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

Matthew J. Ellis[1,2, 5*#], Li Ding[3,4*#], Dong Shen[3,4*], Jingqin Luo[5,6] , Vera J. Suman[7], John W. Wallis[3,4], Brian A. Van Tine[1], Jeremy Hoog[1], Reece J. Goiffon[9,17,18], Theodore C. Goldstein[24], Sam Ng[24], Li Lin[1], Robert Crowder[1], Jacqueline Snider[1], Karla Ballman[7], Jason Weber[1,8,9], Ken Chen[3,4], Daniel C. Koboldt[3,4], Cyriac Kandoth[3,4], William S. Schierding[3,4], Joshua F. McMichael[3,4], Christopher A. Miller[3,4], Charles Lu[3,4], Christopher C. Harris[3,4], Michael D. McLellan[3,4], Michael C. Wendl[3,4], Katherine DeSchryver[1], D. Craig Allred[5,10,], Laura Esserman[11], Gary Unzeitig[12], Julie Margenthaler[2], G.V.Babiera[13], P. Kelly Marcom[14], J.M. Guenther[15], Marilyn Leitch[16], Kelly Hunt[13], John Olson[14], Yu Tao[6], Chris Maher[1,2], Lucinda L. Fulton[3,4], Robert S. Fulton[3,4], Michelle Harrison[3,4], Ben Oberkfell[3,4], Feiyu Du[3,4], Ryan Demeter[3,4], Tammi L. Vickery[3,4], Adnan Elhammali[9,17,18], Helen Piwnica-Worms[8,9,19,20], Sandra McDonald[2,22], Mark Watson[6,10,22], David J. Dooling[3,4], David Ota[23], Li-Wei Chang[5,10], Ron Bose[2,5], Timothy J. Ley[1,2,3], David Piwnica-Worms[8,9,17,18,21], Joshua M. Stuart[24], Richard K. Wilson[2,3,4] and Elaine R. Mardis[2,3,4#]

*These authors contributed equally to this work
[#] Corresponding authors

Institutional Affiliations
[1]Department of Internal Medicine, Division of Oncology, Washington University, St. Louis, MO, USA
[2]Siteman Cancer Center, Washington University, St. Louis, MO, USA
[3]The Genome Institute, Washington University, St. Louis, MO, USA
[4]Department of Genetics, Washington University, St. Louis, MO, USA
[5]Breast Cancer Program, Washington University, St. Louis, MO, USA
[6]Division of Biostatistics, Washington University, St. Louis, MO, USA
[7]ACOSOG Statistical Center, Mayo Clinic, Rochester, MN, USA
[8]Department of Cell Biology and Physiology, Washington University, St. Louis, MO, USA
[9]BRIGHT Institute, Washington University School of Medicine, St. Louis, MO, USA
[10]Department of Pathology and Immunology, Washington University, St. Louis, MO, USA
[11]Helen Diller Cancer Center, University of California, San Francisco, CA, USA

[12]Doctors Hospital of Laredo, Laredo, TX, USA
[13]M. D. Anderson Cancer Center, Houston, TX, USA
[14]Duke University Cancer Center, Durham, NC, USA
[15]Good Samaritan Hospital, Cincinnati, OH, USA
[16]Simmons Cancer Center, University of Texas, Houston, TX, USA
[17]Molecular Imaging Center, Washington University, St. Louis, MO, USA
[18]Malinckrodt Institute of Radiology, Washington University, St. Louis, MO, USA
[19]Department of Internal Medicine, Washington University, St. Louis, MO, USA
[20]Howard Hughes Medical Institute, Chevy Chase, Maryland, USA
[21]Department of Developmental Biology, Washington University, St. Louis, MO, USA
[22]ACOSOG Central Specimen Bank, Washington University, St. Louis, MO, USA
[23]ACOSOG Operations Center, Duke University, Durham, NC, USA
[24]Department of Biomolecular Engineering, University of California, Santa Cruz, CA USA

Table of Contents

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 protocol[2]. 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 BWA[3] v0.5.7 with soft trimming (-q 5). For each sample, individual lane alignments in BAM format were merged together using SAMtools[4] r544. Duplicates were marked in the merged BAM files by the MarkDuplicates class of Picard[5] 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 GATK [7] IndelGenotyper, Pindel [8], and a modified version of SAMtools [4]. Both SNVs and indels were annotated using gene structure and conservation information, and classified by tier as previously described [9]. 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 probably 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 BreakDancer [10] with TIGRA_SV assembly [11], SquareDancer (K. Chen et al, in preparation), and Pindel [8]. Copy number differences with regions of SV were determined by BreakDancer [10]. 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 Pindel [8] 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 method [13], 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 Banjamini-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≤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 software[14]. 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 7*a*) 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 Package[15]. 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 determined 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 Treeview[16].

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*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 patients[17] and *ARID1A* was previously found to be highly mutated in ovarian clear cell carcinoma[18]. 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 myelination[19] 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 morphogenesis[20-22].

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 cancer [23] (**Supplementary Fig. 5**). CMDS[24] 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.

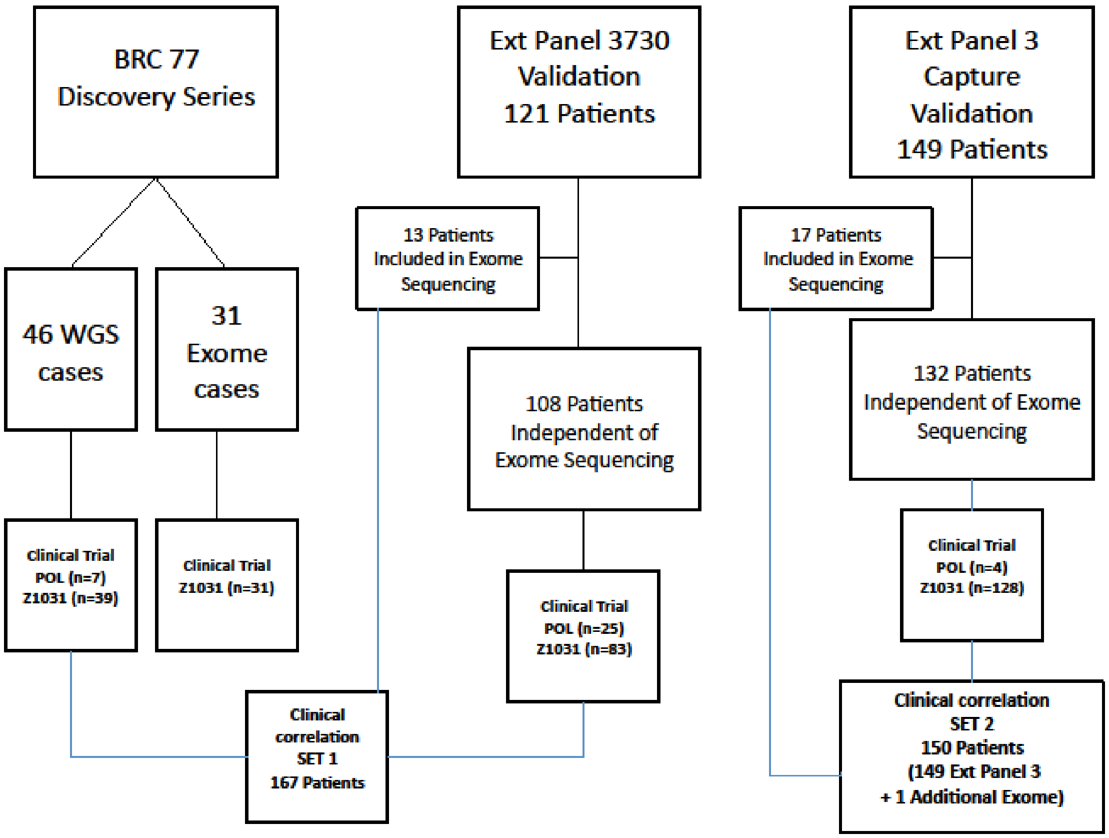
A total of 773 SVs (579 deletions, 189 translocations, and 5 inversions) identified by WGS were validated as somatic in 46 breast cancer genomes by capture validation (**Supplementary Table 11** and Supplementary Information). Paired end reads identified 579 deletions, including 163 events smaller than 1kbp 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*).

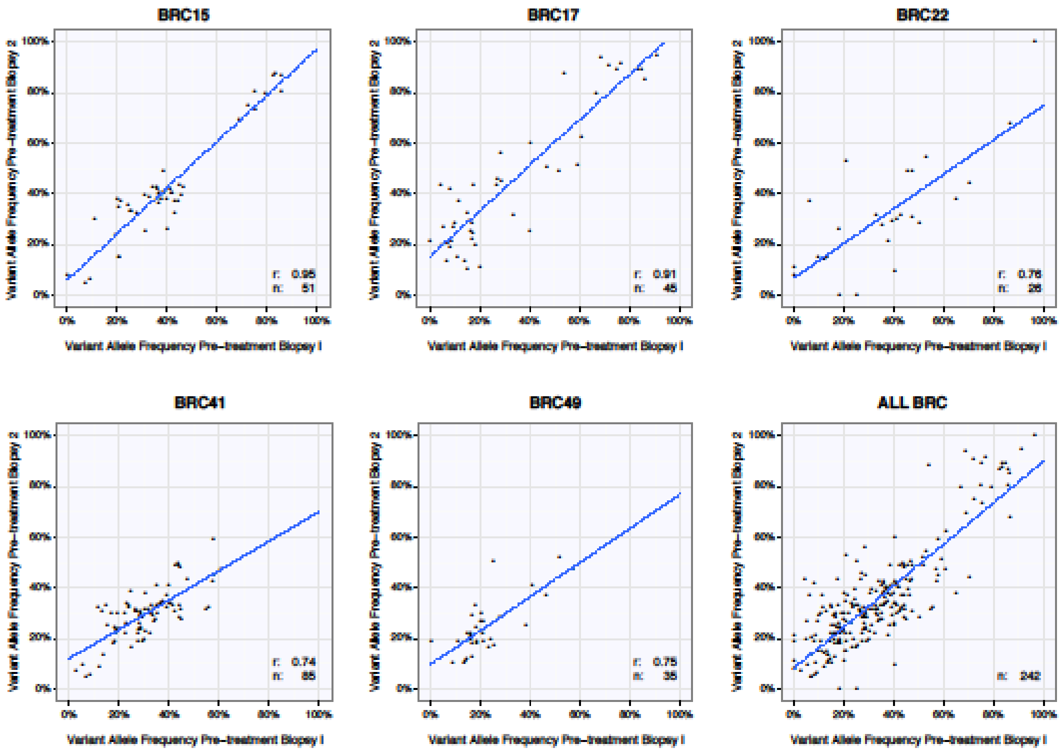
NRG1 encodes a number of isoforms that are ligands of the EGFR family. Gene losses and rearrangements in *NRG1* have been reported[26,27], including our earlier observation in a basal breast tumour of a 109,563 bp heterozygous deletion that removed three exons of *NRG1*[28]. In this series, three *NRG1* 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 line[29] and chimeric transcripts encoding portions of BCAS3 and MET are overexpressed in esophageal adenocarcinoma[30]. Further, BCAS3 overexpression in hormone receptor-positive premenopausal breast cancer has been associated with impaired tamoxifen responses[31].

B. Supplementary Figures

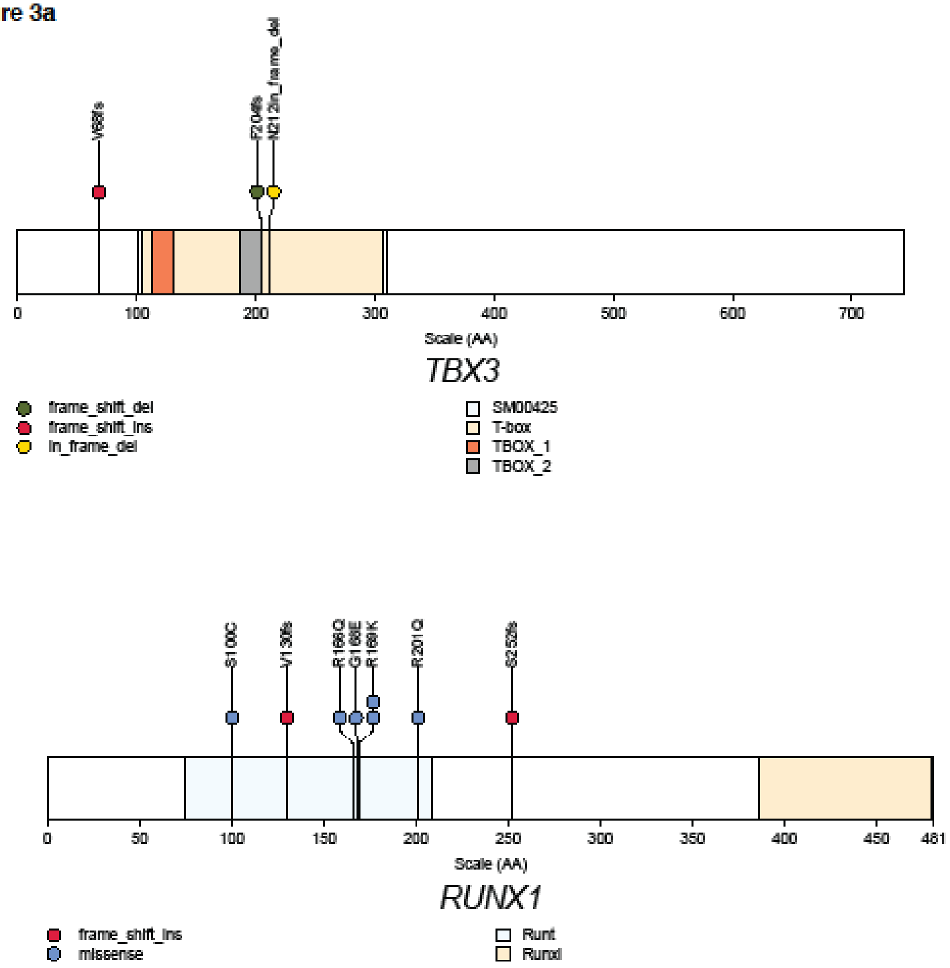
Supplementary Figure 1



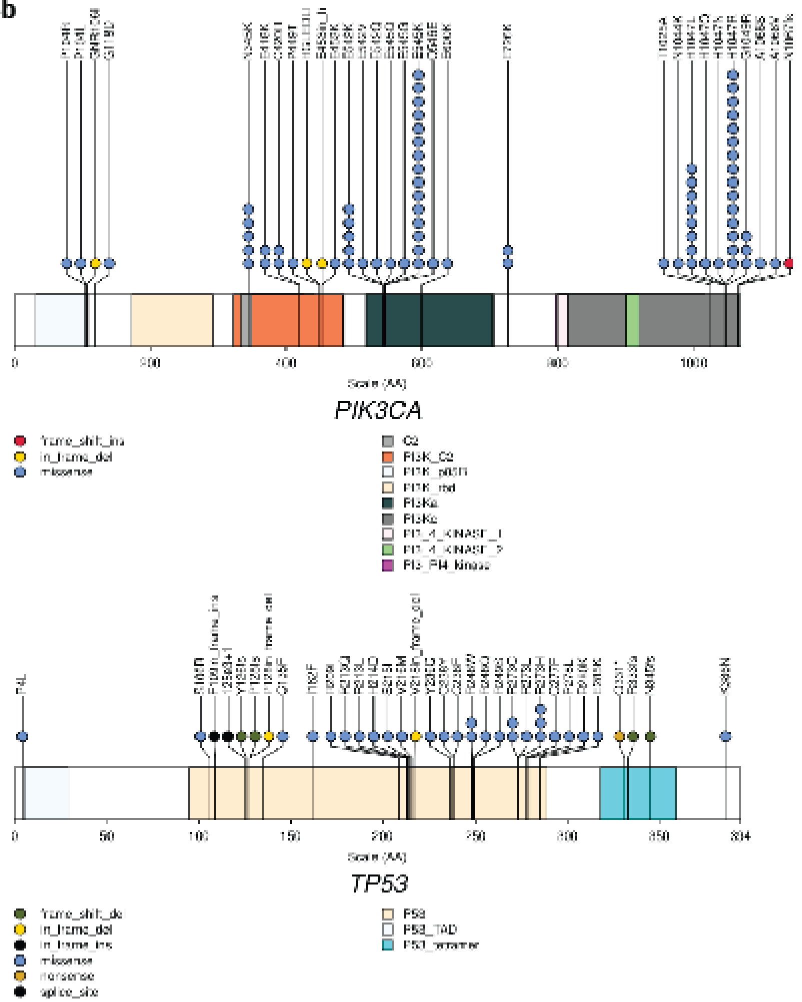
Supplementary Figure 2



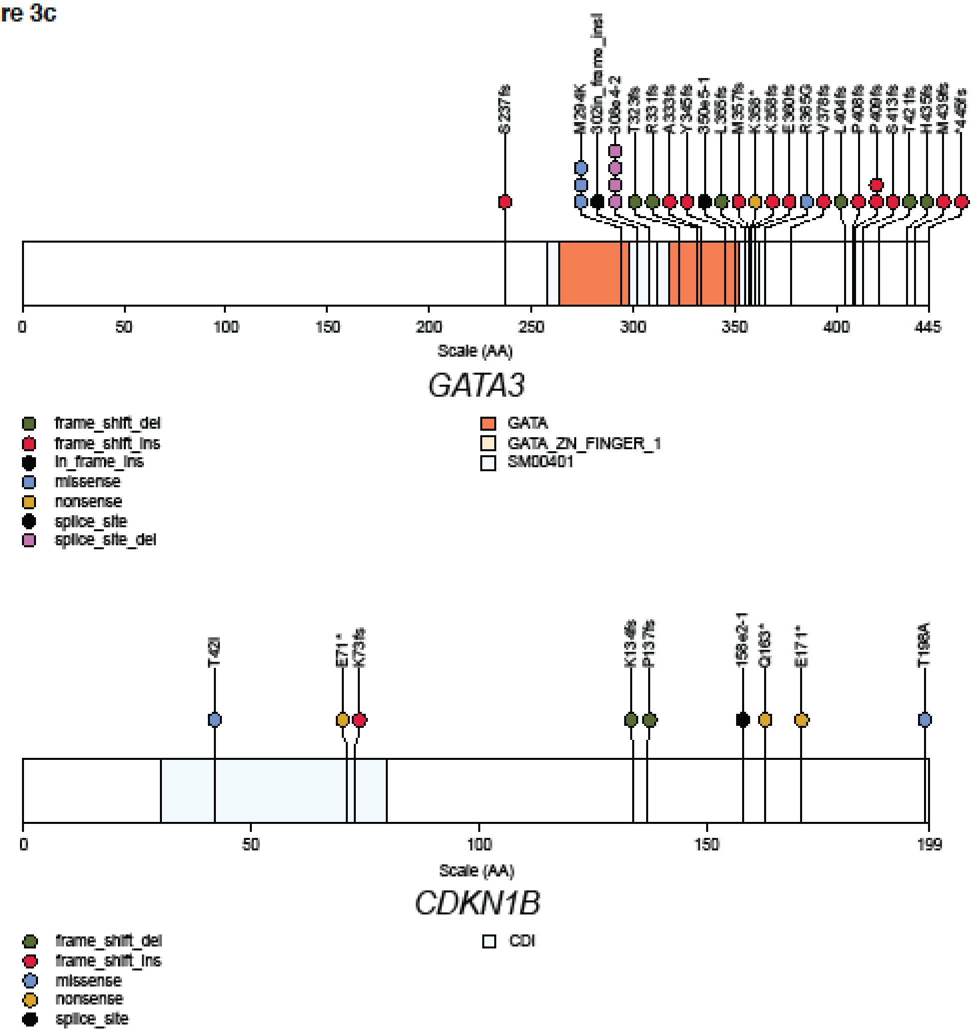
Supplementary Figure 3a



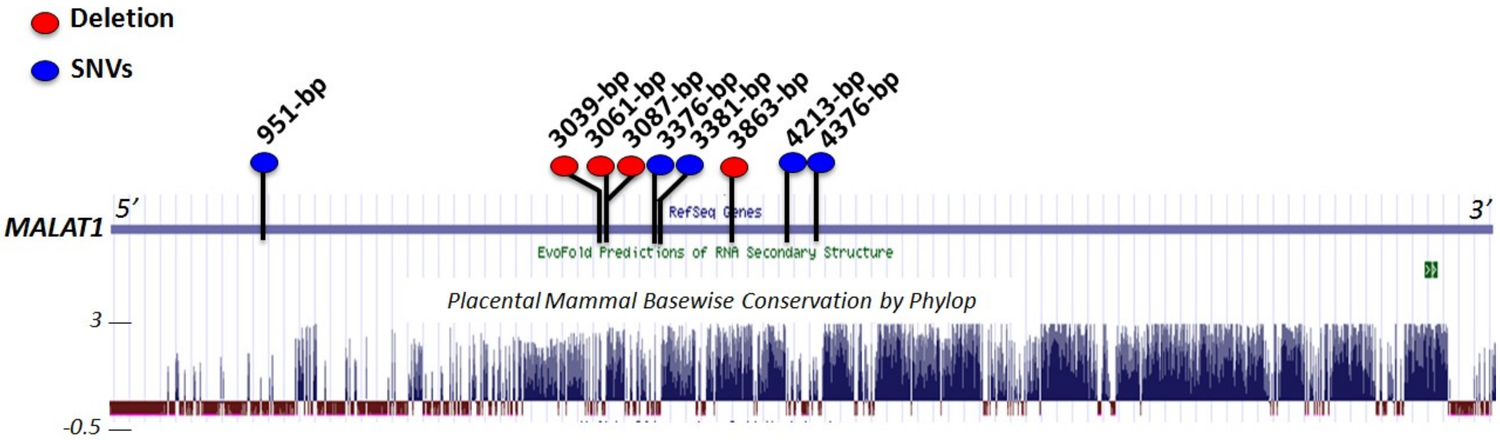
Supplementary Figure 3b



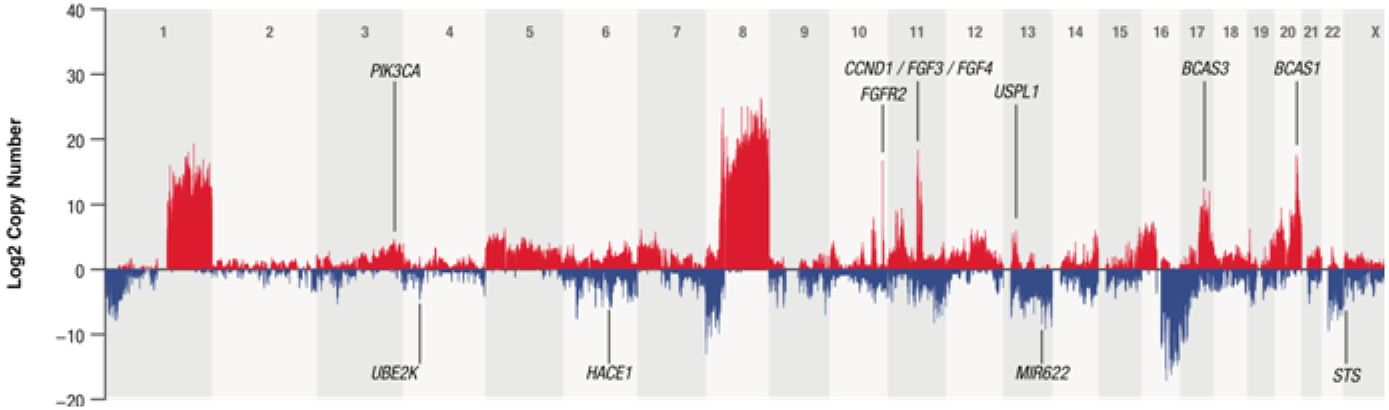
Supplementary Figure 3c



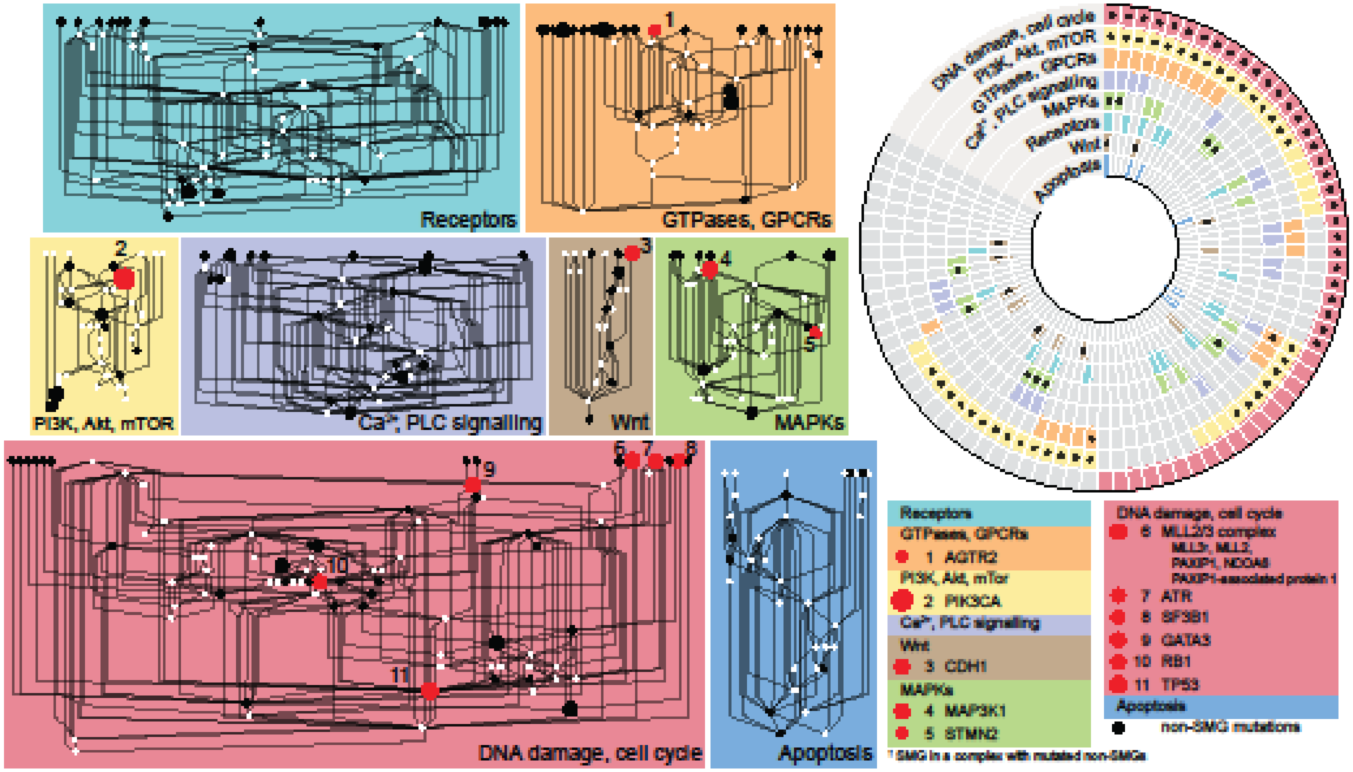
Supplementary Figure 4



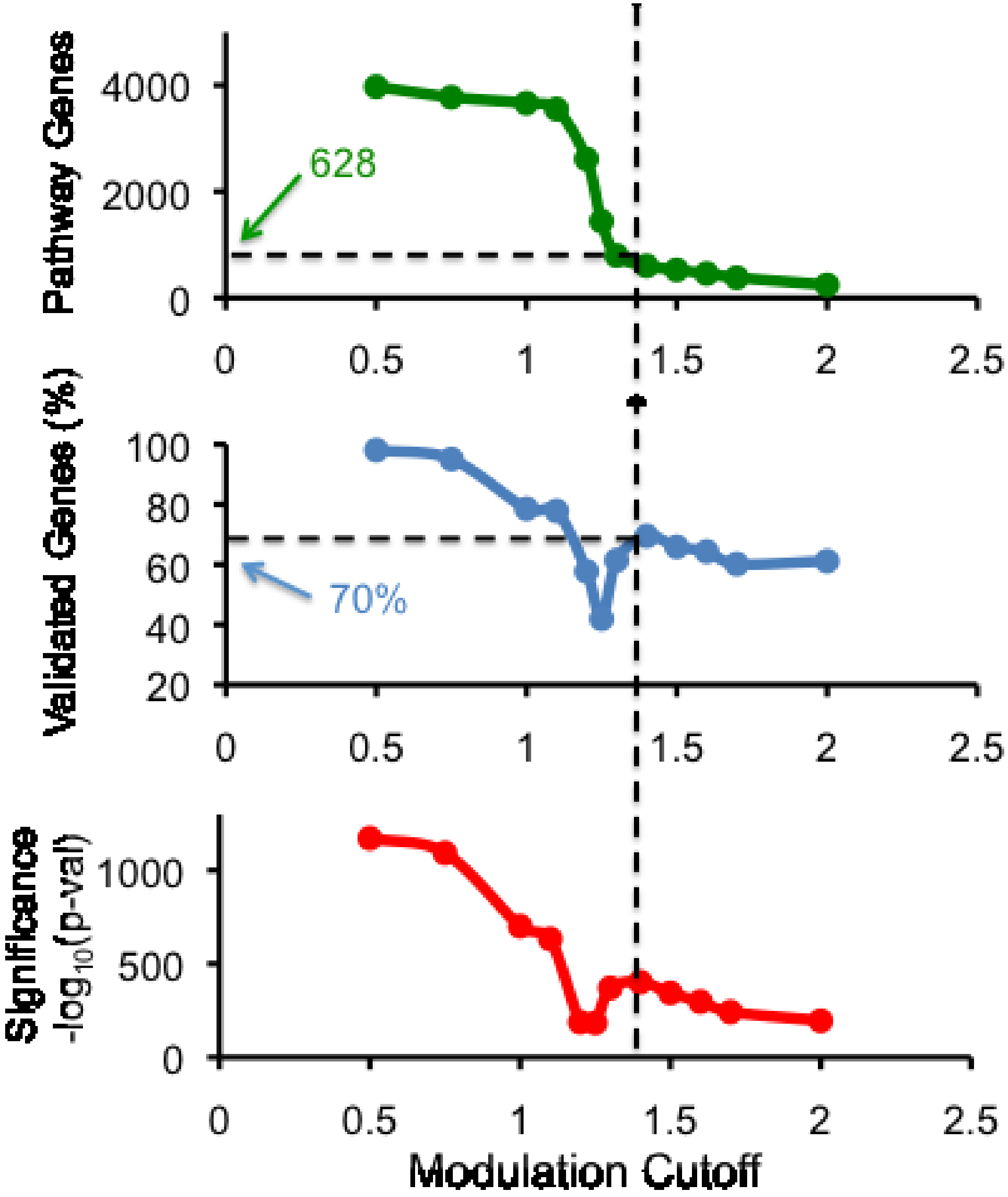
Supplementary Figure 5



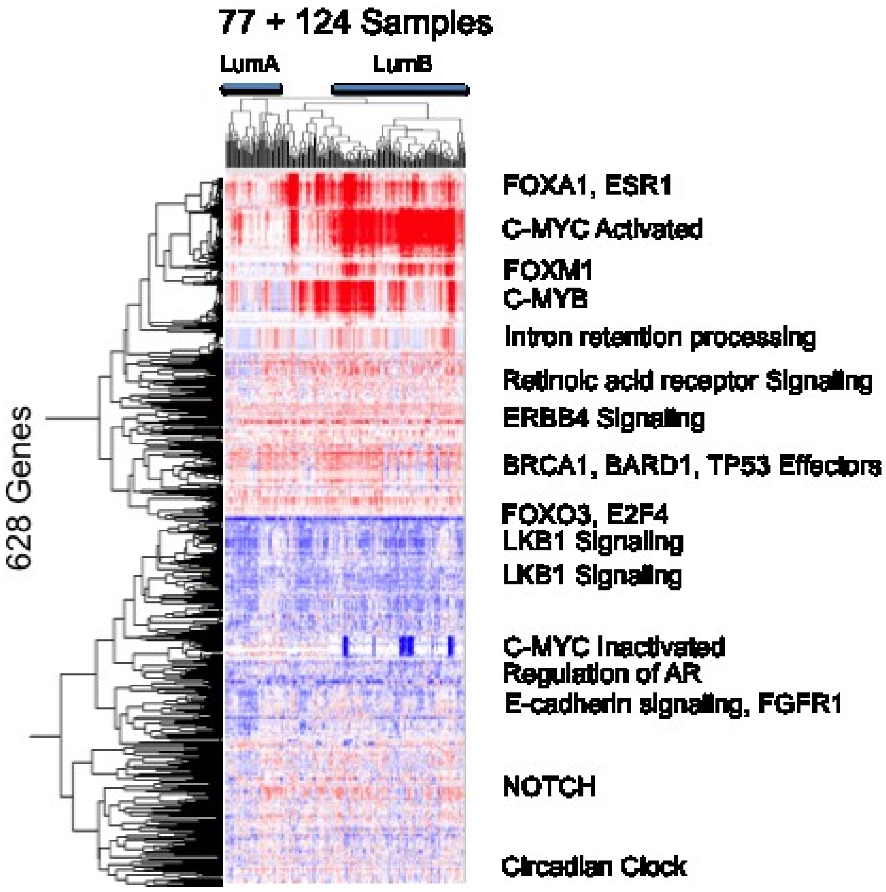
Supplementary Figure 6



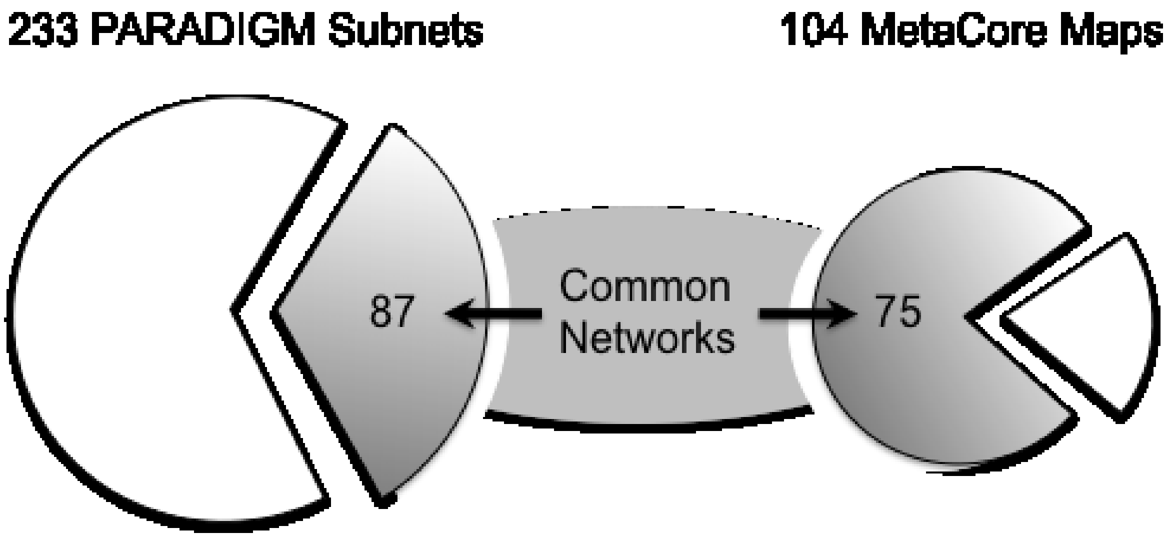
Supplementary Figure 7



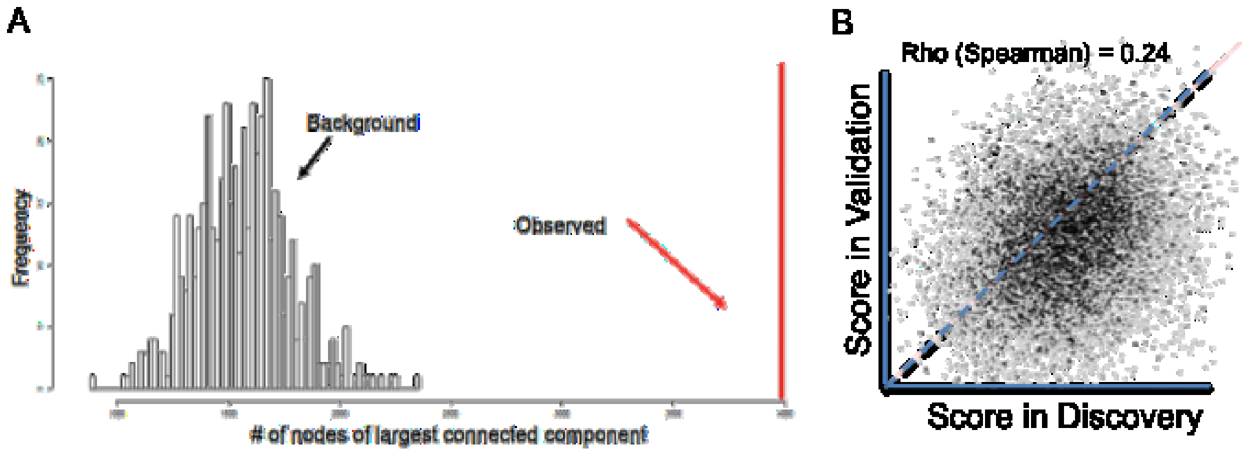
Supplementary Figure 8



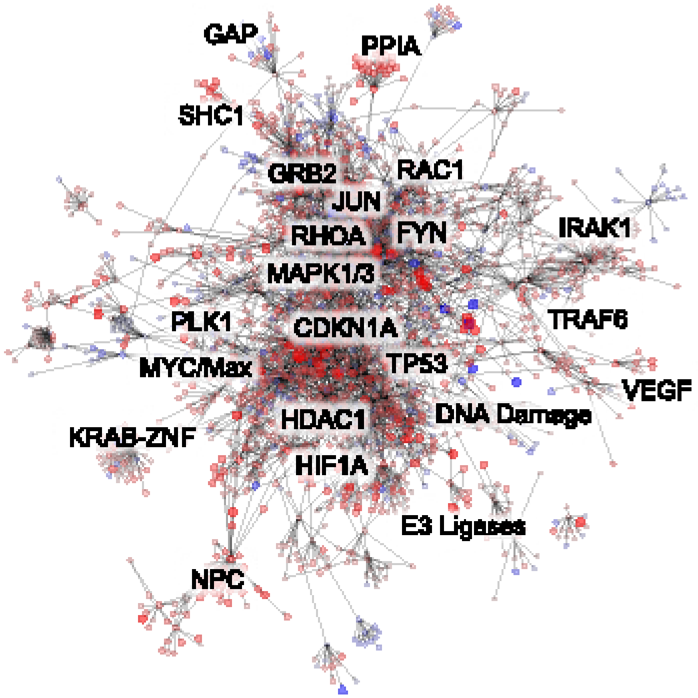
Supplementary Figure 9



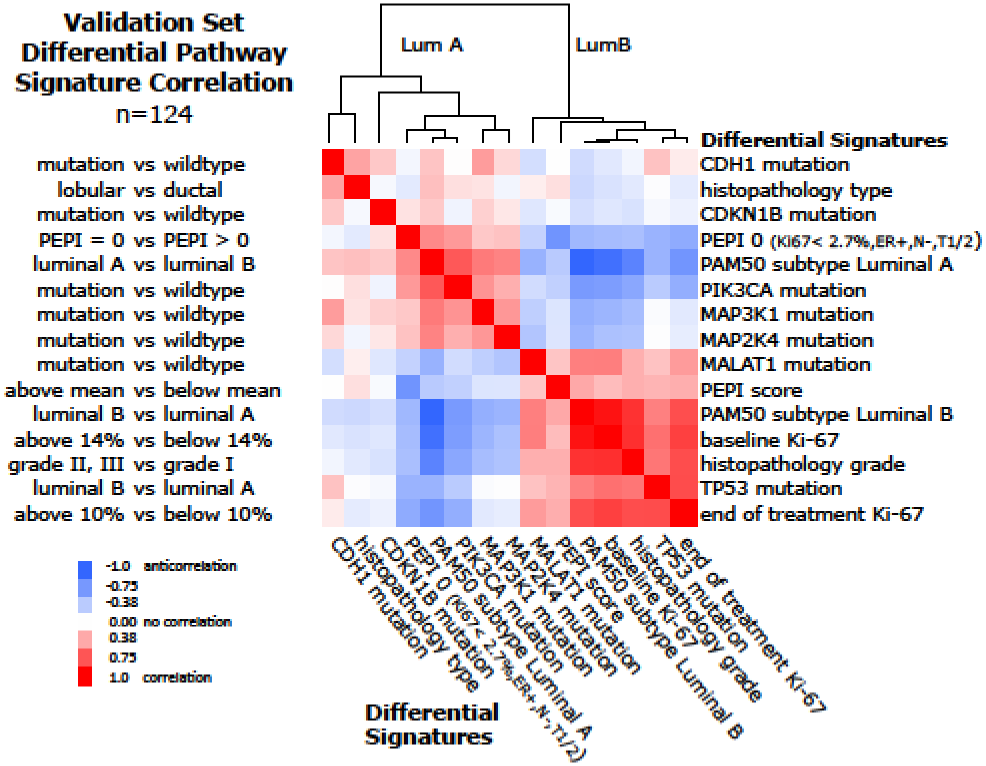
Supplementary Figure 10



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 retains 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 $-\log_{10}$(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 ($P < 4.1\times10^{-6}$) 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 (>=14% vs. <14%), and end-of-treatment Ki67 levels (>=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
Pleasance et al, 2009**	Malignant melanoma	1	292	6.65
Pleasance 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	1	16405149	16405149	Nonsense	SNP	C	A	BRC5	NM_153213.3	p.E439*
ENSG00000186543	1	16832421	16832421	Missense	SNP	G	T	CSB12	ENST00000362058	p.A11D
PADI6	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	SNP	G	A	CSB3	NM_001039775.2	p.R180W
ARID1A	1	26967041	26967041	Frame Shift Ins	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
S100PBP	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	Frame Shift 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
BNIPL	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	GAGAAGGTCACTCCATGA	0	CSB31	NM_000130.4	p.HGVTFS448in 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
AGT	1	228912907	228912907	In Frame Ins	INS	0	TGC	BRC40	NM_000029.3	p.105in Frame insS
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	GGCTCTAGAAGAC	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
ENSG00000202079	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
ENSG00000222279	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	CTAGAGC		0	BRC39	NM_058241.2	p.L114fs
DARS	2	136396834	136396834	Frame Shift Del	DEL	A		0	BRC15	NM_001349.2	p.I268fs
ENSG00000216081	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	SNP	C	T	BRC29	NM_004525.2	p.A2097T
PPIG	2	170179438	170179438	Frame Shift 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
CCDC141	2	179410260	179410260	In Frame Ins	INS	0	AGT	CSB21	NM_173648.2	p.A736in 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
ENSG00000212055	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.L115I
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	SNP	G	T	CSB13	NM_139072.3	p.C123*
TRIP12	2	230432024	230432024	Frame Shift 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	0	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
OXSR1	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	0	T	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	AATCAGGTC	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	Frame Shift 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	Frame Shift 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	SNP	G	A	CSB1	NM_145037.1	p.E36K
NFKBIZ	3	103054957	103054957	Frame Shift 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
ENSG00000222783	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	GGCAACCGT	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	Frame Shift Del	DEL	T	0	CSB7	NM_005612.3	p.S204fs
ENSG00000205682	4	61975771	61975771	Missense	SNP	C	T	BRC39	ENST00000381217	p.E250K
SRD5A2L2	4	64862995	64862995	Nonsense	SNP	C	A	CSB2	NM_001010874.4	p.E173*
CENPC1	4	68038377	68038377	Missense	SNP	A	G	BRC3	NM_001812.2	p.V858A
STAP1	4	68119450	68119450	Silent	SNP	C	T	BRC50	NM_012108.2	p.T58
ENSG00000207428	4	68552228	68552228	RNA	SNP	T	C	BRC15	ENST00000384697	NULL
UGT2B28	4	70191003	70191003	Nonsense	SNP	C	T	BRC50	NM_053039.1	p.Q399*
SULT1B1	4	70655515	70655515	Missense	SNP	G	C	BRC49	NM_014465.3	p.P4A
C4orf35	4	71236213	71236213	Missense	SNP	G	C	CSB1	NM_033122.3	p.E290Q
AMBN	4	71506824	71506824	Missense	SNP	G	A	BRC32	NM_016519.4	p.V378I
RUFY3	4	71874132	71874132	Missense	SNP	G	C	CSB1	NM_001037442.2	p.K432N
NPFFR2	4	73232095	73232095	Missense	SNP	C	T	CSB26	NM_004885.1	p.A424V

ENSG00000210839	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	SNP	G	C	BRC30	NM_002416.1	p.T23
SHROOM3	4	77881026	77881026	Frame Shift 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	SNP	G	A	CSB1	NM_001008388.3	p.L18
TBCKL	4	107236187	107236190	Frame Shift 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
ENSG00000223006	4	122201939	122201939	RNA	SNP	C	G		BRC39	ENST00000411074	NULL
QRFPR	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
PRDM9	5	23558177	23558179	In Frame Del	DEL	GAA	0	BRC32	NM_020227.2	p.K174in 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	Frame Shift Ins	INS	0	A	BRC18	NM_005921.1	p.H393fs
MAP3K1	5	56197437	56197437	Frame Shift Ins	INS	0	TA	CSB14	NM_005921.1	p.H393fs
MAP3K1	5	56197439	56197439	Missense	SNP	C	G	CSB14	NM_005921.1	p.H393Q
MAP3K1	5	56197551	56197552	Frame Shift Del	DEL	TC	0	BRC23	NM_005921.1	p.S431fs
MAP3K1	5	56213653	56213653	Nonsense	SNP	C	T	CSB1	NM_005921.1	p.Q957*
MAP3K1	5	56213820	56213820	Frame Shift Ins	INS	0	A	CSB26	NM_005921.1	p.R1012fs
MAP3K1	5	56213935	56213935	Frame Shift Del	DEL	C	0	CSB27	NM_005921.1	p.L1052fs
MAP3K1	5	56215247	56215247	Frame Shift 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*
MAP3K1	5	56217565	56217567	In Frame Del	DEL	AGT	0	CSB17	NM_005921.1	p.V1346in Frame del
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 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
PIK3R1	5	67626860	67626871	In Frame Del	DEL	TTAAACCAGACC	0	BRC44	NM_181523.2	p.KPDL567in Frame del
BDP1	5	70826934	70826934	Missense	SNP	A	G	BRC26	NM_018429.2	p.N581S
FCHO2	5	72322299	72322301	In Frame Del	DEL	AAG	0	CSB19	NM_138782.1	p.E118in Frame del
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	SNP	C	T	BRC39	NM_173800.4	p.S209L
DMXL1	5	118513201	118513201	Frame Shift 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
PCDHA5	5	140182097	140182099	In Frame Del	DEL	GAA	0	CSB28	NM_018908.2	p.E187in Frame del
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
ENSG00000223270	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	SNP	C	A	CSB2	NM_005565.3	p.K309N
RANBP17	5	170542787	170542787	Frame Shift 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	Frame Shift Del	DEL	CCTGT	0	BRC41	NM_000129.3	p.D140fs
RREB1	6	7156887	7156887	Frame Shift 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.Q4604
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	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
SYTL3	6	159049392	159049397	In Frame Del	DEL	GCAGCC	0	CSB2	NM_001009991.2	p.RS168in Frame del
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
TTLL2	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
GLCCI1	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	SNP	C	G	BRC52	ENST00000409974	p.A7G
HOXA2	7	27107604	27107604	Frame Shift 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	SNP	G	A	BRC8	NM_015198.3	p.R1181*
ECOP	7	55527564	55527564	Frame Shift 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
ENSG00000199231	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
ENSG00000216575	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
ENSG00000211518	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
ENSG00000222149	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	SNP	G	A	BRC6	NM_170606.2	p.R4139*
MLL3	7	151487020	151487023	Frame Shift Del	DEL	CTTC	0	CSB27	NM_170606.2	p.G3843fs
MLL3	7	151508119	151508123	Frame Shift Del	DEL	AGAAT	0	BRC3	NM_170606.2	p.I2391fs
MLL3	7	151550670	151550670	Frame Shift 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	SNP	A	G	BRC15	NM_006197.3	p.K409
LPL	8	19861171	19861172	Frame Shift 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*
INTS8	8	95961563	95961565	In Frame Del	DEL	AGA	0	CSB3	NM_017864.2	p.E973in Frame del
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	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	Frame Shift 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
ENSG00000204562	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
TTLL11	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	Frame Shift 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
GATA3	10	8146086	8146087	In Frame Ins	INS	0	ATT	CSB29	NM_001002295.1	p.302in Frame insI
GATA3	10	8151439	8151440	Splice_Site	DEL	CA	0	CSB7	NM_001002295.1	e4-2
GATA3	10	8151439	8151440	Splice_Site	DEL	CA	0	BRC21	NM_001002295.1	e4-2
GATA3	10	8151512	8151513	Frame Shift Ins	INS	0	T	CSB29	NM_001002295.1	p.A333fs
GATA3	10	8155707	8155707	Splice_Site	SNP	G	C	CSB22	NM_001002295.1	e5-1
GATA3	10	8155724	8155724	Frame Shift Ins	INS	0	TATGA	BRC32	NM_001002295.1	p.K358fs
GATA3	10	8155880	8155880	Frame Shift Ins	INS	0	T	BRC6	NM_001002295.1	p.P409fs
C10orf31	10	11398884	11398884	RNA	SNP	G	A	BRC39	XR_041927.1	NULL
UPF2	10	12049411	12049411	Frame Shift 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*
TMEM26	10	62882705	62882707	In Frame Del	DEL	GAA		0	BRC49	NM_178505.6	p.F47in 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
ATHL1	11	283193	283208	Frame Shift Del	DEL	GGGTCAACAACTCTGT	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
ENSG00000205751	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

ENSG00000180909	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
CAPRIN1	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	Frame Shift 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
FIBP	11	65412045	65412068	In Frame Del	DEL	GCGGCGCATGCAGCAGCCGCTCGA		0	CSB28	NM_198897.4	p.LERLLHAP66in Frame 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
SSH3	11	66835933	66835933	Nonstop 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
XRRA1	11	74316096	74316097	Frame Shift 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	TGCTACATTCC	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
ENSG00000201149	11	94896900	94896900	RNA	SNP	G	A	BRC20	ENST00000364279	NULL
CCDC82	11	95756837	95756837	Missense	SNP	C	G	BRC50	NM_024725.3	p.Q241H
YAP1	11	101605881	101605881	Nonstop 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
ENSG00000200168	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	Frame Shift 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
LOC729025	12	16302041	16302056	Frame Shift Del	DEL	AGTTGCATTTAGGTTC	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	SNP	C	T		BRC13	NM_025003.3	p.E815K
ARID2	12	44530397	44530398	Frame Shift 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	SNP	G	A		CSB1	NM_152319.2	p.R64Q
MLL2	12	47711616	47711616	Frame Shift 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*
ENSG00000202582	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	GGGGCCACTC	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	SNP	C	T	BRC39	NM_032889.3	p.Q310*
PCBP2	12	52148868	52148869	Frame Shift Del	DEL	CA	0	BRC52	NM_005016.2	p.T294fs
MAP3K12	12	52167053	52167054	Frame Shift 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	0	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	SNP	G	T	CSB2	NM_001079910.1	p.E355*
GALNT4	12	88442277	88442277	Frame Shift Del	DEL	G	0	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
TBX3	12	113603087	113603089	In Frame Del	DEL	TGT	0	BRC24	NM_016569.3	p.N212in Frame del
TBX3	12	113603113	113603113	Frame Shift Del	DEL	A	0	CSB30	NM_016569.3	p.F204fs
TBX3	12	113605185	113605185	Frame Shift 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	SNP	C	T	CSB1	NM_016281.3	p.E577K
HSPB8	12	118116045	118116045	Nonstop 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.N921I
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
ENSG00000201793	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

TTLL5	14	75281599	75281599	Missense	SNP	G	A	BRC38	NM_015072.3	p.R470Q
TTLL5	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	Frame Shift 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	Frame Shift 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	SNP	G	A		BRC37	NM_000942.4	p.T156I
ZNF609	15	62757545	62757546	Frame Shift 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*
SEMA7A	15	72496030	72496035	In Frame Del	DEL	TCCTCT		0	BRC32	NM_003612.1	p.ED246in Frame del

ARID3B	15	72670547	72670547	Missense	SNP	A	T	BRC42	NM_006465.2	p.Y295F
ULK3	15	72918681	72918681	Missense	SNP	G	T	CSB19	NM_001099436.1	p.F313L
SIN3A	15	73493702	73493702	Nonsense	SNP	C	A	CSB1	NM_015477.1	p.E124*
SNX33	15	73728769	73728769	Missense	SNP	G	A	BRC36	NM_153271.1	p.A91T
PSTPIP1	15	75116552	75116552	Missense	SNP	T	G	CSB3	NM_003978.3	p.S411A
SGK269	15	75261270	75261270	Missense	SNP	C	G	CSB1	NM_024776.2	p.K18N
HMG20A	15	75558684	75558684	Missense	SNP	G	A	BRC39	NM_018200.2	p.R339Q
CHRNA3	15	76681130	76681130	Silent	SNP	C	T	BRC7	NM_000743.3	p.L303
KIAA1199	15	78959138	78959138	Missense	SNP	G	A	CSB1	NM_018689.1	p.E90K
FSD2	15	81235607	81235607	Missense	SNP	G	A	BRC39	NM_001007122.2	p.H451Y
FAM103A1	15	81449675	81449675	Missense	SNP	G	C	CSB1	NM_031452.2	p.R70T
ENSG00000212374	15	82177273	82177273	RNA	SNP	A	T	BRC42	ENST00000391072	NULL
ADAMTSL3	15	82442609	82442609	Silent	SNP	G	A	BRC18	NM_207517.2	p.L1075
LOC727963	15	82539946	82539961	RNA	DEL	TCGGCGCCGGCTTCCG	0	CSB15	XR_015173.1	NULL
ZSCAN2	15	82965659	82965659	Missense	SNP	G	A	CSB1	NM_181877.1	p.R410K
ALPK3	15	83212458	83212458	Missense	SNP	G	C	CSB12	NM_020778.4	p.E1831Q
AKAP13	15	83925274	83925274	Missense	SNP	C	T	BRC44	NM_006738.4	p.L991F
AGBL1	15	84503262	84503262	Splice_Site	SNP	G	A	BRC38	NM_152336.2	e3+1
AGBL1	15	85018650	85018650	Missense	SNP	C	G	CSB1	NM_152336.2	p.A1021G
NTRK3	15	86277251	86277251	Missense	SNP	G	A	CSB19	NM_001012338.1	p.L629F
ENSG00000221391	15	86882914	86882914	RNA	SNP	G	A	BRC21	ENST00000408464	NULL
ACAN	15	87201681	87201681	Missense	SNP	G	A	BRC18	NM_013227.2	p.E1507K
ZNF710	15	88411919	88411919	Silent	SNP	G	A	BRC47	NM_198526.1	p.L182
ZNF710	15	88412016	88412016	Missense	SNP	G	A	BRC47	NM_198526.1	p.E215K
SEMA4B	15	88572236	88572236	Missense	SNP	G	A	CSB8	NM_020210.3	p.R624H
ZNF774	15	88704709	88704709	Missense	SNP	G	C	CSB1	NM_001004309.2	p.K214N
ZNF774	15	88705095	88705095	Missense	SNP	G	T	CSB1	NM_001004309.2	p.G343V
SV2B	15	89610854	89610854	Missense	SNP	C	A	BRC50	NM_014848.3	p.F349L
CHD2	15	91311623	91311623	Missense	SNP	C	G	CSB1	NM_001271.2	p.L689V
MCTP2	15	92802386	92802386	Missense	SNP	G	T	CSB7	NM_018349.2	p.G756V
LRRC28	15	97645637	97645637	Missense	SNP	C	T	BRC26	NM_144598.2	p.H115Y
ASB7	15	98970063	98970063	Missense	SNP	C	T	BRC4	NM_198243.3	p.P40L

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	TCCAGCTCT		0	CSB1	NM_001040114.1	p.ELE1557in Frame del
ABCC1	16	16142611	16142611	Missense	SNP	G	T		BRC44	NM_004996.3	p.S1523I
NOMO3	16	16257503	16257505	In Frame Del	DEL	ATT		0	BRC33	NM_001004067.2	p.I403in 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.V291
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*
ZNF785	16	30502243	30502245	In Frame Del	DEL	CTC		0	BRC19	NM_152458.5	p.E119in 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
CTCF	16	66203385	66203387	In Frame Del	DEL	GCA	0	BRC24	NM_006565.2	p.S272in Frame del
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
ENSG00000221526	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

CDH1	16	67403177	67403190	Frame Shift Del	DEL	GATCCTGAGCTCCC		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	SNP	G	A		BRC38	NM_004360.3	e8+1
CDH1	16	67407118	67407118	Frame Shift Del	DEL	C		0	CSB30	NM_004360.3	p.Y508fs
CDH1	16	67410696	67410696	Nonsense	SNP	G	A		CSB1	NM_004360.3	p.W526*
CDH1	16	67410725	67410739	In Frame Del	DEL	ATCCGGACACTGGTG		0	CSB28	NM_004360.3	p.NPDTGA536in Frame delT
CIRH1A	16	67751845	67751845	Silent	SNP	C	T		BRC18	NM_032830.2	p.V510
VPS4A	16	67910808	67910808	Missense	SNP	C	T		BRC4	NM_013245.2	p.R161W
AARS	16	68850558	68850559	Frame Shift 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
NPIPL2	16	72982901	72982903	In Frame Del	DEL	CAA		0	CSB30	ENST00000355290	p.Q192in 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
DNAH2	17	7601239	7601250	In Frame Del	DEL	TCTGCGTGAAAA	0	BRC39	NM_020877.2	p.RENL672inFrame 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	Frame Shift 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
ZPBP2	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	DEL	GCACTCATCAAAGAA	0	BRC41	NM_020428.1	p.LIKEA346in Frame del
ILF3	19	10652083	10652083	Frame Shift 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	Frame Shift 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	SNP	C	T		CSB6	ENST00000391940	p.A391T
ERCC2	19	50564241	50564246	Frame Shift 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	SNP	G	T		BRC37	NM_053003.1	p.S47Y
HAS1	19	56908493	56908494	Frame Shift 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	Frame Shift 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	Frame Shift Del	DEL	G	0	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*
CTCFL	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
ENSG00000197934	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	Frame Shift Del	DEL	TCTGTACA	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	TCACAGTCCT	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*
MYH9	22	35011125	35011136	In Frame Del	DEL	TCCAGCTGCTCC		0	CSB28	NM_002473.4	p.EEQL1820in Frame del
MYH9	22	35014898	35014907	Frame Shift Del	DEL	CTAGGGCCCG		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
FLJ23865	22	37900224	37900239	Frame Shift Del	DEL	GTAGATTTTCCATCTG		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
ENSG00000223073	MT	178	178	RNA	SNP	A	G	CSB22	ENST00000411141	NULL
ENSG00000211459	MT	711	711	RNA	SNP	G	A	CSB24	ENST00000389680	NULL
ENSG00000211459	MT	859	859	RNA	SNP	G	A	CSB6	ENST00000389680	NULL
ENSG00000211459	MT	1364	1364	RNA	SNP	G	A	CSB3	ENST00000389680	NULL
ENSG00000210082	MT	1696	1696	RNA	SNP	T	C	BRC39	ENST00000387347	NULL
ENSG00000210082	MT	2151	2151	RNA	SNP	G	A	CSB13	ENST00000387347	NULL
ENSG00000210082	MT	2348	2348	RNA	SNP	T	C	CSB19	ENST00000387347	NULL
ENSG00000210082	MT	2911	2911	RNA	SNP	G	A	CSB28	ENST00000387347	NULL
ENSG00000209082	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
ENSG00000210144	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
KIR2DS2	NT_113949	135024	135024	Missense	SNP	A	T	CSB25	ENST00000400833	p.Q110L
ENSG00000212883	NT_113954	54089	54089	Missense	SNP	T	G	CSB14	ENST00000391570	p.L91R
DHRSX	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	0	GAAGAG	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	ACCCCTCCAGCATGGTCACC	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	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	CCTCATGGATTAGAAGATTTGCTGAAC	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	CTAGTTCAACAACAACAACAACAACAACAACAGAGCAACCAA	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	TGGAACTTACTTATGGTAACCTTTT	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	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	CAAAATC	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	AAAACATCTTGTTGAGGGCAGGGGAGTACTGTAG	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.

