Supplementary Methods

Whole exome sequencing (WES), whole genome sequencing (WGS) and alignment Exome regions were captured by the Agilent SureSelect Human All Exon 50Mb Kit and high-throughput DNA sequencing was performed on Illumina Genome Analyzer IIx (GAIIx) and HiSeq2000 according to the manufacturer's paired-end 2×120bp protocol. Libraries for whole genome sequencing were constructed using Illumina TruSeq Nano DNA Library Prep Kit and then sequenced on the HiSeq XTen platform. Read pairs were aligned to the human reference genome (hg19, downloaded from the UCSC Genome Browser[1] by BWA[2] (version 0.7.5a). Samtools[3] (version 0.1.19)_ were applied to generate chromosomal coordinate-sorted bam files and to remove PCR duplications. Afterwards, the reads were realigned around potential small inversion and deletion (indel) regions by GATK[4] (version 2.6.5) IndelRealigner following the recommended pipeline. For each WES sample, the median depth was 122.8× (range 61.6×~301.5×), with 97.4% (range 76.7%~98.4%) of the target sequence in median being covered sufficiently deep for variant calling (≥ 10× coverage). For WGS, among the 33Mb coding regions according to the RefSeq database, 91.2% in median were covered with sufficient depth (≥10×) (Table S15).

Somatic copy number variation (CNV) detection The DNA from tumor samples and matched germline controls were prepared for hybridization to Illumina high density Genome Wide Human 660W Quad_v1 (~660k probes, for sample ID starting with "A" and "C") and Affymetrix GenomeWide Human SNP 6.0 (~1.85 million probes, for sample ID starting with "B") arrays according to the manufacturer's protocol. The Genotyping Module of Genome Studio software and PennCNV-Affy[5] package were applied to process raw intensity files from Illumina (*.idat) or Affymetrix (*.cel) platforms, respectively. Based on the normalized Log R Ratio (LRR) and B Allele Frequency (BAF) information extracted from the raw intensity files, somatic genomic alterations in paired samples were detected by OncoSNP[6] (version 1.1) and Bioconductor "VanillaICE" package.[7] To verify the reliability of recurrent CNVs events, all the reported regions were plotted based on their LRR and BAF by R statistical software version 3.2.2 and visually checked. CNV segments Gain Or Loss scores were calculated by R "cghMCR" packages. The somatic alterations greater or less than two standard deviations away from the mean were applied as significant amplifications or deletions.

Single nucleotide variation (SNV)/indel calling and filter workflow MuTect[8] (version 1.1.4) and GATK[9] Haplotype Caller were applied to call SNVs and indels, respectively. GATK Unified Genotyper was also used to call both SNVs and indels. SNVs and indels detected by the above softwares were subsequently filtered by a homemade pipeline to exclude: 1) mutations with low consensus confidence score; 2) germline mutations detected from control samples; 3) mutations with low sequencing depth in germline control; 4) mutations reported in dbSNP 138 as common SNPs.

Somatic SNV/indel annotation The potential somatic SNVs and indels were mapped to the genome location using the SeattleSeq Annotation 137 server[10] and Oncotator.[11] All the non-silent mutations, including missense, nonsense and splice site for SNVs, as well as in-frame, frameshift and splice site for indels, were obtained and visually inspected to exclude potential false positive results.

RNA sequencing (RNA-seq) and fusion gene detection Total RNA was purified by TruSeq® RNA Sample Preparation Kit v2 (Illumina), and the quality was verified by Agilent Bioanalyzer 2100. Libraries were prepared according to Illumina standard protocol and paired-end 2×101bp reads were produced by Illumina HiSeq2000. Data were aligned against the human reference genome hg19 using TopHat[12,13] (Version 2.0.13) and Cufflinks[14] (Version 2.2.1) was used to assemble aligned reads into transcripts. HTSeq[15] was used to generate a counts table from Cufflinks output. DESeq2[16,17] (Version v1.8.1) was used to calculate normalized read counts for each gene and/or transcript and to perform expression analysis. FusionCatcher[18] (Version 0.99.3d) and Defuse[19] (Version 0.6.2) were used for finding somatic fusion genes such that there were at least 2 split reads and

3 spanning reads in the analyzed RNA-seq data. For the fusions that may result in fusion proteins, we further estimated their impact to the open reading frames based on the predicted break points and adjacent sequences. Crest[20] (Version 1.0) was used for identifying somatic fusion genes in the WGS data. Recurrent *MEF2D* and *ZNF384* related fusion genes were further assessed by the multiplex-nested reverse transcriptase (RT)-PCR amplification in a large cohort of validated patients using primers listed in Table S16. For the expression of *DUX4*, paired-end reads were mapped to the *DUX4* cDNA sequence (NM_001293798) using the TopHat (Version 2.0.13) computational pipeline using default parameters. Subsequently we counted reads with SAMtools (version 0.1.19).

Gene expression analysis and gene set enrichment analysis (GSEA) All gene expression data from RNA-seq experiment were normalized together using variance stabilizing transformation in the DESeq2 package to remove any technical or spurious background variation.[16,17] The top 864 genes (about 5 percent) were selected only based on the highest variability of gene expression across samples. Unsupervised hierarchical clustering was performed with ward method in R "gplots" package. The distance was based on the Pearson correlation coefficient. The height 1 was applied as the cut-point to generate eight sample groups. GSEA[21] and gene-set collection of KEGG pathways were used for enrichment analysis. *P* values were calculated by 1,000-gene-set two-sided permutation tests.

Mutation validation All the somatic non-silent SNVs, indels and fusion genes discovered by exome or transcriptome sequencing were subject to validation in the original genomic DNA samples. The regions containing the mutation events were amplified by PCR and sequenced by Sanger sequencing. PCR primers were designed by Primer Premier 5.0 (PREMIER Biosoft).

Targeted deep sequencing The genes for targeted deep sequencing were selected mainly on the mutation significance analysis of genomic data[22] (Table S17). Access Array™ System (Fluidigm) and subsequent Illumina Sequencing Platform were used to perform targeted deep sequencing for 48 gene markers from bone marrow (BM) samples at diagnosis in recurrent cohort. The PCR primers were designed by iPLEX AssayDesigner software (Sequenom) for multiplex reaction from uniplex up to 10plex. Multiplexed libraries of tagged amplicons were generated by the 48.48 Access Array microfluidic platform (Fluidigm) and deep sequencing was carried out on Illumina MiSeq. The control DNA was obtained from matching peripheral blood during complete remission or from saliva samples. Among cases without such control samples, the gene mutations were subject to mass spectrum detection in a cohort of 768 normal individuals to eliminate possible single nucleotide polymorphisms.

Plasmids construction The wild type cDNA clones were kindly provided by OriGene, and all of the wild type and fusion plasmids were constructed into Migr1 retroviral vector expressing GFP with a flag or myc tag. All recombinant plasmids were verified by DNA sequencing.

Luciferase assays The promoter region of *HDAC9* was cloned into the pGL4.15 firefly luciferase reporter vector (Promega, Madison, WI). The *HDAC9* reporter construct, a Renilla luciferase vector used for control of transfection efficiency, and wild type *MEF2D* or *MEF2D* fusion expression plasmids were cotransfected into 293T cells using Lipofectamin 2000. Twenty-four hours after transfection, cells were harvested for determination of luciferase activities using the Dual-luciferase reporter assay kit (Promega).

Transient transfection and qPCR Plasmid constructs and *HDAC9* shRNAs (Shanghai Genechem Co., LTD) were co-introduced into JM1 cells using Lipofectamin 2000. Forty-eight hours after transfection, isolated RNA was reversetranscribed into cDNA using random primer and MMLV (Invitrogen). The expression levels of *HDAC9* and *RAG1* were quantified using qRT-PCR with SYBR green (Takara) on ABIPRISM 7500.

Chromatin Immunoprecipitation ChIP assays were performed using the ChIP-IT High Sensitivity Kit (Active Motif) according to the manufacturer's standard protocol. ChIP DNA was quantified using primers specific for *HDAC9* gene promoter.

Mouse keeping, retrovirus packaging, BM transplantation Mice used in this study were housed in the specific pathogen free circumstance in Research Center for Experimental Medicine at Rui Jin Hospital Affiliated to Shanghai Jiao Tong University School of Medicine. Male BALB/c mice (aged 8–10 weeks and weight 25±2 g, n=16) and female BALB/c mice (aged 8–10 weeks and weight 22±2g, n=32) were raised in a temperature (22±1ºC) and humidity (55±5%) controlled room with 12 hours of light and 12 hours of dark a day. All animal experiments were conducted following the institutional ethical guidelines on animal care and were approved by the Animal Care and Use Committee of Shanghai Jiao Tong University School of Medicine.

Retroviral supernatants were generated by co-transfecting 293T cells with recombinant plasmids and ecopac retroviral packaging plasmid using Lipofectamin 2000. BM cells were isolated from male BALB/c mice that received 5-fluorouracil (150 mg/kg) 5 days before harvest. Mobilized cells were infected with retroviruses in IMDM supplemented with 20% FBS, IL-3 (10 ng/mL), IL-6 (10 ng/mL), IL-7 (10 ng/mL), SCF (50 ng/mL), Flt3L (50 ng/mL), and 5ug/mL polybrene. All cytokines were acquired from R&D Systems. After 24-hour infection, cells were randomly injected into lethally irradiated recipient female BALB/c mice through the tail vein (n=8 for each group). Two weeks after transplantation, peripheral blood was collected to analyze the percentage of GFP positive cells to evaluate the efficiency of transplantation. These mice were accessed daily and the peripheral hemogram was monitored every two weeks. For necessary analyzed items, these mice could be sacrificed.

Fluorescence-activated cell sorter analysis of BM cells For flow cytometry analysis, antibodies against Mac-1 (M1/70), Gr-1 (RB6-8C5), CD3(17A2), CD45R/B220 (eBioR2/60), CD19 (1D3), CD117 (2B8), and cocktail of lineage antibodies against Mac-1, Gr-1, B220, Ter119, and CD3 (BD Pharmingen) were used. Analysis was performed on LSR Fortessa^{TM} X-20 (BD Biosciences).

***In vitro* B cell differentiation** Mouse BM lineage negative (Lin$^-$) cells were isolated using a lineage depletion kit (Miltenyi Biotec Inc., Auburn, CA) according to the manufacturer's instructions, then c-Kit^{Low} cells were sorted by MoFlo cell sorter (Dako, Carpinteria, CA). Lin$^-$ c-Kit^{Low} cells were infected with retroviruses in the same condition as mobilized cells. Infected cells were then cultured for 7 days on an OP9 monolayer in IMDM containing SCF (20 ng/mL), Flt3L (50 ng/mL), and IL-7 (20 ng/mL).[23] The lymphoid lineage differentiation capacity of GFP positive cells was assessed by flow cytometry.

Supplementary Results

Characteristic expression profiles of G3, G4, G6, G7 and G8 In addition to the subgroups whose gene expression features were detailed in the main text, other subgroups identified through unsupervised clustering analysis were also bearing distinct expression profile. *BIRC7*, a gene associated with favorable prognosis in pediatric B-ALL,[24] was significantly upregulated in G3 with *ETV6-RUNX1* fusion. The alterations of *ETV6* and *UBA2* were more likely to be found in G3. All 9 patients with *ERG* deletions were clustered in G4, which was characterized by high expression of distinct outlier genes *PCDH17, PTPRM, AGAP1, IGF2* and *CLEC12B*. The dominant cooperating events of G4 was the alterations of *PAX5* (7/11, 63.6%), *NRAS* (5/11, 45.5%) and *IKZF1* (4/11, 36.4%). Most of the patients with hyperdiploidy (16/21, 76.2%) were clustered in G6, which was also characterized by *NRAS/KRAS* mutations (8/21, 38.1%). G7 represented a relative heterogeneous group, including all patients with *MLL* fusions who had a pro-B phenotype with high expression of *MEIS1* and several *HOX* genes. G8 included all but one case of *BCR-ABL1* and all Philadelphia chromosome-like ALL that had frequent *IKZF1* alterations (28/40, 70%). As reported previously,[25] Philadelphia chromosome-like ALL patients had frequent translocations or mutations that activate kinase and cytokine receptor signaling, such as *JAK2*, *ABL1*, *CRLF2* (Table S18).

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Supplementary Figures

Fig. S1 The protein domain plots (left panel) and Sanger sequencing (right panel) of gene fusions involving *MEF2D* (a) and *ZNF384* (b). (a) MEF2D fusion proteins retained the MADS box domain capable of binding DNA and the MEF2 specific type domain influencing DNA-binding affinity and cofactor interactions, yet lacking the TADII domain in C-terminal of MEF2D. (b) ZNF384 related chimeric protein retained all of the functional domains of ZNF384.

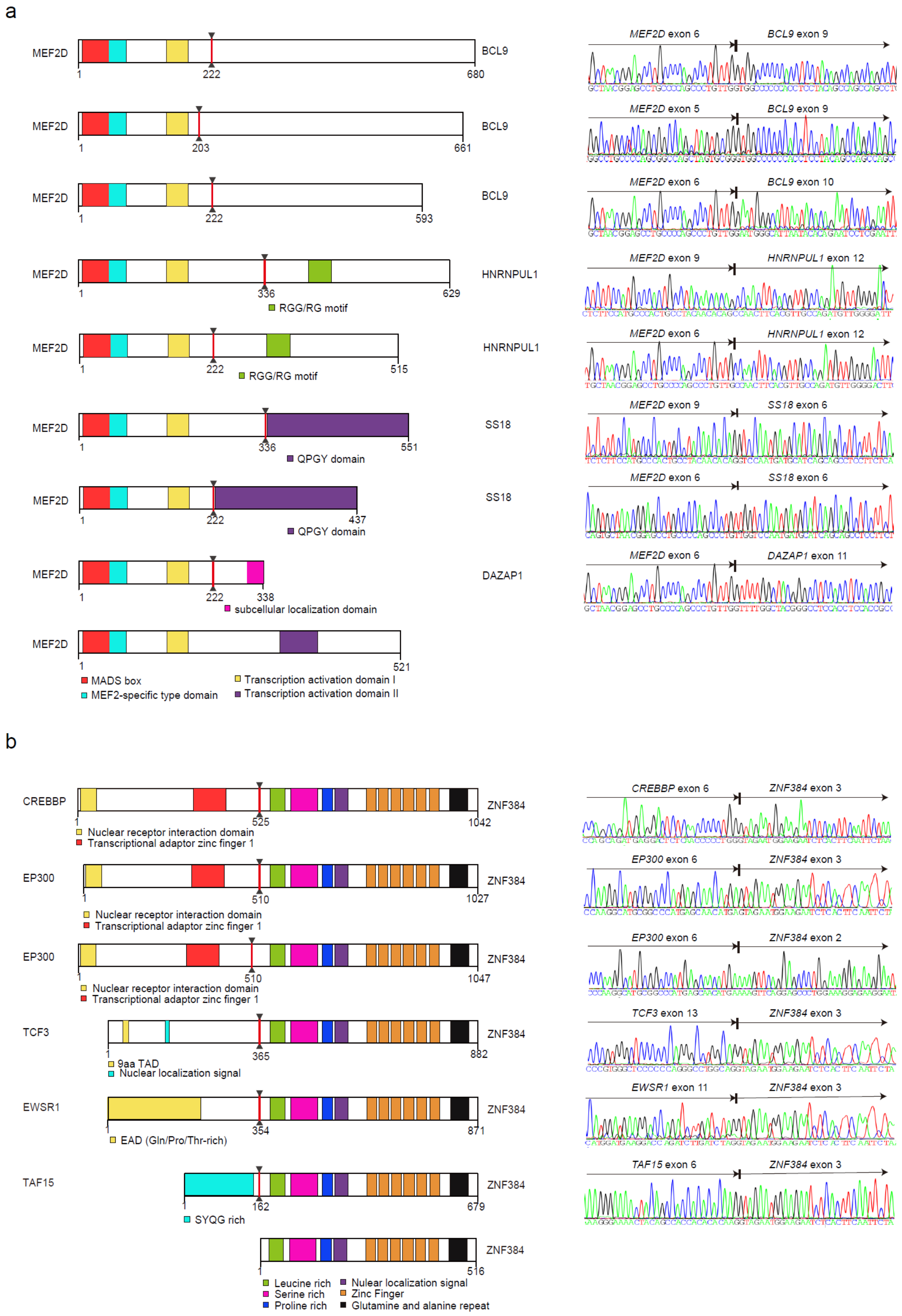

Fig. S2 Sublocalization of MEF2D, HNRNPUL1, MH, BCL9, MB, EP300, ZNF384 and EZ in NIH 3T3 cells. NIH3T3 cells were infected by different retroviruses encoding indicated proteins, and were stained with DAPI and antibody recognizing flag tagged proteins. Upper panels show nuclei as visualized by DAPI staining; middle panels, localization patterns of wild type or fusion proteins; bottom panels, the merged images.

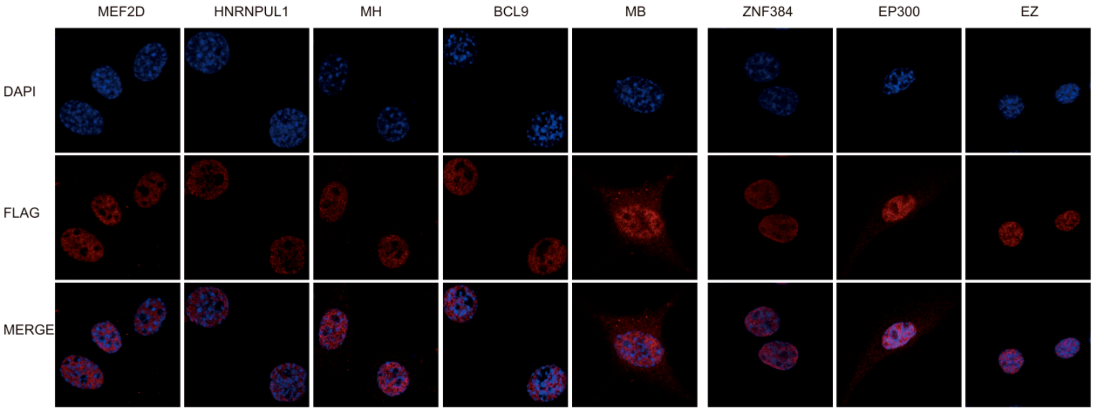

Fig. S3 (a) In vitro differentiation of Lin$^-$c-Kit^{Low} cells expressing wild type MEF2D or fusions. Sorted Lin$^-$c-Kit^{Low} BM cells were infected with retroviruses encoding wild type MEF2D or fusions or GFP only for 24 hours in the presence of SCF, Flt3L, IL-3, IL-6, IL-7 and 5μg/mL polybrene. These cells were plated onto OP9 monolayer and stimulated with SCF, IL-7, and Flt3L for 7 days. The cells were labeled with CD19 and Mac-1, and analyzed by flow cytometry. (b) *HDAC9* (left) and *RAG1* (right) mRNA levels in patients with *MEF2D* fusions and without *MEF2D* fusions as determined by RNA-seq.

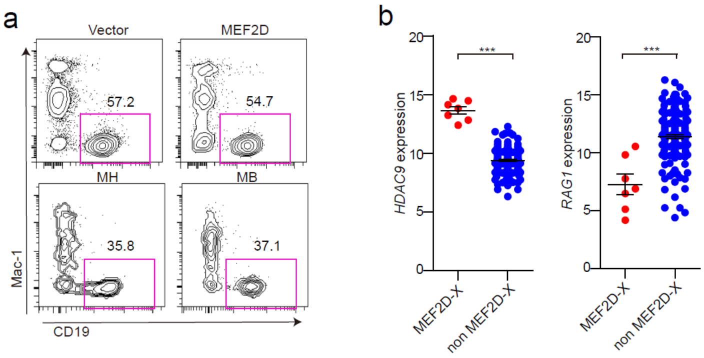

Fig. S4 (a) In vitro differentiation of Lin$^-$c-Kit^{Low} cells expressing wild type ZNF384 or EP300-ZNF384 fusion. (b) Comparison of peripheral blood parameters in control and morbid mice. (c) Gross change of spleen of EP300-ZNF384 mice, and spleen pathological section stained with hematoxylin-eosin (HE) of control and EP300-ZNF384 mice.

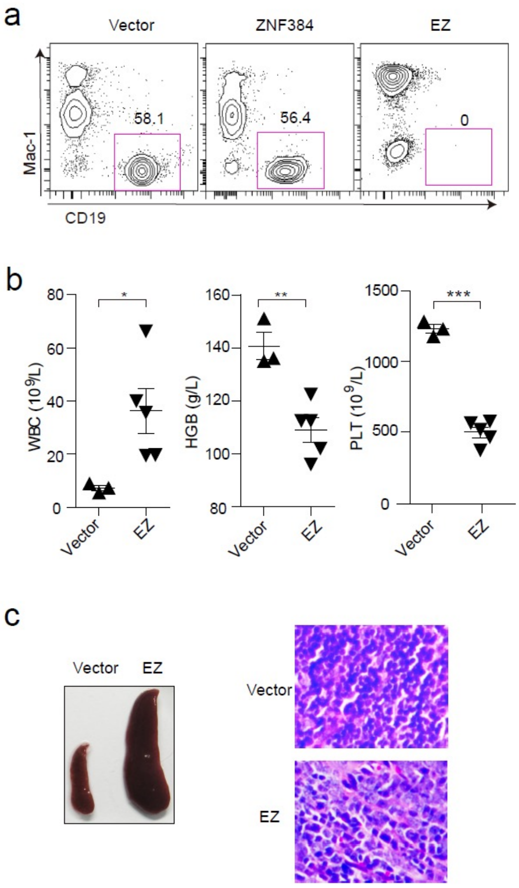

Fig. S5 (a) Heatmap of genes closely related to myeloid or lymphoid cell differentiation in different fusion groups. (b) GSEA of JAK-STAT signaling pathway in samples with or without *ZNF384* fusions (upper panel) and samples with or without *MEF2D* fusions (bottom panel).

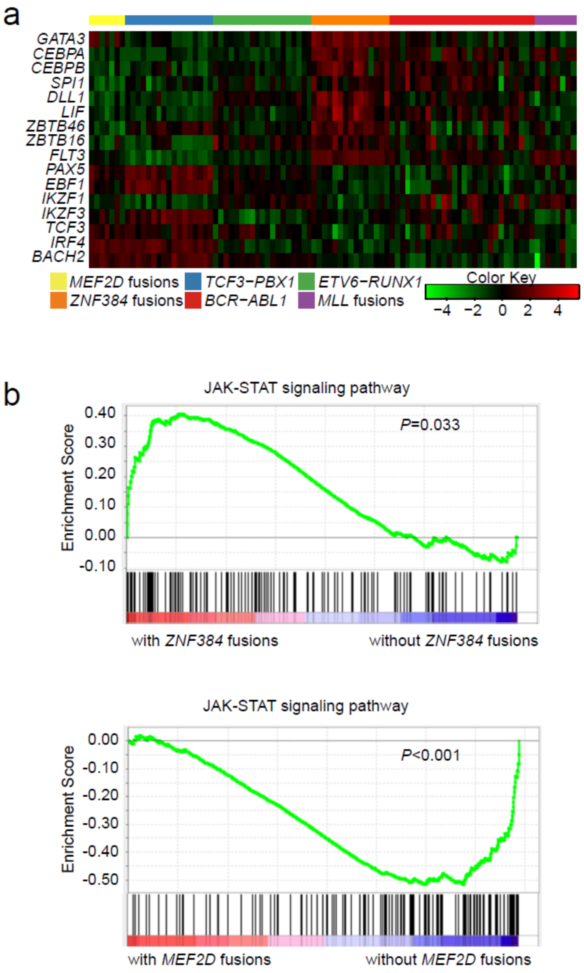

Fig.S6 Comparison of numbers of gene mutations in G1-G8. Each dot represents one sample. * denotes there is a significant difference between adults and children.

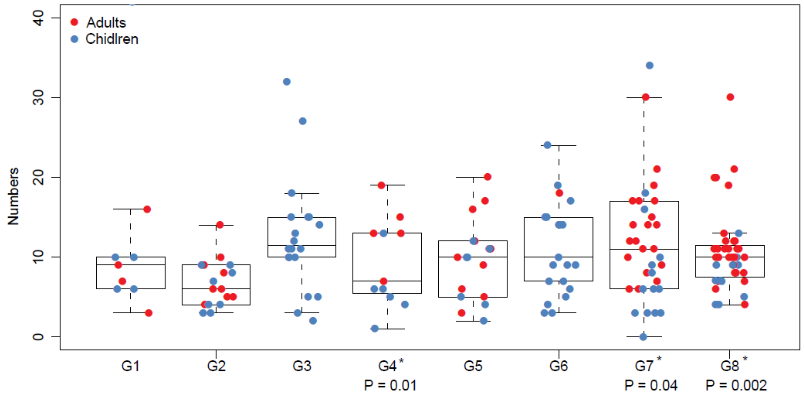

Fig. S7 Comparison of main functional categories of recurrent and crucial gene mutations in different groups between adults and children.

Supplementary tables

Table S1. Clinical and biological data of B-ALL patients in discovery cohort

Abbreviations: CR, complete remission after two courses of induction therapy; CNV, copy number variation; NA, not available
*Last follow up date: 2015/12/3

Patient ID	**Age (yrs)**	**Gender**	**WBC ($\times 10^9$/L)**	**Karyotype**	**CR (0=no, 1=yes)**	**Death* (0=no, 1=yes)**	**Relapse* (0=no, 1=yes)**	**CNV analysis (0=no, 1=yes)**	**RNA-seq (0=no, 1=yes)**
A01	58.2	Female	1.9	46,XX	1	0	0	1	0
A02	18.3	Male	2.7	Fail	1	0	1	1	0
A03	27.5	Male	20.7	46,XY	0	0	1	1	1
A04	68.9	Male	116.9	46,XY	0	1	1	1	1
A05	31.2	Male	6.4	46,XY	1	0	0	1	1
A06	45.6	Male	20.3	46,XY	1	0	1	1	0
A07	39.7	Female	31.5	46,XX	0	1	NA	1	0
A08	49.5	Male	7.1	NA	1	1	1	1	1
A09	45.2	Female	2.7	46,XX	1	0	0	1	1
A10	44.8	Female	89.0	46,XX,Ph[8]/46, XX[1]/[10]	1	0	0	1	1
A11	47.5	Male	18.8	Fail	1	0	1	1	0
A12	52.2	Female	35.6	46,XX,Ph[4]/[6]	1	1	1	1	0
A13	26.5	Male	39.4	46,XY,Ph[4]/46,XY[2]/[6]	1	1	1	1	1
A14	35.8	Male	25.7	Fail	0	1	1	1	1
A15	21.6	Female	1.9	46,XX,hyperdiploidy visible	1	0	1	1	1
A16	47.0	Female	66.8	40~46,XX,der(19)t(1;19)[cp15]/46,XX[5]/[20]	1	0	0	1	1
A17	21.9	Male	12.8	42~46,XY,2q+,-4[cp4]/46,XY[4]/[8]	1	1	1	1	1
A18	32.5	Female	273.3	Fail	1	1	1	1	1
A19	36.3	Male	6.4	Fail	1	1	1	1	1
A20	44.3	Male	46.4	46,XY	1	0	0	1	1
A21	46.8	Male	47.9	Fail	1	0	0	1	1
A22	49.2	Female	256.6	43~46,XX,t(6;12),-20,2Ph[cp7]/[9]	1	1	1	1	1
A23	26.7	Male	61.3	46,XY	1	1	1	1	1

A24	23.7	Male	6.3	46,XY	1	0	0	1	0
A25	30.9	Female	24.6	46,XY	1	1	1	1	1
A26	37.3	Male	22.0	46,XY,der(19)t(1;19)	1	1	1	1	1
A27	19.3	Female	18.9	46,XX	1	1	1	1	1
A28	64.3	Female	280.0	Fail	0	1	NA	1	1
A29	21.8	Male	2.4	46,XY	1	1	1	1	0
A30	31.4	Male	62.7	45~47,XY,der(9),add(9p)t(9;22),Ph,+M[cp5]/45~47,XY,Ph,+M[cp5]/46,XY,Ph[1]/[11]	1	0	0	1	1
A31	18.2	Male	70.0	46,XY,der(19)t(1;19)[5]/[5]	1	0	0	1	1
A32	51.0	Female	6.2	NA	1	0	0	1	1
A33	63.8	Male	23.0	46,XY,1q+,22q-[6]/46,XY,1q+[3]/[10]	1	0	0	0	0
A34	23.6	Male	84.0	45~46,XY,Ph[cp2]/46,XY[2]/[5]	1	1	1	1	1
A35	18.6	Male	4.3	46,XY[6]/[12], 6q- and M chromosome occasionally seen	1	0	0	1	1
A36	23.7	Male	13.0	46,XY	1	0	0	1	1
A37	22.8	Female	10.3	46-47,XX,+M[cp3][3]/46,XX[17]/[20]	1	0	0	1	1
A38	27.8	Female	2.1	Fail	1	0	1	1	1
A39	18.3	Female	27.5	45~46,XX,der(19)t(1;19),+M[cp4]/46,XX[4]	1	1	1	1	1
A40	34.2	Female	2.5	46,XX	1	0	0	1	1
A41	59.1	Female	58.3	47-48,XX,-4,-6,+M1-M5[cp3]/[4]	0	1	NA	1	1
A42	53.4	Female	144.0	46,XX,t(4;11)[5]/[7]	1	0	0	1	1
A43	30.4	Female	3.8	46,XX	1	0	0	1	1
A44	56.3	Female	27.5	46,XX[7]/[9]	0	1	NA	1	1
A46	68.0	Female	112.7	46,XX[6]/[9]	0	1	NA	1	1
A47	38.5	Female	56.6	Fail	1	1	1	1	1
A48	46.8	Female	154.5	46,XX	1	0	0	1	1
A49	18.2	Male	9.7	41-46,XY,1q-, -2, -7, 9q+, -13, -16, -17, -20, -22, +M1～M6[cp12]/46,XY[1]/[18]	1	0	0	1	1
A50	18.2	Female	39.5	45-46,XX,8p-,14q+,-19,+M1～M2[cp2]/46,XX[3]/[6]	1	0	0	1	1
A51	27.3	Male	37.8	Fail	1	0	0	1	1
A52	26.4	Male	31.9	45,XY,-7,der(9)t(7;9)[9]/46,XY[5]/[22]	1	0	0	1	1
A53	28.4	Female	6.4	46,XX	1	0	0	1	0
A54	46.8	Female	3.3	46,XX	1	0	0	1	1
A55	57.1	Female	3.8	48,XX,+13,-19,+21,+mar[cp4]/46,XX[16]/[20]	1	0	0	1	0
A56	47.0	Male	9.4	46,XY,t(9;9;9;22)[4];46,XY[4]/[10]	1	1	1	1	1
A57	42.4	Female	135.4	44,XX,-11,-13,Ph[1]/46,XX[19]/[20]	1	1	1	1	1

A58	25.3	Male	18.0	Fail	1	0	0	1	1
A59	29.2	Male	214.3	Fail	1	0	0	1	1
A60	31.3	Female	7.4	44-46,XX,-22,+M[cp6]/46,XX[1]/[9]	1	0	0	1	1
A61	55.4	Male	1.9	42-43,XY,3q+,Ph,+M1-M2[cp4]/46,XY,Ph[2]/46,XY[4]/[10]	1	0	1	1	1
A62	51.1	Male	62.4	42-46,XY,Ph[cp7]	1	0	0	1	1
A63	21.9	Male	438.6	44~46,XY,Ph[cp3]	1	0	0	1	1
A64	27.0	Male	28.3	44~45,XY,inv(11)?[cp2]/46,XY[18]/[31],occasionally der(9q),20q+,+M	1	0	0	1	1
A65	45.3	Male	3.1	46,XY,Ph[3]/46,XY[6]/[11]	1	0	1	1	1
A66	51.8	Female	92.9	NA	0	0	NA	1	0
A67	25.5	Male	117.7	46,XY[5]	1	0	0	1	0
A68	40.8	Female	50.7	NA	0	0	NA	1	0
A70	19.9	Female	253.9	42-46,XX,t(4;11)[cp2]/46,XX[1]/[4]	1	1	1	1	1
A71	18.4	Female	18.7	46,XX	1	1	1	1	1
A72	18.8	Male	4.0	NA	1	0	0	1	1
A73	18.6	Male	12.3	NA	1	0	0	1	1
A74	22.7	Male	14.0	46,XY, t(1;19)(q23;p13)[10]	1	1	1	1	1
A75	28.0	Male	12.0	NA	1	0	0	1	1
A76	58.1	Female	13.1	Fail	1	0	0	1	1
A77	59.9	Male	99.1	NA	0	0	0	1	1
A78	36.9	Female	36.0	46,XX,+8,9p-,-20,Ph~2ph[cp17]/46,XX[1]/[19]	1	0	0	1	1
A79	46.2	Male	5.9	45,XY,Ph[cp2]/46,XY[6]/[13]	1	0	0	1	1
A81	36.7	Female	2.2	46,XX[12]/[20]	1	0	1	1	1
A82	18.1	Male	30.4	46,XY	1	0	0	1	1
A83	18.2	Male	78.0	46,XY[2]	1	0	0	1	1
A84	57.7	Male	1.5	46,XY[2]/[3]	1	0	0	1	1
A85	18.4	Male	76.5	41~46,XY,9p-[cp7]/45,X,-Y,9p-[4]/46,XY[2]/[15]	1	0	0	1	1
A86	24.8	Female	27.1	43~46,XX,12p+[cp4]/44~45,XX,6q-,12p+[cp3]/46,XX[5]/[18]	1	0	0	1	1
A87	27.5	Male	17.9	46,XY[6]/[9]	1	0	0	1	1
A88	28.3	Female	16.7	38~43,XX[cp8]/46,XX[10]/[20]	1	0	0	1	1
A89	30.0	Female	108.2	46,XX[3]/[4]	1	0	0	1	1
A90	43.9	Female	66.1	43~46,XX,der(2)[cp4]/46,XX[6]/[10]	1	0	0	1	1
A91	45.9	Female	25.4	46,XX[9]/[20],hyperdiploidy visible	1	0	0	1	1
A93	25.2	Male	7.2	46,XX	1	0	0	1	1

A94	28.1	Female	20.1	NA	1	1	1	1	1
A95	57.7	Female	0.4	58~59,XX,-X,-1,-2,-3,-5,6q-,-7,7q+,-11,-13,-14,-15,-18,-20[cp3]/46,XX[7]	1	0	0	1	1
A96	19.3	Male	8.6	NA	1	0	0	1	1
AC04	16.1	Female	24.0	46,XX	1	0	0	1	0
AC06	16.2	Male	4.0	46,XY	1	0	0	1	1
AC09	16.2	Male	2.4	Fail	1	1	1	1	0
AC10	16.8	Male	10.5	40~46,XY,-11,-15,+M1~M3[cp3]/46, XY[16]/[27]	1	0	0	1	0
AC11	16.4	Male	69.3	46,XY,Ph	1	0	1	1	1
AC14	16.7	Male	27.0	NA	1	1	1	1	0
AC16	15.6	Male	2.4	46,XY	1	1	1	1	1
B01	4.6	Female	158.0	46,XX	1	0	1	1	0
B02	0.4	Female	386.8	46,XX,t(4;11)	1	1	1	1	0
B03	5.3	Female	508.8	46,XY,Ph	1	1	1	1	1
B04	4.6	Male	15.5	NA	1	0	1	1	0
B06	6.8	Male	2.9	46,XY	1	1	1	1	0
B12	4.7	Male	20.9	46,XY	1	1	1	1	1
B13	9.2	Male	55.6	46,XY,del(9)(q22)	1	0	1	1	1
B15	7.9	Male	100.9	NA	1	1	1	1	1
B16	7.4	Male	1.9	54-55,XY[cp2]	1	1	1	1	1
B17	3.6	Male	57.1	46,XY	1	1	1	1	1
B18	6.9	Male	16.6	45,XY,Ph	1	1	1	1	1
C01	2.3	Female	104.0	46,XX	1	0	1	1	1
C02	3.1	Female	15.4	Fail, hyperdiploidy visible	1	0	0	1	0
C03	11.6	Male	1.9	46,XY	1	0	0	1	0
C05	4.0	Male	10.9	46,XY,hyperdiploidy visible	1	0	0	1	1
C07	11.1	Female	71.5	Fail	1	0	1	1	0
C08	15.1	Female	6.8	46,XX	1	1	1	1	1
C12	15.2	Female	13.5	54,XX,2Ph,+M1-M2[cp2]/45-46,XX,Ph,+M[cp3]/[5]	1	1	1	1	0
C13	15.4	Female	2.0	46,XX,hyperdiploidy visible	1	0	1	1	0
C15	14.7	Female	10.8	46,XX	1	1	1	1	1
C17	5.8	Male	28.8	46,XY,hyperdiploidy visible	1	0	0	1	1
C18	6.4	Female	25.3	NA	1	0	0	1	1
C19	7.6	Female	21.5	45,XX,i(7q)?,-22/46,XX,i(7q)?/46,XX	1	0	0	1	1

