIK3CA

10k	17	7513676	7523675	14	10	14	TP53	5	166893737	166903736	7	7	3	4	17	7513676	7523675	16	10	14	1	1	TP53	
10k	3	180410761	180420760	9	9	9	PIK3CA	1	164518422	164528421	7	7	0	7	3	180410761	180420760	9	9	9	0	0	PIK3CA	
10k	11	65024869	65034868	4	4	4	MALAT1	9	75988641	75998640	6	6	1	5	6	142747899	142757898	7	7	0	6	1	GPR126	
10k	10	8146064	8156063	4	4	4	GATA3	20	59509086	59519085	6	6	1	5	CDH4	5	166893737	166903736	7	7	0	3	4	
10k	5	56215247	56225246	3	3	3	MAP3K1	11	127867351	127877350	6	6	2	4	ETS1	1	164518422	164528421	7	7	0	0	7	
10k	5	56196978	56206977	3	3	3	MAP3K1	10	84208063	84218062	6	6	1	5	NRG3	9	75988641	75998640	6	6	0	1	5	
10k	4	55259324	55269323	3	3	3	KIT	10	60058774	60068773	7	6	1	6	BICC1	20	59509086	59519085	6	6	0	1	5	CDH4
10k	3	180399618	180409617	3	3	3	PIK3CA	X	4058375	4068374	5	5	2	3		12	83787998	83797997	6	6	1	0	5	SLC6A15
10k	3	143659257	143669256	4	3	4	ATR	X	28829367	28839366	5	5	0	5	IL1RAPL1	11	127867351	127877350	6	6	0	2	4	ETS1

Supplementary Table 7: Whole genome mutation clustering analysis in luminal ER+ breast cancer.

Shown are results from four different sliding windows of 1kbp, 2kbp, 5kbp, and 10kbp, used to identify clusters of somatic mutations. In tier 1 coding regions, somatic mutations cluster in significantly mutated genes (PIK3CA, TP53, MAP3K1, and ATR). In tier 2 and tier 3 noncoding regions, somatic mutations cluster in intronic regions of GPR126 and NRG3.

1584 Z1031 0 A	x	251485033253_3	NA	70 LumB	3.1	1~ 12	1	NEGATIV E	DUCTAL III III I	7	0.26	8 NA	NA	0	0	0.268	-1	Responder	N N A A	7 7 0 3 0	N N N 1 A A A	- - -	N N A A	- - -	N N A A	- - -	N N A A	- - -			
1585 Z1031 8 A	x x	251485054660_2	2.51E+1 1	56 LumA	2.5	1~ 12	1	POSITIV E	LOBULA R I III I	7	0.04	9 NA	NA	0.003	3	0.046	-0.93878	Responder	N N A A	7 7 0 3 0	0 - - - - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -			
1586 Z1031 6 A	x	251485054608_1	2.51E+1 1 x	66 LumB	1.5	1~ 02	0	NEGATIV E	DUCTAL II III I	6	0.15	3 NA	NA	0.035	5	0.118	-0.77124	Responder	N N A A	7 7 1 1 0	1 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -			
1586 Z1031 7 A	x	251485034221_3	2.51E+1 1 x	62 LumA	1.2	1~ 02	0	NEGATIV E	DUCTAL II III I	6	0.06	2 NA	NA	0.039	9	0.023	-0.37097	Responder	N N N N N A A A A A	0 0 A A A	- - -	- - -	- - -	- - -	N N N 0 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1586 Z1031 8 A	x	251485054558_4	NA	86 LumB	1.7	1~ 02	0	NEGATIV E	DUCTAL II III I	8	0.43	4 NA	NA	0.081	1	0.353	-0.81336	Responder	N N A A	8 8 0 1 0	1 A A A	- - -	- - -	- - -	N N N 1 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1587 Z1031 0 A	x	251485036832_1	2.51E+1 1 x	64 LumB	1.3	1~ 02	0	NEGATIV E	DUCTAL II III I	0	0.06	1 NA	NA	0.15	0.15	0.089	1.45901	NonResponde r	N N A A	7 7 7 1 0	1 A A A	- - -	- - -	- - -	N N N A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1587 Z1031 9 A	x	251485036831_3	2.51E+1 1 x	76 LumB	6.3	3~ 14	1	NEGATIV E	DUCTAL III III I	8	0.25	7 NA	NA	0.005	5	0.252	-0.98054	Responder	N N A A	7 7 -1 6 0	0 A A A	- - -	- - -	- - -	N N N 0 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1588 Z1031 0 A	x	251485042959_3	NA	75 LumB	4	1~ 02	0	NEGATIV E	LOBULA R II III I	A	NA	NA	NA	0.019	9	NA	NA	Responder	N N A A	3 3 A 0 1	0 A A A	- - -	- - -	- - -	N N N 0 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1588 Z1031 2 A	x	251485054662_1	2.51E+1 1 x	84 LumB	1.8	1~ 12	1	NEGATIV E	DUCTAL II III I	8	0.39	5 NA	NA	0.153	3	0.242	-0.61266	NonResponde r	N N A A	8 8 0 4 0	1 A A A	- - -	- - -	- - -	N N N A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1589 Z1031 2 A	x	251485035337_3	2.51E+1 1 x	65 LumB	2.4	1~ 12	1	NEGATIV E	DUCTAL II III I	5	0.14	4 NA	NA	0.246	6	0.102	0.70833	NonResponde r	N N A A	5 5 0 5 0	0 A A A	- - -	- - -	- - -	N N N 0 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1589 Z1031 4 A	x	251485034013_1	2.51E+1 1 x	64 LumA	1.7	1~ 02	0	NEGATIV E	DUCTAL II III I	8	0.05	9 NA	NA	0	0	0.059	-1	Responder	N N A A	8 8 0 0 1	1 A A A	- - -	- - -	- - -	N N N 1 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1589 Z1031 7 A	x	251485036831_7	NA	62 LumA	8	3~ 14	1	NEGATIV E	DUCTAL II III I	8	0.12	3 NA	NA	0.121	1	0.002	-0.01626	NonResponde r	N N A A	7 7 -1 7 0	1 A A A	- - -	- - -	- - -	N N N A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1589 Z1031 9 A	x	251485054661_1	NA	84 LumB	2.5	1~ 02	0	NEGATIV E	DUCTAL I III I	8	0.25	6 NA	NA	0.036	6	-0.22	-0.85938	Responder	N N A A	4 4 -4 1 0	1 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -		
1590 Z1031 1 A	x x	251485042140_3	2.51E+1 1	81 LumB	7	3~ 14	1	NEGATIV E	DUCTAL II III I	8	0.21	4 NA	NA	0.04	0.04	0.174	-0.81308	Responder	N N A A	6 6 -2 7 0	0 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -		
1590 Z1031 6 A	x	251485056531_2	NA	58 LumB	2.1	1~ 12	1	NEGATIV E	DUCTAL II III I	2	0.17	2 NA	NA	0.073	3	0.099	-0.57558	Responder	N N A A	3 3 1 4 0	1 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -		
1591 Z1031 0 A	x	251485038540_1	NA	66 LumB	2.3	1~ 12	1	NEGATIV E	DUCTAL II III I	6	0.63	NA	NA	0.178	0.17	-	0.71746	NonResponde r	N N A A	5 5 -1 4 0	1 - - - - -	- - -	- - -	- - -	N N N A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1591 Z1031 3 A	x	251485034016_3	2.51E+1 1 x	86 LumB	1.6	1~ 12	1	NEGATIV E	DUCTAL II III I	8	0.27	4 NA	NA	0.031	1	0.243	-0.88686	Responder	N N A A	8 8 0 4 0	1 A A A	- - -	- - -	- - -	N N N 1 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1591 Z1031 7 A	x	251485042960_1	NA	66 LumA	1.8	1~ 02	0	NEGATIV E	DUCTAL I III I	8	0.07	6 NA	NA	0.008	8	0.068	-0.89474	Responder	N N A A	8 8 0 0 1	1 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -		
1591 Z1031 9 A	x	251485053538_1	NA	72 LumB	1.8	1~ 12	1	NEGATIV E	DUCTAL II III I	5	0.37	6 NA	NA	0.432	0.43	2	0.056	0.14893	NonResponde r	N N A A	7 7 2 5 0	1 A A A	- - -	- - -	- - -	N N N 1 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -
1592 Z1031 1 A	x	251485033452_3	2.51E+1 1 x	78 LumB	3.1	1~ 02	0	NEGATIV E	DUCTAL II III I	6	0.06	2 NA	NA	0.027	0.02	7	0.035	-0.56452	Responder	N N A A	8 8 2 1 0	1 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -	
1593 Z1031 1 A	x	251485036029_1	2.51E+1 1 x	79 LumB	2.2	1~ 2	NA	POSITIV E	DUCTAL II III I	7	0.29	5 NA	NA	0	0	0.295	-1	Responder	N N A A	6 6 -1 A A	0 A A A	- - -	- - -	- - -	N N N 0 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1594 Z1031 5 A	x	251485033453_3	NA	55 LumB	4	1~ 12	1	NEGATIV E	DUCTAL II III I	8	0.41	2 NA	NA	0.008	8	0.404	-0.98058	Responder	N N A A	6 6 -2 3 0	1 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -		
1595 Z1031 0 A	x	251485053312_3	2.51E+1 1 x	53 LumA	0.1	1~ 02	0	NEGATIV E	DUCTAL I III I	8	0.15	2 NA	NA	0	0	0.152	-1	Responder	N N A A	7 7 -1 0 1	1 A A A	- - -	- - -	- - -	N N N 1 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1595 Z1031 2 A	x x	251485054613_4	2.51E+1 1	62 LumB	1.5	1~ 12	1	NEGATIV E	DUCTAL II III I	8	0.38	5 NA	NA	0.336	0.33	6	0.049	-0.12727	NonResponde r	N N A A	6 6 -2 5 0	0 A - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -	
1595 Z1031 3 A	x	251485054661_4	NA	76 LumB	4	1~ 12	1	NEGATIV E	DUCTAL II III I	6	0.41	7 NA	NA	0.192	2	0.225	-0.53957	NonResponde r	N N A A	4 4 -2 4 0	0 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -		
1596 Z1031 8 A	x	251485053312_1	NA	66 LumB	2	1~ 12	1	NA	DUCTAL II III I	6	0.24	1 NA	NA	0.038	8	0.203	-0.84232	Responder	N N A A	5 5 -1 4 0	0 A A A	- - -	- - -	- - -	N N N 0 A A A	- - -	N N N A A A	- - -	N N N A A A	- - -	
1597 Z1031 0 A	x	251485036029_3	2.51E+1 1	56 LumB	2.6	1~ 2	NA	NEGATIV E	DUCTAL II III I	6	0.76	NA	NA	0.308	0.30	8	0.452	-0.59474	NonResponde r	N N A A	4 4 -2 A 0	1 - - - - -	- - -	- - -	- - -	N A	- - -	- - -	- - -	- - -	

nodal
status
unknow
n

1639 Z1031 2 A	x	251485050627_	2.51E+1	1 x	max tumor dim unknow n	84 LumB	3.7	1~ 1 2	NEGATIV 1 E	DUCTAL III III I	II/II	8	0.52 7 NA	NA	0.223	0.22 3 0.304	- -0.57685	NonResponde r	N N A A	8 8 0 5 0	0 0 A A	N N N A A A	- - -	N A	- +	N A	N N A A	+	
1639 Z1031 8 A	x x	251485054557_	2.51E+1	1		67 LumB	NA	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	8	0.11 2 NA	NA	0.064	0.06 4 0.048	- -0.42857	Responder	N N A A	8 8 0 1 0	1 - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1640 Z1031 2 A	x	251485052903_	2.51E+1	1 x		73 LumB	2.4	1~ 1 2	NEGATIV 1 E	DUCTAL II III I	II/II	8	0.32 3 NA	NA	0.106	0.10 6 0.217	- -0.67183	NonResponde r	N N A A	8 8 0 4 0	0 1 A A	N N N A A A	- - -	N A	+ -	N A	N N A A	-	
1640 Z1031 8 A	x	251485054537_	NA			66 LumA	3.8	1~ 1 2	NEGATIV 1 E	DUCTAL II III I	II/II	6	0.02 2 NA	NA	0.346	0.34 6 0.324	14.7272 7 r	NonResponde r	N N A A	6 6 0 5 0	0 - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1641 Z1031 1 A	x	251485054537_	NA			61 LumA	1.9	1~ 1 2	NEGATIV 1 E	DUCTAL III III I	II/II	7	0.10 7 NA	NA	0.024	0.02 4 0.083	- -0.7757	Responder	N N A A	8 8 1 3 0	0 1 A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1643 Z1031 1 A	x	251485053322_	2.51E+1	1		74 LumB	1.9	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	1	0.08 1 NA	NA	0.022	0.02 2 0.059	- -0.7284	Responder	N N A A	8 8 A 0 1	1 + + - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1643 Z1031 9 A	x	251485054608_	2.51E+1	1 x		59 LumB	3.5	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	8	0.44 6 NA	NA	0	0 0.446	- -1	Responder	N N A A	7 7 -1 0 1	1 A A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1644 Z1031 1 A	x	251485052896_	NA			55 LumB	2.3	1~ 1 2	NEGATIV 1 E	DUCTAL III III I	II/II	5	0.10 2 NA	NA	0.007	0.00 7 0.095	- -0.93137	Responder	N N A A	8 8 3 3 0	0 1 A A	N N N A A A	+ - -	- - -	- - -	- - -	- - -	- - -	
1644 Z1031 2 A	x	251485054556_	2.51E+1	1 x		59 LumA	15	3~ 1 2	NEGATIV 1 E	LOBULA R	II III I	8	0.28 9 NA	NA	0.032	0.03 2 0.257	- -0.88927	Responder	N N A A	6 6 -2 7 0	0 1 A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1645 Z1031 0 A	x	251485054659_	NA			62 LumA	4	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	6	0.14 NA	NA	0.031	0.03 1 0.109	- -0.77857	Responder	N N A A	2 2 -4 4 0	0 1 A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1645 Z1031 4 A	x	251485052895_	2.51E+1	1		61 LumB	3	1~ 0 2	NEGATIV 0 E	DUCTAL III III I	II/II	4	0.45 6 NA	NA	0.349	0.34 9 0.107	- -0.23465	NonResponde r	N N A A	6 6 2 2 0	0 1 - - -	- - - + -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1648 Z1031 1 A	x	251485053314_	2.51E+1	1		60 LumB	2	1~ 0 2	NEGATIV 0 E	LOBULA R	II III I	5	0.25 6 NA	NA	0.183	0.18 3 0.073	- -0.28516	NonResponde r	N N A A	5 5 0 1 0	0 - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1648 Z1031 6 A	x	251485054660_	2.51E+1	1 x		76 LumA	2	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	8	0.05 7 NA	NA	0.014	0.01 4 0.043	- -0.75439	Responder	N N A A	8 8 0 0 1	0 A A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1649 Z1031 2 A	x	251485055400_	2.51E+1	1 x		69 LumA	5	1~ 1 2	NEGATIV 1 E	LOBULA R	II III I	8	0.06 4 NA	NA	0	0 0.064	- -1	Responder	N N A A	8 8 0 3 0	0 1 A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1649 Z1031 5 A	x	251485054609_	2.51E+1	1 x		75 LumA	1.3	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	5	0.02 NA	NA	0.027	0.02 7 0.007	0.35	Responder	N N A A	7 7 2 0 1	0 A A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1653 Z1031 1 A	x	251485055266_	2.51E+1	1 x	nodal status unknow n	71 LumA	0.6	1~ 2 A	NEGATIV 2 A	DUCTAL II III I	II/II	8	0.07 6 NA	NA	0.06	0.06 0.016	- -0.21053	Responder	N N A A	8 8 0 A 0	0 1 A A	N N N A A A	- - -	N A	- -	N A	N N A A	-	
1653 Z1031 9 A	x	251485055398_	NA			58 LumB	1	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	7	0.10 7 NA	NA	0.014	0.01 4 0.093	- -0.86916	Responder	N N A A	8 8 1 0 1	1 A A A	N N N A A A	- - -	N A	- -	N A	N N A A	+	
1656 Z1031 1 A	x	251485055265_	2.51E+1	1 x		67 LumA	3.2	1~ 1 2	NEGATIV 1 E	DUCTAL I III I	II/II	8	0.06 2 NA	NA	0.011	0.01 1 0.051	- -0.82258	Responder	N N A A	6 6 -2 3 0	0 A A A	N N N A A A	- - -	N A	+ -	N A	N N A A	-	
1656 Z1031 6 A	x x	251485055266_	2.51E+1	1		58 LumB	5.1	3~ 1 4	NEGATIV 1 E	LOBULA R	I III I	6	NA	NA	0.043	0.04 3 NA	NA	Responder	N N A A	7 7 1 7 0	0 1 - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1657 Z1031 9 A	x	251485055265_	2.51E+1	1 x		59 LumA	4	1~ 1 2	NEGATIV 1 E	DUCTAL III III I	II/II	8	0.11 NA	NA	0.006	0.00 6 0.104	- -0.94545	Responder	N N A A	7 7 -1 3 0	0 1 - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1658 Z1031 9 A	x	251485055264_	2.51E+1	1		56 LumA	1.5	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	8	0.07 7 NA	NA	0.152	0.15 2 0.075	0.97402 6 r	NonResponde r	N N A A	8 8 0 1 0	0 - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1659 Z1031 0 A	x	251485055399_	2.51E+1	1 x		72 LumA	2.8	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	8	0.12 8 NA	NA	0	0 0.128	- -1	Responder	N N A A	8 8 0 0 1	1 - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
1659 Z1031 8 A	x	251485055402_	2.51E+1	1 x		85 LumB	3	1~ 0 2	NEGATIV 0 E	DUCTAL II III I	II/II	8	0.23 NA	NA	0.112	0.11 2 0.118	- -0.51304	NonResponde r	N N A A	8 8 0 1 0	0 1 - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
1670 Z1031 2 B	x	251485060459_	2.51E+1	1 x		62 LumA	NA	1~ 2	NEGATIV 1 E	DUCTAL III III I	II/II	8	0.02 1 NA	NA	0.007	0.00 7 0.014	- -0.66667	Responder	N N A A	7 7 -1 3 0	0 1 - - -	- - - + -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
1672 Z1031 7 B	x x	251485056231_	NA			66 LumB	NA	1~ 2	POSITIVE 0	DUCTAL II III I	II/II	7	0.43 NA	NA	0.153	0.15 3 0.277	- -0.64419	NonResponde r	N N A A	7 7 0 1 0	0 1 - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
1674 Z1031 4 B	x	251485060427_	2.51E+1	1 x		86 LumB	NA	1~ 2	NEGATIV 0 E	DUCTAL III III I	II/II	8	0.75 0.06 NA	NA	0.025	0.02 5 0.725	- -0.96667	Responder	N 8 A	7 7 -1 0 1	1 A - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
1674 Z1031 5 B	x	251485069914_	2.51E+1	1 x		53 LumA	NA	1~ 2	NEGATIV 1 E	DUCTAL II III I	II/II	7	0.12 0.01 NA	NA	0.003	0.00 3 0.124	- -0.97638	Responder	N 7 A	8 8 1 3 0	0 1 - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

2100 Z1031 251485070354_ 1~ NEGATIV II/II 0.00 -
 9 B x 4 NA 57 LumA NA NA 2 0 E DUCTAL II I/II I 8 3 0.01 NA 0 0 0.003 -1 Responder N
 8 A 8 8 0 0 1 1 - - - + - - + A + - - -

Supplementary Table 8: Clinical feature of 317 tumor samples.

Clinical information, tumor characteristics, and sequencing information for all cases.

Mutually exclusively mutated pairs		77 WGS/Exome cases					108 cases from ext 1&2					132 cases from ext 3					77+108 cases					77+132 cases					77+108+132 cases					
Gene A	Gene B	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	
GATA3	PIK3CA	7	37	1	42	0.012	9	42	2	47	0.169	13	52	3	59	0.101	16	79	3	89	0.008	20	89	4	1	10	0.003	29	1	6	8	0.002
MAP3K1	TP53	9	14	0	23	0.058	10	16	2	22	0.844	20	21	1	39	0.094	19	30	2	45	0.308	29	35	1	62	0.004	39	51	3	84	0.095	
MAP2K4 +MAP3K1	TP53	11	14	0	25	0.028	15	16	4	23	0.967	23	21	2	40	0.189	26	30	4	48	0.494	34	35	2	65	0.007	49	51	6	88	0.306	
CDH1	GATA3	8	7	0	15	0.317	N	N	N	N	NA	22	13	0	35	0.068	N	N	N	N	NA	30	20	0	50	0.014	NA	NA	A	NA	NA	
CDH1	TP53	8	14	0	22	0.082	N	N	N	N	NA	22	21	2	39	0.227	N	N	N	N	NA	30	35	2	61	0.021	NA	NA	A	NA	NA	
GATA3	TP53	7	14	0	21	0.110	9	16	1	23	0.603	13	21	2	30	0.635	16	30	1	44	0.171	20	35	2	51	0.147	29	51	3	74	0.319	
CDH1	PIK3CA	8	37	4	37	0.394	A	A	A	A	NA	22	52	8	58	0.326	A	A	A	A	NA	30	89	12	95	0.169	NA	NA	A	NA	NA	
RUNX1	TP53	3	14	0	17	0.422	N	N	N	N	NA	4	21	0	25	0.486	N	N	N	N	NA	7	35	0	42	0.180	NA	NA	A	NA	NA	
PIK3CA	TP53	37	14	9	33	0.764	42	16	6	46	0.449	52	21	6	61	0.097	79	30	15	79	0.721	89	35	15	94	0.257	13	1	51	21	14	0.307
CDH1	RB1	8	4	0	12	0.531	N	N	N	N	NA	22	2	0	24	0.688	N	N	N	N	NA	30	6	0	36	0.294	NA	NA	A	NA	NA	
MAP2K4	MAP3K1	2	9	0	11	0.707	5	10	0	15	0.641	3	20	0	23	0.608	7	19	0	26	0.439	5	29	0	34	0.372	10	39	0	49	0.298	
GATA3	MAP2K4 +MAP3K1	7	11	1	16	0.585	9	15	0	24	0.245	13	23	2	32	0.557	16	26	1	40	0.204	20	34	3	48	0.380	29	49	3	72	0.328	

Concurrently mutated pairs		77 WGS/Exome cases					108 cases from ext 1&2					132 cases from ext 3					77+108 cases					77+132 cases					77+108+132 cases				
Gene A	Gene B	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val	A Mut	B Mut	Both	Excl	p-val
MAP2K4 +MAP3K1	PIK3CA	11	37	9	30	0.101	15	42	10	37	0.017	23	52	13	49	0.097	26	79	19	67	0.001	34	89	22	79	0.030	49	1	32	11	0.000
MAP3K1	PIK3CA	9	37	7	32	0.220	10	42	7	38	0.039	20	52	13	46	0.019	19	79	14	70	0.007	29	89	20	78	0.012	39	1	27	6	0
MAP2K4	PDGFRA	2	2	1	2	0.072	N	N	N	N	NA	3	1	1	2	0.021	N	N	N	N	NA	5	3	2	4	0.002	NA	NA	A	NA	NA
CBFB	MAP2K4 +MAP3K1	2	11	2	9	0.033	N	N	N	N	NA	A	A	A	A	NA	N	N	N	N	NA	A	A	A	NA	NA	NA	A	NA	NA	NA
MAP2K4 +MAP3K1	RUNX1	11	3	2	10	0.091	N	N	N	N	NA	23	4	1	25	0.549	N	N	N	N	NA	34	7	3	35	0.158	NA	NA	A	NA	NA
MAP2K4	PIK3CA	2	37	2	35	0.367	5	42	3	41	0.340	9	52	0	55	0.170	7	79	5	76	0.170	5	89	2	90	0.823	10	13	1	13	0.459

Supplementary Table 9: Mutation Relation. Shown are permutation based mutation-relation test results. Given two genes, and the samples in which these genes are altered by non-silent variants, a permutation-based approach calculates the expected number of samples in which both genes are concurrently altered, and those in which the two genes are altered mutually exclusively. Based on the expected and observed values, p-values are calculated for concurrence and exclusivity. The table shows these calculations for all significantly altered genes, and with MAP2K4 and MAP3K1 variants merged as if affecting the same gene. These calculations are shown separately for the 3 distinct cohorts of cases, and in 3 possible combinations of the cohorts to improve sensitivity. A Mut, B Mut - Number of samples altered in Genes A and B. Both - Number of samples concurrently altered in both genes. Excl - Number of samples altered exclusively in one of the two genes. p-val - P-value for concurrence or mutual exclusivity of variants between Gene A and Gene B.