		Tier 1							Tier 2 and 3								Tier 1, 2, and 3							
Sliding Window	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.

patient.id	cohort	WGS	exome.seq	extpan1.2	extpan3	gex_id	aCGH_id	Test.Set.for.Josh	comment	Age	Baseline_Luminal_Type	*maxsxdim*	posnodes	pathT	pathN	Baseline_HER2_level	Baseline_Lobular_Ductal	Baseline_Grade	Baseline_Grade2	Baseline_Grade3	Baseline_ER	Baseline_Ki67	Ki67_2wk	Ki67_4wk	Ki67_Surg	Ki67_End.of.Treatment	Ki67_Change	Ki67_PercentageChange	Responder_Ki67	ER_2wk	ER_4wk	ER_Surg	ER_End.of.Treatment	ER_Change	PEPI_Score	PEPI_Zero	Clinical_Response	ATR	BIRC6	CDH1	CDKN1B	GATA3	MALAT1	MAP2K4	MAP3K1	MLL3	PIK3CA	RB1	RUNX1	TP53
104	POL			x		251485040709_2	2.51E+11	x		79.175	LumB	*NA*	NA	3~4	1	NEGATIVE	DUCTAL	III	III	II/III	6	0.513	NA	0.315	0.423	0.423	-0.09	-0.17544	NonResponder	NA	6	5	5	-1	8	0	NA	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	+
107	POL			x		251485040709_3	2.51E+11	x		75.75	LumB	*NA*	NA	3~4	1	NEGATIVE	DUCTAL	III	III	II/III	7	0.279	NA	0	0	0	-0.279	-1	Responder	NA	4	7	7	0	6	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	+
111	POL			x		251485040709_4	2.51E+11	x		69.04167	LumB	*NA*	NA	3~4	1	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.291	NA	0.121	0.088	0.088	-0.203	-0.69759	Responder	NA	5	6	6	-2	7	0	1	NA	NA	NA	-	-	NA	+	-	NA	-	NA	NA	-
112	POL			x		251485040721_1	2.51E+11	x		84.23333	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.415	NA	0.133	0.204	0.204	-0.211	-0.50843	NonResponder	NA	7	8	8	1	5	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
115	POL			x		251485040721_3	2.51E+11	x		73.66111	LumA	*NA*	NA	3~4	1	NEGATIVE	LOBULAR	I	I/II	I	8	0.042	NA	0.008	0.016	0.016	-0.026	-0.61905	Responder	NA	4	8	8	0	6	0	0	NA	NA	NA	-	+	NA	-	-	NA	+	NA	NA	-
117	POL			x		251485040704_2	2.51E+11	x		57.66667	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.604	NA	0.214	0.09	0.09	-0.514	-0.85099	Responder	NA	7	2	2	-5	7	0	NA	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
122	POL			x		251485040722_2	2.51E+11	x		71.85833	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	6	0.467	NA	NA	0.155	0.155	-0.312	-0.66809	NonResponder	NA	NA	2	2	-4	7	0	0	NA	NA	NA	-	-	NA	-	+	NA	+	NA	NA	+
125	POL			x		251485040722_4	2.51E+11	x		60.87778	LumB	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	III	III	II/III	4	0.245	NA	0.054	0.286	0.286	0.041	0.167347	NonResponder	NA	2	3	3	-1	5	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
304	POL			x		251485040705_3	2.51E+11	x		63.32778	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	8	0.092	NA	0.048	0.017	0.017	-0.075	-0.81522	Responder	NA	7	8	8	0	3	0	NA	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
306	POL			x		251485040704_4	2.51E+11	x		64.16389	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	6	0.129	NA	0.111	0.094	0.094	-0.035	-0.27132	Responder	NA	7	7	7	1	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
307	POL			x		251485040723_1	2.51E+11	x		55.13889	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.463	NA	0.061	0.19	0.19	-0.273	-0.58963	NonResponder	NA	6	7	7	0	1	0	NA	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	+
308	POL			x		251485067259_2	2.51E+11	x		57.54444	LumB	*NA*	NA	1~2	1	POSITIVE	DUCTAL	III	III	II/III	5	0.375	NA	NA	0.115	0.115	-0.26	-0.69333	NonResponder	NA	NA	5	5	0	4	0	NA	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	+
309	POL			x		251485040723_2	2.51E+11	x		55.74167	LumB	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	5	0.214	NA	0.136	0.02	0.02	-0.194	-0.90654	Responder	NA	6	7	7	2	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
402	POL				x	251485040723_3	2.51E+11	x		83.4	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.124	NA	0.102	0.025	0.025	-0.099	-0.79839	Responder	NA	8	8	8	0	3	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	-
409	POL			x		251485067277_1	2.51E+11	x		78.39722	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	5	0.281	NA	0.163	0.432	0.432	0.151	0.537367	NonResponder	NA	4	4	4	-1	5	0	NA	NA	NA	NA	-	-	NA	+	-	NA	+	NA	NA	+
411	POL			x		2.51E+11	NA			89.35833	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	8	0.338	NA	0.064	0.054	0.054	-0.284	-0.84024	Responder	NA	5	8	8	0	4	0	NA	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
507	POL				x	251485040706_4	NA			68.1	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	6	0.078	NA	0.066	0.056	0.056	-0.022	-0.28205	Responder	NA	8	5	5	-1	1	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
508	POL			x		251485040707_1	2.51E+11	x		77.41667	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.015	NA	0.01	0.013	0.013	-0.002	-0.13333	Responder	NA	5	7	7	-1	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
801	POL			x		251485040706_1	2.51E+11	x		48.06389	LumB	*NA*	NA	1~2	0	POSITIVE	DUCTAL	II	I/II	II/III	4	0.224	NA	0.146	0.145	0.145	-0.079	-0.35268	NonResponder	NA	7	5	5	1	1	0	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
804	POL	x				251485042221_2	2.51E+11			56.98333	LumB	*NA*	NA	1~2	NA	NEGATIVE	DUCTAL	III	III	II/III	7	0.286	NA	0.009	0	0	-0.286	-1	Responder	NA	7	7	7	0	NA	NA	NA	-	-	-	-	-	+	-	-	-	+	-	-	+

807	POL	x				251485042221_4	2.51E+11			72.29167	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.153	NA	0.042	0.002	0.002	-0.151	-0.98693	Responder	NA	8	7	7	0	0	1	1	-	+	-	-	-	+	-	-	-	+	-	-	-
808	POL			x		251485042222_1	2.51E+11	x		64.61944	LumB	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	II	I/II	II/III	5	0.232	NA	0.059	0	0	-0.232	-1	Responder	NA	4	4	4	-1	3	0	1	NA	NA	NA	-	+	NA	-	-	NA	+	NA	NA	+
811	POL			x		251485067259_1	2.51E+11	x		60.37778	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	6	0.226	NA	0.016	0.007	0.007	-0.219	-0.96903	Responder	NA	7	7	7	1	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
814	POL	x				251485042222_3	2.51E+11			57.46667	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.299	NA	0.019	0.023	0.023	-0.276	-0.92308	Responder	NA	8	8	8	1	3	0	1	-	-	-	-	+	-	-	-	+	-	-	-	-
818	POL			x		251485042223_2	2.51E+11	x		65.72778	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.079	NA	0.018	0	0	-0.079	-1	Responder	NA	8	7	7	-1	3	0	1	NA	NA	NA	-	+	NA	-	-	NA	-	NA	NA	-
820	POL	x				251485042223_3	NA			53.75278	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.53	NA	0.12	0.453	0.453	-0.077	-0.14528	NonResponder	NA	7	6	6	-1	5	0	1	-	+	-	-	-	+	-	-	-	+	+	-	+
823	POL			x		251485042959_1	2.51E+11	x		75.46389	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	5	0.361	NA	0.03	0.216	0.216	-0.145	-0.40166	NonResponder	NA	7	7	7	2	5	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
824	POL				x	251485042224_1	NA			78	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	8	0.131	NA	0.063	0.031	0.031	-0.1	-0.76336	Responder	NA	8	8	8	0	4	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
826	POL				x	251485042224_2	2.51E+11	x		57.4	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	II	I/II	II/III	6	0.122	NA	0.016	0.004	0.004	-0.118	-0.96721	Responder	NA	5	3	3	-3	3	0	1	-	-	+	-	-	-	-	-	NA	-	-	-	+
828	POL	x				251485042224_4	2.51E+11			77.72222	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.387	NA	0.045	0.008	0.008	-0.379	-0.97933	Responder	NA	7	7	7	-1	0	1	1	-	-	-	-	-	-	-	-	-	+	-	-	-
829	POL			x		251485042225_1	2.51E+11	x		83.76944	LumB	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	7	0.228	NA	0.083	0.1	0.1	-0.128	-0.5614	NonResponder	NA	6	7	7	0	1	0	NA	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
831	POL			x		251485042225_3	2.51E+11	x		56.725	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.117	NA	0.139	0.071	0.071	-0.046	-0.39316	Responder	NA	6	7	7	0	4	0	0	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
834	POL	x				251485042225_4	2.51E+11			87.225	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	0.147	NA	0.065	0.013	0.013	-0.134	-0.91156	Responder	NA	8	8	8	0	0	1	1	-	-	-	-	-	-	-	+	-	+	-	-	-
837	POL	x				251485042955_1	2.51E+11			64.93611	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.272	NA	0.238	0.293	0.293	0.021	0.077206	NonResponder	NA	6	6	6	-2	5	0	0	-	-	-	-	-	-	-	-	-	+	-	-	-
839	POL			x		251485042955_2	2.51E+11	x		57.68889	LumA	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.644	NA	0.021	0.014	0.014	-0.63	-0.97826	Responder	NA	3	8	8	0	0	1	1	NA	NA	NA	+	-	NA	-	-	NA	-	NA	NA	-
841	POL			x		251485042957_1	2.51E+11	x		55.54722	LumB	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	5	0.439	NA	0.168	0.284	0.284	-0.155	-0.35308	NonResponder	NA	4	6	6	1	2	0	NA	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15386	Z1031A			x		251485014084_3	2.51E+11	x		56	LumB	*1*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	8	0.012	NA	NA	0.028	0.028	0.016	1.333333	Responder	NA	NA	3	3	-5	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	+
15445	Z1031A			x		251485012720_3	2.51E+11	x		79	LumA	*4.4*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.128	NA	NA	0.021	0.021	-0.107	-0.83594	Responder	NA	NA	7	7	-1	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	+
15462	Z1031A		x		x	251485012721_1	2.51E+11			81	LumB	*2.5*	1	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	6	0.192	NA	NA	0.013	0.013	-0.179	-0.93229	Responder	NA	NA	6	6	0	3	0	1	-	-	+	-	-	-	-	-	-	-	-	-	-
15510	Z1031A			x		251485026043_1	NA			69	LumA	*4*	0	1~2	0	NA	LOBULAR	I	I/II	I	6	0	NA	NA	0.005	0.005	0.005	49	Responder	NA	NA	4	4	-2	0	1	0	NA	NA	NA	-	-	NA	-	+	NA	+	NA	NA	-
15544	Z1031A		x	x		251485036031_3	2.51E+11			69	LumA	*2.3*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	5	0.043	NA	NA	0	0	-0.043	-1	Responder	NA	NA	5	5	0	0	1	0	+	-	+	-	-	-	-	+	-	+	-	-	-
15547	Z1031A			x		251485014084_1	2.51E+11	x		60	LumA	*2.1*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	3	0.022	NA	NA	0.07	0.07	0.048	2.181818	Responder	NA	NA	2	2	-1	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15565	Z1031A			x		251485012720_1	2.51E+11	x		63	LumB	*2.1*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.169	NA	NA	0.042	0.042	-0.127	-0.75148	Responder	NA	NA	6	6	-2	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15571	Z1031A				x	251485012719_3	2.51E+11	x		43	LumA	*7*	1	3~4	1	POSITIVE	DUCTAL	II	I/II	II/III	6	0.026	NA	NA	0.051	0.051	0.025	0.961538	Responder	NA	NA	4	4	-2	7	0	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
15574	Z1031A		x	x		251485013244_1	NA		max tumor dim unknown	66	LumB	*NA*	1	NA	1	POSITIVE	DUCTAL	II	I/II	II/III	7	0.377	NA	NA	0.435	0.435	0.058	0.153846	NonResponder	NA	NA	8	8	1	NA	0	1	-	-	-	-	-	-	-	-	-	-	-	-	-
15577	Z1031A				x	251485012719_1	NA			55	LumB	*2.2*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.362	NA	NA	0.023	0.023	-0.339	-0.93646	Responder	NA	NA	7	7	-1	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
15583	Z1031A	x				251485028410_1	2.51E+11			73	LumA	*1.2*	0	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	7	0.058	NA	NA	0.019	0.019	-0.039	-0.67241	Responder	NA	NA	6	6	-1	0	1	0	-	-	-	-	+	-	-	-	+	-	-	-	-

15601	Z1031A	x			251485034014_1	NA			84	LumB	*3.6*	0	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	7	0.25	NA	NA	0.417	0.417		0.167	0.668	NonResponder	NA	NA	6	6	-1	2	0	1	-	-	-	-	-	-	-	-	-	+	-	-	-
15616	Z1031A			x	251485013262_3	2.51E+11	x		68	LumB	*3.2*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.319	NA	NA	0.066	0.066	-	0.253	-0.7931	Responder	NA	NA	7	7	-1	4	0	1	-	-	-	-	-	-	+	-	NA	-	-	-	+
15654	Z1031A		x		251485036032_1	2.51E+11	x		67	LumA	*6.5*	1	3~4	1	NEGATIVE	LOBULAR	I	I/II	I	6	0.024	NA	NA	0	0	-	0.024	-1	Responder	NA	NA	6	6	0	6	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15660	Z1031A		x		251485036032_3	2.51E+11	x		51	LumA	*3.2*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.047	NA	NA	0	0	-	0.047	-1	Responder	NA	NA	7	7	0	0	1	1	NA	NA	NA	-	+	NA	-	-	NA	-	NA	NA	-
15669	Z1031A		x		251485028410_3	2.51E+11	x		60	LumA	*1.5*	1	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	5	0.072	NA	NA	0.034	0.034	-	0.038	-0.52778	Responder	NA	NA	3	3	-2	4	0	0	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15681	Z1031A		x		251485036032_4	2.51E+11	x		80	LumA	*1.5*	0	1~2	0	POSITIVE	DUCTAL	NA	NA	NA	7	0.167	NA	NA	0.05	0.05	-	0.117	-0.7006	Responder	NA	NA	4	4	-3	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15687	Z1031A	x			251485028408_1	2.51E+11			86	LumB	*2.1*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	7	0.442	NA	NA	0.012	0.012		-0.43	-0.97285	Responder	NA	NA	4	4	-3	3	0	1	-	-	-	-	-	-	-	-	-	-	-	-	-
15694	Z1031A		x		251485036593_1	2.51E+11	x		57	LumA	*5.9*	1	3~4	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.18	NA	NA	0.01	0.01		-0.17	-0.94444	Responder	NA	NA	0	0	-7	9	0	0	NA	NA	NA	-	-	NA	-	+	NA	+	NA	NA	-
15714	Z1031A	x			251485035338_3	2.51E+11			64	LumA	*6.5*	1	3~4	1	NEGATIVE	LOBULAR	I	I/II	I	6	0.008	NA	NA	0	0	-	0.008	-1	Responder	NA	NA	7	7	1	6	0	1	-	-	-	-	-	-	-	-	-	-	-	-	-
15715	Z1031A		x		251485035336_1	2.51E+11	x		63	LumB	*1.7*	0	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	5	0.285	NA	NA	0.384	0.384		0.099	0.347368	NonResponder	NA	NA	4	4	-1	2	0	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15721	Z1031A			x	251485036593_3	NA			64	LumA	*2*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.077	NA	NA	0.01	0.01	-	0.067	-0.87013	Responder	NA	NA	7	7	1	0	1	1	-	-	+	-	-	-	-	-	NA	+	-	-	-
15736	Z1031A	x			251485036028_4	2.51E+11			81	LumB	*1.5*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	NA	NA	NA	NA	0.011	0.011		NA	NA	Responder	NA	NA	4	4	NA	0	1	0	-	-	-	-	-	-	-	-	-	-	-	-	-
15750	Z1031A			x	251485035336_3	NA			53	LumB	*2.3*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.095	NA	NA	0.006	0.006	-	0.089	-0.93684	Responder	NA	NA	4	4	-2	3	0	1	-	-	-	-	-	-	-	+	NA	+	-	-	-
15757	Z1031A		x		251485053312_4	2.51E+11	x	nodal status unknown	80	LumB	*2.2*	NA	1~2	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.144	NA	NA	0.03	0.03	-	0.114	-0.79167	Responder	NA	NA	8	8	0	NA	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15760	Z1031A	x			251485036593_4	2.51E+11			61	LumB	*8*	1	3~4	1	NEGATIVE	DUCTAL	III	III	II/III	7	0.127	NA	NA	0.186	0.186		0.059	0.464567	NonResponder	NA	NA	7	7	0	7	0	1	+	-	-	-	-	-	-	-	-	-	-	-	+
15765	Z1031A		x		251485026043_3	NA			60	LumA	*1.5*	1	1~2	1	POSITIVE	DUCTAL	II	I/II	II/III	8	0.276	NA	NA	0.031	0.031	-	0.245	-0.88768	Responder	NA	NA	3	3	-5	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15770	Z1031A		x		251485028411_1	2.51E+11	x	nodal status unknown	64	LumA	*2.1*	NA	1~2	NA	POSITIVE	DUCTAL	I	I/II	I	6	0.087	NA	NA	0.003	0.003	-	0.084	-0.96552	Responder	NA	NA	8	8	2	NA	NA	0	NA	NA	NA	-	-	NA	-	+	NA	-	NA	NA	-
15776	Z1031A		x		251485036870_2	2.51E+11	x		68	LumA	*4*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.153	NA	NA	0.046	0.046	-	0.107	-0.69935	Responder	NA	NA	5	5	-3	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15797	Z1031A		x		251485028411_3	2.51E+11	x		75	LumA	*5.4*	0	3~4	0	NEGATIVE	LOBULAR	II	I/II	II/III	7	0.113	NA	NA	0.012	0.012	-	0.101	-0.89381	Responder	NA	NA	5	5	-2	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15812	Z1031A			x	251485042986_3	NA		max tumor dim unknown	54	LumB	*NA*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.436	NA	NA	0.098	0.098	-	0.338	-0.77523	Responder	NA	NA	7	7	1	4	0	NA	-	-	+	-	-	-	-	-	NA	+	-	-	-
15816	Z1031A		x		251485033252_1	2.51E+11	x		72	LumA	*1.5*	0	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	7	0.271	NA	NA	0.037	0.037	-	0.234	-0.86347	Responder	NA	NA	7	7	0	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15829	Z1031A		x		251485036832_3	2.51E+11	x		59	LumA	*2.5*	1	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	7	0.073	NA	NA	0.035	0.035	-	0.038	-0.52055	Responder	NA	NA	6	6	-1	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15830	Z1031A		x		251485033252_3	2.51E+11	x		55	LumB	*5*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	5	0.074	NA	NA	0.021	0.021	-	0.053	-0.71622	Responder	NA	NA	4	4	-1	3	0	1	NA	NA	NA	-	+	NA	-	-	NA	-	NA	NA	-
15832	Z1031A		x		251485036871_4	2.51E+11	x		71	LumB	*1.7*	1	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.051	NA	NA	0.039	0.039	-	0.012	-0.23529	Responder	NA	NA	8	8	0	4	0	1	NA	NA	NA	+	-	NA	-	-	NA	+	NA	NA	-
15835	Z1031A		x		251485036832_2	NA			76	LumB	*3.4*	0	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	6	0.581	NA	NA	0.021	0.021		-0.56	-0.96386	Responder	NA	NA	5	5	-1	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15838	Z1031A		x		251485033253_1	2.51E+11	x		56	LumB	*1.7*	1	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	7	0.334	NA	NA	0.005	0.005	-	0.329	-0.98503	Responder	NA	NA	5	5	-2	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-

15840	Z1031A			x		251485033253_3	NA			70	LumB	*3.1*		1	1~2		1	NEGATIVE	DUCTAL	III	III	II/III	7	0.268	NA	NA	0	0	-0.268	-1	Responder	NA	NA	7	7	0	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15858	Z1031A		x	x		251485054660_2	2.51E+11			56	LumA	*2.5*		1	1~2		1	POSITIVE	LOBULAR	I	I/II	I	7	0.049	NA	NA	0.003	0.003	-0.046	-0.93878	Responder	NA	NA	7	7	0	3	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
15866	Z1031A				x	251485054608_1	2.51E+11	x		66	LumB	*1.5*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.153	NA	NA	0.035	0.035	-0.118	-0.77124	Responder	NA	NA	7	7	1	1	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	+
15867	Z1031A			x		251485034221_3	2.51E+11	x		62	LumA	*1.2*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.062	NA	NA	0.039	0.039	-0.023	-0.37097	Responder	NA	NA	NA	NA	NA	NA	0	0	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15868	Z1031A			x		251485054558_4	NA			86	LumB	*1.7*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.434	NA	NA	0.081	0.081	-0.353	-0.81336	Responder	NA	NA	8	8	0	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	+
15870	Z1031A			x		251485036832_1	2.51E+11	x		64	LumB	*1.3*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	0	0.061	NA	NA	0.15	0.15	0.089	1.459016	NonResponder	NA	NA	7	7	7	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15879	Z1031A			x		251485036831_3	2.51E+11	x		76	LumB	*6.3*		1	3~4		1	NEGATIVE	DUCTAL	III	III	II/III	8	0.257	NA	NA	0.005	0.005	-0.252	-0.98054	Responder	NA	NA	7	7	-1	6	0	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15880	Z1031A			x		251485042959_3	NA			75	LumB	*4*		0	1~2		0	NEGATIVE	LOBULAR	II	I/II	II/III	NA	NA	NA	NA	0.019	0.019	NA	NA	Responder	NA	NA	3	3	NA	0	1	0	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
15882	Z1031A			x		251485054662_1	2.51E+11	x		84	LumB	*1.8*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.395	NA	NA	0.153	0.153	-0.242	-0.61266	NonResponder	NA	NA	8	8	0	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15892	Z1031A			x		251485035337_3	2.51E+11	x		65	LumB	*2.4*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	5	0.144	NA	NA	0.246	0.246	0.102	0.708333	NonResponder	NA	NA	5	5	0	5	0	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15894	Z1031A			x		251485034013_1	2.51E+11	x		64	LumA	*1.7*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.059	NA	NA	0	0	-0.059	-1	Responder	NA	NA	8	8	0	0	1	1	NA	NA	NA	-	-	NA	-	+	NA	+	NA	NA	-
15897	Z1031A			x		251485036831_1	NA			62	LumA	*8*		1	3~4		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.123	NA	NA	0.121	0.121	-0.002	-0.01626	NonResponder	NA	NA	7	7	-1	7	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15899	Z1031A				x	251485054661_1	NA			84	LumB	*2.5*		0	1~2		0	NEGATIVE	DUCTAL	I	I/II	I	8	0.256	NA	NA	0.036	0.036	-0.22	-0.85938	Responder	NA	NA	4	4	-4	1	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
15901	Z1031A		x	x		251485042140_3	2.51E+11			81	LumB	*7*		1	3~4		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.214	NA	NA	0.04	0.04	-0.174	-0.81308	Responder	NA	NA	6	6	-2	7	0	0	-	-	-	-	-	-	-	-	-	+	-	-	-
15906	Z1031A				x	251485056531_2	NA			58	LumB	*2.1*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	2	0.172	NA	NA	0.073	0.073	-0.099	-0.57558	Responder	NA	NA	3	3	1	4	0	1	-	-	-	-	-	-	-	+	NA	+	-	-	-
15910	Z1031A	x				251485038540_1	NA			66	LumB	*2.3*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.63	NA	NA	0.178	0.178	-0.452	-0.71746	NonResponder	NA	NA	5	5	-1	4	0	1	-	-	-	-	-	+	-	-	-	+	-	-	+
15913	Z1031A			x		251485034016_3	2.51E+11	x		86	LumB	*1.6*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.274	NA	NA	0.031	0.031	-0.243	-0.88686	Responder	NA	NA	8	8	0	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15917	Z1031A	x				251485042960_1	NA			66	LumA	*1.8*		0	1~2		0	NEGATIVE	DUCTAL	I	I/II	I	8	0.076	NA	NA	0.008	0.008	-0.068	-0.89474	Responder	NA	NA	8	8	0	0	1	1	-	-	-	-	-	-	-	-	-	+	-	-	-
15919	Z1031A			x		251485035338_1	NA			72	LumB	*1.8*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	5	0.376	NA	NA	0.432	0.432	0.056	0.148936	NonResponder	NA	NA	7	7	2	5	0	1	NA	NA	NA	-	-	NA	-	+	NA	-	NA	NA	-
15921	Z1031A				x	251485033452_3	2.51E+11	x		78	LumB	*3.1*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.062	NA	NA	0.0271	0.027	-0.035	-0.56452	Responder	NA	NA	8	8	2	1	0	1	-	-	-	-	-	-	-	+	NA	+	-	-	-
15931	Z1031A			x		251485036029_1	2.51E+11	x		79	LumB	*2.2*	NA		1~2	NA		POSITIVE	DUCTAL	II	I/II	II/III	7	0.295	NA	NA	0	0	-0.295	-1	Responder	NA	NA	6	6	-1	NA	NA	0	NA	NA	NA	-	+	NA	-	-	NA	-	NA	NA	-
15945	Z1031A	x				251485033453_3	NA			55	LumB	*4*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.412	NA	NA	0.008	0.008	-0.404	-0.98058	Responder	NA	NA	6	6	-2	3	0	1	-	-	-	-	-	-	-	-	-	-	+	-	-
15950	Z1031A			x		251485053312_3	2.51E+11	x		53	LumA	*0.1*		0	1~2		0	NEGATIVE	DUCTAL	I	I/II	I	8	0.152	NA	NA	0	0	-0.152	-1	Responder	NA	NA	7	7	-1	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
15952	Z1031A		x		x	251485054613_4	2.51E+11			62	LumB	*1.5*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.385	NA	NA	0.336	0.336	-0.049	-0.12727	NonResponder	NA	NA	6	6	-2	5	0	NA	-	-	-	-	-	-	-	-	-	-	-	-	-
15953	Z1031A	x				251485054661_4	NA			76	LumB	*4*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.417	NA	NA	0.192	0.192	-0.225	-0.53957	NonResponder	NA	NA	4	4	-2	4	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
15968	Z1031A			x		251485053312_1	NA			66	LumB	*2*		1	1~2		1	NA	DUCTAL	II	I/II	II/III	6	0.241	NA	NA	0.038	0.038	-0.203	-0.84232	Responder	NA	NA	5	5	-1	4	0	0	NA	NA	NA	-	+	NA	-	-	NA	-	NA	NA	-
15970	Z1031A	x				251485036029_3	2.51E+11		nodal status unknown	56	LumB	*2.6*	NA		1~2	NA		NEGATIVE	DUCTAL	II	I/II	II/III	6	0.76	NA	NA	0.308	0.308	-0.452	-0.59474	NonResponder	NA	NA	4	4	-2	NA	0	1	-	-	-	-	-	-	-	-	-	+	-	-	+

15976	Z1031A		x	x		251485042144_3	NA			58	LumA	*1.8*	1	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.038	NA	NA	0.025	0.025	-0.013	-0.34211	Responder	NA	NA	7	7	-1	3	0	1	-	-	-	-	-	-	-	-	-	+	-	-	-
15977	Z1031A			x		251485052905_3	2.51E+11	x		82	LumA	*5.5*	1	3~4	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.158	NA	NA	0.0271	0.027	-0.131	-0.82911	Responder	NA	NA	5	5	-2	7	0	0	NA	NA	NA	-	-	NA	-	+	NA	+	NA	NA	-
15980	Z1031A		x		x	251485053318_4	NA			61	LumA	*2.3*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.37	NA	NA	0.488	0.488	0.118	0.318919	NonResponder	NA	NA	8	8	0	5	0	1	-	-	-	-	+	-	-	-	-	-	-	-	-
15984	Z1031A	x				251485052905_2	2.51E+11			83	LumA	*NA*	NA	1~2	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.051	NA	NA	0.005	0.005	-0.046	-0.90196	Responder	NA	NA	8	8	0	NA	NA	0	-	-	-	-	-	-	-	+	-	+	-	-	-
15985	Z1031A	x				251485053318_1	2.51E+11		nodal status unknown	64	LumB	*1*	NA	1~2	NA	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.489	NA	NA	0.183	0.183	-0.306	-0.62577	NonResponder	NA	NA	5	5	-2	NA	0	1	-	-	-	-	-	-	-	-	-	-	-	-	+
15990	Z1031A	x				251485038016_3	2.51E+11			68	LumB	*1.5*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.636	NA	NA	0.056	0.056	-0.58	-0.91195	Responder	NA	NA	NA	NA	NA	NA	0	0	-	-	-	-	-	-	-	-	-	+	-	-	-
15991	Z1031A	x				251485034016_1	NA			62	LumB	*2.8*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.217	NA	NA	0.024	0.024	-0.193	-0.8894	Responder	NA	NA	8	8	0	3	0	1	-	-	-	-	-	-	+	-	+	+	-	-	-
15995	Z1031A			x		251485036594_1	2.51E+11	x		74	LumA	*1.5*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.052	NA	NA	0.012	0.012	-0.04	-0.76923	Responder	NA	NA	6	6	0	0	1	0	NA	NA	NA	-	-	NA	-	+	NA	+	NA	NA	-
16002	Z1031A			x		251485036869_3	2.51E+11	x		82	LumB	*4*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.533	NA	NA	0.328	0.328	-0.205	-0.38462	NonResponder	NA	NA	5	5	-2	2	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	+
16004	Z1031A				x	251485036869_2	2.51E+11	x		76	LumA	*2.5*	0	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	5	0.083	NA	NA	0.028	0.028	-0.055	-0.66265	Responder	NA	NA	8	8	3	1	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
16007	Z1031A		x	x		251485038016_2	2.51E+11			59	LumB	*NA*	0	1~2	0	POSITIVE	DUCTAL	I	I/II	I	7	0.496	NA	NA	0.005	0.005	-0.491	-0.98992	Responder	NA	NA	7	7	0	0	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-
16016	Z1031A			x		251485036594_3	2.51E+11	x		81	LumB	*4.1*	0	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.232	NA	NA	0.01	0.01	-0.222	-0.9569	Responder	NA	NA	6	6	-2	0	1	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16024	Z1031A	x				251485036869_1	2.51E+11			51	LumB	*2.6*	0	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	7	0.645	NA	NA	0.081	0.081	-0.564	-0.87442	Responder	NA	NA	8	8	1	1	0	1	-	-	-	-	-	-	-	-	-	+	-	-	+
16025	Z1031A			x		251485036597_1	2.51E+11	x		71	LumB	*2.5*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	6	0.362	NA	NA	0.265	0.265	-0.097	-0.26796	NonResponder	NA	NA	7	7	1	5	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16031	Z1031A			x		251485038018_1	2.51E+11	x		55	LumB	*2.3*	0	1~2	0	POSITIVE	DUCTAL	II	I/II	II/III	5	0.217	NA	NA	0.011	0.011	-0.206	-0.94931	Responder	NA	NA	7	7	2	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16035	Z1031A			x		251485036833_4	2.51E+11	x		84	LumB	*2.8*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.26	NA	NA	0.418	0.418	0.158	0.607692	NonResponder	NA	NA	0	0	-7	5	0	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16040	Z1031A				x	251485036833_3	NA			59	LumA	*2.8*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.057	NA	NA	0.234	0.234	0.177	3.105263	NonResponder	NA	NA	8	8	1	5	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	+
16041	Z1031A	x				251485036596_1	2.51E+11			57	LumB	*2.3*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.492	NA	NA	0.035	0.035	-0.457	-0.92886	Responder	NA	NA	4	4	-2	4	0	1	-	-	-	-	-	-	-	-	-	+	-	-	-
16042	Z1031A			x		251485036595_3	2.51E+11	x		60	LumA	*1.9*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.083	NA	NA	0.016	0.016	-0.067	-0.80723	Responder	NA	NA	5	5	-1	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16043	Z1031A		x		x	251485038540_4	2.51E+11			68	LumB	*4.8*	0	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	6	0.2	NA	NA	0.053	0.053	-0.147	-0.735	Responder	NA	NA	4	4	-2	1	0	1	-	-	-	-	-	-	-	-	-	-	-	-	+
16052	Z1031A			x		251485042144_4	2.51E+11	x		56	LumB	*1.7*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	NA	NA	NA	NA	0.018	0.018	NA	NA	Responder	NA	NA	8	8	NA	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16054	Z1031A				x	251485042139_2	2.51E+11	x		60	LumB	*3.6*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.348	NA	NA	0.009	0.009	-0.339	-0.97414	Responder	NA	NA	6	6	-1	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
16062	Z1031A	x				251485036595_1	2.51E+11			74	LumB	*4*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III	6	0.487	NA	NA	0.224	0.224	-0.263	-0.54004	NonResponder	NA	NA	2	2	-4	8	0	0	-	-	-	-	-	-	-	-	-	-	-	-	+
16063	Z1031A				x	251485042971_1	2.51E+11	x		70	LumA	*10*	1	3~4	1	NEGATIVE	LOBULAR	I	I/II	I	7	0.027	NA	NA	0.006	0.006	-0.021	-0.77778	Responder	NA	NA	3	3	-4	6	0	NA	-	-	-	-	-	-	-	+	NA	+	-	-	-
16064	Z1031A			x		251485036857_1	2.51E+11	x		66	LumA	*1.8*	0	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	7	0.115	NA	NA	0	0	-0.115	-1	Responder	NA	NA	7	7	0	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16067	Z1031A			x		251485036870_4	2.51E+11	x		55	LumB	*2.5*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.732	NA	NA	0.004	0.004	-0.728	-0.99454	Responder	NA	NA	7	7	0	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16069	Z1031A			x		251485036857_4	2.51E+11	x		53	LumA	*1.5*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	5	0.023	NA	NA	0.224	0.224	0.201	8.73913	NonResponder	NA	NA	4	4	-1	2	0	1	NA	NA	NA	-	-	NA	+	-	NA	+	NA	NA	-

16070	Z1031A			x		251485037835_4	2.51E+11	x		55	LumA	*4.6*		1	1~2		1	POSITIVE	DUCTAL	II	I/II	II/III	NA	NA	NA	NA	0.217	0.217	NA	NA	NonResponder	NA	NA	4	4	NA	5	0	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16074	Z1031A		x	x		251485052897_1	2.51E+11			54	LumA	*6.5*		1	3~4		1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.265	NA	NA	0.002	0.002	-0.263	-0.99245	Responder	NA	NA	8	8	1	6	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
16082	Z1031A				x	251485038519_1	NA			74	LumB	*6.6*		0	3~4		0	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.12	NA	NA	0.022	0.022	-0.098	-0.81667	Responder	NA	NA	2	2	-4	6	0	NA	-	-	-	-	-	-	-	+	NA	+	-	-	-
16084	Z1031A			x		251485036856_1	2.51E+11	x		74	LumB	*1.9*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.54	NA	NA	0.24	0.24	-0.3	-0.55556	NonResponder	NA	NA	5	5	-2	2	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16091	Z1031A			x		251485040708_4	NA			63	LumB	*1.7*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	NA	NA	NA	NA	0.229	0.229	NA	NA	NonResponder	NA	NA	5	5	NA	2	0	1	NA	NA	NA	-	-	NA	+	-	NA	-	NA	NA	+
16092	Z1031A			x		251485036856_3	2.51E+11	x		69	LumB	*1.6*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.492	NA	NA	0.034	0.034	-0.458	-0.93089	Responder	NA	NA	7	7	0	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	+
16093	Z1031A			x		251485042139_1	2.51E+11	x		69	LumA	*2.2*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.209	NA	NA	0.003	0.003	-0.206	-0.98565	Responder	NA	NA	5	5	-3	0	1	1	NA	NA	NA	-	+	NA	-	-	NA	-	NA	NA	-
16099	Z1031A			x		251485038002_3	2.51E+11	x		59	LumA	*3.5*		0	1~2		0	NEGATIVE	LOBULAR	II	I/II	II/III	7	0.228	NA	NA	0.08	0.08	-0.148	-0.64912	Responder	NA	NA	6	6	-1	1	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16105	Z1031A			x		251485054612_3	2.51E+11	x		81	LumB	*3.2*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.222	NA	NA	0.018	0.018	-0.204	-0.91892	Responder	NA	NA	7	7	1	3	0	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16107	Z1031A	x				251485038018_3	2.51E+11			78	LumA	*5.2*		0	3~4		0	NEGATIVE	LOBULAR	I	I/II	I	4	0.195	NA	NA	0.104	0.104	-0.091	-0.46667	NonResponder	NA	NA	5	5	1	4	0	1	-	-	-	-	-	-	+	-	-	+	-	-	-
16111	Z1031A	x				251485038519_3	2.51E+11		nodal status unknown	54	LumA	*1*	NA		1~2	NA		NEGATIVE	DUCTAL	I	I/II	I	7	0.1	NA	NA	0	0	-0.1	-1	Responder	NA	NA	6	6	-1	NA	NA	1	-	-	-	-	+	-	-	-	-	-	-	-	-
16127	Z1031A			x		251485038500_1	2.51E+11	x		60	LumA	*1.1*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.119	NA	NA	0.092	0.092	-0.027	-0.22689	Responder	NA	NA	8	8	1	1	0	0	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16135	Z1031A				x	251485042961_1	2.51E+11	x		57	LumA	*3.2*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.233	NA	NA	0.051	0.051	-0.182	-0.78112	Responder	NA	NA	8	8	1	1	0	NA	-	+	-	-	-	-	-	-	NA	+	+	-	+
16136	Z1031A			x		251485038006_2	2.51E+11	x		63	LumB	*2.2*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	5	0.123	NA	NA	0.011	0.011	-0.112	-0.91057	Responder	NA	NA	5	5	0	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16140	Z1031A			x		251485038499_1	2.51E+11	x		67	LumB	*1.5*		0	1~2		0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.517	NA	NA	0.017	0.017	-0.5	-0.96712	Responder	NA	NA	6	6	-2	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16148	Z1031A		x		x	251485038501_4	NA			55	LumB	*15*		0	3~4		0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.154	NA	NA	0.077	0.077	-0.077	-0.5	Responder	NA	NA	7	7	-1	4	0	1	-	-	+	-	-	-	-	-	-	+	-	-	-
16165	Z1031A			x		251485038499_3	2.51E+11	x		53	LumB	*1.8*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.359	NA	NA	0.038	0.038	-0.321	-0.89415	Responder	NA	NA	8	8	0	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16170	Z1031A		x	x		251485038004_1	2.51E+11			62	LumB	*1.3*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.177	NA	NA	0.009	0.009	-0.168	-0.94915	Responder	NA	NA	4	4	-3	3	0	1	-	-	-	-	-	-	-	-	-	+	-	-	-
16171	Z1031A		x	x		251485038016_1	2.51E+11			62	LumB	*0.9*		0	1~2		0	POSITIVE	LOBULAR	II	I/II	II/III	6	0.424	NA	NA	0.103	0.103	-0.321	-0.75708	NonResponder	NA	NA	8	8	2	1	0	1	-	-	+	-	-	-	-	+	-	-	-	+	-
16178	Z1031A	x				251485042985_1	2.51E+11			78	LumB	*3.3*		0	1~2		0	NEGATIVE	DUCTAL	III	III	II/III	8	0.162	NA	NA	0.471	0.471	0.309	1.907407	NonResponder	NA	NA	2	2	-6	5	0	1	-	-	+	-	-	-	-	-	-	-	-	-	-
16180	Z1031A	x				251485042955_3	NA		nodal status unknown	52	LumA	*5*	NA		1~2	NA		NEGATIVE	DUCTAL	I	I/II	I	7	0.006	NA	0	0.006	0.006	0	0	Responder	NA	NA	7	7	0	NA	NA	1	-	-	-	-	-	-	-	-	-	+	-	-	-
16185	Z1031A				x	251485038002_2	NA			75	LumA	*0.7*		1	1~2		1	POSITIVE	DUCTAL	II	I/II	II/III	8	0.005	NA	NA	0.819	0.819	0.814	162.8	NonResponder	NA	NA	3	3	-5	6	0	1	-	-	-	-	+	-	-	-	NA	+	-	-	-
16187	Z1031A	x				251485038501_2	2.51E+11			68	LumA	*3*		0	1~2		0	NEGATIVE	DUCTAL	I	I/II	I	7	0.053	NA	NA	0.193	0.193	0.14	2.641509	NonResponder	NA	NA	8	8	1	1	0	0	-	-	-	-	-	-	-	+	-	-	-	-	-
16189	Z1031A				x	251485054662_4	NA			61	LumB	*6*		0	3~4		0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.187	NA	NA	0.009	0.009	-0.178	-0.95187	Responder	NA	NA	7	7	-1	3	0	1	-	-	-	-	-	+	-	-	NA	+	-	+	-
16202	Z1031A		x		x	251485054610_1	NA			90	LumB	*1.2*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.327	NA	NA	0.254	0.254	-0.073	-0.22324	NonResponder	NA	NA	7	7	-1	5	0	1	-	-	-	-	-	-	-	-	-	+	-	-	+
16208	Z1031A				x	251485042964_3	NA			59	LumB	*3.6*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.145	NA	NA	0.006	0.006	-0.139	-0.95862	Responder	NA	NA	7	7	0	3	0	NA	-	-	-	-	+	-	-	-	NA	-	-	-	-
16216	Z1031A		x			251485054610_4	2.51E+11			76	LumA	*0*		1	1~2		1	NEGATIVE	DUCTAL	II	I/II	II/III	6	0.05	NA	NA	0.042	0.042	-0.008	-0.16	Responder	NA	NA	5	5	-1	4	0	NA	-	-	-	-	-	-	-	-	-	-	-	-	-

1622 Z1031 0 A	x				251485050627_ 4	NA		79	LumA	*0*	1~ 0 2	NEGATIV 0 E	DUCTAL	I	I/II	I	7	0.11 9	NA	NA	0.123	0.12 3	0.004	0.03361 3	NonResponde r	N A	N A	7	7	0	1	0	1	-	-	-	-	-	-	-	-	-	-	-	-	-
1622 Z1031 4 A			x		251485042964_ 1	2.51E+1 1	x	66	LumB	*2.3*	1~ 0 2	NEGATIV 0 E	DUCTAL	I	I/II	I	7	0.13 6	NA	NA	0.03	0.03	- 0.106	-0.77941	Responder	N A	N A	7	7	0	1	0	0	N A	N A	N A	-	+	N A	-	-	N A	-	N A	N A	-
1622 Z1031 7 A	x				251485042144_ 1	2.51E+1 1		63	LumB	*1.8*	1~ 1 2	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	7	0.32	NA	NA	0.019	0.01 9	- 0.301	-0.94063	Responder	N A	N A	8	8	1	3	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
1623 Z1031 7 A		x		x	251485054662_ 2	2.51E+1 1		73	LumA	*1.9*	1~ 1 2	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	7	0.11 2	NA	NA	0.029	0.02 9	- 0.083	-0.74107	Responder	N A	N A	4	4	-3	4	0	1	-	-	-	-	-	-	-	+	-	+	-	-	-
1625 Z1031 2 A	x				251485042962_ 1	2.51E+1 1		83	LumB	*5*	1~ 1 2	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	7	0.23 8	NA	NA	0.01	0.01	- 0.228	-0.95798	Responder	N A	N A	7	7	0	3	0	0	-	+	-	-	-	-	-	-	-	+	-	-	-
1625 Z1031 6 A			x		251485042963_ 3	2.51E+1 1	x	53	LumA	*2.9*	1~ 1 2	NEGATIV 1 E	LOBULA R	II	I/II	II/II I	7	0.13 3	NA	NA	0.55	0.55	0.417	3.13533 8	NonResponde r	N A	N A	5	5	-2	6	0	1	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	+
1627 Z1031 0 A			x		251485040708_ 1	2.51E+1 1	x	81	LumB	*2.1*	1~ 1 2	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	8	0.43 6	NA	NA	0.001	0.00 1	- 0.435	-0.99771	Responder	N A	N A	8	8	0	3	0	0	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-
1627 Z1031 7 A	x				251485054557_ 3	2.51E+1 1		54	LumB	*2.2*	1~ 1 2	NEGATIV 1 E	DUCTAL	III	III	II/II I	5	0.50 1	NA	NA	0.377	0.37 7	- 0.124	-0.2475	NonResponde r	N A	N A	5	5	0	5	0	1	+	-	-	-	-	-	-	-	-	+	+	-	+
1629 Z1031 0 A			x		251485042139_ 3	2.51E+1 1	x	56	LumB	*2*	1~ 1 2	1 NA	DUCTAL	III	III	II/II I	7	0.44	NA	NA	0.022	0.02 2	- 0.418	-0.95	Responder	N A	N A	8	8	1	3	0	1	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-
1629 Z1031 2 A			x		251485050625_ 3	2.51E+1 1	x	63	LumB	*1.7*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	7	0.36	NA	NA	0.039	0.03 9	- 0.321	-0.89167	Responder	N A	N A	7	7	0	1	0	1	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-
1629 Z1031 5 A			x		251485042140_ 1	2.51E+1 1	x	83	LumA	*1.2*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	8	0.52 1	NA	NA	0.005	0.00 5	- 0.516	-0.9904	Responder	N A	N A	8	8	0	0	1	1	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-
1629 Z1031 6 A				x	251485053315_ 2	NA		87	LumA	*3*	1~ 1 2	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	4	0.00 5	NA	NA	0.007	0.00 7	0.002	0.4	Responder	N A	N A	4	4	0	3	0	N A	-	-	+	-	-	-	-	-	N A	-	-	-	-
1630 Z1031 0 A	x				251485053319_ 1	NA		79	LumB	*2.1*	1~ 1 2	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	6	0.35 6	NA	NA	0.124	0.12 4	- 0.232	-0.65169	NonResponde r	N A	N A	5	5	-1	4	0	1	+	-	+	-	-	-	-	-	-	+	-	-	-
1631 Z1031 3 A				x	251485053321_ 1	2.51E+1 1	x	60	LumA	*1.6*	1~ 1 2	NEGATIV 1 E	LOBULA R	II	I/II	II/II I	6	0.00 7	NA	NA	0	0	- 0.007	-1	Responder	N A	N A	7	7	1	3	0	1	-	-	+	-	-	-	-	-	N A	-	-	-	-
1631 Z1031 4 A	x				251485052895_ 4	2.51E+1 1		51	LumB	*2*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	7	0.17 4	NA	NA	0.155	0.15 5	- 0.019	-0.1092	NonResponde r	N A	N A	7	7	0	1	0	1	-	-	-	-	-	-	-	-	-	+	-	+	-
1631 Z1031 5 A		x		x	251485053315_ 1	NA		63	LumB	*5.5*	3~ 1 4	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	7	0.16 3	NA	NA	0.013	0.01 3	-0.15	-0.92025	Responder	N A	N A	4	4	-3	6	0	1	-	-	-	-	-	-	-	-	-	+	-	-	-
1631 Z1031 9 A	x				251485050626_ 1	2.51E+1 1		85	LumB	*4.5*	1~ 1 2	NEGATIV 1 E	DUCTAL	I	I/II	I	8	0.12 5	NA	NA	0	0	- 0.125	-1	Responder	N A	N A	7	7	-1	3	0	1	-	-	-	+	+	-	-	+	-	+	-	+	-
1632 Z1031 4 A			x		251485050626_ 3	NA		61	LumB	*2*	1~ 1 2	NEGATIV 1 E	DUCTAL	II	I/II	II/II I	7	0.19 5	NA	NA	0.086	0.08 6	- 0.109	-0.55897	Responder	N A	N A	8	8	1	4	0	1	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-
1632 Z1031 6 A		x		x	251485052904_ 2	2.51E+1 1		54	LumA	*4*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	8	0.26 1	NA	NA	0	0	- 0.261	-1	Responder	N A	N A	5	5	-3	0	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-
1634 Z1031 2 A				x	251485055399_ 4	2.51E+1 1	x	63	LumA	*3.5*	1~ 1 2	NEGATIV 1 E	LOBULA R	III	III	II/II I	5	0.01 6	NA	NA	0.012	0.01 2	- 0.004	-0.25	Responder	N A	N A	8	8	3	3	0	1	-	-	-	-	-	-	-	-	N A	+	-	-	-
1634 Z1031 7 A	x				251485050627_ 1	NA		75	LumB	*1.5*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	8	0.10 2	NA	NA	0.048	0.04 8	- 0.054	-0.52941	Responder	N A	N A	8	8	0	1	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
1635 Z1031 0 A	x				251485052895_ 2	2.51E+1 1		52	LumB	*0.3*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	5	0.01 5	NA	NA	0.072	0.07 2	0.057	3.8	Responder	N A	N A	7	7	2	1	0	1	-	-	-	-	-	-	-	-	-	-	-	-	-
1635 Z1031 7 A	x				251485052850_ 3	NA		71	LumB	*4*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	7	0.10 1	NA	NA	0.07	0.07	- 0.031	-0.30693	Responder	N A	N A	5	5	-2	1	0	1	-	-	-	-	-	-	-	-	-	-	-	-	-
1636 Z1031 4 A		x	x		251485052897_ 2	NA		55	LumB	*1.8*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	8	0.27	NA	NA	0.045	0.04 5	- 0.225	-0.83333	Responder	N A	N A	4	4	-4	1	0	1	-	-	-	-	-	-	-	-	-	+	-	-	-
1636 Z1031 5 A			x		251485052905_ 1	2.51E+1 1	x	65	LumA	*3.6*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	8	0.40 6	NA	NA	0.097	0.09 7	- 0.309	-0.76108	Responder	N A	N A	7	7	-1	1	0	0	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-
1636 Z1031 8 A			x		251485052897_ 3	2.51E+1 1	x	60	LumA	*1.5*	1~ 0 2	NEGATIV 0 E	LOBULA R	I	I/II	I	6	0.27 7	NA	NA	0.013	0.01 3	- 0.264	-0.95307	Responder	N A	N A	4	4	-2	0	1	1	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-
1637 Z1031 6 A		x	x		251485055399_ 1	NA		55	LumB	*1.8*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	8	0.51 6	NA	NA	0.142	0.14 2	- 0.374	-0.72481	NonResponde r	N A	N A	5	5	-3	1	0	1	-	-	-	-	+	-	-	-	-	-	-	-	-
1638 Z1031 5 A			x		251485053322_ 4	NA		68	LumA	*1*	1~ 0 2	NEGATIV 0 E	DUCTAL	II	I/II	II/II I	8	0.18 3	NA	NA	0.027	0.02 7	- 0.156	-0.85246	Responder	N A	N A	6	6	-2	0	1	0	N A	N A	N A	-	-	N A	-	-	N A	-	N A	N A	-