C20	2.9	Female	10.1	46,XX	1	0	0	1	1
C21	8.9	Female	3.4	NA	1	0	0	1	1
C22	3.9	Male	17.6	46,XY	1	0	0	1	1
C23	13.0	Female	3.6	46,XX	1	0	0	1	1
C24	11.4	Male	2.7	NA	1	0	0	1	1
C25	3.2	Male	16.3	46,XY	1	0	0	1	1
C26	11.1	Male	1.9	46,XY	1	0	0	1	1
C27	1.0	Female	4.4	NA	1	0	0	1	1
C28	2.4	Male	3.0	NA	1	0	0	1	1
C29	2.7	Male	13.6	Fail	1	0	0	1	1
C30	12.9	Male	10.3	44-46,X,-4,-5,-8,+M4~M5/46,XY	1	0	0	1	1
C31	5.2	Male	8.3	NA	1	0	0	1	1
C32	13.8	Female	43.8	45~46,XX,der(1),-2,6q+,-8-19,+M3~M5	1	0	0	1	1
C33	6.1	Male	93.1	NA	1	0	0	1	1
C34	4.4	Female	6.8	NA	1	0	0	1	1
C35	5.6	Male	66.5	NA	1	0	0	1	1
C36	3.7	Male	84.0	44,XY,-7,-18,Ph/46,XY	1	0	0	1	1
C37	13.8	Female	64.8	46,XX,der(1)t(1;14)(q12;q12), -4, +M[6]/46,XX[6]	1	0	0	1	1
C38	10.6	Female	8.3	46,XX	1	0	0	1	1
C39	2.9	Female	7.6	46,XX	1	0	0	1	1
C40	8.9	Male	9.8	46,XY	1	0	0	1	1
C41	14.9	Female	4.2	46,XX,t(1;9)[4]/46,XX[2]/[12]	1	0	0	1	1
C43	8.8	Male	17.9	46,XY,t(10;16)(q11.2;q12)[15]/47,idem,+20[1]/46,XY[4]	1	0	0	1	1
C44	2.1	Female	4.3	56,XX,+dup(1)(q21q31),+4,+5,+7,+8,add(12)(p13),+14,+17,+18,+21,+21[2]/46,XX[18]	1	0	0	1	1
C45	2.2	Female	2.1	52,XX,+X,+6,+14,+17,+18,+21	1	0	0	1	1
C46	4.9	Female	7.4	47,XX,+X	1	0	0	1	0
C47	4.1	Male	96.0	46,XY	1	0	0	1	1
C48	2.9	Male	27.2	46,XY	1	0	0	1	1
C49	13.6	Male	205.6	46,XY,i(17)(q10)[5]/46,XY[15]	0	0	0	1	1
C51	3.2	Male	5.4	46,XY	1	0	0	1	1
C54	6.0	Female	5.7	46,XY	1	0	0	1	1
C55	1.9	Female	9.4	NA	1	0	0	1	1
C56	4.3	Male	2.3	55,XY,+X,+4,der(6)t(5;6)(q13;q21),+10,+14,+17,+18,+21,+21	1	0	0	1	1

C57	3.4	Male	3.5	46,XY	1	0	0	1	1
C58	4.8	Female	0.9	46,XX,del(11)(q14q23)/46,XX	1	0	0	1	1
C59	4.1	Male	13.0	46,XY	1	0	0	1	1
C61	3.0	Male	35.7	60,XY,+X,+4,der(5)t(1;5)q(23;q31),+6,+8,+10,+11,+12,+14,+15,+17,add(19)(p13.3),+21,+21,+22	1	0	0	1	1
C63	1.1	Male	244.3	46,XY,der(9)t(7;9)(q11.2;p13)	1	1	1	1	1
C64	5.1	Male	27.7	NA	1	0	0	1	1
C65	3.7	Female	28.3	46,XX	1	0	0	1	1
C66	2.4	Male	11.9	46,XY[8]	1	0	0	1	1
C67	9.9	Male	506.5	46,XY,t(9;22)	1	0	0	1	1
C68	2.1	Female	3.3	NA	1	0	0	1	1
C69	9.5	Male	2.0	46,XY,del(6)(q13;q23)t(10;13)/46,idem,del(12)(p11.2)/46,XY	1	0	0	1	1
C70	13.8	Male	50.7	46,XY	1	0	0	1	1
C71	4.0	Female	1.5	NA	1	0	0	1	1
C72	7.0	Female	8.0	53,XX,t(2;9)(p12;p21),+4+8,+8,+9,+14,+17,-20,-21,+21[12]	1	0	0	1	1
C73	1.2	Male	32.7	46,XY	1	0	0	1	1
C74	7.8	Female	2.6	54~56,XX,+X,+4,+6,+8,+10,+12,+14,+17,+18,+21[19],+21/46,XX[1]	1	0	1	1	1
C75	2.2	Female	19.0	46,XX[8]	1	0	0	1	1
C76	8.1	Female	6.0	NA	1	0	1	1	1
C77	13.6	Male	2.8	NA	1	0	0	1	1
C78	1.8	Male	1.5	46,XY	1	0	0	1	1
C79	4.6	Male	6.6	46,XY	1	0	0	1	1
C80	2.2	Male	35.1	46,XY	1	0	1	1	1
C81	4.5	Male	37.8	46,XY	1	0	0	1	1
C82	1.7	Male	3.9	46,XY	1	0	0	1	1
C83	7.5	Female	12.2	46,XX	1	0	0	1	1
C84	4.2	Male	163.8	47,XY,+X,t(4;11)(q21;q23)/47,idem,der(5)t(1;5)(p13;q35),der(15)t(1;15)(p13;p11.2), i(17)(q10),der(18)t(1;18)(p13;p11.3)[lp13]	1	0	1	1	1
C85	0.6	Female	16.0	46,XX,t(11;19)(q23;p13)	1	0	0	1	1
C86	3.5	Male	9.4	NA	1	0	0	1	1
C87	8.6	Female	8.7	47,XX,+1,t(1;19)(q23;p13.3)	1	0	0	1	1
C88	11.1	Male	336.0	NA	1	0	0	1	1
C89	3.3	Female	17.3	59,XX,+X,+4,+der(5)t(1,5)(p12;q13),+6+del(8)(q22,q24),+10,+11,+12,+13,+17,+18,+21,+21[18]/46,XX[2]	1	0	0	1	1

C90	5.0	Male	6.2	46,XY,inv(9)(p12,q13)[10]/49,idem,-Y,+8,+13,+20,+22[10]	1	0	0	1	1
C91	1.2	Male	61.7	46,XY,der(19) t(1;19)(q23;p13.3)[5]/46,XY[15]	1	0	0	1	1
C92	5.8	Male	3.4	44,XY,-3,-7,t(9;22)(q34;q11.2)t(p21;p13),der(20)t(3;20)(q21;q13.3)[9]/46,XY[8]	1	0	0	1	0
C93	4.9	Female	11.0	46,XX,+X,t(1;18)(q21;q11.2),del(9)(p22),der(9,10)(q10;q10)[15]/45,XX,t(1;18)(q21;q11.2), t(2;5)(q37;q13),der(9)(p22),der(9;11)(q10;q10)[5]	1	0	0	1	1
C94	3.0	Female	3.6	46,XX ,t(12;22)(p13;q13),i(13)(q10)/46,XX	1	0	0	1	1
C95	3.0	Male	4.8	46,XY	1	0	0	1	1
C96	12.2	Male	1.1	46,XY	1	0	0	1	0
C97	4.2	Male	4.6	46,XY	1	0	0	1	1
C98	6.4	Female	3.8	56,XX,+X,+4,+5,+6,del(q)(p22),+10,+14,+17,+18,+18,+21	1	0	0	1	1
C99	3.9	Female	6.5	46XX	1	0	0	1	0
C100	2.8	Male	17.7	58,XY,+X,+Y<+6,del(7)(q22),+10,+14,+14,+17,+18,+21,+21,+22[17]/46,XY	1	0	0	1	1
C101	2.1	Male	18.0	46,XY	1	0	0	1	1
C102	2.8	Male	5.6	NA	1	0	0	1	1
CA69	17.8	Female	103.8	46,XX[9]/[9]	1	0	0	1	1
CA80	17.5	Female	5.6	46,XX[13]/[20]	1	0	0	1	1
CA92	18.0	Female	3.8	46,XX	1	0	0	1	1
CA97	17.6	Female	47.2	46,XY,4q-,5p+,-7,9p+,+M[2]/46,XY[14]/[17]	1	0	0	1	1

Table S2. Somatic SNVs and indels identified by whole exome and genome sequencing

*Based on UCSC hg19 reference

ID	Chr	Start*	End*	Reference Allele	Variant Allele	Depth	Variant Allele Frequency	Gene	RefSeq	Mutation Type	Amino Acid Change	PROVEAN score	PROVEAN prediction	SIFT score	SIFT prediction	PolyPhen score	PolyPhen prediction
A01	13	111274575	111274575	C	A	35	0.51	*CARKD*	NM_018210	Missense	p.A38E	-1.65	Neutral	0.64	Tolerated	0.983	probably damaging
A01	7	50367240	50367256	AAAGCCCCCCTGTAAGC	AGTGGGG	33	0.21	*IKZF1*	NM_006060	Frame_Shift_Del	p.E16fs	NA	NA	NA	NA	NA	NA
A01	11	7022754	7022754	C	A	107	0.47	*ZNF214*	NM_013249	Nonsense	p.E54_	NA	NA	0.79	Tolerated	NA	NA
A01	22	30403117	30403117	G	T	34	0.50	*MTMR3*	NM_021090	Missense	p.G229V	-8.69	Deleterious	0	Damaging	1	probably damaging
A01	9	125645527	125645527	T	C	139	0.51	*RC3H2*	NM_001100588	Missense	p.I239V	-0.92	Neutral	0.25	Tolerated	0.65	possibly damaging
A01	11	47297481	47297481	C	G	48	0.44	*MADD*	NM_003682	Missense	p.L231V	-0.67	Neutral	0.27	Tolerated	0.999	probably damaging

A01	17	11556230	11556230	C	T	95	0.11	*DNAH9*	NM_001372	Missense	p.L836F	-3.26	Deleterious	0.41	Tolerated	0.031	benign
A01	1	26695017	26695017	T	C	69	0.32	*ZNF683*	NM_001114759	Missense	p.M16V	-0.49	Neutral	0.06	Tolerated	0.004	benign
A01	10	5782047	5782047	G	C	154	0.49	*FAM208B*	NM_017782	Missense	p.M638I	-0.06	Neutral	0.33	Tolerated	0	benign
A01	X	125686271	125686271	G	T	16	0.81	*DCAF12L1*	NM_178470	Missense	p.N107K	-3.41	Deleterious	0.02	Damaging	0.999	probably damaging
A01	5	149008390	149008390	C	T	11	0.55	*ARHGEF37*	NM_001001669	Missense	p.P560L	-1.1	Neutral	0.07	Tolerated	0.999	probably damaging
A01	9	37015165	37015165	G	C	102	0.44	*PAX5*	NM_016734	Missense	p.P80R	-7.7	Deleterious	0	Damaging	1	probably damaging
A01	2	136872498	136872498	G	A	38	0.47	*CXCR4*	NM_001008540	Nonsense	p.R338_	NA	NA	1	Tolerated	NA	NA
A01	2	128339485	128339485	G	A	35	0.46	*MYO7B*	NM_001080527	Missense	p.R367Q	0.35	Neutral	0.59	Tolerated	0.001	benign
A01	20	45000481	45000481	C	A	36	0.47	*ELMO2*	NM_133171	Missense	p.R515M	-4.44	Deleterious	0	Damaging	0.974	probably damaging
A01	2	187626804	187626804	C	T	74	0.50	*FAM171B*	NM_177454	Nonsense	p.R579_	NA	NA	0.63	Tolerated	NA	NA
A01	3	47139423	47139457	TGAAAGAAAAATGCAAACTTACTGAATCCTTCTTA	TAG	40	0.13	*SETD2*	NM_014159	Splice Site	p.KKDSV1711sp	NA	NA	NA	NA	NA	NA
A01	12	56351752	56351752	T	C	45	0.40	*PMEL*	NM_001200054	Missense	p.S196G	-2.13	Neutral	0.08	Tolerated	0.991	probably damaging
A01	1	92445139	92445139	C	T	104	0.09	*BRDT*	NM_001242806	Missense	p.T375M	3.68	Neutral	1	Tolerated	0.016	benign
A01	17	29553477	29553477	A	AC	46	0.72	*NF1*	NM_001042492	Frame_Shift_Ins	p.T676fs	NA	NA	NA	NA	NA	NA
A01	7	141618947	141618947	C	A	102	0.45	*OR9A4*	NM_001001656	Missense	p.T91K	-3.28	Deleterious	0	Damaging	0.608	possibly damaging
A01	1	156828334	156828334	A	G	40	0.48	*INSRR*	NM_014215	Missense	p.V27A	0.82	Neutral	1	Tolerated	0.001	benign
A01	15	51692425	51692425	T	C	97	0.43	*GLDN*	NM_181789	Missense	p.V285A	-0.96	Neutral	0.31	Tolerated	0.002	benign
A01	6	51750732	51750732	C	A	46	0.28	*PKHD1*	NM_138694	Missense	p.W2383L	-2.41	Neutral	0.65	Tolerated	0.92	possibly damaging
A02	12	59266341	59266359	GGTCTCATTCAGTCTATGT	G	74	0.23	*LRIG3*	NM_153377	In_Frame_Del	p.1119_1120T*>fs	NA	NA	NA	NA	NA	NA
A02	13	32735372	32735374	ATT	ACTGACTTACTG	78	0.31	*FRY*	NM_023037	In_Frame_Ins	p.626_626I>TDLL	-10.26	Deleterious	NA	NA	NA	NA
A02	5	63256808	63256808	C	T	53	0.13	*HTR1A*	NM_000524	Missense	p.A247T	-0.53	Neutral	0.57	Tolerated	0.929	possibly damaging
A02	16	77353946	77353946	C	T	33	0.24	*ADAMTS18*	NM_199355	Missense	p.E778K	-0.31	Neutral	0.25	Tolerated	0.615	possibly damaging
A02	X	142596912	142596912	A	C	101	0.41	*SPANXN3*	NM_001009609	Missense	p.F53C	-1.16	Neutral	0	Damaging	0.958	probably damaging
A02	4	156832655	156832655	C	A	77	0.44	*TDO2*	NM_005651	Missense	p.L209M	-1.84	Neutral	0	Damaging	1	probably damaging
A02	9	113169575	113169575	G	A	133	0.30	*SVEP1*	NM_153366	Missense	p.R2769C	-1.92	Neutral	0.05	Damaging	0.996	probably damaging
A02	15	66610820	66610820	G	A	124	0.24	*DIS3L*	NM_001143688	Missense	p.R343Q	-3.49	Deleterious	0.05	Damaging	0.865	possibly damaging
A02	15	71704085	71704085	C	T	59	0.24	*THSD4*	NM_024817	Missense	p.R359W	-4.8	Deleterious	0	Damaging	1	probably damaging
A02	3	143708571	143708571	G	A	68	0.35	*C3orf58*	NM_173552	Missense	p.R394Q	0.07	Neutral	0.63	Tolerated	0.048	benign

A02	20	13251265	13251265	C	T	100	0.58	*ISM1*	NM_080826	Nonsense	p.R85_	NA	NA	1	Tolerated	NA	NA
A02	2	230668294	230668296	TCT	TTTAGGTG	66	0.18	*TRIP12*	NM_004238	Frame_Shift_Ins	p.R922fs	NA	NA	NA	NA	NA	NA
A02	17	44061281	44061281	G	A	47	0.38	*MAPT*	NM_001123066	Missense	p.V371I	-0.25	Neutral	0.17	Tolerated	0.307	benign
A03	6	161152819	161152819	C	T	50	0.36	*PLG*	NM_000301	Missense	p.A494V	-2.38	Neutral	0.01	Damaging	0.992	probably damaging
A03	9	37354767	37354767	G	A	460	0.26	*ZCCHC7*	NM_032226	Missense	p.D382N	-3	Deleterious	0.03	Damaging	1	probably damaging
A03	1	32790094	32790094	G	A	89	0.37	*HDAC1*	NM_004964	Missense	p.D99N	-4.61	Deleterious	0	Damaging	1	probably damaging
A03	12	123333031	123333031	A	G	13	0.54	*HIP1R*	NM_003959	Missense	p.H59R	-5.23	Deleterious	0.31	Tolerated	0.994	probably damaging
A03	22	41735867	41735868	GC	CT	24	0.25	*ZC3H7B*	NM_017590	Missense	p.L288_P289delinsFS	-3.77	Deleterious	NA	NA	NA	NA
A03	8	87470234	87470234	C	A	50	0.50	*WWP1*	NM_007013	Missense	p.Q827K	-3.59	Deleterious	0.06	Tolerated	1	probably damaging
A03	8	30701172	30701172	G	A	78	0.53	*TEX15*	NM_031271	Nonsense	p.R1788_	NA	NA	0	Damaging	NA	NA
A03	5	13717533	13717533	C	T	14	0.43	*DNAH5*	NM_001369	Missense	p.R4199H	-4.79	Deleterious	0	Damaging	1	probably damaging
A03	10	86008679	86008679	C	T	16	0.50	*RGR*	NM_002921	Missense	p.R84C	-1.98	Neutral	0.01	Damaging	0.999	probably damaging
A03	4	76811189	76811189	C	G	51	0.59	*PPEF2*	NM_006239	Missense	p.S113T	-1.4	Neutral	0.19	Tolerated	0.004	benign
A03	16	705126	705126	T	A	12	0.42	*WDR90*	NM_145294	Missense	p.V512D	-5.78	Deleterious	0.01	Damaging	0.993	probably damaging
A04	20	33876701	33876701	C	T	15	0.60	*FAM83C*	NM_178468	Missense	p.A192T	-3.82	Deleterious	0.01	Damaging	0.281	benign
A04	2	160714908	160714908	T	C	114	0.49	*LY75-CD302*	NM_001198759	Missense	p.D783G	-3.58	Deleterious	0.15	Tolerated	1	probably damaging
A04	12	25398285	25398285	C	T	14	0.29	*KRAS*	NM_033360	Missense	p.G12S	-4.44	Deleterious	0.01	Damaging	0.682	possibly damaging
A04	12	50571079	50571079	C	T	163	0.55	*LIMA1*	NM_001113546	Missense	p.G684D	-2.09	Neutral	0.01	Damaging	1	probably damaging
A04	1	226252135	226252135	A	T	29	0.55	*H3F3A*	NM_002107	Missense	p.K28M	-5.39	Deleterious	0	Damaging	1	probably damaging
A04	1	55607394	55607394	G	C	51	0.61	*USP24*	NM_015306	Nonsense	p.S882_	NA	NA	0.25	Tolerated	NA	NA
A04	11	124252956	124252956	A	C	109	0.43	*OR8B2*	NM_001005468	Missense	p.V95G	-1.18	Neutral	0.25	Tolerated	0.02	benign
A05	2	68882419	68882419	C	T	19	0.47	*PROKR1*	NM_138964	Missense	p.A298V	-2.31	Neutral	0.02	Damaging	0.991	probably damaging
A05	X	133551277	133551277	T	C	47	0.96	*PHF6*	NM_001015877	Missense	p.C305R	-2.93	Deleterious	0	Damaging	0.997	probably damaging
A05	12	12037382	12037382	G	A	69	0.42	*ETV6*	NM_001987	Missense	p.C338Y	-8.44	Deleterious	1	Tolerated	1	probably damaging
A05	16	10721631	10721631	C	T	7	0.57	*TEKT5*	NM_144674	Missense	p.D423N	-1	Neutral	0.44	Tolerated	0.001	benign
A05	20	50307291	50307291	C	T	75	0.39	*ATP9A*	NM_006045	Missense	p.G237E	-6.9	Deleterious	0	Damaging	1	probably damaging
A05	1	183091387	183091387	G	C	41	0.44	*LAMC1*	NM_002293	Splice Site	p.G801sp	NA	NA	NA	NA	NA	NA
A05	5	133473786	133473790	CTCTC	CCAGACT	23	0.43	*TCF7*	NM_003202	Frame_Shift_Ins	p.L160fs	NA	NA	NA	NA	NA	NA
A05	1	111146528	111146528	G	A	50	0.52	*KCNA2*	NM_004974	Missense	p.L293F	-3.84	Deleterious	0.12	Tolerated	1	probably damaging
A05	20	31022808	31022808	C	CT	27	0.37	*ASXL1*	NM_015338	Frame_Shift_Ins	p.L765fs	NA	NA	NA	NA	NA	NA
A05	10	78708903	78708903	C	A	83	0.31	*KCNMA1*	NM_001161352	Missense	p.L902F	-3.84	Deleterious	0.04	Damaging	1	probably damaging

A05	19	17949108	17949108	C	G	51	0.41	*JAK3*	NM_000215	Missense	p.M511I	-1.54	Neutral	0.12	Tolerated	0.187	benign
A05	1	116275550	116275556	ATGTAAG	AAGTAA	58	0.12	*CASQ2*	NM_001232	Frame_Shift_Del	p.P191fs	NA	NA	NA	NA	NA	NA
A05	13	23905183	23905183	G	A	77	0.51	*SACS*	NM_014363	Missense	p.P4278S	-1.15	Neutral	0.13	Tolerated	0.013	benign
A05	1	181765825	181765825	G	A	30	0.47	*CACNA1E*	NM_001205293	Missense	p.R2077H	-1.4	Neutral	0.11	Tolerated	0.999	probably damaging
A05	21	36252939	36252940	CG	CTC	34	0.38	*RUNX1*	NM_001001890	Frame_Shift_Ins	p.S114fs	NA	NA	NA	NA	NA	NA
A05	16	67654675	67654675	A	C	55	0.38	*CTCF*	NM_006565	Missense	p.S388R	-4.62	Deleterious	0.03	Damaging	0.997	probably damaging
A05	5	108168508	108168508	G	A	69	0.51	*FER*	NM_005246	Missense	p.S82N	-1.99	Neutral	0	Damaging	0.98	probably damaging
A06	11	5173374	5173374	C	A	50	0.18	*OR52A1*	NM_012375	Missense	p.A76S	1.27	Neutral	1	Tolerated	0.001	benign
A06	2	99766961	99766963	AAC	A	41	0.37	*C2orf15*	NM_144706	Frame_Shift_Del	p.E14fs	NA	NA	NA	NA	NA	NA
A06	12	49428410	49428410	T	TC	37	0.16	*MLL2*	NM_003482	Frame_Shift_Ins	p.G3465fs	NA	NA	NA	NA	NA	NA
A06	5	78586992	78586992	G	A	77	0.45	*JMY*	NM_152405	Missense	p.G466D	-6.41	Deleterious	0	Damaging	1	probably damaging
A06	5	177569646	177569646	A	G	46	0.50	*RMND5B*	NM_022762	Missense	p.I68V	0.02	Neutral	0.33	Tolerated	0.088	benign
A06	14	24785002	24785002	A	T	38	0.61	*LTB4R*	NM_001143919	Nonsense	p.K49_	NA	NA	0.15	Tolerated	NA	NA
A06	17	36484361	36484361	C	A	58	0.57	*GPR179*	NM_001004334	Missense	p.L1697F	-1.2	Neutral	0.09	Tolerated	0.943	possibly damaging
A06	10	105883870	105883870	G	A	85	0.33	*SFR1*	NM_001002759	Missense	p.M178I	-2.81	Deleterious	0.03	Damaging	0.995	probably damaging
A06	2	183066266	183066267	AT	A	66	0.48	*PDE1A*	NM_001003683	Frame_Shift_Del	p.M358fs	NA	NA	NA	NA	NA	NA
A06	1	161011135	161011135	G	T	29	0.34	*USF1*	NM_001276373	Missense	p.P180H	-7.43	Deleterious	0	Damaging	1	probably damaging
A06	3	9743572	9743572	C	G	20	0.40	*MTMR14*	NM_001077525	Missense	p.P623R	-1.78	Neutral	0.04	Damaging	0.974	probably damaging
A06	16	3807360	3807360	C	CTGTG	31	0.26	*CREBBP*	NM_004380	Frame_Shift_Ins	p.Q1209fs	NA	NA	NA	NA	NA	NA
A06	X	29935692	29935692	G	A	101	0.10	*IL1RAPL1*	NM_014271	Missense	p.R297Q	-0.77	Neutral	NA	NA	0.995	probably damaging
A06	5	149006813	149006813	C	T	27	0.56	*ARHGEF37*	NM_001001669	Missense	p.R547C	-7.32	Deleterious	0	Damaging	0.999	probably damaging
A06	1	234565893	234565893	G	A	84	0.44	*TARBP1*	NM_005646	Missense	p.T850M	-0.2	Neutral	0.11	Tolerated	0.096	benign
A07	12	100042290	100042290	A	G	61	0.31	*FAM71C*	NM_153364	Missense	p.E113G	-2.95	Deleterious	NA	NA	0.166	benign
A07	X	115304404	115304404	G	A	135	0.47	*AGTR2*	NM_000686	Missense	p.E291K	0.25	Neutral	0.45	Tolerated	0.128	benign
A07	8	72984020	72984020	A	G	82	0.29	*TRPA1*	NM_007332	Missense	p.F65S	3.2	Neutral	0.25	Tolerated	0	benign
A07	16	15718946	15718946	C	T	81	0.38	*KIAA0430*	NM_014647	Missense	p.G680S	0.84	Neutral	0.74	Tolerated	0	benign
A07	1	82433771	82433771	G	A	109	0.33	*LPHN2*	NM_012302	Missense	p.G787E	-7.18	Deleterious	0	Damaging	1	probably damaging
A07	X	32490307	32490307	T	A	156	0.31	*DMD*	NM_004006	Missense	p.M975L	-1.18	Neutral	0.29	Tolerated	0.963	probably damaging
A07	12	49432738	49432738	G	A	39	0.15	*MLL2*	NM_003482	Nonsense	p.R2801_	NA	NA	0	Damaging	NA	NA
A07	2	74763475	74763475	G	A	26	0.54	*LOXL3*	NM_032603	Missense	p.R346W	-6.85	Deleterious	0	Damaging	1	probably damaging
A07	7	151716786	151716786	G	A	96	0.48	*GALNTL5*	NM_145292	Missense	p.R411H	-0.08	Neutral	0.04	Damaging	0	benign
A07	14	62547891	62547891	C	T	56	0.38	*SYT16*	NM_031914	Nonsense	p.R445_	NA	NA	1	Tolerated	NA	NA
A07	3	179472610	179472610	G	GC	89	0.27	*USP13*	NM_003940	Frame_Shift_Ins	p.S630fs	NA	NA	NA	NA	NA	NA

A07	17	29557344	29557345	TG	TCCC	124	0.56	*NF1*	NM_001042492	Frame_Shift_Ins	p.V1019fs	NA	NA	NA	NA	NA	NA
A08	3	175473064	175473064	G	A	104	0.13	*NAALADL2*	NM_207015	Missense	p.A683T	-0.46	Neutral	0.04	Damaging	0.062	benign
A08	17	39135207	39135207	A	G	38	0.13	*KRT40*	NM_182497	Missense	p.C349R	-4.15	Deleterious	0.36	Tolerated	0.009	benign
A08	1	216251640	216251640	T	C	253	0.26	*USH2A*	NM_206933	Missense	p.D1788G	-2.43	Neutral	0.36	Tolerated	0.801	possibly damaging
A08	1	186064409	186064409	G	C	105	0.15	*HMCN1*	NM_031935	Missense	p.E3443D	-1.02	Neutral	0.23	Tolerated	0.997	probably damaging
A08	1	75072303	75072303	C	A	165	0.50	*C1orf173*	NM_001002912	Nonsense	p.E491_	NA	NA	0.28	Tolerated	NA	NA
A08	4	47954636	47954636	T	C	135	0.40	*CNGA1*	NM_001142564	Missense	p.E97G	-0.71	Neutral	0.41	Tolerated	0.016	benign
A08	11	88780630	88780630	G	T	85	0.26	*GRM5*	NM_001143831	Missense	p.F137L	0	Neutral	NA	NA	0.001	benign
A08	9	138378527	138378527	T	A	15	0.33	*PPP1R26*	NM_014811	Missense	p.F724Y	-2.42	Neutral	0.08	Tolerated	0.997	probably damaging
A08	7	148526841	148526841	C	T	94	0.16	*EZH2*	NM_004456	Missense	p.G155R	-7.72	Deleterious	0.1	Tolerated	0.983	probably damaging
A08	6	51774093	51774093	C	A	95	0.17	*PKHD1*	NM_138694	Nonsense	p.G2224_	NA	NA	0	Damaging	NA	NA
A08	5	66426248	66426248	T	G	141	0.44	*MAST4*	NM_015183	Splice Site	p.G463sp	NA	NA	NA	NA	NA	NA
A08	19	55255446	55255446	C	A	90	0.39	*KIR2DL3*	NM_015868	Missense	p.H192N	-5.25	Deleterious	0	Damaging	0.98	probably damaging
A08	11	125765167	125765167	A	G	88	0.48	*PUS3*	NM_031307	Missense	p.I299T	-4.09	Deleterious	0	Damaging	1	probably damaging
A08	10	20534346	20534346	T	G	75	0.28	*PLXDC2*	NM_032812	Missense	p.I462S	-3.16	Deleterious	0.01	Damaging	0.634	possibly damaging
A08	2	227985831	227985831	T	C	33	0.24	*COL4A4*	NM_000092	Missense	p.I76V	0.01	Neutral	0.29	Tolerated	0.877	possibly damaging
A08	19	59059689	59059689	A	G	83	0.25	*TRIM28*	NM_005762	Missense	p.K377R	0.05	Neutral	0.58	Tolerated	0.996	probably damaging
A08	12	83251034	83251034	T	A	65	0.31	*TMTC2*	NM_152588	Missense	p.L110H	-4.43	Deleterious	0.04	Damaging	0.995	probably damaging
A08	10	91162844	91162844	T	A	189	0.46	*IFIT1*	NM_001548	Missense	p.L271H	-6.64	Deleterious	0.01	Damaging	1	probably damaging
A08	10	18280212	18280212	C	T	128	0.20	*SLC39A12*	NM_001145195	Missense	p.L468F	-1.56	Neutral	0.13	Tolerated	0.406	benign
A08	17	29552143	29552143	C	CT	113	0.39	*NF1*	NM_001042492	Frame_Shift_Ins	p.L626fs	NA	NA	NA	NA	NA	NA
A08	6	154743691	154743691	G	T	104	0.26	*CNKSR3*	NM_173515	Missense	p.N298K	-2	Neutral	0.2	Tolerated	0.02	benign
A08	5	101795467	101795467	T	G	119	0.18	*SLCO6A1*	NM_173488	Missense	p.N305T	-1.88	Neutral	0.48	Tolerated	0.964	probably damaging
A08	12	49444959	49444959	T	TG	22	0.23	*MLL2*	NM_003482	Frame_Shift_Ins	p.Q836fs	NA	NA	NA	NA	NA	NA
A08	11	22248963	22248963	G	A	133	0.21	*ANO5*	NM_213599	Missense	p.R160H	-1.98	Neutral	0.15	Tolerated	0.002	benign
A08	17	7578406	7578406	C	T	8	1.00	*TP53*	NM_000546	Missense	p.R175H	-4.87	Deleterious	0	Damaging	1	probably damaging
A08	9	123927219	123927219	A	G	83	0.24	*CNTRL*	NM_007018	Splice Site	p.R1808sp	NA	NA	NA	NA	NA	NA
A08	2	179436634	179436634	C	T	109	0.42	*TTN*	NM_001267550	Missense	p.R24742H	-3.07	Deleterious	0	Damaging	0.031	benign
A08	20	56140543	56140543	C	T	56	0.41	*PCK1*	NM_002591	Missense	p.R518W	-4.89	Deleterious	0	Damaging	1	probably damaging
A08	8	67590106	67590106	A	T	40	0.23	*C8orf44*	NM_019607	Nonsense	p.R55_	NA	NA	0.61	Tolerated	NA	NA
A08	7	148506429	148506429	A	C	116	0.21	*EZH2*	NM_004456	Missense	p.S695A	-2.62	Deleterious	0.07	Tolerated	0.998	probably damaging
A09	7	20438549	20438549	G	A	62	0.47	*ITGB8*	NM_002214	Missense	p.A405T	-3.26	Deleterious	0.03	Damaging	0.958	probably damaging
A09	1	211966505	211966505	G	C	193	0.59	*LPGAT1*	NM_014873	Missense	p.A89G	-1.12	Neutral	0.34	Tolerated	0.09	benign

A09	16	84456041	84456041	G	A	48	0.50	*ATP2C2*	NM_014861	Missense	p.E224K	-2.35	Neutral	0.71	Tolerated	0.606	possibly damaging
A09	17	15234674	15234674	C	T	89	0.42	*TEKT3*	NM_031898	Missense	p.E77K	-0.48	Neutral	0.78	Tolerated	0.475	possibly damaging
A09	X	27998830	27998830	C	T	23	0.43	*DCAF8L1*	NM_001017930	Missense	p.G208S	-6	Deleterious	0.01	Damaging	1	probably damaging
A09	4	123230424	123230424	A	G	84	0.36	*KIAA1109*	NM_015312	Missense	p.N3353D	-2.61	Deleterious	0.34	Tolerated	0.455	possibly damaging
A09	10	38121212	38121212	A	C	138	0.40	*ZNF248*	NM_021045	Missense	p.N357K	-0.68	Neutral	0	Damaging	0.808	possibly damaging
A09	20	57561861	57561861	A	G	60	0.38	*NELFCD*	NM_198976	Missense	p.N95D	-3.54	Deleterious	0.05	Damaging	0.999	probably damaging
A09	1	76387914	76387914	G	A	90	0.39	*ASB17*	NM_080868	Missense	p.P178S	-1.27	Neutral	0	Damaging	1	probably damaging
A09	6	111688923	111688923	G	A	123	0.10	*REV3L*	NM_002912	Missense	p.P2023L	-1.36	Neutral	0.16	Tolerated	0	benign
A09	11	102815071	102815071	G	T	154	0.31	*MMP13*	NM_002427	Missense	p.P447H	0	Neutral	0.08	Tolerated	0.016	benign
A09	10	30317689	30317689	G	A	51	0.53	*KIAA1462*	NM_020848	Missense	p.P463L	-5.71	Deleterious	0.56	Tolerated	0.987	probably damaging
A09	12	49433004	49433004	C	T	71	0.27	*MLL2*	NM_003482	Splice Site	p.R2789sp	NA	NA	NA	NA	NA	NA
A09	20	42907758	42907758	C	T	46	0.43	*GDAP1L1*	NM_001256737	Missense	p.R327C	-5.97	Deleterious	0	Damaging	1	probably damaging
A09	3	153870621	153870621	C	T	140	0.43	*ARHGEF26*	NM_001251962	Nonsense	p.R463_	NA	NA	0.7	Tolerated	NA	NA
A09	15	48905269	48905269	C	T	99	0.39	*FBN1*	NM_000138	Missense	p.R62H	-3.49	Deleterious	0.03	Damaging	0.999	probably damaging
A09	X	130410972	130410972	C	T	107	0.47	*IGSF1*	NM_001170961	Missense	p.R855Q	-0.55	Neutral	0.12	Tolerated	1	probably damaging
A09	4	7840366	7840366	G	A	73	0.38	*AFAP1*	NM_001134647	Missense	p.T204M	0	Neutral	0.06	Tolerated	0.575	possibly damaging
A09	1	220091782	220091782	G	A	106	0.61	*SLC30A10*	NM_018713	Missense	p.T258M	-2.43	Neutral	NA	NA	1	probably damaging
A09	3	195453044	195453044	A	G	103	0.14	*MUC20*	NM_152673	Missense	p.T353A	-2.47	Neutral	0	Damaging	0.873	possibly damaging
A09	7	123517085	123517085	A	G	105	0.48	*HYAL4*	NM_012269	Missense	p.Y441C	-2.86	Deleterious	0.01	Damaging	0.062	benign
A10	20	32369141	32369141	A	G	39	0.38	*ZNF341*	NM_032819	Missense	p.E549G	-4.21	Deleterious	0.34	Tolerated	0.286	benign
A10	8	71495903	71495903	A	C	78	0.44	*TRAM1*	NM_014294	Missense	p.F291C	-6.33	Deleterious	0.01	Damaging	0.998	probably damaging
A10	6	30624451	30624451	T	C	31	0.61	*DHX16*	NM_003587	Missense	p.H745R	-3.14	Deleterious	0	Damaging	0.411	benign
A10	7	139572087	139572087	A	G	65	0.55	*TBXAS1*	NM_001166253	Missense	p.K49R	-1.36	Neutral	0.24	Tolerated	0.993	probably damaging
A10	12	53553483	53553483	T	C	12	0.50	*CSAD*	NM_015989	Missense	p.N438S	-4.96	Deleterious	0.21	Tolerated	1	probably damaging
A10	9	96212852	96212852	C	T	74	0.49	*FAM120AOS*	NM_198841	Missense	p.R198Q	-1	Neutral	0	Damaging	0.017	benign
A10	16	61687916	61687916	G	A	64	0.50	*CDH8*	NM_001796	Missense	p.R666C	-3.12	Deleterious	0.03	Damaging	0.999	probably damaging
A10	6	155743923	155743923	C	T	55	0.44	*NOX3*	NM_015718	Missense	p.V405I	-0.33	Neutral	0.29	Tolerated	0.003	benign
A11	17	48356273	48356273	C	A	21	0.62	*TMEM92*	NM_001168215	Nonsense	p.C94_	NA	NA	0.24	Tolerated	NA	NA
A11	2	179501157	179501157	T	C	93	0.43	*TTN*	NM_001267550	Missense	p.E13766G	-4.71	Deleterious	0	Damaging	1	probably damaging
A11	1	158612269	158612269	C	T	90	0.54	*SPTA1*	NM_003126	Missense	p.G1557S	-0.99	Neutral	0.93	Tolerated	0.012	benign
A11	6	31914062	31914062	G	T	34	0.50	*CFB*	NM_001710	Missense	p.G22C	-0.06	Neutral	0.13	Tolerated	1	probably damaging
A11	19	55481405	55481405	G	A	57	0.47	*NLRP2*	NM_001174081	Missense	p.G8S	-0.66	Neutral	0.35	Tolerated	0.412	benign
A11	X	84526469	84526469	C	A	54	0.41	*ZNF711*	NM_021998	Missense	p.H641N	-6.88	Deleterious	0	Damaging	0.997	probably damaging