Chr	Start	Stop	# Samples Amp	# Samples Del	Type	Genes
2	23450000	23790000	1	0	AMP	<i>KLHL29</i>
4	73770000	74840000	3	0	AMP	<i>COX18,AFP,ALB,RASSF6,IL8,ANKRD17,AFM</i>
4	75190000	75490000	2	0	AMP	<i>EPGN,EREG,MTHFD2L</i>
4	75690000	76630000	2	0	AMP	<i>LOC441025,RCHY1,AREG,PARM1,BTC</i>
4	126950000	127600000	2	1	AMP	.
4	152410000	152870000	3	2	AMP	<i>PRSS48,PET112L,FAM160A1</i>
4	152780000	153470000	3	0	AMP	<i>PET112L,FAM160A1,FBXW7</i>
5	45910000	46690000	7	1	AMP	.
5	49150000	49470000	2	0	AMP	.
6	20940000	21320000	3	1	AMP	<i>CDKAL1</i>
11	19570000	20200000	7	1	AMP	<i>LOC100126784,DBX1,NAV2</i>
11	20490000	21550000	6	1	AMP	<i>SLC6A5,NELL1</i>
11	34040000	34750000	8	3	AMP	<i>NAT10,CAT,ABTB2,ELF5,CAPRIN1,EHF</i>
11	68850000	69150000	10	3	AMP	.
11	72210000	72560000	5	4	AMP	<i>ATG16L2,FCHSD2</i>
11	74670000	74980000	6	4	AMP	<i>MIR326,SNORD15A,SNORD15B,KLHL35,RPS3,SERPINH1,MAP6,GDPD5,ARRB1</i>
11	75190000	75550000	8	5	AMP	<i>DGAT2,UVRAG</i>
11	76660000	77300000	8	7	AMP	<i>GDPD4,CLNS1A,AQP11,C11orf67,RSF1,PAK1,INTS4</i>
11	77540000	77970000	7	7	AMP	<i>KCTD21,NARS2,GAB2,USP35</i>
11	77810000	78700000	7	2	AMP	<i>NARS2,ODZ4</i>
12	68440000	70220000	6	0	AMP	<i>TSPAN8,KCNMB4,CNOT2,RAB3IP,PTPRR,PTPRB,LGR5</i>
12	87890000	88250000	10	0	AMP	.
12	90410000	90860000	11	0	AMP	.
12	90880000	91250000	11	0	AMP	<i>BTG1</i>
12	91100000	91680000	7	0	AMP	<i>C12orf74,CLLU1OS,CLLU1,PLEKHG7</i>
18	51950000	52310000	5	1	AMP	.
18	52480000	52850000	5	1	AMP	<i>WDR7</i>
18	52850000	53240000	4	3	AMP	<i>BOD1P,ST8SIA3</i>
18	56860000	57360000	6	3	AMP	<i>CDH20</i>
18	57280000	57880000	7	2	AMP	<i>CDH20,PIGN,RNF152</i>
20	51050000	51560000	19	0	AMP	<i>TSHZ2</i>
20	51560000	52040000	18	0	AMP	<i>SUMO1P1,ZNF217,BCAS1</i>
20	51950000	52320000	19	0	AMP	<i>CYP24A1,PFDN4,BCAS1</i>
20	52380000	53240000	18	0	AMP	<i>DOK5</i>

X	61300000	61640000	3	2	AMP	.
2	10190000	10610000	0	2	DEL	<i>MIR4261,SNORA80B,HPCAL1,ODC1,C2orf48</i>
2	120770000	121570000	1	5	DEL	<i>INHBB,LOC84931,GLI2</i>
2	239590000	239890000	0	9	DEL	<i>MGC16025,HDAC4</i>
6	21190000	21610000	3	4	DEL	<i>CDKAL1</i>
6	106210000	106610000	4	7	DEL	.
7	66510000	66980000	2	3	DEL	.
8	31510000	31940000	4	9	DEL	<i>NRG1</i>
8	31900000	32350000	5	9	DEL	<i>NRG1</i>
10	98770000	99330000	2	10	DEL	<i>FRAT1,FRAT2,PGAM1,ANKRD2,ARHGAP19,EXOSC1,ZDHHC16,RRP12,UBTD1,SLIT1,MMS19,ARH GAP19-SLIT1</i>
10	101430000	102960000	2	6	DEL	<i>SNORA12,BLOC1S2,NDUFB8,MIR608,LZTS2,SFXN3,KAZALD1,TLX1,CUTC,COX15,NCRNA00093, CPN1,ERLIN1,PKD2L1,CWF19L1,WNT8B,NCRNA00263,HIF1AN,SEC31B,C10orf2,FAM178A,MRPL4 3,SEMA4G,TLX1NB,ABCC2,ENTPD7,SCD,PAX2,CHUK,DNMBP,PDZD7</i>
10	106510000	106950000	3	4	DEL	<i>SORCS3</i>
10	123070000	123540000	3	5	DEL	<i>ATE1,FGFR2</i>
13	22050000	22490000	2	5	DEL	<i>BASP1P1</i>
13	22520000	23070000	2	5	DEL	<i>SGCG,SACS,TNFRSF19</i>
13	23350000	23890000	3	8	DEL	<i>MIR2276,C1QTNF9B,PCOTH,C1QTNF9,SPATA13,MIPEP</i>
13	26640000	27440000	1	7	DEL	<i>RPL21P28,SNORD102,RPL21,SNORA27,RASL11A,GSX1,ATP5EP2,CDX2,GTF3A,MTIF3,LNX2,POL R1D,USP12,PDX1</i>
13	27580000	28850000	2	7	DEL	<i>LOC100288730,POMP,FLT1,PAN3,SLC46A3,MTUS2</i>
13	29410000	29710000	4	5	DEL	<i>LOC440131,KATNAL1</i>
13	29720000	30440000	4	5	DEL	<i>LOC100188949,HMGB1,USPL1,ALOX5AP,C13orf33,KATNAL1,C13orf26</i>
13	30500000	30850000	3	4	DEL	<i>HSPH1,B3GALT1</i>
18	53340000	54190000	3	5	DEL	<i>FECH,NARS,NEDD4L,ATP8B1</i>
18	54050000	54460000	3	4	DEL	<i>MIR122,ALPK2,NEDD4L</i>
19	61940000	63010000	2	8	DEL	<i>PEG3- AS1,AURKC,ZNF543,TRAPPC2P1,ZNF304,ZNF749,VN1R1,ZNF772,ZNF419,ZNF773,ZNF416,ZIK1, ZNF530,ZNF134,ZNF211,ZNF551,ZNF154,ZNF671,ZNF776,MIMT1,PEG3,ZIM3,DUXA,USP29,ZNF46 0,ZNF264,ZNF805,ZNF548,ZNF547,ZNF17,ZNF549,ZNF550,ZSCAN4,ZNF586,ZIM2 SEZ6L,MIR1302-1,MYO18B,ASPHD2</i>
22	24470000	25160000	1	7	DEL	

Supplementary Table 10: Focal Copy Number Variants

The following regions were identified as recurrent DNA copy number amplifications or deletions in 46 whole-genome samples by the CMDS algorithm. Most regions are small, with a median size of 0.47Mb, and 93% contain less than 10 genes. Several regions contain known cancer-related genes, including ZNF217, BCAS1, GAB2, and ELF5.

ChrA	Outer_startA	Inner_startA	ChrB	Outer_startB	Inner_startB	Event_type	Size	Patient	OrientationA	OrientationB	Inferred_mechanism	GeneA	TranscriptA	StrandA	SubStructureA	GeneB	TranscriptB	StrandB	SubStructureB	DeletedGenes	
2	05 45 90 36	05 45 90 36	2	08 45 79 36	08 45 79 36	D E	2 2	B R				Z M	EN ST								
0	90 000 90 003	90 000 90 003	0	79 112 79 112	79 112 79 112	L E	9 8	0 1	1	1	NH EJ	N D8	112 75	-	intron 3			-1	intron3	N/A	
1	05 90 13 44	05 90 13 44	1	24 90 78 46	24 90 78 46	E L	6 3	1 0	1	1	MM EJ	N/ A	N/A	/	N/ A						
2	13 000 13 003	13 000 13 003	2	78 112 78 112	78 112 78 112	L E	3 2	0 1				A	N/A	A	N/A						N/A ESPL1 VDR THAP2 OR6C6 DGKA ACSS3 AQP5 BLOC1S1 AAAS ITGA5 NXPH4 PPM1H NDUFA4L2 CNPY2 IL26 PTPRR SP7 TMBIM4 RARG KCN3 ACVR1B WNT1 CCDC59 STAT2 OR6C74 DNAJC14 GTSF1 NFE2 SYT1 LRIG3 TMEM194A NAV3 LIMA1 LRR1Q1 OR2AP1 HNRPA1L3 ELA1 C12orf66 PRR13 SENP1 KRT82 RASSF3 SLC11A2 TMTC3 LLP3 SDR9C7 GRIP1 FAM113B GLIPR1 RPS26P53 ATP5G2 RPAP3 MYF5 HOXC13 NPFF IL23A SMARCC2 C12orf28 R3HDM2 LALBA MSRB3 RAB3IP SLC4A8 KRT8P9 PAWR OR6C70 KRT77 SLC38A1 KRT76 OSBPL8 RNF41 KRT80 COQ10A TUBA1A AVIL SMARCD1 KRT72 YEATS4 METTL7B uc001ryd.1 MCRS1 KRT73 DDX23 TBC1D15 ARHGAP9 USP15 C12orf41 LYZ OR6C68 PRIM1 B4GALNT1 NAB2 SLC35E3 CSRP2 GRASP TMEM19 ACVRL1 RHEBL1 CAND1 LGR5 C12orf56 SILV DNAJC22 HOXC11 TBK1 MYO1A DHH CEP290 TAC3 LINTA SLC38A2 KRT1 ZC3H10 H1FNT OR6C65 GLI1 IL22 FAM62A HOXC5 C12orf62 MIP OR6C2 PPP1R1A SCN8A LRFP1 RAP1B KCNC2 SNS CYP27B1 ARF3 KIF5A KRT4 RPSAP52 OR10P1 MLL2 MBD6 DIP2B ANKRD33 ASB8 MDM2 CPM IRAK3 SLC16A7 OR6C1 OBFC2B RBMS1P CACNB3 DAZAP2 TBC1D30 FMNL3 GALNT6 PPFIA2 HOXC12 FAM19A2 KRT5 PCBP2 SP1 PTPRQ MARS CTDSP2 ALX1 ACN2 C12orf26 KRT83 SMUG1 SFRS2IP HOXC8 HOXC9 ZNF740 NR4A1 RASSF9 FRS2 MFSD5 LARP4 KRT6C ZFC3H1 ERBB3 INHBC IGFBP6 STAC3 HDAC7 HOXC4 TFCP2 KITLG NACA SLC6A15 ORMDL2 KRT6B DDI3 CDK4 PLEKHA9 ITGA7 WIF1 FAM186B CBX5 IFNG CCDC65 KRT18P19 C12orf68 TMEM106C KIAA1602 SPRYD4 OR6C76 DPY19L2 CPSF6 TSPAN8 KRT74 MDM1 DBX2 ZNF385A MUCL1 MYL6B BAZ2A FAIM2 HOXC6 PA2G4P4 SLC48A1 RDH16 TMPRSS12 HOXC10 C12orf50 TPH2 CCT2 TRHDE MGAT4C PDE1B DCTN2 COL2A1 ATP5B XPOT GPD1 DDN C12orf61 CCNT1 BIN2 OR9K1P HELB KCNMB4 PFKM MYF6 OS9 STAT6 KRT84 PRPF40B CD63 AQP2 GEFT COPZ1 NCKAP1L GPR182 AVPR1A TSMF SPRYD3 CSRN2P RPL21P18 MMP19 KRT85 DTX3 CSAD NTS C12orf44 PFDN5 TMEM5 RAB5B TUBA1C RAPGEF3 OR8S1 KRT79 RPL14P1 TMBIM6 SRGAP1 PTGES3 PHLDA1 NELL2 ZBTB39 CAPS2 FIGLN2 OR6C4 CS WNT10B PTPRB LEMD3 AQP6 SLC38A4 ATF1 FKBP11 RAGGAP1P RND1 MAP3K12 E2F7 KRT3 FAM119B KRT71 LMBRL1 TARBP2 IKZF4 ARID2 KRT78 POU6F1 CALCOCO1 ATF7 LRRC10 ZNF641 KRR1 ENSG00000202582 KIAA0748 SPATS2 MARCH9 KRT6A OR6C75 BBS10 TSPAN31 AMIGO2 XRC6BP1 MON2 SUXO PAN2 ANHR2 ANO6 GDF11 HSD17B6 PHC1B KRT81 LACRT GLIPR1L1 AGAP2 RBMS2P CNOT2 ADCY6 C12orf10 MYL6 TROAP SHMT2 SLC39A5 KRT86 OR6C3 GLS2 PRKAG1 OR10A7 RDH5 ANP32D INHBE PIP4K2C HMG2A METTL7A APOF RAB21 TENC1 LETMD1 LASS5 TUBA1B KRT75 C12orf29 CDK2 NEUROD4 C1QL4 NUP107 FAM186A TIMELESS PPP1R12A C12orf64 GPR84 PRPH KRT7 TMTC2 WIBG NAP1L1 GLIPR1L2 DYRK2 METTL1 SOAT2 OR10AD1 ITGB7 ANKRD52 BCDIN3D EIF4B KRT2 OR9K2 BEST3 ZDHHC17 C12orf54 DCD
1	32 42 54 42	32 42 54 42	1	32 87 32 87	32 87 32 87	D E	0 1	0 1				NH	M 11		intron						
2	73 000 73 003	73 000 73 003	2	88 112 88 112	88 112 88 112	L E	3 2	0 1	1	1	EJ	EJ	7	34	1	1	N/A				
1	85 71 60 60	85 71 60 60	1	23 55 3 60	23 55 3 60	T X	/	1				NH	N/A	/	N/ A						
1	79 71 79 71	79 71 79 71	1	61 71 61 71	61 71 61 71	C T	/	1				NH	N/A	/	N/ A						
0	11 000 11 003	11 000 11 003	3	37 112 37 112	37 112 37 112	X A	3 2	0 1	-1	-1	EJ	A	N/A	A	N/A						

KIFAP3 TPM3 MRPL55 FLG2 NPHS2 MARK1 MGST3 FAM177B
 RAB3GAP2 INSR ZNF648 C1orf98 ACBD6 CREG1 ATP1A4 JTB
 THBS3 ASCL5 TOR3A PMF1 VHL COPA FAM163A LENEP C1orf2
 C1orf46 MUC1 LEMD1 F13B OR6K1P ITPKB PKLR EFN4 IL24
 MAEL CTSE CLK2 SHISA4 TRIM11 NCF2 SPRR2A TROVE2
 S100A5 GLUL DEGS1 ELF3 RPL26P11 TDRD5 LAD1 EPHX1
 KLHL12 NPR1 CDC42BPA OR10T1P SLC30A10 C1orf157 RGS4
 NR5A2 RCSD1 RPL13AP8 PPP2R5A TSEN15 POP4L1 RAB4A
 MYOC C1orf55 SLC25A44 MTX1 HMCN1 C1orf65 C1orf14 RNASEL
 NAV1 OR10K1 C1orf148 SLAMF1 SLC30A1 RGL1 FCGR3B
 ARHGEP2 CAMSAP1L1 NCRNA00083 PIGR CFH RCOR3 DUSP27
 TCHHL1 RASSF5 CACNA1S FCRL3 ATP8V1G3 RGS13 OR10J9P
 SMG5 GPR52 CYCSF2 C1orf74 SPTA1 ARF1 TMCC2 CCT3
 C1orf111 TNN C1orf58 IER5 UBAP2L C1orf129 S100A2 RALGPS2
 APCS CNTN2 IL6R CHRNB2 SSR2 RD3 MFS04 CHI3L1 C1orf120
 IRF6 C1orf197 RNPEP NIT1 TBX19 CRP TMO1 MOSC2 CD247
 S100A7L2 KKBKE CRNN GPATCH2 FAM72A SYT11 SLC26A9
 SUS4 ATP2B4 ENAH CDC73 FCRL4 CNIH4 POGK SPRR2B ADAR
 ESRRG JMJD4 FLAD1 CD48 C1orf21 GORAB RIT1 SH2D1B MND4
 KIF14 OR10J3 LIN9 SELE C1orf105 PBX1 RAB13 USF1 C1orf25
 SLAMF7 ASH1L UHMK1 FCRL5 VAMP4 RPL17P8 OLFML2B
 S100A10 C1orf35 NOS1AP NMNAT2 IGSF8 FAIM3 RNF2 ADIPOR1
 RGS1 SH2D2A NR113 PRRX1 NEK7 LEFTY1 C1orf189 KIAA1614
 MYBPH LCE5A C1orf112 WNT3A IFI16 DDX59 GJC2 C1orf226
 KRT18P28 TNN1 LCE3A RPL4P3 CFHR2 TIPRL SDHC PROX1
 LGTN ATF6 uc001gud.2 CKS1B ARPC5 C1orf145 FMO2 RPTN
 LAMB3 ZC3H11A NDUFS2 B4GALT3 HIST3H2A SNRPE NVL NENF
 SCAMP3 S100A3 TDRD10 CD1E DTL TOR1AIP1 SPRR2F KCNJ9
 CR2 DPM3 OR6N2 TTC24 C1orf53 SMG7 CSRP1 ANGEL2
 SLC41A1 VANGL2 GLT25D2 IGSF9 TIMM17A TMEM78 FLG
 RAG1AP1 ZNF281 TATDN3 SNAP47 PBXIP1 SLC45A3 OR10T2
 ILDR2 EFNA1 CENPL GPR25 SNFT RASAL2 LCE2D YY1AP1
 PLA2G4A TMEM79 C1orf92 RGS21 TRAF3IP3 TOMM40L RBBP5
 DSTYK CFHR4 PTPRV PMVK RPL4P2 IQWD1 FCER1A LM0D1
 SELP LAMC2 CD84 ETV3L CACYBP S100A14 F5 FAM78B MYOG
 C1orf49 SPFR3 GPATC4 TOR1AIP2 IARS2 ADAMT54 EPRS
 OSOX1 DISP1 KIRREL PPOX FMO8P HSPA6 GUK1 C1orf115
 DENND4B SRGAP2 DCST2 METTL13 OR6N1 APOA1BP SLAMF8
 RABGAP1L SYT14 MPZL1 KLHL20 TNNT2 OR10J1 RGS8 LOR
 APOA2 EFNA3 C1orf192 NES SEMA4A NUKA2 PEX19 PTGS2
 USH2A NSL1 CFHR1 OPTC FCRL2 CABC1 LCE2C C1orf204
 METTL11B NUP133 ASTN1 UCHL5 BLZF1 WNT9A C4BPB OR6K5P
 AIM2 SMCP TLR5 MIA3 RNF187 FAM71A FCGR3A SPRR2G
 C1orf107 HAX1 REN CFHR3 ACTA1 C1orf66 NCSTN PDC LCE2B
 S100A7 NHLH1 PYHIN1 TRIM46 FCRLA FMO9P SPRR4 LCE1D
 CRTC2 FCER1G C1orf77 WDR42A PAPPA2 F11R LY9 HSD11B1
 KCNN3 HDGF S100A7A ZBTB7B ZNF847P DDR2 OR6K6 FMO11P
 BRP44 HAPLN2 SFT2D2 FMOD C4BPA IGFN1 ISG20L2 OBSCN
 GBA TNFSF18 PTPN14 SERPINC1 SLC9A11 PPFIA4 CNIH3
 HHIPL2 uc001fxh.2 RPL26P12 FCAMR TMEM183A ROBLD3
 C1orf186 PRELP S100A12 KIF21B PYGO2 LMNA KCNJ10 CD46
 C1orf147 KPRP CAMK1G OR10K2 HSD17B7 OR6Y1 KCTD3
 C1orf69 POU2F1 KISS1 C1orf97 G0S2 RAB25 FCRLB PCTK3
 GPA33 RRP15 PYCR2 OR2AQ1P SLC39A1 C1orf110 STX6 ZBTB41
 BAT2D1 S100A6 HIST3H2BB PIGC S100A1 TPR LCE2A GATAD2B
 LCE1C FBXO28 PSEN2 SPRR1A LELP1 PGLYRP4 WDR26 OR6K3
 LCE3C UAP1 OR10R1P PEAR1 LMX1A C1orf116 ADAM15 FMO7P
 NPL S100A16 FMO1 KLHDC9 LCE1E S100A8 IVL PLEKHA6 CHIT1
 C1orf125 UBE2Q1 PRC C HCN3 NUF2 SOAT1 MR1 C1orf220 RGS18
 TNR FCRL1 PRR9 LHX9 ZC3H11B PGLYRP3 FDP5 ERVK5 SPHAR
 ARL8A EEF1AL12 CRB1 LCE3B RPS6K1 MSTO1 DUSP10 PVRL4
 C1orf156 EDEM3 DARC LCE4A ALDH9A1 GBAP SPRR2E ADCY10
 S100A11 LAMC1 ZNF678 SRP9 SMYD2 NEK2 OR6K4P OR10R2
 JARID1B CREB3L4 PTPN7 C1orf9 TP53BP2 S100A13 SNAPIN
 LYPLAL1 TMEM206 UBE2T SLAMF6 CENPF UFC1 ELK4 C1orf43
 C1orf68 XCL2 HLX HHAT TMEM81 ANGPTL1 MDM4 RHBG RGS1
 MPN2 CR1 ENSG00000216295 INTS3 SLC19A2 SPRR1B TMEM63A
 PFDN2 CD1C PIGM S100A9 UCK2 LBR PARP1 DHX9 PTPRC
 B3GALT2 ACTBP11 DARS2 C1orf95 DUSP23 CRCT1 RPS27 LCE1F
 HRNR KCNH1 XPR1

	2.	2.		2.	2.		9	B		A	EN		
	28	28		28	28		8	R		B	ST		utr
	E	E		E	E		5	C		C	003		_e
	+0	+0		+0	+0	D	2	1	NH	B1	445	-	xo
1	8	8	1	8	8	E	1	1	EJ	0	17	1	n1
						L	1	1		0	17	1	3
													TAF5L

ENST00000258281

-1 intron0

TAF5L

ZBTB10 PKHD1L1 MAL2 WISP1 TMEM74 OSR2 MED30 TTC35
 TRIM55 C8orf37 IL7 CYP7A1 ANGPT1 C8orf44 RIPK2 POP1
 CHMP4C ZFAT FAM49B FBXO43 SNX31 GRHL2 UBE2W MTERFD1
 HEY1 VPS13B KIAA0196 LACTB2 ST18 PABPCP5 FAM84B
 ATP6V1C1 RSP02 LRP12 FER1L6 NDUFB9 PTDSS1 FAM82B
 YWHAZ TMEM67 WDR67 FAM83A KIAA1429 MTFR1 CDH17

8	1.27	1.27	1.27	1.27	D	1	1	NH	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
8	1.31	1.31	1.31	1.31	D	1	1	NH	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
1	31.79	31.79	31.79	31.79	D	1	1	NH	B	EN	ST	000	003	801	1	1	BRCA2	ENST00000380152	1	intron2	N/A
3	61.1	61.1	94.1	94.1	E	2	2	EJ	A2	52											
7	1E+08	1E+08	1E+08	1E+08	D	1	1	NH	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	29.94	29.94	29.95	29.95	D	6	7	MM	G	RI	K1	000	003	277	1	4	GRIK1	ENST00000327783	-1	intron4	N/A
1	42.96	42.96	1.33	1.33	E	6	2	EJ													
1	78.55	78.55	79.28	79.28	D	9	4	MM	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	60.33	60.33	1.89	1.89	E	4	2	EJ													
1	80.62	80.62	85.27	85.27	D	4	3	MM	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	CCDC83	ENST00000342404	1	intron4	DLG2 CCDC89 ANKRD42 CREBZF TMEM126A FAM181B RAB30 PCF11 PRCP C11orf82 CCDC90B SYTL2 TMEM126B
1	19.51	19.51	1.98	1.98	E	3	2	EJ													
8	40.12	40.12	40.12	40.12	D	3	1	MM	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	74.34	74.34	8.63	8.63	E	5	2	EJ													
8	38.42	38.42	38.50	38.50	D	6	1	NH	F	G	R1	000	003	414	1	1	N/A	N/A	N/A	N/A	N/A
8	35.99	35.99	8.77	8.77	E	7	2	EJ													
2	53.55	53.55	42.92	42.92	C	N	1	MM	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
0	59.12	59.12	2.40	2.40	T	X	A	EJ													
1	20.07	20.07	2.15	2.15	T	X	A	NH	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	33.33	33.33	0.43	0.43	X	A	2	EJ													
2	38.42	38.42	2.20	2.20	C	N	1	MM	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	RUNX1	ENST00000300305	-1	intron1	N/A
0	93.85	93.85	2.41	2.41	T	X	A	EJ													
2	12.96	12.96	2.86	2.86	C	N	1	MM	P	T	87	000	003	731	1	1	CLDN14	ENST00000342108	-1	intron0	N/A
0	62.62	62.62	1.78	1.78	X	A	2	EJ													