16392	Z1031A			x		251485050627_2	2.51E+11	x		84	LumB	*3.7*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III		8	0.527	NA	NA	0.223	0.223	- 0.304	-0.57685	NonResponder	NA	NA	8	8	0	5	0	0	NA	NA	NA	-	-	NA	-	+	NA	-	NA	NA	+
16398	Z1031A		x	x		251485054557_4	2.51E+11		max tumor dim unknown	67	LumB	*NA*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.112	NA	NA	0.064	0.064	- 0.048	-0.42857	Responder	NA	NA	8	8	0	1	0	1	-	-	-	-	-	-	-	-	-	-	-	-	-
16402	Z1031A			x		251485052903_2	2.51E+11	x		73	LumB	*2.4*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.323	NA	NA	0.106	0.106	- 0.217	-0.67183	NonResponder	NA	NA	8	8	0	4	0	1	NA	NA	NA	-	-	NA	+	-	NA	+	NA	NA	-
16408	Z1031A	x				251485054537_1	NA			66	LumA	*3.8*	1	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III		6	0.022	NA	NA	0.346	0.346	0.324	14.72727	NonResponder	NA	NA	6	6	0	5	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
16411	Z1031A			x		251485054537_3	NA			61	LumA	*1.9*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III		7	0.107	NA	NA	0.024	0.024	- 0.083	-0.7757	Responder	NA	NA	8	8	1	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16431	Z1031A	x				251485053322_1	2.51E+11			74	LumB	*1.9*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	NA		0.081	NA	NA	0.022	0.022	- 0.059	-0.7284	Responder	NA	NA	8	8	NA	0	1	1	+	+	-	-	-	-	-	-	-	-	-	-	-
16439	Z1031A			x		251485054608_2	2.51E+11	x		59	LumB	*3.5*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.446	NA	NA	0	0	- 0.446	-1	Responder	NA	NA	7	7	-1	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16441	Z1031A			x		251485052896_1	NA			55	LumB	*2.3*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III		5	0.102	NA	NA	0.007	0.007	- 0.095	-0.93137	Responder	NA	NA	8	8	3	3	0	1	NA	NA	NA	+	-	NA	-	-	NA	-	NA	NA	-
16442	Z1031A			x		251485054556_2	2.51E+11	x		59	LumA	*15*	1	3~4	1	NEGATIVE	LOBULAR	II	I/II	II/III		8	0.289	NA	NA	0.032	0.032	- 0.257	-0.88927	Responder	NA	NA	6	6	-2	7	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16450	Z1031A			x		251485054659_4	NA			62	LumA	*4*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		6	0.14	NA	NA	0.031	0.031	- 0.109	-0.77857	Responder	NA	NA	2	2	-4	4	0	1	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16454	Z1031A	x				251485052895_1	2.51E+11			61	LumB	*3*	0	1~2	0	NEGATIVE	DUCTAL	III	III	II/III		4	0.456	NA	NA	0.349	0.349	- 0.107	-0.23465	NonResponder	NA	NA	6	6	2	2	0	1	-	-	-	+	-	-	-	-	-	+	+	-	+
16481	Z1031A	x				251485053314_1	2.51E+11			60	LumB	*2*	0	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III		5	0.256	NA	NA	0.183	0.183	- 0.073	-0.28516	NonResponder	NA	NA	5	5	0	1	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
16486	Z1031A			x		251485054660_3	2.51E+11	x		76	LumA	*2*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.057	NA	NA	0.014	0.014	- 0.043	-0.75439	Responder	NA	NA	8	8	0	0	1	0	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16492	Z1031A			x		251485055400_2	2.51E+11	x		69	LumA	*5*	1	1~2	1	NEGATIVE	LOBULAR	II	I/II	II/III		8	0.064	NA	NA	0	0	- 0.064	-1	Responder	NA	NA	8	8	0	3	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16495	Z1031A			x		251485054609_1	2.51E+11	x		75	LumA	*1.3*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		5	0.02	NA	NA	0.027	0.027	0.007	0.35	Responder	NA	NA	7	7	2	0	1	0	NA	NA	NA	-	-	NA	-	-	NA	+	NA	NA	-
16531	Z1031A			x		251485055266_4	2.51E+11	x	nodal status unknown	71	LumA	*0.6*	NA	1~2	NA	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.076	NA	NA	0.06	0.06	- 0.016	-0.21053	Responder	NA	NA	8	8	0	NA	0	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	-
16539	Z1031A			x		251485055398_1	NA			58	LumB	*1*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		7	0.107	NA	NA	0.014	0.014	- 0.093	-0.86916	Responder	NA	NA	8	8	1	0	1	1	NA	NA	NA	-	-	NA	-	-	NA	-	NA	NA	+
16561	Z1031A			x		251485055265_1	2.51E+11	x		67	LumA	*3.2*	1	1~2	1	NEGATIVE	DUCTAL	I	I/II	I		8	0.062	NA	NA	0.011	0.011	- 0.051	-0.82258	Responder	NA	NA	6	6	-2	3	0	0	NA	NA	NA	-	-	NA	-	+	NA	+	NA	NA	-
16566	Z1031A		x	x		251485055266_1	2.51E+11			58	LumB	*5.1*	1	3~4	1	NEGATIVE	LOBULAR	I	I/II	I		6	NA	NA	NA	0.043	0.043	NA	NA	Responder	NA	NA	7	7	1	7	0	1	-	-	-	-	-	-	-	-	-	-	-	-	+
16579	Z1031A				x	251485055265_4	2.51E+11	x		59	LumA	*4*	1	1~2	1	NEGATIVE	DUCTAL	III	III	II/III		8	0.11	NA	NA	0.006	0.006	- 0.104	-0.94545	Responder	NA	NA	7	7	-1	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
16589	Z1031A	x				251485055264_1	2.51E+11			56	LumA	*1.5*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.077	NA	NA	0.152	0.152	0.075	0.974026	NonResponder	NA	NA	8	8	0	1	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-
16590	Z1031A				x	251485055399_3	2.51E+11	x		72	LumA	*2.8*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.128	NA	NA	0	0	- 0.128	-1	Responder	NA	NA	8	8	0	0	1	1	-	-	+	-	-	-	-	-	NA	+	-	+	-
16598	Z1031A				x	251485055402_2	2.51E+11	x		85	LumB	*3*	0	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III		8	0.23	NA	NA	0.112	0.112	- 0.118	-0.51304	NonResponder	NA	NA	8	8	0	1	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	-
16702	Z1031B				x	251485060459_2	2.51E+11	x		62	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	III	III	II/III		8	0.021	NA	NA	0.007	0.007	- 0.014	-0.66667	Responder	NA	NA	7	7	-1	3	0	1	-	-	-	-	+	-	-	-	NA	-	-	-	-
16727	Z1031B		x		x	251485056231_1	NA			66	LumB	*NA*	NA	1~2	0	POSITIVE	DUCTAL	II	I/II	II/III		7	0.43	NA	NA	0.153	0.153	- 0.277	-0.64419	NonResponder	NA	NA	7	7	0	1	0	1	-	-	-	-	-	-	-	-	-	+	-	-	+
16744	Z1031B				x	251485060427_3	2.51E+11	x		86	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III		8	0.75	0.06	NA	0.025	0.025	- 0.725	-0.96667	Responder	8	NA	7	7	-1	0	1	NA	-	-	-	-	-	-	-	-	NA	-	-	-	+
16745	Z1031B				x	251485069914_1	2.51E+11	x		53	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III		7	0.127	0.01	NA	0.003	0.003	- 0.124	-0.97638	Responder	7	NA	8	8	1	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-

16751	Z1031B			x	251485060457_2	2.51E+11	x		65	LumB	*NA*	NA	1~2	0	POSITIVE	DUCTAL	II	I/II	II/III	8	0.11	0.025	NA	0.004	0.004	-0.106	-0.96364	Responder	8	NA		7	7	-1	0	1	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
16754	Z1031B		x	x	251485055401_4	2.51E+11			59	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.28	0.21	NA	NA	0.21	-0.07	-0.25	NonResponder	8	NA	NA		8	0	NA	NA	NA	-	-	-	-	-	-	-	-	-	-	-	-	-
16757	Z1031B			x	251485062374_3	2.51E+11	x		61	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.16	0.02	NA	0.018	0.018	-0.142	-0.8875	Responder	8	NA		7	7	-1	3	0	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
16779	Z1031B			x	251485060705_1	2.51E+11	x		59	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	0.107	0.015	NA	0.006	0.006	-0.101	-0.94393	Responder	8	NA		7	7	-1	0	1	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
16786	Z1031B		x	x	251485062373_4	NA			69	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	0.02	0.02	NA	0.002	0.002	-0.018	-0.9	Responder	7	NA		7	7	-1	0	1	1	-	-	-	-	-	-	-	+	-	+	-	-	-
16825	Z1031B			x	251485062373_1	2.51E+11	x		62	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.103	0.02	NA	0	0	-0.103	-1	Responder	8	NA		8	8	0	3	0	1	-	-	-	-	-	-	+	-	NA	-	-	-	-
16837	Z1031B		x	x	251485062371_2	2.51E+11			60	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	0.129	0.004	NA	0.006	0.006	-0.123	-0.95349	Responder	7	NA		7	7	-1	0	1	1	-	-	-	-	-	-	-	+	+	+	-	-	-
16846	Z1031B		x	x	251485062371_1	2.51E+11			69	LumB	*NA*	NA	3~4	1	NEGATIVE	LOBULAR	I	I/II	I	8	0.257	0.01	NA	0.003	0.003	-0.254	-0.98833	Responder	8	NA		8	8	0	6	0	1	-	-	+	-	-	-	-	-	+	-	-	-	-
16847	Z1031B		x	x	251485060709_3	2.51E+11			56	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.159	0.003	NA	0	0	-0.159	-1	Responder	8	NA		8	8	0	0	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-
16880	Z1031B			x	251485062371_3	2.51E+11	x		83	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.104	0.03	NA	0.003	0.003	-0.101	-0.97115	Responder	8	NA		8	8	0	0	1	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
16889	Z1031B			x	251485060706_1	2.15E+11	x		64	LumB	*NA*	NA	NA	NA	POSITIVE	LOBULAR	II	I/II	II/III	8	0.45	0.178	NA	NA	0.178	-0.272	-0.60444	NonResponder	8	NA	NA		8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
16895	Z1031B			x	251485062366_2	NA		tumor stage T1 max dim=1.8	78	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.125	0.006	NA	0.003	0.003	-0.122	-0.976	Responder	8	NA		8	8	0	0	1	1	-	-	-	-	-	-	-	-	NA	+	-	-	-
16912	Z1031B		x	x	251485062375_1	2.51E+11			54	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.088	0.015	NA	0.003	0.003	-0.085	-0.96591	Responder	8	NA		8	8	0	3	0	NA	-	-	-	-	+	-	-	-	-	-	-	-	-
16918	Z1031B	x			251485056229_2	NA			55	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	III	III	II/III	7	0.6	0.8	NA	NA	0.8	0.2	0.333333	NonResponder	7	NA	NA		7	0	NA	NA	NA	-	-	-	-	-	-	-	-	-	+	-	-	-
16921	Z1031B			x	251485062367_1	NA			73	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	7	0.3	0.063	NA	0.378	0.378	0.078	0.26	NonResponder	7	7		7	7	0	2	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
16934	Z1031B			x	251485062368_1	NA			53	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.4	0.016	NA	0.003	0.003	-0.397	-0.9925	Responder	8	NA		8	8	1	3	0	1	-	-	-	-	+	-	-	-	NA	-	-	-	-
16947	Z1031B		x	x	251485065726_3	NA			51	LumA	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	6	0.102	0.063	NA	0.004	0.004	-0.098	-0.96078	Responder	7	NA		7	7	1	0	1	1	-	-	+	-	-	-	-	-	-	+	-	-	-
16956	Z1031B			x	251485063742_1	2.51E+11	x	tumor stage T2; max dim=3.0	61	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.229	0.083	NA	0.059	0.059	-0.17	-0.74236	Responder	7	NA		7	7	0	4	0	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
16957	Z1031B			x	251485069957_1	NA			69	LumA	*NA*	NA	3~4	1	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.005	0.011	NA	0.005	0.005	0	0	Responder	8	NA		7	7	-1	6	0	NA	-	-	+	-	-	-	-	-	NA	-	-	-	-
16959	Z1031B			x	251485065618_1	NA			57	LumA	*NA*	NA	1~2	0	NA	DUCTAL	II	I/II	II/III	8	0.108	0.023	NA	0.012	0.012	-0.096	-0.88889	Responder	8	NA		8	8	0	0	1	1	-	-	+	-	-	-	-	-	NA	+	-	-	-
16965	Z1031B			x	251485060458_2	2.51E+11	x		61	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	8	0.7	0.266	NA	0.133	0.133	-0.567	-0.81	NonResponder	8	NA		7	7	-1	1	0	NA	-	-	-	-	-	+	-	-	NA	+	-	-	-
16970	Z1031B			x	251485063743_1	2.51E+11	x		55	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.103	0.06	NA	0.008	0.008	-0.095	-0.92233	Responder	7	NA		7	7	-1	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
16982	Z1031B			x	251485067280_3	NA			55	LumB	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.121	0.005	NA	0.015	0.015	-0.106	-0.87603	Responder	8	NA		8	8	0	0	1	NA	-	-	-	-	-	-	-	-	NA	-	-	-	+
16986	Z1031B			x	251485067277_4	2.51E+11	x		63	LumB	*NA*	NA	NA	NA	POSITIVE	DUCTAL	III	III	II/III	8	0.251	0.186	NA	NA	0.186	-0.065	-0.25896	NonResponder	8	NA	NA		8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
16990	Z1031B			x	251485065620_4	NA			63	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.118	0.034	NA	0.008	0.008	-0.11	-0.9322	Responder	8	NA		7	7	0	3	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
16992	Z1031B			x	251485065619_3	2.51E+11	x		66	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.214	0.101	NA	NA	0.101	-0.113	-0.52804	NonResponder	7	NA	NA		7	-1	NA	0	NA	-	-	-	-	-	+	-	-	NA	+	-	-	-
16993	Z1031B			x	251485065618_3	NA			55	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.133	0.076	NA	0	0	-0.133	-1	Responder	7	NA		8	8	0	0	1	1	+	-	-	-	+	-	-	-	NA	-	-	-	-

16994	Z1031B	x	251485069915_3	NA			55	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.119	0.008	NA	0.004	0.004	-0.115	-0.96639	Responder	7	NA	7	7	-1	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
16998	Z1031B	x	251485067279_1	NA		max dim=5.0	77	LumA	*NA*	NA	3~4	1	NEGATIVE	DUCTAL	III	III	II/III	8	0.136	0.009	NA	0.005	0.005	-0.131	-0.96324	Responder	8	NA	8	8	0	6	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	-
17050	Z1031B	x	251485067255_1	NA			70	LumA	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.094	0.081	NA	0.023	0.023	-0.071	-0.75532	Responder	8	NA	7	7	-1	0	1	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17055	Z1031B	x	251485069957_2	NA			82	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.141	0.042	NA	0.005	0.005	-0.136	-0.96454	Responder	8	NA	8	8	0	3	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17066	Z1031B	x	251485067278_1	NA			47	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	III	III	II/III	8	0.3	0.125	NA	NA	0.125	-0.175	-0.58333	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	+	-	-	NA	-	-	-	-
17070	Z1031B	x	251485069914_3	NA			64	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.089	0.012	NA	0.002	0.002	-0.087	-0.97753	Responder	8	NA	7	7	-1	0	1	1	-	-	-	-	-	-	-	-	NA	+	-	-	-
17123	Z1031B	x	251485070714_2	2.51E+11	x		85	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.262	0.012	NA	0.013	0.013	-0.249	-0.95038	Responder	8	NA	8	8	0	0	1	1	-	-	-	-	+	-	-	-	NA	-	-	-	-
17124	Z1031B	x	251485067309_3	2.51E+11	x		86	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.3	0.02	NA	0	0	-0.3	-1	Responder	8	NA	8	8	0	0	1	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17138	Z1031B	x	251485069956_1	NA			82	LumA	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.169	0.06	NA	0.012	0.012	-0.157	-0.92899	Responder	8	NA	7	7	-1	0	1	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
17143	Z1031B	x	251485067310_1	NA			67	LumB	*NA*	NA	NA	NA	NEGATIVE	LOBULAR	I	I/II	I	7	0.266	0.117	NA	NA	0.117	-0.149	-0.56015	NonResponder	7	NA	NA	7	0	NA	NA	NA	+	+	-	+	-	-	-	-	NA	+	-	-	-
17157	Z1031B	x	251485067310_3	NA			64	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.398	0.274	NA	NA	0.274	-0.124	-0.31156	NonResponder	7	NA	NA	7	-1	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	+
17170	Z1031B	x	251485069956_2	2.51E+11	x		75	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.151	0.027	NA	0.11	0.11	-0.041	-0.27152	NonResponder	8	NA	7	7	-1	4	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17175	Z1031B	x	251485067309_1	NA			69	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	8	0.171	0.012	NA	0	0	-0.171	-1	Responder	8	NA	7	7	-1	0	1	1	-	-	-	-	-	-	-	-	NA	+	-	-	+
17208	Z1031B	x	251485065621_2	2.51E+11	x		68	LumB	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.202	0.023	NA	0.02	0.02	-0.182	-0.90099	Responder	8	NA	7	7	-1	0	1	1	-	-	+	-	-	-	-	-	NA	-	-	-	-
17232	Z1031B	x	251485070307_2	NA			77	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	8	0.166	NA	0.017	0.008	0.008	-0.158	-0.95181	Responder	NA	8	7	7	-1	0	1	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17233	Z1031B	x	251485070306_1	NA			56	LumA	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.019	0.005	NA	0.003	0.003	-0.016	-0.84211	Responder	8	NA	8	8	0	0	1	1	-	-	+	-	-	-	-	-	NA	-	-	-	-
17250	Z1031B	x	251485070234_1	NA			51	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	I	I/II	I	8	0.243	0.321	NA	NA	0.321	0.078	0.320988	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	-	+	-	NA	-	+	-	-
17278	Z1031B	x	251485070262_4	NA			58	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.143	0.014	NA	0.016	0.016	-0.127	-0.88811	Responder	8	NA	8	8	0	0	1	NA	-	-	-	-	+	-	-	-	NA	-	-	-	+
17292	Z1031B	x	251485070442_1	NA			62	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	III	III	II/III	8	0.22	0.535	NA	NA	0.535	0.315	1.431818	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17327	Z1031B	x	251485070306_3	NA			74	LumA	*NA*	NA	NA	NA	NEGATIVE	LOBULAR	I	I/II	I	8	0.122	0.15	NA	NA	0.15	0.028	0.229508	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	+	-	-	-	-	+	NA	+	-	-	-
17328	Z1031B	x	251485070234_2	NA			61	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.65	0.091	NA	0.006	0.006	-0.644	-0.99077	Responder	8	NA	8	8	0	0	1	1	-	-	-	-	-	-	-	-	NA	+	-	-	+
17329	Z1031B	x	251485070546_1	NA			54	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.533	0.229	NA	NA	0.229	-0.304	-0.57036	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17331	Z1031B	x	251485070443_1	NA			56	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.135	0.01	NA	0.015	0.015	-0.12	-0.88889	Responder	7	NA	7	7	0	3	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	+
17352	Z1031B	x	251485070237_3	NA			58	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.121	0.019	NA	0.023	0.023	-0.098	-0.80992	Responder	6	NA	7	7	-1	3	0	NA	-	-	+	-	-	-	-	+	NA	-	-	-	-
17383	Z1031B	x	251485067280_1	NA			67	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	NA	NA	0.017	0.035	0.035	NA	NA	Responder	NA	8	8	8	0	1	0	1	-	-	-	-	+	-	-	-	NA	-	-	-	-
17384	Z1031B	x	251485070443_3	NA			52	LumA	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	I	I/II	I	8	0.007	0.144	NA	NA	0.144	0.137	19.57143	NonResponder	7	NA	NA	7	-1	NA	NA	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
17407	Z1031B	x	251485069955_1	NA			62	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.2	0.026	NA	0.006	0.006	-0.194	-0.97	Responder	8	NA	8	8	0	3	0	1	-	-	-	+	-	-	-	-	NA	+	-	-	-
17409	Z1031B	x	251485067258_1	NA			61	LumB	*NA*	NA	3~4	1	NEGATIVE	DUCTAL	III	III	II/III	8	0.9	0.224	NA	0.009	0.009	-0.891	-0.99	Responder	8	NA	8	8	0	6	0	NA	-	-	-	-	+	-	-	-	NA	-	-	-	-

17412	Z1031B	x	251485070545_1	NA	tumor stage T1; max dim=1.2	57	LumA	*NA*	NA	NA	1	NEGATIVE	DUCTAL	III	III	II/III	8	0.24	0.032	NA	0.007	0.007	-0.233	-0.97083	Responder	8	NA	8	8	0	NA	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17419	Z1031B	x	251485070263_3	NA		66	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	8	0.205	0.011	NA	0.004	0.004	-0.201	-0.98049	Responder	8	NA	6	6	-2	0	1	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17445	Z1031B	x	251485070262_1	NA		61	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.161	0.04	NA	0.087	0.087	-0.074	-0.45963	Responder	8	NA	7	7	-1	4	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	+
17467	Z1031B	x	251485070546_2	NA		56	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.113	0.01	NA	0.001	0.001	-0.112	-0.99115	Responder	8	NA	8	8	0	3	0	NA	-	-	-	-	+	-	-	-	NA	+	-	-	-
17494	Z1031B	x	251485070263_1	NA		60	LumB	*NA*	NA	3~4	1	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.15	0.04	NA	0.05	0.05	-0.1	-0.66667	Responder	7	NA	6	6	-1	7	0	1	-	-	+	-	-	-	-	-	NA	+	-	-	-
17518	Z1031B	x	251485070547_3	NA		50	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	I	I/II	I	7	0.085	0.2	NA	NA	0.2	0.115	1.352941	NonResponder	7	NA	NA	7	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
17521	Z1031B	x	251485070263_4	NA		69	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.167	0.003	NA	0.096	0.096	-0.071	-0.42515	Responder	7	NA	7	7	-1	4	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	+
17522	Z1031B	x	251485070234_3	NA		58	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.075	0.083	NA	0.005	0.005	-0.07	-0.93333	Responder	8	NA	7	7	-1	3	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17584	Z1031B	x	251485070234_4	NA		52	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	8	0.198	0.098	NA	0.002	0.002	-0.196	-0.9899	Responder	8	NA	8	8	0	0	1	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17586	Z1031B	x	251485070265_1	NA		73	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.09	0.057	NA	0.004	0.004	-0.086	-0.95556	Responder	8	NA	8	8	0	3	0	1	-	-	-	-	-	-	-	+	NA	-	-	-	-
17601	Z1031B	x	251485070549_3	NA		66	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.45	0.031	NA	0.054	0.054	-0.396	-0.88	Responder	8	NA	7	7	0	1	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17611	Z1031B	x	251485070266_3	NA		65	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	I	I/II	I	8	0.086	0.01	NA	0.003	0.003	-0.083	-0.96512	Responder	8	NA	8	8	0	3	0	1	-	-	-	-	-	-	-	+	NA	+	-	-	-
17612	Z1031B	x	251485070547_1	NA		55	LumA	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	I	I/II	I	8	0.035	0.141	NA	NA	0.141	0.106	3.028571	NonResponder	7	NA	NA	7	-1	NA	NA	NA	-	-	-	-	-	-	-	+	NA	+	-	+	-
17636	Z1031B	x	251485070235_2	NA		67	LumA	*NA*	NA	NA	NA	NEGATIVE	LOBULAR	I	I/II	I	7	0.092	0.035	NA	NA	0.035	-0.057	-0.61957	Responder	8	NA	NA	8	1	NA	NA	1	-	-	-	-	-	-	-	+	NA	+	-	-	-
17645	Z1031B	x	251485070265_4	NA		73	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.11	NA	0.089	0.098	0.098	-0.012	-0.10909	Responder	NA	7	7	7	0	1	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17646	Z1031B	x	251485070266_1	NA		69	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.188	0.049	NA	0.004	0.004	-0.184	-0.97872	Responder	7	NA	7	7	-1	3	0	NA	-	-	-	-	-	-	-	+	NA	-	-	-	-
17678	Z1031B	x	251485070570_1	NA		63	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.02	NA	NA	0.003	0.003	-0.017	-0.85	Responder	NA	NA	8	8	0	3	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	-
17688	Z1031B	x	251485070570_2	NA		55	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.134	0.025	NA	0.008	0.008	-0.126	-0.9403	Responder	8	NA	8	8	0	3	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	+
17714	Z1031B	x	251485070238_3	NA		78	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	0.071	0.013	NA	0.047	0.047	-0.024	-0.33803	Responder	8	NA	8	8	0	1	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17733	Z1031B	x	251485070570_3	NA		65	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.124	0.025	NA	0.003	0.003	-0.121	-0.97581	Responder	8	NA	8	8	0	3	0	NA	-	-	-	-	+	-	-	+	NA	-	-	-	-
17738	Z1031B	x	251485070570_4	NA		75	LumA	*NA*	NA	3~4	1	NEGATIVE	LOBULAR	I	I/II	I	8	0.044	0.002	NA	0.003	0.003	-0.041	-0.93182	Responder	7	NA	8	8	0	6	0	1	-	-	+	-	-	-	-	-	NA	-	-	-	-
17739	Z1031B	x	251485070573_1	NA		63	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.143	0.075	NA	0.007	0.007	-0.136	-0.95105	Responder	8	NA	8	8	0	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	+
17740	Z1031B	x	251485070572_1	NA		57	LumB	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	I	I/II	I	7	0.123	0.037	NA	0.007	0.007	-0.116	-0.94309	Responder	8	NA	7	7	0	3	0	1	-	-	+	-	-	-	-	-	NA	-	-	-	-
17746	Z1031B	x	251485070573_2	NA		54	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	I	I/II	I	8	0.204	0.179	NA	NA	0.179	-0.025	-0.12255	NonResponder	7	NA	NA	7	-1	NA	NA	NA	-	-	-	-	+	-	-	-	NA	-	-	-	+
17762	Z1031B	x	251485070572_2	NA		71	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.118	0.041	NA	0.045	0.045	-0.073	-0.61864	Responder	7	NA	7	7	-1	4	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17774	Z1031B	x	251485070573_3	NA		63	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.064	0.007	NA	0	0	-0.064	-1	Responder	8	NA	8	8	0	0	1	1	-	-	-	-	-	-	-	+	NA	-	-	-	+
17776	Z1031B	x	251485070235_3	NA		75	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	III	III	II/III	8	0.45	0.103	NA	NA	0.103	-0.347	-0.77111	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-

17818	Z1031B	x	251485070235_4	NA		51	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.336	0.021	NA	NA	0.021	-0.315	-0.9375	Responder	8	NA	NA	8	0	NA	NA	1	+	-	-	-	-	+	-	+	NA	+	-	-	-
17823	Z1031B	x	251485070236_1	NA		66	LumB	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.277	0.063	NA	0.027	0.027	-0.25	-0.90253	Responder	8	NA	7	7	0	0	1	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17835	Z1031B	x	251485070236_2	NA		68	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.01	0.037	NA	0.016	0.016	0.006	0.6	Responder	8	NA	7	7	-1	3	0	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
17860	Z1031B	x	251485070236_3	NA		69	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.05	0.059	NA	0.082	0.082	0.032	0.64	Responder	8	NA	8	8	0	4	0	1	-	-	-	-	-	-	-	-	NA	+	-	-	-
17868	Z1031B	x	251485070236_4	NA		66	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	0.025	0.035	NA	0.01	0.01	-0.015	-0.6	Responder	8	NA	7	7	-1	0	1	1	-	-	-	-	-	-	-	+	NA	-	-	-	-
17881	Z1031B	x	251485070237_1	NA		73	LumB	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	I	I/II	I	8	0.126	0.055	NA	0.018	0.018	-0.108	-0.85714	Responder	8	NA	8	8	0	3	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17902	Z1031B	x	251485070574_2	NA		63	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	III	III	II/III	7	0.244	0.035	NA	0.005	0.005	-0.239	-0.97951	Responder	8	NA	8	8	1	0	1	1	-	-	-	-	-	-	-	+	NA	+	-	-	-
17913	Z1031B	x	251485070572_3	NA		51	LumA	*NA*	NA	NA	NA	NEGATIVE	LOBULAR	I	I/II	I	8	0.048	0.247	NA	NA	0.247	0.199	4.145833	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
17915	Z1031B	x	251485070237_2	NA		63	LumA	*NA*	NA	3~4	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.106	0.033	NA	0.013	0.013	-0.093	-0.87736	Responder	8	NA	7	7	-1	6	0	NA	-	-	-	-	-	-	-	-	NA	+	-	-	-
17929	Z1031B	x	251485070574_4	NA	tumor stage T1; max dim=0.9	72	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.129	0.005	NA	0.05	0.05	-0.079	-0.6124	Responder	7	NA	8	8	0	4	0	1	-	-	+	-	-	-	-	-	NA	-	-	-	-
17946	Z1031B	x	251485070350_1	NA		64	LumB	*NA*	NA	3~4	0	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.065	0.065	NA	0	0	-0.065	-1	Responder	8	NA	8	8	0	3	0	1	-	-	+	-	-	-	-	-	NA	+	-	-	-
17967	Z1031B	x	251485070350_2	NA		83	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.126	0.006	NA	0.023	0.023	-0.103	-0.81746	Responder	8	NA	8	8	0	3	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
17972	Z1031B	x	251485070350_3	NA		70	LumA	*NA*	NA	1~2	0	NEGATIVE	LOBULAR	I	I/II	I	8	0.242	0.029	NA	0.126	0.126	-0.116	-0.47934	NonResponder	8	NA	8	8	0	1	0	1	-	-	+	-	-	-	-	-	NA	-	-	-	-
18025	Z1031B	x	251485070350_4	NA		56	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.65	0.183	NA	NA	0.183	-0.467	-0.71846	NonResponder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	+
18074	Z1031B	x	251485070351_4	NA		62	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	I	I/II	I	8	0.067	0.002	NA	0.005	0.005	-0.062	-0.92537	Responder	8	NA	8	8	0	3	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
18091	Z1031B	x	251485070353_1	NA		58	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.076	0.066	NA	0.05	0.05	-0.026	-0.34211	Responder	8	NA	8	8	0	4	0	NA	-	-	+	-	-	-	-	-	NA	-	-	-	+
18096	Z1031B	x	251485070353_2	NA		76	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.134	0.014	NA	0.003	0.003	-0.131	-0.97761	Responder	8	NA	8	8	0	0	1	1	-	-	-	-	-	-	-	-	NA	-	-	-	-
18140	Z1031B	x	251485070353_4	NA		60	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	II	I/II	II/III	7	0.142	0.126	NA	NA	0.126	-0.016	-0.11268	NonResponder	8	NA	NA	8	1	NA	NA	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-
18154	Z1031B	x	251485070354_1	NA	tumor stage T0; no disease present; also 0/3 SLN positive; no ALND	72	LumA	*NA*	NA	3~4	1	NEGATIVE	LOBULAR	II	I/II	II/III	8	0.074	0.006	NA	0.026	0.026	-0.048	-0.64865	Responder	6	NA	6	6	-2	6	0	1	-	-	+	-	-	-	-	-	NA	-	-	-	-
18155	Z1031B	x	251485070354_2	NA		72	LumB	*NA*	NA	NA	NA	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.182	0.054	NA	NA	0.054	-0.128	-0.7033	Responder	8	NA	NA	8	0	NA	NA	NA	-	-	-	-	-	-	-	-	NA	+	-	+	-
18156	Z1031B	x	251485070354_3	NA		56	LumB	*NA*	NA	3~4	0	NEGATIVE	LOBULAR	I	I/II	I	8	0.17	0.005	NA	0.006	0.006	-0.164	-0.96471	Responder	8	NA	8	8	0	3	0	1	-	-	+	-	-	-	-	-	NA	+	-	-	-
18161	Z1031B	x	251485070572_4	NA		62	LumA	*NA*	NA	1~2	1	NEGATIVE	LOBULAR	I	I/II	I	8	0.036	0.018	NA	0.012	0.012	-0.024	-0.66667	Responder	8	NA	8	8	0	3	0	1	-	-	+	-	-	-	-	+	NA	-	-	-	-
18182	Z1031B	x	251485070351_1	NA		49	LumA	*NA*	NA	1~2	1	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.21	0.085	NA	0.26	0.26	0.05	0.238095	NonResponder	8	NA	5	5	-3	5	0	1	-	-	-	-	-	-	-	-	NA	-	-	-	+
18183	Z1031B	x	251485070713_3	NA		57	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	I	I/II	I	8	0.056	0.017	NA	0.03	0.03	-0.026	-0.46429	Responder	8	NA	8	8	0	1	0	1	-	-	-	+	-	-	-	+	NA	+	-	-	-
18184	Z1031B	x	251485070351_3	NA		53	LumA	*NA*	NA	3~4	1	NEGATIVE	LOBULAR	I	I/II	I	8	0.3	0.031	NA	0.004	0.004	-0.296	-0.98667	Responder	8	NA	8	8	0	6	0	NA	-	-	-	-	-	-	-	-	NA	-	-	-	-

21009	Z1031B	x	251485070354_4	NA	57	LumA	*NA*	NA	1~2	0	NEGATIVE	DUCTAL	II	I/II	II/III	8	0.003	0.01	NA	0	0	-0.003	-1	Responder	8	NA	8	8	0	0	1	1	-	-	-	-	+	-	-	+	NA	+	-	-	-			

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	0.1697	13	52	3	59	0.1017	16	79	3	89	0.008	20	89	4	101	0.0034	29	131	6	148	0.0026
MAP3K1	TP53	9	14	0	23	0.0585	10	16	2	22	0.8447	20	21	1	39	0.0949	19	30	2	45	0.3082	29	35	1	62	0.0045	39	51	3	84	0.0957
MAP2K4 +MAP3K1	TP53	11	14	0	25	0.028	15	16	4	23	0.9679	23	21	2	40	0.189	26	30	4	48	0.4942	34	35	2	65	0.0076	49	51	6	88	0.3063
CDH1	GATA3	8	7	0	15	0.3174	NA	NA	NA	NA	NA	22	13	0	35	0.0684	NA	NA	NA	NA	NA	30	20	0	50	0.0147	NA	NA	NA	NA	NA
CDH1	TP53	8	14	0	22	0.0822	NA	NA	NA	NA	NA	22	21	2	39	0.2271	NA	NA	NA	NA	NA	30	35	2	61	0.0216	NA	NA	NA	NA	NA
GATA3	TP53	7	14	0	21	0.1103	9	16	1	23	0.6035	13	21	2	30	0.6353	16	30	1	44	0.1711	20	35	2	51	0.1476	29	51	3	74	0.3193
CDH1	PIK3CA	8	37	4	37	0.394	NA	NA	NA	NA	NA	22	52	8	58	0.3268	NA	NA	NA	NA	NA	30	89	12	95	0.1695	NA	NA	NA	NA	NA
RUNX1	TP53	3	14	0	17	0.4228	NA	NA	NA	NA	NA	4	21	0	25	0.4861	NA	NA	NA	NA	NA	7	35	0	42	0.1805	NA	NA	NA	NA	NA
PIK3CA	TP53	37	14	9	33	0.7643	42	16	6	46	0.4493	52	21	6	61	0.0978	79	30	15	79	0.7215	89	35	15	94	0.2575	131	51	21	140	0.3076
CDH1	RB1	8	4	0	12	0.5312	NA	NA	NA	NA	NA	22	2	0	24	0.6886	NA	NA	NA	NA	NA	30	6	0	36	0.2948	NA	NA	NA	NA	NA
MAP2K4	MAP3K1	2	9	0	11	0.707	5	10	0	15	0.6411	3	20	0	23	0.608	7	19	0	26	0.439	5	29	0	34	0.3721	10	39	0	49	0.2984
GATA3	MAP2K4 +MAP3K1	7	11	1	16	0.585	9	15	0	24	0.2452	13	23	2	32	0.5577	16	26	1	40	0.204	20	34	3	48	0.3808	29	49	3	72	0.3281

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	0.0176	23	52	13	49	0.0975	26	79	19	67	0.0016	34	89	22	79	0.0306	49	131	32	116	0.0002
MAP3K1	PIK3CA	9	37	7	32	0.2207	10	42	7	38	0.039	20	52	13	46	0.0193	19	79	14	70	0.0075	29	89	20	78	0.0123	39	131	27	116	0
MAP2K4	PDGFRA	2	2	1	2	0.0721	NA	NA	NA	NA	NA	3	1	1	2	0.0213	NA	NA	NA	NA	NA	5	3	2	4	0.002	NA	NA	NA	NA	NA
CBFB	MAP2K4 +MAP3K1	2	11	2	9	0.0335	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP2K4 +MAP3K1	RUNX1	11	3	2	10	0.091	NA	NA	NA	NA	NA	23	4	1	25	0.5499	NA	NA	NA	NA	NA	34	7	3	35	0.1585	NA	NA	NA	NA	NA
MAP2K4	PIK3CA	2	37	2	35	0.3673	5	42	3	41	0.3409	3	52	0	55	1	7	79	5	76	0.1706	5	89	2	90	0.8235	10	131	5	131	0.4598

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

X	61300000	61640000	3	2	AMP	.
2	10190000	10610000	0	2	DEL	*MIR4261,SNORA80B,HPCAL1,ODC1,C2orf48*
2	120770000	121570000	1	5	DEL	*INHBB,LOC84931,GLI2*
2	239590000	239890000	0	9	DEL	*MGC16025,HDAC4*
6	21190000	21610000	3	4	DEL	*CDKAL1*
6	106210000	106610000	4	7	DEL	.
7	66510000	66980000	2	3	DEL	.
8	31510000	31940000	4	9	DEL	*NRG1*
8	31900000	32350000	5	9	DEL	*NRG1*
10	98770000	99330000	2	10	DEL	*FRAT1,FRAT2,PGAM1,ANKRD2,ARHGAP19,EXOSC1,ZDHHC16,RRP12,UBTD1,SLIT1,MMS19,ARHGAP19-SLIT1*
10	101430000	102960000	2	6	DEL	*SNORA12,BLOC1S2,NDUFB8,MIR608,LZTS2,SFXN3,KAZALD1,TLX1,CUTC,COX15,NCRNA00093,CPN1,ERLIN1,PKD2L1,CWF19L1,WNT8B,NCRNA00263,HIF1AN,SEC31B,C10orf2,FAM178A,MRPL43,SEMA4G,TLX1NB,ABCC2,ENTPD7,SCD,PAX2,CHUK,DNMBP,PDZD7*
10	106510000	106950000	3	4	DEL	*SORCS3*
10	123070000	123540000	3	5	DEL	*ATE1,FGFR2*
13	22050000	22490000	2	5	DEL	*BASP1P1*
13	22520000	23070000	2	5	DEL	*SGCG,SACS,TNFRSF19*
13	23350000	23890000	3	8	DEL	*MIR2276,C1QTNF9B,PCOTH,C1QTNF9,SPATA13,MIPEP*
13	26640000	27440000	1	7	DEL	*RPL21P28,SNORD102,RPL21,SNORA27,RASL11A,GSX1,ATP5EP2,CDX2,GTF3A,MTIF3,LNX2,POLR1D,USP12,PDX1*
13	27580000	28850000	2	7	DEL	*LOC100288730,POMP,FLT1,PAN3,SLC46A3,MTUS2*
13	29410000	29710000	4	5	DEL	*LOC440131,KATNAL1*
13	29720000	30440000	4	5	DEL	*LOC100188949,HMGB1,USPL1,ALOX5AP,C13orf33,KATNAL1,C13orf26*
13	30500000	30850000	3	4	DEL	*HSPH1,B3GALTL*
18	53340000	54190000	3	5	DEL	*FECH,NARS,NEDD4L,ATP8B1*
18	54050000	54460000	3	4	DEL	*MIR122,ALPK2,NEDD4L*
19	61940000	63010000	2	8	DEL	*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,ZNF460,ZNF264,ZNF805,ZNF548,ZNF547,ZNF17,ZNF549,ZNF550,ZSCAN4,ZNF586,ZIM2*
22	24470000	25160000	1	7	DEL	*SEZ6L,MIR1302-1,MYO18B,ASPHD2*

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
20	45360590	45360590	20	45360879	45360879	DEL	289	BRC10	1	1	NHEJ	ZMYND8	ENST00000311275	-1	intron3	ZMYND8	ENST00000311275	-1	intron3	N/A
12	90440513	90440513	12	90462478	90462478	DEL	21963	BRC10	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	42543273	42543273	12	87613288	87613288	DEL	45069013	BRC10	1	1	NHEJ	TMEM117	ENST00000266534	1	intron1	N/A	N/A	N/A	N/A	ESPL1 VDR THAP2 OR6C6 DGKA ACSS3 AQP5 BLOC1S1 AAAS ITGA5 NXPH4 PPM1H NDUFA4L2 CNPY2 IL26 PTPRR SP7 TMBIM4 RARG KCNH3 ACVR1B WNT1 CCDC59 STAT2 OR6C74 DNAJC14 GTSF1 NFE2 SYT1 LRIG3 TMEM194A NAV3 LIMA1 LRRIQ1 OR2AP1 HNRPA1L3 ELA1 C12orf66 PRR13 SENP1 KRT82 RASSF3 SLC11A2 TMTC3 LLPH 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 LIN7A SLC38A2 KRT1 ZC3H10 H1FNT OR6C65 GLI1 IL22 FAM62A HOXC5 C12orf62 MIP OR6C2 PPP1R1A SCN8A LRP1 RAP1B KCNC2 GNS 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 ACCN2 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 DDIT3 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 TSFM SPRYD3 CSRNP2 RPL21P18 MMP19 KRT85 DTX3 CSAD NTS C12orf44 PFDN5 TMEM5 RAB5B TUBA1C RAPGEF3 OR8S1 KRT79 RPL14P1 TMBIM6 SRGAP1 PTGES3 PHLDA1 NELL2 ZBTB39 CAPS2 FIGNL2 OR6C4 CS WNT10B PTPRB LEMD3 AQP6 SLC38A4 ATF1 FKBP11 RACGAP1P RND1 MAP3K12 E2F7 KRT3 FAM119B KRT71 LMBR1L TARBP2 IKZF4 ARID2 KRT78 POU6F1 CALCOCO1 ATF7 LRRC10 ZNF641 KRR1 ENSG00000202582 KIAA0748 SPATS2 MARCH9 KRT6A OR6C75 BBS10 TSPAN31 AMIGO2 XRCC6BP1 MON2 SUOX PAN2 AMHR2 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 HMGA2 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
10	71698560	71698560	13	55612360	55612360	CTX	N/A	BRC10	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	797911	797911	13	716137	716137	CTX	N/A	BRC	-1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

	80	80		72	72			10												
10	79789302	79789302	13	71601318	71601318	CTX	N/A	BRC10	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	52016504	52016504	12	90722363	90722363	CTX	N/A	BRC10	-1	-1	MMEJ	SGMS1	ENST00000361543	-1	intron0	N/A	N/A	N/A	N/A	N/A
10	78996431	78996431	13	61310786	61310786	CTX	N/A	BRC10	1	1	NHEJ	KCNMA1	ENST00000372437	-1	intron1	N/A	N/A	N/A	N/A	N/A
2	71475739	71475739	10	76560798	76560798	CTX	N/A	BRC10	-1	1	NHEJ	ZNF638	ENST00000410075	1	intron11	SAMD8	ENST00000372690	1	intron1	N/A
10	79789705	79789705	13	71603244	71603244	CTX	N/A	BRC10	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	54734836	54734836	8	62997940	62997940	CTX	N/A	BRC10	1	1	NHEJ	SKIV2L2	ENST00000230640	1	intron21	N/A	N/A	N/A	N/A	N/A
1	1.7E+08	1.7E+08	1	1.72E+08	1.72E+08	DEL	2630407	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ANKRD45 PRDX6 RPL26P11 TNFSF4 GOT2L2 C1orf9 KLHL20 VAMP4 BAT2D1 RPL4P3 DNM3 PIGC TNFSF18 RC3H1 SERPINC1 CENPL DARS2 SLC9A11 MYOC FASLG C1orf105 METTL13 ZBTB37
6	1.04E+08	1.04E+08	6	1.07E+08	1.07E+08	DEL	3006798	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	HACE1 PREP POPDC3 C6orf112 RPL35P3 BVES LIN28B
6	1.03E+08	1.03E+08	6	1.09E+08	1.09E+08	DEL	5957430	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	ARMC2	ENST00000368972	1	intron4	SNX3 SCML4 RPL3P7 SOBP ZNF259P BEND3 BVES ATG5 OSTM1 HACE1 PDSS2 SEC63 RPL35P3 NR2E1 AIM1 LACE1 C6orf203 C6orf112 FOXO3 RTN4IP1 PREP POPDC3 QRSL1 PRDM1 LIN28B
6	1.07E+08	1.07E+08	6	1.07E+08	1.07E+08	DEL	284648	BRC11	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ATG5 PRDM1
4	1.04E+08	1.04E+08	4	1.04E+08	1.04E+08	DEL	1537	BRC11	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.17E+08	1.17E+08	1	1.59E+08	1.59E+08	DEL	42150332	BRC11	1	1	NHEJ	C1orf203	ENST00000369492	-1	intron0	N/A	N/A	N/A	N/A	PDE4DIP C1orf189 OTUD7B KRTCAP2 LCE5A ADAM30 IFI16 LCE3A CKS1B RPTN FAM63A IQGAP3 NOTCH2NL CCDC19 CASQ1 RPS10P8 MEF2D C1orf85 NBPF1 OR6P1 ARHGEF11 SCAMP3 PPIAL4A S100A3 CDC42SE1 DCST1 TDRD10 NTRK1 NBPF12 CD1E KCNJ9 SPRR2F HIST2H2AA4 HAO2 OR10Z1 DPM3 OR6N2 CD1B HMGCS2 TTC24 SPAG17 TUFT1 CTSS SRGAP2P1 HIST2H2BD GNRHR2 FCRL6 VANGL2 PRKAB2 LCE3E IGSF9 RFX5 HIST2H3PS2 RAG1AP1 FLG HIST2H3D TMOD4 TRIM45 PTGFRN PBXIP1 OR10T2 FAM108A3 HIST2H2BC NBPF16 EFNA1

																				YY1AP1 LCE2D TMEM79 C1orf92 CRABP2 NUDT17 CD1D NUP210L PRUNE SHE IGSF3 PMVK PI4KB FCER1A ANP32E HFE2 LCE1A CD84 ETV3L MRPS21 S100A14 RBM8A LINGO4 SPRR3 PIP5K1A ATP1A2 SHC1 BCAN GPATCH4 TTF2 ILF2 OR10X1 HSD3B1 C1orf137 PDZK1 KIRREL GDAP2 SV2A S100A4 CA14 C1orf182 DENND4B THEM5 DCST2 KIAA0907 HIST2H3A OR6N1 APOA1BP ETV3 NCRNA00166 VPS72 SLAMF8 TCHH LYSMD1 FCGR1A SNX27 CD160 PHGDH ACP6 CCT8P1 TNRC4 OR10J1 RXFP4 RORC LOR EFNA3 GABPB2 NES CADM3 SEMA4A C1orf61 PEX19 CD1A REG4 ADAMTSL4 FCRL2 LCE2C OR10J5 PEA15 TAGLN2 CD5L CD2 C1orf204 DAP3 ATP8B2 AIM2 OR6K5P SMCP SLC27A3 PLEKHO1 OR6K2 CGN SPRR2G PAQR6 MEX3A HAX1 FAM46C C1orf66 NCSTN WARS2 NHLH1 S100A7 LCE2B HIST2H4A PYHIN1 ANKRD35 SF3B4 AQP10 TRIM46 LCE3D LCE1B CTSK SLAMF9 SPRR2D NOTCH2 UBQLN4 NBPF10 SPRR4 PIAS3 RUSC1 LCE1D SEMA6C CRTC2 HIST2H2BF MRPL24 GON4L WDR42A C1orf77 ANKRD34A KCNN3 HDGF S100A7A TPM3 ARNT FLG2 ZBTB7B INSRR RPL6P2 OR6K6 GPR89A HAPLN2 BOLA1 TARS2 ATP1A4 HIST2H4B APH1A JTB ISG20L2 THBS3 RNF115 GPR89C GBA PMF1 VHLL C1orf138 COPA C1orf2 SETDB1 LENEP MUC1 ENSA C1orf46 ROBLD3 S100A12 POLR3GL PYGO2 LMNA FAM72B OR6K1P HIST2H2AB KCNJ10 PKLR EFNA4 KPRP THEM4 OR10K2 HSD3B2 OR6Y1 CLK2 MLLT11 SPRR2A S100A5 RAB25 C1orf56 OR2AQ1P NPR1 SLC39A1 SEC22B OR10T1P SRGAP2P2 BCL9 FAM108A2 S100A6 S100A1 LCE2A POGZ LCE1C GATAD2B RPS10P6 SPRR1A WDR3 LELP1 PGLYRP4 SLC25A44 MTX1 OR6K3 LCE3C OR10R1P FMO5 PDZK1P2 NBPF8 PEAR1 OR10K1 ADAM15 DRD5P2 SLAMF1 S100A16 POLR3C ZNF687 ARHGEF2 LCE1E S100A8 TCHHL1 IVL FCRL3 GJA8 OR10J9P PSMB4 SMG5 MRPL9 CYCSP52 SPTA1 UBE2Q1 CCT3 PRCC HCN3 TNFAIP8L2 IGSF2 UBAP2L S100A2 C1orf152 APCS FCRL1 HORMAD1 PRR9 IL6R uc001elp.1 CHRNB2 SSR2 BNIPL FDPS PGLYRP3 ERVK5 TBX15 VTCN1 MTMR11 LCE3B CHD1L MSTO1 CRP MCL1 SELENBP1 SCNM1 S100A7L2 CRNN HIST2H2AA3 ZNF697 TXNIP DARC NBPF11 LCE4A SYT11 GBAP GJA5 SPRR2E NBPF7 S100A11 HIST2H2AC MAN1A2 RPRD2 OR6K4P OR10R2 TDRKH HIST2H2BE FCGR1B VPS45 CREB3L4 FCRL4 S100A13 NEFHL LIX1L PEX11B SPRR2B SNAPIN ADAR PPIAL4G SLAMF6 PSMD4 ECM1 CD58 FLAD1 C1orf51 C1orf43 RIT1 C1orf68 MNDA OR10J3 RHBG GOLPH3L NBPF15 ENSG00000216295 INTS3 RAB13 SPRR1B ASH1L HIST2H3C FCRL5 CD1C PRPF3 LASS2 PIGM S100A10 S100A9 IGSF8 C1orf54 SH2D2A ANXA9 GPR89B KIAA1245 DUSP23 OAZ3 CRCT1 RPS27 LCE1F HRNR ITGA10
1	1.54E+08	1.54E+08	1	1.54E+08	1.54E+08	DEL	17394	BRC1	1	1	NHEJ	ASH1L	ENST00000368346	-1	intron11	ASH1L	ENST00000368346	-1	intron6	N/A
6	1.06E+08	1.06E+08	6	1.09E+08	1.09E+08	DEL	3689183	BRC1	1	1	NHEJ	LIN28B	ENST00000392705	1	intron3	ARMC2	ENST00000368972	1	intron4	SNX3 SCML4 RPL3P7 SOBP ZNF259P BEND3 BVES ATG5 OSTM1 PDSS2 SEC63 RPL35P3 NR2E1 AIM1 LACE1 C6orf203 C6orf112 FOXO3 RTN4IP1 PREP POPDC3 QRSL1 PRDM1
1	1.92E+08	1.92E+08	1	2.07E+08	2.07E+08	DEL	14752220	BRC1	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	MYBPH KLHDC8A DDX59 TNNI1 RPL34P1 CFHR2 CD34 LGTN BTG2 C1orf106 C1orf98 uc001gud.2 GOLT1A FMOD C4BPA ZC3H11A IGFN1 ASCL5 IL19 PPFIA4 SNRPE FCAMR TMEM183A C1orf186 PRELP CFHR5 KIF21B LEMD1 F13B CD46 C1orf147 IL24 CR2 CTSE C1orf53 SHISA4 CSRP1 KISS1 KCNT2 SLC41A1 RABIF DYRK3 ELF3 CD46P PCTK3 LGR6 NUCKS1 LAD1 TIMM17A KLHL12 ZBTB41 C1orf157 ZNF281 TMEM9 NR5A2 PKP1 RPL13AP8 SLC45A3 PHLDA3 PPP1R12B GPR25 IL20 ASPM SOX13 RBBP5 PLXNA2 DSTYK CFHR4 PTPRV NAV1 IPO9 C1orf116 PM20D1 LRRN2 LMOD1 PIK3C2B CAMSAP1L1 PIGR CFH NFASC PLEKHA6 CR1L RASSF5 CACNA1S LAX1 CHIT1 ATP6V1G3 MAPKAPK2 MYOG TMCC2 CNTN2 PFKFB2 LHX9 RAB7L1 IL10 CHI3L1 MFSD4 SRGAP2 CRB1 ARL8A RNPEP PPP1R15B IKBKE TNNT2 FAM72A CD55 GPR37L1 SLC26A9 ATP2B4 YOD1 NUAK2 FAM58B CFHR1 JARID1B OPTC PTPN7 C1orf132 UBE2T SYT2 C4BPB ELK4 KIF14 TMEM81 MDM4 DENND1B CR1 CFHR3 REN AVPR1B RPL17P8 ETNK2 FAIM3 ADORA1 NECAP1 ADIPOR1 CYB5R1 NEK7 PTPRC
1	2.28E+08	2.28E+08	1	2.28E+08	2.28E+08	DEL	9912	BRC1	1	1	MMEJ	ABCB10	ENST00000344517	-1	intron13	ABCB10	ENST00000344517	-1	intron1	N/A

17

1	1.7E+08	1.7E+08	1	1.82E+08	1.82E+08	DEL	12209675	BRC11	1	1	MMEJ	N/A	N/A	N/A	N/A	SMG7	ENST00000347615	1	intron2	ANKRD45 PRDX6 KIAA1614 GPR52 TNFSF4 NPHS2 TOR1AIP2 RGS16 ZNF648 SOAT1 MR1 TNN TOP1P1 KRT18P28 IER5 ENSG00000135820 ABL2 RPL4P3 C1orf220 ACBD6 QSOX1 TNR RALGPS2 TOR3A TNFSF18 TEDDM1 SERPINC1 FAM20B RFWD2 SLC9A11 FASLG C1orf120 METTL13 ZBTB37 FAM163A GOT2L2 RABGAP1L KLHL20 FAM5B DNM3 LAMC1 TOR1AIP1 RGS8 CEP350 GLUL RPL26P11 C1orf9 TDRD5 ASTN1 STX6 BAT2D1 LHX4 PIGC CACNA1E FMO4 CENPL ANGPTL1 MYOC ENSG00000216295 C1orf105 RASAL2 C1orf14 RNASEL VAMP4 SEC16B NMNAT2 NPL LAMC2 RGSL1 NCRNA00083 CACYBP DHX9 RC3H1 PAPPA2 DARS2 C1orf49 MRPS14 C1orf125 XPR1
1	1.46E+08	1.46E+08	1	1.46E+08	1.46E+08	DEL	2460	BRC11	1	1	NHEJ	ACP6	ENST00000369238	-1	intron4	ACP6	ENST00000369238	-1	intron1	N/A
8	34289801	34289801	8	34291257	34291257	DEL	1455	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.51E+08	1.51E+08	1	1.57E+08	1.57E+08	DEL	5719677	BRC11	1	1	NHEJ	SPRR2A	ENST00000368752	-1	intron0	MNDA	ENST00000368141	1	intron0	HDGF TPM3 S100A7A C1orf189 KRTCAP2 ZBTB7B INSRR OR6K6 HAPLN2 CKS1B IQGAP3 JTB ISG20L2 THBS3 RPS10P8 GBA MEF2D PMF1 VHLL C1orf85 OR6P1 C1orf2 LENEP MUC1 ROBLD3 ARHGEF11 S100A12 PYGO2 LMNA OR6K1P SCAMP3 S100A3 PKLR DCST1 TDRD10 NTRK1 EFNA4 CD1E OR10K2 OR10Z1 OR6Y1 DPM3 OR6N2 CD1B CLK2 TTC24 S100A5 RAB25 OR2AQ1P NPR1 SLC39A1 OR10T1P RAG1AP1 S100A6 S100A1 GATAD2B PBXIP1 OR10T2 EFNA1 LELP1 PGLYRP4 SLC25A44 YY1AP1 MTX1 OR6K3 TMEM79 C1orf92 CRABP2 OR10R1P CD1D NUP210L SHE PEAR1 PMVK OR10K1 ADAM15 S100A16 ARHGEF2 S100A8 ETV3L S100A14 FCRL3 SHC1 SMG5 CYCSP52 GPATCH4 BCAN ILF2 SPTA1 OR10X1 UBE2Q1 CCT3 HCN3 PRCC UBAP2L S100A2 KIRREL FCRL1 PRR9 IL6R S100A4 CHRNB2 SSR2 PGLYRP3 FDPS C1orf182 ERVK5 DENND4B DCST2 KIAA0907 OR6N1 MSTO1 APOA1BP ETV3 S100A7L2 SYT11 GBAP RXFP4 LOR EFNA3 NES SEMA4A C1orf61 OR6K4P OR10R2 CD1A FCRL2 CREB3L4 FCRL4 S100A13 SNAPIN CD5L ADAR DAP3 ATP8B2 OR6K5P FLAD1 C1orf43 SLC27A3 RIT1 OR6K2 SPRR2G RHBG HAX1 MEX3A PAQR6 ENSG00000216295 RAB13 INTS3 C1orf66 S100A7 AQP10 TRIM46 ASH1L FCRL5 CD1C UBQLN4 S100A9 SH2D2A RUSC1 CRTC2 GON4L MRPL24 C1orf77 RPS27 KCNN3
1	1.53E+08	1.53E+08	1	1.78E+08	1.78E+08	DEL	24771285	BRC11	1	1	NHEJ	KCNN3	ENST00000361147	-1	intron3	C1orf125	ENST00000367618	1	intron22	ANKRD45 KRTCAP2 XCL1 C1orf112 IFI16 TOP1P1 ENSG00000135820 C1orf226 RPL4P3 TIPRL SDHC ATF6 CKS1B FMO2 IQGAP3 CCDC19 DUSP12 CASQ1 RPS10P8 NDUFS2 MEF2D FAM20B FASLG C1orf85 ZBTB37 B4GALT3 OR6P1 RXRG ARHGEF11 DPT SCAMP3 RGS5 DCST1 DNM3 NTRK1 CD1E KCNJ9 C1orf114 OR10Z1 DPM3 OR6N2 CD1B FCGR2A TTC24 FCRL6 VANGL2 IGSF9 DEDD RAG1AP1 PBXIP1 LRRC52 OR10T2 ILDR2 CENPL EFNA1 ITLN2 ITLN1 RASAL2 YY1AP1 TMEM79 C1orf92 CRABP2 TOMM40L CD1D CD244 PMVK RPL4P2 IQWD1 FCER1A SCYL3 FMO10P SELP CD84 CACYBP ETV3L RC3H1 F5 FAM78B MPZ C1orf49 MRPS14 PRDX6 ATP1A2 SHC1 TNFSF4 GPATCH4 BCAN OR10X1 ADAMTS4 ABL2 FCGR2B PPOX KIRREL FMO8P HSPA6 C1orf182 RFWD2 ARHGAP30 METTL13 DCST2 KIAA0907 TADA1L OR6N1 APOA1BP GOT2L2 ETV3 RABGAP1L SLAMF8 MPZL1 KLHL20 FAM5B RXFP4 OR10J1 APOA2 C1orf192 EFNA3 NES HMGB1L11 SEMA4A CADM3 C1orf61 PEX19 CD1A FCRL2 FMO3 SELL OR10J5 PEA15 TAGLN2 CD5L METTL11B C1orf204 DAP3 ASTN1 BLZF1 OR6K5P AIM2 NME7 FCGR3A OR6K2 FMO4 PAQR6 MEX3A FMO6P C1orf66 NCSTN NHLH1 PYHIN1 TRIM46 FCRLA FMO9P SEC16B SLAMF9 GPR161 UBQLN4 RUSC1 FCER1G ATP1B1 GON4L MRPL24 PAPPA2 USP21 WDR42A KIFAP3 F11R LY9 HDGF MGST3 ZBTB7B INSRR DDR2 OR6K6 FMO11P BRP44 HAPLN2 CREG1 SFT2D2 ATP1A4 THBS3 ISG20L2 TOR3A TNFSF18 GBA PMF1 SERPINC1 VHLL SLC9A11 COPA LENEP C1orf2 uc001fxh.2 RPL26P12 MUC1 ROBLD3 PYGO2 LMNA OR6K1P KCNJ10 PKLR EFNA4 MAEL OR10K2 HSD17B7 OR6Y1 CLK2 POU2F1 RAB25 FCRLB RPL26P11 GPA33 OR2AQ1P C1orf110 BAT2D1 OR10T1P RGS4 RCSD1 PIGC PCP4L1 MYOC SLC25A44 MTX1 OR6K3 UAP1 OR10R1P PEAR1 LMX1A ADAM15 OR10K1 FMO7P FMO1 SLAMF1 KLHDC9 FCGR3B ARHGEF2 NCRNA00083 DUSP27 FCRL3 OR10J9P SMG5 GPR52 CYCSP52 SPTA1 CCT3 C1orf111 SOAT1 PRCC HCN3 NUF2 TNN