A11	14	45566201	45566201	A	G	59	0.39	*PRPF39*	NM_017922	Missense	p.I188V	-0.6	Neutral	0.7	Tolerated	0.005	benign
A11	7	26246003	26246003	A	G	26	0.31	*CBX3*	NM_007276	Missense	p.K14E	-1.36	Neutral	0.05	Damaging	0.991	probably damaging
A11	1	110256150	110256150	T	A	79	0.42	*GSTM5*	NM_000851	Missense	p.N74K	-5.44	Deleterious	0.09	Tolerated	0.997	probably damaging
A11	7	140246688	140246688	G	A	31	0.45	*DENND2A*	NM_015689	Missense	p.P697S	-7.27	Deleterious	0.05	Damaging	1	probably damaging
A11	9	14722651	14722651	T	G	41	0.44	*CER1*	NM_005454	Missense	p.Q7P	-1.24	Neutral	0	Damaging	0.994	probably damaging
A11	2	212285167	212285167	C	T	18	0.56	*ERBB4*	NM_005235	Missense	p.R1045K	-0.75	Neutral	0.74	Tolerated	0.002	benign
A11	5	61923102	61923102	C	T	39	0.38	*IPO11*	NM_001134779	Missense	p.T1002M	-1.02	Neutral	0.02	Damaging	0.998	probably damaging
A11	15	60653207	60653207	G	A	44	0.55	*ANXA2*	NM_001002858	Missense	p.T115M	-1.11	Neutral	0.01	Damaging	0.584	possibly damaging
A11	X	111697970	111697970	C	T	71	0.42	*ZCCHC16*	NM_001004308	Missense	p.T5M	-1.12	Neutral	0.05	Damaging	0.931	possibly damaging
A11	9	37020768	37020768	A	AC	70	0.40	*PAX5*	NM_016734	Frame_Shift_Ins	p.V26fs	NA	NA	NA	NA	NA	NA
A11	15	25213117	25213117	T	C	68	0.35	*SNURF*	NM_022804	Missense	p.V50A	-1.92	Neutral	0.19	Tolerated	0.001	benign
A12	11	72466018	72466018	G	A	66	0.55	*STARD10*	NM_006645	Missense	p.A267V	-0.82	Neutral	0.28	Tolerated	0.769	possibly damaging
A12	7	93055801	93055801	G	A	98	0.54	*CALCR*	NM_001164737	Missense	p.A465V	-0.66	Neutral	0.23	Tolerated	0.734	possibly damaging
A12	20	1286025	1286025	G	T	76	0.45	*SNPH*	NM_014723	Missense	p.G271V	-0.98	Neutral	0.57	Tolerated	1	probably damaging
A12	10	114205096	114205096	T	C	110	0.45	*ZDHHC6*	NM_022494	Missense	p.I33M	-0.57	Neutral	0.11	Tolerated	0.958	probably damaging
A12	21	36259198	36259199	AG	A	42	0.40	*RUNX1*	NM_001001890	Frame_Shift_Del	p.L71fs	NA	NA	NA	NA	NA	NA
A12	19	44118276	44118276	C	T	161	0.40	*SRRM5*	NM_001145641	Missense	p.P668L	-1.26	Neutral	0.22	Tolerated	0.002	benign
A12	X	129149895	129149906	GAAAATGGAGAA	GG	112	0.17	*BCORL1*	NM_021946	Frame_Shift_Del	p.V1049fs	NA	NA	NA	NA	NA	NA
A12	19	36018339	36018339	A	G	131	0.37	*SBSN*	NM_001166034	Missense	p.V282A	-0.05	Neutral	0.85	Tolerated	0	benign
A13	16	75611244	75611244	G	A	46	0.28	*GABARAPL2*	NM_007285	Missense	p.G111R	-7.22	Deleterious	0	Damaging	0.942	possibly damaging
A13	3	49412983	49412983	C	T	42	0.14	*RHOA*	NM_001664	Missense	p.G14R	-6.83	Deleterious	0	Damaging	1	probably damaging
A13	19	41021241	41021241	T	A	8	0.38	*SPTBN4*	NM_020971	Missense	p.M930K	-5.45	Deleterious	0	Damaging	0.999	probably damaging
A13	20	13867026	13867026	G	A	53	0.45	*SEL1L2*	NM_001271539	Missense	p.P270S	-0.79	Neutral	0.81	Tolerated	0.061	benign
A13	9	5231714	5231714	C	T	13	0.54	*INSL4*	NM_002195	Missense	p.P64L	-3.35	Deleterious	0.3	Tolerated	0.006	benign
A13	15	81188338	81188338	C	T	63	0.29	*KIAA1199*	NM_018689	Nonsense	p.Q450_	NA	NA	0.03	Damaging	NA	NA
A13	8	113353783	113353783	C	A	89	0.39	*CSMD3*	NM_198123	Missense	p.S2192I	-5.72	Deleterious	0.01	Damaging	1	probably damaging
A13	19	16268225	16268225	A	G	40	0.15	*HSH2D*	NM_032855	Missense	p.T227A	0.19	Neutral	1	Tolerated	0.004	benign
A13	11	19077936	19077936	G	A	104	0.43	*MRGPRX2*	NM_054030	Missense	p.T5I	0.28	Neutral	1	Tolerated	0	benign
A13	5	110712615	110712615	G	A	127	0.26	*CAMK4*	NM_001744	Missense	p.V121I	-0.79	Neutral	0	Damaging	0.985	probably damaging
A14	7	142643320	142643320	C	A	43	0.40	*KEL*	NM_000420	Missense	p.A430S	-0.68	Neutral	0.47	Tolerated	0.27	benign
A14	X	53230850	53230850	A	ATGTCC	27	0.33	*KDM5C*	NM_004187	Frame_Shift_Ins	p.I648fs	NA	NA	NA	NA	NA	NA

A14	13	25670802	25670802	A	T	93	0.09	*PABPC3*	NM_030979	Nonsense	p.K156_	NA	NA	0.47	Tolerated	NA	NA
A14	X	53239864	53239864	A	C	32	0.25	*KDM5C*	NM_004187	Missense	p.L526R	-5.31	Deleterious	0	Damaging	1	probably damaging
A14	20	1559047	1559047	G	A	61	0.31	*SIRPB1*	NM_006065	Missense	p.R124W	-4.62	Deleterious	0	Damaging	0.319	benign
A14	12	6936278	6936278	G	A	39	0.13	*GPR162*	NM_019858	Missense	p.R559H	-0.5	Neutral	0.02	Damaging	0.997	probably damaging
A14	7	143657713	143657713	C	T	43	0.49	*OR2F1*	NM_012369	Missense	p.S217F	-5.96	Deleterious	0	Damaging	1	probably damaging
A14	15	54592571	54592571	C	T	50	0.32	*UNC13C*	NM_001080534	Missense	p.T1423M	-5.84	Deleterious	0.01	Damaging	1	probably damaging
A14	11	62752098	62752098	G	A	25	0.36	*SLC22A6*	NM_004790	Missense	p.T22I	-1.27	Neutral	0.68	Tolerated	0.079	benign
A14	3	124951284	124951285	TG	TTCT	60	0.15	*ZNF148*	NM_021964	Frame_Shift_Ins	p.T762fs	NA	NA	NA	NA	NA	NA
A14	7	98457900	98457900	A	C	50	0.30	*TMEM130*	NM_001134450	Nonsense	p.Y151_	NA	NA	0.89	Tolerated	NA	NA
A14	13	28592620	28592620	T	C	43	0.19	*FLT3*	NM_004119	Missense	p.Y842C	-8.17	Deleterious	0	Damaging	1	probably damaging
A15	11	59811020	59811020	C	T	59	0.25	*PLAC1L*	NM_173801	Missense	p.A48V	-1.04	Neutral	0.17	Tolerated	0.995	probably damaging
A15	1	66384437	66384437	A	G	36	0.81	*PDE4B*	NM_001037341	Missense	p.E67G	-0.8	Neutral	0.45	Tolerated	0	benign
A15	22	29192146	29192154	TCAGCAGAC	T	54	0.44	*XBP1*	NM_001079539	Frame_Shift_Del	p.G160fs	NA	NA	NA	NA	NA	NA
A15	6	13182858	13182858	A	G	67	0.37	*PHACTR1*	NM_001242648	Missense	p.M202V	-0.55	Neutral	0.3	Tolerated	0.021	benign
A15	15	72492875	72492875	G	GT	23	0.48	*PKM*	NM_182471	Frame_Shift_Ins	p.P477fs	NA	NA	NA	NA	NA	NA
A15	6	142691792	142691792	C	T	214	0.33	*GPR126*	NM_198569	Nonsense	p.R311_	NA	NA	1	Tolerated	NA	NA
A15	4	90169365	90169365	G	A	34	0.21	*GPRIN3*	NM_198281	Missense	p.R633C	-4.87	Deleterious	0	Damaging	1	probably damaging
A15	1	236702306	236702306	C	T	54	0.13	*LGALS8*	NM_201545	Missense	p.R88W	-0.99	Neutral	0.05	Damaging	0.008	benign
A15	5	13762917	13762917	C	T	39	0.46	*DNAH5*	NM_001369	Missense	p.V3399I	-1	Neutral	0.05	Damaging	0.991	probably damaging
A16	X	41056715	41056715	G	GA	15	0.93	*USP9X*	NM_001039590	Frame_Shift_Ins	p.E1444fs	NA	NA	NA	NA	NA	NA
A16	6	5404817	5404823	GAACAAA	GTCCTGAGG	39	0.51	*FARS2*	NM_006567	Frame_Shift_Ins	p.E219fs	NA	NA	NA	NA	NA	NA
A16	11	35006228	35006228	A	T	89	0.54	*PDHX*	NM_003477	Nonsense	p.K379_	NA	NA	1	Tolerated	NA	NA
A16	1	152586351	152586351	C	T	13	1.00	*LCE3B*	NM_178433	Missense	p.P22L	-8.89	Deleterious	0.04	Damaging	0.998	probably damaging
A16	3	196792172	196792172	T	G	102	0.49	*DLG1*	NM_004087	Missense	p.Q816P	-4.1	Deleterious	0.05	Damaging	0.998	probably damaging
A16	11	92531151	92531151	C	T	135	0.44	*FAT3*	NM_001008781	Missense	p.R1658C	-3.2	Deleterious	0.03	Damaging	1	probably damaging
A16	10	95553086	95553086	C	T	77	0.52	*LGI1*	NM_005097	Missense	p.R273W	-6.65	Deleterious	0	Damaging	1	probably damaging
A16	3	129247721	129247721	G	A	26	0.58	*RHO*	NM_000539	Missense	p.V49M	-0.52	Neutral	0.05	Damaging	0.013	benign
A16	2	10140749	10140749	G	T	95	0.48	*GRHL1*	NM_198182	Missense	p.V591L	-1.19	Neutral	0.1	Tolerated	0.317	benign
A17	3	47088004	47088005	TG	TCGC	45	0.40	*SETD2*	NM_014159	Frame_Shift_Ins	p.A2357fs	NA	NA	NA	NA	NA	NA
A17	13	28608275	28608277	AAA	CAT	149	0.50	*FLT3*	NM_004119	Missense	p.D593_F594delinsEC	-6.36	Deleterious	NA	NA	NA	NA
A17	10	17026259	17026259	A	C	64	0.47	*CUBN*	NM_001081	Missense	p.F1457C	-3.14	Deleterious	0.2	Tolerated	0.999	probably damaging

A17	7	116422068	116422069	CT	C	119	0.46	*MET*	NM_000245	Frame_Shift_Del	p.G1183fs	NA	NA	NA	NA	NA	NA
A17	1	100584613	100584613	A	T	84	0.50	*SASS6*	NM_194292	Missense	p.H210Q	-4.58	Deleterious	0.25	Tolerated	1	probably damaging
A17	22	29192127	29192127	T	TAGTCTTG	43	0.47	*XBP1*	NM_005080	Frame_Shift_Ins	p.L169fs	NA	NA	NA	NA	NA	NA
A17	19	39899200	39899200	C	G	39	0.41	*ZFP36*	NM_003407	Missense	p.P287R	-0.6	Neutral	0.38	Tolerated	0.995	probably damaging
A17	2	3743321	3743321	C	T	134	0.13	*ALLC*	NM_018436	Nonsense	p.R176_	NA	NA	1	Tolerated	NA	NA
A17	15	42003170	42003171	AG	A	213	0.30	*MGA*	NM_001080541	Frame_Shift_Del	p.R903fs	NA	NA	NA	NA	NA	NA
A17	18	43311054	43311054	G	A	42	0.57	*SLC14A1*	NM_001128588	Missense	p.V132I	0.76	Neutral	0.27	Tolerated	0	benign
A17	9	96051555	96051555	G	A	19	0.47	*WNK2*	NM_006648	Missense	p.V1507I	-0.18	Neutral	0.27	Tolerated	0.429	benign
A17	3	101390039	101390039	T	C	211	0.46	*ZBTB11*	NM_014415	Missense	p.Y238C	-1.89	Neutral	0	Damaging	1	probably damaging
A18	22	50886872	50886872	C	G	58	0.48	*SBF1*	NM_002972	Missense	p.G1718A	-0.64	Neutral	0.73	Tolerated	0.05	benign
A18	1	11015120	11015120	T	C	23	0.35	*C1orf127*	NM_001170754	Missense	p.N301S	-2.29	Neutral	0.12	Tolerated	0.025	benign
A18	5	135587360	135587360	G	A	40	0.33	*TRPC7*	NM_020389	Missense	p.P519L	-2.54	Deleterious	0.64	Tolerated	0.057	benign
A18	9	79635295	79635295	C	T	10	0.40	*FOXB2*	NM_001013735	Missense	p.S242F	-0.85	Neutral	0.01	Damaging	0.019	benign
A18	3	49161296	49161296	G	A	65	0.55	*LAMB2*	NM_002292	Missense	p.T1221M	-2.7	Deleterious	0.11	Tolerated	0.987	probably damaging
A18	4	120240238	120240240	TAC	AAG	54	0.43	*FABP2*	NM_000134	Missense	p.V119L	-0.8	Neutral	NA	NA	NA	NA
A19	5	162932712	162932712	A	C	21	0.33	*MAT2B*	NM_013283	Missense	p.E7A	-0.37	Neutral	0.32	Tolerated	0.705	possibly damaging
A19	7	44189566	44189567	AC	A	53	0.32	*GCK*	NM_000162	Splice Site	p.G193sp	NA	NA	NA	NA	NA	NA
A19	12	49433301	49433302	GC	G	27	0.37	*MLL2*	NM_003482	Frame_Shift_Del	p.G2715fs	NA	NA	NA	NA	NA	NA
A19	8	25226164	25226164	C	T	76	0.09	*DOCK5*	NM_024940	Missense	p.R1121W	-6.98	Deleterious	0	Damaging	1	probably damaging
A19	10	124390771	124390771	G	A	85	0.35	*DMBT1*	NM_007329	Missense	p.R1978H	0.79	Neutral	0.23	Tolerated	0.997	probably damaging
A19	15	41750044	41750044	G	C	43	0.28	*RTF1*	NM_015138	Missense	p.R211P	-6.77	Deleterious	0	Damaging	0.979	probably damaging
A19	17	76816058	76816058	C	CA	92	0.32	*USP36*	NM_025090	Frame_Shift_Ins	p.V289fs	NA	NA	NA	NA	NA	NA
A20	22	17601413	17601413	G	GC	21	0.29	*CECR6*	NM_031890	Frame_Shift_Ins	p.A202fs	NA	NA	NA	NA	NA	NA
A20	19	1461989	1461989	G	A	22	0.68	*APC2*	NM_005883	Missense	p.A556T	-3.76	Deleterious	0	Damaging	1	probably damaging
A20	12	102190484	102190484	G	T	43	0.37	*GNPTAB*	NM_024312	Missense	p.D58E	-2.78	Deleterious	0	Damaging	1	probably damaging
A20	5	121488088	121488088	G	T	48	0.35	*ZNF474*	NM_207317	Nonsense	p.E135_	NA	NA	0.74	Tolerated	NA	NA
A20	7	148511200	148511200	T	C	25	0.28	*EZH2*	NM_004456	Missense	p.K568E	-3.51	Deleterious	0.01	Damaging	0.999	probably damaging
A20	13	111158795	111158795	C	T	22	0.27	*COL4A2*	NM_001846	Missense	p.P1479L	-7.12	Deleterious	0.07	Tolerated	0.999	probably damaging
A20	2	165378603	165378603	G	A	17	0.35	*GRB14*	NM_004490	Missense	p.P235S	-7.13	Deleterious	0	Damaging	1	probably damaging
A20	20	31021535	31021535	C	T	79	0.09	*ASXL1*	NM_015338	Nonsense	p.Q512_	NA	NA	0.32	Tolerated	NA	NA
A20	10	79569450	79569450	C	T	36	0.31	*DLG5*	NM_004747	Missense	p.R1501H	-4.36	Deleterious	0	Damaging	1	probably damaging
A20	18	44262028	44262028	C	T	13	0.62	*ST8SIA5*	NM_013305	Splice Site	p.R190sp	NA	NA	NA	NA	NA	NA

A20	13	42742581	42742581	G	A	32	0.22	*DGKH*	NM_178009	Missense	p.R375K	-2.3	Neutral	0.09	Tolerated	0.992	probably damaging
A20	8	23290530	23290530	C	T	46	0.35	*ENTPD4*	NM_004901	Missense	p.R587H	-2.4	Neutral	0.01	Damaging	0.934	possibly damaging
A20	12	112926884	112926884	T	G	31	0.39	*PTPN11*	NM_002834	Missense	p.S502A	-2.76	Deleterious	0.06	Tolerated	0.726	possibly damaging
A20	6	147684834	147684834	C	A	44	0.30	*STXBP5*	NM_001127715	Missense	p.T970N	-3.44	Deleterious	0	Damaging	1	probably damaging
A20	X	100749138	100749138	G	A	24	0.79	*ARMCX4*	NM_001256155	Nonsense	p.W1854_	NA	NA	NA	NA	NA	NA
A20	3	151107771	151107771	A	G	93	0.37	*MED12L*	NM_053002	Missense	p.Y1784C	-2.21	Neutral	0.01	Damaging	0.999	probably damaging
A21	11	88911158	88911158	T	C	52	0.56	*TYR*	NM_000372	Missense	p.F13L	0.59	Neutral	NA	NA	0.001	benign
A21	1	3413600	3413600	C	T	69	0.39	*MEGF6*	NM_001409	Missense	p.G1189R	-7.18	Deleterious	0.12	Tolerated	0.987	probably damaging
A21	11	3249551	3249551	C	T	49	0.47	*MRGPRE*	NM_001039165	Missense	p.G160D	-0.64	Neutral	0.18	Tolerated	0.997	probably damaging
A21	1	74834736	74834736	G	T	69	0.42	*FPGT-TNNI3K*	NM_001112808	Missense	p.G552V	-0.21	Neutral	0.29	Tolerated	0.763	possibly damaging
A21	1	1572454	1572454	C	T	32	0.31	*CDK11B*	NM_033486	Missense	p.G559S	NA	NA	NA	NA	NA	NA
A21	16	31144629	31144629	T	G	82	0.43	*PRSS8*	NM_002773	Missense	p.I62L	-0.04	Neutral	1	Tolerated	0.009	benign
A21	14	53100374	53100374	G	A	149	0.44	*GPR137C*	NM_001099652	Splice Site	p.L331sp	NA	NA	NA	NA	NA	NA
A21	5	106717051	106717051	G	C	59	0.46	*EFNA5*	NM_001962	Missense	p.P198A	-3.44	Deleterious	0.82	Tolerated	0.134	benign
A21	11	64534542	64534542	G	GCC	108	0.41	*SF1*	NM_004630	Frame_Shift_Ins	p.P471fs	NA	NA	NA	NA	NA	NA
A21	6	39073250	39073250	C	A	85	0.48	*SAYSD1*	NM_018322	Missense	p.Q170H	-4.87	Deleterious	0	Damaging	1	probably damaging
A21	X	148055076	148055076	C	T	54	0.96	*AFF2*	NM_002025	Missense	p.R1115C	-5.72	Deleterious	0.01	Damaging	1	probably damaging
A21	18	7050796	7050796	C	T	79	0.38	*LAMA1*	NM_005559	Missense	p.R162H	-3.39	Deleterious	0.58	Tolerated	0.828	possibly damaging
A21	5	121759339	121759339	C	T	80	0.54	*SNCAIP*	NM_005460	Missense	p.R303W	4.35	Neutral	NA	NA	0.003	benign
A21	12	32134559	32134559	A	G	142	0.46	*KIAA1551*	NM_018169	Missense	p.S224G	-1.83	Neutral	NA	NA	0.007	benign
A21	3	160142671	160142671	C	T	31	0.45	*SMC4*	NM_001002800	Missense	p.S781L	-2.97	Deleterious	0.23	Tolerated	0.348	benign
A21	1	115284260	115284260	G	C	64	0.28	*CSDE1*	NM_001242891	Nonsense	p.S9_	NA	NA	0	Damaging	NA	NA
A21	15	64496703	64496703	T	TG	118	0.42	*CSNK1G1*	NM_022048	Frame_Shift_Ins	p.T312fs	NA	NA	NA	NA	NA	NA
A21	2	179620975	179620975	G	A	102	0.55	*TTN*	NM_001267550	Missense	p.T3743M	-1.29	Neutral	0	Damaging	0.01	benign
A21	12	132510265	132510265	G	A	93	0.46	*EP400*	NM_015409	Missense	p.V1644M	-0.29	Neutral	0.24	Tolerated	0.535	possibly damaging
A22	1	248224920	248224920	T	C	50	0.46	*OR2L3*	NM_001004687	Missense	p._313Q	NA	NA	NA	NA	NA	NA
A22	1	27238557	27238557	C	T	24	0.33	*NR0B2*	NM_021969	Missense	p.A185T	-0.42	Neutral	0.85	Tolerated	0.008	benign
A22	4	155410534	155410534	G	T	51	0.41	*DCHS2*	NM_001142552	Missense	p.D658E	-3.13	Deleterious	0	Damaging	1	probably damaging
A22	4	41749529	41749529	T	C	51	0.65	*PHOX2B*	NM_003924	Missense	p.H89R	-2.97	Deleterious	0.5	Tolerated	0.988	probably damaging
A22	15	77317659	77317659	C	T	38	0.39	*PSTPIP1*	NM_003978	Nonsense	p.Q83_	NA	NA	0.01	Damaging	NA	NA
A22	5	178699963	178699963	G	A	36	0.44	*ADAMTS2*	NM_014244	Missense	p.R213C	-5.63	Deleterious	0	Damaging	0.999	probably damaging
A22	17	79918703	79918703	C	T	12	0.33	*NOTUM*	NM_178493	Missense	p.R28H	-0.04	Neutral	0.39	Tolerated	0.989	probably damaging

A23	17	40362461	40362461	C	T	100	0.52	*STAT5B*	NM_012448	Missense	p.E579K	0.14	Neutral	0.75	Tolerated	0.422	benign
A23	20	31022439	31022439	G	GGA	54	0.17	*ASXL1*	NM_015338	Frame_Shift_Ins	p.G642fs	NA	NA	NA	NA	NA	NA
A23	7	50607642	50607642	C	T	43	0.44	*DDC*	NM_000790	Missense	p.G96R	-2.78	Deleterious	0	Damaging	1	probably damaging
A23	3	183753791	183753791	C	T	56	0.52	*HTR3D*	NM_001163646	Nonsense	p.Q95_	NA	NA	0.24	Tolerated	NA	NA
A23	14	90650562	90650562	C	T	101	0.43	*KCNK13*	NM_022054	Missense	p.R148C	-7.18	Deleterious	0.02	Damaging	1	probably damaging
A23	5	112321534	112321534	G	T	92	0.57	*DCP2*	NM_152624	Missense	p.R19L	-6.4	Deleterious	0	Damaging	1	probably damaging
A23	12	81568670	81568670	G	A	36	0.14	*ACSS3*	NM_024560	Missense	p.R401H	-3.45	Deleterious	0.01	Damaging	1	probably damaging
A23	2	172950440	172950440	G	A	105	0.46	*DLX1*	NM_178120	Missense	p.S12N	-0.97	Neutral	0.03	Damaging	0.936	possibly damaging
A23	19	9072604	9072604	C	A	131	0.10	*MUC16*	NM_024690	Missense	p.V4948L	-0.47	Neutral	0	Damaging	0.001	benign
A23	12	124235681	124235681	G	A	57	0.44	*ATP6V0A2*	NM_012463	Missense	p.V654I	-0.29	Neutral	0.35	Tolerated	0	benign
A23	20	31023625	31023625	G	A	86	0.09	*ASXL1*	NM_015338	Nonsense	p.W1037_	NA	NA	0.46	Tolerated	NA	NA
A24	7	100844060	100844060	C	T	48	0.17	*MOGAT3*	NM_178176	Missense	p.A26T	-0.5	Neutral	0.08	Tolerated	0.086	benign
A24	X	41204467	41204467	G	A	121	0.09	*DDX3X*	NM_001356	Missense	p.D354N	-4.74	Deleterious	0	Damaging	0.999	probably damaging
A24	3	47142972	47142972	A	T	169	0.39	*SETD2*	NM_014159	Missense	p.F1664Y	-2.84	Deleterious	0.04	Damaging	1	probably damaging
A24	1	115258744	115258744	C	T	118	0.34	*NRAS*	NM_002524	Missense	p.G13D	-5.48	Deleterious	0.03	Damaging	0.434	benign
A24	17	46627965	46627966	TC	T	33	0.39	*HOXB3*	NM_002146	Frame_Shift_Del	p.G342fs	NA	NA	NA	NA	NA	NA
A24	3	9798917	9798917	A	G	112	0.39	*OGG1*	NM_016820	Missense	p.M380V	0.03	Neutral	0.72	Tolerated	0.048	benign
A24	14	79432666	79432666	G	T	125	0.40	*NRXN3*	NM_004796	Missense	p.Q525H	-4.01	Deleterious	NA	NA	1	probably damaging
A24	9	119188162	119188162	G	A	71	0.31	*ASTN2*	NM_014010	Nonsense	p.R1279_	NA	NA	1	Tolerated	NA	NA
A24	1	13109020	13109020	G	A	16	0.75	*PRAMEF5*	NM_001013407	Missense	p.R417W	-3.94	Deleterious	0.03	Damaging	1	probably damaging
A24	3	47155487	47155490	GAGA	G	138	0.09	*SETD2*	NM_014159	In_Frame_Del	p.S1531del	-11.45	Deleterious	NA	NA	NA	NA
A24	3	47125756	47125756	A	AG	122	0.39	*SETD2*	NM_014159	Frame_Shift_Ins	p.S1838fs	NA	NA	NA	NA	NA	NA
A24	5	14492884	14492884	C	A	47	0.28	*TRIO*	NM_007118	Missense	p.T2614N	-1.66	Neutral	0.18	Tolerated	0.997	probably damaging
A24	16	19195350	19195350	G	A	112	0.39	*SYT17*	NM_016524	Missense	p.V278M	-2.42	Neutral	0	Damaging	0.851	possibly damaging
A24	12	68708870	68708870	C	G	148	0.40	*MDM1*	NM_017440	Missense	p.V453L	-0.38	Neutral	NA	NA	0	benign
A25	10	64973343	64973343	T	C	113	0.50	*JMJD1C*	NM_032776	Missense	p.I862V	-0.34	Neutral	0.09	Tolerated	0.995	probably damaging
A25	13	28608329	28608329	A	G	115	0.47	*FLT3*	NM_004119	Missense	p.L576P	-3.81	Deleterious	0	Damaging	0.988	probably damaging
A25	16	3293541	3293541	A	G	150	0.42	*MEFV*	NM_000243	Missense	p.L649P	-2.97	Deleterious	0.14	Tolerated	0.977	probably damaging
A25	19	608020	608020	G	C	49	0.45	*HCN2*	NM_001194	Missense	p.M425I	-3.83	Deleterious	0	Damaging	0.774	possibly damaging
A25	16	57416744	57416744	C	T	64	0.44	*CX3CL1*	NM_002996	Missense	p.P332S	-3.1	Deleterious	0	Damaging	0.592	possibly damaging
A25	3	64085424	64085424	T	G	212	0.11	*PRICKLE2*	NM_198859	Missense	p.Q613P	0.1	Neutral	0.27	Tolerated	0.001	benign
A25	10	96466680	96466680	G	T	147	0.57	*CYP2C18*	NM_000772	Missense	p.R261L	-5.57	Deleterious	0	Damaging	0.978	probably damaging
A25	19	30054821	30054821	C	T	110	0.45	*VSTM2B*	NM_001146339	Missense	p.R280C	-0.51	Neutral	0.06	Tolerated	0.733	possibly damaging

A25	3	51297638	51297638	C	T	126	0.50	*DOCK3*	NM_004947	Nonsense	p.R746_	NA	NA	1	Tolerated	NA	NA
A25	1	62516720	62516720	G	T	63	0.33	*INADL*	NM_176877	Missense	p.S1372I	-0.82	Neutral	0	Damaging	0.911	possibly damaging
A25	5	131546066	131546066	G	A	133	0.51	*P4HA2*	NM_004199	Missense	p.S207L	-0.74	Neutral	0.3	Tolerated	0	benign
A25	12	98926879	98926879	T	A	150	0.46	*TMPO*	NM_003276	Missense	p.S282T	0.38	Neutral	0.48	Tolerated	0.003	benign
A25	11	62678427	62678427	G	A	92	0.49	*CHRM1*	NM_000738	Missense	p.S49F	-5.35	Deleterious	0	Damaging	1	probably damaging
A25	19	48220126	48220126	C	T	40	0.55	*EHD2*	NM_014601	Missense	p.S86F	0.75	Neutral	0.15	Tolerated	0.908	possibly damaging
A26	15	89400204	89400204	C	T	46	0.15	*ACAN*	NM_013227	Missense	p.A1463V	-1.11	Neutral	0.04	Damaging	0.996	probably damaging
A26	15	79614332	79614332	T	G	58	0.17	*TMED3*	NM_007364	Missense	p.C144G	-6.34	Deleterious	0	Damaging	0.486	possibly damaging
A26	7	134719055	134719055	G	A	107	0.41	*AGBL3*	NM_178563	Missense	p.G238D	-6.87	Deleterious	0	Damaging	1	probably damaging
A26	22	29192125	29192125	C	CTGGA	38	0.18	*XBP1*	NM_005080	Frame_Shift_Ins	p.L169fs	NA	NA	NA	NA	NA	NA
A27	3	128516848	128516848	C	T	74	0.19	*RAB7A*	NM_004637	Missense	p.A39V	-3.46	Deleterious	0.01	Damaging	0.997	probably damaging
A27	6	56336906	56336906	G	A	147	0.48	*DST*	NM_001144769	Missense	p.A5251V	-3.31	Deleterious	0.09	Tolerated	1	probably damaging
A27	12	112888199	112888199	C	T	90	0.47	*PTPN11*	NM_002834	Missense	p.A72V	-3.45	Deleterious	0	Damaging	0.994	probably damaging
A27	18	74962746	74962746	A	G	7	0.57	*GALR1*	NM_001480	Missense	p.D81G	-6.8	Deleterious	0	Damaging	1	probably damaging
A27	X	101971349	101971349	G	A	110	0.53	*ARMCX5-GPRASP2*	NM_001199818	Missense	p.E518K	0.49	Neutral	0.94	Tolerated	0.085	benign
A27	1	115258748	115258748	C	T	30	0.30	*NRAS*	NM_002524	Missense	p.G12S	-4.44	Deleterious	0.04	Damaging	0.329	benign
A27	4	77192721	77192721	G	A	80	0.40	*FAM47E*	NM_001136570	Missense	p.G224R	-5.21	Deleterious	NA	NA	1	probably damaging
A27	2	198266821	198266821	A	C	73	0.14	*SF3B1*	NM_012433	Missense	p.I704S	-5.65	Deleterious	0.02	Damaging	0.991	probably damaging
A27	19	42192037	42192037	G	T	17	0.47	*CEACAM7*	NM_006890	Missense	p.L20I	-1.66	Neutral	0	Damaging	0.999	probably damaging
A27	9	37020673	37020673	G	A	55	0.15	*PAX5*	NM_016734	Missense	p.L58F	-3.31	Deleterious	0	Damaging	1	probably damaging
A27	9	37020758	37020758	A	C	59	0.19	*PAX5*	NM_016734	Missense	p.N29K	-4.76	Deleterious	0	Damaging	1	probably damaging
A27	3	164907867	164907867	G	A	87	0.52	*SLITRK3*	NM_014926	Missense	p.P251L	-4.01	Deleterious	0.02	Damaging	1	probably damaging
A27	2	25967303	25967303	G	A	74	0.43	*ASXL2*	NM_018263	Nonsense	p.Q635_	NA	NA	0.17	Tolerated	NA	NA
A27	2	179472662	179472662	G	A	154	0.11	*TTN*	NM_001267550	Missense	p.R17618C	-5.96	Deleterious	0	Damaging	1	probably damaging
A27	1	186084058	186084058	G	A	118	0.19	*HMCN1*	NM_031935	Missense	p.R3795Q	-0.78	Neutral	0.62	Tolerated	0.999	probably damaging
A27	4	153247366	153247366	C	T	71	0.14	*FBXW7*	NM_033632	Missense	p.R479Q	-3.97	Deleterious	0.05	Damaging	1	probably damaging
A27	7	121651640	121651640	C	T	82	0.48	*PTPRZ1*	NM_002851	Missense	p.S847L	-0.68	Neutral	0.02	Damaging	0.22	benign
A27	9	138376741	138376741	G	A	20	0.45	*PPP1R26*	NM_014811	Missense	p.V129M	-2.83	Deleterious	0	Damaging	1	probably damaging
A27	10	21120227	21120227	G	T	53	0.43	*NEBL*	NM_006393	Nonsense	p.Y523_	NA	NA	1	Tolerated	NA	NA
A28	22	36863879	36863879	T	A	42	0.43	*TXN2*	NM_012473	Missense	p.E158V	-4.49	Deleterious	0.09	Tolerated	0.18	benign
A28	16	3080732	3080732	C	T	115	0.58	*CCDC64B*	NM_001103175	Missense	p.E194K	-1.81	Neutral	0.2	Tolerated	0.72	possibly damaging
A28	4	13543663	13543663	G	A	85	0.48	*NKX3-2*	NM_001189	Missense	p.P319L	-6.13	Deleterious	0	Damaging	1	probably damaging

A28	7	141643732	141643732	G	A	126	0.38	*CLEC5A*	NM_013252	Missense	p.P58S	-1.16	Neutral	0.99	Tolerated	0.048	benign
A28	22	46125421	46125421	A	T	110	0.44	*ATXN10*	NM_013236	Missense	p.Q282L	-1.67	Neutral	0.37	Tolerated	0.358	benign
A28	4	106164914	106164914	G	A	91	0.47	*TET2*	NM_001127208	Missense	p.R1261H	-4.6	Deleterious	0	Damaging	1	probably damaging
A28	8	29194671	29194671	G	A	93	0.47	*DUSP4*	NM_001394	Missense	p.R353W	-2.04	Neutral	0.04	Damaging	1	probably damaging
A28	6	38854763	38854763	C	T	73	0.10	*DNAH8*	NM_001206927	Missense	p.S2819L	-5.89	Deleterious	0.01	Damaging	1	probably damaging
A28	17	41956732	41956732	C	T	142	0.39	*MPP2*	NM_005374	Missense	p.V465M	-2.62	Deleterious	0	Damaging	1	probably damaging
A28	9	140245587	140245587	A	G	63	0.41	*EXD3*	NM_017820	Missense	p.V466A	1.83	Neutral	0.77	Tolerated	0	benign
A29	22	50961531	50961531	C	T	17	0.29	*NCAPH2*	NM_001185011	Missense	p.A539V	-1.98	Neutral	0.22	Tolerated	0.992	probably damaging
A29	11	65314034	65314034	G	T	5	0.60	*LTBP3*	NM_001130144	Missense	p.D744E	-3.82	Deleterious	0.07	Tolerated	1	probably damaging
A29	2	212812155	212812155	C	A	59	0.39	*ERBB4*	NM_005235	Nonsense	p.E141_	NA	NA	NA	NA	NA	NA
A29	2	201334736	201334736	G	A	122	0.39	*SPATS2L*	NM_015535	Missense	p.E353K	-2.07	Neutral	0.01	Damaging	0.999	probably damaging
A29	1	1737942	1737942	A	T	28	0.43	*GNB1*	NM_002074	Missense	p.I80N	-5.87	Deleterious	0.04	Damaging	1	probably damaging
A29	1	109778659	109778659	A	T	39	0.41	*SARS*	NM_006513	Missense	p.M344L	-2.97	Deleterious	0.16	Tolerated	1	probably damaging
A29	1	155449952	155449952	C	A	120	0.30	*ASH1L*	NM_018489	Missense	p.M903I	-1.03	Neutral	0.08	Tolerated	0.4	benign
A29	13	111532374	111532375	CG	C	65	0.28	*ANKRD10*	NM_017664	Frame_Shift_Del	p.P291fs	NA	NA	NA	NA	NA	NA
A29	8	77766148	77766148	C	G	153	0.35	*ZFHX4*	NM_024721	Missense	p.Q2331E	-2.69	Deleterious	0.01	Damaging	0.979	probably damaging
A29	19	48832705	48832705	G	T	40	0.43	*EMP3*	NM_001425	Missense	p.R93L	-3.94	Deleterious	0.01	Damaging	0.979	probably damaging
A29	1	162731149	162731149	C	T	34	0.32	*DDR2*	NM_001014796	Missense	p.T335M	-4.19	Deleterious	0.01	Damaging	0.996	probably damaging
A30	11	118625578	118625578	C	T	67	0.27	*DDX6*	NM_001257191	Missense	p.G432D	-6.73	Deleterious	0	Damaging	0.982	probably damaging
A30	3	97167425	97167426	TG	CT	82	0.46	*EPHA6*	NM_001080448	Missense	p.L582P	-0.85	Neutral	NA	NA	NA	NA
A30	11	16071445	16071445	G	C	55	0.47	*SOX6*	NM_001145819	Missense	p.P444A	-4.79	Deleterious	0.03	Damaging	0.942	possibly damaging
A30	7	131982906	131982906	G	A	90	0.23	*PLXNA4*	NM_020911	Missense	p.R483W	-5.94	Deleterious	0.07	Tolerated	1	probably damaging
A30	8	131916098	131916098	G	A	42	0.29	*ADCY8*	NM_001115	Missense	p.R611W	-3.05	Deleterious	0.01	Damaging	0.978	probably damaging
A30	17	80373281	80373281	C	G	120	0.71	*OGFOD3*	NM_175902	Missense	p.R99S	-1.91	Neutral	0.1	Tolerated	0.049	benign
A30	1	21938542	21938542	C	T	80	0.15	*RAP1GAP*	NM_001145658	Missense	p.V261I	-0.86	Neutral	0.05	Damaging	0.544	possibly damaging
A30	3	3186303	3186303	T	A	61	0.48	*TRNT1*	NM_182916	Missense	p.Y173N	-6.76	Deleterious	0.04	Damaging	0.978	probably damaging
A31	7	73657513	73657513	G	GCACCCTCTC	45	0.09	*RFC2*	NM_181471	In_Frame_Ins	p.166_167insRGC	-11.9	Deleterious	NA	NA	NA	NA
A31	X	123697623	123697623	C	T	36	0.83	*TENM1*	NM_014253	Splice Site	p.A755sp	NA	NA	NA	NA	NA	NA
A31	6	27776304	27776304	G	A	41	0.34	*HIST1H2AI*	NM_003509	Missense	p.G106D	-5.63	Deleterious	0	Damaging	NA	NA
A31	10	91178020	91178020	G	C	76	0.45	*IFIT5*	NM_012420	Missense	p.S355T	-0.79	Neutral	0.16	Tolerated	0.007	benign
A31	15	87097719	87097719	G	A	22	0.59	*AGBL1*	NM_152336	Missense	p.S936N	-2.51	Deleterious	0	Damaging	1	probably damaging
A32	18	33848646	33848647	TA	T	85	0.32	*MOCOS*	NM_017947	Frame_Shift_Del	p._889fs	NA	NA	NA	NA	NA	NA