7	86 28 15 80	86 28 15 80	7	86 26 21	86 28 26 21	D E L	1 0 4 1 6	B R C	1	1	NH EJ	G R M 3	EN ST 000 003 616 69	1	intr on 2	GRM3	ENST00000361669	1	intron2	N/A
1	1. 74 E +0 8	1. 74 E +0 8	1	1. 74 E +0 8	1. 74 E +0 8	D E L	1 8 0 3	B R C	1	1	NH EJ	R F W D2	EN ST 000 003 676 67	-	intr on 14	RFWD2	ENST00000367667	-1	intron14	N/A
X	73 84 89 49 1. 03 E +0 8	73 84 89 49 1. 03 E +0 8	X	73 85 18 79 1. 03 E +0 8	73 85 18 79 1. 03 E +0 8	D E L	2 9 3 1 6	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A
1	1. 03 E +0 8	1. 03 E +0 8	1	1. 03 E +0 8	1. 03 E +0 8	D E L	1 2 1 6	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A
5	57 31 04 42	57 31 04 42	5	57 31 98 91	57 31 98 91	D E L	9 4 1 6	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A
2	1. 57 E +0 8	1. 57 E +0 8	2	1. 57 E +0 8	1. 57 E +0 8	D E L	4 7 1 6	B R C	1	1	NH EJ	G P D2	EN ST 000 003 104 54	1	intr on 0	GPD2	ENST00000310454	1	intron0	N/A
1	57 42 92 32	57 42 92 32	1	57 42 93 18	57 42 93 18	D E L	8 5 6	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A
2	18 02 25 58	18 02 25 58	2	18 02 49 62	18 02 49 62	D E L	2 4 0 5	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A
3	35 36 19 59	35 36 19 59	3	35 36 62 88	35 36 62 88	D E L	4 3 2 7	B R C	1	1	MM EJ	M M KL	EN ST 000 003 606 31	-	intr on 3	DCAMKL1	ENST00000360631	-1	intron3	N/A
1	97 87 48 88	97 87 48 88	1	97 87 76 98	97 87 76 98	D E L	2 8 0 9	B R C	1	1	NH EJ	FA R P1	EN ST 000 003 195 62	1	cd s_ ex on 15	FARP1	ENST00000319562	1	intron16	N/A
8	1. 35 E +0 8	1. 35 E +0 8	8	1. 35 E +0 8	1. 35 E +0 8	D E L	5 6 1 6	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A
1	55 61 70 8	55 61 70 8	1	55 64 12 8	55 64 12 8	D E L	2 4 1 9	B R C	1	1	NH EJ	A N O 2	EN ST 000 003 270 87	-	intr on 21	ANO2	ENST00000327087	-1	intron21	N/A
4	12 01 64 48	12 01 64 48	4	12 01 70 69	12 01 70 69	D E L	6 2 1 0	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A
6	11 35 30 9	11 35 30 9	6	11 35 47 7	11 35 47 7	D E L	1 6 1 9	B R C	1	1	NH EJ	N/ A	N/A	N	N/ A	N/A	N/A	N/A	N/A	N/A

1	2. 17 E +0 8	2. 17 E +0 8	2. 17 E +0 8	2. 17 E +0 8	D E L	4 6 3 8	B R C 1 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A			
1	85 33 54 01 1. 08 E +0 8	85 33 54 01 1. 08 E +0 8	85 34 30 42 1. 08 E +0 8	85 34 30 42 1. 08 E +0 8	D E L	7 6 3 7	B R C 1 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A			
2	1. 08 E +0 8	1. 08 E +0 8	1. 08 E +0 8	1. 08 E +0 8	D E L	1 9 6 1 5	B R C 1 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A			
1	31 57 03 21	31 57 03 21	31 57 27 42	31 57 27 42	D E L	2 4 2 1	B R C 1 6	1	1	NH EJ	R Y R3	000 892 32	1	1	2	intron	RYR3	ENST00000389232	1	intron2	N/A
5	84 90 51 45	84 90 51 45	84 90 55 35	84 90 55 35	D E L	3 8 1 9	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	22 98 37 69	22 98 37 69	22 98 63 96	22 98 63 96	D E L	2 6 2 6	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2. 11 E +0 8	2. 11 E +0 8	2. 11 E +0 8	2. 11 E +0 8	D E L	4 2 9 1 8	B R C 1 6	1	1	NH EJ	R P S6 K C1	000 003 659 60	1	1	10	intron	RPS6KC1	ENST00000366960	1	cds_exon1 0	N/A
1	1. 17 E +0 8	1. 17 E +0 8	1. 17 E +0 8	1. 17 E +0 8	D E L	1 3 6 1 0	B R C 1 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1. 69 E +0 8	1. 69 E +0 8	1. 69 E +0 8	1. 69 E +0 8	D E L	2 4 5 1 5	B R C 1 6	1	1	NH EJ	W D R4 9	000 003 083 78	-	1	5	intron	WDR49	ENST00000308378	-1	intron5	N/A
2	80 83 52 24	80 83 52 24	80 84 21 68	80 84 21 68	D E L	6 9 4 1 6	B R C 1 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	79 83 06 53	79 83 06 53	79 83 15 76	79 83 15 76	D E L	9 2 1 3	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1. 64 E +0 8	1. 64 E +0 8	1. 64 E +0 8	1. 64 E +0 8	D E L	2 9 2 1 4	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2. 18 E +0 8	2. 18 E +0 8	2. 18 E +0 8	2. 18 E +0 8	D E L	2 9 2 1 0	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	68 69 39 83 32 45	68 69 39 83 32 45	68 82 22 83 32 57	68 82 22 83 32 57	D E L	1 2 1 6 1 2	B R C 1 6	1	1	MM EJ	C P A6	000 002 977 70 EN ST 000 002	-	1	2	intron	CPA6	ENST00000297770	-1	intron2	N/A
X	01 01	X 51 51	01 51 51	01 51 51	D E L	1 1 1 1	B R C 1 6	1	1	NH EJ	R P S6 K	000 002	-	1	1	intron	RPS6KA6	ENST00000262752	-1	intron1	N/A

7	35 63 98 03	35 63 98 03	7	35 64 46 89	35 64 46 89	D E L	4 8 5 6	B R C	1	1	NH EJ	H E R P U D 2	EN ST 000 003 960 81	-	utr _e xo n8	HERPUD2	ENST00000396081	-1	intron4	N/A
1	1. 24 E +0 8	1. 24 E +0 8	1	1. 24 E +0 8	1. 24 E +0 8	D E L	6 6 7 6	B R C	1	1	MM EJ	M M 13 2B	EN ST 000 002 993 08	1	intr on 1	TMEM132B	ENST00000299308	1	intron1	N/A
1	57 58 51 67	57 58 51 67	1	57 59 11 12	57 59 11 12	D E L	5 9 4 5	B R C	1	1	NH EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A
7	68 29 86 00	68 29 86 00	7	68 30 31 25	68 30 31 25	D E L	4 5 2 5	B R C	1	1	NH EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A
3	1. 69 E +0 8	1. 69 E +0 8	3	1. 69 E +0 8	1. 69 E +0 8	D E L	6 2 1 5	B R C	1	1	MM EJ	W R D R4 9	EN ST 000 003 083 78	-	intr on 0	WDR49	ENST00000308378	-1	intron0	N/A
7	1. 32 E +0 8	1. 32 E +0 8	7	1. 32 E +0 8	1. 32 E +0 8	D E L	4 3 5 4	B R C	1	1	NH EJ	C H C D3	EN ST 000 002 625 70	-	intr on 6	CHCHD3	ENST00000262570	-1	intron6	N/A
2	2. 01 E +0 8	2. 01 E +0 8	2	2. 01 E +0 8	2. 01 E +0 8	D E L	4 7 2 2	B R C	1	1	MM EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A
1	86 50 30 89	86 50 30 89	1	86 50 69 69	86 50 69 69	D E L	3 8 7 5	B R C	1	1	MM EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A
4	86 03 51 11	86 03 51 11	4	86 03 78 29	86 03 78 29	D E L	2 7 1 8	B R C	1	1	NH EJ	W D F Y 3	EN ST 000 003 223 66	-	intr on 0	WDFY3	ENST00000322366	-1	intron0	N/A
4	18 13 51 59	18 13 51 59	4	18 13 88 46	18 13 88 46	D E L	3 6 8 7	B R C	1	1	NH EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A
7	1. 59 E +0 8	1. 59 E +0 8	7	1. 59 E +0 8	1. 59 E +0 8	D E L	2 2 0 5	B R C	1	1	MM EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A
1	1. 06 E +0 8	1. 06 E +0 8	1	1. 06 E +0 8	1. 06 E +0 8	D E L	2 2 1 5	B R C	1	1	NH EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A
6	1. 12 E +0 8	1. 12 E +0 8	6	1. 12 E +0 8	1. 12 E +0 8	D E L	1 5 7 6	B R C	1	1	NH EJ	R E V3 L	EN ST 000 003 688 05	-	intr on 2	REV3L	ENST00000368805	-1	intron2	N/A
2	28 91 64 80	28 91 64 80	2	28 91 67 60	28 91 67 60	D E L	2 2 8 1	B R C	1	1	NH EJ	N/ A	N/ A	N/ A	N/ A	N/A	N/A	N/A	N/A	N/A

8	24 62 97 73	24 62 97 73	8	24 63 36 31	24 63 36 31	D E L	3 8 5 8	B R C 1 6	1	1	NH EJ	N/ A	N/A EN ST 000 003 704	N / A	N / A	N/A	N/A	N/A	N/A			
1	1. 02 E +0 8	1. 02 E +0 8	1	1. 02 E +0 8	1. 02 E +0 8	D E L	3 0 7 2	B R C 1 6	1	1	NH EJ	E RL IN 1	10 EN ST 000 003 704	-	1	7	intron	ERLIN1	ENST00000370410	-1	intron6	N/A
1	1. 44 E +0 8	1. 44 E +0 8	1	1. 44 E +0 8	1. 44 E +0 8	D E L	5 7 1 6	B R C 1 6	1	1	NH EJ	P O LR 3C	10 EN ST 000 003 341 63	-	1	4	intron	POLR3C	ENST00000334163	-1	intron3	N/A
1	2. 28 E +0 8	2. 28 E +0 8	1	2. 28 E +0 8	2. 28 E +0 8	D E L	4 1 5 3	B R C 1 6	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	64 31 97 18 1.	64 31 97 18 1.	8	64 32 26 18 1.	64 32 26 18 1.	D E L	2 8 9 6	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	94 E +0 8	94 E +0 8	1	94 E +0 8	94 E +0 8	D E L	3 9 1 6	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	22 99 95 61	22 99 95 61	1	23 00 49 47	23 00 49 47	D E L	5 3 8 6	B R C 1 6	1	1	NH EJ	C H S T 9	000 002 842 24	-	1	0	intron	CHST9	ENST00000284224	-1	intron0	N/A
1	80 43 16 04	80 43 16 04	1	80 43 21 13	80 43 21 13	D E L	5 0 1 9	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1. 91 E +0 8	1. 91 E +0 8	3	1. 91 E +0 8	1. 91 E +0 8	D E L	2 5 4 0	B R C 1 6	1	1	NH EJ	LE P R EL 1	000 003 193 32	-	1	1	intron	LEPREL1	ENST00000319332	-1	intron1	N/A
1	75 14 10 68	75 14 10 68	1	75 39 53 93	75 39 53 93	D E L	3 2 2 6	B R C 1 6	1	1	MM EJ	FL V C R2	000 002 386 67	-	1	1	intron	TTL5	ENST00000393826	1	intron27	C14orf1 TTL5
4	1. 54 E +0 8	1. 54 E +0 8	4	1. 54 E +0 8	1. 54 E +0 8	D E L	7 7 8 7	B R C 1 6	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1. 12 E +0 8	1. 12 E +0 8	3	1. 12 E +0 8	1. 12 E +0 8	D E L	3 6 1 3	B R C 1 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	79 94 91 21	79 94 91 21	2	79 94 95 88	79 94 95 88	D E L	4 4 1 6	B R C 1 6	1	1	MM EJ	C T N A2	000 004 095 36	-	1	3	intron	CTNNA2	ENST00000409536	1	intron3	N/A
1	76 39 32 0	76 39 32 0	1	76 39 73 72	76 39 73 72	D E L	4 1 4 0	B R C 1 6	1	1	NH EJ	M Y S T4	000 003 727 25	-	1	2	intron	MYST4	ENST00000372725	1	intron2	N/A

1	2.1E+08	2.1E+08	2.1E+08	2.1E+08	DELL	158	1	1	NH EJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	25491.09E+08	25491.09E+08	25491.09E+08	25491.09E+08	DELL	863	1	1	MM EJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	1103.72E+08	1103.72E+08	1103.72E+08	1103.72E+08	DELL	542	1	1	MM EJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	9103.72E+08	9103.72E+08	9103.72E+08	9103.72E+08	DELL	863	1	1	NH EJ	NTN0000359640	ENST00000359640	-1	intron1	N/A	N/A	N/A	N/A	N/A
7	1.41E+08	1.41E+08	1.41E+08	1.41E+08	DELL	238	1	1	MM EJ	KIAA1147	ENST00000297761	-1	intron3	N/A	N/A	N/A	N/A	N/A
1	9763.03E+06	9763.03E+06	9763.03E+06	9763.03E+06	DELL	394	1	1	NH EJ	APAF1	ENST00000339433	1	intron20	N/A	N/A	N/A	N/A	N/A
1	1.01E+08	1.01E+08	1.01E+08	1.01E+08	DELL	281	1	1	NH EJ	KIAA1377	ENST00000263468	1	intron4	N/A	N/A	N/A	N/A	N/A
7	2469.25E+19	2469.25E+19	2469.25E+19	2469.25E+19	DELL	196	1	1	MM EJ	MPP6	ENST00000222644	1	cds_exon10	N/A	N/A	N/A	N/A	N/A
1	5548.77E+63	5548.77E+63	5548.77E+63	5548.77E+63	DELL	666	1	1	NH EJ	CCBE1	ENST00000333570	-1	intron2	N/A	N/A	N/A	N/A	N/A
1	8537.42E+82	8537.42E+82	8537.42E+82	8537.42E+82	DELL	666	1	1	MM EJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2622.41E+49	2622.41E+49	2622.41E+49	2622.41E+49	DELL	566	1	1	MM EJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	6953.81E+09	6953.81E+09	6953.81E+09	6953.81E+09	DELL	866	1	1	NH EJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	1.45E+08	1.45E+08	1.45E+08	1.45E+08	DELL	496	1	1	NH EJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	7889.63E+23	7889.63E+23	7889.63E+23	7889.63E+23	DELL	256	1	1	NH EJ	KCNMA1	ENST00000372437	-1	intron1	N/A	N/A	N/A	N/A	N/A

2	1. 15 E +0 8	1. 15 E +0 8	2	1. 15 E +0 8	1. 15 E +0 8	D E L	6 4 1 6	1	1	NH EJ	N/ A R A B G A P1 L	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	N/A
1	1. 73 E +0 8	1. 73 E +0 8	1	1. 73 E +0 8	1. 73 E +0 8	D E L	5 0 1 6	1	1	MM EJ	N/ A P1 L	EN ST 000 004 077 35	1	intr on 16	RABGAP1L	ENST00000407735	1	intron16	N/A	
1	64 20 60 89	64 20 60 89	1	64 20 81 17	64 20 81 17	D E L	2 0 2 7	1	1	NH EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
1	67 98 34 53	67 98 34 53	1	67 98 48 18	67 98 48 18	D E L	1 3 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
3	19 E +0 8	19 E +0 8	3	19 E +0 8	19 E +0 8	D E L	1 5 0 8	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
1	55 E +0 8	55 E +0 8	1	55 E +0 8	55 E +0 8	D E L	2 0 7 3	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
1	14 60 65	14 60 65	1	14 60 70	14 60 70	D E L	4 0 4 6	1	1	MM EJ	SL C4 3A 2	EN ST 000 003 013 35	1	intr on 4	SLC43A2	ENST00000301335	-1	intron3	N/A	
9	8 E +0 8	8 E +0 8	9	8 E +0 8	8 E +0 8	D E L	4 4 6 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
8	16 E +0 8	16 E +0 8	8	16 E +0 8	16 E +0 8	D E L	1 0 1 6	1	1	NH EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
2	18 70 88	18 70 88	2	18 71 02	18 71 02	D E L	1 4 1 7	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
1	31	31	1	50	50	D E L	7 6	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
8	80 73 90 70	80 73 90 70	8	80 73 92 73	80 73 92 73	D E L	2 0 1 6	1	1	MM EJ	ST M N2	EN ST 000 002 208 76	1	intr on 4	STMN2	ENST00000220876	1	intron4	N/A	
8	35 E +0 8	35 E +0 8	8	35 E +0 8	35 E +0 8	D E L	3 3 1 5	1	1	MM EJ	N/ A	N/A	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
1	70 76 70	70 76 70	1	70 78 04	70 78 04	D E L	1 3 3 9	1	1	NH EJ	LA M A1	EN ST 000 003 896 58	1	intr on 1	LAMA1	ENST00000389658	-1	intron1	N/A	
2	48 25 49	48 25 49	2	21 13 49	21 13 49	D E L	8 7 1 5	1	1	NH EJ	N/ A F S	N/A EN ST 000	N / A	N/ A	N/A	N/A	N/A	N/A	N/A	
2	20 93	20 93	2	21 08	21 08	D E L	1 4 C	1	1	NH EJ	H R	EN ST 000	1	intr on 1	FSHR	ENST00000346173	-1	intron1	N/A	

6	1. 07 E +0 8	1. 07 E +0 8	1. 07 E +0 8	1. 07 E +0 8	D E L	2 3 1 6	B R C C	1	1	NH EJ	AI M 1	EN ST 000 003 690 66	1	1	1	intr on	AIM1	ENST00000369066	1	cds_exon1	N/A
2	2. 08 E +0 8	2. 08 E +0 8	45 45 97 09 00	45 45 97 09 00	C T X	N / A	B R C C	-1	1	MM EJ	N/ A	N/A	N	N	N	N/A	N/A	N/A	N/A	N/A	
7	43 71 13 9	43 71 13 9	1 +0 8	1 +0 8	E E X	C T X	N / A	B R C C	1	-1	MM EJ	N/ A	N/A	N	N	N/A	N/A	N/A	N/A	N/A	
9	62 46 94 24	62 46 94 24	1 16 13	1 16 13	E L	D E L	2 1 8 7	B R C C	1	1	MM EJ	N/ A	N/A	N	N	N/A	N/A	N/A	N/A	N/A	
0	46 15 65 28	46 15 65 28	2 16 29	2 16 29	IN V	IN V	1 0 0 7	B R C C	-1	1	NH EJ	N/ A	N/A	N	N	N/A	N/A	N/A	N/A	N/A	
0	51 40 11 01	51 40 11 01	2 54 14	2 54 14	D L	D L	3 3 1 7	B R C C	1	1	NH EJ	TS H Z2	EN ST 000 003 714 97	1	1	intr on	N/A	N/A	N/A	CASS4 CYP24A1 C20orf107 RPL39P AURKA MC3R C20orf106 C20orf43 PPIAP10 BCAS1 GCNT7 DOK5 PTMAP6 TFAP2C ZNF217 PFDN4 C20orf108 CBLN4 CSTF1	
9	61 47 93 77	61 47 93 77	1 88 72 98	1 88 72 98	D L	D L	6 9 1 9	B R C C	1	1	NH EJ	ZS C A	EN ST 000 002 541 65	-	0	intr on	N/A	N/A	N/A	ZNF71 ZNF542 ZFP28 ZNF582 ZNF471 ZNF583 ZNF667 ZNF835 ZNF470	
5	83 02 30 1. 25 E +0 8	83 02 30 1. 25 E +0 8	1 05 53 1. 25 E +0 8	1 05 53 1. 25 E +0 8	D E L	D E L	3 1 0 7	B R C C	1	1	MM EJ	SL C2 8A	EN ST 000 002 867 49	1	13	intr on	ENST00000286749	1	intron13	N/A	
1	2. 37 E +0 8	2. 37 E +0 8	2. 37 E +0 8	2. 37 E +0 8	D E L	D E L	7 1 4	B R C C	1	1	MM EJ	A S B1	EN ST 000 003 308 42	-	1	intr on	ASB18	ENST00000330842	-1	intron1	N/A
1	99 27 95 22	99 27 95 22	1 +0 8	1 +0 8	D E L	D E L	2 0 5 0	B R C C	1	1	MM EJ	N5	EN ST 000 002 794 63	1	3	intr on	ARHGEF12	ENST00000356641	1	intron2	N/A PHLDB1 POU2AF1 C11orf87 MCAM FXYD2 AASDHPPT ARHGAP20 TMEM25 SLC37A4 HYOU1 TAGLN ALG9 USP2 KB1BD3 ABCG4 C11orf1 SIK2 GRIA4 CRYAB IL10RA CASP5 PVRL1 FDACB1 POU2F3 DLAT HTR3B C11orf1 KIAA1377 MPZL2 TMEM123 APOA1 ANGPTL5 C11orf65 TRIM29 AMICA1 RPS25F8 DDX6 RDX CCDC84 MMP7 PDZD3 CD3D MMP13 HSPB2 DIXDC1 C10TNF5 FAM55A C11orf34 SLN ARCN1 BUD13 CASP4 OAF SCN2B DPAGT1 APOA5 MMP3 PDGFD REXO2 FXYD6 FAM55D DRD2 LAYN USP28 BIRC2 NPAT ZC3H12C H2AFX MMP10 TTC12 ZBTB16 KDELC2 BTG4 HTR3A DYNC2H1 C11orf60 C11orf52 TRAPPC4 KIAA1826 ATP5L NCAM1 PPIHP1 MMP8 BACE1 THY1 CASP12 PAFAH1B2 MPZL3 CWF19L2 SLC35F2 TMEM133 SCN4B RBM7 BCO2 CD3E RPL23AP64 TRPC6 TMPRSS4 C2CD2L ANKK1 PCSK7 TMPRSS13 TTC36 PPP2R1B CASP1 TIMM8B CARD17 HINFP SIDT2 CUL5 NNMT CCDC153 C11orf70 FDX1 DSCAML1 PTS MMP1 uc001ppy.1 RNF26 ACAT1 FOXR1 BCL9L C11orf92 DCUN1D5 SDHD DDI1 YAP1 MMP12 VPS11 CARD16 MLL MMP27 GUCY1A2 ELMOD1 CARD18 TREH TMPRSS5 ZNF259 FAM55B CBL APOC3 ZW10 NLRX1 UBE4A UPK2 ENSG00000216295 HMBS MMP20 ENSG00000165895 PGR IL18 DDX10 C11orf88 TMEM136 PIH1D2 MFRP C11orf57 EXPH5 RAB39 ALKBH8 CEP164 BIRC3 CADM1 APOA4 TEX12 CD3G ATM CXCR5 RNF214 C11orf53

8	41 96 21 61	41 96 21 61	1 9	39 60 04 3	39 60 04 3	C T X	N / A	B R C 1 7	-1	1	NH EJ	M Y S T 3	EN S T 000 002 657 13	-	1	intr on 2	PIAS4	ENST00000262971	1	intron1	N/A	
1 9	56 48 76 32	56 48 76 32	2 0	54 68 77 51	54 68 77 51	C T X	N / A	B R C 1 7	-1	1	NH EJ	N/ A	N/A EN S T 000 003 081	N / A A	N / A A	N/A	N/A	N/A	N/A	N/A		
1 9	62 99 61 77	62 99 61 77	2 0	36 28 89 80	36 28 89 80	C T X	N / A	B R C 1 7	1	1	NH EJ	Z N C F5 86	EN S T 000 003 081 37	1	2	intr on	KIAA1755	ENST00000279024	-1	cds_exon6	N/A	
1 9	61 98 67 36	61 98 67 36	2 0	44 37 79 96	44 37 79 96	C T X	N / A	B R C 1 7	1	1	NH EJ	P E G S3A	EN S T 000 003 917 08	-	1	6	intr on	N/A	N/A	N/A	N/A	
1 9	57 99 36 25	57 99 36 25	2 0	43 60 60 68	43 33 60 68	C T X	N / A	B R C 1 7	1	1	NH EJ	Z N C F2 8	EN S T 000 003 602 72	-	1	1	utr _e xo n1	N/A	N/A	N/A	N/A	
1 9	54 28 43 72	54 28 43 72	2 0	51 76 64 11	51 76 64 11	C T X	N / A	B R C 1 7	-1	1	NH EJ	S N R N P7 0	EN S T 000 002 214 48	1	1	intr on	N/A	N/A	N/A	N/A		
3	72 79 54 7	72 79 54 7	1 5	71 47 79 61	71 47 80 12	C T X	N / A	B R C 1 7	1	-1	NA HR	G R M 7	EN S T 000 003 577 16	1	2	intr on	N/A	N/A	N/A	N/A		
8	87 16 47 0 1. 19 E E 0	87 16 47 0 1. 19 E E 8	1 9 0	41 96 16 2 1. 19 E E 8	41 96 16 2 1. 19 E E 8	C T X	N / A	B R C 1 7	-1	1	NH EJ	M F H A S1	EN S T 000 002 762 82	-	1	1	intr on	N/A	N/A	N/A	N/A	
1 0	+0 8	+0 8	1 0	+0 8	+0 8	D E L	4 4 1 3	B R C 1 7	1	1	NH EJ	N/ A	N/A	N / A A	N / A A	N/A	N/A	N/A	N/A	N/A		
3	1. 23 E E +0 8	1. 23 E E +0 8	3	1. 23 E E +0 8	1. 23 E E +0 8	D E L	4 2 0 2	B R C 1 7	1	1	NH EJ	I Q C B1	EN S T 000 003 498 20	-	1	3	intr on	ILDR1	ENST00000383663	-1	cds_exon4	SLC15A2 EAF2
1 3	61 52 41 02	61 52 41 02	1 3	61 52 42 65	61 52 42 65	D E L	1 6 3 0	B R C 1 7	1	1	NH EJ	N/ A	N/A	N / A A	N / A A	N/A	N/A	N/A	N/A	N/A		
1 1	17 89 32 75	17 89 32 75	1 1	22 77 57 79	22 77 57 79	D E L	5 0 2 0	B R C 1 7	1	1	NH EJ	S E R G EF	EN S T 000 002 659 65	-	1	9	intr on	GAS2	ENST00000278187	1	intron6	SLC17A6 SAAL1 ANO5 SPTY2D1 E2F8 LDHA NAV2 MRGPRX3 HPS5 SAA1 SAA2 LDHC MRGPRX1 FAM10A5 DBX1 TMEM86A PTPN5 CSRP3 IGSF22 TSG101 MRGPRX2 HTATIP2 TPH1 ZDHHC13 NELL1 UEVLD PRMT3 SLC6A5 FANCF MRGPRX4 GTF2H1 SAA3P LDHAL6A SAA4
3	1. 23 E E +0 8	1. 23 E E +0 8	3	1. 28 E E +0 8	1. 28 E E +0 8	D E L	9 1 C 8 2	B R C 1 7	1	1	NH EJ	P O L Q	EN S T 000 002 642 33	-	1	14	intr on	CCDC37	ENST00000352312	1	cds_exon1 3	HSPBAP1 SEC22A SEMA5B CSTA ILDR1 CD86 OSBPL1 IQCB1 PARP14 ROPN1B CCDC14 WDR5B ROPN1 SNX4 CCDC58 ZNF148 DTX3L SLC15A2 MUC13 CASR EAF2 MYLK GOLGB1 ADCY5 HEG1 SLC12A8 KPNA1 ARGFX SLC41A3 PARP9 KLF15 HCLS1 ALDH1L1 ITGB5 PARP15 KALRN PTPLB PDIA5 FBXO40 FAM162A UMPS DIRC2