1	1.47E+08	1.47E+08	1	2.38E+08	2.38E+08	DEL	91064724	BRC11	1	1	MMEJ	ENST00000407608	-1	intron0	FMN2	ENST00000406993	1	intron6	C1orf129 C1orf220 TNR RALGPS2 APCS FCRL1 SSR2 FDPS ERVK5 NIT1 MSTO1 CRP TBX19 TMCO1 PVRL4 CD247 C1orf156 DARC SYT11 ALDH9A1 GBAP ADCY10 OR6K4P OR10R2 C1orf9 FCRL4 POGK SLAMF6 UFC1 FLAD1 CD48 GORAB RIT1 MNDA SH2D1B XCL2 OR10J3 ANGPTL1 RHBG SELE C1orf105 ENSG00000216295 PBX1 SLC19A2 USF1 SLAMF7 ASH1L PFDN2 FCRL5 UHMK1 VAMP4 CD1C PIGM OLFML2B NOS1AP IGSF8 UCK2 SH2D2A NR1I3 PRRX1 DARS2 DUSP23 ANKRD45 CAPN8 URB2 KRTCAP2 XCL1 KLHDC8A TOP1P1 RPL34P1 ENSG00000135820 CD34 BTG2 C1orf106 GOLT1A RGS2 FAM63A IQGAP3 CCDC19 DUSP12 CASQ1 RPS10P8 MEF2D VASH2 IL19 FAM20B FASLG C1orf85 ARV1 ZBTB37 OR6P1 MOSC1 RXRG CFHR5 ARHGEF11 TAF5L INTS7 IVNS1ABP TGFB2 KCNK2 DPT ADORA2BP RGS5 DCST1 TOMM20 DNM3 NTRK1 DNAH14 C1orf114 OR10Z1 C1orf96 APOBEC4 CD1B FCGR2A H3F3A NID1 KCNT2 RABIF FCRL6 DYRK3 CD46P LGR6 FAM5C NUCKS1 LCE3E RFX5 RBM34 DEDD MIXL1 TMEM9 PKP1 TMOD4 TAF1A C1orf27 LRRC52 HIST2H2BC PPP1R12B PHLDA3 ITLN2 ITLN1 IL20 ASPM SOX13 CRABP2 IRF2BP2 CD1D NUP210L BPNT1 PLXNA2 CD244 LEFTY2 SHE TRIM67 IPO9 FLVCR1 PM20D1 LRRN2 PI4KB ANP32E PIK3C2B SCYL3 FMO10P LCE1A PRG4 NFASC RC3H1 CR1L LAX1 MPZ MAPKAPK2 MRPS14 PRDX6 ATP1A2 SHC1 FAM129A TNFSF4 BCAN C1orf133 ILF2 OR10X1 UBBP2 RGS16 AIDA ABL2 GPR137B FCGR2B RPLP0P5 PFKFB2 RAB7L1 C1orf26 S100A4 IL10 CA14 C1orf182 TEDDM1 TBCE RFWD2 ARHGAP30 THEM5 KIAA0907 HIST2H3A TADA1L PPP1R15B GOT2L2 ETV3 NCRNA00166 TCHH SNX27 DUSP5P FAM5B CD55 TNRC4 GPR37L1 RXFP4 ADH5P3 GABPB2 ACBD3 RHOU YOD1 HMGB1L11 CADM3 C1orf61 ATF3 CD1A TRAF5 CEP350 FAM58B SERTAD4 C1orf132 FMO3 SELL OR10J5 PEA15 TAGLN2 CD5L DAP3 SYT2 LHX4 ATP8B2 NME7 SLC27A3 HIST3H3 CACNA1E SPATA17 PLEKHO1 OR6K2 FMO4 DENND1B PAQR6 MEX3A FMO6P PGBD5 HIST2H4A AVPR1B AQP10 C1orf227 LPGAT1 LCE3D KIAA1383 LCE1B CAPN2 SEC16B SLAMF9 SPRR2D GPR161 UBQLN4 GLRX2 ETNK2 NECAP1 ADORA1 CYB5R1 RUSC1 SEMA6C TRIM17 ATP1B1 MRPL24 GON4L USP21 KIFAP3 TPM3 MRPL55 ARNT FLG2 NPHS2 MARK1 MGST3 FAM177B RAB3GAP2 INSRR ZNF648 C1orf98 ACBD6 CREG1 TARS2 ATP1A4 HIST2H4B APH1A JTB THBS3 ASCL5 TOR3A PMF1 VHLL C1orf138 COPA FAM163A SETDB1 LENEP C1orf2 ENSA C1orf46 MUC1 LEMD1 F13B OR6K1P ITPKB PKLR EFNA4 IL24 MT1P2 MAEL CTSE CLK2 SHISA4 ABCB10 TRIM11 NCF2 SPRR2A TROVE2 S100A5 GLUL DEGS1 ELF3 RPL26P11 C1orf56 TDRD5 LAD1 EPHX1 KLHL12 NPR1 CDC42BPA OR10T1P SLC30A10 C1orf157 RGS4 NR5A2 RCSD1 RPL13AP8 PPP2R5A TSEN15 POGZ PCP4L1 RPS10P6 RAB4A MYOC C1orf55 SLC25A44 MTX1 HMCN1 C1orf65 C1orf14 RNASEL NAV1 OR10K1 C1orf148 SLAMF1 SLC30A1 RGL1 FCGR3B ZNF687 ARHGEF2 CAMSAP1L1 NCRNA00083 PIGR CFH RCOR3 DUSP27 TCHHL1 RASSF5 CACNA1S FCRL3 ATP6V1G3 RGS13 OR10J9P PSMB4 SMG5 GPR52 CYCSP52 C1orf74 SPTA1 AGT ARF1 TMCC2 CCT3 C1orf111 TNN SIPA1L2 C1orf58 IER5 UBAP2L C1orf129 S100A2 ERO1LB RALGPS2 APCS CNTN2 IL6R CHRNB2 SSR2 RD3 MFSD4 CHI3L1 C1orf120 IRF6 C1orf197 RNPEP NIT1 ZP4 TBX19 CRP TMCO1 MOSC2 CD247 S100A7L2 IKBKE CRNN CAPN9 GPATCH2 HIST2H2AA3 RYR2 FAM72A SYT11 SLC26A9 SUSD4 ATP2B4 ENAH TDRKH CDC73 FCRL4 CNIH4 POGK SPRR2B ADAR PSMD4 ESRRG JMJD4 ECM1 FLAD1 CD48 C1orf51 C1orf21 GORAB RIT1 SH2D1B MNDA KIF14 OR10J3 LIN9 SELE C1orf105 PBX1 RAB13 MTR USF1 C1orf25 SLAMF7 ASH1L UHMK1 FCRL5 VAMP4 PRPF3 RPL17P8 OLFML2B S100A10 C1orf35 NOS1AP NMNAT2 IGSF8 FAIM3 C1orf54 RNF2 ADIPOR1 RGSL1 ANXA9 SH2D2A NR1I3 PRRX1 NEK7 OAZ3 LEFTY1 C1orf189 KIAA1614 MYBPH OTUD7B LCE5A COG2 C1orf112 WNT3A DDX59 IFI16 GJC2 TNNI1 C1orf226 KRT18P28 CFHR2 LCE3A RPL4P3 DISC1 TIPRL SDHC PROX1 LGTN uc001gud.2 ATF6 ARPC5 CKS1B C1orf145 FMO2 RPTN LAMB3 ZC3H11A NDUFS2 B4GALT3 HIST3H2A SNRPE NVL NENF SCAMP3 TTC13 CDC42SE1 S100A3 EDARADD TDRD10 CD1E DTL TOR1AIP1 HIST2H2AA4 SPRR2F KCNJ9 CR2 DPM3 OR6N2 TTC24 C1orf53 CSRP1 CTSS TUFT1 SMG7 HIST2H2BD ANGEL2 SLC41A1 GLT25D2 VANGL2 TIMM17A IGSF9 LYST C1orf198 HIST2H3PS2 TMEM78 FLG RAG1AP1 ZNF281 HIST2H3D TATDN3 SNAP47 PBXIP1 SLC45A3 OR10T2 ILDR2 GPR25 EFNA1 CENPL SNFT RASAL2 LCE2D YY1AP1 PLA2G4A TMEM79 C1orf92 RGS21 TRAF3IP3 TOMM40L RBBP5 PRUNE GGPS1 DSTYK CFHR4 PTPRV PMVK RPL4P2 IQWD1 LMOD1 FCER1A SELP LAMC2 CD84 ETV3L CACYBP MRPS21 S100A14 F5 FAM78B MYOG C1orf49 LINGO4 PIP5K1A SPRR3 GPATCH4 EXOC8 TOR1AIP2 IARS2

																				ADAMTS4 EGLN1 EPRS QSOX1 DISP1 KIRREL PPOX FMO8P SV2A HSPA6 GUK1 C1orf115 DENND4B SRGAP2 DCST2 METTL13 OR6N1 APOA1BP VPS72 SLAMF8 RABGAP1L SYT14 LYSMD1 MPZL1 FCGR1A KLHL20 TNNT2 GNPAT OR10J1 RORC RGS8 LOR APOA2 EFNA3 C1orf192 C1orf57 NES SEMA4A NUAK2 PEX19 PTGS2 USH2A NSL1 CFHR1 ADAMTSL4 OPTC FCRL2 CABC1 LCE2C C1orf204 METTL11B GALNT2 NUP133 ASTN1 UCHL5 BLZF1 GNG4 WNT9A C4BPB OR6K5P AIM2 SMCP TLR5 MIA3 RNF187 FAM71A CGN FCGR3A SPRR2G C1orf107 HAX1 REN CFHR3 CHRM3 ACTA1 C1orf66 PDC NCSTN LCE2B S100A7 NHLH1 C1orf124 SF3B4 PYHIN1 TRIM46 FCRLA FMO9P CTSK SPRR4 TSNAX LCE1D CRTC2 FCER1G HIST2H2BF C1orf77 WDR42A PAPPA2 F11R LY9 KCNK1 HSD11B1 KCNN3 HDGF S100A7A ARID4B ZBTB7B ZNF847P DDR2 OR6K6 FMO11P BRP44 HAPLN2 BOLA1 SFT2D2 FMOD C4BPA LGALS8 IGFN1 ISG20L2 OBSCN GBA TNFSF18 PTPN14 SERPINC1 SLC9A11 PPFIA4 CNIH3 HHIPL2 uc001fxh.2 RPL26P12 FCAMR TMEM183A ROBLD3 C1orf186 PRELP KIF21B S100A12 PYGO2 LMNA HIST2H2AB KCNJ10 CD46 C1orf147 KPRP CAMK1G THEM4 OR10K2 HSD17B7 OR6Y1 KCTD3 B3GALNT2 C1orf69 POU2F1 KISS1 MLLT11 C1orf31 C1orf97 G0S2 RAB25 FCRLB PCTK3 GPA33 RRP15 FAM89A PYCR2 SLC39A1 OR2AQ1P C1orf110 RPS7P5 ZBTB41 STX6 BAT2D1 S100A6 HIST3H2BB PIGC TPR S100A1 LCE2A GATAD2B LCE1C FBXO28 PSEN2 SPRR1A PGLYRP4 LELP1 C1orf131 WDR26 OR6K3 LCE3C UAP1 PCNXL2 OR10R1P PEAR1 LMX1A C1orf116 ADAM15 FMO7P NPL S100A16 FMO1 SLC35F3 KLHDC9 LCE1E S100A8 IVL PLEKHA6 CHIT1 C1orf125 MRPL9 UBE2Q1 PRCC HCN3 NUF2 SOAT1 TNFAIP8L2 MR1 RGS18 C1orf220 TNR FCRL1 HORMAD1 PRR9 LHX9 ZC3H11B BNIPL FDPS PGLYRP3 ERVK5 SPHAR MAP3K19 ARL8A CRB1 EEF1AL12 MTMR11 LCE3B RPS6KC1 MSTO1 DUSP10 MCL1 SELENBP1 SCNM1 PVRL4 C1orf156 EDEM3 ACTN2 DARC LCE4A ALDH9A1 GBAP SPRR2E ADCY10 S100A11 LAMC1 ZNF678 SRP9 HIST2H2AC SMYD2 RPRD2 NEK2 OR10R2 OR6K4P HIST2H2BE JARID1B CREB3L4 VPS45 TARBP1 PTPN7 C1orf9 TP53BP2 S100A13 SNAPIN LYPLAL1 TMEM206 UBE2T SLAMF6 HEATR1 CENPF UFC1 ELK4 C1orf43 C1orf68 XCL2 HLX HHAT TMEM81 ANGPTL1 MDM4 RGS1 RHBG MPN2 GOLPH3L CR1 ENSG00000216295 INTS3 SLC19A2 SPRR1B TMEM63A HIST2H3C PFDN2 CD1C LASS2 PIGM S100A9 UCK2 LBR PARP1 PTPRC DHX9 B3GALT2 ACTBP11 DARS2 C1orf95 RPS27 CRCT1 DUSP23 LCE1F HRNR KCNH1 XPR1
1	1.46E+08	1.46E+08	1	1.46E+08	1.46E+08	DEL	163508	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	GJA5 GJA8
7	84430265	84430265	7	89455137	89455137	DEL	5023871	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ABCB1 RUNDC3B STEAP4 ZNF804B DBF4 CROT uc003ujn.1 SEMA3D C7orf62 ABCB4 SRI GRM3 ADAM22 TP53TG1 SLC25A40 DMTF1 C7orf23 KIAA1324L
1	1.5E+08	1.5E+08	1	2.28E+08	2.28E+08	DEL	77510032	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	ABCB10	ENST00000344517	-1	intron8	ANKRD45 CAPN8 KRTCAP2 XCL1 KLHDC8A TOP1P1 RPL34P1 ENSG00000135820 CD34 BTG2 C1orf106 GOLT1A RGS2 IQGAP3 CCDC19 DUSP12 CASQ1 RPS10P8 MEF2D VASH2 IL19 FAM20B FASLG C1orf85 ZBTB37 OR6P1 MOSC1 RXRG CFHR5 ARHGEF11 INTS7 IVNS1ABP TGFB2 KCNK2 DPT ADORA2BP RGS5 DCST1 DNM3 NTRK1 DNAH14 C1orf114 OR10Z1 C1orf96 APOBEC4 CD1B FCGR2A H3F3A KCNT2 RABIF FCRL6 DYRK3 CD46P LGR6 FAM5C NUCKS1 LCE3E DEDD MIXL1 TMEM9 PKP1 TAF1A C1orf27 LRRC52 PPP1R12B PHLDA3 ITLN2 ITLN1 IL20 ASPM SOX13 CRABP2 CD1D NUP210L BPNT1 PLXNA2 CD244 LEFTY2 SHE IPO9 FLVCR1 PM20D1 LRRN2 PIK3C2B SCYL3 FMO10P LCE1A PRG4 NFASC RC3H1 CR1L LAX1 MPZ MAPKAPK2 MRPS14 PRDX6 ATP1A2 SHC1 FAM129A TNFSF4 BCAN C1orf133 ILF2 OR10X1 UBBP2 RGS16 AIDA ABL2 FCGR2B RPLP0P5 PFKFB2 RAB7L1 C1orf26 S100A4 IL10 C1orf182 TEDDM1 RFWD2 ARHGAP30 KIAA0907 TADA1L PPP1R15B GOT2L2 ETV3 TCHH DUSP5P FAM5B CD55 GPR37L1 RXFP4 ACBD3 RHOU YOD1 HMGB1L11 CADM3 C1orf61 ATF3 CD1A TRAF5 CEP350 FAM58B SERTAD4 C1orf132 FMO3 SELL OR10J5 PEA15 TAGLN2 CD5L DAP3 SYT2 LHX4 ATP8B2 NME7 SLC27A3 HIST3H3 CACNA1E SPATA17 OR6K2 FMO4 DENND1B PAQR6 MEX3A FMO6P AVPR1B AQP10 C1orf227 LPGAT1 LCE3D LCE1B CAPN2 SEC16B SLAMF9 SPRR2D GPR161 UBQLN4 GLRX2 ETNK2 NECAP1 ADORA1 CYB5R1 RUSC1 TRIM17 ATP1B1 MRPL24 GON4L USP21

																				KIFAP3 TPM3 MRPL55 FLG2 NPHS2 MARK1 MGST3 FAM177B RAB3GAP2 INSRR ZNF648 C1orf98 ACBD6 CREG1 ATP1A4 JTB THBS3 ASCL5 TOR3A PMF1 VHLL COPA FAM163A LENEP C1orf2 C1orf46 MUC1 LEMD1 F13B OR6K1P ITPKB PKLR EFNA4 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 PCP4L1 RAB4A MYOC C1orf55 SLC25A44 MTX1 HMCN1 C1orf65 C1orf14 RNASEL NAV1 OR10K1 C1orf148 SLAMF1 SLC30A1 RGL1 FCGR3B ARHGEF2 CAMSAP1L1 NCRNA00083 PIGR CFH RCOR3 DUSP27 TCHHL1 RASSF5 CACNA1S FCRL3 ATP6V1G3 RGS13 OR10J9P SMG5 GPR52 CYCSP52 C1orf74 SPTA1 ARF1 TMCC2 CCT3 C1orf111 TNN C1orf58 IER5 UBAP2L C1orf129 S100A2 RALGPS2 APCS CNTN2 IL6R CHRNB2 SSR2 RD3 MFSD4 CHI3L1 C1orf120 IRF6 C1orf197 RNPEP NIT1 TBX19 CRP TMCO1 MOSC2 CD247 S100A7L2 IKBKE CRNN GPATCH2 FAM72A SYT11 SLC26A9 SUSD4 ATP2B4 ENAH CDC73 FCRL4 CNIH4 POGK SPRR2B ADAR ESRRG JMJD4 FLAD1 CD48 C1orf21 GORAB RIT1 SH2D1B MNDA KIF14 OR10J3 LIN9 SELE C1orf105 PBX1 RAB13 USF1 C1orf25 SLAMF7 ASH1L UHMK1 FCRL5 VAMP4 RPL17P8 OLFML2B S100A10 C1orf35 NOS1AP NMNAT2 IGSF8 FAIM3 RNF2 ADIPOR1 RGSL1 SH2D2A NR1I3 PRRX1 NEK7 LEFTY1 C1orf189 KIAA1614 MYBPH LCE5A C1orf112 WNT3A IFI16 DDX59 GJC2 C1orf226 KRT18P28 TNNI1 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 LMOD1 SELP LAMC2 CD84 ETV3L CACYBP S100A14 F5 FAM78B MYOG C1orf49 SPRR3 GPATCH4 TOR1AIP2 IARS2 ADAMTS4 EPRS QSOX1 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 NUAK2 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 PRCC HCN3 NUF2 SOAT1 MR1 C1orf220 RGS18 TNR FCRL1 PRR9 LHX9 ZC3H11B PGLYRP3 FDPS ERVK5 SPHAR ARL8A EEF1AL12 CRB1 LCE3B RPS6KC1 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
1	2.28E+08	2.28E+08	1	2.28E+08	2.28E+08	DEL	98521	BRC11	1	1	NHEJ	ABCB10	ENST00000344517	-1	utr_exon13	TAF5L	ENST00000258281	-1	intron0	TAF5L

1	1.51E+08	1.51E+08	1	1.53E+08	1.53E+08	DEL	1576969	BRC1	1	1	NHEJ	SPRR2A	ENST00000368752	-1	intron0	N/A	N/A	N/A	N/A	TPM3 S100A7A C1orf189 CREB3L4 ILF2 UBE2Q1 S100A13 SNAPIN ADAR SLC39A1 NPR1 UBAP2L S100A2 ATP8B2 S100A6 S100A1 IL6R C1orf43 JTB PRR9 GATAD2B SLC27A3 CHRNB2 S100A4 PGLYRP3 DENND4B SPRR2G HAX1 ENSG00000216295 PGLYRP4 LELP1 RAB13 INTS3 S100A7 AQP10 S100A12 NUP210L S100A7L2 SHE S100A3 TDRD10 S100A9 S100A16 SPRR2F LOR CRTC2 S100A8 S100A14 C1orf77 RPS27 S100A5
1	1.19E+08	1.19E+08	1	1.93E+08	1.93E+08	DEL	74114972	BRC1	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ANKRD45 KRTCAP2 XCL1 ADAM30 TOP1P1 ENSG00000135820 RGS2 FAM63A IQGAP3 CCDC19 DUSP12 CASQ1 RPS10P8 MEF2D FAM20B FASLG C1orf85 ZBTB37 OR6P1 RXRG ARHGEF11 IVNS1ABP DPT PPIAL4A RGS5 DCST1 DNM3 NTRK1 NBPF12 C1orf114 OR10Z1 APOBEC4 CD1B HMGCS2 FCGR2A SRGAP2P1 FCRL6 FAM5C LCE3E RFX5 DEDD TMOD4 C1orf27 LRRC52 HIST2H2BC ITLN2 ITLN1 CRABP2 NUDT17 CD1D NUP210L CD244 SHE PI4KB ANP32E SCYL3 FMO10P LCE1A PRG4 RC3H1 MPZ MRPS14 PRDX6 ATP1A2 SHC1 FAM129A TNFSF4 BCAN ILF2 OR10X1 RGS16 ABL2 FCGR2B C1orf26 S100A4 CA14 C1orf182 TEDDM1 RFWD2 ARHGAP30 THEM5 KIAA0907 HIST2H3A TADA1L GOT2L2 ETV3 NCRNA00166 TCHH SNX27 CD160 FAM5B TNRC4 RXFP4 GABPB2 HMGB1L11 CADM3 C1orf61 CD1A CEP350 REG4 FMO3 SELL OR10J5 PEA15 TAGLN2 CD5L DAP3 LHX4 ATP8B2 NME7 SLC27A3 CACNA1E PLEKHO1 OR6K2 FMO4 PAQR6 MEX3A FMO6P HIST2H4A ANKRD35 AQP10 LCE3D LCE1B SEC16B SLAMF9 SPRR2D GPR161 UBQLN4 GLRX2 NBPF10 PIAS3 RUSC1 SEMA6C ATP1B1 MRPL24 GON4L USP21 KIFAP3 TPM3 ARNT FLG2 NPHS2 MGST3 INSRR ZNF648 RPL6P2 ACBD6 CREG1 TARS2 ATP1A4 HIST2H4B APH1A JTB GPR89C THBS3 TOR3A PMF1 VHLL C1orf138 COPA FAM163A C1orf2 SETDB1 LENEP ENSA C1orf46 MUC1 FAM72B OR6K1P PKLR EFNA4 MAEL HSD3B2 CLK2 NCF2 SPRR2A TROVE2 S100A5 GLUL RPL26P11 C1orf56 TDRD5 NPR1 OR10T1P BCL9 RGS4 FAM108A2 RCSD1 TSEN15 POGZ PCP4L1 RPS10P6 MYOC SLC25A44 MTX1 HMCN1 C1orf14 FMO5 PDZK1P2 NBPF8 RNASEL OR10K1 DRD5P2 SLAMF1 RGL1 FCGR3B ZNF687 ARHGEF2 NCRNA00083 DUSP27 TCHHL1 FCRL3 GJA8 RGS13 OR10J9P PSMB4 SMG5 GPR52 CYCSP52 SPTA1 CCT3 C1orf111 TNN IER5 UBAP2L C1orf129 S100A2 C1orf152 RALGPS2 APCS IL6R uc001elp.1 CHRNB2 SSR2 C1orf120 NIT1 TBX19 CRP TMCO1 CD247 S100A7L2 CRNN HIST2H2AA3 NBPF11 SYT11 TDRKH FCGR1B CDC73 FCRL4 POGK SPRR2B ADAR PSMD4 ECM1 FLAD1 CD48 C1orf51 C1orf21 GORAB RIT1 SH2D1B MNDA OR10J3 SELE C1orf105 PBX1 RAB13 USF1 C1orf25 SLAMF7 ASH1L UHMK1 FCRL5 VAMP4 PRPF3 OLFML2B S100A10 NOS1AP NMNAT2 IGSF8 C1orf54 RNF2 RGSL1 SH2D2A ANXA9 NR1I3 PRRX1 KIAA1245 OAZ3 PDE4DIP C1orf189 KIAA1614 OTUD7B LCE5A C1orf112 IFI16 KRT18P28 C1orf226 LCE3A RPL4P3 TIPRL SDHC ATF6 ARPC5 CKS1B FMO2 RPTN NOTCH2NL NDUFS2 NBPF1 B4GALT3 SCAMP3 CDC42SE1 S100A3 TDRD10 CD1E TOR1AIP1 HIST2H2AA4 SPRR2F KCNJ9 HAO2 DPM3 OR6N2 TTC24 SMG7 CTSS TUFT1 HIST2H2BD GNRHR2 GLT25D2 PRKAB2 VANGL2 IGSF9 HIST2H3PS2 FLG RAG1AP1 HIST2H3D PBXIP1 FAM108A3 OR10T2 NBPF16 ILDR2 CENPL EFNA1 RASAL2 LCE2D YY1AP1 PLA2G4A TMEM79 C1orf92 RGS21 TOMM40L PRUNE PMVK RPL4P2 IQWD1 FCER1A HFE2 LAMC2 SELP CD84 CACYBP ETV3L MRPS21 S100A14 F5 FAM78B C1orf49 RBM8A LINGO4 PIP5K1A SPRR3 GPATCH4 TOR1AIP2 HSD3B1 ADAMTS4 PDZK1 QSOX1 KIRREL PPOX FMO8P SV2A HSPA6 DENND4B DCST2 METTL13 OR6N1 APOA1BP VPS72 RABGAP1L SLAMF8 LYSMD1 MPZL1 KLHL20 FCGR1A PHGDH ACP6 CCT8P1 OR10J1 RORC RGS8 LOR APOA2 EFNA3 C1orf192 NES SEMA4A PEX19 PTGS2 ADAMTSL4 FCRL2 LCE2C C1orf204 METTL11B ASTN1 UCHL5 BLZF1 OR6K5P AIM2 SMCP CGN FCGR3A SPRR2G HAX1 C1orf66 PDC WARS2 NCSTN LCE2B S100A7 NHLH1 SF3B4 PYHIN1 TRIM46 FCRLA FMO9P CTSK NOTCH2 SPRR4 LCE1D CRTC2 FCER1G HIST2H2BF PAPPA2 C1orf77 WDR42A ANKRD34A F11R LY9 KCNN3 S100A7A HDGF ZBTB7B DDR2 OR6K6 FMO11P GPR89A BRP44 HAPLN2 BOLA1 SFT2D2 RNF115 ISG20L2 GBA TNFSF18 SERPINC1 SLC9A11 uc001fxh.2 RPL26P12 ROBLD3 S100A12 PYGO2 POLR3GL LMNA HIST2H2AB KCNJ10 KPRP THEM4 OR10K2 HSD17B7 OR6Y1 POU2F1 MLLT11 RAB25 FCRLB GPA33 SLC39A1 OR2AQ1P C1orf110 SEC22B STX6 BAT2D1 SRGAP2P2 S100A6 PIGC TPR S100A1 LCE2A GATAD2B LCE1C SPRR1A PGLYRP4 LELP1 OR6K3 LCE3C UAP1 OR10R1P PEAR1 LMX1A ADAM15 NPL FMO7P S100A16 FMO1 POLR3C KLHDC9 LCE1E S100A8 IVL C1orf125 MRPL9 UBE2Q1 SOAT1 HCN3 PRCC NUF2 MR1 TNFAIP8L2 RGS18 C1orf220 TNR FCRL1 PRR9 HORMAD1 BNIPL PGLYRP3 FDPS ERVK5 TBX15 EEF1AL12 MTMR11 LCE3B CHD1L MSTO1 MCL1 SELENBP1 SCNM1 PVRL4 C1orf156 EDEM3 ZNF697

1	1.92E+08	1.92E+08	1	2E+08	2E+08	DEL	8303412	BRC11	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	TXNIP DARC LCE4A ALDH9A1 GBAP GJA5 SPRR2E ADCY10 NBPF7 LAMC1 S100A11 HIST2H2AC RPRD2 OR10R2 OR6K4P HIST2H2BE CREB3L4 VPS45 C1orf9 S100A13 SNAPIN PEX11B LIX1L PPIAL4G SLAMF6 UFC1 C1orf43 C1orf68 XCL2 ANGPTL1 RGS1 RHBG NBPF15 GOLPH3L ENSG00000216295 INTS3 SLC19A2 SPRR1B HIST2H3C PFDN2 CD1C LASS2 PIGM S100A9 UCK2 GPR89B DHX9 B3GALT2 DARS2 RPS27 CRCT1 DUSP23 LCE1F HRNR XPR1 ITGA10 ELF3 TIMM17A LAD1 DDX59 TNNI1 RPL34P1 ZBTB41 CFHR2 TMEM9 C1orf106 ZNF281 C1orf98 uc001gud.2 PKP1 NR5A2 IGFN1 LHX9 ASCL5 PHLDA3 KIF14 GPR25 DENND1B CFHR3 EEF1AL12 CRB1 RNPEP ASPM CFHR5 KIF21B TNNT2 CFHR4 F13B IPO9 NAV1 LMOD1 CAMSAP1L1 CFH NEK7 PTPRC C1orf53 SHISA4 CSRP1 CACNA1S ATP6V1G3 FAM58B KCNT2 CFHR1
20	2574140	2574140	20	4052073	4052073	DEL	1476924	BRC11	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	UBOX5 HSPA12B C20orf141 C20orf29 CENPB GFRA4 FASTKD5 PTPRA CDC25B C20orf194 ITPA RNF24 UBE2V1P1 ADAM33 MRPS26 CPXM1 NOP56 IDH3B RPL19P1 PANK2 FAM113A VPS16 ATRN DDRGK1 SPEF1 AVP SIGLEC1 SF3A3P1 uc002wjw.2 GNRH2 EBF4 SLC4A11 ENSG00000205300 C20orf27 uc002wia.1 OXT
7	4571311	4571360	10	66301902	66301923	CTX	N/A	BRC11	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
21	29956766	29956766	21	35944516	35944516	DEL	5986750	BRC12	1	1	NHEJ	GRIK1	ENST00000327783	-1	intron4	N/A	N/A	N/A	N/A	OLIG1 KRTAP19P2 DONSON OLIG2 RPL8P2 OR7E23P URB1 KRTAP19P1 KCNE2 KRTAP8P2 KRTAP19-4 CRYZL1 KRTAP19-1 ATP5O TCP10L KRTAP21-2 KRTAP13-4 C21orf66 HUNK KRTAP8-1 C21orf45 KRTAP19-2 KRTAP11-1 CLDN8 KRTAP19-5 KRTAP13-3 UBE3AP2 KRTAP21-1 CLDN17 MRPS6 KRTAP22-1 KRTAP27-1 IFNAR2 C21orf59 SON KRTAP26-1 KRTAP19-6 IFNGR2 KRTAP19-3 IFNAR1 KRTAP22-2 RUNX1 CLIC6 ITSN1 RPS5P2 TMEM50B C21orf49 KRTAP15-1 KRTAP13P2 KRTAP20-3 KRTAP19-7 GART KRTAP20-2 KRTAP8P1 KRTAP19P3 KRTAP6-1 KRTAP13P1 KCNE1 FBXW11P1 TIAM1 SLC5A3 KRTAP6-3 KRTAP23-1 KRTAP20-4 C21orf77 KRTAP24-1 C21orf51 C21orf62 KRTAP13-2 RPL34P3 SOD1 KRTAP6-2 SYNJ1 HMGN1L2 C21orf63 IL10RB DSCR1 TPT1P KRTAP19-8 SFRS15 DNAJC28 C21orf9 KRTAP13-1 MRAP KRTAP20-1
8	1.32E+08	1.32E+08	8	1.32E+08	1.32E+08	DEL	1477	BRC12	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	52546546	52546546	8	1.36E+08	1.36E+08	DEL	83434877	BRC12	1	1	NHEJ	PXDNL	ENST00000356297	-1	intron0	N/A	N/A	N/A	N/A	BHLHE22 uc010maq.1 CA3 CPA6 PKIA ASPH CHCHD7 TRMT12 TPD52 ESRP1 ABRA RALYL CNBD1 KCNB2 MYBL1 AZIN1 UBR5 CA8 NBN TMEM64 DECR1 RAB2 C8orf85 C8orf83 GGH EYA1 ZNF572 ZFPM2 RNF139 MRPS28 PRDM14 LRRC6 MOS ZFHX4 SPAG1 SLC7A13 MATN2 RDH10 RPL7 CA13 SLC10A5 MSC REXO1L4P RP1 ASAP1 RB1CC1 EXT1 NCALD SULF1 SLA KCNV1 EBAG9 ANKRD46 TMEM68 C8orf76 uc003ygm.1 RGS20 VCPIP1 C8orf45 COX6C MTSS1 NSMCE2 ATP6V0D2 ZFAND1 PREX2 uc010mco.1 NACAP1 TMEM65 PHF20L1 PI15 TCEA1P2 CALB1 RLBP1L1 PSKH2 CSPP1 UQCRB CSMD3 ARFGEF1 IMPA1 XKR9 GDAP1 COPS5 TG C8orf84 C8orf47 LYN NCOA2 FABP4 FAM164A C8orf71 LRRC67 RIMS2 CRH TMEM55A SEC11B RAD54B RPS20 RRM2B SNX16 SDCBP ATAD2 C8orf39 ODF1 KCNS2 ZNF704 FABP12 CHD7 SLC30A8 SDR16C5 CRISPLD1 KCNQ3 SAMD12 TMEM70 LYPLA1 CYP7B1 DPY19L4 PXMP3 TRPA1 WDSOF1 FZD6 ADHFE1 DSCC1 PTTG3 IMPAD1 SQLE NOV C8orf46 SNORD54 RAD21 POLR2K ST3GAL1 ANXA13 ZHX1 OXR1 SOX17 STAU2 GDF6 DPYS STK3 HAS2 YTHDF3 NDRG1 GSDMC MRPL13 ZNF706 POU5F1P1 OC90 RUNX1T1 RRS1 WDR21C SLCO5A1 HNF4G COLEC10 FAM150A KLHL38 SLC25A32 TM7SF4 EIF3E NSMAF TOX ARMC1 SNTB1 DEPDC6 ATP6V1H HNRNPA1P4 C8orf54 RNF19A ENY2 PMP2 PLAG1 TMEM75 PPM2C FABP5 DERL1 JPH1 ZHX2 TERF1 RPS26P6 TP53INP1 EFR3A TRHR UBXN2B MMP16 NPAL2 TCEB1 TRIB1 TSPYL5 TNFRSF11B TATDN1 TRAM1 WDYHV1 E2F5 KLF10 RBM12B BAALC TTPA OTUD6B CTHRC1 TMEM71 PAG1 IFITM8P ENPP2 MTBP ADCY8 DNAJC5B TAF2 NPBWR1 NECAB1 COL14A1 CPNE3 SGK3 C8orf38 TRPS1 CNGB3 GEM UTP23 CA1 MYC XKR4 STMN2 C8orf34 SLC26A7 PENK FAM110B TCF24 FBXO32 RPL30 NKAIN3 CCNE2 SDC2 PDE7A CA2 PLEKHF2 INTS8 MTDH LRRCC1 PCMTD1 NUDCD1 FAM91A1 uc003yhw.1 LRRC69 OPRK1 RGS22 EIF3H LY96 HRSP12 FABP9 OSGIN2 MRPL15 TGS1 LAPTM4B WWP1

																				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 RSPO2 LRP12 FER1L6 NDUFB9 PTDSS1 FAM82B YWHAZ TMEM67 WDR67 FAM83A KIAA1429 MTFR1 CDH17
8	1.27E+08	1.27E+08	8	1.27E+08	1.27E+08	DEL	1332	BRC12	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	1.31E+08	1.31E+08	8	1.31E+08	1.31E+08	DEL	1011	BRC12	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
13	31790161	31790161	13	31791494	31791494	DEL	1332	BRC12	1	1	NHEJ	BRCA2	ENST00000380152	1	intron1	BRCA2	ENST00000380152	1	intron2	N/A
7	1.1E+08	1.1E+08	7	1.1E+08	1.1E+08	DEL	1092	BRC12	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
21	29949642	29949642	21	29956433	29956433	DEL	6786	BRC12	1	1	MMEJ	GRIK1	ENST00000327783	-1	intron4	GRIK1	ENST00000327783	-1	intron4	N/A
11	78556033	78556033	11	79288978	79288978	DEL	731942	BRC12	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	80621951	80621951	11	85277898	85277898	DEL	4654943	BRC12	1	1	MMEJ	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
8	40123474	40123474	8	40123863	40123863	DEL	385	BRC12	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	38423599	38423599	8	38507277	38507277	DEL	83677	BRC12	1	1	NHEJ	FGFR1	ENST00000341462	-1	intron1	N/A	N/A	N/A	N/A	N/A
20	53551259	53551259	21	42924092	42924092	CTX	N/A	BRC12	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
14	53072033	53072033	20	56021543	56021543	CTX	N/A	BRC12	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	38429385	38429385	21	35204152	35204152	CTX	N/A	BRC12	1	1	MMEJ	N/A	N/A	N/A	N/A	RUNX1	ENST00000300305	-1	intron1	N/A
20	41129662	41129662	21	36868378	36868378	CTX	N/A	BRC12	-1	1	MMEJ	PTPRT	ENST00000373187	-1	intron1	CLDN14	ENST00000342108	-1	intron0	N/A

20	48892971	48892971	21	29949264	29949264	CTX	N/A	BRC12	1	1	NHEJ	BCAS4	ENST00000355583	1	intron4	GRIK1	ENST00000327783		-1	intron4	N/A
20	48381856	48381856	21	45014680	45014680	CTX	N/A	BRC12	1	1	NHEJ	N/A	N/A	N/A	N/A	UBE2G2	ENST00000397904		-1	utr_exon6	N/A
20	57406699	57406699	21	45124730	45124730	CTX	N/A	BRC12	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A		N/A	N/A
20	29513823	29513823	21	34806348	34806348	CTX	N/A	BRC12	-1	1	NHEJ	N/A	N/A	N/A	N/A	KCNE1	ENST00000337385		-1	utr_exon0	N/A
17	11907399	11907399	17	54959348	54959348	DEL	43050938	BRC14	1	1	MMEJ	MAP2K4	ENST00000353533	1	intron2	N/A	N/A	N/A		N/A	MLX C17orf103 KRTAP4-12 OR4D1 FAM187A CNTNAP1 KRTAP2-2 RNF135 TBC1D3F ERAL1 HOXB1 SLC4A1 HSD17B1 MYL4 CDC27 CCL11 VEZF1 PPY uc010crp.1 KRT14 CCL23 AMAC1 GIT1 NUFIP2 MSL1 MRPL10 CDRT4 TTC19 GJD3 SEPT4 RPL19 MMP28 CCDC49 B9D1 LPO HS3ST3A1 KRT9 NOS2 MFAP4 CRKRS KRTAP9-3 CCDC103 RARA C17orf63 UBB SLC6A4 ANKRD13B CDRT1 C17orf67 SKAP1 EPN2 TOP3A ZNF385C C17orf50 MRPL45 CRHR1 SOCS7 CCL18 FOXO3B TBC1D3H EZH1 SSH2 KRTAP1-3 KRTAP4-5 GPR179 SPAG5 KRT27 FAM83G TMEM132E NSF KIF2B DUSP3 RPS16P8 ITGA2B BZRAP1 FLCN RHOT1 C17orf32 DHRS11 ITGA3 NXPH3 BRCA1 SCPEP1 UNC45B HS3ST3B1 KRT42P CNTD1 AARSD1 BLMH NEUROD2 HIGD1B RAI1 MRM1 ACACA NPEPPS EPN3 KRT17P1 CCL4L2 UTP18 C17orf96 SP6 COL1A1 CCL3L3 MLLT6 MEOX1 ALDOC WIPF2 NT5M SFRS1 AKAP1 SUPT4H1 KRTAP9-8 NAGLU FAM117A DHX8 KRTAP4-3 ALDH3A2 NLK KRT39 KRT222P FBXW10 TTLL6 HOXB4 PYY SPOP KRT28 RASL10B KRT13 SLFN12 ANKFN1 ARL17P1 KRTAP3-1 FAM33A MEIS3P1 C17orf73 EVI2A MYO15A THRAP4 KRTAP2-1 SAMD14 ARL4D SGCA MYO19 MTMR4 HDAC5 GRB7 PPARBP LRRC37B2 TBC1D3G ERBB2 KRTAP4-6 PERLD1 ALDH3A1 EIF1 POLDIP2 TMEM98 CCDC43 PNMT RPS28 OSBPL7 GSDMA TMIGD1 KRT26 CCL8 KRTAP4-14 KIAA0100 TADA2L SCRN2 ZNF624 RPL17P43 KRTAP9-1 FZD2 MAP3K14 ENSG00000198274 KRT20 CCL3L1 KRT38 uc002gnr.2 KRTAP9-5 TMEM99 CCDC144B STAT5B LRRC37A2 RPL7P48 PSMD3 LRRC37B ZPBP2 C17orf79 C1QL1 ZNF286 PLEKHM1 KIF18B KRTAP3-2 CA10 COPZ2 ATXN7L3 KRTAP4-4 TRAF4 KRT16 PTRF CCL16 EVI2B ELAC2 PSMD11 NEK8 C17orf42 uc002igz.2 TOP2A DLX3 TMEM92 MRPS23 TOM1L1 KCNJ12 FAM134C SNX11 RPS2P48 FNDC8 HOXB3 NME1-NME2 C17orf69 TNS4 TCAP LGALS9 NCOR1 KRTAP4-9 COIL DBF4B SUZ12P PLD6 TUBG1 SP2 EFTUD2 uc002ibz.1 PSMC3IP EPX MSI2 CACNB1 MBTD1 NFE2L1 CCDC56 IKZF3 WNT3 uc002hxt.1 CASC3 LSM12 PIGS SLC5A10 KRT37 SPACA3 GIP SPATA20 PPP1R9B HOXB13 HOXB6 VPS25 CDC6 UTP6 GSDMB LRRC48 COPS3 SEZ6 SLC47A1 COX10 ORMDL3 TBC1D28 GAS2L2 TMEM97 RAPGEFL1 SUZ12 TBC1D3E ARL5C CDK5R1 FBXO47 DHRS13 CCL1 SH3D20 C17orf65 RASD1 LGALS9C GRN TMEM11 CCL7 ENSG00000197665 KRTAP17-1 CDK5RAP3 SLFN13 LRRC59 HLF C17orf98 MAPT RAB34 KRTAP3-3 TAC4 STAT5A PPY2 FAM18B TBC1D27 SDF2 SLC47A2 RAB5C STXBP4 CCDC144C TOM1L2 TRIM37 CCDC144NL KRTAP9-2 TEKT3 TBC1D3D MRPL27 ENSG00000204913 DLX4 KRT15 MED9 PYY2 C17orf102 C17orf53 KRT17 SLC46A1 RNF126P1 ATAD4 CCDC55 ADORA2B LLGL1 HILS1 HEXIM1 SNF8 ACBD4 DNAJC7 THRA ACSF2 SEBOX GFAP PIGL PRAC IFI35 FLOT2 RPL23 WFIKKN2 KRTAP4-1 KRT19 PPP1R1B HEXIM2 GOSR2 TIAF1 UBE2Z TUBG2 TBX21 ZSWIM7 C17orf75 CCR10 SLFN11 TNFRSF13B TP53I13 CRYBA1 ADAP2 DYNLL2 HOXB5 AOC3 KSR1 TRPV2 MEIS3P2 TTC25 CCL5 STAC2 C17orf66 CENPV STARD3 LRRC37A4 HOXB8 ALKBH5 PLEKHH3 KRT24 JUP PRPSAP2 MPP3 C17orf71 RAD51L3 KRTAP9-6 AKAP10 EME1 NGFR SLC13A2 NBR2 KLHL10 ENSG00000214845 HNF1B ACCN1 MYCBPAP uc002isr.1 FOXN1 ATP6V0A1 TBC1D3B PEMT MMD CCL14 FKBP10 DGKE NOG DUSP14 C17orf45 PLCD3 KCNH4 GPATCH8 MPO FAM27L CPD RNF112 ZNF830 ABCC3 HOXB9 FBXL20 CSF3 ULK2 RHBDL3 GJC1 SARM1 COX11 SPAG9 DCAKD ARL17 PDK2 ETV4 KRTAP1-5 STAT3 KRTAP2-4 CUEDC1 USP22 KRT25 ZNHIT3 NT5C3L LRRC46 KRT36 DDX52 RPS26P8 TMUB2

																				GRAP NMT1 KRT10 MPP2 CBX1 FAM18B2 RAB11FIP4 NF1 RND2 UNC119 CNP TBC1D3C RAD51C CDRT15 KRTAP9-7 LGALS9B PCTP TBKBP1 EFCAB5 uc002hqd.1 SLFN5 KRT35 RSAD1 ITGB3 KRT33A G6PC VTN TLCD1 CCL15 WNK4 RPL23A C17orf78 SLC35B1 KRTAP4-2 CD300LG KRTAP9-4 RFFL PIGW CCL4 AP2B1 MYO18A KLHL11 RAMP2 CCDC144A C17orf39 ACLY SOST PSMB3 SUPT6H MAPK7 ZNF207 MPRIP HSF5 NLE1 TAF15 BECN1 TBC1D26 TBC1D29 SREBF1 PCGF2 ANKRD40 CCT6B CALCOCO2 IGFBP4 UBTF CCL4L1 MYST2 PHB KPNB1 AATF PIP5K2B RNF43 MKS1 PHF12 TMEM106A KRTAP4-8 KRT12 LYZL6 TEX14 XYLT2 PSME3 GNGT2 PEX12 PMP22 IFT20 WSB1 TRIM16L ASB16 PPM1E PHOSPHO1 DHX58 WNT9B SMCR7 VAT1 CYTSB C17orf84 GAST NAGS CCL3 DHRS7B KRT33B LRRC37A HOXB7 KRT34 LIG3 KRT31 ATAD5 ADAM11 HCRT TMEM101 uc002hca.1 GOSR1 OR4D2 MYO1D HAP1 KAT2A KIAA1267 TRIM25 B4GALNT2 ZNF403 HOXB2 TAOK1 PLXDC1 MAP2K3 RUNDC3A OMG RUNDC1 RPL27 FLII CDRT15L2 LASP1 SLC25A39 ATPAF2 ARHGAP23 C17orf57 G6PC3 PNPO GDPD1 RPL29P31 CCL2 CRLF3 PRR11 KRT40 SHMT1 EVPLL HSPB9 PIPOX SMARCE1 COASY C17orf76 TBC1D3 ARHGAP27 NR1D1 ABI3 CHAD C17orf47 NKIRAS2 CORO6 ENSG00000204880 KRTAP1-1 TRIM16 TOB1 MYOCD CACNA1G AOC2 KRT14P CCR7 IGF2BP1 RPL9P2 GHDC YPEL2 ATP5G1 KRTAP16-1 DRG2 FAM171A2 C17orf46 TMEM100 KRT23 ZNF287 RPRML RDM1 FAM106B KRT32 SLFN12L ZNF652 SMCR8 C17orf37 FMNL1 CCL13 LHX1 TNFAIP1 AP1GBP1 HSD17BP1
8	51317594	51317594	8	55261988	55261988	DEL	3943392	BRC14	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ATP6V1H OPRK1 NPBWR1 ST18 SNTG1 TCEA1P2 RGS20 RB1CC1 PCMTD1 MRPL15 PXDNL LYPLA1 FAM150A
2	2.11E+08	2.11E+08	2	2.12E+08	2.12E+08	DEL	783202	BRC14	1	1	NHEJ	N/A	N/A	N/A	N/A	ERBB4	ENST00000342788	-1	intron12	N/A
7	1.52E+08	1.52E+08	7	1.52E+08	1.52E+08	DEL	599	BRC14	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	5273926	5273926	17	21287713	21287713	DEL	16012759	BRC14	1	1	MMEJ	RPAIN	ENST00000381209	1	intron6	N/A	N/A	N/A	N/A	C17orf103 ALDH3A1 MAPK7 C17orf59 ARHGEF15 PIGL AURKB VAMP2 RPS28 CNTROB MPRIP MED31 SHBG TBC1D26 SREBF1 ZSWIM7 ZNF624 MFSD6L NEURL4 DHRS7C uc002gna.2 RPL26 SLC13A5 RPL17P43 TNFRSF13B ASGR2 TMEM220 SLC25A35 ENSG00000198274 MEIS3P2 TRPV2 uc002gnr.2 TP53 AIPL1 C17orf100 CCDC144B CDRT4 TTC19 CENPV MAP2K4 B9D1 C17orf48 NTN1 TXNL5 ALKBH5 HS3ST3A1 CHRNB1 ZNF286 PMP22 C17orf61 MFAP4 PRPSAP2 PIK3R6 TMEM102 MYH8 TRIM16L RNF222 PFAS C1QBP SLC16A11 AKAP10 ALOXE3 ALOX12 DLG4 UBB ELAC2 DERL2 KCTD11 C17orf74 CDRT1 NLRP1 ENSG00000214845 SMCR7 GAS7 SENP3 SPDYE4 KCNAB3 KCNJ12 CYTSB C17orf84 EPN2 TOP3A MPDU1 JMJD3 CLEC10A C17orf81 DHX33 DHRS7B CHD3 MYH3 GABARAP FOXO3B ZNF18 PEMT FBXO39 WSCD1 DNAH9 C17orf45 FAM83G NCOR1 RANGRF ALOX15B SOX15 MIS12 PLD6 WDR16 TMEM88 RNF112 FLCN GLP2R MAP2K3 FLII PITPNM3 ULK2 TMEM95 HES7 HS3ST3B1 SLC5A10 FGF11 STX8 ODF4 CDRT15L2 C17orf49 RCVRN ATPAF2 CYB5D1 ZBTB4 LRRC48 COPS3 YBX2 PIK3R5 GPS2 SLC47A1 COX10 RAI1 ACADVL TBC1D28 USP22 XAF1 DULLARD MYH10 RASD1 LGALS9C KRT17P1 TMEM11 ENSG00000197665 NDEL1 EVPLL SHMT1 SLC2A4 C17orf68 SPEM1 GRAP C17orf76 TNK1 NT5M MYH13 TEKT1 ASGR1 FAM18B2 CCDC42 PER1 MYH1 EIF5A MYH2 ALDH3A2 GUCY2D SCO1 TRIM16 FBXW10 KRBA2 SAT2 MYH4 MYOCD FAM18B CDRT15 LGALS9B TBC1D27 FAM64A KRT14P SLC47A2 CLDN7 EFNB3 KIAA0753 CCDC144C CD68 TOM1L2 RPL9P2 DVL2 CCDC144NL FXR2 TEKT3 BCL6B MED9 NLGN2 DRG2 TNFSF12 PHF23 MEIS3P1 EIF4A1 WRAP53 ALOX12B DNAH2 MYO15A ZNF287 PLSCR3 C17orf44 FAM106B POLR2A TRAPPC1 ADORA2B ATP1B2 LLGL1 SMCR8 LSMD1 ACAP1 ENSG00000215067 RNASEK C17orf39 CCDC144A TMEM107 SLC16A13 USP43
17	200199	200199	17	222940	222940	DEL	227	BRC	1	1	NHEJ	CYTS	ENST000	1	intron2	N/A	N/A	N/A	N/A	MAP2K3 CDRT15L2 C17orf103 CCDC144C KCNJ12 USP22 FAM27L CCDC144NL FAM106B TMEM11 MEIS3P2 DHRS7B LGALS9B

	44	44		75	75		3130	14				B	00395530							
9	1.35E+08	1.35E+08	9	58561646	58561646	CTX	N/A	BRC14	1	-1	NHEJ	GBGT1	ENST00000372043	-1	intron5	N/A	N/A	N/A	N/A	N/A
13	1.1E+08	1.1E+08	13	1.1E+08	1.1E+08	DEL	129	BRC15	1	1	NAHR	CARKD	ENST00000397191	1	intron4	CARKD	ENST00000397191	1	intron4	N/A
11	80125761	80125761	11	80446909	80446909	DEL	320145	BRC15	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	31729116	31729116	11	31771239	31771239	DEL	42122	BRC15	1	1	NHEJ	ELP4	ENST00000350638	1	intron9	PAX6	ENST00000346294	-1	intron5	N/A
12	26125451	26125451	12	34582389	34582389	DEL	8455936	BRC15	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	DDX11 C12orf70 ALG10 PPFIBP1 DNM1L BHLHE41 TSPAN11 SYT10 CAPRIN2 BICD1 AMN1 ITPR2 DENND5B TMTC1 OVCH1 uc001rka.1 IPO8 STK38L FAR2 ERGIC2 FGD4 PKP2 PTHLH MED21 KLHDC5 SSPN C12orf11 C12orf72 FAM60A CCDC91 FGFR1OP2 YARS2 C12orf71 TM7SF3 MRPS35 ARNTL2 C12orf35
10	1.19E+08	1.19E+08	10	1.19E+08	1.19E+08	DEL	1383	BRC15	1	1	MMEJ	KIAA1598	ENST00000355371	-1	intron3	KIAA1598	ENST00000355371	-1	intron3	N/A
12	25255652	25255652	17	18652472	18652472	CTX	N/A	BRC15	1	1	NHEJ	KRAS	ENST00000311936	-1	intron3	N/A	N/A	N/A	N/A	N/A
1	71829487	71829487	1	71831079	71831079	DEL	1590	BRC16	1	1	MMEJ	NEGR1	ENST00000357731	-1	intron6	NEGR1	ENST00000357731	-1	intron6	N/A
6	1.07E+08	1.07E+08	6	1.07E+08	1.07E+08	DEL	688	BRC16	1	1	NHEJ	AIM1	ENST00000369066	1	intron1	AIM1	ENST00000369066	1	intron1	N/A
X	24939889	24939889	X	24944152	24944152	DEL	4262	BRC16	1	1	NHEJ	ARX	ENST00000379044	-1	intron2	N/A	N/A	N/A	N/A	N/A
1	54806151	54806151	1	54809523	54809523	DEL	3372	BRC16	1	1	NHEJ	ACOT11	ENST00000343744	1	intron1	ACOT11	ENST00000343744	1	intron1	N/A
3	67116459	67116459	3	67118983	67118983	DEL	2524	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