A32	21	28216912	28216912	G	A	106	0.36	*ADAMTS1*	NM_006988	Missense	p.A121V	-1.76	Neutral	0.27	Tolerated	0.1	benign
A32	11	133779112	133779112	G	T	103	0.31	*IGSF9B*	NM_001277285	Missense	p.A1389D	-3.44	Deleterious	NA	NA	NA	NA
A32	2	28631732	28631732	C	T	73	0.33	*FOSL2*	NM_005253	Missense	p.A154V	-2.93	Deleterious	NA	NA	0.999	probably damaging
A32	22	23523893	23523893	C	G	145	0.35	*BCR*	NM_004327	Missense	p.A249G	-0.9	Neutral	0.35	Tolerated	0.002	benign
A32	14	73572645	73572657	GGAGCGAGAGAGA	G	73	0.37	*RBM25*	NM_021239	In_Frame_Del	p.ERER420del	-2.28	Neutral	NA	NA	NA	NA
A32	20	9546721	9546721	G	A	116	0.39	*PAK7*	NM_020341	Missense	p.A434V	-3.91	Deleterious	NA	NA	0.999	probably damaging
A32	15	77906423	77906423	G	A	98	0.36	*LINGO1*	NM_032808	Missense	p.A609V	-0.88	Neutral	0.16	Tolerated	0.001	benign
A32	18	60985722	60985722	C	T	70	0.31	*BCL2*	NM_000633	Missense	p.A60T	-0.54	Neutral	0.95	Tolerated	0.442	benign
A32	19	43430107	43430107	C	A	114	0.30	*PSG7*	NM_002783	Missense	p.C354F	NA	NA	NA	NA	NA	NA
A32	14	69259602	69259604	GCA	TCT	94	0.29	*ZFP36L1*	NM_001244701	Missense	p.C87R	-2.49	Neutral	NA	NA	NA	NA
A32	X	118716572	118716572	G	A	96	0.13	*UBE2A*	NM_003336	Missense	p.C88Y	-10.76	Deleterious	0	Damaging	1	probably damaging
A32	1	235973226	235973226	C	T	158	0.32	*LYST*	NM_000081	Missense	p.D298N	-1.74	Neutral	0.2	Tolerated	0.956	possibly damaging
A32	12	57496661	57496661	T	C	126	0.19	*STAT6*	NM_001178079	Missense	p.D419G	-4.83	Deleterious	0	Damaging	1	probably damaging
A32	19	50210851	50210851	G	A	126	0.37	*CPT1C*	NM_152359	Missense	p.D474N	-4.54	Deleterious	0	Damaging	1	probably damaging
A32	20	25249801	25249801	G	A	105	0.25	*PYGB*	NM_002862	Missense	p.E128K	-2.96	Deleterious	0.24	Tolerated	0.433	benign
A32	9	130742357	130742357	C	G	112	0.29	*FAM102A*	NM_001035254	Missense	p.E20D	-0.88	Neutral	0.59	Tolerated	0.997	probably damaging
A32	3	180675693	180675693	G	A	36	0.39	*FXR1*	NM_005087	Missense	p.E323K	-3.17	Deleterious	0	Damaging	0.998	probably damaging
A32	16	85954865	85954866	GA	G	146	0.29	*IRF8*	NM_002163	Frame_Shift_Del	p.E420fs	NA	NA	NA	NA	NA	NA
A32	19	33793152	33793152	C	T	70	0.44	*CEBPA*	NM_004364	Missense	p.E57K	-2.08	Neutral	0.01	Damaging	0.995	probably damaging
A32	7	12683931	12683931	G	A	92	0.46	*SCIN*	NM_001112706	Missense	p.E584K	-0.42	Neutral	0.34	Tolerated	0	benign
A32	3	175345130	175345130	G	T	12	0.25	*NAALADL2*	NM_207015	Nonsense	p.E618_	NA	NA	1	Tolerated	NA	NA
A32	1	216373452	216373452	A	C	67	0.28	*USH2A*	NM_206933	Missense	p.F1110V	-3.86	Deleterious	0.09	Tolerated	0.945	possibly damaging
A32	1	93586164	93586164	T	A	26	0.58	*MTF2*	NM_007358	Missense	p.F286I	-4.45	Deleterious	0	Damaging	0.999	probably damaging
A32	6	37138549	37138549	G	A	117	0.33	*PIM1*	NM_001243186	Missense	p.G119D	-1.3	Neutral	NA	NA	0.791	possibly damaging
A32	6	38548066	38548066	C	T	83	0.29	*BTBD9*	NM_052893	Missense	p.G321D	-5.72	Deleterious	0.03	Damaging	1	probably damaging
A32	1	41949818	41949818	C	T	49	0.33	*EDN2*	NM_001956	Missense	p.G41S	-1.3	Neutral	0.41	Tolerated	0.835	possibly damaging
A32	14	100847382	100847382	G	A	140	0.32	*WDR25*	NM_001161476	Missense	p.G41S	-0.31	Neutral	0.69	Tolerated	0.295	benign
A32	2	133542678	133542678	C	T	150	0.32	*NCKAP5*	NM_207363	Missense	p.G569D	-0.84	Neutral	0.02	Damaging	1	probably damaging
A32	3	5229933	5229933	A	G	122	0.27	*EDEM1*	NM_014674	Missense	p.H148R	-4.14	Deleterious	0.02	Damaging	0.752	possibly damaging
A32	1	22073631	22073631	T	C	16	0.31	*USP48*	NM_032236	Missense	p.H307R	-1.66	Neutral	0.71	Tolerated	0.254	benign
A32	14	48143806	48143806	T	C	142	0.24	*MDGA2*	NM_001113498	Missense	p.H65R	-0.35	Neutral	NA	NA	NA	NA
A32	16	3817720	3817720	C	CT	130	0.28	*CREBBP*	NM_004380	Splice Site	p.I1084sp	NA	NA	NA	NA	NA	NA

A32	18	72176107	72176107	A	T	81	0.33	*CNDP2*	NM_018235	Nonsense	p.K134_	NA	NA	1	Tolerated	NA	NA
A32	X	74273416	74273416	T	G	83	0.30	*ABCB7*	NM_004299	Missense	p.K684T	-3.3	Deleterious	0.17	Tolerated	0.27	benign
A32	2	70457886	70457886	A	T	122	0.37	*TIA1*	NM_022173	Splice Site	p.K74sp	NA	NA	NA	NA	NA	NA
A32	10	73515163	73515163	A	G	124	0.31	*C10orf54*	NM_022153	Missense	p.L210P	-5.21	Deleterious	0	Damaging	1	probably damaging
A32	6	69653877	69653877	C	A	115	0.31	*BAI3*	NM_001704	Missense	p.L396I	-0.53	Neutral	0.11	Tolerated	0.828	possibly damaging
A32	6	134495164	134495164	C	G	75	0.33	*SGK1*	NM_001143676	Missense	p.M164I	-1.19	Neutral	0.22	Tolerated	0.054	benign
A32	9	6413491	6413491	A	G	65	0.48	*UHRF2*	NM_152896	Missense	p.M1V	-3.06	Deleterious	0	Damaging	0.998	probably damaging
A32	6	37138403	37138403	A	G	127	0.35	*PIM1*	NM_001243186	Missense	p.N109D	0.36	Neutral	0.76	Tolerated	0.115	benign
A32	5	131630581	131630581	A	G	64	0.33	*SLC22A4*	NM_003059	Missense	p.N91S	-3.55	Deleterious	0.29	Tolerated	0.884	possibly damaging
A32	X	3238204	3238204	G	T	70	0.26	*MXRA5*	NM_015419	Missense	p.P1841H	-1.93	Neutral	0.19	Tolerated	0.028	benign
A32	X	51638750	51638750	C	A	142	0.24	*MAGED1*	NM_001005333	Missense	p.P272Q	-1.23	Neutral	0.1	Tolerated	0.999	probably damaging
A32	7	82579120	82579120	G	T	185	0.37	*PCLO*	NM_033026	Missense	p.P3595H	-8.85	Deleterious	0	Damaging	1	probably damaging
A32	12	123480005	123480005	G	A	96	0.29	*PITPNM2*	NM_020845	Missense	p.P662L	-3.93	Deleterious	0.05	Damaging	0.034	benign
A32	6	100838287	100838287	G	T	122	0.12	*SIM1*	NM_005068	Missense	p.P751T	0.27	Neutral	0.38	Tolerated	0.099	benign
A32	11	1026405	1026405	G	A	66	0.38	*MUC6*	NM_005961	Missense	p.P823L	-4.39	Deleterious	0.34	Tolerated	0.998	probably damaging
A32	3	185797652	185797652	G	T	121	0.31	*ETV5*	NM_004454	Missense	p.Q202K	-0.57	Neutral	0.91	Tolerated	0.08	benign
A32	1	178442279	178442279	C	T	143	0.43	*RASAL2*	NM_170692	Missense	p.R1250W	-2.55	Deleterious	0	Damaging	1	probably damaging
A32	22	41634666	41634666	C	T	84	0.30	*CHADL*	NM_138481	Missense	p.R137Q	-0.69	Neutral	0.59	Tolerated	0.08	benign
A32	15	41137180	41137180	G	A	159	0.36	*SPINT1*	NM_181642	Missense	p.R143K	-0.12	Neutral	0.38	Tolerated	0.005	benign
A32	12	122261055	122261055	C	T	88	0.30	*SETD1B*	NM_015048	Nonsense	p.R1481_	NA	NA	0.84	Tolerated	NA	NA
A32	1	20517583	20517583	C	T	151	0.38	*UBXN10*	NM_152376	Nonsense	p.R177_	NA	NA	1	Tolerated	NA	NA
A32	1	196434492	196434492	C	T	20	0.35	*KCNT2*	NM_198503	Missense	p.R190H	-3.48	Deleterious	0.22	Tolerated	0.972	probably damaging
A32	3	7188191	7188191	G	A	46	0.30	*GRM7*	NM_181874	Missense	p.R191H	-4.41	Deleterious	0.01	Damaging	1	probably damaging
A32	1	181767497	181767497	C	T	183	0.27	*CACNA1E*	NM_001205293	Missense	p.R2157W	-6.61	Deleterious	0	Damaging	1	probably damaging
A32	5	176883106	176883106	G	C	31	0.35	*PRR7*	NM_001174101	Missense	p.R270T	-2.6	Deleterious	NA	NA	0.949	possibly damaging
A32	22	39709294	39709294	G	A	78	0.35	*RPL3*	NM_000967	Missense	p.R357W	-7.01	Deleterious	0.01	Damaging	0.222	benign
A32	1	231858322	231858322	G	A	136	0.38	*DISC1*	NM_001012958	Missense	p.R362Q	0.63	Neutral	0.8	Tolerated	0	benign
A32	6	56362247	56362247	C	T	72	0.39	*DST*	NM_001144769	Missense	p.R4599H	-2.98	Deleterious	0.12	Tolerated	1	probably damaging
A32	6	63990011	63990011	C	T	112	0.35	*LGSN*	NM_016571	Missense	p.R482Q	-0.12	Neutral	0.27	Tolerated	0.099	benign
A32	20	3677876	3677876	G	A	161	0.42	*SIGLEC1*	NM_023068	Nonsense	p.R746_	NA	NA	0.84	Tolerated	NA	NA
A32	1	193099338	193099338	G	A	31	0.16	*CDC73*	NM_024529	Missense	p.R91Q	-2.95	Deleterious	0	Damaging	1	probably damaging
A32	12	9875411	9875411	T	G	29	0.41	*CLECL1*	NM_001253750	Splice Site	p.S105sp	NA	NA	NA	NA	NA	NA
A32	2	11758642	11758642	C	T	121	0.38	*GREB1*	NM_014668	Missense	p.S1214L	-1.45	Neutral	0.28	Tolerated	0.324	benign

A32	21	30316209	30316209	A	G	62	0.31	*LTN1*	NM_015565	Missense	p.S1380P	-0.86	Neutral	0.1	Tolerated	0.93	possibly damaging
A32	8	110984939	110984939	C	A	99	0.41	*KCNV1*	NM_014379	Missense	p.S180I	-1.51	Neutral	0.02	Damaging	0.984	probably damaging
A32	14	51288720	51288720	T	C	119	0.29	*NIN*	NM_020921	Missense	p.S19G	-3.62	Deleterious	0	Damaging	1	probably damaging
A32	5	158250249	158250249	G	A	126	0.31	*EBF1*	NM_024007	Missense	p.S238F	-5.04	Deleterious	0	Damaging	0.999	probably damaging
A32	9	14150160	14150160	A	G	126	0.34	*NFIB*	NM_001190737	Missense	p.S264P	0.87	Neutral	0.47	Tolerated	0.985	probably damaging
A32	X	140995349	140995349	C	A	186	0.61	*MAGEC1*	NM_005462	Missense	p.S720Y	-0.74	Neutral	0.02	Damaging	0.588	possibly damaging
A32	12	64609734	64609734	G	T	43	0.30	*C12orf66*	NM_152440	Missense	p.S82Y	-1.55	Neutral	NA	NA	0.997	probably damaging
A32	12	49440134	49440139	AGTGTG	A	117	0.39	*MLL2*	NM_003482	Frame_Shift_Del	p.T1496fs	NA	NA	NA	NA	NA	NA
A32	11	6650025	6650025	G	A	123	0.37	*DCHS1*	NM_003737	Missense	p.T1733M	-2.37	Neutral	0.04	Damaging	0.986	probably damaging
A32	6	41903710	41903710	T	G	74	0.35	*CCND3*	NM_001760	Missense	p.T283P	-5.27	Deleterious	0.16	Tolerated	0.999	probably damaging
A32	X	12994482	12994482	T	C	149	0.19	*TMSB4X*	NM_021109	Splice Site	p.T34sp	NA	NA	NA	NA	NA	NA
A32	15	22958189	22958189	C	T	85	0.35	*CYFIP1*	NM_014608	Missense	p.T611M	-3.1	Deleterious	0.03	Damaging	0.999	probably damaging
A32	8	128750681	128750681	C	A	146	0.40	*MYC*	NM_002467	Missense	p.T73N	-3.65	Deleterious	0.01	Damaging	0.997	probably damaging
A32	18	60985881	60985881	T	C	137	0.23	*BCL2*	NM_000633	Missense	p.T7A	-0.54	Neutral	0.27	Tolerated	0.148	benign
A32	11	1031856	1031856	C	T	160	0.33	*MUC6*	NM_005961	Missense	p.V105I	-0.76	Neutral	0.15	Tolerated	0.04	benign
A32	6	41011793	41011793	G	A	121	0.33	*TSPO2*	NM_001010873	Missense	p.V144M	0.2	Neutral	0.08	Tolerated	0.62	possibly damaging
A32	4	69795760	69795760	A	T	31	0.45	*UGT2A3*	NM_024743	Missense	p.V452E	-4.49	Deleterious	0	Damaging	0.994	probably damaging
A32	1	16378855	16378855	T	C	73	0.40	*CLCNKB*	NM_000085	Missense	p.V524A	-3.29	Deleterious	0	Damaging	0.037	benign
A32	1	175324662	175324663	TG	T	137	0.41	*TNR*	NM_003285	Frame_Shift_Del	p.Y1075fs	NA	NA	NA	NA	NA	NA
A32	1	231131518	231131518	A	G	65	0.37	*ARV1*	NM_022786	Missense	p.Y154C	-2.38	Neutral	0.07	Tolerated	0.975	probably damaging
A32	1	27106617	27106617	C	A	173	0.47	*ARID1A*	NM_006015	Nonsense	p.Y2076_	NA	NA	1	Tolerated	NA	NA
A32	9	37034009	37034009	T	C	28	0.21	*PAX5*	NM_016734	Missense	p.Y7C	-0.34	Neutral	0.01	Damaging	0.994	probably damaging
A33	19	6686229	6686229	G	T	53	0.42	*C3*	NM_000064	Missense	p.A1239D	-4.73	Deleterious	0.01	Damaging	1	probably damaging
A33	17	7369097	7369097	A	G	93	0.39	*ZBTB4*	NM_001128833	Missense	p.C342R	-11.59	Deleterious	0.01	Damaging	0.999	probably damaging
A33	18	72228148	72228148	G	A	93	0.45	*CNDP1*	NM_032649	Missense	p.D121N	-3.77	Deleterious	0.08	Tolerated	0.267	benign
A33	2	48037545	48037548	TATC	T	39	0.51	*FBXO11*	NM_025133	In_Frame_Del	p.D665del	-11.46	Deleterious	NA	NA	NA	NA
A33	12	49431499	49431499	C	CA	110	0.37	*MLL2*	NM_003482	Frame_Shift_Ins	p.E3214fs	NA	NA	NA	NA	NA	NA
A33	16	90032347	90032347	G	T	46	0.54	*DEF8*	NM_207514	Missense	p.E505D	-0.41	Neutral	0.18	Tolerated	0.002	benign
A33	17	55193540	55193540	G	A	111	0.20	*AKAP1*	NM_003488	Missense	p.E784K	-0.04	Neutral	1	Tolerated	0.504	possibly damaging
A33	19	11141498	11141498	G	C	67	0.43	*SMARCA4*	NM_001128849	Missense	p.G1159R	-7.45	Deleterious	0	Damaging	1	probably damaging
A33	11	72539781	72539781	G	A	175	0.37	*ATG16L2*	NM_033388	Missense	p.G544S	-3.76	Deleterious	0.23	Tolerated	1	probably damaging
A33	11	46568662	46568662	C	T	25	0.76	*AMBRA1*	NM_017749	Splice Site	p.H126sp	NA	NA	NA	NA	NA	NA
A33	1	27278212	27278212	A	T	122	0.82	*C1orf172*	NM_152365	Missense	p.H220Q	-4.11	Deleterious	0.28	Tolerated	0.077	benign

A33	3	183515838	183515838	A	T	28	0.36	*YEATS2*	NM_018023	Missense	p.K1075N	-1.5	Neutral	0.03	Damaging	0.999	probably damaging
A33	20	3728901	3728901	T	C	80	0.43	*HSPA12B*	NM_052970	Missense	p.L238P	-5.46	Deleterious	0.17	Tolerated	0.997	probably damaging
A33	15	58247454	58247454	A	T	64	0.34	*ALDH1A2*	NM_003888	Missense	p.L500M	-1.63	Neutral	0	Damaging	0.997	probably damaging
A33	18	18964294	18964295	GT	G	107	0.36	*GREB1L*	NM_001142966	Frame_Shift_Del	p.M95fs	NA	NA	NA	NA	NA	NA
A33	11	372943	372943	C	T	94	0.46	*B4GALNT4*	NM_178537	Missense	p.P147L	-8.66	Deleterious	0	Damaging	1	probably damaging
A33	2	107459943	107459943	G	A	97	0.37	*ST6GAL2*	NM_001142351	Missense	p.P164L	-1.29	Neutral	0.29	Tolerated	0.494	possibly damaging
A33	3	71027097	71027098	TG	T	107	0.38	*FOXP1*	NM_032682	Frame_Shift_Del	p.P410fs	NA	NA	NA	NA	NA	NA
A33	1	23885752	23885752	G	A	135	0.84	*ID3*	NM_002167	Missense	p.P56S	-7.65	Deleterious	0	Damaging	1	probably damaging
A33	1	70505463	70505463	G	A	63	0.81	*LRRC7*	NM_020794	Missense	p.R1281K	0.62	Neutral	1	Tolerated	0.1	benign
A33	3	51864449	51864449	A	G	36	0.47	*IQCF3*	NM_001207023	Missense	p.R33G	-3.1	Deleterious	0.46	Tolerated	0.675	possibly damaging
A33	6	160858163	160858163	G	A	101	0.40	*SLC22A3*	NM_021977	Missense	p.R403H	-4.72	Deleterious	0.18	Tolerated	1	probably damaging
A33	7	30490831	30490831	C	A	49	0.37	*NOD1*	NM_006092	Splice Site	p.R734sp	NA	NA	NA	NA	NA	NA
A33	17	39991330	39991330	G	A	118	0.46	*NT5C3B*	NM_052935	Missense	p.R74W	-5.08	Deleterious	0.01	Damaging	1	probably damaging
A33	3	48459734	48459734	T	C	95	0.42	*PLXNB1*	NM_002673	Missense	p.S1030G	-3.3	Deleterious	0.55	Tolerated	0.997	probably damaging
A33	2	203395598	203395598	G	T	95	0.48	*BMPR2*	NM_001204	Missense	p.S350I	-1.64	Neutral	0.04	Damaging	0.688	possibly damaging
A33	17	79430815	79430815	C	T	33	0.70	*BAHCC1*	NM_001080519	Missense	p.T2545M	-4.07	Deleterious	0	Damaging	1	probably damaging
A33	13	25671472	25671472	C	G	121	0.37	*PABPC3*	NM_030979	Missense	p.T379S	-1.3	Neutral	0.23	Tolerated	0.202	benign
A33	8	128750681	128750681	C	T	121	0.55	*MYC*	NM_002467	Missense	p.T73I	-4.43	Deleterious	0	Damaging	0.999	probably damaging
A33	1	197070259	197070259	A	T	82	0.44	*ASPM*	NM_018136	Missense	p.Y2708N	-4.97	Deleterious	0	Damaging	0.999	probably damaging
A33	8	24811750	24811750	A	T	133	0.37	*NEFL*	NM_006158	Missense	p.Y372N	NA	NA	NA	NA	NA	NA
A34	17	64881235	64881235	G	A	112	0.32	*CACNG5*	NM_145811	Missense	p.A236T	-1.03	Neutral	0.2	Tolerated	0.725	possibly damaging
A34	11	113857495	113857495	G	A	141	0.47	*HTR3A*	NM_213621	Missense	p.A327T	-0.03	Neutral	NA	NA	0.013	benign
A34	12	23728630	23728630	G	A	106	0.22	*SOX5*	NM_006940	Missense	p.A436V	-1.02	Neutral	0.16	Tolerated	0.446	benign
A34	2	170063179	170063179	C	T	155	0.46	*LRP2*	NM_004525	Missense	p.G2351S	-4.34	Deleterious	0.08	Tolerated	1	probably damaging
A34	4	91234133	91234133	A	C	126	0.25	*CCSER1*	NM_001145065	Missense	p.I482L	0.18	Neutral	0.24	Tolerated	0	benign
A34	20	31376701	31376701	G	T	76	0.50	*DNMT3B*	NM_006892	Missense	p.K232N	-3.79	Deleterious	0.03	Damaging	1	probably damaging
A34	18	56246069	56246069	G	A	86	0.20	*ALPK2*	NM_052947	Missense	p.P647S	-2.75	Deleterious	0.3	Tolerated	0.441	benign
A34	21	36252866	36252866	G	A	84	0.42	*RUNX1*	NM_001754	Nonsense	p.R166_	NA	NA	1	Tolerated	NA	NA
A34	16	89595944	89595944	G	A	39	0.72	*SPG7*	NM_003119	Missense	p.R273H	-2.75	Deleterious	0.01	Damaging	0.999	probably damaging
A34	19	47193954	47193954	C	T	61	0.51	*PRKD2*	NM_016457	Missense	p.R571Q	-3.6	Deleterious	0	Damaging	1	probably damaging
A34	17	73809189	73809189	C	T	109	0.52	*UNK*	NM_001080419	Missense	p.T218M	-5.95	Deleterious	0	Damaging	1	probably damaging
A35	15	88679210	88679210	T	C	87	0.48	*NTRK3*	NM_001012338	Missense	p.E276G	-1.7	Neutral	0.1	Tolerated	0.967	probably damaging
A35	15	44109639	44109639	A	AATCTGA	53	0.28	*MFAP1*	NM_005926	Frame_Shift_Ins	p.I29fs	NA	NA	NA	NA	NA	NA

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A35	8	100479692	100479692	C	T	135	0.33	*VPS13B*	NM_017890	Missense	p.L1166F	-1.41	Neutral	0.03	Damaging	1	probably damaging
A35	19	51052065	51052065	G	A	25	0.40	*LRRC4B*	NM_001080457	Missense	p.P11S	-0.19	Neutral	1	Tolerated	0	benign
A35	3	151161484	151161484	G	A	99	0.11	*IGSF10*	NM_178822	Missense	p.R1751C	-4.86	Deleterious	NA	NA	0.999	probably damaging
A35	21	47537830	47537830	C	T	35	0.20	*COL6A2*	NM_001849	Nonsense	p.R366_	NA	NA	0.96	Tolerated	NA	NA
A35	12	86373302	86373302	C	T	136	0.38	*MGAT4C*	NM_013244	Missense	p.R401Q	-0.77	Neutral	0.1	Tolerated	0.994	probably damaging
A35	5	65466522	65466522	C	T	96	0.41	*SREK1*	NM_001077199	Missense	p.R411W	-2.92	Deleterious	0	Damaging	0.998	probably damaging
A35	10	62038620	62038620	G	T	138	0.17	*ANK3*	NM_020987	Missense	p.T109K	-5.21	Deleterious	0	Damaging	1	probably damaging
A35	20	47675041	47675041	A	G	40	0.45	*CSE1L*	NM_001316	Missense	p.Y14C	-2.82	Deleterious	0.37	Tolerated	0.037	benign
A36	20	15480436	15480436	G	A	133	0.24	*MACROD2*	NM_080676	Missense	p.A197T	-3.49	Deleterious	0	Damaging	1	probably damaging
A36	X	70604826	70604826	G	T	29	0.83	*TAF1*	NM_004606	Missense	p.C738F	1.85	Neutral	0.74	Tolerated	0.002	benign
A36	1	33360453	33360453	C	T	49	0.41	*TMEM54*	NM_033504	Missense	p.G208S	-1.23	Neutral	0.27	Tolerated	0.011	benign
A36	1	155874263	155874263	T	C	95	0.38	*RIT1*	NM_001256821	Missense	p.M107V	-3.99	Deleterious	0.01	Damaging	1	probably damaging
A36	11	60701149	60701149	C	T	12	0.50	*TMEM132A*	NM_017870	Missense	p.R499C	-4.75	Deleterious	0	Damaging	0.999	probably damaging
A36	2	237489833	237489833	C	T	100	0.31	*CXCR7*	NM_020311	Missense	p.S242F	-3.46	Deleterious	NA	NA	0.999	probably damaging
A36	1	237550611	237550611	G	A	68	0.22	*RYR2*	NM_001035	Missense	p.V203M	-2.19	Neutral	0	Damaging	0.998	probably damaging
A36	2	105858943	105858943	G	A	77	0.29	*GPR45*	NM_007227	Missense	p.V210I	-0.13	Neutral	0.41	Tolerated	0.027	benign
A36	13	28609758	28609758	C	G	202	0.25	*FLT3*	NM_004119	Missense	p.V491L	-0.39	Neutral	0.87	Tolerated	0.792	possibly damaging
A37	2	143742752	143742752	G	A	151	0.10	*KYNU*	NM_003937	Splice Site	p.K276sp	NA	NA	NA	NA	NA	NA
A37	7	107834739	107834739	T	C	134	0.11	*NRCAM*	NM_001037132	Missense	p.M533V	-0.64	Neutral	0.2	Tolerated	0	benign
A37	12	49426603	49426606	TGTT	TGCCAAG GC	29	0.14	*MLL2*	NM_003482	Frame_Shift_Ins	p.Q3961fs	NA	NA	NA	NA	NA	NA
A37	9	104079717	104079717	G	A	98	0.44	*LPPR1*	NM_207299	Missense	p.R295H	-0.67	Neutral	0.16	Tolerated	0.999	probably damaging
A37	6	127796575	127796575	G	A	53	0.11	*SOGA3*	NM_001012279	Missense	p.R866W	-4.42	Deleterious	0	Damaging	0.999	probably damaging
A37	9	140611260	140611260	C	T	151	0.34	*EHMT1*	NM_024757	Missense	p.R90W	-2.22	Neutral	0.01	Damaging	1	probably damaging
A37	2	235950156	235950156	C	T	223	0.10	*SH3BP4*	NM_014521	Missense	p.S248L	-3.04	Deleterious	0	Damaging	1	probably damaging
A37	4	184240941	184240941	G	A	80	0.46	*CLDN22*	NM_001111319	Missense	p.T144M	-2.51	Deleterious	0	Damaging	0.99	probably damaging
A37	12	104728049	104728049	C	T	50	0.22	*TXNRD1*	NM_001093771	Missense	p.T562M	-5.14	Deleterious	0	Damaging	1	probably damaging
A37	2	234365952	234365952	G	C	99	0.35	*DGKD*	NM_152879	Missense	p.W853S	-11.91	Deleterious	0	Damaging	1	probably damaging
A37	16	3786150	3786150	A	C	107	0.12	*CREBBP*	NM_004380	Missense	p.Y1539D	-9.85	Deleterious	0	Damaging	1	probably damaging
A38	X	149101984	149101984	A	T	85	0.19	*CXorf40B*	NM_001013845	Missense	p.C37S	-1.25	Neutral	0.46	Tolerated	0.027	benign
A38	12	100957258	100957258	C	A	66	0.41	*NR1H4*	NM_001206993	Missense	p.D484E	-2.36	Neutral	0.43	Tolerated	0.999	probably damaging
A38	3	97124025	97124025	C	A	53	0.28	*EPHA6*	NM_001080448	Missense	p.D546E	0.14	Neutral	1	Tolerated	NA	NA

A38	8	68084680	68084680	T	G	126	0.42	*CSPP1*	NM_024790	Missense	p.F948C	-4.77	Deleterious	0	Damaging	1	probably damaging
A38	1	16054644	16054644	G	T	50	0.18	*PLEKHM2*	NM_015164	Splice Site	p.K610sp	NA	NA	NA	NA	NA	NA
A38	1	35656487	35656487	C	G	95	0.38	*SFPQ*	NM_005066	Missense	p.R376P	-4.71	Deleterious	0	Damaging	0.998	probably damaging
A38	15	44166570	44166570	C	T	54	0.30	*FRMD5*	NM_032892	Missense	p.R409Q	0.13	Neutral	0.63	Tolerated	0.04	benign
A38	17	58286756	58286756	C	T	60	0.55	*USP32*	NM_032582	Missense	p.R858Q	-3.62	Deleterious	0.01	Damaging	0.999	probably damaging
A38	2	186657538	186657538	C	T	115	0.30	*FSIP2*	NM_173651	Missense	p.T1981M	-4.5	Deleterious	0.01	Damaging	NA	NA
A38	9	35703798	35703798	C	T	76	0.45	*TLN1*	NM_006289	Missense	p.V2111M	3.01	Neutral	1	Tolerated	0.001	benign
A38	19	7684836	7684836	C	T	59	0.25	*XAB2*	NM_020196	Missense	p.V798M	-1.96	Neutral	0	Damaging	0.995	probably damaging
A39	17	7577091	7577091	G	GGCC	91	0.29	*TP53*	NM_001126112	In_Frame_Ins	p.282_283insG	-9.45	Deleterious	NA	NA	NA	NA
A39	1	120311418	120311418	G	A	63	0.30	*HMGCS2*	NM_005518	Missense	p.A17V	-0.07	Neutral	0.55	Tolerated	0.001	benign
A39	6	66005908	66005908	G	A	206	0.46	*EYS*	NM_001142800	Missense	p.S624L	1.69	Neutral	0.83	Tolerated	0	benign
A39	3	47161707	47161710	AAAG	AAATAAC	109	0.33	*SETD2*	NM_014159	In_Frame_Ins	p.Y1472_	NA	NA	NA	NA	NA	NA
A39	13	37678498	37678498	G	A	114	0.31	*CSNK1A1L*	NM_145203	Missense	p.T299M	-3.78	Deleterious	0.01	Damaging	0.999	probably damaging
A40	18	13040879	13040882	CTTA	CTTTTT	107	0.16	*CEP192*	NM_032142	Frame_Shift_Ins	p.A620fs	NA	NA	NA	NA	NA	NA
A40	8	145661150	145661150	G	A	100	0.19	*TONSL*	NM_013432	Missense	p.A889V	-0.56	Neutral	0.31	Tolerated	0.001	benign
A40	X	32459418	32459418	C	T	64	0.17	*DMD*	NM_004006	Missense	p.C1267Y	-5.56	Deleterious	0.07	Tolerated	0.999	probably damaging
A40	4	122853599	122853599	A	T	154	0.47	*TRPC3*	NM_001130698	Missense	p.C272S	-9.29	Deleterious	0	Damaging	1	probably damaging
A40	5	140530535	140530535	G	C	202	0.08	*PCDHB6*	NM_018939	Missense	p.D233H	-6.84	Deleterious	0	Damaging	1	probably damaging
A40	9	118950482	118950482	G	A	35	0.34	*PAPPA*	NM_002581	Missense	p.D489N	-2.4	Neutral	0.04	Damaging	0.948	possibly damaging
A40	18	64197195	64197195	C	T	75	0.27	*CDH19*	NM_021153	Missense	p.E449K	0.3	Neutral	1	Tolerated	0.045	benign
A40	X	99945149	99945149	C	A	170	0.24	*SYTL4*	NM_001174068	Missense	p.G244V	-2	Neutral	NA	NA	0.122	benign
A40	17	67283844	67283844	G	A	200	0.34	*ABCA5*	NM_018672	Missense	p.H651Y	-5.5	Deleterious	NA	NA	0.977	probably damaging
A40	10	99349736	99349736	A	G	111	0.23	*C10orf62*	NM_001009997	Missense	p.K28E	-0.58	Neutral	0.02	Damaging	0.206	benign
A40	19	1993065	1993065	A	G	28	0.39	*BTBD2*	NM_017797	Missense	p.L213P	-6.05	Deleterious	0	Damaging	0.906	possibly damaging
A40	1	150799085	150799085	T	G	27	0.22	*ARNT*	NM_001668	Missense	p.L392F	-3.69	Deleterious	0	Damaging	1	probably damaging
A40	15	93545433	93545433	G	GA	135	0.32	*CHD2*	NM_001271	Frame_Shift_Ins	p.M1388fs	NA	NA	NA	NA	NA	NA
A40	13	92345759	92345760	TG	AT	100	0.28	*GPC5*	NM_004466	Missense	p.M215N	-5.25	Deleterious	NA	NA	NA	NA
A40	6	152652142	152652142	T	G	360	0.21	*SYNE1*	NM_182961	Missense	p.N4560H	-1.16	Neutral	0.54	Tolerated	0.001	benign
A40	4	175898609	175898609	A	C	194	0.11	*ADAM29*	NM_001130704	Missense	p.N645H	-3.33	Deleterious	NA	NA	1	probably damaging
A40	4	1725285	1725285	C	T	122	0.29	*TACC3*	NM_006342	Missense	p.P46L	-7.61	Deleterious	0	Damaging	1	probably damaging
A40	19	57286865	57286865	G	A	123	0.25	*ZIM2*	NM_001146327	Nonsense	p.Q259_	NA	NA	0.17	Tolerated	NA	NA