3	1. 23 E +0 8	1. 23 E +0 8	3	1. 23 E +0 8	1. 23 E +0 8	D E L	5 0 0 8 7 2 3	B R C 2	1	1	NH EJ	P O L Q	EN ST 000 002 642 33	-	1	13	intr on	ILDR1	ENST00000273691	-1	intron5	IQCB1 ARGFX FBXO40 SLC15A2 HCLS1 EAF2 GOLGB1	
2	1. 65 E +0 8	1. 65 E +0 8	2	1. 65 E +0 8	1. 65 E +0 8	D E L	9 9 6 4	B R C 2	1	1	NH EJ	C O B L L	EN ST 000 003 421 93	-	1	1	intr on	COBLL1	ENST00000342193	-1	intron1	N/A	
1 8	96 11 93 8	96 11 93 8	1 8	96 12 26 7	96 12 26 7	D E L	3 0 2 4	B R C 2	1	1	NA HR	N/ A	N/ A	N / A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	87 78 92	87 78 92	3	1. 23 E +0 8	1. 23 E +0 8	D E L	3 5 4 4 9 7 9	B R C 2	1	1	NH EJ	N/ A	N/A	N / A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1 8	25 69 71	25 69 71	1 8	28 93 94	28 93 94	D E L	1 3 5	B R C 2	1	1	MM EJ	N/ A	N/A	N / A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	DSG4 RNF138 B4GALT6 DSC2 FAM59A DSC1 MEP1B DSG1 TTR DSG2 RNF125 KLHL14 DSC3 WBP11P1 MCART2 KIAA1012 DSG3
1 8	49 43 50 31	49 43 50 31	1 8	51 01 64 78	51 01 64 78	D E L	0 4 2 7	B R C 2	1	1	NH EJ	N/ A	N/A	N / A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	STARD6 RAB27B C18orf26 MBD2 C18orf54 CCDC68 POLI
8	49 78 83 03	49 78 83 03	8	49 78 92 77	49 78 92 77	D E L	9 7 2 0	B R C 2	1	1	MM EJ	N/ A	N/A	N / A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	18 73 26 01	18 73 26 01	9	19 60 55 25	19 60 55 25	D E L	1 9 2 3	B R C 2	1	1	NH EJ	N/ A	EN ST 000 003 805 48	1	15	intr on	SLC24A2	ENST00000341998	-1	intron3	ACER2 RPS6 ADFP ADAMTSL1 FAM154A RRAGA FAM29A DENND4C		
1 8	25 52 76 08	25 52 76 08	1 8	28 94 05 26	28 94 05 26	D E L	1 9 1 5	B R C 2	1	1	MM EJ	N/ A	N/A	N / A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	DSG4 RNF138 B4GALT6 DSC2 FAM59A DSC1 MEP1B DSG1 TTR DSG2 RNF125 KLHL14 DSC3 WBP11P1 MCART2 KIAA1012 DSG3 FSTL1 C3orf66 TOMM70A KIAA1524 C3orf15 PVRL3 OR5K1 ZNF80 KTELC1 DHFRL1 RG9MTD1 CRYBG3 WDR52 IFT57 OR5H15 ABHD10 ZPLD1 LRRC58 TAGLN3 CCDC80 GTPBP8 NAT13 NR112 ARL13B CD96 PLA1A GAP43 CBLB DRD3 ALCAM KIAA1407 SIDT1 EPAH6 OR5K3 OR5AC2 OR5H6 EPAH3 RABL3 DPPA4 GUCA1C PROS1 BTLA RETNLB MORC1 TIGIT ZBTB11 IMPG2 GABRR3 C3orf26 TMEM39A NSUN3 CCDC52 HHLA2 NIT2 CD200R1L IGSF11 CGGBP1 ZDHHC23 MYH15 C3orf52 CCDC54 STXBP5L SEN7 TMPPRS7 CPOX C3orf1 GTF2E1 LNP1 TBC1D23 CLDND1 C3orf38 UPK1B COX17 HTR1F HGD STX19 NFKBIZ GSK3B ZBED2 B4GALT4 OR5K4 RPL24P6 C3orf17 SLC35A5 ATG3 ST3GAL6	
3	86 71 14 77	86 71 14 77	3	1. 23 E +0 8	1. 23 E +0 8	D E L	3 6 0 0 0	B R C 2	1	1	NH EJ	N/ A	N/A	N / A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	DSG4 RNF138 B4GALT6 DSC2 FAM59A DSC1 MEP1B DSG1 TTR DSG2 RNF125 KLHL14 DSC3 WBP11P1 MCART2 KIAA1012 DSG3 FSTL1 C3orf66 TOMM70A KIAA1524 C3orf15 PVRL3 OR5K1 ZNF80 KTELC1 DHFRL1 RG9MTD1 CRYBG3 WDR52 IFT57 OR5H15 ABHD10 ZPLD1 LRRC58 TAGLN3 CCDC80 GTPBP8 NAT13 NR112 ARL13B CD96 PLA1A GAP43 CBLB DRD3 ALCAM KIAA1407 SIDT1 EPAH6 OR5K3 OR5AC2 OR5H6 EPAH3 RABL3 DPPA4 GUCA1C PROS1 BTLA RETNLB MORC1 TIGIT ZBTB11 IMPG2 GABRR3 C3orf26 TMEM39A NSUN3 CCDC52 HHLA2 NIT2 CD200R1L IGSF11 CGGBP1 ZDHHC23 MYH15 C3orf52 CCDC54 STXBP5L SEN7 TMPPRS7 CPOX C3orf1 GTF2E1 LNP1 TBC1D23 CLDND1 C3orf38 UPK1B COX17 HTR1F HGD STX19 NFKBIZ GSK3B ZBED2 B4GALT4 OR5K4 RPL24P6 C3orf17 SLC35A5 ATG3 ST3GAL6

SLC9A10 CD80 CD47 C3orf30 OR5H14 NDUFB4 ADPRH POPDC2
 QTRTD1 PLCXD2 ZBTB20 VGLL3 COL8A1 BOC OR5H2 WDR82P1
 TFG FAM172B GCET2 TMEM45A POU1F1 BZW1L1 DZIP3 LSAMP
 ATP6V1A ZNF654 DCBLD2 MINA KIAA2018 GPR156 OR5H1 CD200
 FAM55C GPR128 BBX CHMP2B TRAT1 DPPA2 CD200R1 OR5K2
 ABI3BP ARL6 GPR15 CEP97 PCNP GRAMD1C FILIP1L

3	1. 23 E +0	1. 23 E +0	3	1. 23 E +0	1. 23 E +0	D E L	9 7 2 0	B R C 2 0	1	1	NH EJ	P O L Q	EN ST 000 002 642 33 EN	-	1	intr on 15	ARGFX	ENST00000334384	1	utr_exon4	N/A
6	24 43 88 19	24 43 88 19	7	72 97 64 84	72 97 64 84	C T X	N A	B R C 0	-1	-1	NH EJ	D C C2	EN ST 000 003 784 54	-	1	intr on 2	N/A	N/A	N/A	N/A	
6	1. 07 E +0	1. 07 E +0	2	28 02 04 62	28 02 04 62	C T X	N A	B R C 0	1	-1	NH EJ	N/ A	N/A	N	/	N/ A	N/A	N/A	N/A	N/A	
1 8	56 86 57 55	56 86 57 55	2 1	15 16 57 60	15 16 57 60	C T X	N A	B R C 0	-1	-1	MM EJ	N/ A	N/A	N	/	N/ A	N/A	N/A	N/A	N/A	
1	34 92 02	34 92 02	5	64 64 88 43	64 64 88 43	C T X	N A	B R C 0	1	1	NH EJ	N/ A	N/A	N	/	N/ A	N/A	N/A	N/A	N/A	
1 8	26 34 21 01	26 34 21 01	2 1	30 68 84 99	30 68 84 99	C T X	N A	B R C 0	1	1	NH EJ	N/ A	N/A	N	/	N/ A	N/A	N/A	N/A	N/A	
6	56 E +0	56 E +0	2	53 82 18 50	53 82 18 50	C T X	N A	B R C 0	1	1	NH EJ	N/ A	N/A	N	/	N/ A	N/A	N/A	N/A	N/A	
1 8	51 01 59 03	51 01 59 03	2 1	23 12 04 83	23 12 04 83	C T X	N A	B R C 0	1	1	NH EJ	N/ A	N/A	N	/	N/ A	N/A	N/A	N/A	N/A	
8	74 28 01 54	74 28 01 54	1	34 81 32 03	34 81 32 03	C T X	N A	B R C 0	1	1	MM EJ	N/ A	N/A	N	/	N/ A	N/A	N/A	N/A	N/A	
3	1. 23 E +0	1. 23 E +0	6	57 62 05 23	57 62 05 23	C T X	N A	B R C 0	-1	1	MM EJ	I Q C B1	EN ST 000 003 498 20	-	1	intr on 3	PRIM2	ENST00000389488	1	utr_exon10	N/A
3	1. 23 E +0	1. 23 E +0	6	57 62 51 66	57 62 51 66	C T X	N A	B R C 0	1	-1	NH EJ	H C L S1	EN ST 000 003 145 83	-	1	intr on 5	N/A	N/A	N/A	N/A	
7	29 88 33 28	29 88 33 28	7	29 88 34 68	29 88 34 68	D E L	1 3 2	B R C 2	1	1	NH EJ	W I P F	EN ST 000 004 091	1	intr on 2	WIPF3	ENST00000409123	1	intron2	N/A	
1 3	21 91 72 51	21 91 72 51	3	23 28 59 72	23 28 59 72	D E L	7 7 2	B R C 2	1	1	NH EJ	N/ A	N/A	N	/	N/ A	MIPEP	ENST00000382172	-1	intron14	TNFRSF19 SGCG HMGA1L6 MIPEP SACS

5	1. 77 E +0 8	1. 77 E +0 8	1. 77 E +0 8	1. 77 E +0 8	D E L	1 2 9	B R C 2 3	1	1	NA HR	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
1	2. 18 E +0 8	2. 18 E +0 8	43 13 04 54	43 13 04 54	C T X	N / A	B R C 2 4	-1	1	MM EJ	N/ A	N/A EN ST 000 003 206	N / A	N / A	HGSNAT	ENST00000332689	1	intron2	N/A
5	80 86 23 72	80 86 23 72	80 86 32 64	80 86 32 64	D E L	8 9 2 1	B R C 6	1	1	NH EJ	S S B P2	EN ST 000 003 206 72	-	intr on 4	SSBP2	ENST00000320672	-1	intron4	N/A
6	12 45 49 55	12 45 49 55	12 45 65 39	12 45 65 39	D E L	1 5 8 3	B R C 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A
4	60 30 41 08	60 30 41 08	60 30 42 79	60 30 42 79	D E L	1 7 1	B R C 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A
9	16 17 75 3	16 17 75 3	16 17 97 6	16 17 97 6	D E L	2 2 3	B R C 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A
10	37 66 44 16	37 66 44 16	37 66 47 27	37 66 47 27	D E L	3 1 0	B R C 6	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A
2	32 58 90 58	32 58 90 58	32 58 92 54	32 58 92 54	D E L	1 9 2 7	B R C 6	1	1	NH EJ	BI R C6	EN ST 000 002 613 59	1	intr on 52	BIRC6	ENST00000261359	1	intron53	N/A
4	81 92 27 44	81 92 27 44	81 92 29 23	81 92 29 23	D E L	1 8 0	B R C 6	1	1	VN TR	C4 orf 22	EN ST 000 004 067 49	1	intr on 4	C4orf22	ENST00000406749	1	intron4	N/A
X	1. 35 E +0 8	1. 35 E +0 8	1. 35 E +0 8	1. 35 E +0 8	D E L	1 2 7	B R C 6	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A
2	2. 31 E +0 8	2. 31 E +0 8	13 23 49	13 23 49	C T X	N / A	B R C 6	1	-1	NH EJ	S P1 00	EN ST 000 004 098 24	1	intr on 1	COX10	ENST00000261643	1	intron3	N/A
2	64 14 95 0	64 14 95 0	64 18 04 5	64 18 04 5	D E L	3 0 9	B R C 9	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A
7	90 23 41 28	90 23 41 28	90 23 43 01	90 23 43 01	D E L	1 7 4 3 3 3	B R C 9	1	1	NH EJ	PF TK 1	EN ST 000 003 800 50	1	intr on 4	PFTK1	ENST00000380050	1	intron4	N/A
8	31 52 55 42	31 52 55 42	34 86 44 69	34 86 44 69	D E L	7 9	B R C 9	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	DUSP26 RPL10AP3 MAK16 C8orf41 NRG1 FUT10 RNF122

SLC22A15 KCNA3 DLEU2L CREG1 DDAH1 TARS2 ATP1A4
HIST2H4B CSF1 JTB APH1A THBS3 GPR89C SORT1 SAMD13
PMF1 VHLH C1orf177 HS2S21 C1orf138 LRP8 MCOLN3 COPA
C1orf2 LENEPE SETDB1 MUC1 C1orf46 ENSA GCLM AGL GBP1
FAM72B FAM159A OR6K1P SCP2 PALMD PKLR GNG5 FAM102B
EFNA4 KIAA1324 USP24 MAEL ATG4C HSD3B2 CSDE1 WDR77
ADH5P2 CLK2 SPRR2A C1orf168 SH3GLB1 S100A5 C1orf83
C1orf56 NPR1 ARHGAP29 GSTM4 OR10T1P BCL9 C1orf62
TMEM59 TACSTD2 RGS4 FAM108A2 MAGI3 RCSD1 FAM40A
FOXO3 POGZ PCP4L1 RPS10P6 ALG14 C1orf123 SYPL2
SLC25A44 GPR177 MTX1 FMO5 PDZK1P2 NBPF8 ADOXA3 GBP6
FAM69A EFCAB7 OR10K1 DRD5P2 SLAMF1 DPYD SLC16A4 BRDT
FCGR3B ZNF687 ARHGEF2 DUSP27 HSPB11 TCHHL1 SARS
TNNI3K FCRL3 LRRCA4 GJA8 NEXN OR10J9P PSMB4 SMO5
LRRC7 USP33 CYGSP52 CRYZ SPTA1 OVGP1 WNT2B CTBS
CCT3 C1orf111 UBAP2L SGIP1 S100A2 RSNB1 GNG12 C1orf152
APCS IL6R GTF2B CHRN2 uc001elpl.1 SSR2 EEF1A9 CD53
VTCN1 CNN3 NIT1 TBX19 CRP EXTL2 PPAP2B TMCO1 CD247
S100A7L2 CRNN EVI5 HIST2H2AA3 DCLRE1B NBPF11 MCOLN2
CCDC18 SYT11 SYCP1 CFLP2 HHLA3 ALX3 TDRKH C1orf141
FCGR1B CHIA C1orf175 RTCD1 RPS15P1 PPAPR5 FCRL4 GSTM3
POGK SPRR2B NRAS ADAR PSM2A SLC35D1 DR1 ECM1 TTC22
FLAD1 CD58 CD48 C1orf51 AHCYL1 FUBP1 PTGFR KI12 RIT1
SH2D1B MNDA OR10J3 NTNG1 CCDC76 GF11 PBX1 RAB13 USF1
SLAMF7 OSBPL9 LRRCS3 PDE4B ASH1L UHMK1 FCRL5 PRPF3
LRRC8B OLFML2B S100A10 NOS1AP ATP1A1 C1orf59 IGSF8
C1orf54 IL23R SH2D2A ANXA9 NR1I3 LMO4 ABCA4 KIAA1245
OAZ3 PHTF1 PDE4DIP C1orf189 KCNC4 OTUD7B LCE5A CLCA1
IFI16 C1orf226 LEPR DNTTIP2 LCE3A TIPRL SDHC ATF6 FNDC7
CKS1B NBPF6 RPTN ALG6 NOTCH2NL NDUFS2 CYB5RL NBPF1
B4GALT3 RAVR2 RPE65 GBP3 LEPROT SCAMP3 VCAM1 S100A3
CDC42SE1 PRPF38A TDRD10 CD1E FAF1 KCNJ9 SPRR2F
HIST2H2AA4 HAO2 DPM3 OR6N2 AP4B1 TTC24 TUFT1 CTSS
HIST2H2BD GNRHR2 VANGL2 C1orf68 PRKAB2 IGSF9 ZCCHC11
TLL7 C1orf203 HIST2H3P2 RAG1AP1 FLG HIST2HD TGFB3
TRIM45 C1orf194 PTGFRN PBXIP1 NHLH2 OR10T2 FAM108A3
ILDR2 INSL5 NBPF16 EFNA1 SLC35A3 YY1A1 LCE2D KCND3
LRRC42 TMEM79 C1orf92 TOMM40L PRUNE PMVK DBT RPL4P2
PTBP2 IQWD1 AMY2B OR11I1P FCER1A HFE2 KIAA1107 DIO1
PGM1 CD84 ETV3L JAK1 MRPS21 S100A14 FAM78B RBM8A
LINGO4 SPRR3 PIP5K1A DNAJB4 EPS8L3 VANGL1 GPATCH4
MAGOH AK5 AMY2A OLFML3 HSD3B1 ADAMT54 SYDE2 C1orf137
CELSR2 PDZK1 RWDD3 PPOX KIRREL FMO8P CDMN2C
CYB561D1 HSPA6 SV2A DENND4B ECHDC2 DCST2 TCTEX1D1
DMRTB1 OR6N1 APOA1BP VPS72 HOOK1 SLAMF8 MPZL1
LYSMD1 FCGR1A LRR1Q3 PHGDH ACP6 EPS15 CCT8P1 OR10J1
RORC AMPD1 APOA2 LOR C1orf192 EFNA3 NES LDLRAD1
SEMA4A PEX19 RPL36AP11 ADAMTSL4 FCRL2 LCE2C NEGR1
ELTD1 SXS2IP TM2D1 CD2 C1orf204 UOX UBE2U AIM2 OR6K5P
SMCP RPAP2 GNAT2 GBP2 FCGR3A CGN SPRR2G HAX1 C1orf52
TMEM167B FAM46C C1orf66 LHX8 NCSTN WARS2 NHLH1 S100A7
LCE2B PYHIN1 SF3B4 TRIM46 uc001dmb.1 FCRLA TMEM77
ZNF644 FMO3P CTSK NOTCH2 GSTM5 BSND CTH NR1H5P
SPRR4 SLC30A7 LCE1D FCER1G CRTG2 COBL2 HIST2H2BF
WDR42A C1orf77 ODF2L ANKRD34A F11R LY9 KCNN3 WDR78
HDGF S100A7A BCAS2 ZBTB7B TMED5 COL24A1 DDR2 FMO11P
OR6K6 BRP44 ZNF326 GPR89A HAPLN2 SFT2D2 BOLA1
HSP90B3P SLC44A5 TMEM61 ISG20L2 C1orf103 RNF115 GBA
CLCA2 RNF11 F3 RABGG1B RPL17 ZZZ3 RPL7P8 RPL26P12
uc001fkh.2 COL11A1 ROBLD3 ASB17 S100A12 PYGO2 POLR3GL
LMNA uc001efo.2 C1orf163 HIST2H2AB KCNJ10 TMEM48
HNRNPA1L1 CASQ2 AMPD2 CEPT1 C1orf191 KPRP PRKACB
THEM4 PRMT6 GBP5 OR10K2 HSD17B7 OR6Y1 C1orf87 POU2F1
MLL11 BCAR3 FCRLB RAB25 OLFM3 GPA33 INADL L1TD1
OR2AQ1P SLC39A1 C1orf110 DOCK7 SEC22B SRGAP2P2 S100A6
TSHB S100A1 LCE2A ABHD7 KANK4 GATAD2B LCE1C BCL10
TTC4 UBL4B SPRR1A SERBP1 PGLYRP4 LELP1 WDR3 PRPF38B
HIAT1 C1orf185 GSTM2 TXNDC12 OR6K3 UAP1 LCE3C JUN
OR10R1P CTTNBP2NL LMX1A PEAR1 OMA1 ADAM15 FMO7P
PIGK S100A16 RNPC3 POLR3C KLHDC9 ROR1 LCE1E C1orf180
S100A8 LPHN2 IVL NRD1 TMEM56 MRPL9 TSPAN2 AMYP1
UBE2Q1 PCSK9 CYP2J2 NUF2 PRCC HCN3 TNFAIP8L2 IGSF2
BTBD8 uc001dse.1 FCRL1 PARS2 PRR9 DENND2D HORMAD1
CYR61 BNIPL FDCP3 PGLYRP3 ERVK5 PSRC1 TBX15 VAV3
MTMR11 LCE3B MRPL37 STXBP3 CHD1L MSTO1 SELENBP1
DDX20 MCL1 SCN11 GBP4 PVRL4 PSMA5 AMIGO1 FAM19A3
ZNF697 TXNIP DARC SLC16A1 LCE4A ALDH9A1 GBAP GJA5
ADCY10 SPRR2E LRRC39 ZRANB2 NBPF7 S100A11 ST6GALNAC3

										EN ST 000								
1	12	E	1	12	E	D	3	9	3	AT P1	003	1	1	intr on				
3	+0	8	1	+0	8	L	0	1	1	NH EJ	756	1	1	ATP11A	ENST00000375630	1	intron1	N/A
1	02	E	1	03	E	D	1	1	3	NH N/A	N/A	N	N	SFXN3	ENST00000393459	1	cds_exon5	<p>PDZD7 FAM178A PAX2 LZTS2 SEMA4G PEO1 MRPL43 MMS19 CALHM3 CYP17A1 SMNDC1 HNSE2 PNLI CCDC147 PEO1 KCNIP2 BTRC SORCS3 GBF1 INPP5F KAZALD1 SLC18A2 SUFU FBXW4 FAM178A SFXN4 NFKB2 C10orf95 CUEDC2 CASP7 PDZD8 UBTD1 ENTPD7 SORCS1 VWA2 C10orf82 ADD3 OBFC1 GOLGA7B TDRD1 ADRB1 ACSL5 KIAA1598 GUCY2G PRDX3 PDCD11 CNM2 SEC31B CASC2 PCGF6 DUSP GSTO2 PDZD7 EMX2 MARVELD1 CNM1 MGEA5 LOXL4 TRUB1 NDUFB8 VTI1A ADRA2A NT5C2 PGAM1 ARHGAP19 NCRNA00081 SFRP5 SEC23IP USMG5 PNLI PRP3 PAX2 COX15 CWF19L1 C10orf28 WDR11 NANOS1 PI4K2A GOT1 NEURL C10orf85 FRAT1 FAM180B1 ABCC2 FBXL15 FGF8 HPS1 RPL19P16 TCF7L2 CALHM2 EXOSC1 ANKRD2 MORF4 RAB11FIP2 C10orf33 FGFR2 C10orf81 LBX1 NPM3 C10orf134 SFXN2 GSTO1 BLOC1S2 ITPRIP CPN1 NOLC1 RBM20 RPS84 AVP1 AFAP1L2 RGS10 TEC1B TMEM180 SLC25A28 SCD SLK C10orf78 ACTR1A CHUK uc001kyr.1 CUTC RPS15AP5 C10orf79 C10orf46 C10orf62 FAM45A CRTAC1 XPNPEP1 C10orf118 SMC3 GRK5 NHLRC2 HPS6 SFXN3 C10orf96 NKX2-3 TLX1 EIF3S10 VAX1 INA SEMA4G TAF5 PITX3 PDCD4 PNLI PRP1 HSPA12A PSD TRIM8 ZFYVE27 NRAP ELOVL3 SLIT1 HABP2 WNT8B C10orf32 CALHM1 ZDHHC16 C10orf84 ERLIN1 ABLIM1 LDB1 GFRA1 ATRNL1 RPL13AP6 PRLHR POLL DNMBP HIF1AN AS3MT SHOC2 PPAPDC1A PKD2L1 GPAM FRAT2 ZDHHC6 C10orf76 C10orf65 MX1 TIAL1 PNLI PRP2 BAG3 ARL3 PPRC1 RRP12 C10orf26 SH3PXD2A C10orf119 uc001ktn.1 LZTS2 KCNK18 MRPL43 DCLRE1A COL17A1</p>
1	77	E	1	24	E	D	2	7	3	SL IT	002	-	-	ATE1	ENST00000369043	-1	intron8	
0	88	88	0	8	8	L	0	1	1	EJ	660	1	25					
2	02	E	2	03	E	D	9	3	3	VN TR	N/A	N	N	N/A	N/A	N/A	N/A	N/A
0	61	61	0	67	67	L	3	1	1	TR	N/A	A	A					
5	50	E	5	09	E	D	9	3	3	MM EJ	N/A	N	N	N/A	N/A	N/A	N/A	N/A
	75	E		75	E	D	9	3	3	MM EJ	N/A	N	N	N/A	N/A	N/A	N/A	N/A
	52	E		62	E	D	3	3	3	MM EJ	N/A	N	N	N/A	N/A	N/A	N/A	N/A
	67	67		09	09	L	9	2	2	EJ	N/A	A	A					
1	04	E	1	04	E	D	9	3	3	NH EJ	000	-	-					
8	+0	8	1	+0	8	L	8	2	2	EJ	003	1	1					
	8	8	8	8	8	L	8	2	2	EJ	785	1	1					
3	26	E	3	26	E	D	8	3	3	NH EJ	N/A	N	N	ZNF148	ENST00000360647	-1	intron4	N/A
	8	8	3	8	8	L	2	2	2	EJ	N/A	A	A					
	00	E		01	E	D	1	7	3	SF BT	000	-	-					
3	21	E	3	39	E	D	4	3	3	MM EJ	003	1	0	SFMBT1	ENST00000394750	-1	intron0	N/A
	87	E		38	E	D	2	2	2	EJ	947	1	0					
	1	E		1	E	D	2	2	2	MM EJ	N/A	N	N	N/A	N/A	N/A	N/A	N/A
2	+0	8	1	+0	8	L	2	3	3	EJ	N/A	A	A					