12	122266605	122266605	12	122275571	122275571	DEL	963	BRC16	1	1	MMEJ	BCL2L14	ENST00000298566	1	intron5	BCL2L14	ENST00000298566	1	intron5	N/A
2	48512278	48512278	2	48516945	48516945	DEL	4663	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	80917208	80917208	9	80922108	80922108	DEL	4901	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	11371523	11371523	20	11372181	11372181	DEL	657	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
21	38446173	38446173	21	38448758	38448758	DEL	2584	BRC16	1	1	NHEJ	DSCR8	ENST00000400477	1	intron1	DSCR8	ENST00000400477	1	intron2	N/A
2	12214844	12214844	2	12216487	12216487	DEL	1644	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	53612619	53612619	4	53616545	53616545	DEL	3923	BRC16	1	1	MMEJ	SCFD2	ENST00000401642	-1	intron5	SCFD2	ENST00000401642	-1	intron5	N/A
12	1.03E+08	1.03E+08	12	1.03E+08	1.03E+08	DEL	2763	BRC16	1	1	NHEJ	STAB2	ENST00000388887	1	intron54	STAB2	ENST00000388887	1	intron56	N/A
11	1.29E+08	1.29E+08	11	1.29E+08	1.29E+08	DEL	1170	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.31E+08	1.31E+08	6	1.31E+08	1.31E+08	DEL	4226	BRC16	1	1	MMEJ	EPB41L2	ENST00000392427	-1	intron0	EPB41L2	ENST00000392427	-1	intron0	N/A
12	1.3E+08	1.3E+08	12	1.3E+08	1.3E+08	DEL	2515	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1.29E+08	1.29E+08	4	1.29E+08	1.29E+08	DEL	696	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	1.51E+08	1.51E+08	X	1.51E+08	1.51E+08	DEL	4066	BRC16	1	1	NHEJ	GABRA3	ENST00000370314	-1	intron4	GABRA3	ENST00000370314	-1	intron3	N/A
8	1.05E+08	1.05E+08	8	1.05E+08	1.05E+08	DEL	2188	BRC16	1	1	NHEJ	DPYS	ENST00000351513	-1	intron7	DPYS	ENST00000351513	-1	intron7	N/A

15	61793750	61793750	15	61795060	61795060	DEL	1310	BRC16	1	1	NHEJ	HERC1	ENST00000261887	-1	intron21	HERC1	ENST00000261887	-1	intron21	N/A
6	1.66E+08	1.66E+08	6	1.66E+08	1.66E+08	DEL	755	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	2.15E+08	2.15E+08	2	2.15E+08	2.15E+08	DEL	6172	BRC16	1	1	NHEJ	SPAG16	ENST00000331683	1	intron15	SPAG16	ENST00000331683	1	intron15	N/A
5	14303741	14303741	5	14309858	14309858	DEL	6117	BRC16	1	1	NHEJ	TRIO	ENST00000344204	1	intron1	TRIO	ENST00000344204	1	intron1	N/A
1	1.12E+08	1.12E+08	1	1.12E+08	1.12E+08	DEL	2856	BRC16	1	1	NHEJ	ATP5F1	ENST00000369722	1	utr_exon7	N/A	N/A	N/A	N/A	N/A
2	15681086	15681086	2	15683383	15683383	DEL	2296	BRC16	1	1	NHEJ	DDX1	ENST00000381341	1	cds_exon18	DDX1	ENST00000381341	1	intron19	N/A
7	19077769	19077769	7	19080072	19080072	DEL	2297	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.15E+08	1.15E+08	3	1.15E+08	1.15E+08	DEL	35101	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	GRAMD1C	ENST00000358160	1	intron2	N/A
15	46816808	46816808	15	46817176	46817176	DEL	362	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	1.41E+08	1.41E+08	7	1.41E+08	1.41E+08	DEL	2399	BRC16	1	1	MMEJ	AGK	ENST00000355413	1	intron12	AGK	ENST00000355413	1	intron12	N/A
X	1.36E+08	1.36E+08	X	1.36E+08	1.36E+08	DEL	2992	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	56015349	56015349	1	56016214	56016214	DEL	861	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	38552898	38552898	11	38554946	38554946	DEL	2046	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	1.15E+08	1.15E+08	X	1.15E+08	1.15E+08	DEL	2336	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

7	86281580	86281580	7	86282621	86282621	DEL	1041	BRC16	1	1	NHEJ	GRM3	ENST00000361669	1	intron2	GRM3	ENST00000361669	1	intron2	N/A
1	1.74E+08	1.74E+08	1	1.74E+08	1.74E+08	DEL	1803	BRC16	1	1	NHEJ	RFWD2	ENST00000367667	-1	intron14	RFWD2	ENST00000367667	-1	intron14	N/A
X	73848949	73848949	X	73851879	73851879	DEL	2931	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.03E+08	1.03E+08	1	1.03E+08	1.03E+08	DEL	1211	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	57310442	57310442	5	57319891	57319891	DEL	9449	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	1.57E+08	1.57E+08	2	1.57E+08	1.57E+08	DEL	4778	BRC16	1	1	NHEJ	GPD2	ENST00000310454	1	intron0	GPD2	ENST00000310454	1	intron0	N/A
14	57429232	57429232	14	57429318	57429318	DEL	85	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
22	18022558	18022558	22	18024962	18024962	DEL	2405	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
13	35361959	35361959	13	35366288	35366288	DEL	4327	BRC16	1	1	MMEJ	DCAMKL1	ENST00000360631	-1	intron3	DCAMKL1	ENST00000360631	-1	intron3	N/A
13	97874888	97874888	13	97877698	97877698	DEL	2809	BRC16	1	1	NHEJ	FARP1	ENST00000319562	1	cds_exon15	FARP1	ENST00000319562	1	intron16	N/A
8	1.35E+08	1.35E+08	8	1.35E+08	1.35E+08	DEL	566	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	5561708	5561708	12	5564128	5564128	DEL	2419	BRC16	1	1	NHEJ	ANO2	ENST00000327087	-1	intron21	ANO2	ENST00000327087	-1	intron21	N/A
4	12016448	12016448	4	12017069	12017069	DEL	620	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1135309	1135309	6	1135477	1135477	DEL	169	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

1	2.17E+08	2.17E+08	1	2.17E+08	2.17E+08	DEL	4638	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	85335401	85335401	12	85343042	85343042	DEL	7637	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	1.08E+08	1.08E+08	2	1.08E+08	1.08E+08	DEL	1965	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15	31570321	31570321	15	31572742	31572742	DEL	2421	BRC16	1	1	NHEJ	RYR3	ENST00000389232	1	intron2	RYR3	ENST00000389232	1	intron2	N/A
5	84905145	84905145	5	84905535	84905535	DEL	389	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19	22983769	22983769	19	22986396	22986396	DEL	2626	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.11E+08	2.11E+08	1	2.11E+08	2.11E+08	DEL	4298	BRC16	1	1	NHEJ	RPS6KC1	ENST00000366960	1	intron10	RPS6KC1	ENST00000366960	1	cds_exon10	N/A
11	1.17E+08	1.17E+08	11	1.17E+08	1.17E+08	DEL	1360	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.69E+08	1.69E+08	3	1.69E+08	1.69E+08	DEL	2455	BRC16	1	1	NHEJ	WDR49	ENST00000308378	-1	intron5	WDR49	ENST00000308378	-1	intron5	N/A
2	80835224	80835224	2	80842168	80842168	DEL	6941	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	79830653	79830653	4	79831576	79831576	DEL	923	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1.64E+08	1.64E+08	4	1.64E+08	1.64E+08	DEL	2924	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.18E+08	2.18E+08	1	2.18E+08	2.18E+08	DEL	2920	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	68686939	68686939	8	68688222	68688222	DEL	12181	BRC16	1	1	MMEJ	CPA6	ENST00000297770	-1	intron2	CPA6	ENST00000297770	-1	intron2	N/A
X	83324501	83324501	X	83325751	83325751	DEL	1251	BRC1	1	1	NHEJ	RPS6K	ENST000002	-1	intron1	RPS6KA6	ENST00000262752	-1	intron1	N/A

								6				A6	62752							
1	1.67E+08	1.67E+08	1	1.67E+08	1.67E+08	DEL	347	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	34528112	34528112	11	34528713	34528713	DEL	592	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	61449743	61449743	18	61450221	61450221	DEL	477	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	94114135	94114135	5	94118172	94118172	DEL	4035	BRC16	1	1	MMEJ	MCTP1	ENST00000312202	-1	intron16	MCTP1	ENST00000312202	-1	intron16	N/A
5	28123052	28123052	5	28125494	28125494	DEL	2439	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
14	66203940	66203940	14	66207657	66207657	DEL	3715	BRC16	1	1	MMEJ	GPHN	ENST00000315266	1	intron1	GPHN	ENST00000315266	1	intron1	N/A
3	1.54E+08	1.54E+08	3	1.54E+08	1.54E+08	DEL	1271	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	1.01E+08	1.01E+08	X	1.01E+08	1.01E+08	DEL	1517	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	84741367	84741367	6	84749473	84749473	DEL	8104	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.03E+08	1.03E+08	3	1.03E+08	1.03E+08	DEL	836	BRC16	1	1	MMEJ	NFKBIZ	ENST00000394054	1	utr_exon11	NFKBIZ	ENST00000394054	1	utr_exon11	N/A
8	38696161	38696161	8	38706605	38706605	DEL	10441	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	58039883	58039883	16	58040915	58040915	DEL	1033	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	75283663	75283663	10	75284065	75284065	DEL	401	BRC16	1	1	NHEJ	CAMK2G	ENST00000351293	-1	intron3	CAMK2G	ENST00000351293	-1	intron3	N/A
5	1.55E+08	1.55E+08	5	1.55E+08	1.55E+08	DEL	646	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

7	35639803	35639803	7	35644689	35644689	DEL	4885	BRC16	1	1	NHEJ	HERPUD2	ENST00000396081	-1	utr_exon8	HERPUD2	ENST00000396081	-1	intron4	N/A
12	1.24E+08	1.24E+08	12	1.24E+08	1.24E+08	DEL	6676	BRC16	1	1	MMEJ	TMEM132B	ENST00000299308	1	intron1	TMEM132B	ENST00000299308	1	intron1	N/A
13	57585167	57585167	13	57591112	57591112	DEL	5945	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	68298600	68298600	7	68303125	68303125	DEL	4525	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.69E+08	1.69E+08	3	1.69E+08	1.69E+08	DEL	6225	BRC16	1	1	MMEJ	WDR49	ENST00000308378	-1	intron0	WDR49	ENST00000308378	-1	intron0	N/A
7	1.32E+08	1.32E+08	7	1.32E+08	1.32E+08	DEL	4354	BRC16	1	1	NHEJ	CHCHD3	ENST00000262570	-1	intron6	CHCHD3	ENST00000262570	-1	intron6	N/A
2	2.01E+08	2.01E+08	2	2.01E+08	2.01E+08	DEL	4702	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
14	86503089	86503089	14	86506969	86506969	DEL	3875	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	86035111	86035111	4	86037829	86037829	DEL	2718	BRC16	1	1	NHEJ	WDFY3	ENST00000322366	-1	intron0	WDFY3	ENST00000322366	-1	intron0	N/A
4	18135159	18135159	4	18138846	18138846	DEL	3687	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	1.59E+08	1.59E+08	7	1.59E+08	1.59E+08	DEL	2205	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	1.06E+08	1.06E+08	12	1.06E+08	1.06E+08	DEL	2215	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.12E+08	1.12E+08	6	1.12E+08	1.12E+08	DEL	1576	BRC16	1	1	NHEJ	REV3L	ENST00000368805	-1	intron2	REV3L	ENST00000368805	-1	intron2	N/A
22	28916480	28916480	22	28916760	28916760	DEL	281	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

8	24629773	24629773	8	24633631	24633631	DEL	3858	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	1.02E+08	1.02E+08	10	1.02E+08	1.02E+08	DEL	3072	BRC16	1	1	NHEJ	ERLIN1	ENST00000370410	-1	intron7	ERLIN1	ENST00000370410	-1	intron6	N/A
1	1.44E+08	1.44E+08	1	1.44E+08	1.44E+08	DEL	574	BRC16	1	1	NHEJ	POLR3C	ENST00000334163	-1	intron4	POLR3C	ENST00000334163	-1	intron3	N/A
1	2.28E+08	2.28E+08	1	2.28E+08	2.28E+08	DEL	1513	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	64319718	64319718	8	64322618	64322618	DEL	2899	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.94E+08	1.94E+08	1	1.94E+08	1.94E+08	DEL	3991	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	22999561	22999561	18	23004947	23004947	DEL	5386	BRC16	1	1	NHEJ	CHST9	ENST00000284224	-1	intron0	CHST9	ENST00000284224	-1	intron0	N/A
1	80431604	80431604	1	80432113	80432113	DEL	509	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.91E+08	1.91E+08	3	1.91E+08	1.91E+08	DEL	2540	BRC16	1	1	NHEJ	LEPREL1	ENST00000319332	-1	intron1	LEPREL1	ENST00000319332	-1	intron1	N/A
14	75141068	75141068	14	75395393	75395393	DEL	253322	BRC16	1	1	MMEJ	FLVCR2	ENST00000238667	1	intron1	TTLL5	ENST00000393826	1	intron27	C14orf1 TTLL5
4	1.54E+08	1.54E+08	4	1.54E+08	1.54E+08	DEL	7787	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.12E+08	1.12E+08	3	1.12E+08	1.12E+08	DEL	363	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	79949121	79949121	2	79949588	79949588	DEL	446	BRC16	1	1	MMEJ	CTNNA2	ENST00000409536	1	intron3	CTNNA2	ENST00000409536	1	intron3	N/A
10	76393232	76393232	10	76737372	76737372	DEL	41410	BRC16	1	1	NHEJ	MYST4	ENST00000372725	1	intron2	MYST4	ENST00000372725	1	intron2	N/A

1	2.1E+08	2.1E+08	1	2.1E+08	2.1E+08	DEL	1158	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	25884919	25884919	4	25885785	25885785	DEL	864	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	1.09E+08	1.09E+08	7	1.09E+08	1.09E+08	DEL	5633	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	11910372	11910372	5	11916215	11916215	DEL	5842	BRC16	1	1	NHEJ	CTNND2	ENST00000359640	-1	intron1	CTNND2	ENST00000359640	-1	intron1	N/A
7	1.41E+08	1.41E+08	7	1.41E+08	1.41E+08	DEL	2238	BRC16	1	1	MMEJ	KIAA1147	ENST00000297761	-1	intron4	KIAA1147	ENST00000297761	-1	intron3	N/A
12	97630306	97630306	12	97634252	97634252	DEL	3945	BRC16	1	1	NHEJ	APAF1	ENST00000339433	1	cds_exon18	APAF1	ENST00000339433	1	intron20	N/A
11	1.01E+08	1.01E+08	11	1.01E+08	1.01E+08	DEL	2184	BRC16	1	1	NHEJ	KIAA1377	ENST00000263468	1	intron4	KIAA1377	ENST00000263468	1	intron4	N/A
7	24692519	24692519	7	24693680	24693680	DEL	1149	BRC16	1	1	MMEJ	MPP6	ENST00000222644	1	intron10	MPP6	ENST00000222644	1	cds_exon10	N/A
18	55487763	55487763	18	55490369	55490369	DEL	2606	BRC16	1	1	NHEJ	CCBE1	ENST00000333570	-1	intron2	CCBE1	ENST00000333570	-1	intron2	N/A
14	85374282	85374282	14	85379464	85379464	DEL	5176	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	26224149	26224149	11	26224806	26224806	DEL	653	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	69530981	69530981	3	69533268	69533268	DEL	2288	BRC16	1	1	NHEJ	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	2	1.45E+08	1.45E+08	DEL	419	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	78896323	78896323	10	78898380	78898380	DEL	2057	BRC16	1	1	NHEJ	KCNMA1	ENST00000372437	-1	intron1	KCNMA1	ENST00000372437	-1	intron1	N/A

12	69825516	69825516	12	69826329	69826329	DEL	803	BRC16	1	1	MMEJ	TSPAN8	ENST00000393330	-1	intron1	TSPAN8	ENST00000393330	-1	intron1	N/A
13	1.11E+08	1.11E+08	13	1.11E+08	1.11E+08	DEL	2664	BRC16	1	1	MMEJ	ARHGEF7	ENST00000375739	1	intron5	ARHGEF7	ENST00000375739	1	intron5	N/A
2	1.65E+08	1.65E+08	2	1.65E+08	1.65E+08	DEL	698	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	2.06E+08	2.06E+08	2	2.06E+08	2.06E+08	DEL	3868	BRC16	1	1	NHEJ	PARD3B	ENST00000406610	1	intron2	PARD3B	ENST00000406610	1	intron2	N/A
13	32140752	32140752	13	32142611	32142611	DEL	1857	BRC16	1	1	MMEJ	PDS5B	ENST00000315596	1	intron6	PDS5B	ENST00000315596	1	intron6	N/A
3	47163169	47163169	3	47165309	47165309	DEL	2125	BRC16	1	1	MMEJ	SETD2	ENST00000409792	-1	intron1	SETD2	ENST00000409792	-1	intron1	N/A
13	37068356	37068356	13	37070798	37070798	DEL	2442	BRC16	1	1	NHEJ	POSTN	ENST00000379742	-1	intron2	POSTN	ENST00000379742	-1	cds_exon0	N/A
10	84419592	84419592	10	84420851	84420851	DEL	1256	BRC16	1	1	MMEJ	NRG3	ENST00000372142	1	intron2	NRG3	ENST00000372142	1	intron2	N/A
1	2.09E+08	2.09E+08	1	2.09E+08	2.09E+08	DEL	2177	BRC16	1	1	MMEJ	KCNH1	ENST00000271751	-1	intron10	KCNH1	ENST00000271751	-1	intron10	N/A
4	30637420	30637420	4	30640971	30640971	DEL	3544	BRC16	1	1	MMEJ		ENST00000399870	-1	intron2		ENST00000399870	-1	intron1	N/A
6	98307094	98307094	6	98309321	98309321	DEL	2222	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	57567256	57567256	X	57568978	57568978	DEL	1720	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	14473009	14473009	11	14474284	14474284	DEL	1275	BRC16	1	1	NHEJ	COPB1	ENST00000249923	-1	intron1	COPB1	ENST00000249923	-1	intron1	N/A
4	1.77E	1.77E	4	1.77E	1.77E	DEL	197	BRC	1	1	MMEJ	GPM	ENST000	-1	intron0	GPM6A	ENST00000280187	-1	intron0	N/A

	+08	+08		+08	+08		7	16				6A	00280187							
4	14576014	14576014	4	14577214	14577214	DEL	1199	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	14274645	14274645	3	14276105	14276105	DEL	1457	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	1.55E+08	1.55E+08	5	1.55E+08	1.55E+08	DEL	1349	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	1.09E+08	1.09E+08	X	1.09E+08	1.09E+08	DEL	4859	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	AMMECR1	ENST00000372059	-1	utr_exon5	N/A
3	1.1E+08	1.1E+08	3	1.1E+08	1.1E+08	DEL	6199	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	68678464	68678464	3	68681996	68681996	DEL	3531	BRC16	1	1	NHEJ	FAM19A1	ENST00000327941	1	intron3	FAM19A1	ENST00000327941	1	intron3	N/A
8	1.32E+08	1.32E+08	8	1.32E+08	1.32E+08	DEL	2326	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	2.26E+08	2.26E+08	2	2.26E+08	2.26E+08	DEL	764	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	43860241	43860241	17	43861109	43861109	DEL	867	BRC16	1	1	NHEJ	SKAP1	ENST00000336915	-1	intron1	SKAP1	ENST00000336915	-1	intron1	N/A
X	1.53E+08	1.53E+08	X	1.53E+08	1.53E+08	DEL	1513	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	88557583	88557583	8	88557935	88557935	DEL	353	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.63E+08	1.63E+08	1	1.63E+08	1.63E+08	DEL	3642	BRC16	1	1	NHEJ	LMX1A	ENST00000342310	-1	intron3	LMX1A	ENST00000342310	-1	intron3	N/A
1	55182725	55182725	1	55183293	55183293	DEL	568	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19	7966133	7966133	19	7967824	7967824	DEL	1689	BRC16	1	1	MMEJ	ELAVL1	ENST00000407627	-1	intron0	ELAVL1	ENST00000407627	-1	intron0	N/A

2	1.15E+08	1.15E+08	2	1.15E+08	1.15E+08	DEL	641	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.73E+08	1.73E+08	1	1.73E+08	1.73E+08	DEL	5016	BRC16	1	1	MMEJ	RABGAP1L	ENST00000407735	1	intron16	RABGAP1L	ENST00000407735	1	intron16	N/A
12	64206089	64206089	12	64208117	64208117	DEL	2027	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	67983453	67983453	17	67984818	67984818	DEL	1363	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.19E+08	1.19E+08	3	1.19E+08	1.19E+08	DEL	1508	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.55E+08	1.55E+08	1	1.55E+08	1.55E+08	DEL	2073	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	1460657	1460657	17	1464707	1464707	DEL	4046	BRC16	1	1	MMEJ	SLC43A2	ENST00000301335	-1	intron4	SLC43A2	ENST00000301335	-1	intron3	N/A
9	1.04E+08	1.04E+08	9	1.04E+08	1.04E+08	DEL	3446	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	1.16E+08	1.16E+08	8	1.16E+08	1.16E+08	DEL	1011	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
21	18708831	18708831	21	18710250	18710250	DEL	1417	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	80739070	80739070	8	80739273	80739273	DEL	201	BRC16	1	1	MMEJ	STMN2	ENST00000220876	1	intron4	STMN2	ENST00000220876	1	intron4	N/A
8	1.35E+08	1.35E+08	8	1.35E+08	1.35E+08	DEL	3315	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	7076703	7076703	18	7078043	7078043	DEL	1339	BRC16	1	1	NHEJ	LAMA1	ENST00000389658	-1	intron1	LAMA1	ENST00000389658	-1	intron1	N/A
12	37154825	37154825	12	37192113	37192113	DEL	37287	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	492093	492093	2	492108	492108	DEL	154	BRC	1	1	NHEJ	FSHR	ENST000	-1	intron1	FSHR	ENST00000346173	-1	intron1	N/A

	50	50		92	92		5	16					00346173							
21	27479605	27479605	21	27483036	27483036	DEL	3426	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.98E+08	1.98E+08	3	1.98E+08	1.98E+08	DEL	4103	BRC16	1	1	MMEJ	DLG1	ENST00000359922	-1	intron3	DLG1	ENST00000359922	-1	intron3	N/A
7	1.36E+08	1.36E+08	7	1.36E+08	1.36E+08	DEL	1837	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	83950381	83950381	11	83951700	83951700	DEL	1315	BRC16	1	1	MMEJ	DLG2	ENST00000398309	-1	intron1	DLG2	ENST00000398309	-1	intron1	N/A
16	46431840	46431840	16	46433625	46433625	DEL	1782	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.55E+08	1.55E+08	1	1.55E+08	1.55E+08	DEL	6819	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.89E+08	1.89E+08	3	1.89E+08	1.89E+08	DEL	804	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	8347133	8347133	18	8348770	8348770	DEL	736	BRC16	1	1	NHEJ	PTPRM	ENST00000332175	1	intron21	PTPRM	ENST00000332175	1	intron21	N/A
1	2.2E+08	2.2E+08	1	2.2E+08	2.2E+08	DEL	2786	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	62410895	62410895	12	62413657	62413657	DEL	2762	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.23E+08	1.23E+08	3	1.23E+08	1.23E+08	DEL	8208	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	88170297	88170297	3	88173040	88173040	DEL	2737	BRC16	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	29803381	29803381	17	29807151	29807151	DEL	3766	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	1.06E+08	1.06E+08	12	1.06E+08	1.06E+08	DEL	544	BRC16	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

6	1.07E+08	1.07E+08	6	1.07E+08	1.07E+08	DEL	2326	BRC16	1	1	NHEJ	AIM1	ENST00000369066	1	intron1	AIM1	ENST00000369066	1	cds_exon1	N/A
2	2.08E+08	2.08E+08	15	45970900	45970900	CTX	N/A	BRC16	-1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	43711399	43711399	12	1.13E+08	1.13E+08	CTX	N/A	BRC16	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19	62469424	62469424	19	62471613	62471613	DEL	2182	BRC17	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	46156528	46156528	20	46156629	46156629	INV	100	BRC17	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	51401101	51401101	20	54975414	54975414	DEL	3573311	BRC17	1	1	NHEJ	TSHZ2	ENST00000371497	1	intron2	N/A	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
19	61479377	61479377	19	61887298	61887298	DEL	406919	BRC17	1	1	NHEJ	ZSCAN5A	ENST00000254165	-1	intron0	N/A	N/A	N/A	N/A	ZNF71 ZNF542 ZFP28 ZNF582 ZNF471 ZNF583 ZNF667 ZNF835 ZNF470
15	83280230	83280230	15	83280553	83280553	DEL	310	BRC17	1	1	MMEJ	SLC28A1	ENST00000286749	1	intron13	SLC28A1	ENST00000286749	1	intron13	N/A
11	1.25E+08	1.25E+08	11	1.25E+08	1.25E+08	DEL	154	BRC17	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	2.37E+08	2.37E+08	2	2.37E+08	2.37E+08	DEL	79	BRC17	1	1	MMEJ	ASB18	ENST00000330842	-1	intron1	ASB18	ENST00000330842	-1	intron1	N/A
11	99279522	99279522	11	1.2E+08	1.2E+08	DEL	20502069	BRC17	1	1	MMEJ	CNTN5	ENST00000279463	1	intron3	ARHGEF12	ENST00000356641	1	intron2	PHLDB1 POU2AF1 C11orf87 MCAM FXYD2 AASDHPPT ARHGAP20 TMEM25 SLC37A4 HYOU1 TAGLN ALG9 USP2 KBTBD3 ABCG4 C11orf1 SIK2 GRIA4 CRYAB IL10RA CASP5 PVRL1 FDXACB1 POU2F3 DLAT HTR3B C11orf71 KIAA1377 MPZL2 TMEM123 APOA1 ANGPTL5 C11orf65 TRIM29 AMICA1 RPS25P8 DDX6 RDX CCDC84 MMP7 PDZD3 CD3D MMP13 HSPB2 DIXDC1 C1QTNF5 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	41962161	41962161	19	39600433	39600433	CTX	N/A	BRC17	-1	1	NHEJ	MYST3	ENST00000265713	-1	intron2	PIAS4	ENST00000262971	1	intron1	N/A
19	56487632	56487632	20	54687751	54687751	CTX	N/A	BRC17	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19	62996177	62996177	20	36288980	36288980	CTX	N/A	BRC17	1	1	NHEJ	ZNF586	ENST00000308137	1	intron2	KIAA1755	ENST00000279024	-1	cds_exon6	N/A
19	61986736	61986736	20	44377996	44377996	CTX	N/A	BRC17	1	1	NHEJ	PEG3AS	ENST00000391708	-1	intron6	N/A	N/A	N/A	N/A	N/A
19	57993625	57993625	20	43336068	43336068	CTX	N/A	BRC17	1	1	NHEJ	ZNF28	ENST00000360272	-1	utr_exon1	N/A	N/A	N/A	N/A	N/A
19	54284372	54284372	20	51766411	51766411	CTX	N/A	BRC17	-1	1	NHEJ	SNRNP70	ENST00000221448	1	intron1	N/A	N/A	N/A	N/A	N/A
3	72795477	72795477	15	71477961	71478012	CTX	N/A	BRC17	1	-1	NAHR	GRM7	ENST00000357716	1	intron2	N/A	N/A	N/A	N/A	N/A
8	87164700	87164700	19	41961162	41961162	CTX	N/A	BRC17	-1	1	NHEJ	MFHAS1	ENST00000276282	-1	intron1	N/A	N/A	N/A	N/A	N/A
10	1.19E+08	1.19E+08	10	1.19E+08	1.19E+08	DEL	4438	BRC18	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.23E+08	1.23E+08	3	1.23E+08	1.23E+08	DEL	172612	BRC20	1	1	NHEJ	IQCB1	ENST00000349820	-1	intron3	ILDR1	ENST00000383663	-1	cds_exon4	SLC15A2 EAF2
13	61524102	61524102	13	61524265	61524265	DEL	163	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	17893275	17893275	11	22775779	22775779	DEL	4881502	BRC20	1	1	NHEJ	SERGEF	ENST00000265965	-1	intron9	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	1.23E+08	1.23E+08	3	1.28E+08	1.28E+08	DEL	4939188	BRC20	1	1	NHEJ	POLQ	ENST00000264233	-1	intron14	CCDC37	ENST00000352312	1	cds_exon13	HSPBAP1 SEC22A SEMA5B CSTA ILDR1 CD86 OSBPL11 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	1.23E+08	1.23E+08	3	1.23E+08	1.23E+08	DEL	500873	BRC20	1	1	NHEJ	POLQ	ENST00000264233	-1	intron13	ILDR1	ENST00000273691	-1	intron5	IQCB1 ARGFX FBXO40 SLC15A2 HCLS1 EAF2 GOLGB1
2	1.65E+08	1.65E+08	2	1.65E+08	1.65E+08	DEL	99964	BRC20	1	1	NHEJ	COBLL1	ENST00000342193	-1	intron1	COBLL1	ENST00000342193	-1	intron1	N/A
18	9611930	9611930	18	9612267	9612267	DEL	304	BRC20	1	1	NAHR	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	87789245	87789245	3	1.23E+08	1.23E+08	DEL	35449799	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	FSTL1 C3orf66 TOMM70A KIAA1524 C3orf15 PVRL3 OR5K1 ZNF80 KTELC1 DHFRL1 RG9MTD1 CRYBG3 WDR52 IFT57 OR5H15 ABHD10 ZPLD1 LRRC58 TAGLN3 CCDC80 GTPBP8 NAT13 NR1I2 ARL13B CD96 ARGFX PLA1A GAP43 CBLB DRD3 ALCAM KIAA1407 SIDT1 EPHA6 OR5K3 OR5AC2 OR5H6 EPHA3 RABL3 DPPA4 GUCA1C PROS1 BTLA RETNLB MORC1 TIGIT ZBTB11 IMPG2 SLC15A2 GABRR3 C3orf26 TMEM39A NSUN3 CCDC52 HHLA2 NIT2 CD200R1L IGSF11 CGGBP1 ZDHHC23 MYH15 C3orf52 CCDC54 STXBP5L SENP7 TMPRSS7 CPOX C3orf1 GTF2E1 LNP1 TBC1D23 CLDND1 C3orf38 UPK1B COX17 HTR1F POLQ HGD STX19 NFKBIZ IQCB1 GSK3B ZBED2 B4GALT4 OR5K4 RPL24P6 C3orf17 SLC35A5 GOLGB1 ATG3 ST3GAL6 SLC9A10 CD80 CD47 C3orf30 OR5H14 ADPRH POPDC2 NDUFB4 QTRTD1 PLCXD2 ZBTB20 COL8A1 BOC OR5H2 WDR82P1 TFG FAM172B GCET2 TMEM45A BZW1L1 ILDR1 DZIP3 LSAMP ATP6V1A ZNF654 DCBLD2 MINA KIAA2018 GPR156 EAF2 OR5H1 CD200 FAM55C GPR128 BBX TRAT1 DPPA2 CD200R1 OR5K2 HCLS1 ABI3BP ARL6 GPR15 CEP97 PCNP FBXO40 GRAMD1C FILIP1L
18	25697102	25697102	18	28939456	28939456	DEL	3241351	BRC20	1	1	MMEJ	N/A	N/A	N/A	N/A	C18orf34	ENST00000406524	-1	intron17	DSG4 RNF138 B4GALT6 DSC2 FAM59A DSC1 MEP1B DSG1 TTR DSG2 RNF125 KLHL14 DSC3 WBP11P1 MCART2 KIAA1012 DSG3
18	49435031	49435031	18	51016478	51016478	DEL	1580447	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	STARD6 RAB27B C18orf26 MBD2 C18orf54 CCDC68 POLI
8	49788303	49788303	8	49789277	49789277	DEL	971	BRC20	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	18732601	18732601	9	19605525	19605525	DEL	871923	BRC20	1	1	NHEJ	ADAMTSL1	ENST00000380548	1	intron15	SLC24A2	ENST00000341998	-1	intron3	ACER2 RPS6 ADFP ADAMTSL1 FAM154A RRAGA FAM29A DENND4C
18	25527608	25527608	18	28940526	28940526	DEL	3411915	BRC20	1	1	MMEJ	N/A	N/A	N/A	N/A	C18orf34	ENST00000406524	-1	intron17	DSG4 RNF138 B4GALT6 DSC2 FAM59A DSC1 MEP1B DSG1 TTR DSG2 RNF125 KLHL14 DSC3 WBP11P1 MCART2 KIAA1012 DSG3
3	86711477	86711477	3	1.23E+08	1.23E+08	DEL	36004100	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	POLQ	ENST00000264233	-1	intron9	FSTL1 C3orf66 TOMM70A KIAA1524 C3orf15 PVRL3 OR5K1 ZNF80 KTELC1 DHFRL1 RG9MTD1 CRYBG3 WDR52 IFT57 OR5H15 ABHD10 ZPLD1 LRRC58 TAGLN3 CCDC80 GTPBP8 NAT13 NR1I2 ARL13B CD96 PLA1A GAP43 CBLB DRD3 ALCAM KIAA1407 SIDT1 EPHA6 OR5K3 OR5AC2 OR5H6 EPHA3 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 SENP7 TMPRSS7 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	1.23E+08	1.23E+08	3	1.23E+08	1.23E+08	DEL	972600	BRC20	1	1	NHEJ	POLQ	ENST00000264233	-1	intron15	ARGFX	ENST00000334384	1	utr_exon4	N/A
6	24438819	24438819	7	72976484	72976484	CTX	N/A	BRC20	-1	-1	NHEJ	DCDC2	ENST00000378454	-1	intron2	N/A	N/A	N/A	N/A	N/A
6	1.07E+08	1.07E+08	12	28020462	28020462	CTX	N/A	BRC20	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	56865755	56865755	21	15165760	15165760	CTX	N/A	BRC20	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	34920241	34920241	15	64648843	64648843	CTX	N/A	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	26342101	26342101	21	30688499	30688499	CTX	N/A	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.56E+08	1.56E+08	12	53821850	53821850	CTX	N/A	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	51015903	51015903	21	23120483	23120483	CTX	N/A	BRC20	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	74280154	74280154	11	34813203	34813203	CTX	N/A	BRC20	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.23E+08	1.23E+08	6	57620523	57620523	CTX	N/A	BRC20	-1	1	MMEJ	IQCB1	ENST00000349820	-1	intron3	PRIM2	ENST00000389488	1	utr_exon10	N/A
3	1.23E+08	1.23E+08	6	57625166	57625166	CTX	N/A	BRC20	1	-1	NHEJ	HCLS1	ENST00000314583	-1	intron5	N/A	N/A	N/A	N/A	N/A
7	29883328	29883328	7	29883468	29883468	DEL	139	BRC22	1	1	NHEJ	WIPF3	ENST00000409123	1	intron2	WIPF3	ENST00000409123	1	intron2	N/A
13	21917251	21917251	13	23285972	23285972	DEL	1367719	BRC22	1	1	NHEJ	N/A	N/A	N/A	N/A	MIPEP	ENST00000382172	-1	intron14	TNFRSF19 SGCG HMGA1L6 MIPEP SACS

11	74517005	74517005	11	74843700	74843700	DEL	325695	BRC22	1	1	NHEJ	N/A	N/A	N/A	N/A	GDPD5	ENST00000376282	-1	intron1	RPS3P3 SLCO2B1 KLHL35 ARRB1
14	82204234	82204234	14	82204730	82204730	DEL	495	BRC22	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.84E+08	1.84E+08	3	1.84E+08	1.84E+08	INV	180	BRC22	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	74010046	74010046	11	74964161	74964161	DEL	953114	BRC22	1	1	NHEJ	POLD3	ENST00000263681	1	intron7	N/A	N/A	N/A	N/A	RPS3P3 SERPINH1 NEU3 SPCS2 GDPD5 OR2AT4 RNF169 XRRA1 SLCO2B1 KLHL35 CHRDL2 ARRB1
13	23056388	23056388	13	23142170	23142170	DEL	85778	BRC22	1	1	NHEJ	TNFRSF19	ENST00000248484	1	intron0	TNFRSF19	ENST00000248484	1	intron8	N/A
11	70500352	70500352	11	75317690	75317690	DEL	4816338	BRC22	1	1	NHEJ	SHANK2	ENST00000338508	-1	intron3	UVRAG	ENST00000356136	1	intron6	C11orf59 MAP6 FCHSD2 KRTAP5-10 CLPB PAAF1 FOLR1 FOLR3 OR2AT4 ATG16L2 P2RY2 KRTAP5-7 RNF121 DNAJB13 C11orf51 NADSYN1 C2CD3 INPPL1 DEFB108B IL18BP PDE2A SLCO2B1 RELT CHRDL2 OR7E87P SERPINH1 CHCHD8 RAB6A UCP3 LRTOMT DGAT2 POLD3 UCP2 FAM86C P4HA3 PPME1 XRRA1 ARAP1 STARD10 MOGAT2 ARHGEF17 KCNE3 RPS3P3 KRTAP5-11 PLEKHB1 uc001ouw.1 KRTAP5-9 P2RY6 NEU3 PGM2L1 FAM168A SPCS2 KRTAP5-8 FOLR2 PHOX2A GDPD5 NUMA1 RNF169 KLHL35 MRPL48 ARRB1 DHCR7
13	24075451	24075451	13	24075583	24075583	INV	129	BRC22	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	75371475	75371475	11	76722597	76722597	DEL	1350122	BRC22	1	1	NHEJ	UVRAG	ENST00000356136	1	intron7	PAK1	ENST00000356341	-1	intron12	ACER3 TSKU PRKRIR MYO7A WNT11 C11orf30 GDPD4 CAPN5 LRRC32 B3GNT6 GUCY2E
11	67625117	67625117	11	69724046	69724046	DEL	2097932	BRC22	1	1	NHEJ	CHKA	ENST00000356135	-1	intron1	N/A	N/A	N/A	N/A	LRP5 TPCN2 MTL5 SAPS3 FGF4 MRGPRF C11orf24 ANO1 CCND1 GAL FGF19 MRGPRD CPT1A MYEOV FGF3 SUV420H1 ORAOV1 IGHMBP2 MRPL21
6	27676931	27676931	7	98007491	98007491	CTX	N/A	BRC22	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	67785502	67785502	13	22073570	22073570	CTX	N/A	BRC22	1	1	NHEJ	C11orf24	ENST00000304271	-1	utr_exon2	N/A	N/A	N/A	N/A	N/A
11	78718485	78718485	13	30845612	30845612	CTX	N/A	BRC22	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	1.34E+08	1.34E+08	11	1.34E+08	1.34E+08	DEL	117	BRC23	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

5	1.77E+08	1.77E+08	5	1.77E+08	1.77E+08	DEL	129	BRC23	1	1	NAHR	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.18E+08	2.18E+08	8	43130454	43130454	CTX	N/A	BRC24	-1	1	MMEJ	N/A	N/A	N/A	N/A	HGSNAT	ENST00000332689	1	intron2	N/A
5	80862372	80862372	5	80863264	80863264	DEL	891	BRC26	1	1	NHEJ	SSBP2	ENST00000320672	-1	intron4	SSBP2	ENST00000320672	-1	intron4	N/A
6	12454955	12454955	6	12456539	12456539	DEL	1583	BRC26	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	60304108	60304108	4	60304279	60304279	DEL	171	BRC26	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	1617753	1617753	9	1617976	1617976	DEL	223	BRC26	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	37664416	37664416	10	37664727	37664727	DEL	310	BRC26	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	32589058	32589058	2	32589254	32589254	DEL	197	BRC26	1	1	NHEJ	BIRC6	ENST00000261359	1	intron52	BIRC6	ENST00000261359	1	intron53	N/A
4	81922744	81922744	4	81922923	81922923	DEL	180	BRC26	1	1	VNTR	C4orf22	ENST00000406749	1	intron4	C4orf22	ENST00000406749	1	intron4	N/A
X	1.35E+08	1.35E+08	X	1.35E+08	1.35E+08	DEL	127	BRC26	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	2.31E+08	2.31E+08	17	13922349	13922349	CTX	N/A	BRC26	1	-1	NHEJ	SP100	ENST00000409824	1	intron1	COX10	ENST00000261643	1	intron3	N/A
20	6414955	6414955	20	6418045	6418045	DEL	3089	BRC29	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	90234128	90234128	7	90234301	90234301	DEL	174	BRC29	1	1	NHEJ	PFTK1	ENST00000380050	1	intron4	PFTK1	ENST00000380050	1	intron4	N/A
8	31525542	31525542	8	34864469	34864469	DEL	3337927	BRC29	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	DUSP26 RPL10AP3 MAK16 C8orf41 NRG1 FUT10 RNF122

20	14582335	14582335	20	22795163	22795163	DEL	8211824	BRC29	1	1	MMEJ	C20orf133	ENST00000217246	1	intron4	N/A	N/A	N/A	N/A	FOXA2 GSTM3P XRN2 PCSK2 INSM1 C20orf23 C20orf133 SEC23B ZNF133 RIN2 PPIAP17 RPL15P1 C20orf78 C20orf12 RPS27AP2 C20orf79 RBBP9 C20orf72 BFSP1 NAT5 RPL7AL3 RPL41P1 RPL21P3 OTOR NKX2-4 C20orf74 SNX5 C20orf179 SLC25A6P1 RPL17P1 RRBP1 HARS2 OVOL2 GCNT1P ST13P PAX1 RPLP0P1 MRPS11P1 SNRPB2 C20orf26 DSTN RPS10P2 RPL24P2 CRNKL1 CSRP2BP NCRNA00153 NKX2-2 SLC24A3 TCTE1P POLR3F
5	55260721	55260721	5	55261803	55261803	DEL	1082	BRC29	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	71434366	71434366	5	71444470	71444470	DEL	105	BRC29	1	1	NAHR	TPPP	ENST00000360578	-1	utr_exon3	TPPP	ENST00000360578	-1	utr_exon3	N/A
8	40572937	40572937	17	14834933	14834933	CTX	N/A	BRC3	-1	1	NHEJ	ZMAT4	ENST00000297737	-1	intron4	N/A	N/A	N/A	N/A	N/A
8	38435223	38435223	17	15319937	15319937	CTX	N/A	BRC3	1	-1	MMEJ	FGFR1	ENST00000341462	-1	intron0	CDRT4	ENST00000395926	-1	intron0	N/A
3	47922323	47922323	3	47951717	47951717	DEL	295	BRC30	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	99048497	99048497	6	1.06E+08	1.06E+08	DEL	7076841	BRC30	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	COQ3 BVES SFRS18 HACE1 GRIK2 MCHR2 RPL35P3 SIM1 ASCC3 FBXL4 C6orf168 PRDM13 USP45 C6orf112 POU3F2 PREP POPDC3 CCNC LIN28B
1	1.71E+08	1.71E+08	1	1.71E+08	1.71E+08	DEL	534	BRC30	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.89E+08	1.89E+08	1	1.89E+08	1.89E+08	DEL	484	BRC30	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.62E+08	1.62E+08	6	1.62E+08	1.62E+08	DEL	733	BRC30	1	1	NHEJ	PARK2	ENST00000366898	-1	intron7	PARK2	ENST00000366898	-1	intron7	N/A
17	91664377	91664377	17	9166529	9166529	DEL	93	BRC30	1	1	NHEJ	STX8	ENST00000306357	-1	intron7	STX8	ENST00000306357	-1	intron7	N/A
17	22135721	22135721	17	22135866	22135866	DEL	147	BRC30	1	1	NAHR	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	86545037	86545037	12	13028362	13028362	CTX	N/A	BRC30	1	-1	NHEJ	N/A	N/A	N/A	N/A	HEBP1	ENST00000014930	-1	intron3	N/A
8	55599884	55599884	17	47708898	47708898	CTX	N/A	BRC3	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

								0												
1	77184678	77184678	18	1397103	1397103	CTX	N/A	BRC30	-1	-1	MMEJ	ST6GALNAC5	ENST00000318803	1	intron2	N/A	N/A	N/A	N/A	N/A
1	25173299	25173299	4	1.36E+08	1.36E+08	CTX	N/A	BRC30	-1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	7517910	7517910	21	14535893	14535893	CTX	N/A	BRC30	-1	1	NHEJ	TP53	ENST00000269305	-1	intron6	N/A	N/A	N/A	N/A	N/A
8	40346881	40346881	8	40352841	40352841	DEL	5961	BRC31	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	32016938	32016938	1	43858956	43858956	DEL	11841018	BRC31	1	1	NHEJ	N/A	N/A	N/A	N/A	PTPRF	ENST00000359947	1	intron29	C1orf210 C1orf91 ZNF642 RRAGC YBX1 C1orf216 LEPRE1 C1orf149 ZMYM4 ZNF684 TRAPPC3 FNDC5 NFYC EIF3I ADPRHL2 C1orf94 ZMYND12 SCMH1 C1orf102 MPL MACF1 CTPS FAM167B SYNC COL8A2 TRIT1 FAM183A GJA4 GJB5 A3GALT2 BSDC1 PTP4A2 CLSPN HPCA AKIRIN1 CDC20 ADC PABPC4 KHDRBS1 TEKT2 ZC3H12A ERMAP LCK MANEAL TMCO2 DEM1 YARS ELOVL1 BMP8A GJA9 WDR65 GUCA2B C1orf212 ZNF643 CCDC28B ZSCAN20 FHL3 KPNA6 NCDN PPIH AK2 FOXJ3 THRAP3 uc001chm.2 MARCKSL1 TMEM39B MED8 EPHA10 RIMS3 PPT1 DCDC2B PPCS MRPS15 KCNQ4 PSMB2 RNF19B C1orf84 CCDC23 FTHL1 CSF3R HYI TXLNA MYCBP RBBP4 KIAA1522 SFPQ ZMYM6 S100PBP SMAP2 MAP7D1 IQCC HEYL TMEM125 RSPO1 POU3F1 GJB4 UTP11L EBNA1BP2 C1orf122 MFSD2 SNIP1 NT5C1A COL9A2 PHC2 NDUFS5 ENSG00000221042 ZBTB8OS DLGAP3 TSSK3 HMGB4 OXCT2 LSM10 C1orf113 STK40 C1orf50 KIAA0319L ZNF691 CITED4 CAP1 EDN2 GJB3 HDAC1 FAM176B FOXO6 GUCA2A YRDC PTPRF SLC2A1 EIF2C4 SLFNL1 TRIM62 GRIK3 SF3A3 MYCL1 ZNF362 INPP5B TFAP2E BMP8B HIVEP3 ZMYM1 TMEM54 C1orf109 CLDN19 RIMKLA GNL2 PPIE SPOCD1 EIF2C1 RPL18AP4 MTF1 EIF2C3 ZMPSTE24 TIE1 RHBDL2 DNALI1 CSMD2 HPCAL4 RLF CDCA8 ZBTB8
1	59182849	59182849	1	59830711	59830711	DEL	646861	BRC31	1	1	NHEJ	N/A	N/A	N/A	N/A	FGGY	ENST00000371218	1	intron7	N/A
10	98918410	98918410	10	1.26E+08	1.26E+08	DEL	26797466	BRC31	1	1	NHEJ	SLIT1	ENST00000266058	-1	intron1	N/A	N/A	N/A	N/A	MMS19 CALHM3 CYP17A1 SMNDC1 HPSE2 PNLIP CCDC147 PEO1 KCNIP2 BTRC SORCS3 GBF1 INPP5F TACC2 KAZALD1 BTBD16 SLC18A2 SUFU FBXW4 BUB3 C10orf88 FAM178A SFXN4 NFKB2 C10orf95 CUEDC2 CASP7 PDZD8 UBTD1 ENTPD7 SORCS1 ATE1 VWA2 C10orf82 ADD3 OBFC1 GOLGA7B HMX2 TDRD1 ADRB1 ACSL5 KIAA1598 GUCY2G PRDX3 CPXM2 PDCD11 CNNM2 SEC31B CASC2 PCGF6 DUSP GSTO2 NSMCE4A PDZD7 EMX2 MARVELD1 CNNM1 LOXL4 MGEA5 TRUB1 NDUFB8 VTI1A ADRA2A NT5C2 PGAM1 ARHGAP19 NCRNA00081 SFRP5 SEC23IP USMG5 PSTK PNLIPRP3 PAX2 COX15 CWF19L1 C10orf28 WDR11 NANOS1 PI4K2A GOT1 NEURL C10orf85 FRAT1 IKZF5 FAM160B1 ABCC2 FBXL15 FGF8 HPS1 RPL19P16 TCF7L2 CALHM2 EXOSC1 ANKRD2 MORN4 RAB11FIP2 C10orf33 FGFR2 C10orf81 LBX1 NPM3 C10orf134 SFXN2 GSTO1 FAM24A BLOC1S2 ITPRIP ACADSB FAM24B CPN1 NOLC1 RBM20 RPS8P4 AVPI1 AFAP1L2 RGS10 TECTB HMX3 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 HTRA1 EIF3S10 VAX1 INA SEMA4G TAF5 PITX3 PDCD4 PNLIPRP1 HSPA12A PSD TRIM8 ZFYVE27 NRAP ELOVL3 HABP2 WNT8B C10orf32 CALHM1 ZDHHC16 GPR26 C10orf84 ERLIN1 ABLIM1 LDB1 GFRA1 ATRNL1 RPL13AP6 PRLHR POLL DNMBP HIF1AN AS3MT SHOC2 PPAPDC1A PKD2L1 GPAM FRAT2 ZDHHC6 C10orf76 DMBT1 C10orf65 MXI1 CUZD1 C10orf120 TIAL1

																				PNLIPRP2 BAG3 ARL3 PPRC1 RRP12 C10orf26 SH3PXD2A C10orf119 uc001ktn.1 LZTS2 PLEKHA1 KCNK18 MRPL43 DCLRE1A COL17A1
4	1.32E+08	1.32E+08	4	1.33E+08	1.33E+08	DEL	290699	BRC31	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	1.02E+08	1.02E+08	10	1.03E+08	1.03E+08	DEL	852553	BRC31	1	1	NHEJ	CHUK	ENST00000370397	-1	intron19	N/A	N/A	N/A	N/A	PDZD7 FAM178A BLOC1S2 NDUFB8 WNT8B PEO1 SCD SFXN3 PAX2 HIF1AN LZTS2 SEMA4G CWF19L1 MRPL43 SEC31B PKD2L1
11	62524184	62524184	11	67865861	67865861	DEL	5340674	BRC31	1	1	MMEJ	SLC22A8	ENST00000336232	-1	intron2	LRP5	ENST00000294304	1	intron1	PCNXL3 NUDT22 GPR152 LRFN4 NDUFV1 EIF1AD TM7SF2 SIPA1 CCDC85B NDUFS8 RBM4 PTPRCAP FIBP C11orf84 SLC22A24 RARRES3 ACTN3 CFL1 HRASLS5 RCOR2 SYT12 KCNK7 RPS6KA4 TMEM151A RTN3 ALDH3B1 PRDX5 C11orf24 TBC1D10C RAB1B SSSCA1 DNAJC4 RHOD MARK2 ADRBK1 PYGM FAU SLC22A11 RBM4B NAALADL1 GAL3ST3 HRASLS2 SLC29A2 CATSPER1 SF3B2 OTUB1 COX8A TBX10 KAT5 EHBP1L1 ANKRD13D MEN1 C11orf72 CST6 CTSW MAP4K2 GPR137 RAD9A CCDC88B ARL2 CDK2AP2 CCS MRPL11 ZNHIT2 CD248 EHD1 BATF2 C11orf80 EFEMP2 DPP3 SLC22A25 DRAP1 ESRRA MUS81 CAPN1 PLCB3 C11orf85 RASGRP2 CDC42BPG FBXL11 RPS6KB2 STIP1 PELI3 CHKA AIP SART1 MAP3K11 CABP4 FERMT3 CLCF1 SLC22A10 MRPL49 RNASEH2C BBS1 ATL3 CTSF PC SLC22A9 FRMD8 GPHA2 RCE1 CNIH2 TCIRG1 LTBP3 POLA2 C11orf2 CABP2 RELA FOSL1 SPDYC ALDH3B2 PPP1R14B SLC22A12 UNC93B1 TMEM134 MACROD1 SAC3D1 SCYL1 TRPT1 FKBP2 SPTBN2 DPF2 SSH3 GSTP1 SUV420H1 PLA2G16 SLC22A20 NPAS4 KCNK4 POLD4 KLC2 CDCA5 TMEM137 PPP2R5B ATG2A CDC42EP2 ZDHHC24 C11orf68 VEGFB NRXN2 TSGA10IP BANF1 ATPGD1 OVOL1 SYVN1 BAD SLC25A45 FLRT1 SF1 PACS1 C11orf20 BRMS1 CCDC87 SNX15 ACY3 PITPNM1 PPP1CA TIGD3 YIF1A SNX32 NUDT8 CORO1B FAM89B NAT11 C11orf86 ZFPL1 LGALS12 RIN1
1	34407350	34407350	1	37767609	37767609	DEL	3359258	BRC31	1	1	NHEJ	C1orf94	ENST00000373374	1	intron10	N/A	N/A	N/A	N/A	FAM176B GJB3 SFPQ ZMYM6 C1orf216 C1orf149 EIF2C4 GRIK3 MAP7D1 ZMYM4 C1orf212 TRAPPC3 TFAP2E GJB4 NCDN ADPRHL2 C1orf94 ZMYM1 THRAP3 C1orf102 DLGAP3 COL8A2 GJA4 GJB5 MRPS15 EIF2C1 CLSPN LSM10 PSMB2 C1orf113 STK40 EIF2C3 CSF3R KIAA0319L TEKT2 ZC3H12A
13	37380437	37380437	13	39957364	39957364	DEL	2575924	BRC31	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	STOML3 C13orf23 LHFP NHLRC3 COG6 FREM2 UFM1 ENSG00000215483
1	50444375	50444375	1	1.67E+08	1.67E+08	DEL	1.17E+08	BRC31	1	1	NHEJ	N/A	N/A	N/A	N/A	NME7	ENST00000367811	-1	intron11	DNAJC6 HFM1 PTGER3 KRTCAP2 XCL1 ADAM30 BARHL2 ABCD3 FAM63A C1orf183 IQGAP3 MTF2 CCDC19 DUSP12 CASQ1 RPS10P8 DHCR24 MEF2D GLIS1 C1orf85 ATP5F1 OR6P1 DPH5 DIRAS3 RXRG ARHGEF11 PRKAA2 DPT PPIAL4A RGS5 DCST1 RBM15 C1orf161 NTRK1 NBPF12 HBXIP OR10Z1 CD1B HMGCS2 FCGR2A RAP1A SPAG17 SRGAP2P1 GPSM2 MOV10 GOT2L1 FCRL6 ATXN7L2 FNBP1L C8A LCE3E RFX5 TRIM33 DEDD TYW3 TMOD4 MIER1 GNAI3 LRRC52 HIST2H2BC NBPF5 ITLN2 ITLN1 LPAR3 AMY1C CRABP2 NUDT17 ZYG11B CD1D NUP210L CD244 NGF SHE C1orf173 IGSF3 AMY1A ORC1L PI4KB ACADM ANP32E DENND2C PPM1J FMO10P GIPC2 LCE1A CAPZA1 CDCP2 NFIA C1orf178 AK3L1 CLCA4 MPZ ST6GALNAC5 SLC44A3 SSBP3 ATP1A2 SHC1 BCAN TTF2 ILF2 OR10X1 PTPN22 ST7L RPS2P8 GPX7 ZYG11A FCGR2B GDAP2 CLCC1 GSTM1 S100A4 CA14 C1orf182 ARHGAP30 CDC14A THEM5 KIAA0907 HIST2H3A TADA1L PROK1 ETV3 NCRNA00166 ENSG00000221042 TCHH GADD45A SNX27 CD160 MSH4 SYT6 LRRC8C TNRC4 RXFP4 TAF13 FGGY GABPB2 IL12RB2 CADM3 C1orf61 CD1A REG4 FAM73A RHOC MYSM1 SLC1A7 OR10J5 PEA15 TAGLN2 CD5L DAP3 DAB1 NBPF4 SPATA1 C8B SASS6 ATP8B2 GBP7 SLC27A3 PLEKHO1 OR6K2 RPL5 BXDC5 PAQR6 MEX3A ACOT11 HIST2H4A PODN ANKRD35 KCNA2 AQP10 LCE3D RPL5P6 HBXIPL S1PR1 LCE1B LRRC8D ANGPTL3 SLAMF9 SPRR2D GPR161 YIPF1 UBQLN4 CHI3L2 NBPF10 ANKRD13C CACHD1 PIAS3 RAB3B TTC39A RUSC1 SEMA6C GLMN AMY1B ATP1B1 MRPL24 GON4L USP21 TPM3 FLG2 ARNT IFI44L MGST3 INSRR FRRS1 RPL6P2