A40	1	94461694	94461694	G	A	97	0.29	*ABCA4*	NM_000350	Nonsense	p.R2263_	NA	NA	1	Tolerated	NA	NA
A40	1	163044246	163044246	C	T	106	0.11	*RGS4*	NM_001102445	Nonsense	p.R269_	NA	NA	0.49	Tolerated	NA	NA
A40	1	237586429	237586429	C	T	170	0.21	*RYR2*	NM_001035	Nonsense	p.R296_	NA	NA	1	Tolerated	NA	NA
A40	3	135721683	135721683	G	A	76	0.38	*PPP2R3A*	NM_002718	Missense	p.R448K	0.18	Neutral	0.59	Tolerated	0	benign
A40	2	160714940	160714940	T	G	65	0.25	*LY75-CD302*	NM_001198759	Missense	p.R772S	-0.88	Neutral	0.65	Tolerated	0.837	possibly damaging
A40	4	152021651	152021651	C	T	78	0.40	*RPS3A*	NM_001006	Missense	p.S26F	-3.21	Deleterious	0	Damaging	0.105	benign
A40	X	47918248	47918248	G	A	91	0.19	*ZNF630*	NM_001037735	Missense	p.S528L	-4.98	Deleterious	0.01	Damaging	0.022	benign
A40	1	201186484	201186484	C	T	75	0.24	*IGFN1*	NM_001164586	Missense	p.T3222I	-3.44	Deleterious	0.23	Tolerated	0.55	possibly damaging
A40	4	87653830	87653830	C	T	264	0.40	*PTPN13*	NM_080685	Missense	p.T590I	0.56	Neutral	0.96	Tolerated	0.041	benign
A40	17	74465275	74465275	G	A	148	0.36	*AANAT*	NM_001166579	Missense	p.V107I	-0.42	Neutral	0.23	Tolerated	0.001	benign
A40	4	26491053	26491053	C	T	141	0.20	*CCKAR*	NM_000730	Missense	p.V56M	-2.11	Neutral	0.19	Tolerated	0.801	possibly damaging
A40	1	248512303	248512303	T	C	352	0.18	*OR14C36*	NM_001001918	Missense	p.V76A	-3.37	Deleterious	0.11	Tolerated	0.502	possibly damaging
A41	12	25380282	25380282	G	T	65	0.49	*KRAS*	NM_033360	Missense	p.A59E	-4.71	Deleterious	0	Damaging	1	probably damaging
A41	1	93300428	93300440	TTATGCTGCAGCA	T	104	0.31	*RPL5*	NM_000969	In_Frame_Del	p.YAAA95del	-29.54	Deleterious	NA	NA	NA	NA
A41	19	42224844	42224844	G	T	53	0.36	*CEACAM5*	NM_004363	Missense	p.G592W	-1.22	Neutral	0	Damaging	0.998	probably damaging
A41	22	46614228	46614228	G	GA	97	0.55	*PPARA*	NM_005036	Frame_Shift_Ins	p.Q146fs	NA	NA	NA	NA	NA	NA
A41	4	59992	59992	C	T	241	0.11	*ZNF718*	NM_001039127	Nonsense	p.Q58_	NA	NA	0.03	Damaging	NA	NA
A41	16	19126394	19126394	G	A	51	0.57	*ITPRIPL2*	NM_001034841	Missense	p.R204H	0.26	Neutral	0.46	Tolerated	0	benign
A41	11	64600152	64600152	G	A	84	0.33	*CDC42BPG*	NM_017525	Missense	p.R977C	-5.33	Deleterious	0	Damaging	1	probably damaging
A41	21	41447089	41447089	G	A	83	0.40	*DSCAM*	NM_001389	Missense	p.T1588M	-0.2	Neutral	0.3	Tolerated	0.521	possibly damaging
A41	17	62850745	62850745	G	A	36	0.36	*LRRC37A3*	NM_199340	Missense	p.T1626M	-1.25	Neutral	0.05	Damaging	0.994	probably damaging
A42	15	22369012	22369012	C	T	801	0.17	*OR4M2*	NM_001004719	Missense	p.A146V	0.55	Neutral	1	Tolerated	0.016	benign
A42	X	153763446	153763446	G	T	39	0.51	*G6PD*	NM_000402	Missense	p.A171D	-5.67	Deleterious	0	Damaging	1	probably damaging
A42	17	78164675	78164675	G	A	55	0.40	*CARD14*	NM_024110	Missense	p.E356K	-3.59	Deleterious	0.01	Damaging	0.901	possibly damaging
A42	1	115258747	115258747	C	G	58	0.31	*NRAS*	NM_002524	Missense	p.G12A	-4.62	Deleterious	0	Damaging	0.775	possibly damaging
A42	10	103563716	103563722	ATAATCT	A	110	0.40	*MGEA5*	NM_012215	In_Frame_Del	p.KI269del	-15.36	Deleterious	NA	NA	NA	NA
A42	2	32735011	32735011	T	G	61	0.43	*BIRC6*	NM_016252	Missense	p.L3396R	-5.58	Deleterious	0	Damaging	0.998	probably damaging
A42	3	129546893	129546893	C	T	182	0.48	*TMCC1*	NM_001017395	Missense	p.R110Q	-0.63	Neutral	0	Damaging	0.034	benign
A42	2	85051137	85051137	C	T	32	0.53	*TRABD2A*	NM_001277053	Missense	p.R425Q	-0.97	Neutral	0.03	Damaging	0.681	possibly damaging
A42	3	69168023	69168023	G	A	107	0.45	*LMOD3*	NM_198271	Missense	p.R495C	-2.13	Neutral	0.04	Damaging	1	probably damaging
A42	8	74526158	74526158	T	C	72	0.56	*STAU2*	NM_001164380	Missense	p.S238G	-2.65	Deleterious	0.1	Tolerated	0.735	possibly damaging
A42	18	61256920	61256920	T	A	124	0.52	*SERPINB13*	NM_012397	Missense	p.S66T	0.9	Neutral	0.93	Tolerated	0	benign

A42	7	105664932	105664932	G	A	78	0.41	*CDHR3*	NM_152750	Missense	p.V728M	-0.25	Neutral	0.07	Tolerated	0.943	possibly damaging
A43	12	100811834	100811834	C	T	121	0.17	*SLC17A8*	NM_139319	Missense	p.A442V	-3.97	Deleterious	0	Damaging	1	probably damaging
A43	13	28592642	28592642	C	A	50	0.24	*FLT3*	NM_004119	Missense	p.D835Y	-8.17	Deleterious	0	Damaging	1	probably damaging
A43	1	3329021	3329021	G	A	109	0.42	*PRDM16*	NM_022114	Missense	p.E754K	-1.85	Neutral	0	Damaging	0.997	probably damaging
A43	X	3241049	3241049	C	T	89	0.40	*MXRA5*	NM_015419	Missense	p.E893K	-0.79	Neutral	0.7	Tolerated	0.98	probably damaging
A43	4	183601761	183601761	G	A	73	0.12	*TENM3*	NM_001080477	Missense	p.G569S	-5.19	Deleterious	0	Damaging	0.998	probably damaging
A43	18	32833809	32833809	T	G	58	0.22	*ZSCAN30*	NM_001112734	Missense	p.K364Q	-3.54	Deleterious	0.03	Damaging	1	probably damaging
A43	1	38056339	38056339	T	C	67	0.40	*GNL2*	NM_013285	Missense	p.M118V	-0.44	Neutral	0.3	Tolerated	0.045	benign
A43	9	73152206	73152206	T	C	51	0.35	*TRPM3*	NM_001007471	Missense	p.M1263V	-0.79	Neutral	0.37	Tolerated	0.012	benign
A43	10	99640143	99640143	T	C	92	0.50	*CRTAC1*	NM_018058	Missense	p.N561S	-0.72	Neutral	0.18	Tolerated	0.011	benign
A43	6	46761203	46761203	C	T	76	0.29	*MEP1A*	NM_005588	Missense	p.P23L	-1.56	Neutral	0.1	Tolerated	0.118	benign
A43	7	88963668	88963668	C	T	191	0.43	*ZNF804B*	NM_181646	Missense	p.P458S	-7.82	Deleterious	0.01	Damaging	1	probably damaging
A43	1	212870325	212870326	TG	T	55	0.27	*BATF3*	NM_018664	Frame_Shift_Del	p.Q58fs	NA	NA	NA	NA	NA	NA
A43	14	68244307	68244307	C	T	17	0.35	*ZFYVE26*	NM_015346	Missense	p.R1648H	-0.74	Neutral	0.23	Tolerated	0.002	benign
A43	20	41385239	41385239	C	T	42	0.40	*PTPRT*	NM_133170	Missense	p.R241H	-2.45	Neutral	0	Damaging	0.999	probably damaging
A43	14	69994623	69994623	G	A	62	0.56	*PLEKHD1*	NM_001161498	Missense	p.R442H	-1.65	Neutral	NA	NA	0.94	possibly damaging
A43	6	25850392	25850392	G	T	183	0.43	*SLC17A3*	NM_001098486	Missense	p.S336Y	-5.89	Deleterious	0	Damaging	1	probably damaging
A43	1	183516320	183516320	C	G	43	0.42	*SMG7*	NM_201569	Missense	p.S896C	-1.15	Neutral	0.1	Tolerated	0.957	probably damaging
A43	1	82372828	82372828	C	T	111	0.43	*LPHN2*	NM_012302	Missense	p.T67M	-4.57	Deleterious	0.01	Damaging	1	probably damaging
A43	3	184008969	184008969	C	T	64	0.28	*ECE2*	NM_014693	Missense	p.T777M	-5.71	Deleterious	0	Damaging	1	probably damaging
A43	1	169694895	169694895	T	A	114	0.43	*SELE*	NM_000450	Missense	p.Y608F	-0.37	Neutral	0.69	Tolerated	0	benign
A44	6	12161939	12161939	C	T	108	0.10	*HIVEP1*	NM_002114	Missense	p.A2252V	-1.65	Neutral	0.05	Damaging	0.999	probably damaging
A44	8	75932247	75932247	G	T	114	0.58	*CRISPLD1*	NM_031461	Missense	p.A393S	-0.06	Neutral	0.73	Tolerated	0.976	probably damaging
A44	2	97507820	97507820	T	TG	37	0.30	*ANKRD23*	NM_144994	Frame_Shift_Ins	p.A93fs	NA	NA	NA	NA	NA	NA
A44	3	42738525	42738525	C	G	86	0.45	*HHATL*	NM_020707	Missense	p.K326N	-2.97	Deleterious	0.13	Tolerated	1	probably damaging
A44	12	50747660	50747660	C	G	196	0.33	*FAM186A*	NM_001145475	Missense	p.K985N	-1.98	Neutral	0.04	Damaging	0.764	possibly damaging
A44	2	209113113	209113113	G	A	61	0.52	*IDH1*	NM_005896	Missense	p.R132C	-6.68	Deleterious	0	Damaging	0.259	benign
A44	5	169145774	169145774	G	A	251	0.49	*DOCK2*	NM_004946	Missense	p.R749Q	-0.77	Neutral	0.68	Tolerated	1	probably damaging
A44	2	25457242	25457242	C	T	35	0.69	*DNMT3A*	NM_022552	Missense	p.R882H	-4.72	Deleterious	0.03	Damaging	0.651	possibly damaging
A46	9	13119520	13119520	G	A	251	0.47	*MPDZ*	NM_003829	Missense	p.A1787V	-1.24	Neutral	0.3	Tolerated	1	probably damaging
A46	16	9857510	9857510	G	C	92	0.48	*GRIN2A*	NM_001134407	Missense	p.D1297E	-0.9	Neutral	NA	NA	0.005	benign
A46	14	21360262	21360262	C	A	96	0.47	*RNASE3*	NM_002935	Missense	p.D139E	-1.85	Neutral	0.32	Tolerated	0	benign
A46	1	196694409	196694409	G	C	163	0.47	*CFH*	NM_000186	Missense	p.D619H	-0.09	Neutral	0.12	Tolerated	0.943	possibly damaging

A46	X	144906057	144906057	A	G	102	0.52	*SLITRK2*	NM_032539	Missense	p.E705G	-2.44	Neutral	0.03	Damaging	0.009	benign
A46	9	127089677	127089677	G	C	56	0.50	*NEK6*	NM_001145001	Missense	p.G226A	-5.54	Deleterious	0	Damaging	1	probably damaging
A46	15	35274855	35274855	T	G	25	0.52	*ZNF770*	NM_014106	Missense	p.N261H	0.98	Neutral	0.11	Tolerated	0.006	benign
A46	3	195513413	195513413	G	A	14	0.14	*MUC4*	NM_018406	Missense	p.P1680S	-0.27	Neutral	NA	NA	0.544	possibly damaging
A46	11	6524048	6524048	C	A	44	0.34	*DNHD1*	NM_144666	Missense	p.P271H	-2.01	Neutral	0.07	Tolerated	0.122	benign
A46	14	73945501	73945501	G	A	56	0.43	*HEATR4*	NM_001220484	Missense	p.P964L	-0.35	Neutral	1	Tolerated	0	benign
A46	1	78383437	78383437	C	A	68	0.46	*NEXN*	NM_144573	Missense	p.Q72K	-1.14	Neutral	0.06	Tolerated	0.033	benign
A46	3	48612929	48612929	C	T	30	0.27	*COL7A1*	NM_000094	Missense	p.R2008H	-1.64	Neutral	0.12	Tolerated	0.995	probably damaging
A46	12	7864237	7864237	G	A	79	0.15	*DPPA3*	NM_199286	Missense	p.R24Q	1.38	Neutral	0.62	Tolerated	0.017	benign
A46	4	156764844	156764844	G	A	116	0.19	*ASIC5*	NM_017419	Missense	p.R284C	-4.13	Deleterious	0.03	Damaging	0.995	probably damaging
A46	7	5338706	5338706	C	T	16	0.69	*SLC29A4*	NM_153247	Missense	p.R324C	-2.29	Neutral	0.07	Tolerated	1	probably damaging
A46	9	5078362	5078362	A	T	46	0.09	*JAK2*	NM_004972	Missense	p.R683S	-5.16	Deleterious	0	Damaging	1	probably damaging
A46	12	69085768	69085768	T	G	92	0.17	*NUP107*	NM_020401	Missense	p.S108R	-1.26	Neutral	NA	NA	0.495	possibly damaging
A46	9	5089726	5089726	C	A	94	0.22	*JAK2*	NM_004972	Missense	p.T875N	-4.59	Deleterious	0.04	Damaging	0.922	possibly damaging
A46	3	128348896	128348896	C	T	54	0.39	*RPN1*	NM_002950	Missense	p.V312I	-0.58	Neutral	0.19	Tolerated	0.867	possibly damaging
A46	20	55027281	55027281	A	G	110	0.40	*CASS4*	NM_001164116	Missense	p.Y350C	-8.12	Deleterious	0	Damaging	1	probably damaging
A47	9	135926366	135926366	G	A	17	0.12	*GTF3C5*	NM_001122823	Splice Site	p.K256sp	NA	NA	NA	NA	NA	NA
A47	22	40066215	40066215	G	A	18	0.61	*CACNA1I*	NM_021096	Missense	p.R1456H	-4.47	Deleterious	0.03	Damaging	1	probably damaging
A47	14	25102230	25102230	G	A	47	0.34	*GZMB*	NM_004131	Missense	p.R32C	-7	Deleterious	0	Damaging	0.977	probably damaging
A47	14	22038134	22038134	C	T	58	0.33	*OR10G3*	NM_001005465	Missense	p.V248M	-1.82	Neutral	0.03	Damaging	0.243	benign
A47	19	17943502	17943502	C	T	39	0.33	*JAK3*	NM_000215	Missense	p.V836M	-2.8	Deleterious	0	Damaging	1	probably damaging
A48	10	94018	94018	T	C	16	0.19	*TUBB8*	NM_177987	Missense	p.H105R	-4.78	Deleterious	0	Damaging	0.926	possibly damaging
A48	11	320606	320606	G	T	23	0.22	*IFITM3*	NM_021034	Missense	p.P70T	0.65	Neutral	0.4	Tolerated	0	benign
A48	9	19058075	19058075	C	T	154	0.44	*HAUS6*	NM_017645	Missense	p.R897H	-1.82	Neutral	0.12	Tolerated	0.025	benign
A49	5	140573648	140573648	C	T	14	0.21	*PCDHB10*	NM_018930	Missense	p.A508V	-3.19	Deleterious	0.03	Damaging	0.966	probably damaging
A49	X	92927826	92927826	C	T	47	0.70	*NAP1L3*	NM_004538	Missense	p.E160K	-2.99	Deleterious	0.09	Tolerated	0.573	possibly damaging
A49	17	80210955	80210955	G	A	79	0.48	*CSNK1D*	NM_001893	Missense	p.R168C	-7.2	Deleterious	0.01	Damaging	1	probably damaging
A49	11	47201086	47201086	G	A	70	0.09	*PACSIN3*	NM_001184975	Missense	p.R219C	-4.97	Deleterious	0.03	Damaging	1	probably damaging
A49	X	133549136	133549136	C	T	31	0.71	*PHF6*	NM_001015877	nonsense	p.R274_	NA	NA	1	Tolerated	NA	NA
A49	4	367442	367442	C	T	161	0.38	*ZNF141*	NM_003441	Missense	p.R406W	-1.97	Neutral	NA	NA	1	probably damaging
A49	5	52403013	52403013	C	T	133	0.21	*MOCS2*	NM_176806	Missense	p.R60H	0.63	Neutral	0	Damaging	1	probably damaging
A49	20	17240946	17240946	G	A	55	0.36	*PCSK2*	NM_002594	Missense	p.R80K	-0.15	Neutral	0.66	Tolerated	0	benign
A49	13	103398840	103398840	T	C	184	0.16	*CCDC168*	NM_001146197	Missense	p.T1403A	NA	NA	NA	NA	NA	NA

A49	16	72153863	72153863	G	A	76	0.14	*PMFBP1*	NM_031293	Missense	p.T965M	-0.39	Neutral	0.07	Tolerated	0.216	benign
A50	12	23687338	23687338	C	A	75	0.37	*SOX5*	NM_006940	nonsense	p.E703_	NA	NA	0.02	Damaging	NA	NA
A50	6	37626117	37626117	C	G	78	0.50	*MDGA1*	NM_153487	Missense	p.E96Q	-0.66	Neutral	0.55	Tolerated	0.998	probably damaging
A50	1	115258744	115258744	C	A	44	0.32	*NRAS*	NM_002524	Missense	p.G13V	-7.65	Deleterious	0	Damaging	0.998	probably damaging
A50	2	179582020	179582020	C	T	150	0.38	*TTN*	NM_001267550	Missense	p.G8481R	-4.35	Deleterious	0	Damaging	1	probably damaging
A50	2	145147550	145147550	T	C	118	0.53	*ZEB2*	NM_014795	Missense	p.H1038R	-7.28	Deleterious	0.08	Tolerated	0.992	probably damaging
A50	9	109694775	109694775	C	T	102	0.29	*ZNF462*	NM_021224	Missense	p.R2021C	-3.76	Deleterious	0.02	Damaging	1	probably damaging
A50	17	40695147	40695147	C	T	88	0.45	*NAGLU*	NM_000263	Missense	p.R375C	-1.24	Neutral	0.18	Tolerated	0.996	probably damaging
A50	11	22281108	22281108	G	A	191	0.49	*ANO5*	NM_213599	Missense	p.R484H	-4.76	Deleterious	0	Damaging	1	probably damaging
A50	9	79634721	79634721	C	T	128	0.54	*FOXB2*	NM_001013735	Missense	p.R51C	-7.7	Deleterious	0	Damaging	1	probably damaging
A50	3	3072567	3072567	G	A	98	0.46	*CNTN4*	NM_175607	Missense	p.R564Q	-2.82	Deleterious	0.12	Tolerated	1	probably damaging
A50	11	70194471	70194471	G	A	91	0.46	*PPFIA1*	NM_003626	Missense	p.R703Q	-1.89	Neutral	0.19	Tolerated	0.996	probably damaging
A50	1	176903320	176903320	C	T	55	0.38	*ASTN1*	NM_004319	Missense	p.R880Q	0.33	Neutral	1	Tolerated	0	benign
A50	2	11053417	11053417	G	A	68	0.44	*KCNF1*	NM_002236	Missense	p.V289M	-2.73	Deleterious	0.03	Damaging	0.992	probably damaging
A50	19	15288380	15288380	G	T	56	0.36	*NOTCH3*	NM_000435	nonsense	p.Y1453_	NA	NA	0.38	Tolerated	NA	NA
A51	10	50339936	50339936	C	G	65	0.49	*FAM170B*	NM_001164484	Missense	p.E192Q	-0.39	Neutral	0.37	Tolerated	0.256	benign
A51	11	94759122	94759122	G	A	53	0.44	*KDM4E*	NM_001161630	Missense	p.G134D	-6.83	Deleterious	0	Damaging	1	probably damaging
A51	10	105823571	105823571	C	T	39	0.38	*COL17A1*	NM_000494	Missense	p.G258R	-3.92	Deleterious	0	Damaging	1	probably damaging
A51	3	195507925	195507925	C	T	14	0.14	*MUC4*	NM_018406	Missense	p.G3509D	0.22	Neutral	NA	NA	0.003	benign
A51	2	145147550	145147550	T	C	94	0.43	*ZEB2*	NM_014795	Missense	p.H1038R	-7.28	Deleterious	0.08	Tolerated	0.992	probably damaging
A51	2	204245097	204245097	A	C	42	0.50	*ABI2*	NM_005759	Missense	p.H151P	-9.27	Deleterious	0	Damaging	1	probably damaging
A51	2	86509349	86509349	G	A	83	0.48	*REEP1*	NM_001164730	Missense	p.L24F	-3.93	Deleterious	0.05	Damaging	0.999	probably damaging
A51	12	3018711	3018711	A	G	98	0.51	*TULP3*	NM_001160408	Missense	p.M20V	-0.6	Neutral	0.44	Tolerated	0.178	benign
A51	9	37015165	37015165	G	C	34	1.00	*PAX5*	NM_016734	Missense	p.P80R	-7.7	Deleterious	0	Damaging	1	probably damaging
A51	14	104642791	104642792	TG	T	54	0.50	*KIF26A*	NM_015656	Frame_Shift_Del	p.R1222fs	NA	NA	NA	NA	NA	NA
A51	3	10970960	10970960	C	T	74	0.39	*SLC6A11*	NM_014229	Missense	p.R436W	-7.19	Deleterious	0	Damaging	1	probably damaging
A51	15	65621883	65621883	G	A	50	0.42	*IGDCC3*	NM_004884	Missense	p.R684W	-1.34	Neutral	0.04	Damaging	0.996	probably damaging
A51	11	4703421	4703421	G	A	70	0.44	*OR51E2*	NM_030774	Missense	p.S174L	-3.5	Deleterious	0.3	Tolerated	0.839	possibly damaging
A51	13	103053922	103053922	G	A	132	0.38	*FGF14*	NM_175929	Missense	p.S36L	-1.35	Neutral	0.09	Tolerated	0.997	probably damaging
A51	15	69325561	69325561	G	A	60	0.48	*NOX5*	NM_024505	Missense	p.V267I	-0.07	Neutral	0.84	Tolerated	0.002	benign
A52	1	36554587	36554587	G	C	43	0.47	*ADPRHL2*	NM_017825	Missense	p.A28P	-2.02	Neutral	0.01	Damaging	0.999	probably damaging
A52	13	28592629	28592629	T	C	96	0.30	*FLT3*	NM_004119	Missense	p.D839G	-6.36	Deleterious	0.04	Damaging	0.827	possibly damaging
A52	9	133589796	133589796	A	C	154	0.36	*ABL1*	NM_007313	Missense	p.E30D	-0.13	Neutral	0.53	Tolerated	0	benign

A52	12	25398284	25398284	C	T	99	0.08	*KRAS*	NM_033360	Missense	p.G12D	-5.37	Deleterious	0	Damaging	0.517	possibly damaging
A52	12	112926887	112926887	G	C	49	0.27	*PTPN11*	NM_002834	Missense	p.G503R	-7.26	Deleterious	0.01	Damaging	1	probably damaging
A52	16	1306971	1306971	A	G	18	0.39	*TPSD1*	NM_012217	Missense	p.H143R	-3.36	Deleterious	0.28	Tolerated	0.003	benign
A52	19	35941582	35941582	G	A	49	0.45	*FFAR2*	NM_005306	Missense	p.M322I	0.2	Neutral	0.42	Tolerated	0.002	benign
A52	9	37015165	37015165	G	C	19	0.84	*PAX5*	NM_016734	Missense	p.P80R	-7.7	Deleterious	0	Damaging	1	probably damaging
A52	19	6678454	6678454	C	T	44	0.39	*C3*	NM_000064	Missense	p.R1548Q	-1.3	Neutral	0.18	Tolerated	0.271	benign
A52	X	26157898	26157898	C	T	43	0.84	*MAGEB18*	NM_173699	Missense	p.R266C	-2.1	Neutral	0.39	Tolerated	0.056	benign
A52	17	2908678	2908678	C	T	76	0.18	*RAP1GAP2*	NM_015085	Missense	p.R406W	-7.49	Deleterious	0	Damaging	1	probably damaging
A52	12	50037934	50037934	C	T	61	0.23	*PRPF40B*	NM_001031698	Missense	p.R880W	-4.4	Deleterious	0	Damaging	0.999	probably damaging
A52	6	72962473	72962473	G	A	69	0.32	*RIMS1*	NM_014989	Missense	p.R903Q	-3.49	Deleterious	0.01	Damaging	1	probably damaging
A52	4	56730536	56730536	C	A	16	0.19	*EXOC1*	NM_001024924	Missense	p.S133R	-1.34	Neutral	0.33	Tolerated	0.673	possibly damaging
A52	11	28352252	28352252	C	T	74	0.28	*METTL15*	NM_001113528	Missense	p.T363M	-0.11	Neutral	NA	NA	0.016	benign
A52	17	33738775	33738775	A	G	166	0.27	*SLFN12*	NM_018042	Missense	p.V440A	-3.43	Deleterious	0.06	Tolerated	0.999	probably damaging
A52	1	93300403	93300403	A	AGCCCC	77	0.31	*RPL5*	NM_000969	Frame_Shift_Ins	p.Y86fs	NA	NA	NA	NA	NA	NA
A53	10	5416147	5416147	C	T	21	0.33	*UCN3*	NM_053049	Missense	p.A155V	-4	Deleterious	0	Damaging	1	probably damaging
A53	15	24921247	24921247	C	T	36	0.25	*NPAP1*	NM_018958	Missense	p.A78V	-1.02	Neutral	0.31	Tolerated	0.324	benign
A53	7	31008756	31008756	A	G	16	0.44	*GHRHR*	NM_000823	Missense	p.D80G	-1.65	Neutral	0.27	Tolerated	0.002	benign
A53	X	9905397	9905397	G	A	97	0.34	*SHROOM2*	NM_001649	Missense	p.E1271K	-2.15	Neutral	0.04	Damaging	0.999	probably damaging
A53	7	150820924	150820924	A	G	45	0.33	*AGAP3*	NM_031946	Missense	p.E391G	-3.23	Deleterious	0.11	Tolerated	0.11	benign
A53	3	195497223	195497223	C	T	52	0.25	*MUC4*	NM_018406	Missense	p.G4421D	-0.07	Neutral	0.68	Tolerated	0.033	benign
A53	10	116698249	116698249	G	GC	56	0.25	*TRUB1*	NM_139169	Frame_Shift_Ins	p.G79fs	NA	NA	NA	NA	NA	NA
A53	3	47059130	47059130	T	G	47	0.28	*SETD2*	NM_014159	Missense	p.K2511Q	-3.55	Deleterious	0	Damaging	0.999	probably damaging
A53	3	195509756	195509756	G	C	18	0.17	*MUC4*	NM_018406	Missense	p.L2899V	0.12	Neutral	NA	NA	0.034	benign
A53	16	87790069	87790069	A	T	41	0.41	*KLHDC4*	NM_017566	Missense	p.L69H	-5.55	Deleterious	0.19	Tolerated	1	probably damaging
A53	16	48290541	48290541	G	T	110	0.32	*LONP2*	NM_031490	Missense	p.M163I	-1.16	Neutral	0.15	Tolerated	0.003	benign
A53	3	195513413	195513413	G	A	16	0.25	*MUC4*	NM_018406	Missense	p.P1680S	-0.27	Neutral	NA	NA	0.544	possibly damaging
A53	3	148558742	148558742	C	T	71	0.27	*CPB1*	NM_001871	Missense	p.R152C	-6.51	Deleterious	0	Damaging	1	probably damaging
A53	9	115759981	115759981	G	A	97	0.26	*ZNF883*	NM_001101338	Missense	p.R187W	NA	NA	NA	NA	NA	NA
A53	1	38227313	38227313	C	T	49	0.24	*EPHA10*	NM_001099439	Missense	p.R205H	-3.69	Deleterious	0.01	Damaging	1	probably damaging
A53	12	6936088	6936088	C	T	118	0.28	*GPR162*	NM_019858	Missense	p.R496W	0.1	Neutral	0.03	Damaging	0.996	probably damaging
A53	1	155753776	155753776	C	T	64	0.28	*GON4L*	NM_001037533	Splice Site	p.R631sp	NA	NA	NA	NA	NA	NA
A53	7	100687041	100687041	C	T	90	0.28	*MUC17*	NM_001040105	Missense	p.T4115M	-0.98	Neutral	0.12	Tolerated	0.521	possibly damaging
A53	9	37020768	37020768	A	C	48	0.48	*PAX5*	NM_016734	Missense	p.V26G	-4.49	Deleterious	0	Damaging	1	probably damaging

A53	5	35873646	35873646	A	G	131	0.35	*IL7R*	NM_002185	Missense	p.Y201C	-8.56	Deleterious	0	Damaging	1	probably damaging
A53	9	99581577	99581577	T	TCCCC	76	0.25	*ZNF782*	NM_001001662	Frame_Shift_Ins	p.Y243fs	NA	NA	NA	NA	NA	NA
A54	12	49415864	49415864	T	TGAG	45	0.40	*MLL2*	NM_003482	In_Frame_Ins	p.5494_5495insL	-9.04	Deleterious	NA	NA	NA	NA
A54	4	7776519	7776519	G	A	35	0.23	*AFAP1*	NM_001134647	Missense	p.A670V	-0.73	Neutral	0.61	Tolerated	0.999	probably damaging
A54	9	21968243	21968243	T	G	12	0.67	*CDKN2A*	NM_001195132	Splice Site	p.D153sp	NA	NA	NA	NA	NA	NA
A54	11	93417292	93417292	A	T	67	0.30	*KIAA1731*	NM_033395	Missense	p.D371V	-3.83	Deleterious	0.07	Tolerated	0.102	benign
A54	3	98216555	98216555	G	C	84	0.42	*OR5K2*	NM_001004737	Missense	p.E11Q	-2.32	Neutral	0.02	Damaging	0.303	benign
A54	19	1622324	1622324	A	AG	30	0.63	*TCF3*	NM_003200	Frame_Shift_Ins	p.F214fs	NA	NA	NA	NA	NA	NA
A54	8	128750684	128750684	C	A	70	0.24	*MYC*	NM_002467	Missense	p.P74Q	-6.31	Deleterious	0	Damaging	1	probably damaging
A54	19	43382086	43382086	G	A	87	0.54	*PSG1*	NM_006905	Missense	p.R137C	-1.79	Neutral	0.03	Damaging	0.967	probably damaging
A54	13	23911374	23911374	C	T	115	0.32	*SACS*	NM_014363	Missense	p.R2214H	-0.14	Neutral	0.01	Damaging	0.389	benign
A54	12	65134449	65134449	C	T	49	0.47	*GNS*	NM_002076	Missense	p.R271K	-1.86	Neutral	NA	NA	1	probably damaging
A54	7	158663888	158663888	G	A	50	0.50	*WDR60*	NM_018051	Missense	p.R42H	-0.09	Neutral	0.41	Tolerated	0.001	benign
A54	14	20404090	20404090	C	T	367	0.23	*OR4K1*	NM_001004063	Missense	p.R89C	-3.46	Deleterious	0.12	Tolerated	0.001	benign
A54	X	153940920	153940920	G	C	29	0.34	*GAB3*	NM_001081573	nonsense	p.S218_	NA	NA	0.06	Tolerated	NA	NA
A54	11	77103484	77103484	T	C	40	0.60	*PAK1*	NM_001128620	Missense	p.S28G	-0.38	Neutral	0.68	Tolerated	0	benign
A54	1	182555100	182555100	A	G	48	0.23	*RNASEL*	NM_021133	Missense	p.V281A	-0.43	Neutral	0.53	Tolerated	0.972	probably damaging
A55	16	90095597	90095597	T	TGGGGCAGCCTACGGGGCAGGCTGC	51	0.24	*C16orf3*	NM_001214	In_Frame_Ins	p.51_52insAACPVGCP	11	Neutral	NA	NA	NA	NA
A55	11	65146930	65146930	C	T	111	0.37	*SLC25A45*	NM_182556	Missense	p.A86T	-0.53	Neutral	0.41	Tolerated	0.061	benign
A55	3	137749921	137749921	G	C	50	0.30	*CLDN18*	NM_001002026	Missense	p.D242H	-0.18	Neutral	0.25	Tolerated	0.664	possibly damaging
A55	5	82835717	82835717	G	T	103	0.52	*VCAN*	NM_004385	nonsense	p.E2299_	NA	NA	0.71	Tolerated	NA	NA
A55	13	76419512	76419512	A	G	44	0.48	*LMO7*	NM_015842	Missense	p.N1150D	-2.97	Deleterious	0.02	Damaging	0.974	probably damaging
A55	19	1037781	1037781	C	A	21	0.19	*CNN2*	NM_004368	Missense	p.P271H	-4.44	Deleterious	0	Damaging	0.999	probably damaging
A55	1	115256530	115256530	G	T	142	0.35	*NRAS*	NM_002524	Missense	p.Q61K	-3.38	Deleterious	0.03	Damaging	0.948	possibly damaging
A55	11	61607827	61607827	C	T	26	0.42	*FADS2*	NM_004265	Missense	p.R114W	-5.39	Deleterious	0	Damaging	0.999	probably damaging
A55	19	39964709	39964709	T	C	46	0.40	*SUPT5H*	NM_001111020	Missense	p.S867P	-0.78	Neutral	NA	NA	0.036	benign
A55	3	75713618	75713618	A	T	19	0.21	*FRG2C*	NM_001124759	Missense	p.T30S	-0.84	Neutral	0.13	Tolerated	0	benign
A56	22	45740439	45740439	A	G	54	0.46	*SMC1B*	NM_148674	Missense	p._1236Q	NA	NA	NA	NA	NA	NA
A56	1	249106236	249106236	C	T	31	0.39	*SH3BP5L*	NM_030645	Missense	p.D349N	-1.52	Neutral	0.08	Tolerated	1	probably damaging

A56	19	42824472	42824472	C	A	52	0.50	*TMEM145*	NM_173633	Missense	p.F359L	-5.3	Deleterious	0.1	Tolerated	0.997	probably damaging
A56	3	64085328	64085328	A	G	101	0.38	*PRICKLE2*	NM_198859	Missense	p.F645S	-0.41	Neutral	0.18	Tolerated	0.09	benign
A56	4	77134668	77134668	C	T	46	0.35	*SCARB2*	NM_005506	Missense	p.G10E	-4.81	Deleterious	0.02	Damaging	1	probably damaging
A56	6	109484040	109484040	A	G	38	0.45	*CEP57L1*	NM_001083535	Missense	p.K417R	-1.52	Neutral	0.21	Tolerated	0.021	benign
A56	6	155635525	155635525	G	A	28	0.50	*TFB1M*	NM_016020	Missense	p.P13L	-9.16	Deleterious	0	Damaging	0.997	probably damaging
A56	19	1529818	1529818	C	T	36	0.39	*PLK5*	NM_001243079	Missense	p.P188L	NA	NA	NA	NA	NA	NA
A56	7	50450244	50450244	G	A	23	0.87	*IKZF1*	NM_006060	Missense	p.R143Q	-3.45	Deleterious	0	Damaging	1	probably damaging
A56	21	41137635	41137635	C	T	73	0.44	*IGSF5*	NM_001080444	Missense	p.R92C	-6.77	Deleterious	0	Damaging	1	probably damaging
A56	16	83636135	83636135	C	T	67	0.46	*CDH13*	NM_001220488	Missense	p.T393M	-5.09	Deleterious	0	Damaging	1	probably damaging
A56	5	135583358	135583358	C	T	68	0.47	*TRPC7*	NM_020389	Missense	p.V549M	-2.82	Deleterious	0.16	Tolerated	1	probably damaging
A57	X	51075851	51075851	G	A	83	0.41	*NUDT10*	NM_153183	Missense	p.D12N	-3.76	Deleterious	0.02	Damaging	0.995	probably damaging
A57	10	29762792	29762792	T	A	26	0.38	*SVIL*	NM_021738	Missense	p.E1835V	-6.04	Deleterious	0.01	Damaging	0.978	probably damaging
A57	19	48183560	48183560	T	C	65	0.38	*GLTSCR1*	NM_015711	Missense	p.L378P	-2.8	Deleterious	0.09	Tolerated	1	probably damaging
A57	4	9784642	9784642	C	T	39	0.56	*DRD5*	NM_000798	Missense	p.P330L	-0.95	Neutral	0.19	Tolerated	0.131	benign
A57	7	142479917	142479917	C	T	30	0.20	*PRSS2*	NM_002770	Missense	p.P4S	NA	NA	NA	NA	NA	NA
A57	5	156770114	156770114	C	T	87	0.45	*FNDC9*	NM_001001343	Missense	p.R144Q	-0.4	Neutral	0.06	Tolerated	0.974	probably damaging
A57	11	93535032	93535032	C	T	49	0.37	*MED17*	NM_004268	nonsense	p.R454_	NA	NA	0.87	Tolerated	NA	NA
A57	3	126708044	126708044	G	A	114	0.53	*PLXNA1*	NM_032242	Missense	p.S203N	-2.38	Neutral	0	Damaging	0.542	possibly damaging
A57	19	10561573	10561573	A	G	41	0.54	*PDE4A*	NM_001111307	Missense	p.T247A	-4.18	Deleterious	0.02	Damaging	0.167	benign
A57	15	75122688	75122688	T	A	23	0.43	*CPLX3*	NM_001030005	Missense	p.V157D	-4.84	Deleterious	0	Damaging	0.265	benign
A58	4	2696747	2696747	C	T	61	0.61	*FAM193A*	NM_001256666	Missense	p.A765V	-0.57	Neutral	0.22	Tolerated	0.634	possibly damaging
A58	2	49210073	49210073	C	T	121	0.39	*FSHR*	NM_000145	Missense	p.G216R	-6.48	Deleterious	NA	NA	1	probably damaging
A58	1	196965323	196965323	T	A	51	0.33	*CFHR5*	NM_030787	Missense	p.M321K	1.46	Neutral	0.98	Tolerated	0	benign
A58	4	94436507	94436507	A	G	29	0.48	*GRID2*	NM_001510	Missense	p.N713S	-0.4	Neutral	1	Tolerated	0.014	benign
A58	15	74365127	74365127	T	G	19	0.26	*GOLGA6A*	NM_001038640	Missense	p.Q486P	-2.83	Deleterious	0.09	Tolerated	0.383	benign
A58	17	56833744	56833744	G	T	29	0.59	*PPM1E*	NM_014906	Missense	p.R129L	-1.28	Neutral	0.65	Tolerated	0.868	possibly damaging
A58	21	44514780	44514780	C	T	94	0.28	*U2AF1*	NM_001025203	Missense	p.R156H	-4.43	Deleterious	0	Damaging	0.947	possibly damaging
A58	4	88536868	88536886	TAGTGACAGCAGCAATAGC	T	12	0.50	*DSPP*	NM_014208	In_Frame_Del	p.SDSSNS1025del	-2.31	Neutral	NA	NA	NA	NA
A58	20	76650	76650	C	A	65	0.42	*DEFB125*	NM_153325	Missense	p.NSSDSS1029del	-1.28	Neutral	0.04	Damaging	0.989	probably damaging
A58	20	43561803	43561803	C	T	66	0.35	*PABPC1L*	NM_001124756	Missense	p.208_209AL>V	-0.49	Neutral	0.18	Tolerated	0.688	possibly damaging