8	39 40 19 82	39 40 19 82	1	74 62 74 96 1.	74 62 74 96 1.	C T X A	N / / / A	B R C 3 5 B R C 3 5 B R C 3 7	1	1	NH EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	
1 2	94 09 51	94 09 51	1 3	08 E +0 8 1.	08 E +0 8 1.	C T X A	N / / / A	B R C 3 5 B R C 3 7	-1	-1	MM EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	
X	26 E +0 8	26 E +0 8	X	1. E +0 8	1. E +0 8	D E L	1 6 3 7	B R C 3 7	1	1	NH EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	
X	38 46 91 03	38 46 91 03	X	51 60 13 17	51 60 13 17	IN V	9 3 0 7	B R C 3 7	-1	1	MM EJ	N/ A	N/A	N / / / A	N / / / A	MAGED1	ENST00000375772	1	intron0	N/A
1 4	99 37 95 70	99 37 95 70	1 4	1. E +0 8	1. E +0 8	D E L	5 2 3 7	B R C 3 7	1	1	MM EJ	E M L1	EN ST 000 002 622 33	1 1	intr on 1	RAGE	ENST00000193029	-1	intron1	DEGS2 C14orf68 DYNC1H1 BEGAIN HSP90AA2 YY1 RTL1 EVL C14orf70 WDR20 WARS EML1 DIO3 DLK1 WDR25 PPP2R5C SLC25A29
1 4	49 29 47 95	49 29 47 95	1 4	49 E 48 82	49 E 48 82	D E L	8 3 0 7	B R C 3 7	1	1	MM EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	
1	71 99 94 08	71 99 94 08	3	1. E +0 8	1. E +0 8	C T X A	7 3 A	B R C 3 7	1	-1	NH EJ	N E R1	EN ST 000 003 577 31	1 3	intr on 3	N/A	N/A	N/A	N/A	
1 6	60 00 30 08	60 00 30 08	1 9	32 81 57 15	32 81 57 15	C T X A	7 3 A	B R C 3 7	1	-1	NH EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	
1	64 25 63 30	64 25 63 30	3	1. E +0 8	1. E +0 8	C T X A	7 3 A	B R C 3 7	1	1	NH EJ	R O R1	EN ST 000 003 710 80	1 2	intr on 2	N/A	N/A	N/A	N/A	
1 1	29 E +0 8	29 E +0 8	1 4	91 45 11 38	91 45 11 38	C T X A	7 3 A	B R C 3 7	-1	-1	MM EJ	N/ A	N/A	N / / / A	N / / / A	FBLN5	ENST00000267620	-1	intron5	N/A
1 1	49 07 99 21	49 07 99 21	1 4	03 E +0 8	03 E +0 8	C T X A	7 3 A	B R C 3 7	1	-1	MM EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	
1 1	49 07 96 36	49 07 96 36	1 4	72 50 88 89	72 50 88 89	C T X A	7 3 A	B R C 3 7	-1	1	NH EJ	N/ A	N/A	N / / / A	N / / / A	ZFYVE1	ENST00000394207	-1	intron7	N/A
6	19 63 23 99	19 63 23 99	6	19 63 31 89	19 63 31 89	D E L	7 9 3 8	B R C 3 8	1	1	NH EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	
8	55 85 72 31	55 85 72 31	8	55 85 75 00	55 85 75 00	D E L	2 6 3 7	B R C 3 8	1	1	MM EJ	N/ A	N/A	N / / / A	N / / / A	N/A	N/A	N/A	N/A	

1	43 04 24 61	43 04 24 61	1	43 04 66 58	43 04 66 58	D E L	4 1 9 8	B R C	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
2	70 38 45 24	70 38 45 24	2	70 40 19 20	70 40 19 20	D E L	7 3 9 8	B R C	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
8	52 66 77 22	52 66 77 22	8	74 11 44 92	74 11 44 92	D E L	5 7 6 8	B R C	1	1	NH EJ	P X D NL	EN ST 000 003 562 97	-	intr on	TERF1	ENST00000276602	1	intron8	N/A BHLHE22 ATP6V1H CPA6 COPS5 ASPH CHCHD7 LYN NCOA2 PCMTD1 C8orf71 PLAG1 LRRC67 KCNB2 OPRK1 MYBL1 TERF1 CRH CA8 SEC11B RPS20 RAB2 SDCBP GGH EYA1 UBXN2B CHD7 SDR16C5 MRPL15 PRDM14 TGS1 CYP7B1 LYPLA1 MOS TRAM1 TRPA1 TTPA ADHFE1 PTTG3 TRIM55 MSC IMPAD1 RP1 CYP7A1 SNORD54 C8orf46 IFITM8P RB1CC1 C8orf44 SULF1 DNAJC5B NPBWR1 SOX17 TMEM68 YTHDF3 SGK3 RGS20 VCP1P1 C8orf45 XKR4 LACTB2 PREX2 ST18 C8orf34 TCEA1P2 RRS1 SLC05A1 PENK FAM110B FAM150A TCF24 RLB1P1 NKAIN3 CSPP1 TOX NSMAF ARFGEF1 ARMC1 PDE7A XKR9 MTRF1
1	2. 23 E +0 8	2. 23 E +0 8	1	2. 23 E +0 8	2. 23 E +0 8	D E L	8 8 9 3 7	B R C	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	CNIH3	
8	1. 13 E +0 8	1. 13 E +0 8	8	1. 13 E +0 8	1. 13 E +0 8	D E L	6 5 4 7	B R C	1	1	NH EJ	N/ A	N/A	N / A	N / A	CSMD3	ENST00000395717	-1	intron59	N/A
5	13 76 27 4	13 76 27 4	5	13 76 51 7	13 76 51 7	D E L	2 3 3 1	B R C	1	1	NA HR	CL PT M 1L	000 003 208 95	-	intr on	CLPTM1L	ENST00000320895	-1	intron12	N/A
1	1. 24 E +0 8	1. 24 E +0 8	1	1. 24 E +0 8	1. 24 E +0 8	D E L	1 4 3 7	B R C	1	1	NA HR	A A C S	000 003 165 19	1	intr on	AACS	ENST00000316519	1	intron9	N/A
6	19 11 26 68	19 11 26 68	6	19 11 60 70	19 11 60 70	D E L	3 3 9 2	B R C	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
8	1. 13 E +0 8	1. 13 E +0 8	X	1. 18 E +0 8	1. 18 E +0 8	C T X	N / A	B R C	1	-1	MM EJ	N/ A	N/A	N / A	N / A	DOCK11	ENST00000276202	1	intron30	N/A
5	90 58 37 25	90 58 37 25	9	82 93 83 66	82 93 83 66	C T X	N / A	B R C	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
1	73 61 75	73 61 75	1	73 62 70	73 62 70	D E L	8 3 7	B R C	1	1	NA HR	H A G HL	000 003 897 01	1	intr on	HAGHL	ENST00000389701	1	intron6	N/A
1	66 78 52 61	66 78 52 61	2	27 39 57 53	27 39 57 53	C T X	N / A	B R C	1	-1	NH EJ	N/ A	N/A	N / A	N / A	TTC28	ENST00000397906	-1	intron1	N/A
8	1. 37 E +0 8	1. 37 E +0 8	1	1. 68 X 77	1. 68 X 77	C T D	N / A	B R C	-1	1	VN TR	N/ A	N/A	N / A	N / A	NINJ2	ENST00000305108	-1	intron1	N/A
1	32 86 24	32 86 24	1	32 86 76	32 86 76	D E L	4 4 9	B R C	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
5	86 24	86 24	5	86 76	86 76	D E L	4 4 9	B R C	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	

8	1. 33 E +0 8	1. 33 E +0 8	1. 38 +0 8	1. 33 E +0 8	D E L	1 0 6 5 3 9 2 3 7 8 0 9 0 5 5 8 9 1 4 2 7 1	B R C 4	1	1	MM EJ	N/ A	N/A EN ST 000 003 562 64	N / A A	N/ A A	EFR3A	ENST00000254624	1	intron1	N/A
7	38 45 95 41	38 45 95 41	39 38 43 23	39 38 43 23	D E L	3 3 7 8 0 9 0 5 5 8 9 1 4 2 7 1	B R C 4	1	1	NH EJ	A M P H	A M P H	- 1	intr on 11	POU6F2	ENST00000403058	1	intron5	FAM183B VPS41
7	38 46 56 92	38 46 56 92	39 37 21 99	39 37 21 99	D E L	3 3 7 8 0 9 0 5 5 8 9 1 4 2 7 1	B R C 4	1	1	NH EJ	A M P H	A M P H	- 1	intr on 11	POU6F2	ENST00000403058	1	intron5	FAM183B VPS41
1	56 36 32 15 1. 1. 16 E +0 8	56 36 32 15 1. 1. 16 E +0 8	56 95 33 62 1. 1. 16 E +0 8	56 95 33 62 1. 1. 16 E +0 8	D E L	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	MM EJ	N/ A	N/A	N / A A	N/ A A	N/A	N/A	N/A	N/A	OR5AK2 P2RX3 PRG3 OR5AK3P SSRP1 SLC43A3 APLNR LRRCS5 PRG2 TNKS1BP1
2	16 E +0 8	16 E +0 8	16 E +0 8	16 E +0 8	D E L	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	NH EJ	N/ A	N/A	N / A A	N/ A A	N/A	N/A	N/A	N/A	N/A BHLHE22 ATP6V1H CPA6 COPS5 PKIA C8orf84 ASPH CHCHD7 LYN NCOA2 FAM164A PCMTD1 C8orf71 PXDNL PLAG1 LRRRC67 KCN2 OPRK1 JPH1 MYBL1 TERF1 CRH CA8 SEC11B LY96 RPS20 RAB2 SDCBP GGH EYA1 UBXN2B TCEB1 CHD7 SDR16C5 EFCAB1 CRISPLD1 MRPL15 TMEM70 PRDM14 TGS1 CYP7B1 LYPLA1 MOS PXMP3 TRAM1 ZFHx4 TRPA1 TTPA ADHFE1 RDH10 RPL7 PTTG3 TRIM55 IL7 MSC IMPAD1 RP1 CYP7A1 SNORD54 C8orf46 IFITM8P RB1CC1 C8orf44 SULF1 DNAJC5B NPBWIR1 STAU2 SOX17 TMEM88 YTHDF3 SGK3 UBE2W C8orf45 RGS20 VCPPI1 HEY1 XKR4 STMN2 LACTB2 PREX2 ST18 SNTG1 C8orf34 P15 TCEA1P2 RRS1 HNF4G SLC05A1 PENK FAM110B FAM150A C8orf22 TCF24 RLBPL11 CSPP1 NKAIN3 SNAI2 NSMAF TOX ARFGF1 ARMC1 PDE7A XKR9 GDAP1 MTFR1
8	49 36 34 88	49 36 34 88	81 03 26 53	81 03 26 53	D E L	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	MM EJ	N/ A	N/A	N / A A	N/ A A	MRPS28	ENST00000276585	-1	intron2	N/A
1	57 42 77 46 49 26 80 15 85 35 02 16	57 42 77 46 49 26 80 15 85 35 02 16	59 07 80 82 49 26 10 04 10 89 15 56	59 07 80 82 49 26 10 04 10 89 15 56	D E L	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	NH EJ	N/ A	N/A	N / A A	N/ A A	N/A	N/A	N/A	N/A	FAM111B OR6Q1 OR5A2 OR1S1 DTX4 ZFP91 LPXN GLYATL1 OR5AZ1P OR5B17 OR5AN1 GLYATL2 OR10Q1 OR1S2 OR4D11 OR5B12 OR9Q1 FAM111A GLYAT OR5B3 OR4D6 OR9Q2 OR10W1 MPEG1 OR9I1 OR5B21 OR5B2 OR4D9 OR5A1
7	49 26 80 15 85 35 02 16	49 26 80 15 85 35 02 16	86 26 10 04 10 89 15 56	86 26 10 04 10 89 15 56	D E L	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	MM EJ	N/ A	N/A	N / A A	N/ A A	N/A	N/A	N/A	N/A	N/A
4	44 06 23 8 12 04 48 80	44 06 23 8 12 04 48 80	56 2 +0 8 91 81 51 9	56 2 +0 8 91 81 51 9	C N X	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	MM EJ	N/ A	N/A	N / A A	N/ A A	N/A	N/A	N/A	N/A	N/A
6	81 85 82 49	81 85 82 49	81 84 84 09	81 84 84 09	D E L	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	NH EJ	N/ A	N/A	N / A A	N/ A A	N/A	N/A	N/A	N/A	N/A
X	22 E +0 8	22 E +0 8	22 E +0 8	22 E +0 8	D E L	3 1 6 6 8 8 1 4 2 7 1	B R C 4	1	1	MM EJ	M R P L	000 003 061 85	- 1	intr on 2	MRPL13	ENST00000306185	-1	intron2	N/A

8	1.07 E +0 8	1.07 E +0 8	1.07 E +0 8	1.07 E +0 8	D E L	9 1 1 4 9	B R C 1 B R C	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A
5	1.55 E +0 8	1.55 E +0 8	1.55 E +0 8	1.55 E +0 8	D E L	1 4 4 0	B R C 1 B R C	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A
4	59.55 23 6	59.55 23 6	59.55 23 6	59.55 23 6	D E L	2 6 4 5	B R C 2 C 6 4 5	1	1	MM EJ	N/A	ENST 000 003 978 88	-	intr on 7	-1	intron7	N/A	ENST00000397888
1	14.84 38 49	14.84 38 49	14.84 38 49	14.84 38 49	D E L	1 7 4 0	B R C 1 B R C	1	1	NH EJ	W B P1	ENST 000 002 611 67	-	cd s_ ex on 2	-1	intron2	N/A	ENST00000261167
3	1.4E +0 8	1.4E +0 8	1.4E +0 8	1.4E +0 8	D E L	5 3 2 4	B R C 5 3 2 4	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A
2	22.65 96 47	22.65 96 47	22.65 96 47	22.65 96 47	D E L	4 8 4 5	B R C 4 8 4 5	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A
6	1.42E +0 8	1.42E +0 8	1.42E +0 8	1.42E +0 8	D E L	3 1 4 8	B R C 3 1 4 8	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A
1	78.90 16 02	78.90 16 02	78.90 16 02	78.90 16 02	D E L	2 4 4 2	B R C 2 4 4 2	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A
7	14.86 35 2.	14.86 35 2.	14.86 35 2.	14.86 35 2.	D E L	6 4 1 4	B R C 6 4 1 4	1	1	MM EJ	D G K B	ENST 000 004 039 51	-	intr on 20	-1	intron20	N/A	ENST00000403951
1	2.2E +0 8	2.2E +0 8	2.2E +0 8	2.2E +0 8	D E L	1 8 4 9	B R C 1 8 4 9	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A
1	2.14E +0 8	2.14E +0 8	2.14E +0 8	2.14E +0 8	D E L	4 4 4 2	B R C 4 4 4 2	1	1	NH EJ	U S H2	ENST 000 003 669 43	-	intr on 37	-1	intron37	N/A	ENST00000366943
4	20.64 51 49	20.64 51 49	20.64 51 49	20.64 51 49	D E L	5 1 4 5	B R C 5 1 4 5	1	1	NH EJ	K C NIP4	ENST 000 003 821 52	-	intr on 1	-1	intron1	N/A	ENST00000382152
1	1.01E +0 8	1.01E +0 8	1.01E +0 8	1.01E +0 8	D E L	1 7 4 9	B R C 1 7 4 9	1	1	MM EJ	F G F1	ENST 000 003 761 31	-	intr on 1	-1	intron1	N/A	ENST00000376131
2	2.21E +0 8	2.21E +0 8	2.21E +0 8	2.21E +0 8	D E L	5 3 4 1	B R C 5 3 4 1	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A

6	23 34 89 07	23 34 89 07	6	23 34 91 11	23 34 91 11	D E L	2 0 0	B R C 4	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
3	89 97 27 56	89 97 27 56	3	89 97 32 36	89 97 32 36	D E L	4 7 6	B R C 4	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
9	1. 03 E +0 8	1. 03 E +0 8	9	1. 03 E +0 8	1. 03 E +0 8	D E L	2 1 1	B R C 4	1	1	MM EJ	R3	P P A R 74	EN ST 000 003 748	1	1	PPAPR3	ENST00000374874	1	intron1	N/A
1	1. 07 E +0 8	1. 07 E +0 8	1	1. 07 E +0 8	1. 07 E +0 8	D E L	4 6 4	B R C 4	1	1	NH EJ	1	N T G 76	EN ST 000 003 700 76	1	1	NTNG1	ENST00000370076	1	intron1	N/A
7	1. 37 E +0 8	1. 37 E +0 8	7	1. 37 E +0 8	1. 37 E +0 8	D E L	1 9 4	B R C 4	1	1	MM EJ	D G KI	EN ST 000 002 884 90	-	1	30	DGKI	ENST00000288490	-1	intron30	N/A
4	62 72 96 09	62 72 96 09	4	62 73 10 11	62 73 10 11	D E L	1 3 9	B R C 4	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
5	1. 78 E +0 8	1. 78 E +0 8	5	1. 78 E +0 8	1. 78 E +0 8	D E L	7 8 4	B R C 4	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
1	2. 23 E +0 8	2. 23 E +0 8	1	2. 23 E +0 8	2. 23 E +0 8	D E L	4 7 2	B R C 4	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
4	1. 74 E +0 8	1. 74 E +0 8	4	1. 74 E +0 8	1. 74 E +0 8	D E L	5 6 8	B R C 4	1	1	NH EJ	G A L N T7	EN ST 000 002 650 00	1	1	GALNT7	ENST00000265000	1	intron2	N/A	
3	1. 9E +0 8	1. 9E +0 8	3	1. 9E +0 8	1. 9E +0 8	D E L	5 2 4	B R C 4	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
6	1. 68 E +0 8	1. 68 E +0 8	6	1. 68 E +0 8	1. 68 E +0 8	D E L	6 0 4	B R C 4	1	1	NH EJ	M L L T4	EN ST 000 003 668 09	1	1	MLLT4	ENST00000366809	1	intron19	N/A	
1	20 58 16 11	20 58 16 11	1	20 59 78 61	20 59 78 61	D E L	6 2 4	B R C 4	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
5	94 18 95 23	94 18 95 23	5	94 18 96 68	94 18 96 68	D E L	1 4 4	B R C 4	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A		
7	84 55 71 79	84 55 71 79	7	84 55 75 37	84 55 75 37	D E L	3 5 4	B R C 4	1	1	NH EJ	S E M A3 D	EN ST 000 002 841 36	-	1	2	SEMA3D	ENST00000284136	-1	intron2	N/A

6	1.34 E +0 8	1.34 E +0 8	1.34 E +0 8	1.34 E +0 8	D E L	1 6 9	1	1	NH EJ	N/ A	N/A EN ST 000 004 096 64	N / A	N / A	N/A	N/A	N/A	N/A	
2	1.66 E +0 8	1.66 E +0 8	1.66 E +0 8	1.66 E +0 8	D E L	4 4 7	1	1	NH EJ	C S R N P3	EN ST 000 004 096 64	1	intr on 0	CSRNP3	ENST00000409664	1	intron0	N/A
1	67 45 49 46	67 45 49 46	67 45 72 91	67 45 72 91	D E L	2 3 4 5	1	1	NH EJ	IL 23 R	EN ST 000 003 473 10	1	intr on 5	IL23R	ENST00000347310	1	intron5	N/A
3	45 32 51 34	45 32 51 34	45 32 53 55	45 32 53 55	D E L	2 2 2 0	1	1	NH EJ	N/ A	N/A EN ST 000 003 669 35	N / A	N / A	N/A	N/A	N/A	N/A	
1	2.16 E +0 8	2.16 E +0 8	2.16 E +0 8	2.16 E +0 8	D E L	3 4 7	1	1	MM EJ	G P A T C H2	EN ST 000 003 669 35	-	intr on 6	GPATCH2	ENST00000366935	-1	intron6	N/A
3	60 85 31 32	60 85 31 32	60 85 39 60	60 85 39 60	D E L	8 2 2 6	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
5	10 82 55 23	10 82 55 23	10 82 76 02	10 82 76 02	D E L	2 0 7 4	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
2	16 73 27 04	16 73 27 04	16 73 92 11	16 73 92 11	D E L	6 4 2 1	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
8	98 41 59 23	98 41 59 23	98 42 30 14	98 42 30 14	D E L	7 0 8 1	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
1	50 36 60 60	50 36 60 60	50 36 62 13	50 36 62 13	D E L	1 4 4 9	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
4	1.06 E +0 8	1.06 E +0 8	1.06 E +0 8	1.06 E +0 8	D E L	9 0 6 5	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
4	1.17 E +0 8	1.17 E +0 8	1.17 E +0 8	1.17 E +0 8	D E L	4 5 4 1	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	
4	44 06 95 16	44 06 95 16	44 07 89 27	44 07 89 27	D E L	9 4 1 2	1	1	NH EJ	K C D T8	EN ST 000 003 600 29	-	intr on 1	KCTD8	ENST00000360029	-1	intron1	N/A
7	1.41 E +0 8	1.41 E +0 8	1.41 E +0 8	1.41 E +0 8	D E L	0 4 3 4	1	1	MM EJ	KI A A1 14	EN ST 000 002 977 61	-	intr on 4	KIAA1147	ENST00000297761	-1	intron3	N/A
2	17 17	17 17	17 17	17 17	D E L	1 4 4 C	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	

1
1

PRKAR2B C7orf66 AASS RPL31P37 IRF5 ATXN7L1 ST7OT4 FSCN3
 PBEF1 COPG2 FOXP2 ZC3HC1 EFCAB10 WNT16 LMOD2 NDUFA5
 PIK3CG CFTR ANKRD7 COG5 KLF14 RNF133 CADPS2 SYPL1
 TSGA14 KCP SLC26A4 FAM71F2 DOCK4 FAM40B C7orf58 CAV2
 TSPAN3 ST7 SND1 CTTNBP2 MET MEST IMP2L TES ING3
 CAV1 DLD CAPZA2 KCND2 RINT1 TSPAN12 PNPLA8 THAP5
 METTL2B ASB15 SLC13A1 BCAP29 uc003vdi.2 CPA5 TNPO3 PAX4
 HYAL4 C7orf60 UBE2H GPR37 LRRN3 NRF1 LRRC4 WNT2 LEP
 POT1 MLL5 TMEM209 ASZ1 KLHDC10 ZNF800 LAMB4 SRPK2

3	1 57 E +0 8	1 57 E +0 8	3	1 57 E +0 8	1 57 E +0 8	D E L	2 3 2 1 4 6	B R C C 1	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A			
7	27 98 64 90	27 98 64 90	7	27 98 64 90	27 98 64 90	D E L	7 6 7 1	B R C C 1	1	1	NH EJ	JA ZF 1	N/A EN ST 000 002 839 28	-	1	2	intr on	JAZF1	ENST00000283928	-1	intron2	N/A
6	15 90 30 58	15 90 30 58	6	15 90 30 58	15 90 30 58	D E L	1 1 3 5 4 8	B R C C 1	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	60 99 33 68	60 99 33 68	6	60 99 33 68	61 01 01 16	D E L	1 6 7 3 4 7	B R C C 1	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	31 92 24 45	31 92 24 45	8	31 92 24 45	31 92 30 00	D E L	5 4 4 9	B R C C 1	1	1	MM EJ	N R G 1	N/A EN ST 000 004 056 06	1	1	intr on	NRG1	ENST00000405606	1	intron1	N/A	
2	71 80 74 83	71 80 74 83	2	71 80 74 83	71 80 78 44	D E L	3 3 6 4 1	B R C C 1	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	
3	12 41 01 42	12 41 01 42	3	12 41 01 42	12 41 05 37	D E L	3 3 9 2	B R C C 1	1	1	MM EJ	P P A R G	N/A EN ST 000 003 970 10 EN ST	1	3	intr on	PPARG	ENST00000397010	1	intron3	N/A	
1	57 78 07 8	57 78 07 8	1	57 78 07 8	57 78 18 3	D E L	1 0 4 6	B R C C 1	1	1	NH EJ	T R I M 5	N/A EN ST 000 003 800 27	-	1	0	intr on	TRIM5	ENST00000380027	-1	intron0	N/A
4	1 83 E +0 8	1 83 E +0 8	4	1 83 E +0 8	1 83 E +0 8	D E L	5 4 1 5	B R C C 1	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	
3	1 47 E +0 8	1 47 E +0 8	3	1 47 E +0 8	1 47 E +0 8	D E L	6 4 4 2	B R C C 1	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	
8	77 77 79 43	77 77 79 43	8	77 77 79 43	77 77 81 20	D E L	1 7 4 3	B R C C 1	1	1	MM EJ	ZF H X4	N/A EN ST 000 000 509 61 EN ST	1	0	intr on	ZFHx4	ENST0000050961	1	intron0	N/A	
0	1 67 72 23	1 67 72 23	0	1 67 72 23	1 69 51 23	D E L	1 7 4 1	B R C C 1	1	1	MM EJ	M Y S T 4	N/A EN ST 000 003 727 25	1	1	intr on	MYST4	ENST00000372725	1	intron1	N/A	
9	31 37	31 37	9	31 37	31 49	D E L	2 0	B R C C 1	1	1	MM EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A	