SLC22A15 KCNA3 DLEU2L CREG1 DDAH1 TARS2 ATP1A4 HIST2H4B CSF1 JTB APH1A THBS3 GPR89C SORT1 SAMD13 PMF1 VHLL C1orf177 HS2ST1 C1orf138 LRP8 MCOLN3 COPA C1orf2 LENEP 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 FOXD3 POGZ PCP4L1 RPS10P6 ALG14 C1orf123 SYPL2 SLC25A44 GPR177 MTX1 FMO5 PDZK1P2 NBPF8 ADORA3 GBP6 FAM69A EFCAB7 OR10K1 DRD5P2 SLAMF1 DPYD SLC16A4 BRDT FCGR3B ZNF687 ARHGEF2 DUSP27 HSPB11 TCHHL1 SARS TNNI3K FCRL3 LRRC40 GJA8 NEXN OR10J9P PSMB4 SMG5 LRRC7 USP33 CYCSP52 CRYZ SPTA1 OVGP1 WNT2B CTBS CCT3 C1orf111 UBAP2L SGIP1 S100A2 RSBN1 GNG12 C1orf152 APCS IL6R GTF2B CHRNB2 uc001elp.1 SSR2 EEF1AL9 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 PSMD4 SLC35D1 DR1 ECM1 TTC22 FLAD1 CD58 CD48 C1orf51 AHCYL1 FUBP1 PTGFR KTI12 RIT1 SH2D1B MNDA OR10J3 NTNG1 CCDC76 GFI1 PBX1 RAB13 USF1 SLAMF7 OSBPL9 LRRC53 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 RAVER2 RPE65 GBP3 LEPROT SCAMP3 VCAM1 S100A3 CDC42SE1 PRPF38A TDRD10 CD1E FAF1 KCNJ9 SPRR2F HIST2H2AA4 HAO2 DPM3 OR6N2 AP4B1 TTC24 TUFT1 CTSS HIST2H2BD GNRHR2 VANGL2 C1orf88 PRKAB2 IGSF9 ZCCHC11 TTLL7 C1orf203 HIST2H3PS2 RAG1AP1 FLG HIST2H3D TGFBR3 TRIM45 C1orf194 PTGFRN PBXIP1 NHLH2 OR10T2 FAM108A3 ILDR2 INSL5 NBPF16 EFNA1 SLC35A3 YY1AP1 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 ADAMTS4 SYDE2 C1orf137 CELSR2 PDZK1 RWDD3 PPOX KIRREL FMO8P CDKN2C CYB561D1 HSPA6 SV2A DENND4B ECHDC2 DCST2 TCTEX1D1 DMRTB1 OR6N1 APOA1BP VPS72 HOOK1 SLAMF8 MPZL1 LYSMD1 FCGR1A LRRIQ3 PHGDH ACP6 EPS15 CCT8P1 OR10J1 RORC AMPD1 APOA2 LOR C1orf192 EFNA3 NES LDLRAD1 SEMA4A PEX19 RPL36AP11 ADAMTSL4 FCRL2 LCE2C NEGR1 ELTD1 SSX2IP 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 FMO9P CTSK NOTCH2 GSTM5 BSND CTH NR1H5P SPRR4 SLC30A7 LCE1D FCER1G CRTC2 CCBL2 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 RABGGTB RPL17 ZZZ3 RPL7P8 RPL26P12 uc001fxh.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 MLLT11 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 FDPS PGLYRP3 ERVK5 PSRC1 TBX15 VAV3 MTMR11 LCE3B MRPL37 STXBP3 CHD1L MSTO1 SELENBP1 DDX20 MCL1 SCNM1 GBP4 PVRL4 PSMA5 AMIGO1 FAM19A3 ZNF697 TXNIP DARC SLC16A1 LCE4A ALDH9A1 GBAP GJA5 ADCY10 SPRR2E LRRC39 ZRANB2 NBPF7 S100A11 ST6GALNAC3

																					HIPK1 MAN1A2 HIST2H2AC RBMXL1 GPR88 LRIG2 RPRD2 MYBPHL OR6K4P OR10R2 C1orf162 USP1 SFRS11 HIST2H2BE KCNA10 CYMP CREB3L4 VPS45 C1orf146 S100A13 SNAPIN CDC7 NEFHL LIX1L PEX11B SNX7 CPT2 PPIAL4G SLAMF6 IFI44 UFC1 FAM151A C1orf43 C1orf68 DMRTA2 GPR61 XCL2 RHBG SLC6A17 NBPF15 GOLPH3L ENSG00000216295 INTS3 SPRR1B DNASE2B SLC25A24 PFDN2 HIST2H3C CD1C LASS2 PIGM ITGB3BP ZFYVE9 S100A9 CC2D1B UCK2 DEPDC1 GPR89B CLCA3 ZNHIT6 WDR63 BTF3L4 DUSP23 RPS27 CRCT1 WDR47 LCE1F HRNR PKN2 ITGA10
13	1.12E+08	1.12E+08	13	1.12E+08	1.12E+08	DEL	3950	BRC31	1	1	NHEJ	ATP11A	ENST00000375630	1	intron1	ATP11A	ENST00000375630		1	intron1	N/A
10	1.02E+08	1.02E+08	10	1.03E+08	1.03E+08	DEL	41315	BRC31	1	1	NHEJ	N/A	N/A	N/A	N/A	SFXN3	ENST00000393459		1	cds_exon5	PDZD7 FAM178A PAX2 LZTS2 SEMA4G PEO1 MRPL43
10	98771788	98771788	10	1.24E+08	1.24E+08	DEL	24828720	BRC31	1	1	MMEJ	SLIT1	ENST00000266058	-1	intron25	ATE1	ENST00000369043		-1	intron8	MMS19 CALHM3 CYP17A1 SMNDC1 HPSE2 PNLIP 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 CNNM2 SEC31B CASC2 PCGF6 DUSP GSTO2 PDZD7 EMX2 MARVELD1 CNNM1 MGEA5 LOXL4 TRUB1 NDUFB8 VTI1A ADRA2A NT5C2 PGAM1 ARHGAP19 NCRNA00081 SFRP5 SEC23IP USMG5 PNLIPRP3 PAX2 COX15 CWF19L1 C10orf28 WDR11 NANOS1 PI4K2A GOT1 NEURL C10orf85 FRAT1 FAM160B1 ABCC2 FBXL15 FGF8 HPS1 RPL19P16 TCF7L2 CALHM2 EXOSC1 ANKRD2 MORN4 RAB11FIP2 C10orf33 FGFR2 C10orf81 LBX1 NPM3 C10orf134 SFXN2 GSTO1 BLOC1S2 ITPRIP CPN1 NOLC1 RBM20 RPS8P4 AVPI1 AFAP1L2 RGS10 TECTB 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 PNLIPRP1 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 MXI1 TIAL1 PNLIPRP2 BAG3 ARL3 PPRC1 RRP12 C10orf26 SH3PXD2A C10orf119 uc001ktn.1 LZTS2 KCNK18 MRPL43 DCLRE1A COL17A1
20	25690261	25690261	20	25690367	25690367	DEL	93	BRC31	1	1	VNTR	N/A	N/A	N/A	N/A	N/A	N/A	N/A		N/A	N/A
5	50755267	50755267	5	50756209	50756209	DEL	939	BRC32	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A		N/A	N/A
8	1.04E+08	1.04E+08	8	1.04E+08	1.04E+08	DEL	978	BRC32	1	1	NHEJ		ENST00000378537	-1	intron1		ENST00000378537		-1	intron1	N/A
3	1.26E+08	1.26E+08	3	1.26E+08	1.26E+08	DEL	23882	BRC32	1	1	NHEJ	N/A	N/A	N/A	N/A	ZNF148	ENST00000360647		-1	intron4	N/A
3	53002187	53002187	3	53013938	53013938	DEL	11742	BRC32	1	1	MMEJ	SFMBT1	ENST00000394750	-1	intron0	SFMBT1	ENST00000394750		-1	intron0	N/A
12	1.27E+0	1.27E+0	12	1.27E+0	1.27E+0	DEL	5212	BRC3	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A		N/A	N/A

	8	8		8	8			2												
15	50164924	50164924	15	50165051	50165051	DEL	127	BRC32	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	68678611	68678611	11	68678694	68678694	DEL	76	BRC32	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	84931802	84931802	5	84933710	84933710	DEL	1906	BRC32	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	72892992	72893360	6	87267575	87267735	CTX	N/A	BRC33	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	21052748	21052748	20	21284204	21284204	DEL	230456	BRC35	1	1	NHEJ	N/A	N/A	N/A	N/A	XRN2	ENST00000377191	1	intron21	NCRNA00153
17	47318360	47318360	17	50681691	50681691	DEL	3362328	BRC35	1	1	MMEJ	CA10	ENST00000340813	-1	intron3	N/A	N/A	N/A	N/A	STXBP4 TOM1L1 KIF2B COX11 RPS2P48
X	66207272	66207272	X	66207628	66207628	DEL	348	BRC35	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	20681963	20681963	20	21053176	21053176	DEL	370211	BRC35	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	RPL24P2 MRPS11P1
X	66029496	66029496	X	66029638	66029638	DEL	141	BRC35	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	21194444	21194444	20	22439220	22439220	DEL	1243773	BRC35	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SLC25A6P1 GSTM3P XRN2 ST13P PAX1 RPL41P1 NKX2-2 NKX2-4
17	51453440	51453440	17	54596095	54596095	DEL	3141649	BRC35	1	1	MMEJ	N/A	N/A	N/A	N/A	PRR11	ENST00000262293	1	intron0	RAD51C SCPEP1 PPM1E OR4D1 HSF5 C17orf67 ANKFN1 MRPS23 TRIM37 FAM33A CUEDC1 DGKE DYNLL2 RNF126P1 NOG VEZF1 COIL MPO MTMR4 RNF43 MKS1 OR4D2 SEPT4 SFRS1 AKAP1 LPO TRIM25 EPX MSI2 SUPT4H1 C17orf47 TEX14 BZRAP1
11	74649654	74649654	11	74670244	74670244	DEL	20591	BRC35	1	1	NHEJ	N/A	N/A	N/A	N/A	ARRB1	ENST00000360025	-1	intron6	N/A
11	77312191	77312191	11	78262417	78262417	DEL	949226	BRC35	1	1	NHEJ	INTS4	ENST00000354849	-1	intron12	ODZ4	ENST00000278550	-1	intron5	ALG8 USP35 NARS2 THRSP KCTD21 GAB2 KCTD14 NDUFC2

2	60891329	60891329	2	61339729	61339729	DEL	447398	BRC35	1	1	NHEJ	N/A	N/A	N/A	N/A	USP34	ENST00000398569	-1	intron43	KIAA1841 REL PUS10 AHSA2 C2orf74 PEX13
14	29069616	29069616	14	29436876	29436876	DEL	366260	BRC35	1	1	NHEJ	N/A	N/A	N/A	N/A	PRKD1	ENST00000389985	-1	intron1	N/A
17	55351304	55351304	17	73897045	73897045	DEL	18544740	BRC35	1	1	MMEJ	RPS6KB1	ENST00000225577	1	intron4	PGS1	ENST00000262764	1	intron1	ACE BTBD17 TLK2 MXRA7 KIF19 RGS9 KCNJ2 C17orf99 GALR2 C17orf77 CCDC45 EXOC7 SRP68 ICT1 CD79B SLC16A5 WIPI1 SYNGR2 ABCA8 MFSD11 LLGL2 RNF157 SDK2 TK1 METTL2A C17orf95 CDC42EP4 KCNH6 OTOP2 QRICH2 MRPS7 GPR142 SNORD1C CD300LD DDX42 SOX9 PRCD MYO15B ACOX1 AMZ2 SEC14L1 PITPNC1 CD300C CCDC46 SFRS2 TMC6 FTSJ3 ST6GALNAC2 CDR2L NACA2 PSMC5 HN1 TBC1D3P2 UBE2O DDX5 COG1 C17orf54 CSHL1 PRPSAP1 PECAM1 ABCA5 CD300E CPSF4L THA1P TBX2 CASKIN2 POLG2 MED13 KIAA0195 GALK1 TMEM104 TBX4 KCTD2 FAM20A MAP3K3 KCNJ16 ERN1 UNC13D SOCS3 MRPL38 FALZ C17orf28 TMC8 CD300LF TANC2 APPBP2 SLC39A11 CD300LB SCN4A CACNG5 FBF1 H3F3B CYB561 USP32 GH2 LIMD2 ABCA10 UNK ARSG RPL38 PRKAR1A DNAI2 ATP5H WBP2 CSH1 TTYH2 NUP85 C17orf82 LRRC37A3 C17orf58 MARCH10 ICAM2 C17orf60 GNA13 CACNG1 HELZ GRIN2C CD300A AANAT CA4 EFCAB3 RPL36AP46 RNFT1 BCAS3 WDR68 USH1G SPHK1 EVPL NT5C PRKCA CCDC44 KPNA2 FAM104A FADS6 TRIM65 TSEN54 JMJD6 CACNG4 BRIP1 SMARCD2 ZACN SLC25A19 SLC16A6 FDXR OTOP3 CDK3 ARMC7 SSTR2 SLC9A3R1 BIRC5 SEPT9 PPM1D CSH2 TEX2 C17orf80 FAM100B MGAT5B GPRC5C ABCA6 GH1 FOXJ1 ITGB4 TNRC6C CYGB NAT9 RECQL5 TRIM47 MRC2 RHBDF2 AXIN2 SMURF2 AFMID GGA3 CCDC47 PLEKHM1P HEATR6 INTS2 MIF4GD STRADA ST6GALNAC1 C17orf64 SAP30BP NOL11 PSMD12 RAB37 APOH ABCA9 MAP2K6 GRB2
17	62126148	62126148	17	73761829	73761829	DEL	11634683	BRC35	1	1	NHEJ	PRKCA	ENST00000284384	1	intron8	THA1P	ENST00000401961	-1	intron0	ABCA10 UNK BTBD17 RPL38 ARSG PRKAR1A MXRA7 KIF19 DNAI2 KCNJ2 C17orf99 GALR2 ATP5H C17orf77 WBP2 TTYH2 EXOC7 SRP68 NUP85 ICT1 C17orf58 SLC16A5 WIPI1 SYNGR2 ABCA8 MFSD11 CACNG1 LLGL2 GRIN2C HELZ RNF157 SDK2 TK1 CD300A AANAT C17orf95 CDC42EP4 USH1G SPHK1 OTOP2 EVPL QRICH2 MRPS7 GPR142 SNORD1C CD300LD NT5C SOX9 PRCD MYO15B ACOX1 FADS6 KPNA2 FAM104A AMZ2 TRIM65 TSEN54 SEC14L1 JMJD6 PITPNC1 CACNG4 CD300C SFRS2 TMC6 ZACN SLC25A19 OTOP3 FDXR SLC16A6 CDK3 ARMC7 ST6GALNAC2 CDR2L SLC9A3R1 SSTR2 BIRC5 SEPT9 HN1 UBE2O COG1 C17orf54 C17orf80 PRPSAP1 FAM100B MGAT5B GPRC5C ABCA6 ABCA5 CD300E FOXJ1 ITGB4 CPSF4L TNRC6C CYGB NAT9 RECQL5 TRIM47 CASKIN2 RHBDF2 KIAA0195 GALK1 TMEM104 AFMID KCTD2 GGA3 FAM20A KCNJ16 UNC13D MIF4GD MRPL38 ST6GALNAC1 FALZ C17orf28 TMC8 CD300LF SAP30BP NOL11 PSMD12 RAB37 SLC39A11 CACNG5 CD300LB FBF1 H3F3B MAP2K6 ABCA9 GRB2
X	66327321	66327321	X	66346879	66346879	DEL	19555	BRC35	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	38279841	38279841	17	53293976	53293976	CTX	N/A	BRC35	-1	-1	MMEJ	WHSC1L1	ENST00000317025	-1	intron13	N/A	N/A	N/A	N/A	N/A
X	66327483	66327483	22	39133883	39133883	CTX	N/A	BRC35	-1	1	NHEJ	N/A	N/A	N/A	N/A	SGSM3	ENST00000248929	1	intron13	N/A
8	36874884	36874884	19	2105641	2105641	CTX	N/A	BRC35	1	1	MMEJ		ENST00000399881	1	intron21	N/A	N/A	N/A	N/A	N/A

8	39401982	39401982	11	74627496	74627496	CTX	N/A	BRC35	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	94310951	94310951	13	1.08E+08	1.08E+08	CTX	N/A	BRC35	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	1.26E+08	1.26E+08	X	1.26E+08	1.26E+08	DEL	160	BRC37	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	38469103	38469103	X	51601317	51601317	INV	13131190	BRC37	-1	1	MMEJ	N/A	N/A	N/A	N/A	MAGED1	ENST00000375772	1	intron0	N/A
14	99379570	99379570	14	1.02E+08	1.02E+08	DEL	2385527	BRC37	1	1	MMEJ	EML1	ENST00000262233	1	intron1	RAGE	ENST00000193029	-1	intron1	DEGS2 C14orf68 DYNC1H1 BEGAIN HSP90AA2 YY1 RTL1 EVL C14orf70 WDR20 WARS EML1 DIO3 DLK1 WDR25 PPP2R5C SLC25A29
14	49294795	49294795	14	49294882	49294882	DEL	80	BRC37	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	71999408	71999408	3	1.12E+08	1.12E+08	CTX	N/A	BRC37	1	-1	NHEJ	NEGR1	ENST00000357731	-1	intron3	N/A	N/A	N/A	N/A	N/A
16	60003008	60003008	19	32815715	32815715	CTX	N/A	BRC37	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	64256330	64256330	3	1.49E+08	1.49E+08	CTX	N/A	BRC37	1	1	NHEJ	ROR1	ENST00000371080	1	intron2	N/A	N/A	N/A	N/A	N/A
11	1.29E+08	1.29E+08	14	91451138	91451138	CTX	N/A	BRC37	-1	-1	MMEJ	N/A	N/A	N/A	N/A	FBLN5	ENST00000267620	-1	intron5	N/A
11	49079921	49079921	14	1.03E+08	1.03E+08	CTX	N/A	BRC37	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	49079636	49079636	14	72508889	72508889	CTX	N/A	BRC37	-1	1	NHEJ	N/A	N/A	N/A	N/A	ZFYVE1	ENST00000394207	-1	intron7	N/A
6	19632399	19632399	6	19633189	19633189	DEL	790	BRC38	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	55857231	55857231	8	55857500	55857500	DEL	267	BRC38	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

14	43042461	43042461	14	43046658	43046658	DEL	4191	BRC38	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	70384524	70384524	2	70401920	70401920	DEL	17393	BRC38	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	52667722	52667722	8	74114492	74114492	DEL	21445768	BRC38	1	1	NHEJ	PXDNL	ENST00000356297	-1	intron0	TERF1	ENST00000276602	1	intron8	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 VCPIP1 C8orf45 XKR4 LACTB2 PREX2 ST18 C8orf34 TCEA1P2 RRS1 SLCO5A1 PENK FAM110B FAM150A TCF24 RLBP1L1 NKAIN3 CSPP1 TOX NSMAF ARFGEF1 ARMC1 PDE7A XKR9 MTFR1
1	2.23E+08	2.23E+08	1	2.23E+08	2.23E+08	DEL	288967	BRC38	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	CNIH3
8	1.13E+08	1.13E+08	8	1.13E+08	1.13E+08	DEL	316547	BRC38	1	1	NHEJ	N/A	N/A	N/A	N/A	CSMD3	ENST00000395717	-1	intron59	N/A
5	1376274	1376274	5	1376517	1376517	DEL	231	BRC38	1	1	NAHR	CLPTM1L	ENST00000320895	-1	intron12	CLPTM1L	ENST00000320895	-1	intron12	N/A
12	1.24E+08	1.24E+08	12	1.24E+08	1.24E+08	DEL	147	BRC38	1	1	NAHR	AACS	ENST00000316519	1	intron9	AACS	ENST00000316519	1	intron9	N/A
6	19112668	19112668	6	19116070	19116070	DEL	3392	BRC38	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	1.13E+08	1.13E+08	X	1.18E+08	1.18E+08	CTX	N/A	BRC38	1	-1	MMEJ	N/A	N/A	N/A	N/A	DOCK11	ENST00000276202	1	intron30	N/A
5	90583725	90583725	9	82938366	82938366	CTX	N/A	BRC38	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	736175	736175	16	736270	736270	DEL	87	BRC39	1	1	NAHR	HAGHL	ENST00000389701	1	intron6	HAGHL	ENST00000389701	1	intron6	N/A
18	66785261	66785261	22	27395753	27395753	CTX	N/A	BRC39	1	-1	NHEJ	N/A	N/A	N/A	N/A	TTC28	ENST00000397906	-1	intron1	N/A
8	1.37E+08	1.37E+08	12	556844	556875	CTX	N/A	BRC39	-1	1	VNTR	N/A	N/A	N/A	N/A	NINJ2	ENST00000305108	-1	intron1	N/A
15	328624	328624	15	777976	777976	DEL	449	BRC	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	DPP8 STRC SCG3 uc002aog.1 ANXA2 SRP14P1 SPESP1 PSMA4 DISP2 C15orf27 NARG2 GNB5 PSTPIP1 HERC1 CYP11A1 TIPIN PRTG ETFA COX5A CYP19A1 UBR1 CSPG4 PKM2 CRABP1

	58	58		98	98		34238	4												C15orf33 CASC4 LBXCOR1 SLTM CSK VPS39 KIAA1024 BMF WDR61 CGNL1 TRPM7 CILP MTFMT SCAPER C15orf48 BRUNOL6 TBC1D2B TMED3 C15orf56 C15orf21 PLCB2 CAPN3 PLA2G4D ITGA11 ATP8B4 CEP27 GLDN PML RPS27L AQP9 SPATA5L1 RAD51 SQRDL COMMD4 LEO1 CKMT1B COPS2 CD276 TSPAN3
15	19981980	19981980	15	56883313	56883313	DEL	36900331	BRC4	1	1	NHEJ	N/A	N/A	N/A	N/A	FAM63B	ENST00000316848	1	intron3	RAB11A HCN4 RORA PTPLAD1 PLDN SNX1 TNFAIP8L3 OAZ2 LIPC C15orf15 MNS1 MPI ZFP106 APH1B C15orf41 RAB8B CHRNA3 ISLR2 ITPKA CYP1A2 ONECUT1 EXD1 TLN2 DUOXA1 FAM148A GCNT3 DNAJC17 UNC13C SLC28A2 C15orf60 RPP25 MYO9A MAPK6 NPTN MAP2K5 SCAMP2 SENP8 TGM7 TEX9 CIB2 HISPPD2A CATSPER2 SERF2 STARD9 ISLR ANKDD1A TLE3 HIGD2B PARP16 ADAL ZSCAN29 PDIA3 GPR176 GTF2A2 RASGRP1 DENND4A SMAD3 RAB27A CTDSPL2 CALML4 DMXL2 B2M FBXO22 IMP3 C15orf52 EID1 CHRNA5 FAM63B THAP10 uc010bld.1 SPRED1 MAP1A NEIL1 MYO5A CPLX3 PARP6 ADAM10 FGF7 ULK3 NEDD4 MAP2K1 CLK3 GOLGA6B RASL12 DYX1C1 DNM1P34 SNAP23 SLC27A2 RTF1 PPCDC CEP152 MFAP1 USP50 MGA UACA SHC4 TPM1 LDHAL6B MAPKBP1 LINGO1 DUOXA2 LMAN1L ODF3L1 GRAMD2 GALK2 DNAJA4 ACSBG1 CCNB2 ADPGK RASGRF1 SEMA7A NR2E3 BCL2L10 SLC30A4 ANP32A SPTBN5 UBE2Q2 DIS3L DTWD1 PYGO1 D4ST1 CCNDBP1 SNUPN TBC1D21 TMEM84 EPB42 DAPK2 SCAMP5 SIN3A NEO1 CASC5 FRMD5 SPG21 CTSH AQR IQCH EIF3S1 TMOD2 CCPG1 ZNF770 PAK6 TRIM69 SH3PX3 LCTL RHOV EDC3 CLN6 SLC12A1 LRRC49 C15orf43 LRRC57 MEGF11 FAM98B PPIB KIAA1370 C15orf23 JMJD7-PLA2G4B PLA2G4E MEIS2 LTK SLC24A5 BBS4 THSD4 RPLP1 IGDCC4 SECISBP2L FEM1B STOML1 FAM82A2 TMCO5A CCDC33 NDUFAF1 RPSAP55 HMG20A MORF4L1 C15orf53 GABPB1 FAM148B FBXL22 PPP1R14D C15orf57 MYEF2 FAM96A EHD4 GCHFR NOX5 VPS18 RFX7 TMEM202 TP53BP1 KIAA0101 GRINL1A MAN2C1 VPS13C WDR72 HSP90AB4P INO80 RBPMS2 ATPBD4 C15orf54 CKMT1A DNM1P33 ZFYVE19 THBS1 CYP1A1 LCMT2 FOXB1 FSIP1 SH2D7 SNAPC5 GLCE OIP5 LARP6 SPINT1 DUOX2 PLEKHQ1 PAQR5 FBN1 MYO5C ACTC1 PLA2G4F TYRO3 FAM81A PTPN9 BNIP2 ZNF609 GATM HEXA AP4E1 GOLGA6D RPAP1 C15orf39 SEMA6D TCF12 ARIH1 LACTB FAM92A1 HDC C15orf17 TUBGCP4 SORD TMOD3 CORO2B ISL2 ELL3 CDAN1 uc001znl.1 ZWILCH LYSMD2 USP8 PIAS1 C15orf62 DUT CA12 STRA6 TMEM62 RNF111 CLPX C15orf59 TTBK2 IGDCC3 RCN2 TRIP4 SLC24A1 RPL17P33 ALDH1A2 SERINC4 BAHD1 DLL4 C15orf20 SMAD6 IVD SPG11 CHRNB4 C15orf44 ADAMTS7 NUSAP1 ZNF280D CHAC1 NRG4 IREB2 PDCD7 CATSPER2P1 UBL7 BUB1B USP3 RPL4 GANC IDH3A C15orf61 SHF GOLGA6C SNX22 CSNK1G1 LOXL1 ENSG00000184935 EIF2AK4 PIGB DUOX1 WDR76 TGM5 RPUSD2 KIF23 ARID3B MYO1E TMEM87A STRC NIPA1 EPB42 ENSG00000188626 SCG3 CASC5 SRP14P1 FRMD5 RYR3 DISP2 AQR GABRB3 KLF13 CCPG1 GNB5 TMOD2 EIF3S1 ZNF770 MKRN3 PAK6 TRIM69 NOLA3 RHOV SLC12A1 C15orf43 LRRC57 FMN1 FAM98B KIAA1370 C15orf55 PRTG C15orf23 PLA2G4E JMJD7-PLA2G4B MEIS2 CYP19A1 LTK UBR1 SLC24A5 MTMR10 ARHGAP11A TJP1 SECISBP2L C15orf33 CASC4 FAM82A2 TMCO5A RPSAP55 NDUFAF1 VPS39 TRPM1 MAGEL2 BMF C15orf53 GABPB1 CGNL1 TRPM7 SLC12A6 AVEN C15orf48 GOLGA8E PPP1R14D GOLGA8G APBA2 C15orf57 C15orf56 MYEF2 C15orf21 PLCB2 CAPN3 PLA2G4D EHD4 ATP8B4 GCHFR CEP27 RFX7 VPS18 TP53BP1 GLDN GRINL1A HSP90AB4P WDR72 AQP9 SPATA5L1 INO80 RAD51 GREM1 SQRDL CHRM5 ATPBD4 LEO1 CKMT1A C15orf54 ZFYVE19 LPCAT4 THBS1 CKMT1B LCMT2 COPS2 FSIP1 OIP5 PLDN DUOX2 SPINT1 TNFAIP8L3 GOLGA9P FBN1 LIPC HERC2P2 C15orf15 MYO5C MNS1 GOLGA8A ACTC1 ZFP106 PLA2G4F TYRO3 C15orf41 SNRPN NDNL2 CHRFAM7A GATM AP4E1 RPAP1 ITPKA ONECUT1 EXD1 DUOXA1 HERC2 NIPA2 TCF12 SEMA6D DNAJC17 UNC13C SLC28A2 SCG5 HDC FAM7A1 FAM92A1 GABRA5 GJD2 TMEM85 TUBGCP4 MAPK6 SORD OCA2 TMOD3 TGM7 TEX9 HISPPD2A CATSPER2 TMCO5B SERF2 STARD9 ELL3 CDAN1 C15orf29 uc001znl.1 LYSMD2 USP8 ZSCAN29 ADAL PDIA3 SNURF WHAMML1 OTUD7A C15orf62 DUT GPR176 TMEM62 RASGRP1 RAB27A CTDSPL2 ARHGAP11B DMXL2 B2M TTBK2 C15orf52 EID1 ALDH1A2 SPRED1 MTMR15 MAP1A MYO5A GOLGA8F ADAM10 FGF7 SERINC4 BAHD1 DLL4 IVD NEDD4 SPG11 DYX1C1 C15orf24 ZNF280D NUSAP1 CHAC1 SNAP23 SLC27A2 RTF1 CEP152 PGBD4 MFAP1 CATSPER2P1 USP50 MGA SHC4 BUB1B MAPKBP1 DUOXA2 GANC NDN TUBGCP5 ATP10A SHF CHRNA7 CYFIP1 PIGB GALK2 EIF2AK4 ENSG00000184935 DUOX1 WDR76 GOLGA8B TGM5 C15orf2 RPUSD2 BCL2L10 SLC30A4 SPTBN5 UBE3A GABRG3 TMEM87A DTWD1 PYGO1 CCNDBP1 D4ST1

8	1.33E+08	1.33E+08	8	1.33E+08	1.33E+08	DEL	110653	BRC4	1	1	MMEJ	N/A	N/A	N/A	N/A	EFR3A	ENST00000254624	1	intron1	N/A
7	38459541	38459541	7	39384323	39384323	DEL	923780	BRC4	1	1	NHEJ	AMPH	ENST00000356264	-1	intron11	POU6F2	ENST00000403058	1	intron5	FAM183B VPS41
7	38465692	38465692	7	39372199	39372199	DEL	905505	BRC4	1	1	NHEJ	AMPH	ENST00000356264	-1	intron11	POU6F2	ENST00000403058	1	intron5	FAM183B VPS41
11	56363215	56363215	11	56953362	56953362	DEL	589142	BRC4	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	OR5AK2 P2RX3 PRG3 OR5AK3P SSRP1 SLC43A3 APLNR LRRC55 PRG2 TNKS1BP1
12	1.16E+08	1.16E+08	12	1.16E+08	1.16E+08	DEL	271	BRC4	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	49363488	49363488	8	81032653	81032653	DEL	31668148	BRC4	1	1	MMEJ	N/A	N/A	N/A	N/A	MRPS28	ENST00000276585	-1	intron2	BHLHE22 ATP6V1H CPA6 COPS5 PKIA C8orf84 ASPH CHCHD7 LYN NCOA2 FAM164A PCMTD1 C8orf71 PXDNL PLAG1 LRRC67 KCNB2 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 NPBWR1 STAU2 SOX17 TMEM68 YTHDF3 SGK3 UBE2W C8orf45 RGS20 VCPIP1 HEY1 XKR4 STMN2 LACTB2 PREX2 ST18 SNTG1 C8orf34 PI15 TCEA1P2 RRS1 HNF4G SLCO5A1 PENK FAM110B FAM150A C8orf22 TCF24 RLBP1L1 CSPP1 NKAIN3 SNAI2 NSMAF TOX ARFGEF1 ARMC1 PDE7A XKR9 GDAP1 MTFR1
11	57427746	57427746	11	59078082	59078082	DEL	1649335	BRC4	1	1	NHEJ	N/A	N/A	N/A	N/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	49268015	49268015	7	49268604	49268604	DEL	587	BRC4	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	85350216	85350216	6	10891556	10891556	CTX	N/A	BRC4	1	1	MMEJ	N/A	N/A	N/A	N/A	MAK	ENST00000354489	-1	intron10	N/A
6	44062238	44062238	8	1.2E+08	1.2E+08	CTX	N/A	BRC4	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	12044880	12044919	10	9181519	9181528	CTX	N/A	BRC4	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	81858249	81858249	X	81858409	81858409	DEL	160	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	1.22E+08	1.22E+08	8	1.22E+08	1.22E+08	DEL	246	BRC41	1	1	MMEJ	MRPL13	ENST00000306185	-1	intron2	MRPL13	ENST00000306185	-1	intron2	N/A

8	1.07E+08	1.07E+08	8	1.07E+08	1.07E+08	DEL	9119	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	1.55E+08	1.55E+08	5	1.55E+08	1.55E+08	DEL	140	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	5955236	5955236	4	5955503	5955503	DEL	265	BRC41	1	1	MMEJ		ENST00000397888	-1	intron7		ENST00000397888	-1	intron7	N/A
12	14843849	14843849	12	14844020	14844020	DEL	170	BRC41	1	1	NHEJ	WBP11	ENST00000261167	-1	cds_exon2	WBP11	ENST00000261167	-1	intron2	N/A
3	1.4E+08	1.4E+08	3	1.4E+08	1.4E+08	DEL	5324	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	22659647	22659647	20	22660134	22660134	DEL	485	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.42E+08	1.42E+08	6	1.42E+08	1.42E+08	DEL	1318	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
13	78901602	78901602	13	78901845	78901845	DEL	242	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	14448635	14448635	7	14461301	14461301	DEL	12664	BRC41	1	1	MMEJ	DGKB	ENST00000403951	-1	intron20	DGKB	ENST00000403951	-1	intron20	N/A
1	2.2E+08	2.2E+08	1	2.2E+08	2.2E+08	DEL	189	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.14E+08	2.14E+08	1	2.14E+08	2.14E+08	DEL	442	BRC41	1	1	NHEJ	USH2A	ENST00000366943	-1	intron37	USH2A	ENST00000366943	-1	intron37	N/A
4	20645149	20645149	4	20645663	20645663	DEL	515	BRC41	1	1	NHEJ	KCNIP4	ENST00000382152	-1	intron1	KCNIP4	ENST00000382152	-1	intron1	N/A
13	1.01E+08	1.01E+08	13	1.01E+08	1.01E+08	DEL	179	BRC41	1	1	MMEJ	FGF14	ENST00000376131	-1	intron1	FGF14	ENST00000376131	-1	intron1	N/A
2	2.21E+08	2.21E+08	2	2.21E+08	2.21E+08	DEL	534	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

6	23348907	23348907	6	23349111	23349111	DEL	20	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	89972756	89972756	3	89973236	89973236	DEL	476	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	1.03E+08	1.03E+08	9	1.03E+08	1.03E+08	DEL	211	BRC41	1	1	MMEJ	PPAPR3	ENST00000374874	1	intron1	PPAPR3	ENST00000374874	1	intron1	N/A
1	1.07E+08	1.07E+08	1	1.07E+08	1.07E+08	DEL	463	BRC41	1	1	NHEJ	NTNG1	ENST00000370076	1	intron1	NTNG1	ENST00000370076	1	intron1	N/A
7	1.37E+08	1.37E+08	7	1.37E+08	1.37E+08	DEL	195	BRC41	1	1	MMEJ	DGKI	ENST00000288490	-1	intron30	DGKI	ENST00000288490	-1	intron30	N/A
4	62729609	62729609	4	62731011	62731011	DEL	1399	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	1.78E+08	1.78E+08	5	1.78E+08	1.78E+08	DEL	783	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.23E+08	2.23E+08	1	2.23E+08	2.23E+08	DEL	4722	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1.74E+08	1.74E+08	4	1.74E+08	1.74E+08	DEL	50689	BRC41	1	1	NHEJ	GALNT7	ENST00000265000	1	intron1	GALNT7	ENST00000265000	1	intron2	N/A
3	1.9E+08	1.9E+08	3	1.9E+08	1.9E+08	DEL	529	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.68E+08	1.68E+08	6	1.68E+08	1.68E+08	DEL	607	BRC41	1	1	NHEJ	MLLT4	ENST00000366809	1	intron18	MLLT4	ENST00000366809	1	intron19	N/A
18	20581611	20581611	18	20597861	20597861	DEL	16248	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15	94189523	94189523	15	94189668	94189668	DEL	142	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	84557179	84557179	7	84557537	84557537	DEL	357	BRC41	1	1	NHEJ	SEMA3D	ENST00000284136	-1	intron2	SEMA3D	ENST00000284136	-1	intron2	N/A

2	40322650	40322650	2	40323530	40323530	DEL	880	BRCA1	1	1	NHEJ	SLC8A1	ENST00000332839	-1	intron1	SLC8A1	ENST00000332839	-1	intron1	N/A
14	29818008	29818008	14	29837143	29837143	DEL	19133	BRCA1	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	8744781	8744781	12	8761575	8761575	DEL	16793	BRCA1	1	1	NHEJ	RIMKLB	ENST00000357529	1	intron10	RIMKLB	ENST00000357529	1	intron1	N/A
1	42858235	42858235	1	42858413	42858413	DEL	177	BRCA1	1	1	NHEJ	uc001chm.2	ENST00000390640	1	intron4	uc001chm.2	ENST00000390640	1	intron4	N/A
17	51735699	51735699	17	51735887	51735887	DEL	186	BRCA1	1	1	MMEJ	ANKFN1	ENST00000318698	1	intron2	ANKFN1	ENST00000318698	1	intron2	N/A
3	18442851	18442851	3	18442983	18442983	DEL	131	BRCA1	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
14	89479844	89479844	14	89517376	89517376	DEL	37530	BRCA1	1	1	MMEJ	C14orf143	ENST00000316738	-1	intron3	TDP1	ENST00000393454	1	intron6	N/A
3	19384801	19384801	3	19445004	19445004	DEL	60204	BRCA1	1	1	NHEJ	KCNH8	ENST00000328405	1	intron5	KCNH8	ENST00000328405	1	intron7	N/A
8	1.25E+08	1.25E+08	8	1.25E+08	1.25E+08	DEL	1044	BRCA1	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	66820172	66820172	18	66834778	66834778	DEL	14606	BRCA1	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	88641320	88641320	7	88656384	88656384	DEL	15064	BRCA1	1	1	NHEJ	ZNF804B	ENST00000333190	1	intron1	ZNF804B	ENST00000333190	1	intron1	N/A
3	1.02E+08	1.02E+08	3	1.02E+08	1.02E+08	DEL	22605	BRCA1	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1.08E+08	1.08E+08	4	1.08E+08	1.08E+08	DEL	31105	BRCA1	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.56E+08	1.56E+08	1	1.56E+08	1.56E+08	DEL	331	BRCA1	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

6	1.34E+08	1.34E+08	6	1.34E+08	1.34E+08	DEL	169	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	1.66E+08	1.66E+08	2	1.66E+08	1.66E+08	DEL	417	BRC41	1	1	NHEJ	CSRNP3	ENST00000409664	1	intron0	CSRNP3	ENST00000409664	1	intron0	N/A
1	67454946	67454946	1	67457291	67457291	DEL	2345	BRC41	1	1	NHEJ	IL23R	ENST00000347310	1	intron5	IL23R	ENST00000347310	1	intron5	N/A
3	45325134	45325134	3	45325355	45325355	DEL	220	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.16E+08	2.16E+08	1	2.16E+08	2.16E+08	DEL	347	BRC41	1	1	MMEJ	GPATCH2	ENST00000366935	-1	intron6	GPATCH2	ENST00000366935	-1	intron6	N/A
3	60853132	60853132	3	60853960	60853960	DEL	826	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	10825523	10825523	5	10827602	10827602	DEL	2074	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	16732747	16732747	20	16739211	16739211	DEL	6462	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	98415923	98415923	8	98423014	98423014	DEL	7088	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	50366060	50366060	18	50366213	50366213	DEL	149	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1.06E+08	1.06E+08	4	1.06E+08	1.06E+08	DEL	9065	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1.17E+08	1.17E+08	4	1.17E+08	1.17E+08	DEL	451	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	44069516	44069516	4	44078927	44078927	DEL	9412	BRC41	1	1	NHEJ	KCTD8	ENST00000360029	-1	intron1	KCTD8	ENST00000360029	-1	intron1	N/A
7	1.41E+08	1.41E+08	7	1.41E+08	1.41E+08	DEL	10434	BRC41	1	1	MMEJ	KIAA1147	ENST00000297761	-1	intron4	KIAA1147	ENST00000297761	-1	intron3	N/A
21	171720	171720	21	171721	171721	DEL	144	BRC	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

2	474413150	474413150	2	934413714	934413714	DEL	564	41 BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	68259145	68259145	6	1.18E+08	1.18E+08	DEL	50103268	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	SLC35F1	ENST00000360388	1	intron1	C6orf51 PM20D2 GJA10 C6orf162 SOBP FAM46A VGLL2 OSTM1 FUT9 LMBRD1 SART2 TUBE1 DCBLD1 USP45 C6orf112 IMPG1 DOPEY1 LAMA4 WASF1 RWDD1 PREP FIG4 IRAK1BP1 COQ3 PNRC1 UBE2CBP COL9A1 BEND3 SFRS18 MRAP2 NT5DC1 BXDC1 KIAA0776 FAM26D TRAF3IP2 PDSS2 C6orf161 SEC63 SIM1 LACE1 PRDM13 FAM162B C6orf203 OGFRL1 FOXO3 C6orf152 RIMS1 PHIP HS3ST5 RPL30P8 HMGN3 LIN28B GABRR2 ZNF259P TSPYL4 FHL5 AIM1 GPRC6A RSPH4A SYNCRIP NCUBE1 MDN1 GJB7 C6orf186 MAP3K7 C6orf164 POPDC3 FYN BAI3 C6orf184 MARCKS SENP6 BVES GOPC SPACA1 GRIK2 MCHR2 BACH2 TMEM30A AKD1 KIAA1009 WISP3 FBXL4 C6orf150 ME1 C6orf168 TTK LYRM2 POU3F2 PGM3 SNX14 RTN4IP1 COX7A2 NUS1 HDAC2 CCNC FAM135A HTR1E RARS2 REV3L RPL3P7 ZUFSP CYB5R4 ORC3L C6orf57 ATG5 DPPA5 SLC35A1 HACE1 BET3L CGA EPHA7 C6orf225 ASCC3 TBX18 C6orf221 TSPYL1 KPNA5 C6orf163 KIAA1919 SNAP91 ZNF292 GPR6 RWDD2A SLC22A16 FRK OOEP RPL17P25 CDC2L6 SCML4 C6orf182 C6orf59 GABRR1 AMD1 RPL35P3 SLC17A5 KCNQ5 HTR1B FILIP1 KHDC1 SH3BGRL2 FAM26F MANEA DDX43 TPBG IBTK KRT18P30 FAM26E PRSS35 CASP8AP2 SNX3 ELOVL4 C6orf167 CDC40 RRAGD ANKRD6 MTO1 COL12A1 GPR63 MICAL1 RPSAP45 C6orf183 EEF1A1 ROS1 CD164 SLC16A10 RFPL4B CD109 SESN1 ZBTB24 KLHL32 SMPD2 BCKDHB PPIL6 C6orf66 C6orf165 QRSL1 NT5E PRDM1 DDO C6orf185 SMAP1 CNR1 COL19A1 ARMC2 MYO6 B3GAT2 NR2E1 RFX6 COL10A1 C6orf224 AKIRIN2 AKD2 RNGTT
6	30563831	30563831	6	30564208	30564208	DEL	376	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	33119452	33119452	4	33119768	33119768	DEL	314	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15	34892639	34892639	15	34898775	34898775	DEL	6135	BRC41	1	1	NHEJ		ENST00000322237	-1	intron1	N/A	N/A	N/A	N/A	N/A
5	1.43E+08	1.43E+08	5	1.43E+08	1.43E+08	DEL	15043	BRC41	1	1	NHEJ	ARHGAP26	ENST00000378004	1	intron20	ARHGAP26	ENST00000378004	1	intron22	N/A
5	1.65E+08	1.65E+08	5	1.65E+08	1.65E+08	DEL	23923	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	1E+08	1E+08	8	1E+08	1E+08	DEL	684	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	1.08E+08	1.08E+08	8	1.08E+08	1.08E+08	DEL	271	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	1.04E+08	1.04E+08	7	1.3E+08	1.3E+08	DEL	260669	BRC41	1	1	MMEJ	LHFPL3	ENST00000335925	1	intron1	N/A	N/A	N/A	N/A	TMEM168 C7orf68 TAS2R16 TSGA13 CCDC136 ARF5 FEZF1 DNAJB9 FLNC AHCYL2 RPL31P39 NRCAM CPA2 OPN1SW RPS10P15 CALU TFEC PTPRZ1 FAM71F1 GPR85 RBM28 GCC1 GPR22 GRM8 CPA4 SMO DUS4L CPA1 SPAM1 PUS7 ATP6V1F IFRD1 C7orf53 CBLL1 LAMB1 LSM8 WASL FAM3C PPP1R3A SLC26A3 IQUB C7orf45 C7orf54 ZNF277 HBP1 IMPDH1 MDFIC

							11													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 TSPAN33 ST7 SND1 CTTNBP2 MET MEST IMMP2L TES ING3 CAV1 DLD CAPZA2 KCND2 RINT1 TSPAN12 PNPLA8 THAP5 METTL2B ASB15 SLC13A1 BCAP29 uc003vdl.2 CPA5 TNPO3 PAX4 HYAL4 C7orf60 UBE2H GPR37 LRRN3 NRF1 LRRC4 WNT2 LEP POT1 MLL5 TMEM209 ASZ1 KLHDC10 ZNF800 LAMB4 SRPK2
3	1.57E+08	1.57E+08	3	1.57E+08	1.57E+08	DEL	23216	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	27986490	27986490	7	27987256	27987256	DEL	767	BRC41	1	1	NHEJ	JAZF1	ENST00000283928	-1	intron2	JAZF1	ENST00000283928	-1	intron2	N/A
16	15903058	15903058	16	15914423	15914423	DEL	11358	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	60993368	60993368	16	61010116	61010116	DEL	16737	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	31922445	31922445	8	31923000	31923000	DEL	549	BRC41	1	1	MMEJ	NRG1	ENST00000405606	1	intron1	NRG1	ENST00000405606	1	intron1	N/A
2	71807483	71807483	2	71807844	71807844	DEL	361	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	12410142	12410142	3	12410537	12410537	DEL	392	BRC41	1	1	MMEJ	PPARG	ENST00000397010	1	intron3	PPARG	ENST00000397010	1	intron3	N/A
11	5778078	5778078	11	5778183	5778183	DEL	106	BRC41	1	1	NHEJ	TRIM5	ENST00000380027	-1	intron0	TRIM5	ENST00000380027	-1	intron0	N/A
4	1.83E+08	1.83E+08	4	1.83E+08	1.83E+08	DEL	515	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.47E+08	1.47E+08	3	1.47E+08	1.47E+08	DEL	642	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	77777943	77777943	8	77778120	77778120	DEL	173	BRC41	1	1	MMEJ	ZFHX4	ENST00000050961	1	intron0	ZFHX4	ENST00000050961	1	intron0	N/A
10	76376772	76376772	10	76376951	76376951	DEL	177	BRC41	1	1	MMEJ	MYST4	ENST00000372725	1	intron1	MYST4	ENST00000372725	1	intron1	N/A
9	233137	233137	9	233149	233149	DEL	120	BRC	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

	00	00		11	11		9	41												
2	22335770	22335770	2	22348180	22348180	DEL	12409	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	80544671	80544671	4	80545219	80545219	DEL	541	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	93293739	93293739	X	93294186	93294186	DEL	447	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	18436771	18436771	5	18443655	18443655	DEL	6880	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	65159348	65159348	18	65159581	65159581	DEL	232	BRC41	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	70128852	70128852	8	70149010	70149010	DEL	20156	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.46E+08	1.46E+08	3	1.46E+08	1.46E+08	DEL	4757	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	38099936	38099936	3	38100165	38100165	DEL	228	BRC41	1	1	NHEJ	DLEC1	ENST00000346219	1	intron6	DLEC1	ENST00000346219	1	intron6	N/A
4	97643116	97643116	4	97644693	97644693	DEL	1575	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	32285924	32285924	X	32286026	32286026	DEL	100	BRC41	1	1	MMEJ	DMD	ENST00000378684	-1	intron9	DMD	ENST00000378684	-1	intron9	N/A
3	83247223	83247223	3	83247382	83247382	DEL	155	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	7869125	7869133	3	25138467	25138496	CTX	N/A	BRC41	-1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	1.02E+08	1.02E+08	16	17489409	17489409	CTX	N/A	BRC41	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	48276207	48276207	X	28821570	28821570	CTX	N/A	BRC41	-1	-1	MMEJ	N/A	N/A	N/A	N/A	IL1RAPL1	ENST00000378993	1	intron1	N/A
1	2.16E	2.16E	11	1.09E	1.09E	CTX	N/A	BRC	-1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

	+08	+08		+08	+08			41												
8	499518	499521	15	93543473	93543486	CTX	N/A	BRC41	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	1.24E+08	1.24E+08	14	96673340	96673340	CTX	N/A	BRC41	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.59E+08	1.59E+08	3	98883009	98883009	CTX	N/A	BRC41	1	-1	MMEJ	ARHGAP30	ENST00000368018	-1	intron1	EPHA6	ENST00000389672	1	intron14	N/A
2	7867752	7867771	3	25136937	25136952	CTX	N/A	BRC41	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
22	21390396	21390396	22	23951061	23951061	DEL	2559661	BRC42	1	1	MMEJ	N/A	N/A	N/A	N/A	CRYBB2	ENST00000398215	1	intron2	IGLV3-7 IGLV3-12 IGLV2-18 SHFM3P1 IGLV3-19 IGLV3-15 IGLV2-5 PIWIL3 IGLV3-17 SGSM1 IGLC5 CABIN1 UPB1 GSTT2 MIF ZDHHC8P ADORA2A CRYBB3 CHCHD10 IGLC4 IGLV2-14 IGLL1 CYTSA SMARCB1 C22orf36 GSTT2B IGLV3-2 DDT TMEM211 IGLV3-4 RAB36 VPREB3 GGT1 uc003abl.1 DDTL ZNF70 IGL@ IGLV3-13 IGLV3-6 BCR SNRPD3 GSTTP1 GSTT1 C22orf15 C22orf13 GGTLA1 POM121L9P SLC2A11 RGL4 SUSD2 POM121L10P IGLV3-1 RTDR1 IGLV4-3 uc002zwr.1 MMP11 DERL3 GNAZ IGLV3-16
2	1E+08	1E+08	2	1E+08	1E+08	DEL	233	BRC42	1	1	NHEJ	AFF3	ENST00000356421	-1	intron1	AFF3	ENST00000356421	-1	intron1	N/A
22	25249507	25249507	22	25252376	25252376	DEL	2867	BRC42	1	1	MMEJ	N/A	N/A	N/A	N/A	TPST2	ENST00000403880	-1	intron4	N/A
15	55374397	55374397	15	55374996	55374996	DEL	5932	BRC42	1	1	NAHR	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	67922562	67922562	11	68579241	68579241	DEL	655678	BRC42	1	1	NHEJ	LRP5	ENST00000294304	1	intron7	TPCN2	ENST00000294309	1	cds_exon3	MRGPRD MTL5 SAPS3 CPT1A MRGPRF GAL IGHMBP2 MRPL21
3	31974211	31974211	16	79239616	79239616	CTX	N/A	BRC42	-1	-1	NHEJ	OSBPL10	ENST00000396556	-1	intron1	CDYL2	ENST00000299564	-1	intron2	N/A
9	1.35E+08	1.35E+08	17	39620722	39620722	CTX	N/A	BRC42	1	-1	NHEJ	TSC1	ENST00000298552	-1	intron14	TMUB2	ENST00000357984	1	intron0	N/A
1	2.07E+08	2.07E+08	15	84725803	84725803	CTX	N/A	BRC42	1	1	NHEJ	N/A	N/A	N/A	N/A	AGBL1	ENST00000299974	1	intron15	N/A
1	1.19E+08	1.19E+08	2	1.42E+08	1.42E+08	CTX	N/A	BRC42	1	-1	MMEJ	N/A	N/A	N/A	N/A	LRP1B	ENST00000389484	-1	intron7	N/A

6	86006264	86006264	16	79217034	79217034	CTX	N/A	BRC42	1	1	NHEJ	N/A	N/A	N/A	N/A	CDYL2	ENST00000299564	-1	intron3	N/A
2	2.18E+08	2.18E+08	8	1.41E+08	1.41E+08	CTX	N/A	BRC42	-1	-1	MMEJ	N/A	N/A	N/A	N/A	TRAPPC9	ENST00000389327	-1	intron16	N/A
6	1.18E+08	1.18E+08	8	10363680	10363680	CTX	N/A	BRC42	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
13	36599790	36599790	20	35287380	35287380	CTX	N/A	BRC42	1	1	MMEJ	N/A	N/A	N/A	N/A	RPN2	ENST00000237530	1	intron10	N/A
X	1.26E+08	1.26E+08	X	1.26E+08	1.26E+08	DEL	43537	BRC44	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	1.65E+08	1.65E+08	4	1.7E+08	1.7E+08	DEL	5015982	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	DDX60L	ENST00000284630	-1	intron13	TKTL2 CPE C4orf39 DDX60 TMEM192 ANP32C C4orf43 SPOCK3 TLL1 NACA3P SC4MOL TRIM75 TRIM60 ANXA10 TRIM61 MARCH1 KLHL2
X	1.45E+08	1.45E+08	X	1.45E+08	1.45E+08	DEL	73222	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	52810288	52810288	4	55850342	55850342	DEL	3039054	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	CHIC2 GSH2 KIT PDGFRA KDR SCFD2 USP46 RASL11B FIP1L1 LNX1
16	46614788	46614788	16	74405862	74405862	DEL	27790073	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	NFAT5 MT1G PARD6A MMP2 FTS CDH3 CDH1 WWP2 GOT2 MT1B ZNF821 TPPP3 KIFC3 CALB2 COQ9 DHX38 EXOSC6 SLC6A2 DDX19A C16orf70 CSNK2A2 VPS4A LYPLA3 RRAD FAM65A RSPRY1 GFOD2 DUS2L ELMO3 SALL1 FUK SLC7A6 NRN1L BRD7 NFATC3 DOK4 RANBP10 APPBP1 RBL2 GPR114 VAC14 ADCY7 NUTF2 CCDC113 HAS3 ST3GAL2 BBS2 ATP6V0D1 DPEP2 RLTPR CNGB1 TEPP MT1F PMFBP1 TSNAXIP1 LRRC29 KIAA0895L TMEM170A RFWD3 MT1DP COG4 CBLN1 TOX3 NIP7 FA2H PLLP MMP15 CDH11 CES7 AP1G1 CX3CL1 CNOT1 CBFB CHD9 EXOC3L COG8 ZDHHC1 LDHD DDX28 CMTM2 SNX20 PAPD5 CHST4 ABCC12 NOB1 DHODH DYNC1LI2 TMEM188 MT1X C16orf48 C16orf80 SLC9A5 MT2A CHST6 CLEC18A MT3 CTRL GINS3 PSMB10 IRX6 SMPD3 GABARAPL2 CTRB1 CENPT LONP2 SLC12A3 HYDIN ZNF423 PDXDC2 CCL22 ZFP1 CCDC102A ZNF319 PDPR IRX5 NPIPL2 MT1E HERPUD1 NDRG4 HSD11B2 DDX19B SLC12A4 SLC38A7 CHST5 EDC4 HEATR3 N4BP1 uc010ccw.1 CMTM4 FAM96B AGRP CLEC18C MARVELD3 CIAPIN1 CES3 TMEM208 TERF2 AMFR GLG1 CDH5 CTCF ADAT1 ARL2BP GPR97 SNTB2 MLKL CMTM3 TERF2IP FTSJD1 IL34 SF3B3 CHTF8 CARD15 PRMT7 KIAA0174 CES1 CDH8 C16orf86 NUDT21 MT1M FBXL8 C16orf57 HSF4 AARS DPEP3 FTO NUP93 CFDP1 NLRC5 uc002fek.1 POLR2C ABCC11 PSMD7 LRRC36 CES2 CETP TK2 CDH16 KARS KATNB1 BCAR1 ZNF23 CCL17 RPGRIP1L MT1CP GPR56 SETD6 CTRB2 TAT THAP11 NKD1 RBM35B TRADD ACD CYB5B CYLD NQO1 PSKH1 FHOD1 AYTL1 ZNRF1 ENSG00000216295 WDR59 PHLPPL CMTM1 ATBF1 CPNE2 SLC7A6OS C16orf78 CES8 PKD1L3 IRX3 ZNF19 MTSS1L OGFOD1 MT4 LCAT MT1H CLEC18B CKLF CA7 KCTD19 TMCO7 ZFP90 CIRH1A SIAH1 E2F4 CCDC79 TMED6 NOL3 C16orf47 TXNL4B C16orf50 HP GNAO1 PLEKHG4 MT1A
4	1.32E+0	1.32E+0	4	1.57E+0	1.57E+0	DEL	2463	BRC44	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	FGA SMAD1 ABCE1 LRBA DCLK2 FREM3 ZNF330 SH3D19 ZNF827 INPP4B MAML3 C4orf49 TRIM2 SFRP2 FGG MAB21L2 NR3C2 ANAPC10P OTUD4 NPY2R FAM160A1 TTC29 NDUFC1 CCRN4L DCHS2 SLC10A7 MMAA KIAA0922 ELF2 RPS3AP47