A58	11	132306061	132306061	C	T	144	0.09	*OPCML*	NM_002545	Missense	p.K216del	-0.81	Neutral	0	Damaging	0.997	probably damaging
A59	10	115384635	115384635	C	T	58	0.43	*NRAP*	NM_001261463	Missense	p.KKK73del	-4.8	Deleterious	0	Damaging	1	probably damaging
A59	12	83526035	83526035	G	T	77	0.49	*TMTC2*	NM_152588	Missense	p.I33del	-7.56	Deleterious	0	Damaging	1	probably damaging
A59	12	351866	351866	A	G	101	0.37	*SLC6A13*	NM_016615	Missense	p.EPGCTKVP95del	-3.42	Deleterious	0.09	Tolerated	0.85	possibly damaging
A59	7	25200877	25200877	T	C	23	0.52	*C7orf31*	NM_138811	Missense	p.K105R	-0.62	Neutral	0.42	Tolerated	0.99	probably damaging
A59	16	1270702	1270702	G	A	81	0.49	*CACNA1H*	NM_021098	Missense	p.R2257Q	-1.23	Neutral	0.09	Tolerated	0.997	probably damaging
A59	2	128253656	128253656	C	T	118	0.48	*IWS1*	NM_017969	Missense	p.R545Q	-3.26	Deleterious	0.07	Tolerated	1	probably damaging
A59	4	88536862	88536880	TAATAGTAGTGACAGCAGC	T	14	0.43	*DSPP*	NM_014208	In_Frame_Del	p.NSSDSS1029del	-2.31	Neutral	NA	NA	NA	NA
A59	2	241621869	241621869	G	A	13	0.23	*AQP12B*	NM_001102467	Missense	p.T129M	-1.45	Neutral	0.3	Tolerated	0.998	probably damaging
A59	16	7568374	7568374	G	A	67	0.45	*RBFOX1*	NM_145891	Missense	p.V105I	-0.16	Neutral	0.86	Tolerated	0.998	probably damaging
A59	3	13538275	13538275	G	A	126	0.45	*HDAC11*	NM_024827	Missense	p.V98I	-0.29	Neutral	0	Damaging	0.968	probably damaging
A60	18	55024415	55024415	G	A	193	0.30	*ST8SIA3*	NM_015879	Missense	p.A192T	-2.52	Deleterious	0.03	Damaging	1	probably damaging
A60	19	38229883	38229883	C	T	53	0.23	*ZNF573*	NM_001172690	Missense	p.C503Y	-10.42	Deleterious	0	Damaging	0.961	probably damaging
A60	1	235345029	235345029	T	C	109	0.30	*ARID4B*	NM_001206794	Missense	p.I1069V	0.03	Neutral	0.13	Tolerated	0.948	possibly damaging
A60	11	17317759	17317759	G	A	30	0.23	*NUCB2*	NM_005013	Splice Site	p.K82sp	NA	NA	NA	NA	NA	NA
A60	21	36231783	36231783	G	A	92	0.25	*RUNX1*	NM_001754	nonsense	p.R201_	NA	NA	1	Tolerated	NA	NA
A60	4	186545240	186545240	C	T	168	0.31	*SORBS2*	NM_001270771	Missense	p.R544H	2.86	Neutral	1	Tolerated	0	benign
A60	10	82182259	82182259	C	T	60	0.25	*FAM213A*	NM_001243779	nonsense	p.R89_	NA	NA	1	Tolerated	NA	NA
A60	15	56719836	56719836	G	A	21	0.38	*TEX9*	NM_198524	Missense	p.V333M	0.02	Neutral	0.1	Tolerated	0.493	possibly damaging
A60	6	143093769	143093769	C	T	104	0.25	*HIVEP2*	NM_006734	Missense	p.V703I	-0.4	Neutral	0.07	Tolerated	0.999	probably damaging
A61	16	21049198	21049198	G	T	69	0.45	*DNAH3*	NM_017539	Missense	p.A1612D	-5.58	Deleterious	0	Damaging	1	probably damaging
A61	1	2939186	2939186	T	A	122	0.41	*ACTRT2*	NM_080431	Missense	p.D312E	0.47	Neutral	0	Damaging	0.248	benign
A61	12	3702274	3702274	G	A	94	0.24	*PRMT8*	NM_019854	Missense	p.D371N	-3.88	Deleterious	0.04	Damaging	0.901	possibly damaging
A61	1	22903209	22903209	G	A	81	0.26	*EPHA8*	NM_020526	Missense	p.G220E	-4.76	Deleterious	0.11	Tolerated	1	probably damaging
A62	3	195512665	195512665	G	A	17	0.24	*MUC4*	NM_018406	Missense	p.A1929V	-0.23	Neutral	NA	NA	0.805	possibly damaging
A62	22	46785332	46785332	G	A	40	0.40	*CELSR1*	NM_014246	Missense	p.A2137V	-0.33	Neutral	0.32	Tolerated	0.206	benign
A62	9	133942559	133942559	G	A	53	0.32	*LAMC3*	NM_006059	Missense	p.A854T	-2.77	Deleterious	0.03	Damaging	0.999	probably damaging
A62	1	225239282	225239282	G	A	45	0.36	*DNAH14*	NM_001373	Missense	p.E737K	-1.97	Neutral	0.41	Tolerated	0.222	benign
A62	10	134942011	134942011	G	A	32	0.38	*GPR123*	NM_001083909	Missense	p.G227S	-1.27	Neutral	0.08	Tolerated	0.933	possibly damaging
A62	21	36164771	36164785	CATGCCGATG	C	58	0.14	*RUNX1*	NM_001754	Frame_Shift_Del	p.I337fs	NA	NA	NA	NA	NA	NA

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A62	14	23313673	23313673	A	T	61	0.46	*MMP14*	NM_004995	Missense	p.N369Y	-4.03	Deleterious	0	Damaging	0.999	probably damaging
A62	3	74313607	74313607	G	C	106	0.32	*CNTN3*	NM_020872	Missense	p.P1011R	-2.35	Neutral	0.32	Tolerated	0.002	benign
A63	11	101362381	101362381	A	G	107	0.52	*TRPC6*	NM_004621	Missense	p.I345T	-3.41	Deleterious	0	Damaging	0.982	probably damaging
A63	6	76024806	76024806	G	C	108	0.52	*FILIP1*	NM_015687	Missense	p.L248V	-1.49	Neutral	0.1	Tolerated	1	probably damaging
A63	3	132409450	132409450	A	G	86	0.40	*NPHP3*	NM_153240	Missense	p.L872P	-1.85	Neutral	0.03	Damaging	0.977	probably damaging
A63	15	81585205	81585205	C	CGGGT	29	0.48	*IL16*	NM_172217	Frame_Shift_Ins	p.P577fs	NA	NA	NA	NA	NA	NA
A63	6	43251728	43251728	C	T	40	0.40	*TTBK1*	NM_032538	Missense	p.R1084W	-1.93	Neutral	0.02	Damaging	0.997	probably damaging
A63	8	3057290	3057290	G	A	78	0.45	*CSMD1*	NM_033225	nonsense	p.R1714_	NA	NA	1	Tolerated	NA	NA
A63	9	34976562	34976562	G	A	34	0.65	*KIAA1045*	NM_015297	Missense	p.R225H	0.16	Neutral	0.29	Tolerated	0.023	benign
A63	10	112572152	112572152	G	A	59	0.39	*RBM20*	NM_001134363	Missense	p.R666Q	-1.61	Neutral	0.07	Tolerated	1	probably damaging
A63	3	152058464	152058464	T	TGGCAAG	126	0.34	*TMEM14E*	NM_001123228	In_Frame_Ins	p.77_77Y>SCH	-4.44	Deleterious	NA	NA	NA	NA
A63	9	125797594	125797594	A	G	98	0.45	*GPR21*	NM_005294	Missense	p.Y250C	-0.52	Neutral	0.01	Damaging	1	probably damaging
A64	16	83813678	83813678	C	T	92	0.48	*CDH13*	NM_001220488	Missense	p.A643V	-1.49	Neutral	0.28	Tolerated	0.977	probably damaging
A64	22	23615875	23615875	G	A	71	0.46	*BCR*	NM_004327	Missense	p.A677T	-2.74	Deleterious	0	Damaging	1	probably damaging
A64	11	60776033	60776033	G	A	66	0.50	*CD6*	NM_006725	Missense	p.G166D	-5.88	Deleterious	0	Damaging	1	probably damaging
A64	13	114538522	114538522	C	A	67	0.40	*GAS6*	NM_000820	Missense	p.G226C	-7.2	Deleterious	0	Damaging	1	probably damaging
A64	9	35106609	35106609	C	T	77	0.45	*FAM214B*	NM_025182	Missense	p.G329S	0.31	Neutral	0.64	Tolerated	0.002	benign
A64	20	44691204	44691204	C	A	125	0.43	*NCOA5*	NM_020967	Missense	p.G492V	-0.76	Neutral	0.23	Tolerated	1	probably damaging
A64	3	47059126	47059126	A	AC	64	0.41	*SETD2*	NM_014159	Splice Site	p.K2511sp	NA	NA	NA	NA	NA	NA
A64	6	50696956	50696956	C	T	129	0.51	*TFAP2D*	NM_172238	Missense	p.L272F	-2.04	Neutral	0	Damaging	0.905	possibly damaging
A64	9	23705006	23705006	G	A	133	0.44	*ELAVL2*	NM_004432	Missense	p.P133S	-7.46	Deleterious	0.03	Damaging	1	probably damaging
A64	14	39784004	39784006	GTA	G	21	0.29	*CTAGE5*	NM_001247989	Splice Site	p.Q452sp	NA	NA	NA	NA	NA	NA
A64	16	57180165	57180165	C	G	138	0.46	*CPNE2*	NM_152727	Missense	p.R491G	-4.96	Deleterious	0.03	Damaging	0.719	possibly damaging
A64	3	47098971	47098971	T	TC	51	0.27	*SETD2*	NM_014159	Frame_Shift_Ins	p.T2101fs	NA	NA	NA	NA	NA	NA
A65	16	66621862	66621862	T	TGCGAAA	21	0.29	*CMTM2*	NM_144673	In_Frame_Ins	p.196_197insRK	-6.72	Deleterious	NA	NA	NA	NA
A65	1	98293728	98293728	A	AGATTCC	94	0.19	*DPYD*	NM_000110	In_Frame_Ins	p.58_59insGI	-9.11	Deleterious	NA	NA	NA	NA
A65	3	38950583	38950583	C	T	46	0.33	*SCN11A*	NM_014139	Missense	p.A402T	-3.17	Deleterious	0.1	Tolerated	0.246	benign
A65	17	37566912	37566912	T	C	41	0.34	*MED1*	NM_004774	Missense	p.D521G	-1.39	Neutral	0.12	Tolerated	1	probably damaging
A65	19	54135374	54135374	A	T	31	0.32	*DPRX*	NM_001012728	Missense	p.E5V	-1.68	Neutral	0.04	Damaging	0.789	possibly damaging
A65	3	47161764	47161764	G	GGCTTT	69	0.32	*SETD2*	NM_014159	Frame_Shift_Ins	p.F1454fs	NA	NA	NA	NA	NA	NA

A65	6	69646509	69646509	G	A	40	0.45	*BAI3*	NM_001704	Missense	p.G323R	-2.92	Deleterious	0	Damaging	1	probably damaging
A65	19	35622927	35622927	T	C	82	0.38	*LGI4*	NM_139284	Missense	p.I112V	-0.75	Neutral	0.04	Damaging	0.914	possibly damaging
A65	19	38376118	38376118	C	G	200	0.46	*WDR87*	NM_031951	Missense	p.K2692N	-2.63	Deleterious	0	Damaging	1	probably damaging
A65	6	33146696	33146696	C	A	45	0.51	*COL11A2*	NM_080680	Splice Site	p.K448sp	NA	NA	NA	NA	NA	NA
A65	1	151509267	151509267	G	T	57	0.33	*CGN*	NM_020770	Missense	p.R1123L	-6.33	Deleterious	0.02	Damaging	1	probably damaging
A65	9	33246723	33246723	G	A	34	0.26	*SPINK4*	NM_014471	Missense	p.R71Q	-1.91	Neutral	0.28	Tolerated	0.999	probably damaging
A65	3	195513493	195513493	C	A	25	0.20	*MUC4*	NM_018406	Missense	p.S1653I	-0.13	Neutral	NA	NA	0.797	possibly damaging
A65	17	7350889	7350889	C	G	106	0.36	*CHRNB1*	NM_000747	Missense	p.S177W	-4.25	Deleterious	0.04	Damaging	1	probably damaging
A65	11	124294029	124294029	C	G	105	0.33	*OR8B4*	NM_001005196	Missense	p.V247L	-2.52	Deleterious	0.05	Damaging	0.971	probably damaging
A65	16	75269677	75269677	C	T	68	0.49	*BCAR1*	NM_001170714	Missense	p.V420M	-1.54	Neutral	0.13	Tolerated	1	probably damaging
A65	17	42168683	42168683	C	T	42	0.38	*HDAC5*	NM_001015053	Missense	p.V449M	0.13	Neutral	0.62	Tolerated	0.999	probably damaging
A65	3	47058711	47058711	A	AG	74	0.34	*SETD2*	NM_014159	Frame_Shift_Ins	p.Y2523fs	NA	NA	NA	NA	NA	NA
A65	21	31933589	31933589	T	C	105	0.36	*KRTAP19-7*	NM_181614	Missense	p.Y7C	-5.06	Deleterious	0	Damaging	0.011	benign
A66	3	190573431	190573431	C	T	60	0.42	*GMNC*	NM_001146686	Missense	p.A220T	-0.03	Neutral	0.72	Tolerated	0	benign
A66	6	84895045	84895045	G	A	51	0.51	*KIAA1009*	NM_014895	Missense	p.A508V	-1.09	Neutral	0.24	Tolerated	0.99	probably damaging
A66	19	9088055	9088055	C	T	126	0.52	*MUC16*	NM_024690	Missense	p.G1254R	-1.93	Neutral	0	Damaging	0.519	possibly damaging
A66	14	64892742	64892742	T	C	11	0.36	*MTHFD1*	NM_005956	Missense	p.I320T	-4.54	Deleterious	0	Damaging	0.995	probably damaging
A66	2	133541770	133541770	G	T	74	0.41	*NCKAP5*	NM_207363	Missense	p.L872I	-1.12	Neutral	0.18	Tolerated	0.822	possibly damaging
A66	3	47371553	47371553	A	G	42	0.17	*KLHL18*	NM_025010	Missense	p.M172V	-0.99	Neutral	0.18	Tolerated	0	benign
A66	19	56041480	56041481	AG	A	23	0.52	*SBK2*	NM_001101401	Frame_Shift_Del	p.P222fs	NA	NA	NA	NA	NA	NA
A66	11	28112994	28112994	G	C	83	0.45	*KIF18A*	NM_031217	Missense	p.Q184E	-0.7	Neutral	0.15	Tolerated	0.013	benign
A66	12	6697096	6697096	C	G	84	0.40	*CHD4*	NM_001273	Missense	p.R1162P	-6.29	Deleterious	0	Damaging	0.999	probably damaging
A66	4	42895323	42895323	C	T	34	0.38	*GRXCR1*	NM_001080476	Missense	p.R14W	-2.27	Neutral	0	Damaging	0.998	probably damaging
A66	9	84228342	84228342	C	T	42	0.38	*TLE1*	NM_005077	Missense	p.R338H	-2.64	Deleterious	0.01	Damaging	1	probably damaging
A66	10	101567839	101567839	G	A	152	0.45	*ABCC2*	NM_000392	Splice Site	p.R631sp	NA	NA	NA	NA	NA	NA
A66	9	5078360	5078360	A	G	26	0.46	*JAK2*	NM_004972	Missense	p.R683G	-5.88	Deleterious	0	Damaging	1	probably damaging
A66	10	115804724	115804724	C	T	14	0.36	*ADRB1*	NM_000684	Missense	p.S278L	-1.15	Neutral	0.28	Tolerated	0.11	benign
A66	3	185252860	185252860	G	A	104	0.45	*LIPH*	NM_139248	Missense	p.T37M	-3.47	Deleterious	0.01	Damaging	1	probably damaging
A66	1	152192219	152192219	G	C	27	0.11	*HRNR*	NM_001009931	Missense	p.T629S	1.5	Neutral	0.78	Tolerated	0	benign
A66	19	36322580	36322581	AC	A	15	0.47	*NPHS1*	NM_004646	Frame_Shift_Del	p.V1084fs	NA	NA	NA	NA	NA	NA
A67	21	26969689	26969692	AAAG	A	20	0.30	*MRPL39*	NM_080794	In_Frame_Del	p.208_209AL>V	-10.49	Deleterious	NA	NA	NA	NA
A67	X	101159223	101159223	C	A	55	0.95	*ZMAT1*	NM_001011657	nonsense	p.E68_	NA	NA	0.05	Damaging	NA	NA

A67	17	43005428	43005428	C	T	96	0.45	*KIF18B*	NM_001265577	Missense	p.E748K	-0.71	Neutral	0.63	Tolerated	0.873	possibly damaging
A67	2	27324371	27324371	C	T	24	0.21	*CGREF1*	NM_001166239	Missense	p.G243E	-0.08	Neutral	0.34	Tolerated	0.36	benign
A67	1	248524992	248524992	A	G	79	0.13	*OR2T4*	NM_001004696	Missense	p.N37S	-3.3	Deleterious	0.01	Damaging	0.028	benign
A67	6	71562360	71562361	CA	C	73	0.36	*SMAP1*	NM_001044305	Frame_Shift_Del	p.P261fs	NA	NA	NA	NA	NA	NA
A67	11	1093631	1093631	G	C	70	0.09	*MUC2*	NM_002457	Missense	p.S1817T	0.48	Neutral	0.5	Tolerated	0	benign
A68	19	12858277	12858277	C	CGGG	49	0.22	*ASNA1*	NM_004317	In_Frame_Ins	p.262_263insG	-9.71	Deleterious	NA	NA	NA	NA
A68	X	54949351	54949351	C	A	47	0.11	*TRO*	NM_001039705	Missense	p.A129D	-2	Neutral	0.04	Damaging	0.745	possibly damaging
A68	3	195508009	195508009	G	A	12	0.25	*MUC4*	NM_018406	Missense	p.A3481V	-0.48	Neutral	NA	NA	0.735	possibly damaging
A68	1	115258747	115258747	C	T	43	0.23	*NRAS*	NM_002524	Missense	p.G12D	-5.35	Deleterious	0	Damaging	0.372	benign
A68	1	160340606	160340606	G	A	28	0.68	*NHLH1*	NM_005598	Missense	p.G29R	-0.44	Neutral	0.26	Tolerated	0.01	benign
A68	1	228557668	228557668	G	A	73	0.19	*OBSCN*	NM_001271223	Missense	p.G7622S	-3.41	Deleterious	0.45	Tolerated	1	probably damaging
A68	19	12858275	12858275	A	G	53	0.23	*ASNA1*	NM_004317	Missense	p.I262V	0.06	Neutral	0.77	Tolerated	0.278	benign
A68	11	71724224	71724224	T	G	44	0.50	*NUMA1*	NM_006185	Missense	p.K1442T	-0.97	Neutral	0.08	Tolerated	0.493	possibly damaging
A68	1	7890026	7890026	A	G	83	0.20	*PER3*	NM_016831	Missense	p.K998E	0.66	Neutral	1	Tolerated	0	benign
A68	3	187086326	187086326	C	G	61	0.51	*RTP4*	NM_022147	Missense	p.L33V	-2.03	Neutral	0.07	Tolerated	0.995	probably damaging
A68	16	28914643	28914643	G	A	83	0.12	*ATP2A1*	NM_173201	Splice Site	p.M830sp	NA	NA	NA	NA	NA	NA
A68	1	7890024	7890024	T	G	85	0.18	*PER3*	NM_016831	Missense	p.M997R	-0.32	Neutral	0.65	Tolerated	0	benign
A68	19	14717804	14717804	G	T	38	0.11	*CLEC17A*	NM_001204118	Splice Site	p.N299sp	NA	NA	NA	NA	NA	NA
A68	17	79410417	79410417	C	T	43	0.37	*BAHCC1*	NM_001080519	Missense	p.P626L	-6.91	Deleterious	0.02	Damaging	0.991	probably damaging
A68	2	88409913	88409913	G	A	45	0.56	*SMYD1*	NM_198274	Missense	p.R452H	-0.86	Neutral	0.01	Damaging	0.001	benign
A68	15	74179971	74179971	C	T	43	0.44	*TBC1D21*	NM_153356	Missense	p.T263M	-5.49	Deleterious	0	Damaging	0.996	probably damaging
A68	11	119185731	119185731	G	A	53	0.47	*MCAM*	NM_006500	Missense	p.T71M	-0.13	Neutral	0.12	Tolerated	0.084	benign
A68	12	21422655	21422655	C	A	49	0.49	*SLCO1A2*	NM_021094	Missense	p.V614F	-0.68	Neutral	0.55	Tolerated	0	benign
A70	1	78958472	78958472	C	T	88	0.49	*PTGFR*	NM_000959	Missense	p.A15V	-0.4	Neutral	0.3	Tolerated	0.001	benign
A70	7	56045958	56045962	TGTGA	T	101	0.24	*GBAS*	NM_001483	Splice Site	p.F78sp	NA	NA	NA	NA	NA	NA
A70	X	47083137	47083137	G	T	43	0.44	*CDK16*	NM_001170460	Missense	p.G135C	-1	Neutral	0.01	Damaging	0.983	probably damaging
A70	1	51829571	51829571	C	T	150	0.47	*EPS15*	NM_001981	Missense	p.G776R	-3.49	Deleterious	0.31	Tolerated	1	probably damaging
A70	15	34648797	34648797	T	C	73	0.47	*NUTM1*	NM_175741	Missense	p.L835P	-2.24	Neutral	0	Damaging	0.385	benign
A70	10	106166477	106166477	C	T	112	0.49	*CCDC147*	NM_001008723	nonsense	p.Q728_	NA	NA	0.75	Tolerated	NA	NA
A70	12	129028546	129028546	G	A	50	0.34	*TMEM132C*	NM_001136103	Missense	p.R340H	-0.82	Neutral	0.05	Damaging	0.994	probably damaging
A70	7	50367243	50367243	G	GC	68	0.34	*IKZF1*	NM_006060	Frame_Shift_Ins	p.S17fs	NA	NA	NA	NA	NA	NA
A70	12	49920033	49920033	T	A	98	0.45	*SPATS2*	NM_023071	Missense	p.S545T	-0.53	Neutral	0.06	Tolerated	0.596	possibly damaging

A70	19	38948930	38948930	C	T	245	0.42	*RYR1*	NM_000540	Missense	p.T722I	-3.74	Deleterious	0.01	Damaging	0.944	possibly damaging
A70	16	71668362	71668362	G	A	104	0.47	*MARVELD3*	NM_052858	Missense	p.V288I	0.26	Neutral	0.29	Tolerated	0.002	benign
A71	5	114879163	114879163	C	T	47	0.21	*FEM1C*	NM_020177	Missense	p.A10T	-2.27	Neutral	0.01	Damaging	1	probably damaging
A71	10	105963507	105963507	A	T	54	0.17	*WDR96*	NM_025145	Missense	p.F340I	-0.53	Neutral	0.5	Tolerated	0.944	possibly damaging
A71	1	115258747	115258747	C	G	57	0.35	*NRAS*	NM_002524	Missense	p.G12A	-4.62	Deleterious	0	Damaging	0.775	possibly damaging
A71	11	74873698	74873698	A	G	54	0.13	*SLCO2B1*	NM_007256	Splice Site	p.G6sp	NA	NA	NA	NA	NA	NA
A71	17	691247	691247	A	G	23	0.30	*RNMTL1*	NM_018146	Missense	p.K201R	-0.5	Neutral	0.26	Tolerated	0.001	benign
A71	9	21994329	21994329	A	T	65	0.29	*CDKN2A*	NM_058195	Missense	p.M1K	-5.18	Deleterious	0	Damaging	0.51	possibly damaging
A71	6	31540617	31540617	A	G	62	0.39	*LTA*	NM_001159740	Missense	p.Q33R	-1.15	Neutral	0.01	Damaging	0.58	possibly damaging
A71	2	189859787	189859787	C	T	65	0.28	*COL3A1*	NM_000090	nonsense	p.R491_	NA	NA	1	Tolerated	NA	NA
A71	1	145293566	145293566	G	A	22	0.32	*NBPF10*	NM_001039703	Missense	p.R54Q	0.82	Neutral	1	Tolerated	NA	NA
A71	4	9892247	9892247	G	A	39	0.46	*SLC2A9*	NM_020041	Missense	p.T401M	-2.37	Neutral	0	Damaging	0.257	benign
A71	12	121682942	121682942	C	T	25	0.24	*CAMKK2*	NM_001270485	Splice Site	p.T516sp	NA	NA	NA	NA	NA	NA
A71	5	38407063	38407063	T	C	67	0.31	*EGFLAM*	NM_001205301	Missense	p.V321A	-0.07	Neutral	0.84	Tolerated	0.001	benign
A71	10	126691583	126691583	C	T	22	0.27	*CTBP2*	NM_022802	Missense	p.V642M	-2.45	Neutral	0.04	Damaging	0.97	probably damaging
A72	7	50605676	50605676	G	A	54	0.22	*DDC*	NM_000790	Missense	p.A106V	-0.85	Neutral	0.1	Tolerated	0.048	benign
A72	2	31600051	31600051	G	A	48	0.31	*XDH*	NM_000379	Missense	p.A432V	-3.5	Deleterious	0	Damaging	0.996	probably damaging
A72	1	115258747	115258747	C	T	33	0.21	*NRAS*	NM_002524	Missense	p.G12D	-5.35	Deleterious	0	Damaging	0.372	benign
A72	15	55652331	55652331	T	C	83	0.16	*CCPG1*	NM_001204450	Missense	p.K547R	-1.17	Neutral	0.37	Tolerated	0.993	probably damaging
A72	19	18705208	18705208	C	A	50	0.22	*CRLF1*	NM_004750	Missense	p.R354L	-0.33	Neutral	0.66	Tolerated	0.649	possibly damaging
A72	2	153512896	153512896	G	C	137	0.26	*PRPF40A*	NM_017892	Missense	p.S906C	-2.46	Neutral	0.01	Damaging	0.997	probably damaging
A72	3	130744066	130744066	C	A	166	0.23	*ASTE1*	NM_014065	Missense	p.V29F	-3.66	Deleterious	0.03	Damaging	0.988	probably damaging
A73	7	20784913	20784913	C	A	69	0.39	*ABCB5*	NM_001163941	Missense	p.A1094E	-2.18	Neutral	0	Damaging	0.602	possibly damaging
A73	1	19062154	19062154	C	T	37	0.24	*PAX7*	NM_002584	Missense	p.A395V	-1.77	Neutral	0.14	Tolerated	0.926	possibly damaging
A73	16	57197939	57197939	T	G	94	0.40	*FAM192A*	NM_024946	Missense	p.D174A	0.03	Neutral	0.75	Tolerated	0	benign
A73	5	78340206	78340206	A	T	229	0.38	*DMGDH*	NM_013391	Missense	p.D305E	-1.36	Neutral	0.16	Tolerated	0.929	possibly damaging
A73	14	75266060	75266060	G	C	115	0.36	*YLPM1*	NM_019589	Missense	p.E1354Q	-1.16	Neutral	0.07	Tolerated	0.986	probably damaging
A73	17	39768802	39768802	C	T	19	0.32	*KRT16*	NM_005557	Missense	p.G47R	-3.57	Deleterious	0.24	Tolerated	0.671	possibly damaging
A73	7	100645834	100645834	A	G	28	0.11	*MUC12*	NM_001164462	Missense	p.H3997R	-1.86	Neutral	0.54	Tolerated	NA	NA
A73	1	1737942	1737942	A	C	71	0.37	*GNB1*	NM_002074	Missense	p.I80S	-4.95	Deleterious	0.03	Damaging	0.997	probably damaging
A73	7	140453134	140453134	T	C	45	0.29	*BRAF*	NM_004333	Missense	p.K601E	-3.71	Deleterious	0	Damaging	0.784	possibly damaging
A73	9	139569199	139569202	ACTT	A	103	0.36	*AGPAT2*	NM_006412	In_Frame_Del	p.K216del	-9.84	Deleterious	NA	NA	NA	NA
A73	6	55147095	55147095	G	A	125	0.42	*HCRTR2*	NM_001526	Missense	p.R393Q	-1.14	Neutral	0.57	Tolerated	0.027	benign

A73	1	47284367	47284367	C	T	57	0.39	*CYP4B1*	NM_001099772	Missense	p.R474C	-6.2	Deleterious	NA	NA	0.999	probably damaging
A73	17	32961826	32961826	G	A	43	0.40	*TMEM132E*	NM_207313	Missense	p.R476Q	-3.46	Deleterious	0.05	Damaging	1	probably damaging
A73	4	23815345	23815345	T	A	104	0.37	*PPARGC1A*	NM_013261	Missense	p.R587S	-0.9	Neutral	0.34	Tolerated	0.982	probably damaging
A73	12	52845435	52845435	C	T	45	0.15	*KRT6B*	NM_005555	Missense	p.S143N	-1.42	Neutral	0.05	Damaging	0.053	benign
A73	12	100496586	100496586	C	T	72	0.29	*UHRF1BP1L*	NM_015054	Missense	p.S99N	-1.4	Neutral	0.21	Tolerated	0.073	benign
A73	1	236645825	236645825	C	T	57	0.35	*EDARADD*	NM_145861	Missense	p.T175M	-4.54	Deleterious	NA	NA	0.999	probably damaging
A74	16	1706649	1706649	G	A	128	0.52	*CRAMP1L*	NM_020825	Missense	p.D631N	-1.02	Neutral	0.1	Tolerated	0.675	possibly damaging
A74	12	16043552	16043552	G	A	29	0.28	*STRAP*	NM_007178	Missense	p.G118R	-7	Deleterious	0	Damaging	1	probably damaging
A74	3	52402764	52402764	G	A	26	0.46	*DNAH1*	NM_015512	Missense	p.G1925R	-7.7	Deleterious	0	Damaging	1	probably damaging
A74	1	240371913	240371913	G	T	91	0.46	*FMN2*	NM_020066	Missense	p.L1267F	-2.6	Deleterious	NA	NA	1	probably damaging
A74	4	148406949	148406949	C	T	172	0.48	*EDNRA*	NM_001957	Missense	p.T39I	-0.36	Neutral	0.14	Tolerated	0.589	possibly damaging
A74	7	57187764	57187764	G	A	63	0.41	*ZNF479*	NM_033273	Missense	p.T453I	-5.11	Deleterious	0.27	Tolerated	0.116	benign
A74	2	201469525	201469525	A	G	114	0.41	*AOX1*	NM_001159	Missense	p.Y259C	-6.79	Deleterious	0.01	Damaging	0.997	probably damaging
A75	5	137347496	137347496	G	T	54	0.28	*FAM13B*	NM_016603	Missense	p.A170E	-1.9	Neutral	0.05	Damaging	0.998	probably damaging
A75	5	140724975	140724975	G	A	155	0.32	*PCDHGA3*	NM_018916	Missense	p.A459T	-1.35	Neutral	0.19	Tolerated	0.504	possibly damaging
A75	X	41495908	41495908	C	G	47	0.60	*CASK*	NM_003688	Missense	p.D280H	-2.97	Deleterious	0	Damaging	1	probably damaging
A75	19	41944181	41944181	C	A	108	0.24	*ATP5SL*	NM_001167867	nonsense	p.E59_	NA	NA	0.1	Tolerated	NA	NA
A75	11	66392254	66392254	G	A	66	0.21	*RBM14*	NM_006328	Missense	p.G303S	0.54	Neutral	0.29	Tolerated	1	probably damaging
A75	7	48285506	48285506	A	C	93	0.30	*ABCA13*	NM_152701	Missense	p.K513T	-0.59	Neutral	0.02	Damaging	0.213	benign
A75	6	35945010	35945010	G	T	76	0.30	*SLC26A8*	NM_001193476	Missense	p.L382I	-0.68	Neutral	0.15	Tolerated	0.473	possibly damaging
A75	11	55406609	55406609	C	T	98	0.55	*OR4P4*	NM_001004124	Missense	p.P259L	-8.58	Deleterious	0	Damaging	0.772	possibly damaging
A75	17	77757645	77757645	C	T	81	0.31	*CBX2*	NM_005189	Missense	p.R135W	-3.89	Deleterious	0.01	Damaging	1	probably damaging
A75	X	41495910	41495910	C	T	48	0.58	*CASK*	NM_003688	Missense	p.R279Q	-2.38	Neutral	0.01	Damaging	0.998	probably damaging
A75	12	52884454	52884454	G	A	140	0.23	*KRT6A*	NM_005554	Missense	p.R326C	-7.15	Deleterious	0.01	Damaging	0.989	probably damaging
A75	10	99517399	99517399	C	T	68	0.18	*ZFYVE27*	NM_001002261	Missense	p.R369W	-4.06	Deleterious	NA	NA	1	probably damaging
A75	5	73153591	73153591	G	A	30	0.27	*ARHGEF28*	NM_001080479	Missense	p.R634Q	-1.88	Neutral	0.05	Damaging	1	probably damaging
A75	X	104464853	104464853	G	A	20	0.75	*TEX13A*	NM_031274	Missense	p.R77C	-7.48	Deleterious	0	Damaging	1	probably damaging
A75	7	130021607	130021607	C	T	145	0.26	*CPA1*	NM_001868	Missense	p.S95L	-0.65	Neutral	0.29	Tolerated	0.004	benign
A75	2	203420606	203420606	A	G	118	0.21	*BMPR2*	NM_001204	Missense	p.T740A	-0.16	Neutral	0.84	Tolerated	0	benign
A76	11	92599980	92599980	C	T	101	0.33	*FAT3*	NM_001008781	Missense	p.A3911V	-0.01	Neutral	0.5	Tolerated	0.199	benign
A76	1	148011037	148011037	C	G	48	0.13	*NBPF8*	NM_001037501	Missense	p.D625H	-0.43	Neutral	0.01	Damaging	0.918	possibly damaging

A76	1	154842199	154842199	G	GGCTGCTGCTGCTGCTGCTGCTGCTGCT	14	0.14	*KCNN3*	NM_001204087	In_Frame_Ins	p.80_81insQQQQQQQQQ	-1.5	Neutral	NA	NA	NA	NA
A76	10	23244839	23244839	A	G	40	0.40	*ARMC3*	NM_173081	Missense	p.I90M	-1.21	Neutral	0.13	Tolerated	0.988	probably damaging
A76	17	29214270	29214270	A	G	52	0.31	*ATAD5*	NM_024857	Missense	p.K1380E	-1.29	Neutral	0.47	Tolerated	0.483	possibly damaging
A76	13	47469878	47469878	A	C	86	0.35	*HTR2A*	NM_000621	Missense	p.L55R	-1.56	Neutral	0.34	Tolerated	0.856	possibly damaging
A76	8	77767964	77767964	T	A	144	0.37	*ZFHX4*	NM_024721	Missense	p.M2936K	-5.6	Deleterious	0	Damaging	0.947	possibly damaging
A76	12	66709139	66709139	A	G	21	0.29	*HELB*	NM_033647	Missense	p.Q659R	-1.48	Neutral	NA	NA	0.136	benign
A76	17	9066277	9066277	G	A	24	0.50	*NTN1*	NM_004822	Missense	p.R389H	-4.51	Deleterious	0.03	Damaging	1	probably damaging
A76	15	40861552	40861552	C	A	46	0.33	*RPUSD2*	NM_152260	Missense	p.R6S	0.05	Neutral	0.6	Tolerated	0.001	benign
A76	2	102992512	102992512	C	A	24	0.38	*IL18R1*	NM_003855	Missense	p.T205K	-2.11	Neutral	1	Tolerated	0.211	benign
A76	12	49937785	49937785	C	T	52	0.42	*KCNH3*	NM_012284	Missense	p.T304I	-4.27	Deleterious	0.03	Damaging	0.967	probably damaging
A76	17	35825723	35825723	G	T	53	0.30	*TADA2A*	NM_133439	Missense	p.V301L	0.43	Neutral	NA	NA	0	benign
A76	4	17826660	17826660	G	A	74	0.30	*NCAPG*	NM_022346	Missense	p.V485I	-0.42	Neutral	0.34	Tolerated	0	benign
A77	2	51254919	51254919	C	T	92	0.12	*NRXN1*	NM_001135659	Missense	p.A165T	-0.26	Neutral	0.58	Tolerated	0.599	possibly damaging
A77	6	93956694	93956694	C	T	82	0.44	*EPHA7*	NM_004440	Missense	p.A848T	-3.01	Deleterious	0	Damaging	1	probably damaging
A77	11	9202620	9202620	G	C	31	0.32	*DENND5A*	NM_015213	Missense	p.C383W	-9.29	Deleterious	0	Damaging	1	probably damaging
A77	4	187197453	187197453	G	A	99	0.41	*F11*	NM_000128	Missense	p.D222N	-2.89	Deleterious	0.05	Damaging	1	probably damaging
A77	10	90362351	90362351	T	G	52	0.44	*LIPJ*	NM_001010939	Missense	p.F248V	0.65	Neutral	0.5	Tolerated	0	benign
A77	2	21229928	21229928	C	T	178	0.43	*APOB*	NM_000384	Missense	p.G3271D	-2.75	Deleterious	0.03	Damaging	0.216	benign
A77	11	88242508	88242508	C	T	44	0.55	*GRM5*	NM_001143831	Missense	p.G964D	-0.02	Neutral	NA	NA	0.065	benign
A77	3	154024012	154024012	G	A	62	0.52	*DHX36*	NM_020865	Missense	p.L296F	-3.32	Deleterious	0.05	Damaging	0.915	possibly damaging
A77	17	2218996	2218996	C	A	130	0.46	*SRR*	NM_021947	Missense	p.L48I	-0.37	Neutral	0.05	Damaging	0.007	benign
A77	17	37627965	37627965	T	C	90	0.29	*CDK12*	NM_016507	Missense	p.L627S	-3.76	Deleterious	0.08	Tolerated	1	probably damaging
A77	14	20345201	20345201	A	C	230	0.41	*OR4K2*	NM_001005501	Missense	p.M259L	0.22	Neutral	0.35	Tolerated	0	benign
A77	X	129148441	129148441	C	T	39	0.59	*BCORL1*	NM_021946	nonsense	p.Q565_	NA	NA	0.53	Tolerated	NA	NA
A77	5	169535116	169535116	G	A	114	0.42	*FOXI1*	NM_012188	Missense	p.R213H	-4.37	Deleterious	0.01	Damaging	1	probably damaging
A77	13	113333772	113333772	C	T	41	0.59	*C13orf35*	NM_207440	Missense	p.R27C	-8	Deleterious	0	Damaging	0.009	benign
A77	7	128478704	128478704	C	T	62	0.50	*FLNC*	NM_001458	Missense	p.R420W	-4.52	Deleterious	0	Damaging	0.996	probably damaging
A77	7	14880851	14880851	G	A	110	0.50	*DGKB*	NM_004080	Missense	p.S13L	-1.68	Neutral	0.13	Tolerated	0.001	benign
A77	2	55277417	55277417	G	GCC	54	0.44	*RTN4*	NM_020532	Frame_Shift_Ins	p.S7fs	NA	NA	NA	NA	NA	NA
A77	6	10956435	10956435	C	A	48	0.58	*SYCP2L*	NM_001040274	Missense	p.T708N	-1.81	Neutral	0.04	Damaging	0.125	benign