1	5	65 28 24 80	65 28 24 80	1	25 20 3	25 28 20 3	C T X	N / A	B R C 4	1	1	NH EJ		EN ST 000 002 618 80	- 1	intr on 9	PAFAH1B1	ENST00000006951	1	intron8	N/A	
1	5	65 83 47 84	65 83 47 84	2	39 68 11 16	39 68 11 16	C T X	N / A	B R C 4	1	1	NH EJ	M A P2 K5	EN ST 000 003 544 98	1	intr on 18	WRB	ENST000000333781	1	intron1	N/A	
X		89 96 52 03 1. 47 E +0 8	89 96 52 03 1. 47 E +0 8	1	20 80 3	20 06 80 3	C T X	N / A	B R C 4	1	-1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	N/A
6		47 E +0 8	47 E +0 8	1	13 70 93 27	13 70 94 58	C T X	N / A	B R C 4	-1	1	NA HR	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	
2		2. 42 E +0 8	2. 42 E +0 8	2	20 58 02 55	20 58 02 55	C T X	N / A	B R C 4	1	1	NH EJ	S N D1	EN ST 000 003 103 97	1	intr on 27	N/A	N/A	N/A	N/A	N/A	
6		63 75 90 55	63 75 90 55	1	25 93 45 33	25 93 45 33	C T X	N / A	B R C 4	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	LRRC37B2	ENST00000398849	1	intron0	N/A
1	5	95 06 79 72 1. 07 E +0 8	95 06 79 72 1. 07 E +0 8	2	19 31 18 22	19 31 18 22	C T X	N / A	B R C 4	1	1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	
6		07 E +0 8	07 E +0 8	1	42 18 94 55	42 18 94 55	C T X	N / A	B R C 4	1	-1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	
5		11 E +0 8	11 E +0 8	1	55 18 82 66	55 18 82 66	C T X	N / A	B R C 4	1	-1	NH EJ	N/ A	N/A	N / A	N / A	N/A	VRK3	ENST00000316763	-1	intron7	N/A
1	6	54 89 96 88	54 89 96 88	2	17 04 01 66	17 04 01 66	C T X	N / A	B R C 4	1	1	NH EJ	G N A O 1	EN ST 000 002 624 94	1	intr on 3	N/A	N/A	N/A	N/A	N/A	
6		39 57 91 55 1. 46 E +0 8	39 57 91 55 1. 46 E +0 8	1	54 67 91 22 0	54 67 91 22 0	C T X	N / A	B R C 4	1	1	NH EJ	KI F6	EN ST 000 003 732 13	- 1	intr on 12	NET1	ENST000003355029	1	intron3	N/A	
X		46 E +0 8	46 E +0 8	1	77 16 26 13	77 16 26 13	C T X	N / A	B R C 4	1	-1	NH EJ	N/ A	N/A	N / A	N / A	N/A	N/A	N/A	N/A	N/A	
1	7	11 62 14 85	11 62 14 85	1	12 51 87 48	12 51 87 48	D E L	N / A	B R C 4	1	1	MM EJ	D N A H9	EN ST 000 002 624 42	1	intr on 38	MYOCD	ENST00000343344	1	intron1	MAP2K4 DNAH9 ZNF18 RPL29P26 HYAL3 DALRD3 STAB1 TEX264 UBA7 GLT8D1 SFMBT1 RAD54L2 VIPR1 MAP4 HIGD1D ITIH3 GNL3 USP4 RPL17P16 PTPN23 ITIH1 VPRBP CAMP LYZL4 ZNF662 PPM1M TKT MST1R PFKFB4 C3orf18 ZBTB47 SLC38A3 QARS ZNF502 DOCK3 PCBP4 CACNA1D NISCH ABHD14A GNAT1 FBXW12 NME6 KBTBD5 SS18L2 CYP8B1 KIAA1143 ZNF501 CELSR3 LARS2 CCK C3orf23 MON1A TMEM115 SETD2 CCDC36 ZNF35 AMIGO3 LIMD1 IFRD2	
3		41 41 69 36	41 41 69 36	3	53 84 84 99	53 84 84 99	D E L	N / A	B R C 4	1	1	MM EJ	UL K4	EN ST 000 003 018 31	- 1	intr on 33	CHDH	ENST00000315251	-1	intron0	N/A	

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Gene	Accession	Start	End	Strand	Orientation	Feature	Gene	Accession	Start	End	Strand	Orientation	Feature	Gene	Accession	Start	End	Strand	Orientation	Feature
PCNXL3	LRFN4	TMEM216	TM7SF2	BSCL2	STX3	GLYATL1														
POLR2G	MS4A7	OR5B17	PTPRCAP	FIBP	TUT1	FAM111A	ACTN3													
OR9Q2	SSRP1	RCOR2	SLC43A3	TMEM151A	OR5A2	SLC22A8														
C11orf24	RAB1B	SSSCA1	RHOD	ROM1	ADRBK1	SMTNL1	DDB1													
FAU	SLC22A11	RBM4B	MTA2	GAL3ST3	SLC29A2	CATSPER1														
OTUB1	TBX10	MRPL21	EHBP1L1	DAK	MEN1	OR5AK3P	GANAB													
MAP4K2	GPR137	MS4A13	C11orf48	CCDC88B	MS4A1	OR5AK2														
ARL2	CCS	CD248	EHD1	BATF2	LRRN4	CL	DPP3	VPS37C	VWCE											
OR9I1	MS4A10	YPEL4	DAGLA	DRAP1	SAPS3	C11orf85	CDC42BP6													
FADS1	CTNND1	SCGB1D1	FBXL11	LRRC55	OR5B2	PELI3														
RTN4RL2	BEST1	CABP4	RNASEH2C	ZFP91	SCGB1A1	OR5B12														
FRMD8	TCN1	MPEG1	MS4A5	CNIH2	OR4D9	CYBASC3	C11orf2													
CCDC86	TMX2	MS4A12	SLC22A12	PPP1R14B	UNC93B1	SCYL1														
MACROD1	TRPT1	TMEM179B	GNG3	SCGB1D4	SSH3	PLA2G16														
NPAS4	LRP5	KLC2	TMM10	MS4A4A	C11orf66	PPP2R5B	ATG2A													
CDC42EP2	FTHL16	MRPL16	OVOL1	SLC25A45	SYVN1	BAD														
MS4A2	PGA3	PACS1	BRMS1	SNX15	TIGD3	SNX32	OR4D11													
MS4A8B	NUDT8	WDR74	TMEM223	FAM89B	ZFPL1	LGALS12														
C11orf31	ZBTB3	NUDT22	GPR152	OR1S1	NDUUF1	EIF1AD	SIPA1													
PRPF19	CCDC85B	NDUFS8	PGA4	uc001nrq.1	RBM4	P2RX3	TTC9C													
C11orf84	CPT1A	SLC22A24	RARRES3	MED19	HRA5L5	CFL1														
OR10V1	SYT12	C11orf79	RPS6KA4	KCNK7	PRG2	SERPING1	RTN3													
ALDH3B1	MS4A15	PRDX5	TBC1D10C	FADS3	ASRGL1	DNAJC4														
MARK2	OR5A21P	PYGM	OR10C1	OR5A1	GPR44	NAALADL1														
SLC43A1	HRA5L2	STX5	OR10W1	OR4D6	SF3B2	SLC22A6														
COX8A	KAT5	TNKS1BP1	FAM111B	NXF1	MTL5	ZDHHC5														
ANKRD13D	CD6	C11orf72	CTSW	CST6	RAD9A	FEN1	CDK2AP2													
MRPL11	ZNHIT2	C11orf80	PLAC1L	EFEMP2	GIF	SCGB2A2														
SLC22A25	ESRRA	RAB31L1	CAPN1	MUS81	CLP1	PLCB3	OR1S2													
RASGRP2	OR9Q1	TMEM132A	RPS6KB2	STIP1	CHKA	EML3														
SCGB2A1	AIP	TMEM109	SART1	MAP3K11	FERMT3	CLCF1														
SLC3A2	SLC22A10	GAL	MRPL49	SCGB1D2	BBS1	ATL3	TMEM138													
CHRM1	CTSF	PC	SLC22A9	APLN	R	GPHA2	OR5B21	RCE1	OR5A1											
TCIRG1	LTPB3	OR6Q1	POLA2	CABP2	RELA	FOSL1	SPDYC													
ALDH3B2	LPXN	TMEM134	C11orf64	SAC3D1	B3GAT3	UBE2L6														
C11orf83	FKBP2	SPTBN2	DPF2	GLYAT	TAF6L	GSTP1	ZP1													
SUV420H1	FADS2	SLC22A20	MS4A6E	MS4A4E	KCNK4	POLD4														
OSBP	CDCA5	METTL12	TMEM137	C11orf9	SLC15A3	MS4A14														
UBXN1	EEF1G	ZDHHC24	C11orf10	C11orf68	INCEPN	VEGFB														
AHNAK	NRXN2	TSGA10IP	BANF1	INTS5	PATL1	ATPGD1	FLRT1													
PRG3	SF1	C11orf20	MS4A3	DTX4	CCDC87	ACY3	PITPNM1													
PPP1CA	YIF1A	MS4A6A	GLYATL2	HNRNPUL2	CD5	OR5B3														
CORO1B	PGA5	NAT11	C11orf86	RIN1																

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Gene	ChrA	Breakpoint_A	ChrB	Breakpoint_B	Event	Size	Patient
AIM1	6	105624358	6	109314541	DEL	3689183	BRC11
AIM1	6	107072226	6	107074553	DEL	2326	BRC16
ANK1	8	41857756	8	41909046	DEL	51287	BRC6
ANK1	8	41869287	20	59090675	CTX	N/A	BRC36
ANK1	8	40457726	8	43462159	DEL	3003427	BRC49
ANKFN1	17	51735699	17	51735887	DEL	186	BRC41
ANKFN1	17	51453440	17	54596095	DEL	3141649	BRC35
ARRB1	11	74649654	11	74670244	DEL	20591	BRC35
ARRB1	11	70500352	11	75317690	DEL	4816338	BRC22
BCAS1	20	48611427	20	52279539	DEL	3667110	BRC44
BCAS1	20	51401101	20	54975414	DEL	3573311	BRC17
BCAS4	20	48611427	20	52279539	DEL	3667110	BRC44
BCAS4	20	48892971	21	29949264	CTX	N/A	BRC12
C11orf24	11	67595847	11	68472617	DEL	875767	BRC5
C11orf24	11	67785502	13	22073570	CTX	N/A	BRC22
C11orf24	11	67625117	11	69724046	DEL	2097932	BRC22
C11orf59	11	70950698	11	74508544	DEL	3556845	BRC13
C11orf59	11	70500352	11	75317690	DEL	4816338	BRC22
C19orf45	19	6633971	19	7988053	DEL	1353078	BRC44
C19orf45	9	134958218	19	7475834	CTX	N/A	BRC52
C20orf133	20	14773699	20	14794308	DEL	20608	BRC36
C20orf133	20	12821024	20	14070158	DEL	1248134	BRC5
CA10	17	46093811	17	47526550	DEL	1431739	BRC44
CA10	17	47318360	17	50681691	DEL	3362328	BRC35
CHKA	11	67595847	11	68472617	DEL	875767	BRC5
CHKA	11	67625117	11	69724046	DEL	2097932	BRC22
CLDN14	21	35457106	21	36815535	DEL	1357429	BRC44
CLDN14	20	41129662	21	36868378	CTX	N/A	BRC12
CPT1A	11	67922562	11	68579241	DEL	655678	BRC42

CPT1A	11	67595847	11	68472617	DEL	875767	BRC5
CPT1A	11	67625117	11	69724046	DEL	2097932	BRC22
CSRP3	11	18652360	11	19574158	DEL	920798	BRC44
CSRP3	11	17893275	11	22775779	DEL	4881502	BRC20
CYP24A1	20	48611427	20	52279539	DEL	3667110	BRC44
CYP24A1	20	51401101	20	54975414	DEL	3573311	BRC17
DLG2	11	80621951	11	85277898	DEL	4654943	BRC12
DLG2	11	83950381	11	83951700	DEL	1315	BRC16
DMXL2	15	49607827	17	54247128	CTX	N/A	BRC6
DMXL2	15	49627289	20	16121757	CTX	N/A	BRC44
DNM3	1	170126033	4	177525371	CTX	N/A	BRC44
DNM3	1	169606621	1	172238029	DEL	2630407	BRC11
E2F8	11	18652360	11	19574158	DEL	920798	BRC44
E2F8	11	17893275	11	22775779	DEL	4881502	BRC20
ELAVL1	19	6633971	19	7988053	DEL	1353078	BRC44
ELAVL1	19	7966133	19	7967824	DEL	1689	BRC16
ELP4	10	21395714	11	31752224	CTX	N/A	BRC13
ELP4	11	31729116	11	31771239	DEL	42122	BRC15
FAM10A5	11	18194497	11	18647778	DEL	452279	BRC44
FAM10A5	11	17893275	11	22775779	DEL	4881502	BRC20
FGFR1	8	38435223	17	15319937	CTX	N/A	BRC3
FGFR1	8	38423599	8	38507277	DEL	83677	BRC12
GAL	11	67922562	11	68579241	DEL	655678	BRC42
GAL	11	67595847	11	68472617	DEL	875767	BRC5
GAL	11	67625117	11	69724046	DEL	2097932	BRC22
GTF2H1	11	18194497	11	18647778	DEL	452279	BRC44
GTF2H1	11	17893275	11	22775779	DEL	4881502	BRC20
HGSNAT	1	218131972	8	43130454	CTX	N/A	BRC24
HGSNAT	8	40457726	8	43462159	DEL	3003427	BRC49
HPS5	11	18194497	11	18647778	DEL	452279	BRC44
HPS5	11	17893275	11	22775779	DEL	4881502	BRC20
IGHMBP2	11	67922562	11	68579241	DEL	655678	BRC42

IGHMBP2	11	67595847	11	68472617	DEL	875767	BRC5
IGHMBP2	11	67625117	11	69724046	DEL	2097932	BRC22
IGSF22	11	18652360	11	19574158	DEL	920798	BRC44
IGSF22	11	17893275	11	22775779	DEL	4881502	BRC20
KCNMA1	10	78896323	10	78898380	DEL	2057	BRC16
KCNMA1	10	78996431	13	61310786	CTX	N/A	BRC10
KIAA1147	7	141016525	7	141026965	DEL	10434	BRC41
KIAA1147	7	141018378	7	141020618	DEL	2238	BRC16
LDHA	11	18194497	11	18647778	DEL	452279	BRC44
LDHA	11	17893275	11	22775779	DEL	4881502	BRC20
LDHAL6A	11	18194497	11	18647778	DEL	452279	BRC44
LDHAL6A	11	17893275	11	22775779	DEL	4881502	BRC20
LDHC	11	18194497	11	18647778	DEL	452279	BRC44
LDHC	11	17893275	11	22775779	DEL	4881502	BRC20
LRP5	11	67922562	11	68579241	DEL	655678	BRC42
LRP5	11	67595847	11	68472617	DEL	875767	BRC5
LRP5	11	67625117	11	69724046	DEL	2097932	BRC22
MRGPRD	11	67922562	11	68579241	DEL	655678	BRC42
MRGPRD	11	67625117	11	69724046	DEL	2097932	BRC22
MRGPRF	11	67922562	11	68579241	DEL	655678	BRC42
MRGPRF	11	67625117	11	69724046	DEL	2097932	BRC22
MRGPRX1	11	18652360	11	19574158	DEL	920798	BRC44
MRGPRX1	11	17893275	11	22775779	DEL	4881502	BRC20
MRGPRX2	11	18652360	11	19574158	DEL	920798	BRC44
MRGPRX2	11	17893275	11	22775779	DEL	4881502	BRC20
MRPL21	11	67922562	11	68579241	DEL	655678	BRC42
MRPL21	11	67595847	11	68472617	DEL	875767	BRC5
MRPL21	11	67625117	11	69724046	DEL	2097932	BRC22
MTL5	11	67922562	11	68579241	DEL	655678	BRC42
MTL5	11	67595847	11	68472617	DEL	875767	BRC5
MTL5	11	67625117	11	69724046	DEL	2097932	BRC22
MYST3	8	41857756	8	41909046	DEL	51287	BRC6

MYST3	8	40457726	8	43462159	DEL	3003427	BRC49
MYST3	8	41962161	19	3960043	CTX	N/A	BRC17
MYST4	10	76376772	10	76376951	DEL	177	BRC41
MYST4	10	76393232	10	76397372	DEL	4140	BRC16
NEGR1	1	71829487	1	71831079	DEL	1590	BRC16
NEGR1	1	71999408	3	111518038	CTX	N/A	BRC37
NRG1	8	31922445	8	31923000	DEL	549	BRC41
NRG1	8	28097654	8	32351503	DEL	4252845	BRC49
NRG1	8	31525542	8	34864469	DEL	3337927	BRC29
PFDN4	20	48611427	20	52279539	DEL	3667110	BRC44
PFDN4	20	51401101	20	54975414	DEL	3573311	BRC17
PPIAP10	20	48611427	20	52279539	DEL	3667110	BRC44
PPIAP10	20	51401101	20	54975414	DEL	3573311	BRC17
PPM1E	15	49607827	17	54247128	CTX	N/A	BRC6
PPM1E	17	51453440	17	54596095	DEL	3141649	BRC35
PTPN5	11	18652360	11	19574158	DEL	920798	BRC44
PTPN5	11	17893275	11	22775779	DEL	4881502	BRC20
RAB6A	11	73102097	20	53299710	CTX	N/A	BRC5
RAB6A	11	70500352	11	75317690	DEL	4816338	BRC22
RPN2	17	33169841	20	35278169	CTX	N/A	BRC13
RPN2	20	35278158	20	35278284	INV	118	BRC13
RPN2	13	36599790	20	35287380	CTX	N/A	BRC42
SAA1	11	18194497	11	18647778	DEL	452279	BRC44
SAA1	11	17893275	11	22775779	DEL	4881502	BRC20
SAA2	11	18194497	11	18647778	DEL	452279	BRC44
SAA2	11	17893275	11	22775779	DEL	4881502	BRC20
SAA4	11	18194497	11	18647778	DEL	452279	BRC44
SAA4	11	17893275	11	22775779	DEL	4881502	BRC20
SAPS3	11	67922562	11	68579241	DEL	655678	BRC42
SAPS3	11	67595847	11	68472617	DEL	875767	BRC5
SAPS3	11	67625117	11	69724046	DEL	2097932	BRC22
SCFD2	4	52810288	4	55850342	DEL	3039054	BRC44

SCFD2	4	53612619	4	53616545	DEL	3923	BRC16
SHANK2	11	70500352	11	75317690	DEL	4816338	BRC22
SHANK2	11	70125563	11	70421278	DEL	294715	BRC49
SPTY2D1	11	18194497	11	18647778	DEL	452279	BRC44
SPTY2D1	11	17893275	11	22775779	DEL	4881502	BRC20
SUV420H1	11	67595847	11	68472617	DEL	875767	BRC5
SUV420H1	11	67625117	11	69724046	DEL	2097932	BRC22
TMEM86A	11	18652360	11	19574158	DEL	920798	BRC44
TMEM86A	11	17893275	11	22775779	DEL	4881502	BRC20
TPCN2	11	67922562	11	68579241	DEL	655678	BRC42
TPCN2	11	67625117	11	69724046	DEL	2097932	BRC22
TRIM37	15	52537209	17	54446827	CTX	N/A	BRC6
TRIM37	17	51453440	17	54596095	DEL	3141649	BRC35
TSG101	11	18194497	11	18647778	DEL	452279	BRC44
TSG101	11	17893275	11	22775779	DEL	4881502	BRC20
TSHZ2	20	48611427	20	52279539	DEL	3667110	BRC44
TSHZ2	20	51401101	20	54975414	DEL	3573311	BRC17
TTC28	18	66785261	22	27395753	CTX	N/A	BRC39
TTC28	4	121465798	22	27395518	CTX	N/A	BRC50
UEVLD	11	18194497	11	18647778	DEL	452279	BRC44
UEVLD	11	17893275	11	22775779	DEL	4881502	BRC20
UVRAG	11	75510259	20	54698973	CTX	N/A	BRC5
UVRAG	11	75371475	11	76722597	DEL	1350122	BRC22
ZDHHC13	11	18652360	11	19574158	DEL	920798	BRC44
ZDHHC13	11	17893275	11	22775779	DEL	4881502	BRC20
ZMAT4	8	40740842	20	60184832	CTX	N/A	BRC36
ZMAT4	8	40572937	17	14834933	CTX	N/A	BRC3
ZMAT4	8	40457726	8	43462159	DEL	3003427	BRC49
ZNF148	3	126424684	3	126448567	DEL	23882	BRC32
ZNF148	3	122695629	3	127635819	DEL	4939188	BRC20
ZNF217	20	48611427	20	52279539	DEL	3667110	BRC44
ZNF217	20	51401101	20	54975414	DEL	3573311	BRC17

ZNF259P	6	105624358	6	109314541	DEL	3689183	BRC11
ZNF259P	6	109214259	10	90840813	CTX	N/A	BRC21
ZSCAN5A	3	27727151	19	61472558	CTX	N/A	BRC47
ZSCAN5A	19	61479377	19	61887298	DEL	406919	BRC17

Supplementary Table 12: Recurrent SVs

This table shows structural-variation-affected genes found in more than one patient with chromosomal positions of each breakpoint (A, B), type of event (DEL deletion, CTX translocation), size of event in bp and patient ID. Only events less than 5 Mbp in size are listed.

5' sequence	3' sequence	Event type	Number of possible in-frame proteins
<i>MAP2K5</i>	<i>WRB</i>	CTX	8
<i>LIN28B</i>	<i>ARMC2</i>	DEL	9
<i>GLI3</i>	<i>ITPR2</i>	CTX	4
<i>CHDH</i>	<i>ULK4</i>	DEL	1
<i>ELP3</i>	<i>NRG1</i>	DEL	2
<i>NAV2</i>	<i>C11orf49</i>	DEL	20
<i>DNAH9</i>	<i>MYOCD</i>	DEL	3
<i>BCAS3</i>	<i>ATP8B4</i>	CTX	12
<i>LIMK2</i>	<i>TGIF2</i>	CTX	2
<i>APIP</i>	<i>ABTB2</i>	DEL	1
<i>ITPK1</i>	<i>ACTN1</i>	DEL	8
<i>EXOC6</i>	<i>MAGI1</i>	CTX	2
<i>EXOSC1</i>	<i>C6orf97</i>	CTX	2
<i>ZMAT4</i>	<i>SS18L1</i>	CTX	6

Supplementary Table 13: Predicted fusions

The 5' and 3' portions of gene fusions that could produce in-frame protein(s) are listed with the type of event (DEL deletion, CTX translocation) and number of unique protein sequences that could result.

Mechanism	Germline (n=5667)	Somatic (n=773)	P-value
MMEJ	0.538	0.380	1.16E-006
NAHR	0.100	0.019	1.57E-015
VNTR	0.106	0.004	< 2.2e-16
NHEJ	0.256	0.596	< 2.2e-16

Supplementary Table 14: Somatic/germline SVs and mechanism

Inferred mechanisms are reported for 5,667 germline and 773 somatic structural variants (NHEJ non-homologous end joining, MMEJ microhomology mediated end joining, NAHR non-allelic homologous recombination, VNTR variable number tandem repeats). The p-value from Fisher's exact test comparing the frequency of each mechanism shows significantly more NHEJ in somatic cells.