	8	8		8	8		4439	4												RAB33B FHDC1 SCOC GUCY1A3 TMEM184C TLR2 ARFIP1 POU4F2 RPL14P3 PLRG1 MGST2 SLC7A11 CLGN RNF175 GYPB SMARCA5 EDNRA PET112L LRAT HHIP TMEM154 FBXW7 RNF150 MND1 PCDH18 TBC1D9 GAB1 UCP1 GUCY1B3 ELMOD2 ARHGAP10 PCDH10 TIGD4 MAP9 IL15 SETD7 GYPA USP38 NARG1 LSM6 FGB RBM46
X	79596911	79596911	X	79619409	79619409	DEL	22496	BRC44	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
14	40843766	40843766	14	40846900	40846900	DEL	3134	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15	34122032	34122032	15	61887744	61887744	DEL	27764709	BRC44	1	1	MMEJ	N/A	N/A	N/A	N/A	HERC1	ENST00000261887	-1	intron0	STRC EPB42 SCG3 CASC5 ANXA2 SRP14P1 FRMD5 DISP2 NARG2 CCPG1 GNB5 TMOD2 EIF3S1 PAK6 TRIM69 RHOV SLC12A1 C15orf43 LRRC57 FAM98B KIAA1370 PRTG C15orf23 PLA2G4E JMJD7-PLA2G4B MEIS2 CYP19A1 LTK UBR1 SLC24A5 SECISBP2L C15orf33 CASC4 FAM82A2 TMCO5A RPSAP55 NDUFAF1 SLTM VPS39 BMF C15orf53 GABPB1 FBXL22 FAM148B CGNL1 TRPM7 C15orf48 PPP1R14D C15orf56 C15orf57 MYEF2 C15orf21 PLCB2 PLA2G4D CAPN3 EHD4 ATP8B4 GCHFR CEP27 RFX7 VPS18 TP53BP1 GLDN RPS27L GRINL1A VPS13C HSP90AB4P WDR72 AQP9 SPATA5L1 INO80 RAD51 SQRDL LEO1 CKMT1A C15orf54 ZFYVE19 THBS1 CKMT1B LCMT2 FOXB1 COPS2 FSIP1 RORA OIP5 PLDN DUOX2 SPINT1 TNFAIP8L3 FBN1 LIPC C15orf15 MYO5C MNS1 ZFP106 TYRO3 PLA2G4F APH1B FAM81A C15orf41 RAB8B BNIP2 GATM AP4E1 ITPKA RPAP1 ONECUT1 EXD1 TLN2 DUOXA1 FAM148A GCNT3 TCF12 DNAJC17 SEMA6D LACTB UNC13C SLC28A2 HDC FAM92A1 TUBGCP4 MAPK6 SORD TMOD3 TGM7 TEX9 HISPPD2A CATSPER2 SERF2 STARD9 uc001znl.1 CDAN1 ELL3 LYSMD2 USP8 ADAL ZSCAN29 PDIA3 C15orf62 CA12 DUT GPR176 GTF2A2 RNF111 RASGRP1 TMEM62 RAB27A CTDSPL2 DMXL2 TTBK2 B2M C15orf52 EID1 FAM63B ALDH1A2 SPRED1 MAP1A MYO5A ADAM10 FGF7 DLL4 BAHD1 SERINC4 IVD NEDD4 SPG11 DYX1C1 ZNF280D NUSAP1 CHAC1 SNAP23 SLC27A2 RTF1 CEP152 CATSPER2P1 MFAP1 USP50 MGA USP3 BUB1B SHC4 TPM1 LDHAL6B MAPKBP1 GANC DUOXA2 SHF PIGB EIF2AK4 ENSG00000184935 GALK2 DUOX1 WDR76 CCNB2 TGM5 RPUSD2 BCL2L10 SLC30A4 SPTBN5 MYO1E TMEM87A DTWD1 PYGO1 D4ST1 CCNDBP1
11	18652360	18652360	11	19574158	19574158	DEL	920798	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	IGSF22 MRGPRX1 E2F8 MRGPRX2 TMEM86A ZDHHC13 PTPN5 CSRP3
17	46093811	46093811	17	47526550	47526550	DEL	1431739	BRC44	1	1	NHEJ	ABCC3	ENST00000285238	1	intron8	CA10	ENST00000340813	-1	intron1	SPAG9 C17orf73 RPL7P48 NME1-NME2 uc002isr.1 TOB1 WFIKKN2 UTP18 MBTD1 ANKRD40
9	81162815	81162815	9	82443638	82443638	DEL	1279823	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	TLE4 CHCHD9
4	63446015	63446015	4	1.65E+08	1.65E+08	DEL	1.01E+08	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SMR3A C4orf35 NPY5R C4orf45 SH3D19 C4orf49 TNIP3 TMPRSS11B CCDC109B DSPP CXCL10 SFRP2 NR3C2 NHEDC1 C4orf12 EMCN TACR3 FSTL5 SPATA5 HERC5 ADAMTS3 DMP1 LEF1 SLC39A8 MTHFD2L DCHS2 SLC10A7 SEC24D NPFFR2 NUP54 PITX2 CXCL3 SULT1E1 PRDM8 GC ABCG2 FRAS1 AFF1 RAPGEF2 FHDC1 CSN1S1 CCNI GUCY1A3 ODAM uc003hyf.1 POU4F2 RPL14P3 PHF17 DCK GLRB C4orf22 CLGN HNRNPD NAF1 EIF4E FAT4 PRDM5 TMEM155 ADH7 SMARCA5 PET112L HTN1 EGF PAQR3 HHIP OSTC PPA2 UGT2B17 CENPE ADH1B ANK2 BANK1 TIGD2 GSTCD SYNPO2 CASP6 METTL14 C4orf3 TMPRSS11E2 MRPL1 CXCL13 uc003hkb.2 NUDT6 MYOZ2 MOBKL1A QRFPR CXCL5 SETD7 DKK2 LSM6 IL8 HNRPDL NUDT9 GK2 ABCE1 LRBA DCLK2 AGXT2L1 ZNF827 PRSS12 INPP4B MAML3 UGT2B11 BMP3 HSP90AB3P CSN3 CXCL6 PKD2 BTC NPY2R LIN54 HERC6 ART3 SDAD1 ANXA3 FNIP2 BBS12 ATOH1

																				G3BP2 LARP7 SPP1 C4orf31 WDFY3 CYP2U1 GPRIN3 UGT2B7 CXXC4 RPS3AP47 RG9MTD2 RAB33B SCOC INTU RCHY1 TMSL3 CFI SPRY1 UBE2D3 PPP3CA SMARCAD1 PLRG1 MEPE C4orf7 ETFDH USO1 NDST3 SEC24B CXCL2 NFKB1 ADH1C ANKRD17 PPID MANBA ANKRD56 ARD1B FAM177A2 BBS7 MND1 RNF150 SLC10A6 PGRMC2 BMPR1B MFSD8 RASGEF1B UNC5C CENPC1 ADH6 HPSE SEPT11 UTP3 UBA6 PF4 UCP1 TIGD4 IL15 IL2 NPY1R UGT2A3 GYPA NARG1 CSN2 RBM46 TDO2 FGA SMAD1 MMRN1 EREG FREM3 ZNF330 CTSO PIG-Y C4orf32 TRIM2 NAAA NAP1L5 ADH5 BRDG1 SMR3B FGG MAB21L2 PLAC8 UGT2B10 ALB ARHGAP24 OTUD4 COX18 CISD2 UGT2B15 HERC3 PPM1K COPS4 FAM47E LARP2 C4orf21 IL21 SNCA MMAA RPL34 NKX6-1 AMBN USP53 NPNT PLA2G12A FGF2 C4orf29 ENPEP PRKG2 MUC7 HADH CDS1 C4orf33 TMPRSS11E TET2 TMEM184C C4orf17 RRH LRIT3 TLR2 ARFIP1 AFM SLC25A31 DDIT4L ELOVL6 MGST2 TMPRSS11D SLC7A11 RNF175 HTN3 SYT14L AREG C4orf16 PDE5A NDST4 KLHL8 GYPB DNAJB14 EDNRA CDKL2 COL25A1 LRAT ENOPH1 DHRS8 CAMK2D RIPX THAP6 ANKRD50 CXCL9 YTHDC1 SCLT1 H2AFZ CEP170L PLK4 SCARB2 C4orf26 BDH2 FABP2 RXFP1 PCDH18 CCNA2 GNRHR TBC1D9 GAB1 PPBP MAP2K1IP1 SHROOM3 ELMOD2 ARHGAP10 SULT1B1 PCDH10 BMP2K MAPK10 ALPK1 UGT8 PPEF2 MRPS18C PGDS FGB SPARCL1 GRID2 SLC4A4 EPHA5 DAPP1 CCNG2 RASSF6 SCD5 TRAM1L1 ANAPC10P CXCL1 INTS12 TIFA PTPN13 PDHA2 C4orf37 FAM160A1 SGMS2 TTC29 NDUFC1 RPL7AP26 ACCN5 CCRN4L TSPAN5 ADH4 PAPSS1 NEUROG2 IBSP KIAA0922 C4orf40 ELF2 COQ2 CXCL11 ENAM C4orf18 C4orf46 ANTXR2 ARSJ EPGN TRPC3 UGT2B4 AREGB HSPA4L SCYE1 TMPRSS11F ANXA5 STBD1 FGF5 RPS26P54 PDGFC THAP9 STATH MTTP GRIA2 SEC31A IGJ PDLIM5 METAP1 UGT2A1 TMEM144 TMEM154 PF4V1 GAR1 AFP FBXW7 PROL1 FAM175A GRSF1 EXOSC9 UGT2B28 ADAD1 FAM13A MAD2L1 CNOT6L TMPRSS11A HELQ AMTN HSD17B13 NHEDC2 C4orf36 GUCY1B3 RAP1GDS1 MAP9 KIAA1109 AGPAT9 USP38
12	82772020	82772020	12	83212865	83212865	DEL	439844	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	48611427	48611427	20	52279539	52279539	DEL	3667110	BRC44	1	1	NHEJ	PTPN1	ENST0000371621	1	intron2	N/A	N/A	N/A	N/A	ATP9A PSMD10P CYP24A1 RPL36P1 ZFP64 BCAS4 TSHZ2 DPM1 TMSL6 RPSAP1 C20orf175 RPL36P2 ADNP RNU7 NFATC2 SALL4 PPIAP10 BCAS1 ZNF217 PFDN4 PARD6B MOCS3 KCNG1
11	21477995	21477995	11	29476208	29476208	DEL	7997212	BRC44	1	1	NHEJ	NELL1	ENST0000357134	1	intron15	N/A	N/A	N/A	N/A	CCDC34 SLC17A6 BDNF ANO5 ANO3 FIBIN SVIP GAS2 LGR4 METT5D1 BBOX1 KIF18A MUC15 LUZP2 FANCF LIN7C SLC5A12
2	53426165	53426165	2	58963736	58963736	DEL	5536571	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	CCDC104 TSPYL6 BTF3L2 C2orf30 EFEMP1 MTIF2 CCDC88A C2orf63 CHAC2 CCDC85A ACYP2 PNPT1 GPR75 VRK2 SPTBN1 RPL23AP32 C2orf73 ASB3 FANCL RTN4 NCRNA00117 IK SMEK2 EML6 PSME4 RPS27A
4	74318182	74318182	4	1.37E+08	1.37E+08	DEL	62948871	BRC44	1	1	NHEJ	ANKRD17	ENST0000330838	-1	intron1	N/A	N/A	N/A	N/A	MMRN1 EREG TNIP3 C4orf32 PIG-Y CCDC109B NAAA NAP1L5 ADH5 DSPP CXCL10 PLAC8 NHEDC1 ARHGAP24 ALB C4orf12 CISD2 EMCN TACR3 HERC3 PPM1K COPS4 SPATA5 HERC5 FAM47E LARP2 C4orf21 IL21 DMP1 LEF1 SLC39A8 SNCA MTHFD2L SEC24D NUP54 PITX2 CXCL3 RPL34 NKX6-1 PRDM8 USP53 PLA2G12A NPNT FGF2 ABCG2 FRAS1 C4orf29 ENPEP AFF1 PRKG2 HADH CDS1 CCNI C4orf33 TET2 C4orf17 RRH uc003hyf.1 LRIT3 AFM PHF17 SLC25A31 DDIT4L ELOVL6 C4orf22 HNRNPD C4orf16 EIF4E AREG FAT4 PRDM5 PDE5A NDST4 KLHL8 TMEM155 DNAJB14 ADH7 COL25A1 CDKL2 EGF PAQR3 DHRS8 ENOPH1 OSTC PPA2 CAMK2D THAP6 ANKRD50 CENPE ADH1B CXCL9 ANK2 BANK1 TIGD2 GSTCD SCLT1 SYNPO2 CASP6 CEP170L H2AFZ PLK4 METTL14 SCARB2 BDH2 C4orf26 C4orf3 FABP2 CCNA2 CXCL13 MRPL1 MAP2K1IP1 PPBP uc003hkb.2 SHROOM3 PCDH10 NUDT6 MYOZ2 UGT8 ALPK1 MAPK10 BMP2K MRPS18C PPEF2 QRFPR CXCL5 DKK2 PGDS SPARCL1 IL8 GRID2 HNRPDL GK2 NUDT9 AGXT2L1 PRSS12 BMP3 DAPP1 CCNG2

																				RASSF6 SCD5 HSP90AB3P TRAM1L1 CXCL1 INTS12 TIFA CXCL6 PTPN13 BTC PKD2 PDHA2 C4orf37 LIN54 SGMS2 HERC6 ART3 SDAD1 ANXA3 RPL7AP26 BBS12 TSPAN5 ADH4 NEUROG2 PAPSS1 G3BP2 ATOH1 LARP7 SPP1 C4orf31 WDFY3 IBSP CYP2U1 GPRIN3 CXXC4 COQ2 CXCL11 RG9MTD2 ANTXR2 ARSJ INTU EPGN TRPC3 RCHY1 TMSL3 CFI AREGB HSPA4L SPRY1 SCYE1 UBE2D3 PPP3CA ANXA5 STBD1 FGF5 RPS26P54 SMARCAD1 THAP9 MEPE MTTP USO1 SEC31A NDST3 SEC24B CXCL2 PDLIM5 NFKB1 ADH1C MANBA ANKRD56 METAP1 ARD1B PF4V1 FAM177A2 GAR1 BBS7 AFP SLC10A6 FAM175A PGRMC2 EXOSC9 BMPR1B MFSD8 ADAD1 RASGEF1B FAM13A UNC5C MAD2L1 HPSE ADH6 SEPT11 CNOT6L NHEDC2 HELQ HSD17B13 PF4 C4orf36 RAP1GDS1 IL2 KIAA1109 AGPAT9
5	93422955	93422955	5	93535357	93535357	DEL	2398	BRC44	1	1	MMEJ	FAM172A	ENST00000395965	-1	intron1	FAM172A	ENST00000395965	-1	intron1	N/A
15	39769248	39769248	15	49597382	49597382	DEL	9827133	BRC44	1	1	NHEJ	MGA	ENST00000219905	1	intron10	DMXL2	ENST00000251076	-1	intron13	STRC EPB42 DUOXA1 FRMD5 SEMA6D SLC28A2 HDC EIF3S1 TUBGCP4 TRIM69 SLC12A1 C15orf43 SORD LRRC57 TGM7 HISPPD2A PLA2G4E JMJD7-PLA2G4B CYP19A1 CATSPER2 UBR1 SLC24A5 SERF2 STARD9 SECISBP2L ELL3 CDAN1 C15orf33 CASC4 USP8 ADAL ZSCAN29 PDIA3 DUT VPS39 TMEM62 CTDSPL2 GABPB1 TRPM7 B2M TTBK2 EID1 C15orf48 MYEF2 MAP1A C15orf21 PLA2G4D CAPN3 FGF7 EHD4 SERINC4 ATP8B4 CEP27 SPG11 TP53BP1 GLDN SNAP23 SLC27A2 SPATA5L1 SQRDL CEP152 CATSPER2P1 MFAP1 CKMT1A USP50 SHC4 MAPKBP1 CKMT1B LCMT2 GANC DUOXA2 COPS2 SHF GALK2 ENSG00000184935 DUOX2 PLDN TNFAIP8L3 DUOX1 WDR76 FBN1 TGM5 PLA2G4F ZFP106 SLC30A4 SPTBN5 GATM AP4E1 TMEM87A DTWD1 CCNDBP1
X	1.36E+08	1.36E+08	X	1.36E+08	1.36E+08	DEL	83412	BRC44	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	20070578	20070578	11	46963130	46963130	DEL	26891549	BRC44	1	1	MMEJ	NAV2	ENST00000349880	1	intron28	C11orf49	ENST00000378615	1	intron1	SYT13 LMO2 CREB3L1 FSHB C11orf55 QSER1 CCDC34 CD44 CSTF3 BDNF FJX1 EXT2 ACCS ANO3 FBXO3 TSPAN18 FIBIN SVIP CHRM4 CRY2 uc001mwf.1 PEX16 DCDC1 BBOX1 PRRG4 LUZP2 C11orf91 SLC35C1 ELP4 CD82 C11orf41 DBX1 PRDM11 WT1 uc001mwp.1 TRIM44 MPPED2 ZNF408 F2 LRRC4C HTATIP2 EHF GYLTL1B HSD17B12 LDLRAD3 API5L1 KIF18A APIP HARBI1 ACCSL ABTB2 uc001msu.1 LIN7C RCN1 HIPK3 DCDC5 PAX6 IMMP1L COMMD9 SLC17A6 CAPRIN1 MDK DNAJC24 LRP4 ANO5 CKAP5 TTC17 GAS2 RAG2 METT5D1 AMBRA1 PHF21A WIT1 TP53I11 DEPDC7 DGKZ C11orf46 PDHX RAG1 TCP11L1 EIF3M ARHGAP1 ALKBH3 ENSG00000216295 TRAF6 MAPK8IP1 CAT CHST1 CCDC73 KCNA4 KIAA0652 NELL1 SLC1A2 CD59 LGR4 PRMT3 MUC15 NAT10 SLC6A5 FANCF ALX4 ELF5 C11orf74 SLC5A12
5	1.68E+08	1.68E+08	5	1.78E+08	1.78E+08	DEL	9990414	BRC44	1	1	MMEJ	SLIT3	ENST00000332966	-1	intron4	N/A	N/A	N/A	N/A	FAM153B C5orf25 RANBP17 KCNIP1 ERGIC1 B4GALT7 DOK3 RAB24 UIMC1 RPL26L1 SFXN1 FAM153A STK10 AGXT2L2 ZNF454 ATP6V0E PDLIM7 KIAA1191 UBTD2 GRK6 THOC3 GPRIN1 LCP2 MXD3 CLK4 TLX3 HRH2 DBN1 FAM153C FAF2 NHP2 C5orf50 ZNF354A CLTB NOP16 ZNF354B TMED9 NKX2-5 SH3PXD2B LMAN2 PRELID1 C5orf41 RNF44 CPLX2 NPM1 DUSP1 FGFR4 FAM44B ZFP2 PROP1 CCDC99 ZNF346 GRM6 HNRNPAB GABRP EFCAB9 ARL10 COL23A1 NSD1 PCDH24 TSPAN17 HIGD2A FOXI1 RGS14 CPEB4 DOCK2 ENSG00000216295 MSX2 FBXW11 NEURL1B HK3 RMND5B UNC5A FGF18 SNCB EIF4E1B STC2 SLC34A1 DDX41 uc003mhv.1 C5orf47 BNIP1 KCNMB1 DRD1 PRR7 F12 PFN3
11	30748829	30748829	11	30855471	30855471	DEL	105642	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	DCDC5	ENST00000303697	-1	intron9	N/A
16	54055293	54055293	16	57953992	57953992	DEL	3897699	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	CCL22 ZNF319 CCDC102A MT1G CETP MMP2 NDRG4 HERPUD1 MT1E SLC38A7 PLLP MMP15 KATNB1 GOT2 MT1B CCL17 uc010ccw.1 CES7 KIFC3 SETD6 GPR56 COQ9 CX3CL1 MT1CP SLC6A2 CNOT1 CSNK2A2 CIAPIN1 AYTL1 AMFR RSPRY1 GPR97 ARL2BP DOK4 CPNE2 GPR114 MT1X C16orf80 CCDC113 OGFOD1 MT2A CES1 MT4 NUDT21 MT1M C16orf57 BBS2 MT3 MT1H GINS3 CNGB1 TEPP MT1F NUP93 SLC12A3 NLRC5 C16orf50 POLR2C GNAO1 MT1DP MT1A

11	18194497	18194497	11	18647778	18647778	DEL	452279	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	UEVLD HPS5 TSG101 SAA1 LDHC SAA2 SPTY2D1 FAM10A5 GTF2H1 LDHAL6A LDHA SAA4
17	22725062	22725062	17	22735433	22735433	DEL	103370	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	4738365	4738365	10	6119596	6119596	DEL	1380230	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	IL2RA	ENST00000397243	-1	intron1	AKR1CL2 UCN3 AKR1C3 AKR1C4 ANKRD16 TUBAL3 C10orf18 CALML3 ASB13 AKR1C2 AKR1CL1 GDI2 NET1 IL15RA CALML5 FBXO18 AKR1C1
19	6633971	6633971	19	7988053	7988053	DEL	1353078	BRC44	1	1	MMEJ	C3	ENST00000245907	-1	intron33	ELAVL1	ENST00000351593	-1	intron0	INSR VAV1 KIAA1543 ELAVL1 STXBP2 CD209 ZNF358 PEX11G PNPLA6 EVI5L LRRC8E TRAPPC5 RETN GPR108 CLEC4G SH2D3A EMR1 EMR4P TIMM44 TRIP10 C19orf59 MAP2K7 C19orf45 CLEC4GP1 ZNF557 MCOLN1 CLEC4M MBD3L2 FCER2 XAB2 PCP2 ARHGEF18 CTXN1 SNAPC2
21	35457106	35457106	21	36815535	36815535	DEL	1357429	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	CLDN14	ENST00000399136	-1	intron0	CBR3 RPS20P1 CBR1 RPL34P3 CHAF1B PPP1R2P2 RPL3P1 PSMD15 MORC3 DOPEY2 RIMKLB2 CLDN14 ATP5J2LP SETD4
16	25367022	25367022	16	33416120	33416120	DEL	8048093	BRC44	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ATXN2L COX6A2 PHKG2 FAM57B ATP2A1 MYLPF ZNF48 GSG1L SH2B1 ITGAM GDPD3 ALDOA CCDC101 LAT ZNF720P1 STX1B2 CDIPT RUNDC2B PRSS36 INO80E KIF22 EIF3CL DOC2A PRR14 GTF3C1 ZNF668 DCTPP1 TRIM72 C16orf58 ZNF267 ARMC5 VKORC1 ZNF646 SEPT1 FBXL19 IL4R SEPHS2 SRCAP ORAI3 ASPHD1 QPRT MAZ IL27 SLC6A10P RNF40 GIYD1 CLN3 JMJD5 PYCARD STX4 ITGAD BCKDK GIYD2 ZNF629 ITGAL KIAA0556 PYDC1 ZNF771 BOLA2B ERAF SEZ6L2 TAOK2 YPEL3 CORO1A FUS NPIPL1 ZNF688 TP53TG3 SETD1A NSMCE1 SLC5A2 TBC1D10B PPP4C EIF3S8 SULT1A3 RABEP2 NFATC2IP ZNF764 CD2BP2 IL21R TUFM TBX6 ZNF843 C16orf54 MVP HS3ST4 TMEM219 C16orf53 ZNF720 ITGAX SBK1 MYST1 BCL7C SULT1A1 ENSG00000169203 ZNF768 SPN HIRIP3 CD19 BOLA2 IGHV2OR16-5 SULT1A4 MAPK3 CTF1 C16orf67 FBRS XPO6 PRRT2 uc002dqe.1 SULT1A2 KCTD13 ZNF689 PRSS8 ZNF747 TGFB1I1 HSD3B7 SPNS1
1	21007157	21007157	1	21008272	21008272	DEL	1089	BRC44	1	1	NAHR	EIF4G3	ENST00000264211	-1	intron29	EIF4G3	ENST00000264211	-1	intron29	N/A
5	65165571	65165571	5	68834271	68834271	DEL	3667705	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	OCLN	ENST00000355237	1	intron0	CCDC125 CD180 ERBB2IP SLC30A5 RAD17 PIK3R1 MAST4 uc003jwb.1 CDK7 CENPH CCNB1 TAF9 MARVELD2 MRPS36 SFRS12
5	1.18E+08	1.18E+08	8	72888587	72888587	CTX	N/A	BRC44	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	60664324	60664324	21	15127832	15127832	CTX	N/A	BRC44	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.7E+08	1.7E+08	4	1.78E+08	1.78E+08	CTX	N/A	BRC44	-1	-1	NHEJ	DNM3	ENST00000367732	1	intron1	N/A	N/A	N/A	N/A	N/A

16	25564213	25564213	21	18953877	18953877	CTX	N/A	BRC44	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	58498114	58498114	17	47957312	47957312	CTX	N/A	BRC44	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.08E+08	2.08E+08	3	34637947	34637947	CTX	N/A	BRC44	1	-1	NHEJ	SYT14	ENST00000271745	1	intron2	N/A	N/A	N/A	N/A	N/A
6	1.54E+08	1.54E+08	X	1.26E+08	1.26E+08	CTX	N/A	BRC44	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	2.42E+08	2.42E+08	16	57979027	57979027	CTX	N/A	BRC44	-1	1	NHEJ	SNED1	ENST00000401884	1	utr_exon27	N/A	N/A	N/A	N/A	N/A
12	1.15E+08	1.15E+08	17	46414785	46414785	CTX	N/A	BRC44	-1	1	NHEJ	N/A	N/A	N/A	N/A	SPAG9	ENST00000356471	-1	intron16	N/A
6	1.02E+08	1.02E+08	13	42835875	42835875	CTX	N/A	BRC44	1	1	MMEJ	GRIK2	ENST00000369138	1	intron6	ENOX1	ENST00000261488	-1	intron2	N/A
3	1.27E+08	1.27E+08	5	18356898	18356898	CTX	N/A	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15	57380248	57380248	21	18656227	18656227	CTX	N/A	BRC44	1	-1	NHEJ	MYO1E	ENST00000288235	-1	intron1	PRSS7	ENST00000284885	-1	intron7	N/A
15	49627289	49627289	20	16121757	16121757	CTX	N/A	BRC44	-1	1	MMEJ	DMXL2	ENST00000251076	-1	intron6	N/A	N/A	N/A	N/A	N/A
3	29838413	29838413	20	6083837	6083837	CTX	N/A	BRC44	-1	1	NHEJ	RBMS3	ENST00000273139	1	intron6	N/A	N/A	N/A	N/A	N/A
2	2.42E+08	2.42E+08	16	74408261	74408261	CTX	N/A	BRC44	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	25275953	25275953	21	18687322	18687322	CTX	N/A	BRC44	-1	1	MMEJ	N/A	N/A	N/A	N/A	PRSS7	ENST00000284885	-1	intron3	N/A
3	1.36E+08	1.36E+08	6	37021750	37021750	CTX	N/A	BRC44	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

15	65282480	65282480	17	2528203	2528203	CTX	N/A	BRC44	1	1	NHEJ		ENST00000261880	-1	intron9	PAFAH1B1	ENST00000006951		1	intron8	N/A
15	65834784	65834784	21	39681116	39681116	CTX	N/A	BRC44	1	1	NHEJ	MAP2K5	ENST00000354498	1	intron18	WRB	ENST00000333781		1	intron1	N/A
X	89965203	89965203	10	2006803	2006803	CTX	N/A	BRC44	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.47E+08	1.47E+08	19	13709327	13709458	CTX	N/A	BRC44	-1	1	NAHR	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	2.42E+08	2.42E+08	21	20580255	20580255	CTX	N/A	BRC44	1	1	NHEJ	SNED1	ENST00000310397	1	intron27	N/A	N/A	N/A	N/A	N/A	N/A
6	63759055	63759055	17	25934533	25934533	CTX	N/A	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	LRRC37B2	ENST00000398849		1	intron0	N/A
15	95067972	95067972	21	19311822	19311822	CTX	N/A	BRC44	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.07E+08	1.07E+08	13	42189455	42189455	CTX	N/A	BRC44	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	1.11E+08	1.11E+08	19	55188266	55188266	CTX	N/A	BRC44	1	-1	NHEJ	N/A	N/A	N/A	N/A	VRK3	ENST00000316763		-1	intron7	N/A
16	54899688	54899688	21	17040166	17040166	CTX	N/A	BRC44	1	1	NHEJ	GNAO1	ENST00000262494	1	intron3	N/A	N/A	N/A	N/A	N/A	N/A
6	39579155	39579618	10	5467910	5468228	CTX	N/A	BRC44	1	1	NHEJ	KIF6	ENST00000373213	-1	intron12	NET1	ENST00000355029		1	intron3	N/A
X	1.46E+08	1.46E+08	12	77162613	77162613	CTX	N/A	BRC44	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	11621485	11621485	17	12518748	12518748	DEL	896256	BRC47	1	1	MMEJ	DNAH9	ENST00000262442	1	intron38	MYOCD	ENST00000343344		1	intron1	MAP2K4 DNAH9 ZNF18
3	41416936	41416936	3	53848499	53848499	DEL	12430555	BRC47	1	1	MMEJ	ULK4	ENST00000301831	-1	intron33	CHDH	ENST00000315251		-1	intron0	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

							7													SLC6A20 TLR9 SEMA3B GPX1 IP6K2 TMEM158 SACM1L RTP3 KIF9 KLHDC8B SEMA3G ABHD5 TMEM42 LAMB2 CCDC12 UQCRC1 LRRC2 SMARCC1 ARMET NDUFAF3 TSP50 ALS2CL PLXNB1 CCR2 ZNF589 uc003cqq.1 NAT6 WDR51A IQCF6 PHF7 GRM2 ATRIP PTH1R MST1 DUSP7 TREX1 DAG1 UCN2 KLHL18 TGM4 USP19 P4HTM CCR1 SPCS1 GLYCTK CAMKV RNF123 DHX30 PARP3 GNAI2 NT5DC2 ZNF660 LTF SNORD13 SCAP TWF2 ACY1 CISH C3orf39 SLC25A20 GMPPB CCDC71 CCBP2 RBM5 C3orf75 BSN SNRK WDR6 COL7A1 TRAK1 ABHD14B ALAS1 CLEC3B IQCF2 CCR5 IMPDH2 RHOA RRP9 ITIH4 WDR82 PRKCD CCR9 QRICH1 GPR62 HEMK1 TNNC1 ZNF197 RASSF1 TMIE RFT1 HYAL2 DCP1A TUSC2 CDCP1 LZTFL1 TCTA C3orf45 CDH29 NICN1 MUSTN1 KIF15 CCR3 ZMYND10 NKTR TUSC4 C3orf41 CSPG5 CYB561D2 BAP1 IQCF5 ZDHHC3 NEK4 PRKAR2A SEMA3F MYL3 ANO10 NCKIPSD IQCF1 ZNF445 DNAH1 ZNF167 HHATL APEH HYAL1 FYCO1 MAPKAPK3 PBRM1 CXCR6 TMEM89 C3orf71 EXOSC7 XCR1 SEC22C TDGF1 RBM6 CCDC13 RBM15B CCRL2 CACNA2D2 ARIH2 C3orf54 AMT CCDC51 C3orf62 IP6K1 SHISA5 CDC25A TRAIP
8	54249259	54249259	8	54249417	54249417	DEL	157	BRC47	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	21582966	21582966	3	74217457	74217457	DEL	52633490	BRC47	1	1	NHEJ	ZNF385D	ENST00000281523	-1	intron2	N/A	N/A	N/A	N/A	RPL29P26 C3orf14 HYAL3 DALRD3 TEX264 SLMAP SYNPR MAP4 GNL3 USP4 OSBPL10 PTPN23 ITIH1 ACVR2B LRTM1 PPM1M ASB14 TKT MST1R C3orf18 QARS ZNF502 CMTM8 DNAH12L CACNA1D RBMS3 FBXW12 NME6 KBTBD5 SS18L2 SUSD5 CELSR3 MITF TMEM115 SETD2 CCDC36 TGFBR2 LRRFIP2 EXOG TLR9 KBTBD8 IP6K2 RTP3 TMEM158 KLHDC8B DCLK3 SEMA3G PPP4R2 TMEM42 ABHD5 UBE2E2 LAMB2 CCDC12 MYD88 LRRC2 SMARCC1 ARMET NDUFAF3 TSP50 CCR8 ALS2CL CCR2 OXSR1 NAT6 WDR51A C3orf49 GRM2 IL17RD DUSP7 UCN2 CADPS TGM4 P4HTM SPATA12 CCR1 MYRIP CAMKV EIF1B C3orf63 PARP3 GNAI2 ZNF660 ITGA9 SNORD13 ARHGEF3 ACTR8 TWF2 ACY1 ZNF619 C3orf39 SLC25A26 GMPPB GADL1 CCBP2 FHIT BSN WDR48 ENTPD3 CMC1 TRAK1 NKIRAS1 FOXP1 IQCF2 CCDC66 CCR5 IMPDH2 STAC CCR9 FAM19A1 PROK2 FAM107A SHQ1 GPR62 HEMK1 ZNF197 WNT5A UBA3 TMIE RFT1 GPR27 DCP1A THOC7 AZI2 TCTA CDCP1 NICN1 MUSTN1 OXSM TUSC4 C3orf41 DYNC1LI1 ZNF620 ENSG00000132967 CYB561D2 CTNNB1 IQCF5 ZDHHC3 ATXN7 NEK4 PRKAR2A SEMA3F MYL3 ANO10 APPL IQCF1 C3orf35 ZNF167 APEH FYCO1 MAPKAPK3 CXCR6 EXOSC7 XYLB UBP1 SEC22C FLNB XIRP1 RBM15B PDCD6IP AMT LMOD3 RPL15 CHDH IP6K1 C3orf64 TRAIP PLCD1 TOP2B FAM19A4 STAB1 UBA7 IL17RB GLT8D1 SFMBT1 VIPR1 RAD54L2 ULK4 HIGD1D FAM116A ITIH3 RPL17P16 LYZL4 CAMP VPRBP ZNF662 PFKFB4 DNASE1L3 ZBTB47 SLC38A3 SUCLG2 DOCK3 PCBP4 NISCH MLH1 HESX1 ABHD14A LRIG1 NR1D2 ZNF860 GNAT1 ERC2 CYP8B1 SCN10A KIAA1143 PSMD6 ARF4 SNTN CX3CR1 ZNF501 CCK C3orf23 LARS2 MON1A ARL6IP5 SLC22A13 SLC25A38 PDZRN3 KCTD6 GLT8D4 ZNF35 LIMD1 AMIGO3 IFRD2 SLC4A7 SLC6A20 SEMA3B THRB GPX1 NGLY1 SACM1L KIF9 ADAMTS9 UBE2E1 UQCRC1 EOMES uc003dmp.1 PLXNB1 GLB1 ACOX2 uc003cqq.1 ZNF589 IQCF6 PDHB PHF7 C3orf53 CMTM6 ATRIP PTH1R PTPRG MST1 TREX1 DAG1 ZNF621 KLHL18 USP19 TTC21A SPCS1 GLYCTK DNHD2 DHX30 RNF123 ACAA1 NT5DC2 FAM3D ARPP-21 LTF uc003dis.1 SCAP CISH SLC22A14 CNOT10 SLC25A20 PXK EPM2AIP1 CCDC71 ABHD6 RBM5 C3orf75 C3orf51 MOBP GOLGA4 SNRK RPL14 WDR6 COL7A1 GPD1L ABHD14B TMF1 ALAS1 CLEC3B GORASP1 ZCWPW2 RHOA RRP9 ITIH4 WDR82 RARB PRKCD TRIM71 NEK10 FEZF2 QRICH1 TNNC1 CLASP2 RASSF1 LRRC3B HYAL2 TUSC2 LZTFL1 RPSA CDH29 C3orf45 KIF15 CCR3 FBXL2 ZMYND10 NKTR SCN5A CRTAP PRICKLE2 CSPG5 CMTM7 BAP1 TMPPE RPP14 NCKIPSD ZNF445 DNAH1 SCN11A RYBP HHATL STT3B HYAL1 EIF4E3 PBRM1 FRMD4B AXUD1 VILL TMEM89 C3orf71 RPL32P11 DLEC1 C3orf67 XCR1 TDGF1 PDE12 RBM6 CACNA2D3 CCDC13 CTDSPL CCRL2 ARIH2 C3orf54 CACNA2D2 CCR4 CCDC51 C3orf62 SHISA5 CDC25A
8	51222463	51222463	8	51883003	51883003	DEL	659538	BRC47	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

3	27120116	27120116	3	28005558	28005558	DEL	884440	BRC47	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	NEK10 EOMES SLC4A7
7	1.24E+08	1.24E+08	7	1.24E+08	1.24E+08	DEL	187024	BRC47	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	GPR37 POT1
8	35255524	35255524	8	54284949	54284949	DEL	19028421	BRC47	1	1	MMEJ	UNC5D	ENST00000404895	1	intron1	N/A	N/A	N/A	N/A	ANK1 MYST3 LSM1 PCMTD1 PXDNL HOOK3 UBE2V2 POTEA EIF4EBP1 SFRP1 ADRB3 LETM2 KIAA0146 ZNF703 ASH2L VDAC3 ADAM2 EFCAB1 C8orf4 ADAM9 IDO1 C8orf86 MCM4 CEBPD TACC1 ERLIN2 POLB ADAM32 PLAT HTRA4 RB1CC1 HGSNAT RNF170 FNTA NPBWR1 IKBKB ADAM5P FGFR1 CHRNB3 GOT1L1 STAR ZMAT4 IDO2 BAG4 ST18 SNTG1 GINS4 ADAM18 AGPAT6 C8orf40 PROSC WHSC1L1 CHRNA6 DDHD2 DKK4 RAB11FIP1 THAP1 SLC20A2 AP3M2 PRKDC FAM150A PPAPDC1B C8orf22 UNC5D GPR124 NKX6-3 BRF2 SNAI2 TM2D2 PLEKHA2 GOLGA7
13	53612254	53612254	13	54513164	54513164	DEL	899909	BRC47	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	24846834	24846834	3	27160987	27160987	DEL	2313153	BRC47	1	1	NHEJ	N/A	N/A	N/A	N/A	NEK10	ENST00000383770	-1	intron8	OXSM RARB LRRC3B TOP2B RPL32P11 NGLY1
3	27985119	27985119	3	27985284	27985284	DEL	161	BRC47	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	17515685	17515685	3	27596361	27596361	DEL	10079672	BRC47	1	1	MMEJ	TBC1D5	ENST00000253692	-1	intron1	N/A	N/A	N/A	N/A	OXSM SLC4A7 TOP2B RPL32P11 THRB ENSG00000132967 NGLY1 SGOL1 KAT2B RARB NR1D2 NEK10 UBE2E1 UBE2E2 EFHB LRRC3B RAB5A RPL15 ZNF385D NKIRAS1 C3orf48 KCNH8 SATB1
8	1.17E+08	1.17E+08	8	1.17E+08	1.17E+08	DEL	589	BRC47	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	1.24E+08	1.24E+08	8	33743007	33743007	CTX	N/A	BRC47	-1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	1.16E+08	1.16E+08	9	1.3E+08	1.3E+08	CTX	N/A	BRC47	1	-1	MMEJ	DPP10	ENST00000410059	1	intron5	N/A	N/A	N/A	N/A	N/A
7	65695039	65695039	8	1.17E+08	1.17E+08	CTX	N/A	BRC47	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	16360199	16360199	8	33736711	33736711	CTX	N/A	BRC47	-1	-1	NHEJ	RFTN1	ENST00000334133	-1	intron6	N/A	N/A	N/A	N/A	N/A
7	78846083	78846083	8	36760596	36760596	CTX	N/A	BRC4	1	1	MMEJ	MAGI2	ENST000003	-1	intron1	N/A	N/A	N/A	N/A	N/A

								7					54212							
3	16340081	16340081	7	1.24E+08	1.24E+08	CTX	N/A	BRC47	-1	1	MMEJ	RFTN1	ENST00000334133	-1	intron7	N/A	N/A	N/A	N/A	N/A
7	1.07E+08	1.07E+08	8	29893381	29893381	CTX	N/A	BRC47	1	1	NHEJ	CBLL1	ENST00000222597	1	intron4	N/A	N/A	N/A	N/A	N/A
3	16341814	16341814	7	1.24E+08	1.24E+08	CTX	N/A	BRC47	1	1	MMEJ	RFTN1	ENST00000334133	-1	intron7	N/A	N/A	N/A	N/A	N/A
5	1.59E+08	1.59E+08	8	33786970	33786970	CTX	N/A	BRC47	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	27727151	27727151	19	61472558	61472558	CTX	N/A	BRC47	-1	-1	MMEJ	N/A	N/A	N/A	N/A	ZSCAN5A	ENST00000254165	-1	intron0	N/A
20	34651268	34651268	22	29952665	29952665	CTX	N/A	BRC47	-1	-1	MMEJ	TGIF2	ENST00000373874	1	intron1	LIMK2	ENST00000331728	1	intron2	N/A
8	35646564	35646564	8	43309281	43309281	DEL	7661715	BRC49	1	1	NHEJ	UNC5D	ENST00000404895	1	intron4	POTEA	ENST00000344403	1	intron8	POLB ADAM32 PLAT ANK1 HTRA4 MYST3 LSM1 HOOK3 HGSNAT FNTA RNF170 IKBKB EIF4EBP1 ADAM5P FGFR1 CHRNB3 SFRP1 ADRB3 GOT1L1 ZMAT4 STAR IDO2 LETM2 BAG4 GINS4 ZNF703 C8orf40 AGPAT6 ASH2L ADAM18 VDAC3 PROSC CHRNA6 WHSC1L1 ADAM2 DKK4 DDHD2 C8orf4 THAP1 RAB11FIP1 SLC20A2 ADAM9 IDO1 AP3M2 C8orf86 PPAPDC1B GPR124 NKX6-3 BRF2 TACC1 ERLIN2 GOLGA7 PLEKHA2 TM2D2
5	56215381	56215381	5	56322730	56322730	DEL	1063348	BRC49	1	1	NHEJ	MAP3K1	ENST00000399503	1	intron15	N/A	N/A	N/A	N/A	MIER3 C5orf35
12	69650935	69650935	12	69657594	69657594	DEL	6660	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	36209803	36209803	8	73448635	73448635	DEL	37237830	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	BHLHE22 ATP6V1H CPA6 ASPH CHCHD7 PXDNL PLAG1 UBE2V2 POTEA MYBL1 CA8 LETM2 RAB2 GGH KIAA0146 ZNF703 EYA1 UBXN2B ASH2L VDAC3 EFCAB1 C8orf4 IDO1 PRDM14 MOS TRAM1 CEBPD TTPA ERLIN2 MSC RP1 ADAM32 IFITM8P RB1CC1 SULF1 DNAJC5B HGSNAT RNF170 FNTA NPBWR1 ADAM5P TMEM68 SGK3 C8orf45 VCPIP1 RGS20 FGFR1 CHRNB3 GOT1L1 STAR XKR4 IDO2 BAG4 PREX2 C8orf34 C8orf40 PROSC TCEA1P2 CHRNA6 DDHD2 THAP1 SLC20A2 PENK FAM110B PPAPDC1B TCF24 RLBP1L1 GPR124 CSPP1 NKAIN3 SNAI2 ARFGEF1 PDE7A XKR9 TM2D2 COPS5 ANK1 LYN NCOA2 MYST3 LSM1 PCMTD1 HOOK3 C8orf71 LRRC67 OPRK1 EIF4EBP1 CRH SEC11B ADRB3 SFRP1 RPS20 SDCBP CHD7 ADAM2 SDR16C5 ADAM9 MRPL15 TGS1 C8orf86 LYPLA1 CYP7B1 MCM4 TRPA1 TACC1 ADHFE1 TRIM55 PTTG3 IMPAD1 POLB PLAT CYP7A1 HTRA4 SNORD54 C8orf46 C8orf44 IKBKB SOX17 YTHDF3 ZMAT4 LACTB2 GINS4 SNTG1 ST18 AGPAT6 ADAM18 WHSC1L1 DKK4 RRS1 RAB11FIP1 SLCO5A1 AP3M2 PRKDC FAM150A C8orf22 NKX6-3 BRF2 NSMAF TOX ARMC1 GOLGA7 PLEKHA2 MTFR1
8	28097654	28097654	8	32351503	32351503	DEL	422528	BRC49	1	1	MMEJ	ELP3	ENST000003803	1	intron14	NRG1	ENST00000405606	1	intron1	TMEM66 DUSP4 PPP2CB GTF2E2 RBPMS INTS9 KIF13B WRN MBOAT4 UBXN8 PNOC FZD3 LEPROTL1 TEX15 ZNF395 GSR PURG EXTL3 DCTN6 FBXO16 HMBOX1

							45						53							
11	56405633	56405633	11	68450682	68450682	DEL	12044047	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	IGHMBP2	ENST00000255078	1	intron7	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 LRRN4CL DPP3 VPS37C VWCE OR9I1 MS4A10 YPEL4 DAGLA DRAP1 SAPS3 C11orf85 CDC42BPG 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 TIMM10 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 NDUFV1 EIF1AD SIPA1 PRPF19 CCDC85B NDUFS8 PGA4 uc001nrq.1 RBM4 P2RX3 TTC9C C11orf84 CPT1A SLC22A24 RARRES3 MED19 HRASLS5 CFL1 OR10V1 SYT12 C11orf79 RPS6KA4 KCNK7 PRG2 SERPING1 RTN3 ALDH3B1 MS4A15 PRDX5 TBC1D10C FADS3 ASRGL1 DNAJC4 MARK2 OR5AZ1P PYGM OR10Q1 OR5AN1 GPR44 NAALADL1 SLC43A1 HRASLS2 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 RAB3IL1 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 APLNR GPHA2 OR5B21 RCE1 OR5A1 TCIRG1 LTBP3 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 INCENP 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
8	43461129	43461129	8	43680436	43680436	DEL	218307	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	81275162	81275162	12	81282828	81282828	DEL	7667	BRC49	1	1	NHEJ	CCDC59	ENST00000256151	-1	cds_exon1	C12orf26	ENST00000248306	1	intron1	N/A
11	70125563	70125563	11	70421278	70421278	DEL	294715	BRC49	1	1	NHEJ	SHANK2	ENST00000338508	-1	intron23	SHANK2	ENST00000338508	-1	intron16	C11orf76
12	58127359	58127359	12	61944111	61944111	DEL	3815751	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	USP15 SLC16A7 AVPR1A PPM1H MON2 C12orf61 FAM19A2 RPL14P1
8	41029093	41029093	8	65934274	65934274	DEL	2490418	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	BHLHE22 ATP6V1H ASPH CHCHD7 LYN ANK1 MYST3 PCMTD1 C8orf71 PXDNL HOOK3 PLAG1 UBE2V2 POTEA OPRK1 CA8 SEC11B SFRP1 RPS20 RAB2 SDCBP GGH KIAA0146 UBXN2B CHD7 VDAC3 SDR16C5 EFCAB1 MRPL15 TGS1 CYP7B1 MOS LYPLA1 MCM4 CEBPD TTPA IMPAD1 POLB RP1 PLAT CYP7A1 SNORD54 IFITM8P RB1CC1 HGSNAT RNF170 FNTA NPBWR1 IKBKB SOX17 TMEM68 YTHDF3 RGS20 CHRNB3 XKR4 GINS4

							1													SNTG1 ST18 C8orf40 AGPAT6 CHRNA6 TCEA1P2 DKK4 THAP1 SLC20A2 AP3M2 PENK PRKDC FAM110B FAM150A C8orf22 RLBP1L1 NKX6-3 NKAIN3 TOX NSMAF SNAI2 GOLGA7
8	40457726	40457726	8	43462159	43462159	DEL	3003427	BRC49	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	POLB GINS4 C8orf40 PLAT AGPAT6 ANK1 VDAC3 CHRNA6 MYST3 DKK4 THAP1 SLC20A2 HOOK3 AP3M2 POTEA HGSNAT FNTA RNF170 NKX6-3 IKBKB CHRNB3 SFRP1 ZMAT4 GOLGA7
12	81276305	81276305	12	81459948	81459948	DEL	182637	BRC49	1	1	MMEJ	CCDC59	ENST00000256151	-1	utr_exon0	N/A	N/A	N/A	N/A	N/A
8	73054786	73054786	8	88829887	88829887	DEL	15774100	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	REXO1L4P CA2 HNRNPA1P4 CA3 LRRCC1 PAG1 PKIA C8orf84 TPD52 FABP4 FAM164A RALYL PMP2 CNBD1 CHMP4C FABP5 KCNB2 STAU2 JPH1 CPNE3 TERF1 UBE2W HEY1 CNGB3 LY96 CA1 ATP6V0D2 ZFAND1 SNX16 STMN2 FABP9 FABP12 ZNF704 TCEB1 PI15 CRISPLD1 TMEM70 HNF4G MRPS28 WWP1 PXMP3 ZBTB10 ZFHX4 FAM82B PSKH2 E2F5 TRPA1 SLC7A13 IMPA1 RDH10 RPL7 CA13 SLC10A5 GDAP1 IL7
12	78253114	78253114	12	80564150	80564150	DEL	2310036	BRC49	1	1	NHEJ	SYT1	ENST00000393240	1	intron5	PPFIA2	ENST00000333447	-1	intron2	MYF6 PPP1R12A C12orf64 MYF5 ACSS3 PTPRQ LIN7A PAWR
12	61940939	61940939	12	69655569	69655569	DEL	7713630	BRC49	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	LLPH HELB KCNMB4 GRIP1 MDM2 CPM IRAK3 SLC35E3 WIF1 RBMS1P IFNG C12orf28 LRRC10 TBC1D30 CAND1 RPL21P18 C12orf56 HMGA2 MSRB3 TBK1 RAB3IP IL26 DPY19L2 CPSF6 PTPRR TMBIM4 MDM1 NUP107 TMEM5 IL22 YEATS4 SRGAP1 DYRK2 CCT2 RAP1B CNOT2 GNS FRS2 LYZ C12orf66 XPOT PTPRB BEST3 LEMD3 RASSF3 RPSAP52
12	74176905	74176905	12	77304176	77304176	DEL	3126271	BRC49	1	1	NHEJ	GLIPR1	ENST00000266659	1	intron4	N/A	N/A	N/A	N/A	KRR1 NAV3 PHLDA1 E2F7 OSBPL8 BBS10 CSRP2 ZDHHC17 NAP1L1
5	1.72E+08	1.72E+08	5	1.74E+08	1.74E+08	DEL	1856146	BRC49	1	1	MMEJ	SH3PXD2B	ENST00000311601	-1	intron1	N/A	N/A	N/A	N/A	ATP6V0E FAM44B C5orf47 BNIP1 ERGIC1 NKX2-5 CPEB4 RPL26L1 STC2 C5orf41 NEURL1B DUSP1
10	62525865	62525865	12	68367877	68367877	CTX	N/A	BRC49	-1	1	NHEJ	N/A	N/A	N/A	N/A	BEST3	ENST00000393372	-1	intron1	N/A
10	43879894	43879894	12	76976138	76976138	CTX	N/A	BRC49	1	-1	NHEJ	N/A	N/A	N/A	N/A	NAV3	ENST00000397909	1	intron11	N/A
10	62526782	62526782	12	48515935	48515935	CTX	N/A	BRC49	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.02E+08	2.02E+08	4	36542834	36542834	CTX	N/A	BRC49	1	1	NHEJ	PLEKHA6	ENST00000367191	-1	intron11	N/A	N/A	N/A	N/A	N/A
13	88219969	88219969	13	88220938	88220938	DEL	957	BRC5	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

20	15324531	15324531	20	16343372	16343372	DEL	1017838	BRC5	1	1	MMEJ	C20orf133	ENST00000217246	1	intron6	C20orf23	ENST00000377997	-1	intron15	PPIAP17 C20orf23 C20orf133
20	17619410	17619410	20	18933390	18933390	DEL	1312978	BRC5	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	HARS2 SEC23B GCNT1P ZNF133 OVOL2 RPL15P1 C20orf78 C20orf12 C20orf79 C20orf72 RBBP9 CSRP2BP RPL21P3 SNX5 C20orf179 POLR3F
20	12936577	12936577	20	14594034	14594034	DEL	1656456	BRC5	1	1	NHEJ	N/A	N/A	N/A	N/A	C20orf133	ENST00000217246	1	intron4	RPS3P1 C20orf133 RNF11B GAPDP2 FLRT3 SPTLC3 C20orf6 ISM1 C20orf7 SCYE1P TASP1 SEL1L2
18	36370301	36370301	18	36374361	36374361	DEL	4058	BRC5	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	15216189	15216189	20	56631360	56631360	DEL	41414170	BRC5	1	1	NHEJ	C20orf133	ENST00000217246	1	intron6	N/A	N/A	N/A	N/A	CASS4 ELMO2 ZFP64 RPS3P2 CEP250 HCK SFRS6 C20orf175 ZHX3 IFT52 SPINT3 BFSP1 RAE1 SLA2 NCOA5 RPL37P1 KCNG1 C20orf173 C20orf179 SNAI1 NCOA3 RPL36P1 EIF6 L3MBTL SEMG1 CST4 TMSL6 C20orf95 C20orf114 RPLP0P1 ACSS1 C20orf134 FAM83D VAPB MAP1LC3A TPX2 CRNKL1 WISP2 DEFB117 C20orf70 TSPYL3 MOCS3 CSTF1 C20orf62 WFDC10A PKIG SEC23B DHX35 HSPEP1 DEFB124 HNRPA1P3 ZSWIM1 RPL5P2 CTNNBL1 PTPN1 PPP1R16B JPH2 SLC2A10 MYL9 ZNF337 C20orf24 C20orf160 C20orf91 KRT18P4 GCNT1P WFDC3 PAX1 SERINC3 SDC4 RPS3AP3 MRPS11P1 CST9L CYB5P4 C20orf185 C20orf111 ENTPD6 CPNE1 ITCH C20orf3 PSMD10P INSM1 NAPB RPS2L1 KCNB1 ZNF840 HMGB3L1 XKR7 TGM2 FER1L4 GINS1 ROMO1 TM9SF4 DOK5 MANBAL PXMP4 RPL41P1 C20orf4 CST8 ATP9A C20orf10 POFUT1 WFDC5 PYGB DPM1 SNRPFP1 C20orf152 PHF20 KCNS1 FRG1B CDH22 CDK5RAP1 NEURL2 RPS27AP3 GSS PLUNC ASXL1 uc002xda.2 SLC9A8 RALY WFDC12 SAMHD1 C20orf85 APCDD1L BMP7 RBM39 DEFB116 DBNDD2 C20orf199 C20orf133 DDX27 CST7 PCK1 ARFGEF2 PLCG1 SLPI EIF2S2 NPM1P19 RPL15P1 RPSAP1 WFDC10B SPO11 C20orf71 RPS27AP2 RBPSUHL PABPC1L FAM83C SNTA1 RBBP9 WFDC8 UBE2C C20orf172 FTLP CSTP2 ZNF217 TGIF2 C20orf108 OTOR DUSP15 PREX1 CST11 SNX5 CTSA HARS2 PLTP C20orf186 GLRXP RPL37AP1 SGK2 TTPAL CDC91L1 ADNP RPL36P2 UBE2V1 C20orf100 COX6CP2 SULF2 CD93 SNRPB2 CST2 DSTN PTMAP6 PFDN4 SLC24A3 C20orf127 POLR3F DEFB123 GSTM3P FOXA2 uc002wxy.2 KIAA0406 RIN2 GGT7 ADIG RPN2 RNF114 RIMS4 C20orf191 BPIL1 REM1 C20orf43 TRPC4AP C20orf72 C20orf79 NAT5 FAM182B GCNT7 SYS1 RPL7AL3 PMEPA1 MLLT10L C20orf132 SPINT4 RRBP1 OVOL2 EFCAB8 ASIP TTLL9 CSE1L ST13P SPAG4L EDEM2 HMGB3L2 BLCAP SLC13A3 CDC42P1 PTPRT ZNFX1 SNHG11 C20orf106 ANKRD60 ID1 WFDC13 RPL24P2 LBP CSRP2BP CTCFL TFAP2C NKX2-2 DEFB115 PPP4R1L TOMM34 ZSWIM3 DEFB121 HM13 XRN2 DEFB119 ENSG00000215443 KIAA0980 DNMT3B C20orf165 TNNC2 PPIAP17 NNAT FAM112A B4GALT5 CEBPB EMILIN3 BPI COMMD7 ZNF341 SPATA2 ZNF334 RPL17P1 CHD6 RPL12P3 RPL31P2 BCL2L1 CD40 RPL35AP SLC35C2 WFDC6 COX4I2 E2F1 HNRPA3P2 CSTP1 MAPRE1 ZMYND8 UQCC SNAP23P C20orf26 DLGAP4 C20orf123 STK4 CSTL1 NANP PLAGL2 RPL36P4 C20orf118 COX7BP2 HMGB1L1 C20orf144 MYH7B FOXS1 ZBP1 TCTE1P R3HDML RPL24P1 PCSK2 EIF4EBP2P PI3 ZNF133 ACOT8 ABHD12 DYNLRB1 SPAG4 RNU7 C20orf78 KCNK15 GDAP1L1 C20orf142 BCAS1 CST3 RPL31P3 PIGT C20orf74 HNF4A CST5 TP53RK CYP24A1 DNTTIP1 MATN4 SEMG2 PPIAP2 CST1 C20orf107 C20orf39 PROCR GDF5OS RPL39P SSTR4 C20orf168 C20orf102 CBFA2T2 ADA TP53INP2 NCOA6 MYBL2 BPIL3 CHMP4B PARD6B RAB22A CBLN4 RPS2P1 NXT1 ZNF663 PPIAP3 STAU1 DEFB118 NDRG3 KIAA1219 GDF5 ERGIC3 WFDC11 C20orf23 KIF3B GGTLA3 VSX1 RPRD1B AHCY TSHZ2 RBL1 AURKA ZNF335 KIAA1755 WFDC2 NFATC2 C20orf12 EPB41L1 PPIAP10 WFDC9 ENSG00000204663 MMP24 SNX21 SRC ACTR5 PTGIS RPL21P3 NECAB3 NKX2-4 ENSG00000216295 NFS1 C20orf112 SLC25A6P1 LPIN3 MYLK2 PDRG1 SCAND1 SOCS2P1 BCAS4 EYA2 SLC12A5