A77	2	175436688	175436688	A	C	31	0.39	*WIPF1*	NM_003387	Missense	p.V282G	-0.53	Neutral	0.43	Tolerated	0	benign
A77	18	50866208	50866208	G	A	121	0.36	*DCC*	NM_005215	Missense	p.V764I	0.03	Neutral	0.97	Tolerated	0.009	benign
A78	19	56125165	56125165	G	GC	14	0.14	*ZNF865*	NM_001195605	Frame_Shift_Ins	p.A61fs	NA	NA	NA	NA	NA	NA
A78	3	51459856	51459856	T	C	78	0.44	*VPRBP*	NM_014703	Missense	p.D572G	-5.9	Deleterious	0	Damaging	0.996	probably damaging
A78	3	4829742	4829742	G	A	122	0.45	*ITPR1*	NM_001168272	Missense	p.E2228K	-3.45	Deleterious	0.55	Tolerated	0.31	benign
A78	1	119964611	119964611	A	G	72	0.49	*HSD3B2*	NM_001166120	Missense	p.K163E	-1.78	Neutral	NA	NA	0.333	benign
A78	9	37020673	37020673	G	A	38	0.61	*PAX5*	NM_016734	Missense	p.L58F	-3.31	Deleterious	0	Damaging	1	probably damaging
A78	2	238249317	238249317	G	A	56	0.43	*COL6A3*	NM_004369	Missense	p.P2748S	1.52	Neutral	0.65	Tolerated	0.896	possibly damaging
A78	12	133158342	133158342	C	T	43	0.37	*FBRSL1*	NM_001142641	Missense	p.P686L	-5.17	Deleterious	0.03	Damaging	0.997	probably damaging
A78	1	228033691	228033691	C	T	94	0.49	*PRSS38*	NM_183062	Missense	p.R255C	-2.89	Deleterious	0.06	Tolerated	0.993	probably damaging
A78	7	82389989	82389989	C	T	66	0.59	*PCLO*	NM_033026	Missense	p.R5085Q	-1.87	Neutral	0	Damaging	1	probably damaging
A78	6	34985808	34985808	C	T	36	0.42	*ANKS1A*	NM_015245	Missense	p.S661L	-1.11	Neutral	0	Damaging	0.993	probably damaging
A79	2	160803306	160803306	A	T	107	0.48	*PLA2R1*	NM_001007267	Missense	p._1325R	NA	NA	NA	NA	NA	NA
A79	6	159134895	159134895	G	A	87	0.44	*SYTL3*	NM_001242384	Missense	p.A194T	1.84	Neutral	0.9	Tolerated	0	benign
A79	1	117150792	117150792	C	T	92	0.14	*IGSF3*	NM_001542	Missense	p.A332T	-2.38	Neutral	0.06	Tolerated	1	probably damaging
A79	5	35694388	35694388	AG	A	128	0.48	*SPEF2*	NM_024867	Splice Site	p.D634sp	NA	NA	NA	NA	NA	NA
A79	3	113002338	113002338	G	C	44	0.43	*BOC*	NM_033254	Missense	p.E838Q	-0.57	Neutral	0.4	Tolerated	0.763	possibly damaging
A79	4	70146573	70146573	T	C	19	0.84	*UGT2B28*	NM_053039	Missense	p.F119L	-2.77	Deleterious	0.32	Tolerated	0	benign
A79	14	105349434	105349434	C	T	66	0.48	*CEP170B*	NM_001112726	Missense	p.P214S	-1.97	Neutral	0.08	Tolerated	0.437	benign
A79	20	51872999	51872999	G	A	77	0.43	*TSHZ2*	NM_173485	Missense	p.R1001Q	-2.33	Neutral	0	Damaging	1	probably damaging
A79	22	35478615	35478615	C	T	112	0.47	*ISX*	NM_001008494	Missense	p.R112C	-7.97	Deleterious	0	Damaging	1	probably damaging
A79	4	84222252	84222252	A	G	34	0.41	*HPSE*	NM_001098540	Missense	p.Y445H	-3.75	Deleterious	0.24	Tolerated	1	probably damaging
A81	11	396953	396953	C	A	33	0.52	*PKP3*	NM_007183	Missense	p.A151D	-1.15	Neutral	0.22	Tolerated	0.01	benign
A81	20	33570359	33570359	G	A	67	0.16	*MYH7B*	NM_020884	Splice Site	p.A250sp	NA	NA	NA	NA	NA	NA
A81	11	64118671	64118671	G	C	33	0.42	*CCDC88B*	NM_032251	Missense	p.A968P	-2.1	Neutral	0.21	Tolerated	0.764	possibly damaging
A81	7	148801201	148801201	C	T	103	0.50	*ZNF425*	NM_001001661	Missense	p.D588N	0.98	Neutral	0	Damaging	0.009	benign
A81	8	10467581	10467581	C	CTTTAGTCCCCTCTAACTGCACCCCCTCTTCTTGCAGCCCTTCTTCTGT	242	0.50	*RP1L1*	NM_178857	In_Frame_Ins	p.1341_1342insKTEEGLQEEGVQLEGT	2.53	Neutral	NA	NA	NA	NA

A81	17	29667602	29667602	G	A	48	0.73	*NF1*	NM_001042492	Missense	p.G2334D	-5.74	Deleterious	0	Damaging	1	probably damaging
A81	2	74317152	74317152	T	C	25	0.24	*TET3*	NM_144993	Missense	p.L871P	-6.61	Deleterious	0	Damaging	1	probably damaging
A81	X	23748991	23748991	G	T	53	0.25	*ACOT9*	NM_001037171	Missense	p.P102T	-7.48	Deleterious	0	Damaging	1	probably damaging
A81	17	18138002	18138002	G	A	68	0.10	*LLGL1*	NM_004140	Missense	p.R297Q	-0.6	Neutral	0.58	Tolerated	0.473	possibly damaging
A81	X	135741495	135741495	C	T	50	0.52	*CD40LG*	NM_000074	Missense	p.S236L	-2.22	Neutral	0.34	Tolerated	1	probably damaging
A81	3	14862098	14862098	C	T	111	0.12	*FGD5*	NM_152536	Missense	p.S507L	-0.29	Neutral	0.16	Tolerated	0.014	benign
A81	19	15073150	15073150	G	A	73	0.48	*SLC1A6*	NM_005071	Missense	p.T200M	-5.18	Deleterious	0	Damaging	1	probably damaging
A81	17	73500739	73500739	C	T	28	0.54	*CASKIN2*	NM_020753	Missense	p.V410M	-1.12	Neutral	0.19	Tolerated	0.93	possibly damaging
A82	14	73678524	73678524	G	A	130	0.22	*PSEN1*	NM_000021	Missense	p.G335R	-4.34	Deleterious	0.14	Tolerated	1	probably damaging
A82	9	101507924	101507924	C	T	41	0.37	*ANKS6*	NM_173551	Missense	p.G810S	-2.55	Deleterious	0.12	Tolerated	1	probably damaging
A82	2	79385823	79385823	T	G	30	0.30	*REG3A*	NM_138938	Missense	p.H50P	-5.18	Deleterious	0.04	Damaging	0.653	possibly damaging
A82	10	67680133	67680133	A	C	104	0.10	*CTNNA3*	NM_001127384	Missense	p.H881Q	-0.57	Neutral	0.31	Tolerated	0.92	possibly damaging
A82	11	6661346	6661346	G	C	45	0.31	*DCHS1*	NM_003737	Missense	p.P500R	-0.21	Neutral	0.58	Tolerated	0.394	benign
A82	19	758297	758297	T	A	57	0.53	*C19orf21*	NM_173481	Missense	p.S451T	-0.93	Neutral	0.25	Tolerated	0.782	possibly damaging
A83	22	46860089	46860089	G	A	90	0.43	*CELSR1*	NM_014246	Missense	p.A1233V	-2.52	Deleterious	0.02	Damaging	0.599	possibly damaging
A83	2	3651923	3651923	C	T	67	0.46	*COLEC11*	NM_001255985	Missense	p.A12V	-0.82	Neutral	0.77	Tolerated	NA	NA
A83	5	179393977	179393977	C	T	117	0.13	*RNF130*	NM_018434	Missense	p.D327N	-2.79	Deleterious	0.1	Tolerated	1	probably damaging
A83	8	28196924	28196924	A	AG	129	0.39	*PNOC*	NM_006228	Frame_Shift_Ins	p.G165fs	NA	NA	NA	NA	NA	NA
A83	2	179486730	179486730	CTT	C	72	0.43	*TTN*	NM_001267550	Frame_Shift_Del	p.K13332fs	NA	NA	NA	NA	NA	NA
A83	X	76937435	76937435	G	A	80	0.98	*ATRX*	NM_000489	nonsense	p.Q1105_	NA	NA	1	Tolerated	NA	NA
A83	17	12862139	12862139	G	A	121	0.50	*ARHGAP44*	NM_014859	Missense	p.R483H	-1.95	Neutral	0.05	Damaging	0.996	probably damaging
A83	9	131122742	131122742	G	A	73	0.11	*SLC27A4*	NM_005094	Missense	p.R635H	-1.71	Neutral	0.12	Tolerated	0.417	benign
A83	X	78216060	78216060	A	G	81	0.94	*P2RY10*	NM_198333	Missense	p.S15G	-0.42	Neutral	0.2	Tolerated	0	benign
A83	16	86544959	86544959	G	A	31	0.39	*FOXF1*	NM_001451	Missense	p.V262I	-0.4	Neutral	0.39	Tolerated	0.939	possibly damaging
A83	7	148504766	148504766	C	CCTCGTCGA	35	0.14	*EZH2*	NM_004456	Frame_Shift_Ins	p.G738fs	NA	NA	NA	NA	NA	NA
A84	5	878576	878576	C	T	24	0.25	*BRD9*	NM_023924	Missense	p.A389T	-0.44	Neutral	0.09	Tolerated	0.304	benign
A84	21	47676815	47676815	C	T	28	0.21	*MCM3AP*	NM_003906	Missense	p.D1274N	-0.29	Neutral	0.47	Tolerated	0.002	benign
A84	9	138011881	138011881	G	A	77	0.22	*OLFM1*	NM_014279	Missense	p.D421N	-2.85	Deleterious	0.02	Damaging	1	probably damaging
A84	17	73234397	73234397	T	C	35	0.34	*GGA3*	NM_138619	Missense	p.D712G	-4.45	Deleterious	0.03	Damaging	0.732	possibly damaging
A84	19	40392585	40392585	T	G	20	0.20	*FCGBP*	NM_003890	Missense	p.E2640A	-1.4	Neutral	0.49	Tolerated	0.057	benign
A84	11	47611462	47611462	C	T	81	0.15	*C1QTNF4*	NM_031909	Missense	p.G301S	-0.77	Neutral	0.41	Tolerated	0.999	probably damaging
A84	4	109784483	109784483	C	T	33	0.18	*COL25A1*	NM_198721	Missense	p.G382R	-7.43	Deleterious	NA	NA	1	probably damaging

A84	11	82705142	82705142	C	G	80	0.19	*RAB30*	NM_014488	Missense	p.G39A	-2.89	Deleterious	NA	NA	0.977	probably damaging
A84	3	6903265	6903265	G	A	53	0.17	*GRM7*	NM_181874	Missense	p.G64R	-3.98	Deleterious	0.21	Tolerated	1	probably damaging
A84	11	120298874	120298874	A	C	34	0.35	*ARHGEF12*	NM_015313	Missense	p.H168P	-2.01	Neutral	0.12	Tolerated	0.01	benign
A84	2	238402172	238402172	C	T	24	0.21	*MLPH*	NM_024101	Missense	p.R35W	-7.22	Deleterious	0.02	Damaging	1	probably damaging
A84	3	194080646	194080646	C	T	41	0.20	*LRRC15*	NM_001135057	Missense	p.R382H	-2.7	Deleterious	0.18	Tolerated	0.054	benign
A84	12	121177160	121177160	G	A	41	0.17	*ACADS*	NM_000017	Missense	p.R383H	-4.89	Deleterious	0	Damaging	1	probably damaging
A84	18	24127308	24127308	C	A	104	0.23	*KCTD1*	NM_001142730	Missense	p.R398L	0.22	Neutral	1	Tolerated	NA	NA
A84	12	41946474	41946474	G	A	28	0.21	*PDZRN4*	NM_001164595	Missense	p.R407H	-3.95	Deleterious	0	Damaging	1	probably damaging
A84	5	140221099	140221099	C	T	27	0.26	*PCDHA8*	NM_018911	Missense	p.R65W	-7.28	Deleterious	0	Damaging	1	probably damaging
A84	4	175898762	175898762	C	T	40	0.18	*ADAM29*	NM_001130704	nonsense	p.R696_	NA	NA	NA	NA	NA	NA
A84	19	48342778	48342778	T	C	73	0.11	*CRX*	NM_000554	Missense	p.S152P	-1.57	Neutral	0.35	Tolerated	0.015	benign
A84	10	93771059	93771059	T	TA	34	0.29	*BTAF1*	NM_003972	Frame_Shift_Ins	p.Y1400fs	NA	NA	NA	NA	NA	NA
A84	11	30255160	30255160	C	T	38	0.37	*FSHB*	NM_000510	Missense	p.T68I	0.83	Neutral	0.21	Tolerated	0.001	benign
A84	X	153581667	153581667	C	T	52	0.77	*FLNA*	NM_001110556	Missense	p.V2007M	-1.88	Neutral	0.04	Damaging	1	probably damaging
A85	19	36125228	36125228	C	T	32	0.44	*RBM42*	NM_024321	Missense	p.A363V	-3.38	Deleterious	0.02	Damaging	0.984	probably damaging
A85	1	155874287	155874287	A	G	32	0.53	*RIT1*	NM_001256821	Missense	p.F99L	-5.29	Deleterious	0.05	Damaging	0.996	probably damaging
A85	1	115258747	115258747	C	T	37	0.35	*NRAS*	NM_002524	Missense	p.G12D	-5.35	Deleterious	0	Damaging	0.372	benign
A85	22	44277505	44277505	C	T	22	0.41	*PNPLA5*	NM_138814	Missense	p.G378S	-1.13	Neutral	0.75	Tolerated	0.976	probably damaging
A85	7	50132775	50132775	G	A	15	0.27	*ZPBP*	NM_007009	Missense	p.L6F	-0.62	Neutral	NA	NA	0.454	possibly damaging
A85	19	35719114	35719114	G	A	69	0.57	*FAM187B*	NM_152481	Missense	p.P157L	-5.5	Deleterious	0.19	Tolerated	0.606	possibly damaging
A85	3	97311534	97311534	C	T	37	0.54	*EPHA6*	NM_001080448	Missense	p.P822L	-0.57	Neutral	0.01	Damaging	0.957	probably damaging
A85	12	58152021	58152021	G	A	60	0.53	*MAR9*	NM_138396	Missense	p.R215Q	-3.09	Deleterious	0.04	Damaging	1	probably damaging
A85	19	6495758	6495758	C	T	25	0.40	*TUBB4A*	NM_006087	Missense	p.R251H	-4.36	Deleterious	0	Damaging	0.414	benign
A85	2	158991382	158991382	C	T	40	0.38	*UPP2*	NM_001135098	Missense	p.R369W	-2.48	Neutral	0.04	Damaging	0.012	benign
A85	16	88677775	88677775	C	T	32	0.56	*ZC3H18*	NM_144604	nonsense	p.R436_	NA	NA	1	Tolerated	NA	NA
A85	11	47362770	47362770	C	T	41	0.49	*MYBPC3*	NM_000256	Missense	p.V606I	-0.8	Neutral	0.01	Damaging	0.897	possibly damaging
A85	9	35295775	35295775	C	G	27	0.93	*UNC13B*	NM_006377	nonsense	p.Y203_	NA	NA	1	Tolerated	NA	NA
A86	20	2308958	2308958	C	T	47	0.21	*TGM3*	NM_003245	Missense	p.A427V	-3.12	Deleterious	0.02	Damaging	1	probably damaging
A86	15	98982959	98982959	T	G	50	0.26	*FAM169B*	NM_182562	Missense	p.E160D	-1.18	Neutral	0.23	Tolerated	0.939	possibly damaging
A86	4	126242091	126242091	C	T	137	0.42	*FAT4*	NM_024582	Missense	p.R1509W	-2.52	Deleterious	0.03	Damaging	1	probably damaging
A86	20	56137878	56137878	C	T	39	0.51	*PCK1*	NM_002591	Missense	p.T178M	-1.18	Neutral	0.12	Tolerated	0.007	benign
A86	14	93424630	93424630	C	T	45	0.42	*ITPK1*	NM_014216	Missense	p.V196I	-0.34	Neutral	0.21	Tolerated	0.814	possibly damaging
A86	2	1440127	1440127	C	A	75	0.21	*TPO*	NM_001206744	nonsense	p.Y151_	NA	NA	1	Tolerated	NA	NA

A87	2	44051371	44051371	C	G	146	0.23	*ABCG5*	NM_022436	Missense	p.G369R	-1.83	Neutral	0.35	Tolerated	0.75	possibly damaging
A87	1	8422743	8422743	C	A	30	0.30	*RERE*	NM_001042681	Missense	p.K634N	-3.69	Deleterious	NA	NA	1	probably damaging
A87	7	131853086	131853086	GT	G	39	0.49	*PLXNA4*	NM_020911	Frame_Shift_Del	p.N1421fs	NA	NA	NA	NA	NA	NA
A87	15	75656919	75656919	C	T	29	0.31	*MAN2C1*	NM_001256494	Missense	p.M170I	-1.42	Neutral	0.39	Tolerated	0.076	benign
A87	7	50468140	50468140	ATGAAGGTGT ACAAG	A	51	0.24	*IKZF1*	NM_006060	Frame_Shift_Del	p.M459fs	NA	NA	NA	NA	NA	NA
A87	11	5969343	5969343	G	A	131	0.50	*OR56A3*	NM_001003443	Missense	p.S256N	-0.98	Neutral	0	Damaging	0.976	probably damaging
A87	7	82791676	82791676	G	T	19	0.68	*PCLO*	NM_033026	nonsense	p.S78_	NA	NA	0	Damaging	NA	NA
A87	X	41064585	41064585	T	TGA	34	0.68	*USP9X*	NM_001039590	Frame_Shift_Ins	p.G1619fs	NA	NA	NA	NA	NA	NA
A87	12	83290111	83290111	C	T	213	0.30	*TMTC2*	NM_152588	Missense	p.T390M	-1.62	Neutral	0.15	Tolerated	1	probably damaging
A87	6	116821802	116821802	T	C	40	0.18	*BET3L*	NM_001139444	Missense	p.T90A	-3.77	Deleterious	0.02	Damaging	0.98	probably damaging
A87	1	155206089	155206089	C	CACGT	46	0.28	*GBA*	NM_000157	Frame_Shift_Ins	p.V391fs	NA	NA	NA	NA	NA	NA
A88	1	11217303	11217303	C	G	95	0.23	*MTOR*	NM_004958	Missense	p.A1459P	-4.35	Deleterious	0	Damaging	0.856	possibly damaging
A88	12	25378562	25378562	C	T	40	0.28	*KRAS*	NM_033360	Missense	p.A146T	-3.63	Deleterious	0.01	Damaging	1	probably damaging
A88	7	77824190	77824190	C	T	20	0.65	*MAGI2*	NM_012301	Splice Site	p.A155sp	NA	NA	NA	NA	NA	NA
A88	15	78568008	78568008	G	A	55	0.55	*DNAJA4*	NM_018602	Missense	p.C301Y	-10.52	Deleterious	0.02	Damaging	0.988	probably damaging
A88	2	97817617	97817617	T	C	72	0.15	*ANKRD36*	NM_001164315	Missense	p.I368T	-0.09	Neutral	1	Tolerated	0	benign
A88	17	30300238	30300238	C	CA	27	0.41	*SUZ12*	NM_015355	Frame_Shift_Ins	p.L194fs	NA	NA	NA	NA	NA	NA
A88	17	48538118	48538118	A	G	114	0.45	*ACSF2*	NM_025149	Missense	p.N70S	1.04	Neutral	0.25	Tolerated	0	benign
A88	5	137221838	137221838	C	T	33	0.42	*MYOT*	NM_006790	Missense	p.P376S	-7.21	Deleterious	0	Damaging	1	probably damaging
A88	12	49446026	49446026	AG	A	62	0.50	*MLL2*	NM_003482	Frame_Shift_Del	p.P480fs	NA	NA	NA	NA	NA	NA
A88	21	47805823	47805823	G	A	142	0.44	*PCNT*	NM_006031	Missense	p.R1130Q	-3.19	Deleterious	0.16	Tolerated	0.999	probably damaging
A88	2	209113113	209113113	G	A	37	0.54	*IDH1*	NM_005896	Missense	p.R132C	-6.68	Deleterious	0	Damaging	0.259	benign
A88	22	38318086	38318086	G	A	64	0.50	*MICALL1*	NM_033386	Missense	p.R226Q	-0.99	Neutral	0.6	Tolerated	0.013	benign
A88	9	119461030	119461030	A	T	91	0.19	*TRIM32*	NM_012210	Missense	p.R337W	-2.21	Neutral	NA	NA	0.613	possibly damaging
A88	17	47869344	47869344	C	T	26	0.35	*KAT7*	NM_007067	nonsense	p.R38_	NA	NA	0.71	Tolerated	NA	NA
A88	19	6919676	6919676	C	A	30	0.20	*EMR1*	NM_001974	Missense	p.S513Y	-4.93	Deleterious	0	Damaging	1	probably damaging
A88	16	2224261	2224261	A	G	52	0.29	*TRAF7*	NM_032271	Missense	p.T425A	-1.8	Neutral	0.35	Tolerated	0.045	benign
A88	2	210560393	210560393	G	A	145	0.38	*MAP2*	NM_002374	Missense	p.V1167I	-0.36	Neutral	0.99	Tolerated	0.004	benign
A89	11	57886004	57886004	C	T	34	0.29	*OR9I1*	NM_001005211	Missense	p.A305T	0.11	Neutral	0.26	Tolerated	0	benign
A89	1	89279387	89279387	T	A	133	0.44	*PKN2*	NM_006256	Missense	p.H750Q	-7.49	Deleterious	0.15	Tolerated	0.966	probably damaging
A89	12	6701206	6701206	A	G	25	0.16	*CHD4*	NM_001273	Missense	p.I989T	-4.62	Deleterious	0	Damaging	0.99	probably damaging
A89	15	93545433	93545433	G	GA	41	0.24	*CHD2*	NM_001271	Frame_Shift_Ins	p.K1389fs	NA	NA	NA	NA	NA	NA

A89	1	175129924	175129924	CCTTCTTCTT	C	15	0.67	*KIAA0040*	NM_014656	In_Frame_Del	p.KKK73del	NA	NA	NA	NA	NA	NA
A89	19	13226834	13226834	T	C	27	0.52	*TRMT1*	NM_017722	Missense	p.Q96R	-0.84	Neutral	0.46	Tolerated	0.003	benign
A89	X	138882259	138882259	G	A	49	0.16	*ATP11C*	NM_173694	nonsense	p.R227_	NA	NA	0.43	Tolerated	NA	NA
A89	1	162824686	162824686	G	A	86	0.45	*C1orf110*	NM_178550	Missense	p.R260W	-5.6	Deleterious	0.09	Tolerated	0.877	possibly damaging
A89	3	52668826	52668826	G	A	50	0.34	*PBRM1*	NM_018313	Missense	p.R365C	-0.62	Neutral	0.05	Damaging	0.999	probably damaging
A89	6	47846760	47846760	C	T	136	0.29	*PTCHD4*	NM_001013732	Missense	p.R607H	-4.14	Deleterious	0.4	Tolerated	1	probably damaging
A89	2	27276857	27276857	T	C	80	0.30	*AGBL5*	NM_021831	Missense	p.Y161H	-4.67	Deleterious	NA	NA	1	probably damaging
A90	13	92345963	92345963	C	T	54	0.43	*GPC5*	NM_004466	Missense	p.A283V	-3.5	Deleterious	0.07	Tolerated	0.987	probably damaging
A90	14	72818810	72818810	ACAT	A	61	0.34	*RGS6*	NM_001204424	In_Frame_Del	p.I33del	-9.03	Deleterious	NA	NA	NA	NA
A90	3	193176998	193176998	C	A	44	0.57	*ATP13A4*	NM_032279	Missense	p.A516S	-0.49	Neutral	0.82	Tolerated	0.002	benign
A90	3	12858083	12858083	C	G	57	0.54	*CAND2*	NM_001162499	Missense	p.A551G	-2.88	Deleterious	0.08	Tolerated	0.136	benign
A90	8	43147845	43147845	C	T	21	0.57	*POTEA*	NM_001005365	Missense	p.A73V	NA	NA	NA	NA	NA	NA
A90	10	55913034	55913034	T	A	37	0.46	*PCDH15*	NM_001142763	Missense	p.D542V	-7.25	Deleterious	0	Damaging	1	probably damaging
A90	1	236917271	236917271	G	A	41	0.46	*ACTN2*	NM_001103	Missense	p.D622N	-4.07	Deleterious	0	Damaging	0.999	probably damaging
A90	20	34526809	34526809	G	A	104	0.49	*PHF20*	NM_016436	Missense	p.E831K	-1.11	Neutral	0.05	Damaging	0.976	probably damaging
A90	14	21821665	21821665	C	T	22	0.55	*SUPT16H*	NM_007192	Missense	p.E994K	-3.47	Deleterious	0	Damaging	0.956	possibly damaging
A90	12	25398285	25398285	C	G	53	0.38	*KRAS*	NM_033360	Missense	p.G12R	-6.18	Deleterious	0.02	Damaging	0.802	possibly damaging
A90	13	111155584	111155584	G	A	95	0.54	*COL4A2*	NM_001846	Missense	p.G1332R	-6.08	Deleterious	0	Damaging	1	probably damaging
A90	16	67289679	67289679	G	A	22	0.45	*SLC9A5*	NM_004594	Missense	p.G253S	-5.83	Deleterious	0	Damaging	1	probably damaging
A90	2	158978067	158978067	A	G	110	0.47	*UPP2*	NM_001135098	Missense	p.K258E	-1.18	Neutral	0.89	Tolerated	0.001	benign
A90	12	34176906	34176906	A	C	139	0.44	*ALG10*	NM_032834	Missense	p.M61L	-2.27	Neutral	0.56	Tolerated	0.196	benign
A90	5	140710637	140710637	A	G	39	0.62	*PCDHGA1*	NM_018912	Missense	p.N129S	-4.62	Deleterious	0.04	Damaging	0.978	probably damaging
A90	X	123514933	123514933	T	C	93	0.46	*TENM1*	NM_001163278	Missense	p.N2551S	-1.66	Neutral	0.31	Tolerated	0.027	benign
A90	11	65829363	65829363	A	G	51	0.45	*SF3B2*	NM_006842	Missense	p.N624S	-2.69	Deleterious	0.05	Damaging	0.437	benign
A90	8	145106352	145106352	G	T	14	0.29	*OPLAH*	NM_017570	Missense	p.P1248T	NA	NA	0	Damaging	1	probably damaging
A90	6	17292010	17292010	C	T	31	0.48	*RBM24*	NM_001143942	Missense	p.P124L	-5.02	Deleterious	0.06	Tolerated	0.983	probably damaging
A90	7	49815474	49815474	C	A	53	0.47	*VWC2*	NM_198570	Missense	p.P148Q	-2.27	Neutral	0.17	Tolerated	0.997	probably damaging
A90	19	4538386	4538386	G	A	60	0.53	*LRG1*	NM_052972	Missense	p.P204S	-4.84	Deleterious	0.3	Tolerated	0.91	possibly damaging
A90	1	152975658	152975658	AGAGCCAGGCTGTACCAAGGTCCCT	A	31	0.42	*SPRR3*	NM_005416	In_Frame_Del	p.EPGCTKVP95del	-9.33	Deleterious	NA	NA	NA	NA
A90	3	101039204	101039204	G	T	34	0.44	*IMPG2*	NM_016247	Missense	p.P5T	-1.09	Neutral	0.18	Tolerated	0.483	possibly damaging
A90	3	64587693	64587693	C	T	56	0.50	*ADAMTS9*	NM_182920	Missense	p.R1315H	-0.01	Neutral	0.54	Tolerated	0.001	benign

A90	X	103349414	103349414	C	T	36	0.44	*SLC25A53*	NM_001012755	Missense	p.R176H	-4.73	Deleterious	0.05	Damaging	0.062	benign
A90	22	50546667	50546667	G	T	79	0.49	*MOV10L1*	NM_018995	Missense	p.R182L	-4.38	Deleterious	0.01	Damaging	0.994	probably damaging
A90	20	31672780	31672780	C	T	38	0.42	*BPIFB4*	NM_182519	Missense	p.R254C	-3.02	Deleterious	0.21	Tolerated	0.019	benign
A90	12	124359880	124359880	C	T	138	0.40	*DNAH10*	NM_207437	nonsense	p.R2563_	NA	NA	0.56	Tolerated	NA	NA
A90	22	32480560	32480560	C	T	39	0.28	*SLC5A1*	NM_000343	nonsense	p.R267_	NA	NA	1	Tolerated	NA	NA
A90	X	152967490	152967490	C	T	11	0.55	*BCAP31*	NM_001139457	Missense	p.R292H	-2.53	Deleterious	0.09	Tolerated	0.994	probably damaging
A90	1	26440918	26440918	G	T	81	0.42	*PDIK1L*	NM_001243532	Missense	p.R40L	-3.4	Deleterious	0.04	Damaging	0.501	possibly damaging
A90	16	2120571	2120571	C	T	58	0.84	*TSC2*	NM_000548	Missense	p.R611W	-7.26	Deleterious	0	Damaging	1	probably damaging
A90	7	140246715	140246715	G	A	40	0.40	*DENND2A*	NM_015689	nonsense	p.R688_	NA	NA	1	Tolerated	NA	NA
A90	2	180809887	180809887	C	T	98	0.43	*CWC22*	NM_020943	Missense	p.R899Q	-1.17	Neutral	0.06	Tolerated	0.995	probably damaging
A90	9	4118594	4118594	G	A	64	0.56	*GLIS3*	NM_001042413	Missense	p.S295L	-1.98	Neutral	0.31	Tolerated	1	probably damaging
A90	12	124393912	124393912	C	T	53	0.51	*DNAH10*	NM_207437	Missense	p.S3189F	-5.3	Deleterious	0	Damaging	0.997	probably damaging
A90	1	156642553	156642553	C	T	75	0.45	*NES*	NM_006617	Missense	p.S476N	-1.83	Neutral	0.02	Damaging	0.969	probably damaging
A90	X	76888829	76888829	T	TATGGC	81	0.36	*ATRX*	NM_000489	Frame_Shift_Ins	p.Y1667fs	NA	NA	NA	NA	NA	NA
A90	9	13109981	13109981	G	A	38	0.50	*MPDZ*	NM_003829	Missense	p.T1942M	-1.9	Neutral	0.02	Damaging	1	probably damaging
A90	2	102957262	102957262	C	T	84	0.42	*IL1RL1*	NM_016232	Missense	p.T195M	-4.36	Deleterious	0.03	Damaging	1	probably damaging
A90	2	207176153	207176153	G	A	91	0.36	*ZDBF2*	NM_020923	Missense	p.V2301I	-0.54	Neutral	0.2	Tolerated	0	benign
A90	3	3067887	3067887	G	A	108	0.42	*CNTN4*	NM_175607	Missense	p.V530M	-0.5	Neutral	0.09	Tolerated	0.358	benign
A90	20	7915251	7915251	C	T	61	0.33	*HAO1*	NM_017545	Missense	p.V57I	-0.88	Neutral	0.06	Tolerated	0.006	benign
A90	4	54231848	54231848	C	CG	30	0.63	*SCFD2*	NM_152540	Frame_Shift_Ins	p.V86fs	NA	NA	NA	NA	NA	NA
A91	17	17062146	17062146	G	A	19	0.26	*MPRIP*	NM_015134	Missense	p.D626N	-3.01	Deleterious	0.01	Damaging	0.871	possibly damaging
A91	1	159505715	159505715	A	G	87	0.14	*OR10J5*	NM_001004469	Missense	p.F28S	-7.12	Deleterious	0.01	Damaging	1	probably damaging
A91	3	142279172	142279172	C	T	85	0.15	*ATR*	NM_001184	Missense	p.G492R	-1.87	Neutral	0	Damaging	1	probably damaging
A91	7	81340797	81340797	G	A	30	0.17	*HGF*	NM_000601	Missense	p.H482Y	-1.28	Neutral	NA	NA	0.98	probably damaging
A91	16	51173879	51173879	G	T	98	0.15	*SALL1*	NM_002968	Missense	p.H752N	-6.71	Deleterious	0	Damaging	0.991	probably damaging
A91	6	54191662	54191662	G	A	159	0.16	*TINAG*	NM_014464	Missense	p.R191H	-4.56	Deleterious	0.04	Damaging	0.84	possibly damaging
A91	11	77911209	77911209	C	T	83	0.10	*USP35*	NM_020798	Missense	p.R323W	-7.38	Deleterious	0	Damaging	1	probably damaging
A91	6	31753094	31753094	G	A	74	0.19	*VARS*	NM_006295	Missense	p.R426W	-6.4	Deleterious	0	Damaging	1	probably damaging
A93	X	137939775	137939775	G	A	67	0.16	*FGF13*	NM_001139500	Missense	p.A39V	-0.26	Neutral	1	Tolerated	0.999	probably damaging
A93	12	112888166	112888166	A	G	98	0.10	*PTPN11*	NM_002834	Missense	p.D61G	-5.64	Deleterious	0.03	Damaging	0.908	possibly damaging
A93	2	23980369	23980369	C	A	205	0.27	*ATAD2B*	NM_017552	nonsense	p.E1333_	NA	NA	0.44	Tolerated	NA	NA
A93	3	159606659	159606659	A	C	89	0.25	*IQCJ-SCHIP1*	NM_001197113	Missense	p.K491N	-1.16	Neutral	0.09	Tolerated	1	probably damaging

A93	16	88694525	88694525	A	T	32	0.31	*ZC3H18*	NM_144604	nonsense	p.K823_	NA	NA	1	Tolerated	NA	NA
A93	19	36884569	36884569	G	GT	122	0.25	*ZFP82*	NM_133466	Frame_Shift_Ins	p.L225fs	NA	NA	NA	NA	NA	NA
A93	19	19656685	19656685	C	T	65	0.29	*CILP2*	NM_153221	nonsense	p.R1111_	NA	NA	1	Tolerated	NA	NA
A93	10	95380727	95380727	G	T	82	0.29	*PDE6C*	NM_006204	Missense	p.R238L	-5.83	Deleterious	0	Damaging	1	probably damaging
A93	19	614001	614001	C	A	28	0.43	*HCN2*	NM_001194	Missense	p.R659S	-5.57	Deleterious	0.03	Damaging	1	probably damaging
A93	7	138394490	138394490	G	A	53	0.17	*ATP6V0A4*	NM_130841	nonsense	p.R770_	NA	NA	0.59	Tolerated	NA	NA
A93	4	628553	628553	G	A	44	0.16	*PDE6B*	NM_000283	Missense	p.V186I	-0.68	Neutral	0.24	Tolerated	0.232	benign
A93	7	140453136	140453136	A	T	36	0.11	*BRAF*	NM_004333	Missense	p.V600E	-4.78	Deleterious	0	Damaging	0.971	probably damaging
A94	17	76490787	76490787	T	C	85	0.26	*DNAH17*	NM_173628	Missense	p.D2053G	-6.33	Deleterious	0	Damaging	NA	NA
A94	7	120428872	120428872	C	A	32	0.09	*TSPAN12*	NM_012338	Missense	p.G231V	-2.59	Deleterious	0	Damaging	0.974	probably damaging
A94	17	47038277	47038277	C	G	45	0.36	*GIP*	NM_004123	Missense	p.L141F	-1.36	Neutral	0.02	Damaging	0.421	benign
A94	6	152751697	152751697	G	A	169	0.28	*SYNE1*	NM_182961	nonsense	p.R1537_	NA	NA	0.58	Tolerated	NA	NA
A94	18	56411581	56411581	A	G	29	0.28	*MALT1*	NM_006785	Missense	p.S589G	-3.11	Deleterious	0.02	Damaging	0.582	possibly damaging
A94	17	74902195	74902195	G	T	20	0.15	*MGAT5B*	NM_198955	Missense	p.W328C	-11.61	Deleterious	0	Damaging	1	probably damaging
A95	3	55508604	55508604	C	T	19	0.42	*WNT5A*	NM_003392	Missense	p.A149T	-1.93	Neutral	0.05	Damaging	0.983	probably damaging
A95	8	10467589	10467589	T	C	331	0.39	*RP1L1*	NM_178857	Missense	p.E1340G	-1.12	Neutral	0.47	Tolerated	0.948	possibly damaging
A95	2	125232388	125232388	G	A	92	0.40	*CNTNAP5*	NM_130773	Missense	p.E331K	-3.51	Deleterious	0.45	Tolerated	1	probably damaging
A95	1	109839501	109839501	C	T	43	0.53	*MYBPHL*	NM_001010985	Missense	p.G212S	-5.85	Deleterious	0.03	Damaging	1	probably damaging
A95	1	22843939	22843939	C	T	47	0.40	*ZBTB40*	NM_014870	Missense	p.H939Y	-5.91	Deleterious	0	Damaging	1	probably damaging
A95	3	40529262	40529262	A	G	32	0.47	*ZNF619*	NM_001145082	Missense	p.I461V	-0.66	Neutral	0.29	Tolerated	0.894	possibly damaging
A95	2	11742584	11742584	T	C	24	0.38	*GREB1*	NM_014668	Missense	p.I861T	-0.55	Neutral	0.42	Tolerated	0.763	possibly damaging
A95	5	149502699	149502699	T	C	45	0.87	*PDGFRB*	NM_002609	Missense	p.K697E	-2.56	Deleterious	0.01	Damaging	0.999	probably damaging
A95	8	132052315	132052315	G	T	18	0.61	*ADCY8*	NM_001115	Missense	p.L89M	0.03	Neutral	0.3	Tolerated	0.617	possibly damaging
A95	14	86088405	86088405	C	A	108	0.27	*FLRT2*	NM_013231	Missense	p.Q183K	-0.51	Neutral	0.28	Tolerated	0.004	benign
A95	1	201182692	201182692	C	T	76	0.45	*IGFN1*	NM_001164586	Missense	p.R2891W	-2.55	Deleterious	0.02	Damaging	0.999	probably damaging
A95	10	61894114	61894114	G	A	158	0.31	*ANK3*	NM_020987	Missense	p.S919L	-5.17	Deleterious	0	Damaging	1	probably damaging
A95	14	92537379	92537379	T	C	27	0.33	*ATXN3*	NM_001164778	Missense	p.T136A	0	Neutral	NA	NA	NA	NA
A95	2	197172746	197172746	G	A	21	0.43	*HECW2*	NM_020760	Missense	p.T833M	-5.58	Deleterious	0	Damaging	1	probably damaging
A96	11	20699549	20699549	C	T	15	0.33	*NELL1*	NM_006157	Missense	p.L43F	-0.78	Neutral	0.1	Tolerated	0.074	benign
A96	12	12037444	12037444	C	T	33	0.58	*ETV6*	NM_001987	nonsense	p.R359_	NA	NA	0.8	Tolerated	NA	NA
A96	14	42356700	42356700	G	A	25	0.32	*LRFN5*	NM_152447	Missense	p.R291H	-2.17	Neutral	0.21	Tolerated	0.869	possibly damaging
A96	2	27324371	27324371	C	T	11	0.18	*CGREF1*	NM_001166239	Missense	p.G243E	-0.08	Neutral	0.34	Tolerated	0.36	benign
A96	2	125521571	125521571	G	A	21	0.52	*CNTNAP5*	NM_130773	Missense	p.V793I	-0.94	Neutral	0.19	Tolerated	0.813	possibly damaging