Pathway	Name	Class	Samples Affected	Total Variations	p-value	FDR
hsa05218	Melanoma - Homo sapiens (human)	Human Diseases; Cancers	51	77	1.37E-42	1.87E-41
hsa05223	Non-small cell lung cancer - Homo sapiens (human)	Human Diseases; Cancers	48	68	5.33E-36	1.06E-34
hsa05213	Endometrial cancer - Homo sapiens (human)	Human Diseases; Cancers	50	71	1.5E-35	1.57E-34
hsa05220	Chronic myeloid leukemia - Homo sapiens (human)	Human Diseases; Cancers	49	73	2.32E-35	3.64E-34
hsa05214	Glioma - Homo sapiens (human)	Human Diseases; Cancers	48	70	8.69E-35	9.52E-34
hsa05215	Prostate cancer - Homo sapiens (human)	Human Diseases; Cancers	49	79	9.04E-34	1.04E-32
hsa05212	Pancreatic cancer - Homo sapiens (human)	Human Diseases; Cancers	50	69	1.48E-30	1.47E-29
hsa05210	Colorectal cancer - Homo sapiens (human)	Human Diseases; Cancers	47	65	3.16E-30	2.89E-29
hsa04722	Neurotrophin signaling pathway - Homo sapiens (human)	-	48	78	1.67E-26	5.63E-26
hsa04210	Apoptosis - Homo sapiens (human)	Cellular Processes; Cell Growth and Death	46	62	1.65E-24	3.65E-24
hsa05222	Small cell lung cancer - Homo sapiens (human)	Human Diseases; Cancers	46	76	3.01E-24	5.50E-23
hsa05221	Acute myeloid leukemia - Homo sapiens (human)	Human Diseases; Cancers	43	53	8.81E-23	1.48E-21
hsa05200	Pathways in cancer - Homo sapiens (human)	Human Diseases; Cancers	56	124	2.89E-22	2.53E-21
hsa04150	mTOR signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	44	50	3.68E-22	8.06E-22
hsa05211	Renal cell carcinoma - Homo sapiens (human)	Human Diseases; Cancers	44	56	9.28E-22	8.84E-21
hsa05160	Hepatitis C - Homo sapiens (human)	Human Diseases; Infectious Diseases	47	68	1.71E-21	1.44E-20
hsa04664	Fc epsilon RI signaling pathway - Homo sapiens (human)	Organismal Systems; Immune System	42	52	1.97E-19	6.07E-19
hsa04012	ErbB signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	43	58	4.42E-19	8.21E-19
hsa04960	Aldosterone-regulated sodium reabsorption - Homo sapiens (human)	Organismal Systems; Excretory System	41	44	7.67E-19	3.29E-18
hsa04620	Toll-like receptor signaling pathway - Homo sapiens (human)	Organismal Systems; Immune System	43	54	1.84E-18	5.04E-18
hsa04973	Carbohydrate digestion and absorption - Homo sapiens (human)	Organismal Systems; Digestive System	42	46	7.12E-18	3.54E-17
hsa04662	B cell receptor signaling pathway - Homo sapiens (human)	Organismal Systems; Immune System	41	50	1.52E-16	4.64E-16
hsa05100	Bacterial invasion of epithelial cells - Homo sapiens (human)	Human Diseases; Infectious Diseases	42	51	3.57E-16	2.12E-15
hsa04370	VEGF signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	41	47	1.29E-15	3.15E-15
hsa04930	Type II diabetes mellitus - Homo sapiens (human)	Human Diseases; Metabolic Diseases	42	46	2.58E-15	1.05E-14

hsa04660	T cell receptor signaling pathway - Homo sapiens (human)	Organismal Systems; Immune System	42	53	6E-15	1.80E-14
hsa04910	Insulin signaling pathway - Homo sapiens (human)	Organismal Systems; Endocrine System	49	65	9.34E-15	3.47E-14
hsa04650	Natural killer cell mediated cytotoxicity - Homo sapiens (human)	Organismal Systems; Immune System	43	54	1.4E-14	4.14E-14
hsa05142	Chagas disease - Homo sapiens (human)	Human Diseases; Infectious Diseases	43	51	1.87E-14	1.32E-13
hsa00562	Inositol phosphate metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	42	47	2.84E-14	3.70E-14
hsa05219	Bladder cancer - Homo sapiens (human)	Human Diseases; Cancers	28	33	8.07E-14	1.18E-12
hsa04810	Regulation of actin cytoskeleton - Homo sapiens (human)	Cellular Processes; Cell Motility	49	80	1.94E-13	7.07E-13
hsa04666	Fc gamma R-mediated phagocytosis - Homo sapiens (human)	Organismal Systems; Immune System	42	51	2.13E-13	6.67E-13
hsa04914	Progesterone-mediated oocyte maturation - Homo sapiens (human)	Organismal Systems; Endocrine System	45	50	3.86E-13	1.48E-12
hsa04510	Focal adhesion - Homo sapiens (human)	Cellular Processes; Cell Communication	54	96	4.73E-13	1.16E-12
hsa05216	Thyroid cancer - Homo sapiens (human)	Human Diseases; Cancers	26	28	1.85E-12	2.25E-11
hsa04630	Jak-STAT signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	42	55	3.49E-12	1.01E-11
hsa04670	Leukocyte transendothelial migration - Homo sapiens (human)	Organismal Systems; Immune System	41	50	3.62E-11	1.15E-10
hsa05146	Amoebiasis - Homo sapiens (human)	Human Diseases; Infectious Diseases	48	62	5.18E-11	4.05E-10
hsa04070	Phosphatidylinositol signaling system - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	43	50	5.59E-11	1.07E-10
hsa04062	Chemokine signaling pathway - Homo sapiens (human)	Organismal Systems; Immune System	46	58	2.09E-10	3.99E-10
hsa05145	Toxoplasmosis - Homo sapiens (human)	Human Diseases; Infectious Diseases	43	53	4.4E-10	3.33E-09
hsa04110	Cell cycle - Homo sapiens (human)	Cellular Processes; Cell Growth and Death	25	39	1.09E-06	2.13E-06
hsa04010	MAPK signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	41	63	4.18E-06	7.70E-06
hsa04115	p53 signaling pathway - Homo sapiens (human)	Cellular Processes; Cell Growth and Death	19	23	2.45E-05	4.88E-05
hsa05217	Basal cell carcinoma - Homo sapiens (human)	Human Diseases; Cancers	19	21	0.000119	0.001539
hsa05014	Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human)	Human Diseases; Neurodegenerative Diseases	18	19	0.000231	0.001266
hsa04310	Wnt signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	29	36	0.000324	0.000739
hsa04622	RIG-I-like receptor signaling pathway - Homo sapiens (human)	Organismal Systems; Immune System	14	17	0.001069	0.003001
hsa05016	Huntington's disease - Homo sapiens (human)	Human Diseases; Neurodegenerative Diseases	28	33	0.006591	0.037013

hsa04912	GnRH signaling pathway - Homo sapiens (human)	Organismal Systems; Endocrine System	17	25	0.007411	0.027981
hsa04120	Ubiquitin mediated proteolysis - Homo sapiens (human)	Genetic Information Processing; Folding; Sorting and Degradation	24	32	0.012756	0.025629
hsa03420	Nucleotide excision repair - Homo sapiens (human)	Genetic Information Processing; Replication and Repair	10	12	0.017104	0.030453
hsa05416	Viral myocarditis - Homo sapiens (human)	Human Diseases; Cardiovascular Diseases	14	20	0.02079	1
hsa04080	Neuroactive ligand-receptor interaction - Homo sapiens (human)	Environmental Information Processing; Signaling Molecules and Interaction	24	37	0.028058	0.054378
hsa04974	Protein digestion and absorption - Homo sapiens (human)	Organismal Systems; Digestive System	18	23	0.031882	0.162376
hsa00130	Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	4	4	0.034949	0.037155
hsa04950	Maturity onset diabetes of the young - Homo sapiens (human)	Human Diseases; Metabolic Diseases	6	6	0.041644	0.175385
hsa00561	Glycerolipid metabolism - Homo sapiens (human)	Metabolism; Lipid Metabolism	11	11	0.054869	0.071102
hsa05130	Pathogenic Escherichia coli infection - Homo sapiens (human)	Human Diseases; Infectious Diseases	10	11	0.067036	0.431791
hsa03440	Homologous recombination - Homo sapiens (human)	Genetic Information Processing; Replication and Repair	6	8	0.067147	0.121531
hsa04530	Tight junction - Homo sapiens (human)	Cellular Processes; Cell Communication	17	26	0.070028	0.180425
hsa04350	TGF-beta signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	12	15	0.07945	0.189126
hsa04740	Olfactory transduction - Homo sapiens (human)	-	21	33	0.082354	0.286278
hsa03450	Non-homologous end-joining - Homo sapiens (human)	Genetic Information Processing; Replication and Repair	5	6	0.087573	0.159821
hsa04512	ECM-receptor interaction - Homo sapiens (human)	Environmental Information Processing; Signaling Molecules and Interaction	21	30	0.095315	0.237204
hsa04270	Vascular smooth muscle contraction - Homo sapiens (human)	Organismal Systems; Circulatory System	22	25	0.10101	0.228054
hsa04141	Protein processing in endoplasmic reticulum - Homo sapiens (human)	Genetic Information Processing; Folding; Sorting and Degradation	10	20	0.10784	0.224923
hsa04916	Melanogenesis - Homo sapiens (human)	Organismal Systems; Endocrine System	15	17	0.12045	0.471046
hsa03030	DNA replication - Homo sapiens (human)	Genetic Information Processing; Replication and Repair	7	8	0.12229	0.207609
hsa04514	Cell adhesion molecules (CAMs) - Homo sapiens (human)	Environmental Information Processing; Signaling Molecules and Interaction	19	22	0.13817	0.347807
hsa00061	Fatty acid biosynthesis - Homo sapiens (human)	Metabolism; Lipid Metabolism	3	4	0.15058	0.155552
hsa03430	Mismatch repair - Homo sapiens (human)	Genetic Information Processing; Replication and Repair	6	6	0.15527	0.278722
hsa04520	Adherens junction - Homo sapiens (human)	Cellular Processes; Cell Communication	18	18	0.1574	0.400821
hsa04360	Axon guidance - Homo sapiens (human)	-	16	25	0.15912	0.382937

hsa04962	Vasopressin-regulated water reabsorption - Homo sapiens (human)	Organismal Systems; Excretory System	8	9	0.17427	0.763303
hsa00533	Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	2	3	0.19315	0.247368
hsa04730	Long-term depression - Homo sapiens (human)	-	15	15	0.21034	0.719757
hsa03040	Spliceosome - Homo sapiens (human)	Genetic Information Processing; Transcription	13	16	0.21902	0.37473
hsa00472	D-Arginine and D-ornithine metabolism - Homo sapiens (human)	Metabolism; Metabolism of Other Amino Acids	1	1	0.22913	0.275711
hsa00260	Glycine; serine and threonine metabolism - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	3	5	0.24078	0.264979
hsa00524	Butirosin and neomycin biosynthesis - Homo sapiens (human)	Metabolism; Biosynthesis of Other Secondary Metabolites	2	2	0.24425	0.307418
hsa04614	Renin-angiotensin system - Homo sapiens (human)	Organismal Systems; Endocrine System	4	4	0.24757	0.669356
hsa05120	Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human)	Human Diseases; Infectious Diseases	9	10	0.25031	1
hsa03018	RNA degradation - Homo sapiens (human)	Genetic Information Processing; Folding; Sorting and Degradation	9	9	0.26945	0.447042
hsa04720	Long-term potentiation - Homo sapiens (human)	-	13	14	0.27912	0.926171
hsa00190	Oxidative phosphorylation - Homo sapiens (human)	Metabolism; Energy Metabolism	7	8	0.30397	0.326321
hsa04623	Cytosolic DNA-sensing pathway - Homo sapiens (human)	Organismal Systems; Immune System	6	6	0.31928	0.908082
hsa04130	SNARE interactions in vesicular transport - Homo sapiens (human)	Genetic Information Processing; Folding; Sorting and Degradation	3	3	0.32475	0.664675
hsa00600	Sphingolipid metabolism - Homo sapiens (human)	Metabolism; Lipid Metabolism	5	5	0.33016	0.4491
hsa00601	Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	2	3	0.33896	0.463952
hsa03022	Basal transcription factors - Homo sapiens (human)	Genetic Information Processing; Transcription	5	5	0.35028	0.590087
hsa04710	Circadian rhythm - mammal - Homo sapiens (human)	-	4	4	0.35245	1
hsa00052	Galactose metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	5	5	0.35556	0.363867
hsa03320	PPAR signaling pathway - Homo sapiens (human)	Organismal Systems; Endocrine System	6	8	0.35624	0.624132
hsa00270	Cysteine and methionine metabolism - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	2	4	0.35883	0.396888
hsa00531	Glycosaminoglycan degradation - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	3	3	0.36053	0.456393
hsa00400	Phenylalanine; tyrosine and tryptophan biosynthesis - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	1	1	0.37022	0.431267
hsa00650	Butanoate metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	4	4	0.3739	0.531715

hsa05320	Autoimmune thyroid disease - Homo sapiens (human)	Human Diseases; Immune System Diseases	3	4	0.38364	1
hsa00350	Tyrosine metabolism - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	5	5	0.38915	0.446198
hsa00750	Vitamin B6 metabolism - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	1	1	0.39913	0.58273
hsa04122	Sulfur relay system - Homo sapiens (human)	Genetic Information Processing; Folding; Sorting and Degradation	1	1	0.4063	0.823886
hsa04920	Adipocytokine signaling pathway - Homo sapiens (human)	Organismal Systems; Endocrine System	9	9	0.40959	1
hsa00512	O-Glycan biosynthesis - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	4	4	0.41715	0.516135
hsa04621	NOD-like receptor signaling pathway - Homo sapiens (human)	Organismal Systems; Immune System	7	7	0.42044	1
hsa00062	Fatty acid elongation in mitochondria - Homo sapiens (human)	Metabolism; Lipid Metabolism	1	1	0.4261	0.442255
hsa00360	Phenylalanine metabolism - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	2	2	0.44158	0.508979
hsa00790	Folate biosynthesis - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	1	1	0.44436	0.671137
hsa03060	Protein export - Homo sapiens (human)	Genetic Information Processing; Folding; Sorting and Degradation	2	2	0.44509	0.773609
hsa00450	Selenoamino acid metabolism - Homo sapiens (human)	Metabolism; Metabolism of Other Amino Acids	3	3	0.45061	0.533425
hsa05150	Staphylococcus aureus infection - Homo sapiens (human)	-	6	6	0.45257	1
hsa05322	Systemic lupus erythematosus - Homo sapiens (human)	Human Diseases; Immune System Diseases	8	8	0.45652	1
hsa04964	Proximal tubule bicarbonate reclamation - Homo sapiens (human)	Organismal Systems; Excretory System	3	3	0.45975	1
hsa05410	Hypertrophic cardiomyopathy (HCM) - Homo sapiens (human)	Human Diseases; Cardiovascular Diseases	14	21	0.46456	1
hsa05110	Vibrio cholerae infection - Homo sapiens (human)	Human Diseases; Infectious Diseases	6	7	0.46538	1
hsa00770	Pantothenate and CoA biosynthesis - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	2	2	0.46829	0.692943
hsa00532	Glycosaminoglycan biosynthesis - chondroitin sulfate - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	2	2	0.47127	0.600047
hsa00520	Amino sugar and nucleotide sugar metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	5	5	0.47475	0.594116
hsa04114	Oocyte meiosis - Homo sapiens (human)	Cellular Processes; Cell Growth and Death	10	14	0.47695	0.941009
hsa00430	Taurine and hypotaurine metabolism - Homo sapiens (human)	Metabolism; Metabolism of Other Amino Acids	1	1	0.48956	0.576417
hsa03020	RNA polymerase - Homo sapiens (human)	Genetic Information Processing; Transcription	3	3	0.49087	0.820615
hsa05010	Alzheimer's disease - Homo sapiens (human)	Human Diseases; Neurodegenerative Diseases	16	18	0.49259	1

hsa04940	Type I diabetes mellitus - Homo sapiens (human)	Human Diseases; Metabolic Diseases	3	3	0.4936	1
hsa00511	Other glycan degradation - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	2	2	0.49798	0.612683
hsa05140	Leishmaniasis - Homo sapiens (human)	Human Diseases; Infectious Diseases	7	7	0.50129	1
hsa04260	Cardiac muscle contraction - Homo sapiens (human)	Organismal Systems; Circulatory System	8	9	0.50663	1
hsa00340	Histidine metabolism - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	3	3	0.50715	0.578468
hsa05012	Parkinson's disease - Homo sapiens (human)	Human Diseases; Neurodegenerative Diseases	7	7	0.51304	1
hsa00603	Glycosphingolipid biosynthesis - globo series - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	1	1	0.52013	0.716405
hsa00740	Riboflavin metabolism - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	1	1	0.52051	0.754912
hsa04020	Calcium signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	25	31	0.52108	0.975355
hsa05332	Graft-versus-host disease - Homo sapiens (human)	Human Diseases; Immune System Diseases	2	2	0.5223	1
hsa05414	Dilated cardiomyopathy - Homo sapiens (human)	Human Diseases; Cardiovascular Diseases	15	22	0.5245	1
hsa05020	Prion diseases - Homo sapiens (human)	Human Diseases; Neurodegenerative Diseases	4	4	0.52686	1
hsa04340	Hedgehog signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	5	6	0.5382	1
hsa04145	Phagosome - Homo sapiens (human)	Cellular Processes; Transport and Catabolism	12	16	0.53888	1
hsa04612	Antigen processing and presentation - Homo sapiens (human)	Organismal Systems; Immune System	5	5	0.54111	1
hsa00900	Terpenoid backbone biosynthesis - Homo sapiens (human)	Metabolism; Metabolism of Terpenoids and Polyketides	1	1	0.55602	0.857524
hsa05340	Primary immunodeficiency - Homo sapiens (human)	Human Diseases; Immune System Diseases	3	3	0.5711	1
hsa03050	Proteasome - Homo sapiens (human)	Genetic Information Processing; Folding; Sorting and Degradation	3	3	0.57383	0.989518
hsa00051	Fructose and mannose metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	2	3	0.58473	0.595609
hsa04140	Regulation of autophagy - Homo sapiens (human)	Cellular Processes; Transport and Catabolism	2	2	0.59623	1
hsa04966	Collecting duct acid secretion - Homo sapiens (human)	Organismal Systems; Excretory System	2	2	0.60016	1
hsa00240	Pyrimidine metabolism - Homo sapiens (human)	Metabolism; Nucleotide Metabolism	9	9	0.60128	0.655126
hsa04971	Gastric acid secretion - Homo sapiens (human)	Organismal Systems; Digestive System	11	11	0.60183	1
hsa04320	Dorso-ventral axis formation - Homo sapiens (human)	-	4	4	0.6063	1

hsa01040	Biosynthesis of unsaturated fatty acids - Homo sapiens (human)	Metabolism; Lipid Metabolism	1	1	0.61504	0.997732
hsa00630	Glyoxylate and dicarboxylate metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	1	1	0.61559	0.864194
hsa04972	Pancreatic secretion - Homo sapiens (human)	Organismal Systems; Digestive System	14	15	0.61876	1
hsa00100	Steroid biosynthesis - Homo sapiens (human)	Metabolism; Lipid Metabolism	1	1	0.62298	0.655926
hsa00120	Primary bile acid biosynthesis - Homo sapiens (human)	Metabolism; Lipid Metabolism	1	1	0.62438	0.660576
hsa05144	Malaria - Homo sapiens (human)	Human Diseases; Infectious Diseases	4	5	0.62611	1
hsa00310	Lysine degradation - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	4	6	0.64772	0.731189
hsa03410	Base excision repair - Homo sapiens (human)	Genetic Information Processing; Replication and Repair	3	3	0.65427	1
hsa05330	Allograft rejection - Homo sapiens (human)	Human Diseases; Immune System Diseases	1	1	0.66143	1
hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Homo sapiens (human)	Human Diseases; Cardiovascular Diseases	10	13	0.67364	1
hsa04742	Taste transduction - Homo sapiens (human)	-	5	5	0.68341	1
hsa00510	N-Glycan biosynthesis - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	4	4	0.68493	0.837987
hsa00910	Nitrogen metabolism - Homo sapiens (human)	Metabolism; Energy Metabolism	1	1	0.68645	1
hsa04060	Cytokine-cytokine receptor interaction - Homo sapiens (human)	Environmental Information Processing; Signaling Molecules and Interaction	14	17	0.69724	1
hsa05131	Shigellosis - Homo sapiens (human)	Human Diseases; Infectious Diseases	5	5	0.71297	1
hsa00670	One carbon pool by folate - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	1	1	0.71387	1
hsa00500	Starch and sucrose metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	6	6	0.71468	0.869527
hsa00760	Nicotinate and nicotinamide metabolism - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	1	1	0.72169	1
hsa04970	Salivary secretion - Homo sapiens (human)	Organismal Systems; Digestive System	13	13	0.72221	1
hsa00410	beta-Alanine metabolism - Homo sapiens (human)	Metabolism; Metabolism of Other Amino Acids	1	1	0.73154	0.856723
hsa04640	Hematopoietic cell lineage - Homo sapiens (human)	Organismal Systems; Immune System	7	7	0.73655	1
hsa00620	Pyruvate metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	3	3	0.73911	1
hsa00591	Linoleic acid metabolism - Homo sapiens (human)	Metabolism; Lipid Metabolism	1	1	0.74455	1
hsa04744	Phototransduction - Homo sapiens (human)	Organismal Systems; Sensory System	1	1	0.75416	1
hsa04540	Gap junction - Homo sapiens (human)	Cellular Processes; Cell Communication	11	11	0.75479	1

hsa04144	Endocytosis - Homo sapiens (human)	Cellular Processes; Transport and Catabolism	20	23	0.75718	1
hsa00534	Glycosaminoglycan biosynthesis - heparan sulfate - Homo sapiens (human)	Metabolism; Glycan Biosynthesis and Metabolism	1	1	0.76293	0.982833
hsa04672	Intestinal immune network for IgA production - Homo sapiens (human)	Organismal Systems; Immune System	1	1	0.77124	1
hsa00010	Glycolysis / Gluconeogenesis - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	3	4	0.77731	0.77731
hsa00230	Purine metabolism - Homo sapiens (human)	Metabolism; Nucleotide Metabolism	13	16	0.7811	0.842665
hsa00983	Drug metabolism - other enzymes - Homo sapiens (human)	Metabolism; Xenobiotics Biodegradation and Metabolism	2	3	0.79294	1
hsa04610	Complement and coagulation cascades - Homo sapiens (human)	Organismal Systems; Immune System	7	7	0.79399	1
hsa00565	Ether lipid metabolism - Homo sapiens (human)	Metabolism; Lipid Metabolism	1	1	0.79534	1
hsa00053	Ascorbate and aldarate metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	1	1	0.80491	0.827584
hsa00564	Glycerophospholipid metabolism - Homo sapiens (human)	Metabolism; Lipid Metabolism	5	5	0.80602	1
hsa00830	Retinol metabolism - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	4	4	0.80621	1
hsa00140	Steroid hormone biosynthesis - Homo sapiens (human)	Metabolism; Lipid Metabolism	3	3	0.80836	0.863565
hsa03010	Ribosome - Homo sapiens (human)	Genetic Information Processing; Translation	1	1	0.81469	1
hsa00380	Tryptophan metabolism - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	2	2	0.82688	0.958131
hsa00020	Citrate cycle (TCA cycle) - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	1	1	0.82941	0.833215
hsa00590	Arachidonic acid metabolism - Homo sapiens (human)	Metabolism; Lipid Metabolism	1	2	0.83072	1
hsa02010	ABC transporters - Homo sapiens (human)	Environmental Information Processing; Membrane Transport	8	9	0.83499	1
hsa00860	Porphyryn and chlorophyll metabolism - Homo sapiens (human)	Metabolism; Metabolism of Cofactors and Vitamins	2	2	0.83624	1
hsa00040	Pentose and glucuronate interconversions - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	1	1	0.83643	0.848047
hsa00071	Fatty acid metabolism - Homo sapiens (human)	Metabolism; Lipid Metabolism	2	2	0.83722	0.873101
hsa00480	Glutathione metabolism - Homo sapiens (human)	Metabolism; Metabolism of Other Amino Acids	1	1	0.83856	1
hsa00980	Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human)	Metabolism; Xenobiotics Biodegradation and Metabolism	3	3	0.8753	1
hsa00640	Propanoate metabolism - Homo sapiens (human)	Metabolism; Carbohydrate Metabolism	1	1	0.8776	1
hsa04146	Peroxisome - Homo sapiens (human)	Cellular Processes; Transport and Catabolism	4	4	0.88583	1

hsa00330	Arginine and proline metabolism - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	2	2	0.8914	1
hsa00280	Valine; leucine and isoleucine degradation - Homo sapiens (human)	Metabolism; Amino Acid Metabolism	1	1	0.89371	0.993515
hsa04142	Lysosome - Homo sapiens (human)	Cellular Processes; Transport and Catabolism	9	9	0.90046	1
hsa00982	Drug metabolism - cytochrome P450 - Homo sapiens (human)	Metabolism; Xenobiotics Biodegradation and Metabolism	3	3	0.90717	1
hsa00970	Aminoacyl-tRNA biosynthesis - Homo sapiens (human)	Genetic Information Processing; Translation	2	2	0.90926	1
hsa04330	Notch signaling pathway - Homo sapiens (human)	Environmental Information Processing; Signal Transduction	3	3	0.9289	1

Supplementary Table 15: Standard pathway analysis

Significantly altered pathways were identified by PathScan. Those classified by KEGG (Kyoto Encyclopedia of Genes and Genomes) as cancer pathways were removed, since they dominated the list and provided no new information. “Samples Affected” represents the number of samples in which one or more gene from this pathway has a non-silent variant and “Total Variations” denotes the total number of variations that alter this pathway across all samples (variants altering the same gene in a sample are treated as one variant). Multiple-testing correction is again calculated by the Benjamini-Hochberg FDR.