																				RBM38 CST9 MC3R SALL4 GHRH MAFB YWHAB MMP9 ACSS2 THBD TOP1 PCIF1 NCRNA00153 C20orf117 GZF1 SLC32A1
20	12821024	12821024	20	14070158	14070158	DEL	1248134	BRC5	1	1	NHEJ	N/A	N/A	N/A	N/A	C20orf133	ENST00000217246	1	intron3	RPS3P1 C20orf133 GAPDP2 SPTLC3 C20orf6 ISM1 C20orf7 SCYE1P TASP1 SEL1L2
1	1.09E+08	1.09E+08	1	1.09E+08	1.09E+08	DEL	3909	BRC5	1	1	MMEJ	SLC25A24	ENST00000264128	-1	intron1	SLC25A24	ENST00000264128	-1	intron1	N/A
20	16383611	16383611	20	44902503	44902503	DEL	28517891	BRC5	1	1	NHEJ	C20orf23	ENST00000377997	-1	intron12	N/A	N/A	N/A	N/A	ELMO2 RPS3P2 CEP250 HCK SFRS6 ZHX3 IFT52 SPINT3 BFSP1 SLA2 NCOA5 RPL37P1 C20orf173 C20orf179 EIF6 L3MBTL SEMG1 CST4 C20orf95 C20orf114 RPLP0P1 ACSS1 C20orf134 FAM83D MAP1LC3A TPX2 CRNKL1 WISP2 DEFB117 C20orf70 TSPYL3 C20orf62 WFDC10A PKIG SEC23B DHX35 HSPEP1 DEFB124 HNRPA1P3 ZSWIM1 RPL5P2 CTNNBL1 PPP1R16B JPH2 SLC2A10 MYL9 ZNF337 C20orf24 C20orf160 C20orf91 GCNT1P WFDC3 PAX1 SERINC3 SDC4 RPS3AP3 MRPS11P1 CST9L CYB5P4 C20orf185 C20orf111 ENTPD6 CPNE1 ITCH C20orf3 INSM1 NAPB RPS2L1 ZNF840 HMGB3L1 XKR7 TGM2 FER1L4 GINS1 ROMO1 TM9SF4 MANBAL PXMP4 RPL41P1 C20orf4 CST8 C20orf10 POFUT1 WFDC5 PYGB C20orf152 PHF20 KCNS1 FRG1B CDH22 CDK5RAP1 NEURL2 RPS27AP3 GSS PLUNC ASXL1 uc002xda.2 RALY WFDC12 SAMHD1 RBM39 DEFB116 DBNDD2 CST7 PLCG1 SLPI EIF2S2 NPM1P19 RPL15P1 WFDC10B C20orf71 RPS27AP2 RBPSUHL PABPC1L FAM83C SNTA1 RBBP9 WFDC8 UBE2C C20orf172 FTLP CSTP2 TGIF2 OTOR DUSP15 CST11 SNX5 CTSA HARS2 PLTP C20orf186 GLRXP RPL37AP1 SGK2 TTPAL CDC91L1 C20orf100 CD93 SNRPB2 CST2 DSTN SLC24A3 C20orf127 POLR3F DEFB123 GSTM3P FOXA2 uc002wxy.2 KIAA0406 RIN2 GGT7 ADIG RPN2 RIMS4 C20orf191 BPIL1 REM1 TRPC4AP C20orf72 C20orf79 NAT5 FAM182B SYS1 RPL7AL3 MLLT10L C20orf132 SPINT4 RRBP1 OVOL2 EFCAB8 ASIP TTLL9 ST13P SPAG4L EDEM2 HMGB3L2 BLCAP SLC13A3 CDC42P1 PTPRT SNHG11 ID1 WFDC13 RPL24P2 LBP CSRP2BP NKX2-2 DEFB115 TOMM34 ZSWIM3 DEFB121 HM13 XRN2 DEFB119 KIAA0980 DNMT3B C20orf165 TNNC2 NNAT FAM112A EMILIN3 BPI COMMD7 ZNF341 ZNF334 RPL17P1 CHD6 RPL12P3 RPL31P2 BCL2L1 CD40 SLC35C2 WFDC6 COX4I2 E2F1 HNRPA3P2 CSTP1 MAPRE1 UQCC C20orf26 DLGAP4 C20orf123 STK4 CSTL1 NANP PLAGL2 RPL36P4 C20orf118 COX7BP2 C20orf144 MYH7B FOXS1 TCTE1P R3HDML RPL24P1 PCSK2 EIF4EBP2P PI3 ZNF133 ACOT8 ABHD12 DYNLRB1 SPAG4 C20orf78 KCNK15 GDAP1L1 C20orf142 CST3 RPL31P3 PIGT C20orf74 HNF4A CST5 TP53RK DNTTIP1 MATN4 SEMG2 PPIAP2 CST1 C20orf39 PROCR GDF5OS SSTR4 C20orf168 C20orf102 CBFA2T2 ADA TP53INP2 NCOA6 MYBL2 BPIL3 CHMP4B RPS2P1 NXT1 ZNF663 PPIAP3 DEFB118 NDRG3 KIAA1219 GDF5 ERGIC3 WFDC11 KIF3B GGTLA3 VSX1 RPRD1B AHCY RBL1 ZNF335 KIAA1755 WFDC2 C20orf12 EPB41L1 WFDC9 ENSG00000204663 MMP24 SNX21 SRC ACTR5 RPL21P3 NECAB3 NKX2-4 NFS1 C20orf112 SLC25A6P1 LPIN3 MYLK2 PDRG1 SCAND1 SOCS2P1 SLC12A5 CST9 GHRH MAFB YWHAB MMP9 ACSS2 THBD TOP1 PCIF1 NCRNA00153 C20orf117 GZF1 SLC32A1
11	67595847	67595847	11	68472617	68472617	DEL	875767	BRC5	1	1	MMEJ	CHKA	ENST00000356135	-1	intron3	N/A	N/A	N/A	N/A	LRP5 MTL5 SAPS3 CPT1A C11orf24 GAL SUV420H1 IGHMBP2 MRPL21
11	74413510	74413510	11	74422277	74422277	DEL	8767	BRC5	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	37118778	37118778	18	37122341	37122341	DEL	3545	BRC5	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	80108267	80108310	16	80108401	80108419	DEL	93	BRC5	1	1	MMEJ		ENST00000283930	1	intron1		ENST00000283930	1	intron1	N/A

													30							
14	36839363	36839363	16	59636796	59636796	CTX	N/A	BRC5	1	-1	MMEJ	MIPOL1	ENST00000280999	1	intron4		ENST00000321498	-1	intron0	N/A
11	93032043	93032043	20	29750562	29750562	CTX	N/A	BRC5	1	-1	NHEJ	N/A	N/A	N/A	N/A	BCL2L1	ENST00000376062	-1	intron1	N/A
11	63597030	63597030	20	29341116	29341116	CTX	N/A	BRC5	-1	1	NHEJ	MACROD1	ENST00000255681	-1	intron3	N/A	N/A	N/A	N/A	N/A
3	1.21E+08	1.21E+08	14	58966020	58966046	CTX	N/A	BRC5	1	1	NAHR	GSK3B	ENST00000264235	-1	intron9	GPR135	ENST00000343189	-1	intron1	N/A
11	73787862	73787862	20	21543020	21543020	CTX	N/A	BRC5	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	73827598	73827598	20	4913990	4913990	CTX	N/A	BRC5	1	-1	NHEJ	N/A	N/A	N/A	N/A	SLC23A2	ENST00000338244	-1	intron0	N/A
11	66034548	66034548	20	16091240	16091240	CTX	N/A	BRC5	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	74635587	74635587	20	53938221	53938221	CTX	N/A	BRC5	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.59E+08	1.59E+08	16	51392945	51392945	CTX	N/A	BRC5	-1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	67575042	67575042	20	4913505	4913505	CTX	N/A	BRC5	-1	1	NHEJ	N/A	N/A	N/A	N/A	SLC23A2	ENST00000338244	-1	intron0	N/A
2	2.32E+08	2.32E+08	14	43956519	43956519	CTX	N/A	BRC5	-1	1	MMEJ	PSMD1	ENST00000409643	1	intron16	N/A	N/A	N/A	N/A	N/A
11	75510259	75510259	20	54698973	54698973	CTX	N/A	BRC5	1	-1	NHEJ	UVRAG	ENST00000356136	1	intron14	N/A	N/A	N/A	N/A	N/A
11	65745851	65745851	20	47457930	47457930	CTX	N/A	BRC5	1	1	NHEJ	PACS1	ENST00000320580	1	intron10	KCNB1	ENST00000371741	-1	intron1	N/A
11	73102097	73102097	20	53299710	53299710	CTX	N/A	BRC5	1	-1	NHEJ	RAB6A	ENST00000336083	-1	intron5	N/A	N/A	N/A	N/A	N/A
11	66992811	66992811	11	66996357	66996357	DEL	3547	BRC5	1	1	NHEJ	TMEM	ENST000003	-1	intron1	N/A	N/A	N/A	N/A	N/A

								0				134	93877							
5	63850651	63850651	5	63851218	63851218	DEL	567	BRC50	1	1	NHEJ	RGS7BP	ENST00000334025	1	intron2	RGS7BP	ENST00000334025	1	intron2	N/A
7	1.3E+08	1.3E+08	10	73412294	73412351	CTX	N/A	BRC50	1	1	NHEJ	N/A	N/A	N/A	N/A	CHST3	ENST00000373115	1	intron0	N/A
10	87461502	87461502	22	27395277	27395277	CTX	N/A	BRC50	1	1	NHEJ	GRID1	ENST00000327946	-1	intron12	TTC28	ENST00000397906	-1	intron1	N/A
4	1.21E+08	1.21E+08	22	27395518	27395518	CTX	N/A	BRC50	-1	-1	NHEJ	N/A	N/A	N/A	N/A	TTC28	ENST00000397906	-1	intron1	N/A
6	96429793	96429793	17	41701142	41701142	CTX	N/A	BRC50	-1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	1.59E+08	1.59E+08	8	1.4E+08	1.4E+08	CTX	N/A	BRC50	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.54E+08	1.54E+08	20	25836628	25836628	CTX	N/A	BRC50	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	1.27E+08	1.27E+08	4	9186076	9186076	CTX	N/A	BRC50	-1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
X	99958603	99958603	X	99958812	99958812	DEL	209	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	1.05E+08	1.05E+08	2	1.05E+08	1.05E+08	DEL	930	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	79344140	79344140	11	79553482	79553482	DEL	208337	BRC51	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	12269628	12269628	6	12819292	12819292	DEL	548660	BRC51	1	1	MMEJ	HIVEP1	ENST00000379388	1	intron6	N/A	N/A	N/A	N/A	RPL15P3 EDN1
6	65766133	65766133	6	67604044	67604044	DEL	182789	BRC51	1	1	NHEJ	LY86	ENST00000379953	1	intron3	N/A	N/A	N/A	N/A	N/A
18	61520069	61520069	18	62020726	62020726	DEL	49965	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

							6													
14	19626039	19626039	14	35802924	35802924	DEL	16175883	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	GMPR2 CMTM5 RNASE7 TMEM55B DHRS1 ACIN1 CFL2 NFKBIA STRN3 PARP2 TSSK4 OR4E2 OR11H4 PSMA6 TGM1 uc001wnm.1 JPH4 RNASE12 FAM12B CBLN3 SLC7A7 DHRS4 RNASE1 MYH6 C14orf94 THTPA SCFD1 OR6S1 BRMS1L ISGF3G CCNB1IP1 ZFHX2 CHD8 GARNL1 CHMP4A HOMEZ NP ANG C14orf119 OR4N5 METT11D1 NDRG2 TM9SF1 GZMH PCK2 SDR39U1 PSME2 G2E3 CIDEB C14orf10 AP4S1 LTB4R2 APEX1 SNX6 HEATR5A PRKD1 TINF2 METTL3 SRP54 CMA1 ZNF409 C14orf23 FOXG1B RNASE2 RNASE8 PPP1R3E REC8 SUPT16H OR11H6 C14orf93 KLHL33 GZMB CPNE6 SLC22A17 RNASE6 RNF31 OR4K17 HECTD1 LRP10 FAM12A C14orf165 ZNF219 DAD1 CEBPE RNASE13 RABGGTA C14orf147 COCH BCL2L2 EAPP TEP1 OR10G2 PSMB5 NFATC4 TTC5 ADCY4 LRRC16B PRMT5 IL25 DHRS4L2 MYH7 RNASE11 CTSG KIAA1305 PSMB11 NPAS3 TRDV2 SLC7A8 ABHD4 ENSG00000215277 NUBPL NGDN NOVA1 RPGRIP1 RIPK3 C14orf126 WDR23 TRA@ RNASE4 TPPP2 EGLN3 OR6J1 ARHGAP5 RNASE3 MMP14 INSM2 RNASE9 REM2 MRPL52 RAB2B PSME1 OR5AU1 FAM158A RNASE10 OR11H7 C14orf167 STXBP6 NRL TOX4 OR11G2 HNRNPC OSGEP JUB CDH24 KIAA0323 LTB4R SLC39A2 C14orf21 SALL2 OXA1L uc001vzp.1 AP1G2 EFS OR10G3 NEDD8 AKAP6 C14orf128 PABPN1 BAZ1A DHRS2 KIAA0391 RBM23 IPO4 C14orf24
10	90746159	90746159	10	1.11E+08	1.11E+08	DEL	19786625	BRC51	1	1	MMEJ	FAS	ENST00000371875	1	intron1	N/A	N/A	N/A	N/A	MMS19 CALHM3 CYP17A1 HPSE2 IFIT5 LCOR PLCE1 PDE6C CCDC147 PEO1 KCNIP2 BTRC CC2D2B IFIT1 SORCS3 GBF1 CYP26A1 ANKRD1 KAZALD1 BLNK DNTT IDE SUFU RPL13AP5 FBXW4 FAM178A CYP2C8 CPEB3 KIF11 NFKB2 C10orf95 CUEDC2 CEP55 TM9SF3 ENTPD7 UBTD1 SORCS1 OBFC1 GOLGA7B C10orf131 ENTPD1 C10orf4 PDCD11 CNNM2 SEC31B PCGF6 GSTO2 MYOF TNKS2 TLL2 PDZD7 CNNM1 MARVELD1 MGEA5 LOXL4 NDUFB8 LGI1 NT5C2 PGAM1 ARHGAP19 SFRP5 USMG5 KIF20B PAX2 COX15 TMEM20 CWF19L1 C10orf28 IFIT1L PI4K2A GOT1 NEURL HELLS FRAT1 PIK3AP1 ABCC2 FBXL15 FGF8 HPS1 CALHM2 EXOSC1 ANKRD2 MORN4 C10orf12 C10orf33 HHEX NPM3 LBX1 SFXN2 GSTO1 BLOC1S2 ITPRIP CYP26C1 NOLC1 FGFBP3 CPN1 AVPI1 TMEM180 GPR120 RBP4 ZNF518 SLC25A28 SCD SLK C10orf78 SRP9L1 ACTR1A CYP2C19 CHUK CUTC RPS27P1 PANK1 C10orf79 PDLIM1 MARCH5 C10orf62 PIPSL CRTAC1 HPS6 SFXN3 PCGF5 NKX2-3 TLX1 C10orf129 INA OPALIN TAF5 SEMA4G PITX3 TBC1D12 PSD CCNJ TRIM8 ZFYVE27 ELOVL3 RPP30 SORBS1 PPP1R3C CH25H SLIT1 WNT8B CALHM1 C10orf32 LIPA ZDHHC16 ERLIN1 NOC3L BTAF1 LDB1 DNMBP POLL AS3MT HIF1AN HTR7 CYP2C9 PKD2L1 FRAT2 C10orf76 C10orf65 ARL3 ALDH18A1 IFIT3 SLC16A12 TCTN3 PPRC1 IFIT2 RRP12 SH3PXD2A C10orf26 HECTD2 uc001ktn.1 LZTS2 RPS3AP36 EXOC6 MRPL43 CYP2C18 COL17A1
4	1.27E+08	1.27E+08	4	1.27E+08	1.27E+08	DEL	112	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	4038595	4038595	8	4066747	4066747	DEL	28152	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	7828344	7828344	6	12972312	12972312	DEL	5142968	BRC51	1	1	NHEJ	TXNDC5	ENST00000379757	-1	utr_exon10	PHACTR1	ENST00000332995	1	intron2	GCM2 SLC35B3 RPL15P3 PAK1IP1 SYCP2L MAK RPL21P62 C6orf52 TXNDC5 RPL7AP36 GCNT6 C6orf218 NEDD9 OFCC1 TMEM14B HIVEP1 EDN1 ELOVL2 C6orf105 TMEM170B GCNT2 TFAP2A EEF1E1 TMEM14C
12	97711554	97711554	12	98016383	98016383	DEL	303827	BRC51	1	1	NHEJ	ANKS1B	ENST00000404492	-1	intron11	ANKS1B	ENST00000404492	-1	intron6	N/A
7	16918427	16918427	7	16923506	16923506	DEL	5080	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1201	1201	6	5883	5883	DE	57	BR	1	1	NHEJ	N/A	N/A	N/	N/A	N/A	N/A	N/A	N/A	HUS1B SERPINB1 WRNIP1 IRF4 FAM50B GMDS LYRM4 C6orf50 FOXC1 C6orf195 FOXQ1 SERPINB6 RIPK1 EXOC2 PRPF4B

	10	10		783	783	L	626	C51						A						SERPINB9 TUBB2A FOXF2 FARS2 BPHL FAM136B C6orf202 MYLK4 uc010jnm.1 NQO2 C6orf201 DUSP22 RPP40 SLC22A23 PECI C6orf145 TUBB2B PSMG4 C6orf146 CDYL
7	1.04E+08	1.04E+08	7	1.05E+08	1.05E+08	DEL	72219751	BRC51	1	1	NHEJ	MLL5	ENST00000257745	1	intron1	SRPK2	ENST00000393651	-1	intron2	MLL5 SRPK2
10	35587284	35587284	10	60925746	60925746	DEL	25337461	BRC51	1	1	NHEJ	CCNY	ENST00000374706	1	intron0	N/A	N/A	N/A	N/A	AGAP6 FAM25E PARG OGDHL FAM21A OR13A1 ANXA8L2 ZNF33A GDF10 IPMK CTSLL4 RPL13AP19 ZNF485 C10orf25 ASAH2B FAM35B2 C10orf136 GLUDP2 ZNF488 GPRIN2 ZNF25 CHAT RPL23AP61 NCOA4 ZNF37A BMS1 ANKRD30A RASSF4 CISD1 ENSG00000120555 ARHGAP22 GJD4 BICC1 ZNF487 ZNF239 A1CF FAM170B ANTXRL CTGLF13P PHYHIPL FRMPD2L2 OR6D2P FZD8 PRKG1 SLC18A3 CSGALNACT2 FAM35B CXCL12 FAM13C GLUDP8 RASGEF1A TIMM23 C10orf128 RET uc009xnl.1 ANUBL1 CTSLL2 TIMM23B BMS1P7 ZNF37B LRRC18 ZWINT SGMS1 C10orf53 FXYD4 DRGX GDF2 ASAH2 uc009xnf.1 PGBD3 C10orf10 CTSLL5 ENSG00000185904 HNRNPF FAM25B MAPK8 C10orf72 CSTF2T BMS1P1 FRMPD2L1 CTSLL7 HSD17B7P2 MARCH8 RBP3 ANXA8L1 ZNF22 RPS19P7 ZNF248 FAM21B CTSLL3 SYT15 CCNY FAM21C UBE2D1 ZNF32 MBL2 MSMB DKK1 FRMPD2 GLUDP7 PPYR1 TMEM72 FAM25HP TFAM ERCC6 BMS1P5 WDFY4 C10orf71 CTGLF9P ZNF33B AGAP4 ALOX5 AGAP8 CTGLF10P AGAP7 ANXA8 PCDH15 PTPN20B GLUDP6 PTPN20A
18	42485096	42485096	18	56621632	56621632	DEL	14135540	BRC51	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ST8SIA5 LIPG ST8SIA3 NARS C18orf26 PMAIP1 C18orf54 TCEB3CL TXNL1 ZBTB7C POLI TCEB3C SMAD2 NEDD4L DYM GRP ZNF532 FECH MEX3C MBD2 DCC TCEB3B CCDC11 IER3IP1 CXXC1 ALPK2 CPLX4 MRO RAX C18orf24 STARD6 SMAD7 LMAN1 MYO5B ONECUT2 WDR7 PIAS2 KIAA0427 ACAA2 CCDC68 C18orf32 KATNAL2 ATP8B1 ME2 RAB27B MALT1 MC4R CCBE1 SEC11L3 MAPK4 HDHD2 MBD1 ELAC1 TCF4 SMAD4
17	75846008	75846008	17	75846146	75846146	DEL	71	BRC51	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	67821443	67821443	16	67822426	67822426	DEL	956	BRC51	1	1	MMEJ	SNTB2	ENST00000360496	1	intron1	SNTB2	ENST00000360496	1	intron1	N/A
8	33986644	33986644	8	42939728	42939728	DEL	8952082	BRC52	1	1	NHEJ	N/A	N/A	N/A	N/A	HOOK3	ENST00000307602	1	intron9	POLB ADAM32 PLAT ANK1 HTRA4 MYST3 LSM1 RNF170 IKBKB RPL10AP3 EIF4EBP1 ADAM5P FGFR1 CHRNB3 SFRP1 ADRB3 GOT1L1 ZMAT4 STAR IDO2 LETM2 BAG4 GINS4 ZNF703 C8orf40 AGPAT6 ASH2L ADAM18 VDAC3 PROSC CHRNA6 WHSC1L1 ADAM2 DKK4 C8orf4 DDHD2 THAP1 RAB11FIP1 SLC20A2 ADAM9 IDO1 AP3M2 C8orf86 PPAPDC1B UNC5D GPR124 NKX6-3 BRF2 TACC1 ERLIN2 GOLGA7 PLEKHA2 TM2D2
19	6598316	6598316	19	6601668	6601668	DEL	3351	BRC52	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	1.27E+08	1.27E+08	9	1.27E+08	1.27E+08	DEL	36680	BRC52	1	1	NHEJ	PPP6C	ENST00000373546	-1	intron3		ENST00000401825	-1	utr_exon0	N/A
13	1.06E+08	1.06E+08	14	34849885	34849885	CTX	N/A	BRC52	1	-1	NHEJ	EFNB2	ENST00000245323	-1	intron1	KIAA0391	ENST00000321130	1	intron6	N/A
9	1.35E+08	1.35E+08	19	7475834	7475834	CTX	N/A	BRC52	-1	-1	MMEJ	N/A	N/A	N/A	N/A	C19orf45	ENST00000361664	1	intron3	N/A

8	41857756	41857756	8	41909046	41909046	DEL	51287	BRC6	1	1	MMEJ	ANK1	ENST00000265709	-1	intron1	MYST3	ENST00000396930		-1	utr_exon10	N/A
4	1.71E+08	1.71E+08	4	1.71E+08	1.71E+08	DEL	234	BRC6	1	1	MMEJ	NEK1	ENST00000308881	-1	intron27	NEK1	ENST00000308881		-1	intron27	N/A
3	56090753	56090753	3	56090900	56090900	DEL	143	BRC6	1	1	MMEJ	ERC2	ENST00000288221	-1	intron5	ERC2	ENST00000288221		-1	intron5	N/A
15	54435984	54435984	15	54436102	54436102	DEL	119	BRC6	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A		N/A	N/A
1	1.65E+08	1.65E+08	1	1.65E+08	1.65E+08	DEL	976	BRC6	1	1	NHEJ	DUSP27	ENST00000361200	1	intron1	DUSP27	ENST00000361200		1	intron1	N/A
14	36584259	36584259	14	36584378	36584378	DEL	118	BRC6	1	1	NHEJ	SLC25A21	ENST00000331299	-1	intron1	SLC25A21	ENST00000331299		-1	intron1	N/A
15	41034860	41034860	15	49606904	49606904	DEL	8571041	BRC6	1	1	MMEJ	UBR1	ENST00000290650	-1	intron44	DMXL2	ENST00000251076		-1	intron13	STRC EPB42 DUOXA1 FRMD5 SEMA6D SLC28A2 HDC EIF3S1 TUBGCP4 TRIM69 SLC12A1 C15orf43 SORD TGM7 HISPPD2A CYP19A1 CATSPER2 SLC24A5 SERF2 SECISBP2L ELL3 C15orf33 CASC4 USP8 ZSCAN29 ADAL PDIA3 DUT TMEM62 CTDSPL2 GABPB1 TRPM7 B2M EID1 C15orf48 MAP1A MYEF2 C15orf21 SERINC4 FGF7 ATP8B4 SPG11 TP53BP1 GLDN SPATA5L1 SLC27A2 SQRDL CEP152 CATSPER2P1 MFAP1 CKMT1A USP50 SHC4 CKMT1B LCMT2 DUOXA2 COPS2 SHF GALK2 DUOX2 PLDN TNFAIP8L3 DUOX1 WDR76 FBN1 TGM5 SLC30A4 GATM AP4E1 DTWD1 CCNDBP1
15	50562231	50562231	15	51367386	51367386	DEL	804152	BRC6	1	1	MMEJ	MYO5A	ENST00000399233	-1	intron1	N/A	N/A	N/A		N/A	ONECUT1 RPSAP55 KIAA1370
3	86041650	86041650	3	86041778	86041778	DEL	127	BRC6	1	1	NHEJ	CADM2	ENST00000405615	1	intron5	CADM2	ENST00000405615		1	intron5	N/A
1	1.49E+08	1.49E+08	1	1.67E+08	1.67E+08	DEL	17828452	BRC6	1	1	NHEJ	RPRD2	ENST00000401001	1	intron8	TBX19	ENST00000367821		1	intron1	C1orf189 KRTCAP2 LCE5A IFI16 C1orf226 LCE3A TIPRL SDHC ATF6 CKS1B RPTN FAM63A IQGAP3 CCDC19 DUSP12 CASQ1 RPS10P8 NDUFS2 MEF2D C1orf85 B4GALT3 OR6P1 RXRG ARHGEF11 SCAMP3 RGS5 S100A3 CDC42SE1 DCST1 TDRD10 NTRK1 CD1E KCNJ9 SPRR2F OR10Z1 DPM3 OR6N2 CD1B FCGR2A TTC24 TUFT1 CTSS FCRL6 VANGL2 LCE3E IGSF9 RFX5 DEDD RAG1AP1 FLG TMOD4 PBXIP1 LRRC52 OR10T2 ILDR2 EFNA1 ITLN2 ITLN1 YY1AP1 LCE2D TMEM79 C1orf92 CRABP2 TOMM40L CD1D NUP210L CD244 PRUNE SHE PMVK RPL4P2 PI4KB IQWD1 FCER1A FMO10P LCE1A CD84 ETV3L S100A14 FAM78B MPZ LINGO4 SPRR3 PIP5K1A ATP1A2 SHC1 BCAN GPATCH4 ILF2 OR10X1 ADAMTS4 FCGR2B PPOX KIRREL FMO8P HSPA6 S100A4 C1orf182 ARHGAP30 DENND4B THEM5 DCST2 KIAA0907 TADA1L OR6N1 APOA1BP ETV3 VPS72 NCRNA00166 SLAMF8 MPZL1 LYSMD1 TCHH SNX27 TNRC4 OR10J1 RXFP4 RORC APOA2 LOR C1orf192 EFNA3 GABPB2 NES CADM3 SEMA4A C1orf61 PEX19 CD1A ADAMTSL4 FCRL2 LCE2C OR10J5 PEA15 TAGLN2 CD5L C1orf204 DAP3 ATP8B2 AIM2 OR6K5P SMCP SLC27A3 FCGR3A OR6K2 CGN SPRR2G PAQR6 MEX3A HAX1 C1orf66 NCSTN NHLH1 LCE2B S100A7 PYHIN1 AQP10 TRIM46 LCE3D FCRLA FMO9P LCE1B CTSK SLAMF9 SPRR2D GPR161 UBQLN4 SPRR4 RUSC1 SEMA6C LCE1D FCER1G CRTC2

																				MRPL24 GON4L USP21 WDR42A C1orf77 F11R LY9 KCNN3 S100A7A TPM3 HDGF ARNT FLG2 MGST3 ZBTB7B INSRR DDR2 FMO11P OR6K6 BRP44 HAPLN2 SFT2D2 CREG1 TARS2 ATP1A4 JTB THBS3 ISG20L2 GBA PMF1 VHLL C1orf138 COPA RPL26P12 uc001fxh.2 SETDB1 LENEP C1orf2 ENSA C1orf46 MUC1 ROBLD3 S100A12 PYGO2 LMNA OR6K1P KCNJ10 PKLR EFNA4 KPRP THEM4 MAEL OR10K2 HSD17B7 OR6Y1 CLK2 POU2F1 MLLT11 SPRR2A S100A5 FCRLB RAB25 C1orf56 GPA33 NPR1 SLC39A1 OR2AQ1P C1orf110 OR10T1P RGS4 RCSD1 S100A6 S100A1 LCE2A POGZ LCE1C GATAD2B PCP4L1 RPS10P6 SPRR1A LELP1 PGLYRP4 SLC25A44 MTX1 OR6K3 UAP1 LCE3C OR10R1P LMX1A PEAR1 ADAM15 OR10K1 FMO7P SLAMF1 S100A16 KLHDC9 FCGR3B ZNF687 LCE1E ARHGEF2 S100A8 DUSP27 TCHHL1 IVL FCRL3 OR10J9P PSMB4 SMG5 MRPL9 CYCSP52 SPTA1 UBE2Q1 CCT3 C1orf111 NUF2 HCN3 PRCC TNFAIP8L2 UBAP2L S100A2 APCS FCRL1 PRR9 HORMAD1 IL6R CHRNB2 BNIPL SSR2 PGLYRP3 FDPS ERVK5 LCE3B NIT1 MSTO1 CRP TMCO1 SELENBP1 MCL1 SCNM1 CD247 PVRL4 S100A7L2 CRNN DARC LCE4A ALDH9A1 SYT11 GBAP ADCY10 SPRR2E S100A11 OR10R2 OR6K4P TDRKH CREB3L4 FCRL4 S100A13 POGK SNAPIN SPRR2B ADAR SLAMF6 PSMD4 UFC1 ECM1 FLAD1 CD48 C1orf43 C1orf68 RIT1 SH2D1B MNDA OR10J3 RHBG GOLPH3L ENSG00000216295 PBX1 RAB13 INTS3 SPRR1B USF1 SLAMF7 PFDN2 ASH1L UHMK1 FCRL5 CD1C LASS2 PIGM OLFML2B S100A10 NOS1AP S100A9 UCK2 IGSF8 ANXA9 SH2D2A NR1I3 DUSP23 RPS27 OAZ3 CRCT1 LCE1F HRNR
6	86416310	86416310	6	92413409	92413409	DEL	599698	BRC6	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	PNRC1 CNR1 CASP8AP2 PM20D2 GJA10 C6orf162 GABRR1 ORC3L SPACA1 ANKRD6 RRAGD SLC35A1 CGA C6orf161 BACH2 NCUBE1 MDN1 LYRM2 AKIRIN2 GJB7 C6orf163 MAP3K7 C6orf164 ZNF292 RNGTT HTR1E C6orf165 RARS2 GABRR2
15	45673253	45673253	15	57014928	57014928	DEL	11340681	BRC6	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ONECUT1 SCG3 TCF12 SEMA6D UNC13C HDC CCPG1 GNB5 TMOD2 MAPK6 SLC12A1 KIAA1370 TMOD3 TEX9 PRTG CYP19A1 SLC24A5 SECISBP2L C15orf33 LYSMD2 USP8 DUT RPSAP55 SLTM RAB27A GABPB1 CGNL1 TRPM7 DMXL2 EID1 FAM63B ALDH1A2 MYEF2 MYO5A FGF7 ADAM10 ATP8B4 NEDD4 RFX7 DYX1C1 GLDN ZNF280D GRINL1A WDR72 HSP90AB4P SLC27A2 AQP9 CEP152 LEO1 USP50 SHC4 COPS2 GALK2 PIGB TNFAIP8L3 FBN1 LIPC MYO5C C15orf15 MNS1 BCL2L10 AP4E1 DTWD1 PYGO1
6	70873267	70873267	6	1.22E+08	1.22E+08	DEL	51244904	BRC6	1	1	MMEJ	COL19A1	ENST00000393333	1	intron0	N/A	N/A	N/A	N/A	C6orf51 PM20D2 GJA10 C6orf162 SOBP FAM46A MCM9 VGLL2 OSTM1 FUT9 SART2 TUBE1 DCBLD1 USP45 C6orf112 IMPG1 DOPEY1 LAMA4 WASF1 RWDD1 PREP FIG4 IRAK1BP1 COQ3 PNRC1 UBE2CBP COL9A1 BEND3 SFRS18 MRAP2 NT5DC1 BXDC1 KIAA0776 FAM26D TRAF3IP2 PDSS2 C6orf161 SEC63 SIM1 SLC35F1 LACE1 PRDM13 FAM162B C6orf203 OGFRL1 FOXO3 MAN1A1 RIMS1 PHIP C6orf152 HS3ST5 RPL30P8 HMGN3 LIN28B GABRR2 ZNF259P C6orf204 TSPYL4 FHL5 AIM1 GPRC6A RSPH4A SYNCRIP NCUBE1 MDN1 GJB7 C6orf186 MAP3K7 C6orf164 POPDC3 FYN C6orf184 MARCKS SENP6 BVES GOPC SPACA1 GRIK2 MCHR2 BACH2 TMEM30A AKD1 KIAA1009 WISP3 FBXL4 C6orf150 ME1 C6orf168 TTK LYRM2 POU3F2 PGM3 SNX14 RTN4IP1 COX7A2 NUS1 GJA1 HDAC2 CCNC FAM135A HTR1E RARS2 FAM184A REV3L RPL3P7 ZUFSP CYB5R4 ORC3L C6orf57 ATG5 DPPA5 SLC35A1 HACE1 BET3L CGA EPHA7 C6orf170 C6orf225 ASCC3 TBX18 C6orf221 TSPYL1 KPNA5 C6orf163 KIAA1919 SNAP91 ZNF292 GPR6 RWDD2A SLC22A16 FRK OOEP RPL17P25 CDC2L6 SCML4 C6orf182 C6orf59 GABRR1 AMD1 RPL35P3 SLC17A5 KCNQ5 PLN HTR1B FILIP1 KHDC1 SH3BGRL2 FAM26F MANEA DDX43 TPBG IBTK KRT18P30 FAM26E PRSS35 CASP8AP2 ELOVL4 SNX3 C6orf167 CDC40 RRAGD ANKRD6 MTO1 COL12A1 GPR63 MICAL1 RPSAP45 C6orf183 EEF1A1 ROS1 CD164 SLC16A10 RFPL4B CD109 SESN1 ZBTB24 KLHL32 SMPD2 BCKDHB PPIL6 C6orf66 C6orf165 QRSL1 NT5E PRDM1 DDO C6orf185 SMAP1 CNR1 ASF1A ARMC2 MYO6 B3GAT2 NR2E1 RFX6 COL10A1 C6orf224 AKIRIN2 SLC25A5P7 BRD7P3 AKD2 RNGTT
15	82033075	82033075	15	88601453	88601453	DEL	6567378	BRC6	1	1	NHEJ	SH3GL3	ENST00000324537	1	intron5	TTLL13	ENST00000339615	1	cds_exon5	WDR93 MESP2 ACAN ISG20 AKAP13 ENSG00000186702 DET1 SCAND2 CIB1 PEX11A HAPLN3 C15orf38 MFGE8 POLG MESP1 RHCG SLC28A1 ZNF592 ZSCAN2 AP3S2 PDE8A AEN MRPL46 NMB NTRK3 MRPS11 FANCI SEC11A ALPK3 AGBL1 C15orf58 ADAMTSL3 ABHD2 ZNF710 RLBP1 SEMA4B TMEM83 PLIN ANPEP C15orf42 IDH2 KLHL25 KIF7 WDR73

15	52537209	52537209	17	54446827	54446827	CTX	N/A	BRC6	-1	-1	NHEJ	UNC13C	ENST00000260323	1	intron15	TRIM37	ENST00000393066	-1	intron20	N/A
15	48021407	48021407	17	56380254	56380254	CTX	N/A	BRC6	1	-1	NHEJ	ATP8B4	ENST00000284509	-1	intron13	BCAS3	ENST00000360207	1	intron13	N/A
15	94589679	94589679	17	55508669	55508669	CTX	N/A	BRC6	1	-1	NHEJ	N/A	N/A	N/A	N/A	HEATR6	ENST00000393017	-1	intron1	N/A
15	45318924	45318924	17	48346437	48346437	CTX	N/A	BRC6	-1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	19704762	19704762	5	1.16E+08	1.16E+08	CTX	N/A	BRC6	1	-1	NHEJ	N/A	N/A	N/A	N/A	COMMD10	ENST00000274458	1	intron5	N/A
2	1.66E+08	1.66E+08	15	1E+08	1E+08	CTX	N/A	BRC6	1	-1	NHEJ	SCN2A	ENST00000375437	1	intron10	N/A	N/A	N/A	N/A	N/A
15	41455810	41455810	17	57788941	57788941	CTX	N/A	BRC6	-1	1	MMEJ	TUBGCP4	ENST00000260383	1	intron2	N/A	N/A	N/A	N/A	N/A
15	49607827	49607827	17	54247128	54247128	CTX	N/A	BRC6	1	1	MMEJ	DMXL2	ENST00000251076	-1	intron13	PPM1E	ENST00000308249	1	intron1	N/A
15	47994573	47994573	17	55745695	55745695	CTX	N/A	BRC6	1	-1	NHEJ	ATP8B4	ENST00000284509	-1	intron19	USP32	ENST00000393005	-1	intron2	N/A
15	96148968	96148968	17	66143576	66143576	CTX	N/A	BRC6	-1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	55168973	55168973	13	26015841	26015841	CTX	N/A	BRC6	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.07E+08	1.07E+08	17	66640271	66640271	CTX	N/A	BRC6	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.04E+08	1.04E+08	17	55195870	55195870	CTX	N/A	BRC6	-1	1	MMEJ	N/A	N/A	N/A	N/A	TMEM49	ENST00000262291	1	intron4	N/A
15	75547028	75547028	17	55067738	55067738	CTX	N/A	BRC6	-1	1	MMEJ	HMG20A	ENST00000336216	1	intron3	CLTC	ENST00000269122	1	intron1	N/A
X	64482271	64482271	14	30308709	30308709	CTX	N/A	BRC6	-1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

1	90994064	90994064	17	62979110	62979110	CTX	N/A	BRC6	1	1	NHEJ	N/A	N/A	N/A	N/A	PITPNC1	ENST00000299954	1	intron3	N/A
4	37940673	37940673	4	37941895	37941895	DEL	1193	BRC7	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	51561807	51561807	7	51566183	51566183	DEL	4372	BRC7	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	46494367	46494367	2	46494601	46494601	DEL	234	BRC7	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	42062951	42062951	12	26849956	26849956	CTX	N/A	BRC7	-1	-1	MMEJ	GLI3	ENST00000395925	-1	intron3	ITPR2	ENST00000381340	-1	intron1	N/A
17	28534418	28534418	17	28534599	28534599	DEL	181	BRC9	1	1	NHEJ	ACCN1	ENST00000225823	-1	intron1	ACCN1	ENST00000225823	-1	intron1	N/A
14	78882068	78882068	14	79695337	79695337	DEL	812267	BRC9	1	1	NHEJ	NRXN3	ENST00000332068	1	intron13	N/A	N/A	N/A	N/A	N/A
3	1.54E+08	1.54E+08	3	1.54E+08	1.54E+08	DEL	13251	BRC9	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	97571194	97571194	7	97572520	97572520	DEL	1325	BRC9	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7	78982382	78982382	8	42765917	42765917	CTX	N/A	BRC9	1	-1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	2.08E+08	2.08E+08	3	1.68E+08	1.68E+08	CTX	N/A	BRC9	1	1	MMEJ	TRAF3IP3	ENST00000341173	1	intron0	N/A	N/A	N/A	N/A	N/A
10	1.31E+08	1.31E+08	10	1.31E+08	1.31E+08	DEL	3625	BRC13	1	1	NHEJ	MGMT	ENST00000306010	1	intron1	MGMT	ENST00000306010	1	intron1	N/A
11	37302592	37302592	11	39065385	39065385	DEL	1761792	BRC13	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	70950698	70950698	11	74508544	74508544	DEL	3556845	BRC13	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	C11orf59
11	34132292	34132292	11	34889863	34889863	DEL	75656	BRC13	1	1	MMEJ	ABTB2	ENST000002989	-1	intron16	APIP	ENST00000278359	-1	intron1	ELF5

							8						92							
1	1.19E+08	1.19E+08	1	1.19E+08	1.19E+08	DEL	1225	BRC13	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	27086531	27086531	11	27209717	27209717	DEL	122186	BRC13	1	1	NHEJ	BBOX1	ENST00000263182	1	intron3	N/A	N/A	N/A	N/A	N/A
20	49370657	49370657	20	58673070	58673070	DEL	9301413	BRC13	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	CASS4
20	35278158	35278158	20	35278284	35278284	INV	118	BRC13	1	-1	NAHR	RPN2	ENST00000237530	1	intron9	RPN2	ENST00000237530	1	intron9	N/A
10	13706236	13706236	11	31760786	31760786	CTX	N/A	BRC13	1	-1	NHEJ	PRPF18	ENST00000378572	1	intron9	ELP4	ENST00000350638	1	intron9	N/A
9	2665143	2665143	20	45989723	45989723	CTX	N/A	BRC13	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	33169841	33169841	20	35278169	35278169	CTX	N/A	BRC13	1	1	NHEJ	HNF1B	ENST00000225893	-1	intron2	RPN2	ENST00000237530	1	intron9	N/A
10	21395714	21395714	11	31752224	31752224	CTX	N/A	BRC13	1	1	NHEJ	NEBL	ENST00000377159	-1	intron2	ELP4	ENST00000350638	1	intron9	N/A
13	38941487	38941487	13	48209687	48209687	DEL	9267198	BRC21	1	1	NHEJ	LHFP	ENST00000379589	-1	intron1	N/A	N/A	N/A	N/A	DGKH
6	99022200	99022200	6	1.5E+08	1.5E+08	DEL	509091773	BRC21	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	ADAT2
14	68493475	68493475	14	92552173	92552173	DEL	24057695	BRC21	1	1	MMEJ	ACTN1	ENST00000193403	-1	intron1	ITPK1	ENST00000311458	-1	intron3	PNMA1
1	1.63E+08	1.63E+08	1	2.43E+08	2.43E+08	DEL	80535	BRC21	1	1	NHEJ	PBX1	ENST00000401015	1	intron2	KIF26B	ENST00000407071	1	intron2	ANKRD45

													34							
6	1.09E+08	1.09E+08	6	1.38E+08	1.38E+08	DEL	44328333957	BRC21	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	C6orf51
21	45746302	45746302	21	45746462	45746462	DEL	130	BRC21	1	1	NAHR	COL18A1	ENST00000400347	1	intron32	COL18A1	ENST00000400347	1	intron32	N/A
6	1.55E+08	1.55E+08	10	94760032	94760032	CTX	N/A	BRC21	1	-1	MMEJ	MAGI1	ENST00000367213	-1	intron1	EXOC6	ENST00000371552	1	intron19	N/A
6	1.09E+08	1.09E+08	10	57550536	57550536	CTX	N/A	BRC21	1	-1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	1.36E+08	1.36E+08	10	90534447	90534447	CTX	N/A	BRC21	1	-1	MMEJ	AHI1	ENST00000265602	-1	intron5	N/A	N/A	N/A	N/A	N/A
1	1.63E+08	1.63E+08	X	1.3E+08	1.3E+08	CTX	N/A	BRC21	1	-1	NHEJ	PBX1	ENST00000401534	1	intron2	N/A	N/A	N/A	N/A	N/A
6	1.09E+08	1.09E+08	10	90840813	90840813	CTX	N/A	BRC21	1	1	NHEJ	ZNF259P	ENST00000407656	-1	utr_exon0	N/A	N/A	N/A	N/A	N/A
1	18960215	18960215	10	84975323	84975323	CTX	N/A	BRC21	1	1	NHEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	1.56E+08	1.56E+08	X	1.3E+08	1.3E+08	CTX	N/A	BRC21	1	1	NHEJ	FCRL3	ENST00000368186	-1	intron9	N/A	N/A	N/A	N/A	N/A
6	1.62E+08	1.62E+08	10	82110951	82110951	CTX	N/A	BRC21	1	1	NHEJ	N/A	N/A	N/A	N/A	DYDC2	ENST00000372198	1	intron1	N/A
6	1.52E+08	1.52E+08	10	99188486	99188486	CTX	N/A	BRC21	-1	1	NHEJ	C6orf97	ENST00000367290	1	intron1	EXOSC1	ENST00000370902	-1	intron4	N/A
8	1.38E+08	1.38E+08	8	1.39E+08	1.39E+08	DEL	329408	BRC36	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20	14694143	14694143	20	14734381	14734381	DEL	4023	BRC3	1	1	NHEJ	C20orf133	ENST000002	1	intron5	C20orf133	ENST00000217246	1	intron5	N/A

							9	6					17246							
20	14773699	14773699	20	14794308	14794308	DEL	20608	BRC36	1	1	NHEJ	C20orf133	ENST00000217246	1	intron5	C20orf133	ENST00000217246	1	intron5	N/A
20	59087846	59087846	20	59091008	59091008	DEL	3159	BRC36	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	1.3E+08	1.3E+08	11	1.3E+08	1.3E+08	DEL	19223	BRC36	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	40483117	40483117	20	59086636	59086636	CTX	N/A	BRC36	-1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	41869287	41869287	20	59090675	59090675	CTX	N/A	BRC36	1	1	NHEJ	ANK1	ENST00000265709	-1	intron1	N/A	N/A	N/A	N/A	N/A
8	40740842	40740842	20	60184832	60184832	CTX	N/A	BRC36	-1	1	MMEJ	ZMAT4	ENST00000297737	-1	intron2	SS18L1	ENST00000331758	1	intron10	N/A
12	34104229	34104229	13	56832248	56832248	CTX	N/A	BRC36	1	1	MMEJ	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Supplementary Table 11: Validated SVs

Validated structural variants in 46 whole genome sequenced cases are listed with chromosomal positions of each breakpoint (A, B), the type of event (DEL deletion, CTX translocation, INV inversion, INS insertion, ITX tandem duplication), size of event in bp, patient ID, orientation of each sequence, inferred mechanism (NHEJ non-homologous end joining, MMEJ microhomology mediated end joining, NAHR non-allelic homologous recombination, VNTR variable number tandem repeats). If a breakpoint is within a gene, the gene and transcript name are given with the direction of transcription and transcript substructure where the breakpoint is found (intron numbering is relative to the first translated exon). Genes completely deleted are listed in the final column.

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
MAP2K5	*WRB*	CTX	8
LIN28B	*ARMC2*	DEL	9
GLI3	*ITPR2*	CTX	4
CHDH	*ULK4*	DEL	1
ELP3	*NRG1*	DEL	2
NAV2	*C11orf49*	DEL	20
DNAH9	*MYOCD*	DEL	3
BCAS3	*ATP8B4*	CTX	12
LIMK2	*TGIF2*	CTX	2
APIP	*ABTB2*	DEL	1
ITPK1	*ACTN1*	DEL	8
EXOC6	*MAGI1*	CTX	2
EXOSC1	*C6orf97*	CTX	2
ZMAT4	*SS18L1*	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	Porphyrin 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 NFBD1 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
Tyrosine Kinases				
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	
Raf mutations				
BRAF	K601E	KD	BRC15	vemurafenib
	G104W	na	CSB2	
PI3-kinase / AKT pathway				
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 methytransferase, demethylase, and acetyltransferases.

PARADIGM SubNetwork[a]	MetaCore Map ID[b]	-log10 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 na√Øve 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[g]	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

[a] Name of the constituent sub-network from the PARADIGM SuperPathway,
[b] Identifier for the GeneGO MetaCore map.
[c] The 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.
[d] The number of genes in common between a sub-network and a map.
[e] Number of modulated genes in the PARADIGM sub-network.
[f] Number of genes returned in the map from the MetaCore analysis.
[g] ModulatedAll is the set of all modulated PARADIGM sub-networks merged into a single gene list.
[h] All 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).

E. Supplementary References

1 Mardis, E. R. *et al.* Recurring mutations found by sequencing an acute myeloid leukemia genome. *N Engl J Med* **361**, 1058-1066, doi:NEJMoa0903840 [pii]10.1056/NEJMoa0903840 (2009).

2 Gnirke, A. *et al.* Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. *Nat Biotechnol* **27**, 182-189, doi:nbt.1523 [pii]10.1038/nbt.1523 (2009).

3 Getz, G. *et al.* Comment on "The consensus coding sequences of human breast and colorectal cancers". *Science* **317**, 1500 (2007).

4 Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078-2079 (2009).

5 McKenna, A. H. *et al.* The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res*.

6 Ding, L. *et al.* Genome remodelling in a basal-like breast cancer metastasis and xenograft. *Nature* **464**, 999-1005, doi:10.1038/nature08989 (2010).

7 McKenna, A. *et al.* The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res* **20**, 1297-1303, doi:gr.107524.110 [pii]
10.1101/gr.107524.110.

8 Ye, K., Schulz, M. H., Long, Q., Apweiler, R. & Ning, Z. Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. *Bioinformatics* **25**, 2865-2871, doi:btp394 [pii]10.1093/bioinformatics/btp394 (2009).

9 Ley, T. J. *et al.* DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. *Nature* **456**, 66-72 (2008).

10 Chen, K. *et al.* BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. *Nat Methods* **6**, 677-681, doi:nmeth.1363 [pii]10.1038/nmeth.1363 (2009).

11 Chen, L. TIGRA_SV. *http://genome.wustl.edu/software/tigra_sv* **Unpublished** (2011).

12 Dees, N. *et al.* Mutation Significance in Cancer (MuSiC) analysis package. *http://gmt.genome.wustl.edu/download/* **In Preparation** (2011).

13 Fisher, R. A. *Statistical Methods for Research Workers*. (Oliver and Boyd, 1925).

14 Vaske, C. J. *et al.* Inference of patient-specific pathway activities from multi-dimensional cancer genomics data using PARADIGM. *Bioinformatics* **26**, i237-245, doi:10.1093/bioinformatics/btq182 (2010).

15 Eisen, M. B., Spellman, P. T., Brown, P. O. & Botstein, D. Cluster analysis and display of genome-wide expression patterns. *Proc Natl Acad Sci U S A* **95**, 14863-14868 (1998).

16 Saldanha, A. J. Java Treeview--extensible visualization of microarray data. *Bioinformatics* **20**, 3246-3248, doi:10.1093/bioinformatics/bth349 (2004).

17 Parsons, D. W. *et al.* The genetic landscape of the childhood cancer medulloblastoma. *Science* **331**, 435-439, doi:10.1126/science.1198056 (2011).

18 Jones, S. *et al.* Frequent mutations of chromatin remodeling gene ARID1A in ovarian clear cell carcinoma. *Science* **330**, 228-231, doi:10.1126/science.1196333 (2010).

19 Monk, K. R., Oshima, K., Jors, S., Heller, S. & Talbot, W. S. Gpr126 is essential for peripheral nerve development and myelination in mammals. *Development*, doi:10.1242/dev.062224 (2011).

20 Howard, B., Panchal, H., McCarthy, A. & Ashworth, A. Identification of the scaramanga gene implicates Neuregulin3 in mammary gland specification. *Genes Dev* **19**, 2078-2090, doi:10.1101/gad.338505 (2005).

21 Howard, B. A. The role of NRG3 in mammary development. *Journal of mammary gland biology and neoplasia* **13**, 195-203, doi:10.1007/s10911-008-9082-8 (2008).

22 van Bon, B. W. *et al.* The phenotype of recurrent 10q22q23 deletions and duplications. *European journal of human genetics : EJHG* **19**, 400-408, doi:10.1038/ejhg.2010.211 (2011).

23 Haverty, P. M. *et al.* High-resolution genomic and expression analyses of copy number alterations in breast tumors. *Genes Chromosomes Cancer* **47**, 530-542, doi:10.1002/gcc.20558 (2008).

24 Zhang, Q. *et al.* CMDS: a population-based method for identifying recurrent DNA copy number aberrations in cancer from high-resolution data. *Bioinformatics* **26**, 464-469, doi:btp708 [pii]

25 Stephens, P. J. *et al.* Complex landscapes of somatic rearrangement in human breast cancer genomes. *Nature* **462**, 1005-1010, doi:10.1038/nature08645 (2009).

26 Prentice, L. M. *et al.* NRG1 gene rearrangements in clinical breast cancer: identification of an adjacent novel amplicon associated with poor prognosis. *Oncogene* **24**, 7281-7289, doi:10.1038/sj.onc.1208892 (2005).

27 Huang, H. E. *et al.* A recurrent chromosome breakpoint in breast cancer at the NRG1/neuregulin 1/heregulin gene. *Cancer Res* **64**, 6840-6844, doi:10.1158/0008-5472.CAN-04-1762 (2004).

28 Ding, L. *et al.* Genome remodelling in a basal-like breast cancer metastasis and xenograft. *Nature* **464**, 999-1005, doi:10.1038/nature08989 (2010).

29 Barlund, M. *et al.* Cloning of BCAS3 (17q23) and BCAS4 (20q13) genes that undergo amplification, overexpression, and fusion in breast cancer. *Genes Chromosomes Cancer* **35**, 311-317, doi:10.1002/gcc.10121 (2002).

30 Lin, L. *et al.* Multiple forms of genetic instability within a 2-Mb chromosomal segment of 3q26.3-q27 are associated with development of esophageal adenocarcinoma. *Genes Chromosomes Cancer* **45**, 319-331, doi:10.1002/gcc.20293 (2006).

31 Gururaj, A. E., Holm, C., Landberg, G. & Kumar, R. Breast cancer-amplified sequence 3, a target of metastasis-associated protein 1, contributes to tamoxifen resistance in premenopausal patients with breast cancer. *Cell Cycle* **5**, 1407-1410 (2006).