Significantly mutated pathways in AI Responders	Samples_Affected	Total_Variations	p-value	FDR	Significantly mutated pathways in AI Nonresponders	Samples_Affected	Total_Variations	p-value	FDR
Neurotrophin signaling pathway	28	44	1.34E-16	4.5E-16	Apoptosis	18	29	1.64E-13	3.62E-13
mTOR signaling pathway	27	31	5.22E-16	1.14E-15	Neurotrophin signaling pathway	20	34	2.53E-12	8.51E-12
Aldosterone-regulated sodium reabsorption	26	29	4.3E-15	1.84E-14	mTOR signaling pathway	17	19	1.3E-08	2.84E-08
ErbB signaling pathway	27	36	3.48E-14	6.45E-14	Fc epsilon RI signaling pathway	16	21	1.74E-08	5.36E-08
Carbohydrate digestion and absorption	27	30	3.5E-14	1.74E-13	Toll-like receptor signaling pathway	15	22	2.24E-08	6.14E-08
Apoptosis	28	33	2.49E-13	5.5E-13	ErbB signaling pathway	16	22	2.93E-07	5.43E-07
Fc epsilon RI signaling pathway	26	31	3.59E-13	1.11E-12	Jak-STAT signaling pathway	15	24	1.5E-06	4.31E-06
Inositol phosphate metabolism	26	31	2.95E-12	3.84E-12	B cell receptor signaling pathway	15	19	1.69E-06	5.13E-06
Toll-like receptor signaling pathway	28	32	2.95E-12	8.07E-12	Natural killer cell mediated cytotoxicity	17	22	2.43E-06	7.18E-06
B cell receptor signaling pathway	26	31	2.93E-12	8.93E-12	Fc gamma R-mediated phagocytosis	16	21	2.71E-06	8.47E-06
VEGF signaling pathway	26	30	3.87E-12	9.41E-12	Aldosterone-regulated sodium reabsorption	15	15	2.8E-06	1.2E-05
T cell receptor signaling pathway	26	33	1.73E-11	5.18E-11	**p53 signaling pathway	11	15	7.75E-06	1.54E-05
Insulin signaling pathway	31	40	3.58E-11	1.33E-10	Carbohydrate digestion and absorption	15	16	3.85E-06	1.92E-05
Focal adhesion	33	58	1.52E-10	3.75E-10	VEGF signaling pathway	15	17	9.71E-06	2.36E-05
Natural killer cell mediated cytotoxicity	26	32	2.9E-10	8.59E-10	Insulin signaling pathway	18	25	9.42E-06	3.5E-05
Phosphatidylinositol signaling system	26	33	4.78E-10	9.18E-10	T cell receptor signaling pathway	16	20	1.19E-05	3.58E-05
Progesterone-mediated oocyte maturation	28	31	5.06E-10	1.94E-09	Cell cycle	12	21	2.53E-05	4.95E-05
Regulation of actin cytoskeleton	30	47	5.91E-10	2.16E-09	Regulation of actin cytoskeleton	19	33	1.75E-05	6.38E-05
Fc gamma R-mediated phagocytosis	26	30	4.69E-09	1.47E-08	Leukocyte transendothelial migration	16	21	2.06E-05	6.55E-05
Chemokine signaling pathway	28	34	1.71E-07	3.26E-07	Progesterone-mediated oocyte maturation	17	19	3.39E-05	0.00013
Leukocyte transendothelial migration	25	29	1.35E-07	4.29E-07	Chemokine signaling pathway	18	24	9.52E-05	0.000181
Jak-STAT signaling pathway	27	31	1.71E-07	4.92E-07	Inositol phosphate metabolism	16	16	0.000193	0.000252
MAPK signaling pathway	21	33	0.000357	0.000657	Focal adhesion	21	38	0.00011	0.00027
Cell cycle	13	18	0.0037	0.007234	MAPK signaling pathway	20	30	0.001953	0.003594
*GnRH signaling pathway	10	17	0.002288	0.008637	Phosphatidylinositol signaling system	17	17	0.00277	0.005321

*Protein processing in endoplasmic reticulum	7	16	0.005747	0.011987	Wnt signaling pathway	15	18	0.004688	0.010694
RIG-I-like receptor signaling pathway	8	10	0.005919	0.016618	**Ubiquitin mediated proteolysis	11	17	0.012135	0.024381
*Non-homologous end-joining	5	6	0.012215	0.022292	**Axon guidance	11	17	0.015777	0.037969
Wnt signaling pathway	14	18	0.011883	0.027108	**Glycosaminoglycan biosynthesis - keratan sulfate	2	3	0.039696	0.050839
*Ubiquinone and other terpenoid-quinone biosynthesis	3	3	0.033653	0.035777	**TGF-beta signaling pathway	6	9	0.026357	0.062741
*Fatty acid biosynthesis	3	4	0.042149	0.043541	RIG-I-like receptor signaling pathway	6	7	0.033013	0.09269
*Protein digestion and absorption	12	16	0.009906	0.05045	**DNA replication	4	5	0.066204	0.112393
*Neuroactive ligand-receptor interaction	16	23	0.026388	0.051141	**Glycosphingolipid biosynthesis - lacto and neolacto series	2	3	0.09023	0.123502
*Tight junction	10	17	0.02306	0.059413	**Galactose metabolism	4	4	0.12658	0.129537
*Nucleotide excision repair	6	7	0.043346	0.077177	Mismatch repair	4	4	0.083318	0.149563
*Spliceosome	9	12	0.054089	0.092543					
*Glycine, serine and threonine metabolism	2	4	0.1176	0.129419					
*Homologous recombination	3	5	0.071767	0.129892					

Supplementary Table 16: Pathway responder vs non-responder

Significantly altered pathways were also identified by PathScan among responders versus non-responders. The response is based on surgical Ki67 levels. KEGG cancer pathways were removed, as discussed in methods. *Significantly mutated only among AI Responders, **Significantly mutated only among AI Nonresponders.

Map	p value	mutated objects	total objects
Development_Neurotrophin family signaling	3.38E-08	15	40
Neurophysiological process_ACM regulation of nerve impulse	2.89E-07	15	46
DNA damage_Role of Brca1 and Brca2 in DNA repair	3.57E-07	12	30
Cell cycle_Influence of Ras and Rho proteins on G1/S Transition	3.84E-07	16	53
Cytoskeleton remodeling_Cytoskeleton remodeling	4.36E-07	23	102
Development_Melanocyte development and pigmentation	7.28E-07	15	49
Development_Gastrin in cell growth and proliferation	7.67E-07	17	62
Development_WNT signaling pathway. Part 2	2.22E-06	15	53
Development_EGFR signaling pathway	4.88E-06	16	63
Development_Flt3 signaling	6.26E-06	13	44
Transcription_P53 signaling pathway	8.95E-06	12	39
DNA damage_Role of NFB1 in DNA damage response	9.82E-06	7	13
Translation_Non-genomic (rapid) action of Androgen Receptor	1.20E-05	12	40
Development_HGF signaling pathway	1.39E-05	13	47
Cell adhesion_Chemokines and adhesion	1.69E-05	20	100
Muscle contraction_ACM regulation of smooth muscle contraction	2.32E-05	14	56
Development_Beta-adrenergic receptors transactivation of EGFR	3.05E-05	11	37
Neurophysiological process_NMDA-dependent postsynaptic long-term potentiation in CA1 hippocampal neurons	3.19E-05	17	80
Transcription_Androgen Receptor nuclear signaling	4.45E-05	12	45
Development_Thrombopoietin-regulated cell processes	4.45E-05	12	45
Translation_Regulation of EIF4F activity	5.63E-05	13	53
Signal transduction_PTEN pathway	5.64E-05	12	46
G-protein signaling_Regulation of CDC42 activity	5.86E-05	10	33
Development_SSTR2 in regulation of cell proliferation	0.000133	10	36
DNA damage_Brca1 as a transcription regulator	0.00015	9	30
Muscle contraction_GPCRs in the regulation of smooth muscle tone	0.000184	16	83
DNA damage_NHEJ mechanisms of DSBs repair	0.000198	7	19

G-protein signaling_Proinsulin C-peptide signaling	0.000203	12	52
Development_VEGF signaling via VEGFR2 - generic cascades	0.000213	16	84
Development_EPO-induced MAPK pathway	0.000216	11	45
Development_Endothelin-1/EDNRA signaling	0.000246	12	53
Development_WNT5A signaling	0.000266	11	46
G-protein signaling_Regulation of p38 and JNK signaling mediated by G-proteins	0.000274	10	39
Cell cycle_Regulation of G1/S transition (part 2)	0.00029	8	26
PGE2 pathways in cancer	0.000355	12	55
Development_CNTF receptor signaling	0.000427	9	34
Apoptosis and survival_Role of CDK5 in neuronal death and survival	0.000427	9	34
Apoptosis and survival_Cytoplasmic/mitochondrial transport of proapoptotic proteins Bid, Bmf and Bim	0.000427	9	34
Development_Regulation of epithelial-to-mesenchymal transition (EMT)	0.000429	13	64
Translation_Insulin regulation of translation	0.000523	10	42
Signal transduction_JNK pathway	0.000523	10	42
Development_Growth hormone signaling via PI3K/AKT and MAPK cascades	0.000523	10	42
Development_S1P3 receptor signaling pathway	0.000639	10	43
Apoptosis and survival_nAChR in apoptosis inhibition and cell cycle progression	0.00066	8	29
Apoptosis and survival_p53-dependent apoptosis	0.00066	8	29
Signal transduction_PKA signaling	0.000688	11	51
Some pathways of EMT in cancer cells	0.000688	11	51
Development_Slit-Robo signaling	0.000845	8	30
Development_Ligand-independent activation of ESR1 and ESR2	0.000936	10	45
Transport_RAN regulation pathway	0.001064	6	18
Development_FGFR signaling pathway	0.001141	11	54
Development_ERBB-family signaling	0.001258	9	39
G-protein signaling_K-RAS regulation pathway	0.001304	7	25
Cell cycle_Initiation of mitosis	0.001304	7	25

Regulation of lipid metabolism_Insulin signaling:generic cascades	0.001337	10	47
Development_PIP3 signaling in cardiac myocytes	0.001337	10	47
Development_PDGF signaling via MAPK cascades	0.001337	10	47
Apoptosis and survival_Granzyme B signaling	0.00134	8	32
Cell cycle_Role of Nek in cell cycle regulation	0.00134	8	32
Cell cycle_Start of DNA replication in early S phase	0.00134	8	32
Muscle contraction_Regulation of eNOS activity in endothelial cells	0.001483	12	64
Apoptosis and survival_Ceramides signaling pathway	0.001524	9	40
Development_S1P1 receptor signaling via beta-arrestin	0.001661	8	33
Development_EGFR signaling via small GTPases	0.001661	8	33
G-protein signaling_Ras family GTPases in kinase cascades (scheme)	0.001678	7	26
Development_A3 receptor signaling	0.001868	10	49
Chemotaxis_CXCR4 signaling pathway	0.002041	8	34
G-protein signaling_G-Protein alpha-i signaling cascades	0.00213	7	27
Transcription_Role of Akt in hypoxia induced HIF1 activation	0.00213	7	27
Apoptosis and survival_BAD phosphorylation	0.00219	9	42
Development_EDNRB signaling	0.002192	10	50
Development_GM-CSF signaling	0.002192	10	50
Development_A2B receptor: action via G-protein alpha s	0.002192	10	50
Cell cycle_Cell cycle (generic schema)	0.002592	6	21
Cell cycle_Chromosome condensation in prometaphase	0.002592	6	21
Development_ACM2 and ACM4 activation of ERK	0.002601	9	43
Development_EPO-induced PI3K/AKT pathway and Ca(2+) influx	0.002601	9	43
Development_Angiotensin signaling via PYK2	0.002601	9	43
Development_VEGF signaling and activation	0.002601	9	43
Apoptosis and survival_TNFR1 signaling pathway	0.002601	9	43
Apoptosis and survival_DNA-damage-induced apoptosis	0.00283	5	15
Signal transduction_Activation of PKC via G-Protein coupled receptor	0.002972	10	52
Development_FGF-family signaling	0.002972	10	52
Development_Membrane-bound ESR1: interaction with growth factors	0.003603	9	45

signaling			
Cell adhesion_Ephrin signaling	0.003603	9	45
Development_Role of HDAC and calcium/calmodulin-dependent kinase (CaMK) in control of skeletal myogenesis	0.003961	10	54
Translation_Regulation of EIF2 activity	0.005065	8	39
Cytoskeleton remodeling_FAK signaling	0.005911	10	57
Signal transduction_IP3 signaling	0.006499	9	49
Apoptosis and survival_Caspase cascade	0.007092	7	33
Development_Activation of astroglial cells proliferation by ACM3	0.007092	7	33
Cell cycle_ESR1 regulation of G1/S transition	0.007092	7	33
Signal transduction_Erk Interactions: Inhibition of Erk	0.008401	7	34
G-protein signaling_RhoA regulation pathway	0.008401	7	34
Regulation of metabolism_Role of Adiponectin in regulation of metabolism	0.009318	8	43
Signal transduction_AKT signaling	0.009318	8	43
Development_A2A receptor signaling	0.009318	8	43
Development_IGF-1 receptor signaling	0.009647	9	52
Translation_Regulation of translation initiation	0.009856	6	27
Development_EPO-induced Jak-STAT pathway	0.00988	7	35
Cell cycle_The metaphase checkpoint	0.01154	7	36
Immune response_Innate immune response to RNA viral infection	0.01182	6	28
Development_G-Proteins mediated regulation MAPK-ERK signaling	0.01393	8	46
Development_TGF-beta-dependent induction of EMT via RhoA, PI3K and ILK.	0.01393	8	46

Supplementary Table 17: Metacore map network p-values.

Gene	Mutation	Domain	Patient	Candidate Drugs
<i>Tyrosine Kinases</i>				
Her2 (ERBB2)	V777L	KD	BRC14	Lapatinib, Trastuzumab
	755-759 ^{LRENT} in frame deletion	KD	16757	
KIT	Q152L	EC	BRC33	Imatinib, Masitinib (AB1010)
	R281K	EC	BRC39	
	M541L	TM	18115	
PDGFRA	E279K	EC	BRC50	
	E924K	KD	BRC31	
	e12+1	JM/KD	16825	
DDR1	A829V	KD	BRC20	Imatinib, Nilotinib, and Bafetinib (INNO-406)
	R611C	KD	17733	
DDR2	E583D	KD	CSB22	
MET	T263M	EC	BRC20	Foretinib, Tivantinib (ARQ 197), MetMAb (PRO143966), and others
	I316M	EC	18115	
	D864N	EC	17818	
	E1275*	KD	16744	
JAK1	F1134L	KD	17327	ruxolitinib (INCB018424 or INC424)
	E637K	Pseudo-kinase	17787	
CSF1R	D735H	KD	BRC13	Imatinib, Nilotinib, and Sunitinib
	M875L	KD	17066	
	H506P	EC	17807	
	R378H	EC	16751	
	R142H	EC	17881	
LTK	W391R	EC	CSB7	Crizotinib
	W391R	EC	15980	
	E399K	EC	16189	
	M460I	JM	16189	
<i>Raf mutations</i>				
BRAF	K601E	KD	BRC15	vemurafenib
	G104W	na	CSB2	
<i>PI3-kinase / AKT pathway</i>				
PIK3CA	Most common mutations at codons 542,545, 1047	Helical and catalytic	Multiple patients	BKM120, GDC-0941, and others
AKT1	C77F	PH	CSB25	MK2206 and others
AKT2	S11F	PH	BRC21	
RPS6KB1 (S6 kinase)	S375F	KD	BRC44	PF-4708671 (in pre-clinical only)

KD=kinase domain, EC=extracellular domain, TM=transmembrane, JM juxtamembrane, PH = pleckstrin homology, na=outside a known domain

Supplementary Table 18. Druggable mutations with Tyrosine Kinase inhibitors

UPN	ARID1A	ARID2	ARID3B	ARID4B	JARID1B	JARID1C	JMJD2A	MLL2	MLL3	MLL5	MYST1	MYST3	MYST4	SETDB1	UTX
BRC4	-	-	Del	-	-	-	-	-	-	-	-	-	-	-	-
BRC10	-	Del	-	-	-	-	-	Del	-	-	-	-	-	-	-
BRC11	p.A1239T	-	-	Del	p.R119S, Complex	-	-	-	-	-	-	-	-	Complex	-
BRC13	-	-	-	-	p.R1453K	-	-	-	-	-	-	-	-	-	-
BRC15	-	p.S742fs	-	-	-	-	-	-	-	-	-	-	-	-	-
BRC16	-	-	-	-	-	-	-	-	-	-	-	-	-	Complex	-
BRC17	-	-	-	-	-	-	-	-	-	-	-	CTX	-	-	-
BRC18	p.R1989*	-	-	-	-	p.F697S	-	-	-	-	-	-	-	-	-
BRC19	-	-	-	-	-	-	-	p.Q356*	-	-	-	-	-	-	-
BRC21	-	-	-	-	-	-	-	-	p.T1118fs	-	-	-	-	-	-
BRC29	-	-	-	-	-	-	-	-	-	-	-	-	-	-	p.S1068*
BRC3	-	-	-	-	-	-	-	-	p.I2391fs	-	-	-	-	-	-
BRC32	-	-	-	-	-	-	-	p.P4380fs	-	-	-	-	-	-	-
BRC39	-	-	-	-	-	-	-	-	-	-	p.R377Q	-	-	-	-
BRC41	-	-	-	-	-	-	-	-	-	Del	-	-	-	Complex	-
BRC42	-	-	p.Y295F	-	-	-	-	-	-	-	-	-	-	-	-
BRC44	-	-	-	-	-	-	-	-	-	-	Complex	-	p.S975F	-	-
BRC47	-	-	-	-	-	-	-	-	-	-	-	Complex	-	-	-
BRC49	-	-	-	-	-	-	-	-	-	-	-	Complex	-	-	-
BRC5	-	-	-	-	-	-	p.V680A	-	-	-	-	-	-	-	-
BRC51	-	-	-	-	-	-	-	-	-	Del	-	-	-	-	-
BRC52	-	-	-	-	-	-	-	-	-	-	-	Del	-	-	-
BRC6	-	-	-	-	-	-	-	-	p.R4139*	-	-	Complex	-	Complex	-
BRC9	-	-	-	-	-	-	-	-	-	p.M1108T	-	-	-	-	-

Supplementary Table 19. Histone modification. Validated nonsynonymous somatic mutations and structural variants identified in genes related to histone modification from 46 cases with whole genome sequence data. Selected genes include histone methyltransferase, demethylase, and acetyltransferases.

PARADIGM SubNetwork ^a	MetaCore Map ID ^b	-log ₁₀ P-val ^c	Gene Overlap ^d	Size PARADIGM ^e	Size Metacore ^f
GMCSF-mediated signaling events	175	15.8	8	12	31
BARD1 signaling events	4	14.5	7	9	31
ErbB2/ErbB3 signaling events	76	14.3	8	12	45
Mitotic Prometaphase	178	14.3	8	15	34
mTOR signaling pathway	55	14.0	9	16	59
Fc-epsilon receptor I signaling in mast cells	108	13.4	8	13	51
IL2-mediated signaling events	108	13.4	8	13	51
Insulin Pathway	82	13.3	7	7	72
Regulation of nuclear SMAD2/3 signaling	190	12.8	12	31	108
PDGFR-beta signaling pathway	108	12.2	9	26	51
BCR signaling pathway	58	12.0	8	18	50
Activation of mRNA	55	11.9	6	6	59
E2F transcription factor network	32	11.9	7	28	18
ErbB1 downstream signaling	108	11.9	8	18	51
Ras signaling in the CD4+ TCR pathway	92	11.6	5	5	29
Regulation of retinoblastoma protein	12	11.5	8	26	38
Presenilin action in Notch and Wnt signaling	9	11.3	9	25	66
Signaling by Stem cell factor receptor (c-Kit)	40	11.3	8	12	103
Trk receptor signaling mediated by the MAPK pathway	92	11.3	6	11	29
Ribosomal scanning and start codon recognition	55	11.1	6	7	59
Cyclin A/B1 associated events during G2/M transition	79	11.1	6	8	48
Endothelins	116	11.0	6	9	41
FOXM1 transcription factor network	All	10.7	25	31	1288
Nongenotropic Androgen signaling	116	10.6	6	10	41
Translation initiation complex formation	55	10.5	6	8	59
ATM mediated phosphorylation of repair proteins	13	10.4	4	5	11
Neurotrophic factor-mediated Trk receptor signaling	2	10.3	6	10	46
CXCR3-mediated signaling events	92	10.2	5	7	29
HIF-2-alpha transcription factor network	105	10.1	7	22	39
EPO signaling pathway	175	10.1	5	7	31

Ceramide signaling pathway	76	10.0	6	11	45
FGF signaling pathway	108	10.0	6	10	51
GTP hydrolysis of the 60S ribosomal subunit	55	10.0	6	9	59
Regulation of Telomerase	32	10.0	6	26	18
VEGFR3 signaling in lymphatic endothelium	126	10.0	5	6	41
Cyclin D associated events in G1	160	9.9	5	7	33
L13a-mediated silencing of Ceruloplasmin	55	9.6	6	10	59
Hypoxic and oxygen regulation of HIF-1-alpha	105	9.6	5	7	39
Signaling mediated by HGFR (c-Met)	55	9.5	7	18	59
ATR signaling pathway	118	9.4	5	15	17
Noncanonical Wnt signaling pathway	9	9.3	6	10	66
Signaling events regulated by Ret tyrosine kinase	109	9.3	5	5	78
Signaling events mediated by VEGFR1 and VEGFR2	39	9.3	8	16	122
Angiopoietin receptor Tie2-mediated signaling	11	9.2	6	12	55
IFN-gamma pathway	126	9.0	5	8	41
Regulation of Androgen receptor activity	190	8.8	8	20	108
Downstream signaling in naive CD8+ T cells	92	8.7	5	12	29
Meiotic Recombination	4	8.3	5	13	31
IGF1 pathway	49	8.3	4	5	33
PathMarkResponseAll	All	8.3	418	1451	1288
EGF receptor (ErbB1) signaling pathway	91	8.2	4	5	35
HIV-1 Nef: Negative effector of Fas and TNF-alpha	117	8.1	4	5	37
ATF-2 transcription factor network	190	8.1	7	16	108
Signaling events mediated by focal adhesion kinase	24	8.1	5	9	54
Notch-mediated HES/HEY network	12	8.0	6	25	38
IL6-mediated signaling events	58	7.9	5	10	50
Caspase cascade in apoptosis	84	7.9	4	6	31
a6b1 and a6b4 Integrin signaling	76	7.9	5	11	45
TRKR signaling mediated by PI3K and PLC-gamma	108	7.9	5	10	51
Signaling events mediated by PTP1B	65	7.8	6	21	49
ModulatedAll ⁹	32	7.7	13	742	18
Integrins in angiogenesis	39	7.7	6	10	122
Internalization of ErbB1	91	7.7	4	6	35
AP-1 transcription factor network	190	7.6	7	18	108

Retinoic acid receptors-mediated signaling	70	7.6	5	10	59
TGF-beta receptor signaling	65	7.5	5	12	49
Signaling events mediated by TCPTP	All ^h	7.5	17	21	1288
HIF-1-alpha transcription factor network	105	7.3	7	51	39
Class I PI3K signaling events mediated by Akt	173	7.3	5	11	58
Beta1 integrin cell surface interactions	16	7.2	5	6	144
ErbB4 signaling events	76	7.1	5	15	45
Plasma membrane estrogen receptor signaling	126	7.1	4	7	41
S1P1 pathway	116	7.1	4	7	41
Cyclin A:Cdk2-associated events at S phase entry	111	7.0	3	7	9
Signal transduction by L1	90	7.0	4	6	53
CDC42 signaling events	92	6.9	4	10	29
Calcineurin-dependent NFAT signaling in lymphocytes	190	6.9	6	14	108
FOXA1 transcription factor network	190	6.7	8	34	108
IL3-mediated signaling events	175	6.6	4	11	31
PLK1 signaling events	79	6.5	5	18	48
p73 transcription factor network	190	6.5	7	25	108
Regulation of SMAD2/3 signaling	71	6.5	3	5	19
Insulin-mediated glucose transport	82	6.4	4	6	72
Validated targets of C-MYC transcriptional repression	190	6.4	8	37	108
Deadenylation of mRNA	55	6.4	4	7	59
p53 pathway	12	6.3	5	24	38
Aurora A signaling	All	6.3	10	10	1288
Aurora B signaling	178	6.2	4	12	34
Signaling events mediated by HDAC Class I	12	6.2	4	11	38

^aName of the constituent sub-network from the PARADIGM SuperPathway,

^bIdentifier for the GeneGO MetaCore map.

^cThe negative base-10 logarithm of the P-value associated with the hypergeometric test to gauge the significance of the overlap between the PARADIGM sub-network and the MetaCore map. A background set of 5541 genes was assumed, which was the size of the SuperPathway.

^dThe number of genes in common between a sub-network and a map.

^eNumber of modulated genes in the PARADIGM sub-network.

^fNumber of genes returned in the map from the MetaCore analysis.

^gModulatedAll is the set of all modulated PARADIGM sub-networks merged into a single gene list.

^hAll is the set of all GeneGO MetaCore genes across all maps merged into a single gene list.

Supplementary Table 20: Overlap statistics of all PARADIGM sub-networks matching to at least one GeneGO MetaCore map and vice versa (all maps matching to at least one PARADIGM sub-network).

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