A96	20	60894740	60894740	C	T	18	0.22	*LAMA5*	NM_005560	Missense	p.E2291K	-2.2	Neutral	NA	NA	0.962	probably damaging
A96	3	63542307	63542307	G	C	30	0.53	*SYNPR*	NM_001130003	Missense	p.E100Q	-1.85	Neutral	0.53	Tolerated	0.999	probably damaging
A96	3	96533790	96533790	G	C	24	0.46	*EPHA6*	NM_001080448	Missense	p.G108A	0.13	Neutral	0.54	Tolerated	0.999	probably damaging
A96	4	79460451	79460451	C	T	25	0.32	*FRAS1*	NM_025074	Missense	p.R3768C	-6.39	Deleterious	0	Damaging	1	probably damaging
A96	5	23526894	23526894	A	T	11	0.27	*PRDM9*	NM_020227	Missense	p.H566L	-1.58	Neutral	0.31	Tolerated	0.005	benign
A96	5	179765522	179765522	C	T	20	0.50	*GFPT2*	NM_005110	Missense	p.R29Q	-3.69	Deleterious	NA	NA	1	probably damaging
A96	6	30298612	30298612	C	T	28	0.14	*TRIM39*	NM_021253	Missense	p.R170C	-4.08	Deleterious	0.04	Damaging	0.829	possibly damaging
A96	6	32946102	32946102	G	A	23	0.26	*BRD2*	NM_001199455	Missense	p.S593N	-0.32	Neutral	0.41	Tolerated	0.01	benign
A96	9	132876942	132876942	G	T	19	0.16	*GPR107*	NM_001136557	Missense	p.A484S	-2.22	Neutral	0.27	Tolerated	0.043	benign
AC04	1	180283826	180283826	C	G	95	0.35	*ACBD6*	NM_032360	Splice Site	p.A232sp	NA	NA	NA	NA	NA	NA
AC04	1	151265362	151265362	T	TCGGCC	13	0.23	*PI4KB*	NM_002651	Frame_Shift_Ins	p.D806fs	NA	NA	NA	NA	NA	NA
AC04	12	92538058	92538071	CAGAGTGTGA GTTC	CAGTTCC CCCCG	57	0.14	*BTG1*	NM_001731	Frame_Shift_Del	p.E101fs	NA	NA	NA	NA	NA	NA
AC04	1	115258747	115258747	C	A	60	0.45	*NRAS*	NM_002524	Missense	p.G12V	-7.05	Deleterious	0.01	Damaging	0.613	possibly damaging
AC04	11	124829113	124829113	C	A	61	0.46	*CCDC15*	NM_025004	Missense	p.Q94K	-1.74	Neutral	0.16	Tolerated	0.617	possibly damaging
AC04	4	177094487	177094487	G	A	49	0.39	*WDR17*	NM_170710	Missense	p.R1144H	-1.58	Neutral	0.01	Damaging	0.996	probably damaging
AC04	12	52374840	52374840	G	A	44	0.43	*ACVR1B*	NM_020328	Missense	p.R223Q	-3.27	Deleterious	0.05	Damaging	0.999	probably damaging
AC04	21	10934955	10934955	G	A	146	0.11	*TPTE*	NM_199261	Nonsense	p.R280_	NA	NA	0.81	Tolerated	NA	NA
AC04	17	79078380	79078380	G	A	12	0.42	*BAIAP2*	NM_017451	Missense	p.R378Q	-2.65	Deleterious	0.46	Tolerated	1	probably damaging
AC06	12	25398211	25398211	T	C	38	0.34	*KRAS*	NM_033360	Missense	p.I36M	-2.35	Neutral	0	Damaging	0.999	probably damaging
AC06	1	201352505	201352505	C	A	37	0.49	*LAD1*	NM_005558	Missense	p.K396N	-1.95	Neutral	0.06	Tolerated	0.372	benign
AC06	19	56185384	56185384	G	A	23	0.61	*U2AF2*	NM_007279	Missense	p.V460I	-0.84	Neutral	0.24	Tolerated	0.247	benign
AC09	4	90035046	90035046	T	A	73	0.25	*TIGD2*	NM_145715	Missense	p.D307E	-1.83	Neutral	0.48	Tolerated	0.983	probably damaging
AC09	21	46642083	46642083	G	A	25	0.40	*ADARB1*	NM_015833	Missense	p.E733K	-3.44	Deleterious	0	Damaging	1	probably damaging
AC09	9	36353292	36353292	C	T	42	0.48	*RNF38*	NM_022781	Missense	p.G316R	-2.87	Deleterious	0	Damaging	1	probably damaging
AC09	2	145147550	145147550	T	C	19	0.16	*ZEB2*	NM_014795	Missense	p.H1038R	-7.28	Deleterious	0.08	Tolerated	0.992	probably damaging
AC09	21	45194128	45194128	G	C	117	0.24	*CSTB*	NM_000100	Missense	p.N84K	-2.12	Neutral	0.19	Tolerated	0.002	benign
AC09	5	149782167	149782167	G	A	43	0.47	*CD74*	NM_001025159	Missense	p.P280L	-1.23	Neutral	1	Tolerated	0.001	benign
AC09	11	61112764	61112764	C	T	13	0.77	*DAK*	NM_015533	Missense	p.P425S	-1.74	Neutral	0.42	Tolerated	0.759	possibly damaging
AC09	11	57261560	57261560	C	A	17	0.65	*SLC43A1*	NM_001198810	Missense	p.Q259H	-2.58	Deleterious	0.13	Tolerated	0.005	benign
AC09	1	197552341	197552341	G	A	60	0.33	*DENND1B*	NM_001195215	Missense	p.R364C	-6.59	Deleterious	0	Damaging	1	probably damaging
AC09	1	222713535	222713535	G	A	37	0.46	*HHIPL2*	NM_024746	Missense	p.R423C	-7.43	Deleterious	0	Damaging	1	probably damaging
AC09	12	13716673	13716673	C	T	26	0.31	*GRIN2B*	NM_000834	Missense	p.V1167I	-0.27	Neutral	0.18	Tolerated	0	benign

AC10	12	25398284	25398284	C	A	43	0.33	*KRAS*	NM_033360	Missense	p.G12V	-7.11	Deleterious	0.01	Damaging	0.999	probably damaging
AC10	3	47129680	47129680	G	A	89	0.47	*SETD2*	NM_014159	Nonsense	p.Q1734_	NA	NA	0.1	Tolerated	NA	NA
AC10	22	42474013	42474013	G	A	19	0.37	*FAM109B*	NM_001002034	Missense	p.R239Q	-2.8	Deleterious	0.03	Damaging	0.704	possibly damaging
AC10	19	41235200	41235200	G	A	25	0.48	*ITPKC*	NM_025194	Missense	p.R450Q	-2.7	Deleterious	0.17	Tolerated	0.247	benign
AC10	3	47155366	47155366	G	T	89	0.34	*SETD2*	NM_014159	Nonsense	p.S1572_	NA	NA	NA	NA	NA	NA
AC10	10	29821081	29821081	G	A	34	0.41	*SVIL*	NM_021738	Missense	p.S620L	-1.75	Neutral	NA	NA	0.994	probably damaging
AC10	4	177649009	177649009	C	T	60	0.47	*VEGFC*	NM_005429	Missense	p.V159I	-0.2	Neutral	0.23	Tolerated	0.029	benign
AC10	1	92606722	92606722	T	C	65	0.34	*BTBD8*	NM_183242	Missense	p.V295A	-3.41	Deleterious	0.24	Tolerated	0.999	probably damaging
AC10	19	7677298	7677298	T	C	7	0.71	*CAMSAP3*	NM_001080429	Missense	p.V667A	-2.73	Deleterious	0	Damaging	0.865	possibly damaging
AC11	9	133753889	133753889	A	G	76	0.32	*ABL1*	NM_007313	Missense	p.E472G	-6.52	Deleterious	0	Damaging	0.998	probably damaging
AC11	21	36252866	36252866	G	A	74	0.45	*RUNX1*	NM_001754	Nonsense	p.R166_	NA	NA	1	Tolerated	NA	NA
AC11	11	59863044	59863044	G	A	71	0.35	*MS4A2*	NM_000139	Missense	p.R217H	-1.79	Neutral	0.19	Tolerated	0.999	probably damaging
AC11	2	107446647	107446647	C	T	96	0.45	*ST6GAL2*	NM_001142351	Missense	p.R398H	-4.7	Deleterious	0.03	Damaging	1	probably damaging
AC11	1	202880291	202880291	C	A	116	0.45	*KLHL12*	NM_021633	Missense	p.W203L	-12.3	Deleterious	0	Damaging	1	probably damaging
AC11	8	24178792	24178792	A	C	119	0.38	*ADAM28*	NM_014265	Missense	p.Y237S	-4.56	Deleterious	0.16	Tolerated	0.998	probably damaging
AC14	9	94172680	94172680	C	T	164	0.34	*NFIL3*	NM_005384	Missense	p.A113T	-2.73	Deleterious	0.06	Tolerated	0.955	possibly damaging
AC14	6	168999557	168999557	G	A	80	0.18	*SMOC2*	NM_022138	Missense	p.D244N	-1.57	Neutral	0.4	Tolerated	0.996	probably damaging
AC14	1	115258748	115258748	C	T	94	0.05	*NRAS*	NM_002524	Missense	p.G12S	-4.44	Deleterious	0.04	Damaging	0.329	benign
AC14	1	115258744	115258744	C	T	92	0.08	*NRAS*	NM_002524	Missense	p.G13D	-5.48	Deleterious	0.03	Damaging	0.434	benign
AC14	6	31132556	31132556	C	T	19	0.47	*POU5F1*	NM_002701	Missense	p.G302E	-2.53	Deleterious	0.02	Damaging	0.997	probably damaging
AC14	2	84811276	84811276	G	A	150	0.15	*DNAH6*	NM_001370	Missense	p.G795S	-1.49	Neutral	0.65	Tolerated	0.141	benign
AC14	8	10466600	10466600	T	A	99	0.28	*RP1L1*	NM_178857	Missense	p.M1670L	-0.33	Neutral	0.18	Tolerated	0	benign
AC14	12	52215029	52215029	T	C	38	0.24	*FIGNL2*	NM_001013690	Missense	p.Q390R	NA	NA	NA	NA	NA	NA
AC14	9	37006526	37006526	C	T	110	0.27	*PAX5*	NM_016734	Missense	p.R140Q	-3.45	Deleterious	0	Damaging	1	probably damaging
AC14	9	4576054	4576054	G	A	123	0.27	*SLC1A1*	NM_004170	Missense	p.R310Q	-3.05	Deleterious	0	Damaging	0.998	probably damaging
AC16	9	123370072	123370072	T	C	86	0.37	*MEGF9*	NM_001080497	Missense	p.E435G	-4.65	Deleterious	0.04	Damaging	0.993	probably damaging
AC16	11	68855396	68855396	A	T	10	0.60	*TPCN2*	NM_139075	Missense	p.H745L	-8.07	Deleterious	0	Damaging	1	probably damaging
AC16	17	7574003	7574003	G	A	34	0.62	*TP53*	NM_000546	Nonsense	p.R342_	NA	NA	0.73	Tolerated	NA	NA
AC16	8	131826440	131826440	G	A	37	0.49	*ADCY8*	NM_001115	Nonsense	p.R930_	NA	NA	0.46	Tolerated	NA	NA
AC16	1	38184352	38184352	C	T	27	0.48	*EPHA10*	NM_001099439	Missense	p.V965M	-2.18	Neutral	0	Damaging	0.999	probably damaging
AC16	9	97869390	97869390	C	G	29	0.28	*FANCC*	NM_001243743	Missense	p.W497C	-5.01	Deleterious	0.01	Damaging	0.997	probably damaging
B01	7	100693850	100693850	G	A	71	0.54	*MUC17*	NM_001040105	Missense	p.E4270K	0.27	Neutral	0.37	Tolerated	0.362	benign
B01	22	30662785	30662785	C	G	8	0.63	*OSM*	NM_020530	Missense	p.G2R	1.82	Neutral	0.87	Tolerated	0	benign

B01	19	6713420	6713420	G	T	34	0.59	*C3*	NM_000064	Missense	p.P292T	-1.57	Neutral	0.59	Tolerated	0.003	benign
B01	6	46684253	46684253	G	A	103	0.34	*PLA2G7*	NM_005084	Missense	p.R82C	-7.83	Deleterious	0.02	Damaging	1	probably damaging
B01	11	114450895	114450895	G	A	168	0.51	*NXPE4*	NM_001077639	Missense	p.T353M	-4.8	Deleterious	0.01	Damaging	0.999	probably damaging
B01	1	39854025	39854025	G	A	91	0.40	*MACF1*	NM_012090	Missense	p.V3109I	-0.69	Neutral	0.12	Tolerated	0.301	benign
B01	7	150647271	150647271	C	T	25	0.52	*KCNH2*	NM_000238	Missense	p.V795I	-0.96	Neutral	0.03	Damaging	1	probably damaging
B02	5	19747107	19747107	G	A	109	0.40	*CDH18*	NM_004934	Missense	p.A156V	-1.47	Neutral	NA	NA	0.802	possibly damaging
B02	X	85128074	85128074	C	T	66	0.29	*CHM*	NM_000390	Missense	p.D585N	-2.79	Deleterious	0.04	Damaging	0.361	benign
B02	1	115256529	115256529	T	A	83	0.30	*NRAS*	NM_002524	Missense	p.Q61L	-6.32	Deleterious	0.01	Damaging	0.973	probably damaging
B02	8	100779116	100779116	G	A	83	0.40	*VPS13B*	NM_017890	Missense	p.V2414M	-0.61	Neutral	0.08	Tolerated	0.621	possibly damaging
B03	X	29959905	29959905	G	A	135	0.58	*IL1RAPL1*	NM_014271	Missense	p.D399N	-0.75	Neutral	NA	NA	0.061	benign
B03	9	117808823	117808823	A	C	171	0.38	*TNC*	NM_002160	Missense	p.L1664R	0.9	Neutral	0.96	Tolerated	0.011	benign
B03	12	113730861	113730861	C	G	52	0.42	*TPCN1*	NM_001143819	Missense	p.Q818E	-0.51	Neutral	1	Tolerated	0.546	possibly damaging
B03	18	56033309	56033309	G	A	17	0.41	*NEDD4L*	NM_001144967	Missense	p.V638M	-1.97	Neutral	0.03	Damaging	0.992	probably damaging
B04	3	39226481	39226481	C	T	16	0.56	*XIRP1*	NM_194293	Missense	p.A1486T	0.53	Neutral	0.57	Tolerated	0.007	benign
B04	15	41988816	41988816	T	TC	13	0.62	*MGA*	NM_001080541	Frame_Shift_Ins	p.D536fs	NA	NA	NA	NA	NA	NA
B04	18	74617368	74617368	A	AGCC	76	0.32	*ZNF236*	NM_007345	In_Frame_Ins	p.763_763H>QP	-13.96	Deleterious	NA	NA	NA	NA
B04	13	42461363	42461363	T	A	117	0.43	*VWA8*	NM_015058	Missense	p.Q262H	-4.28	Deleterious	0	Damaging	1	probably damaging
B04	19	34925779	34925779	G	A	30	0.53	*UBA2*	NM_005499	Missense	p.R122Q	-3.52	Deleterious	0	Damaging	1	probably damaging
B04	3	164906290	164906290	G	A	88	0.27	*SLITRK3*	NM_014926	Missense	p.R777C	-0.26	Neutral	0.18	Tolerated	0.946	possibly damaging
B04	1	24388564	24388564	G	A	43	0.47	*MYOM3*	NM_152372	Missense	p.T1269M	-1.15	Neutral	0.12	Tolerated	0.825	possibly damaging
B04	1	153066169	153066169	G	A	115	0.16	*SPRR2E*	NM_001024209	Missense	p.T20M	-4	Deleterious	0.07	Tolerated	0.001	benign
B04	11	113287657	113287657	C	T	18	0.33	*DRD2*	NM_000795	Missense	p.V154I	0.14	Neutral	0.32	Tolerated	0.986	probably damaging
B04	12	78582046	78582046	T	A	128	0.45	*NAV3*	NM_014903	Missense	p.Y1915N	-5.15	Deleterious	0.07	Tolerated	0.959	probably damaging
B06	11	6647863	6647863	G	T	81	0.38	*DCHS1*	NM_003737	Missense	p.A2095E	-0.4	Neutral	1	Tolerated	0.012	benign
B06	5	35644628	35644628	G	C	33	0.27	*SPEF2*	NM_024867	Splice Site	p.K195sp	NA	NA	NA	NA	NA	NA
B06	3	47098907	47098907	T	TC	51	0.31	*SETD2*	NM_014159	Frame_Shift_Ins	p.K2123fs	NA	NA	NA	NA	NA	NA
B06	5	72147135	72147135	T	G	40	0.35	*TNPO1*	NM_002270	Nonsense	p.L65_	NA	NA	1	Tolerated	NA	NA
B06	11	35515694	35515694	G	A	38	0.47	*PAMR1*	NM_015430	Missense	p.P67L	-2.02	Neutral	0	Damaging	1	probably damaging
B12	5	79025919	79025919	C	A	108	0.48	*CMYA5*	NM_153610	Missense	p.A444E	-1.52	Neutral	0	Damaging	0.028	benign
B12	2	97749512	97749512	T	C	35	0.40	*FAHD2B*	NM_199336	Missense	p.I309V	-0.75	Neutral	0.23	Tolerated	0.924	possibly damaging
B12	16	15178499	15178499	G	A	30	0.13	*RRN3*	NM_018427	Missense	p.S199L	-0.5	Neutral	NA	NA	0.496	possibly damaging
B12	3	1369199	1369199	C	A	52	0.12	*CNTN6*	NM_014461	Missense	p.S381Y	-4.31	Deleterious	0	Damaging	1	probably damaging

B12	10	127525293	127525293	G	A	35	0.14	*DHX32*	NM_018180	Missense	p.T732M	-0.17	Neutral	0	Damaging	0.698	possibly damaging
B12	9	37020768	37020768	A	C	72	0.13	*PAX5*	NM_016734	Missense	p.V26G	-4.49	Deleterious	0	Damaging	1	probably damaging
B13	17	73626700	73626700	C	T	19	0.42	*RECQL5*	NM_004259	Missense	p.E573K	-0.74	Neutral	1	Tolerated	0.01	benign
B13	6	161528978	161528978	G	A	20	0.20	*MAP3K4*	NM_005922	Missense	p.G1366R	-6.56	Deleterious	0	Damaging	1	probably damaging
B13	9	37020673	37020673	G	A	30	0.20	*PAX5*	NM_016734	Missense	p.L58F	-3.31	Deleterious	0	Damaging	1	probably damaging
B13	3	196664445	196664445	C	T	38	0.47	*NCBP2*	NM_007362	Missense	p.R112H	-4.23	Deleterious	0.11	Tolerated	1	probably damaging
B15	15	59961496	59961496	G	A	64	0.36	*BNIP2*	NM_004330	Missense	p.A379V	-3.84	Deleterious	NA	NA	0.354	benign
B15	2	113875606	113875606	G	A	36	0.28	*IL1RN*	NM_173841	Splice Site	p.A4sp	NA	NA	NA	NA	NA	NA
B15	1	154031094	154031094	C	T	37	0.38	*NUP210L*	NM_207308	Missense	p.A976T	-2.61	Deleterious	0.09	Tolerated	1	probably damaging
B15	19	38900728	38900728	G	C	14	0.29	*RASGRP4*	NM_170604	Missense	p.C658W	-1.19	Neutral	0.01	Damaging	0.96	probably damaging
B15	7	120969766	120969766	T	G	12	0.42	*WNT16*	NM_057168	Missense	p.C81G	-10.49	Deleterious	0	Damaging	1	probably damaging
B15	19	11687264	11687264	C	T	16	0.44	*ACP5*	NM_001611	Missense	p.D177N	-0.89	Neutral	0.59	Tolerated	0	benign
B15	8	25246634	25246634	G	A	37	0.43	*DOCK5*	NM_024940	Missense	p.E1387K	-3.6	Deleterious	0	Damaging	0.999	probably damaging
B15	1	115258748	115258748	C	A	24	0.33	*NRAS*	NM_002524	Missense	p.G12C	-7.09	Deleterious	0.01	Damaging	0.675	possibly damaging
B15	11	59211105	59211105	G	A	65	0.43	*OR5A1*	NM_001004728	Missense	p.G155D	-6.96	Deleterious	0	Damaging	1	probably damaging
B15	7	33192340	33192340	G	A	30	0.47	*BBS9*	NM_198428	Missense	p.G47E	-7.38	Deleterious	0	Damaging	1	probably damaging
B15	17	4575583	4575586	CTCT	C	13	0.46	*PELP1*	NM_014389	In_Frame_Del	p.E900del	-1.22	Neutral	NA	NA	NA	NA
B15	17	39274087	39274087	G	C	20	0.25	*KRTAP4-11*	NM_033059	Missense	p.L161V	-1.22	Neutral	0.64	Tolerated	0.267	benign
B15	11	22284521	22284521	G	T	20	0.25	*ANO5*	NM_213599	Missense	p.L610F	-3.88	Deleterious	0	Damaging	1	probably damaging
B15	2	105883974	105883974	G	A	33	0.33	*TGFBRAP1*	NM_004257	Missense	p.L817F	-1	Neutral	0.7	Tolerated	0.683	possibly damaging
B15	11	74644868	74644868	A	G	6	0.67	*XRRA1*	NM_182969	Splice Site	p.N109sp	-2.25	Neutral	0.02	Damaging	NA	NA
B15	5	60999838	60999838	C	T	45	0.60	*C5orf64*	NM_173667	Missense	p.P124L	-6.67	Deleterious	0	Damaging	0.844	possibly damaging
B15	17	4841715	4841715	G	C	20	0.25	*SLC25A11*	NM_003562	Missense	p.P186A	-7.48	Deleterious	0.13	Tolerated	0.966	probably damaging
B15	4	71063662	71063662	C	G	60	0.43	*ODAM*	NM_017855	Missense	p.P55A	-6.48	Deleterious	0	Damaging	1	probably damaging
B15	12	130649174	130649174	C	T	13	0.38	*FZD10*	NM_007197	Missense	p.P563S	-0.89	Neutral	0.08	Tolerated	0.02	benign
B15	13	24797756	24797756	A	G	25	0.56	*SPATA13*	NM_001166271	Missense	p.Q230R	-0.78	Neutral	0.42	Tolerated	NA	NA
B15	14	103412945	103412945	C	T	20	0.60	*CDC42BPB*	NM_006035	Missense	p.R1203K	-0.39	Neutral	0.23	Tolerated	0.001	benign
B15	2	64779333	64779333	G	A	48	0.42	*AFTPH*	NM_203437	Missense	p.R242K	-0.16	Neutral	0.91	Tolerated	0.01	benign
B15	7	151875096	151875096	C	A	25	0.48	*MLL3*	NM_170606	Splice Site	p.R2481sp	NA	NA	NA	NA	NA	NA
B15	11	123813765	123813765	G	A	48	0.38	*OR6T1*	NM_001005187	Missense	p.R261C	-5.25	Deleterious	0	Damaging	1	probably damaging
B15	6	127836029	127836029	C	T	30	0.40	*SOGA3*	NM_001012279	Missense	p.R422H	-3.72	Deleterious	0	Damaging	0.999	probably damaging
B15	5	131534035	131534035	C	A	13	0.62	*P4HA2*	NM_001017973	Missense	p.R448S	-5.62	Deleterious	0	Damaging	1	probably damaging
B15	18	42281472	42281472	G	A	45	0.51	*SETBP1*	NM_015559	Missense	p.R54H	-1.41	Neutral	0.08	Tolerated	0.391	benign

B15	1	185951514	185951514	C	T	40	0.48	*HMCN1*	NM_031935	Missense	p.S928L	-3.92	Deleterious	0.01	Damaging	0.794	possibly damaging
B15	16	87367634	87367634	T	A	6	0.50	*FBXO31*	NM_024735	Missense	p.T419S	-0.34	Neutral	0.81	Tolerated	0.001	benign
B15	7	31683521	31683521	C	T	40	0.40	*CCDC129*	NM_001257968	Missense	p.T872M	-0.63	Neutral	0.08	Tolerated	0.155	benign
B15	10	112362652	112362652	G	GTAGC	55	0.53	*SMC3*	NM_005445	Frame_Shift_Ins	p.V1123fs	NA	NA	NA	NA	NA	NA
B15	9	37020768	37020768	A	C	21	0.19	*PAX5*	NM_016734	Missense	p.V26G	-4.49	Deleterious	0	Damaging	1	probably damaging
B15	1	11217333	11217333	A	G	16	0.19	*MTOR*	NM_004958	Missense	p.W1449R	-12.18	Deleterious	0	Damaging	0.99	probably damaging
B15	2	31571834	31571834	C	T	13	0.46	*XDH*	NM_000379	Nonsense	p.W994_	NA	NA	1	Tolerated	NA	NA
B16	4	74318320	74318320	C	A	20	0.35	*AFP*	NM_001134	Missense	p.A544E	3.3	Neutral	1	Tolerated	0.22	benign
B16	3	12623366	12623366	G	A	76	0.14	*MKRN2*	NM_014160	Missense	p.C343Y	-10.08	Deleterious	0	Damaging	1	probably damaging
B16	9	36966713	36966713	C	A	14	0.21	*PAX5*	NM_016734	Nonsense	p.E205_	NA	NA	0.48	Tolerated	NA	NA
B16	1	211842635	211842635	G	T	82	0.30	*NEK2*	NM_002497	Missense	p.P269T	-4.1	Deleterious	0.02	Damaging	0.209	benign
B16	7	123269304	123269304	C	A	40	0.30	*ASB15*	NM_080928	Missense	p.P419H	-8.75	Deleterious	0	Damaging	1	probably damaging
B16	2	179611208	179611211	GAGA	G	38	0.13	*TTN*	NM_133379	In_Frame_Del	p.S5306del	1.38	Neutral	NA	NA	NA	NA
B16	9	136217106	136217106	G	A	29	0.21	*RPL7A*	NM_000972	Missense	p.V143I	-0.61	Neutral	0.22	Tolerated	0.128	benign
B16	16	15872658	15872658	C	T	26	0.27	*MYH11*	NM_001040114	Missense	p.V264M	-1.81	Neutral	0	Damaging	0.997	probably damaging
B17	1	180022162	180022162	A	C	72	0.43	*CEP350*	NM_014810	Missense	p.D1617A	-4.45	Deleterious	NA	NA	1	probably damaging
B17	6	160679545	160679545	C	T	25	0.24	*SLC22A2*	NM_003058	Missense	p.G82D	-2.87	Deleterious	0.15	Tolerated	0.282	benign
B17	8	52321417	52321417	C	A	49	0.08	*PXDNL*	NM_144651	Missense	p.G923C	-8.78	Deleterious	0	Damaging	1	probably damaging
B17	9	139108552	139108552	G	A	21	0.43	*QSOX2*	NM_181701	Missense	p.P368L	-7.38	Deleterious	0.09	Tolerated	0.018	benign
B17	3	186980366	186980366	C	T	39	0.26	*MASP1*	NM_139125	Missense	p.R127H	-2.73	Deleterious	0.03	Damaging	0.974	probably damaging
B17	9	119976799	119976799	G	A	54	0.43	*ASTN2*	NM_014010	Missense	p.R285W	-4.66	Deleterious	NA	NA	1	probably damaging
B17	14	105405283	105405283	C	T	67	0.36	*AHNAK2*	NM_138420	Missense	p.R5502Q	-1.1	Neutral	0.56	Tolerated	1	probably damaging
B17	2	149866706	149866706	C	T	9	0.56	*KIF5C*	NM_004522	Missense	p.R870C	-6.27	Deleterious	NA	NA	1	probably damaging
B17	10	99330156	99330156	C	T	26	0.12	*UBTD1*	NM_024954	Missense	p.S187L	-2.61	Deleterious	0.32	Tolerated	0.153	benign
B17	1	65311203	65311203	C	G	66	0.21	*JAK1*	NM_002227	Missense	p.S703T	-1.5	Neutral	0.4	Tolerated	0.999	probably damaging
B17	19	1466086	1466086	G	A	10	0.40	*APC2*	NM_005883	Missense	p.S929N	-2.05	Neutral	0.01	Damaging	1	probably damaging
B17	3	155198866	155198866	G	A	52	0.29	*PLCH1*	NM_001130960	Missense	p.T1658M	-2.07	Neutral	0	Damaging	0.09	benign
B17	19	36685207	36685207	C	T	17	0.35	*ZNF565*	NM_152477	Missense	p.V54I	-0.69	Neutral	0.03	Damaging	0.003	benign
B18	12	126135456	126135456	G	A	15	0.60	*TMEM132B*	NM_052907	Missense	p.G619D	-4.4	Deleterious	0.02	Damaging	1	probably damaging
B18	2	177016609	177016609	G	A	8	0.75	*HOXD4*	NM_014621	Missense	p.G83D	-0.15	Neutral	0.15	Tolerated	0	benign
B18	5	110454715	110454715	A	C	36	0.42	*WDR36*	NM_139281	Missense	p.I657L	-1.73	Neutral	0	Damaging	0.002	benign
B18	5	149406613	149406613	T	C	12	0.33	*HMGXB3*	NM_014983	Missense	p.L556P	-2.79	Deleterious	0	Damaging	1	probably damaging
B18	X	3228955	3228955	G	A	15	0.87	*MXRA5*	NM_015419	Missense	p.T2430M	0.46	Neutral	0.37	Tolerated	0.381	benign

C01	1	152816231	152816231	G	T	33	0.24	*LCE6A*	NM_001128600	Missense	p.G79C	-3	Deleterious	0	Damaging	1	probably damaging
C01	6	135314961	135314961	T	C	82	0.13	*HBS1L*	NM_006620	Missense	p.I340V	-0.25	Neutral	1	Tolerated	0.003	benign
C01	2	189907942	189907942	G	A	63	0.30	*COL5A2*	NM_000393	Nonsense	p.R1136_	NA	NA	0.63	Tolerated	NA	NA
C01	1	82409214	82409214	T	C	105	0.17	*LPHN2*	NM_012302	Missense	p.V320A	-3.25	Deleterious	0	Damaging	0.998	probably damaging
C02	4	42895345	42895345	C	T	86	0.26	*GRXCR1*	NM_001080476	Missense	p.A21V	-1.5	Neutral	0.05	Damaging	1	probably damaging
C02	5	35712967	35712967	G	T	73	0.29	*SPEF2*	NM_024867	Nonsense	p.E965_	NA	NA	0.52	Tolerated	NA	NA
C02	12	25398281	25398281	C	T	29	0.17	*KRAS*	NM_033360	Missense	p.G13D	-5.4	Deleterious	0	Damaging	0.803	possibly damaging
C02	4	144446640	144446640	G	A	118	0.14	*SMARCA5*	NM_003601	Missense	p.R186Q	-2.04	Neutral	0.8	Tolerated	0.504	possibly damaging
C02	2	220396544	220396544	G	A	8	0.38	*ASIC4*	NM_182847	Missense	p.R343Q	-0.57	Neutral	0.54	Tolerated	0.99	probably damaging
C02	1	184677381	184677381	C	T	34	0.29	*EDEM3*	NM_025191	Missense	p.R648Q	-1.34	Neutral	0.32	Tolerated	0.474	possibly damaging
C02	X	153906497	153906497	G	T	108	0.25	*GAB3*	NM_001081573	Missense	p.S574R	-2.95	Deleterious	0.08	Tolerated	0.361	benign
C02	4	165961591	165961591	A	G	90	0.26	*TRIM60*	NM_001258025	Missense	p.T123A	0.18	Neutral	1	Tolerated	0.003	benign
C02	12	112888202	112888202	C	T	79	0.16	*PTPN11*	NM_002834	Missense	p.T73I	-5.04	Deleterious	0	Damaging	0.999	probably damaging
C03	22	31332524	31332524	G	GTTCC	58	0.14	*MORC2*	NM_014941	Frame_Shift_Ins	p.Q509fs	NA	NA	NA	NA	NA	NA
C03	1	115256528	115256528	T	G	63	0.10	*NRAS*	NM_002524	Missense	p.Q61H	-4.43	Deleterious	0.01	Damaging	0.294	benign
C05	7	157926523	157926523	C	T	20	0.40	*PTPRN2*	NM_002847	Missense	p.A468T	0.2	Neutral	0.37	Tolerated	0.083	benign
C05	16	58619318	58619318	C	A	66	0.23	*CNOT1*	NM_016284	Nonsense	p.G244_	NA	NA	NA	NA	NA	NA
C05	16	23546315	23546315	C	A	6	0.67	*EARS2*	NM_001083614	Missense	p.K284N	-4.99	Deleterious	0	Damaging	1	probably damaging
C05	6	52344552	52344552	G	A	48	0.48	*EFHC1*	NM_018100	Missense	p.R536Q	-0.29	Neutral	0.37	Tolerated	0.017	benign
C05	5	140222026	140222026	G	A	66	0.32	*PCDHA8*	NM_018911	Missense	p.V374M	-2.91	Deleterious	0	Damaging	1	probably damaging
C05	11	66358410	66358410	C	A	72	0.50	*CCDC87*	NM_018219	Missense	p.V693F	-2.53	Deleterious	0.02	Damaging	1	probably damaging
C05	8	12957706	12957706	C	T	52	0.17	*DLC1*	NM_182643	Missense	p.V714M	-1.98	Neutral	0.01	Damaging	1	probably damaging
C07	2	152732944	152732944	C	T	181	0.44	*CACNB4*	NM_000726	Missense	p.G173R	-0.41	Neutral	0.14	Tolerated	1	probably damaging
C07	5	61676982	61676982	T	C	271	0.42	*KIF2A*	NM_001098511	Missense	p.L684S	-3.16	Deleterious	0.38	Tolerated	1	probably damaging
C07	3	120363231	120363231	G	A	94	0.46	*HGD*	NM_000187	Missense	p.R237C	-4.61	Deleterious	0.02	Damaging	0.054	benign
C07	7	72734145	72734145	C	T	54	0.39	*TRIM50*	NM_178125	Splice Site	p.V165sp	NA	NA	NA	NA	NA	NA
C08	16	3789597	3789597	C	A	35	0.14	*CREBBP*	NM_004380	Missense	p.C1421F	-10.76	Deleterious	0.01	Damaging	1	probably damaging
C08	2	212543887	212543887	G	T	25	0.20	*ERBB4*	NM_005235	Missense	p.N504K	-2.19	Neutral	0.08	Tolerated	0.673	possibly damaging
C08	X	142122028	142122028	A	T	37	0.27	*SPANXN4*	NM_001009613	Missense	p.N99I	0.42	Neutral	0.01	Damaging	0.563	possibly damaging
C08	5	177715547	177715547	G	A	19	0.16	*COL23A1*	NM_173465	Missense	p.P138L	NA	NA	NA	NA	NA	NA
C08	13	49039435	49039435	C	A	51	0.24	*RB1*	NM_000321	Nonsense	p.S807_	NA	NA	1	Tolerated	NA	NA
C08	15	44856807	44856807	G	T	117	0.13	*SPG11*	NM_025137	Nonsense	p.Y2363_	NA	NA	1	Tolerated	NA	NA
C12	9	117266893	117266893	G	T	7	0.71	*DFNB31*	NM_015404	Missense	p.N63K	-1.59	Neutral	0.19	Tolerated	0.997	probably damaging

C12	4	85662997	85662997	G	A	107	0.64	*WDFY3*	NM_014991	Missense	p.R2051C	-7.21	Deleterious	0.04	Damaging	1	probably damaging
C12	11	61732971	61732971	C	T	96	0.39	*FTH1*	NM_002032	Missense	p.R44H	-3.77	Deleterious	0.03	Damaging	0.044	benign
C12	20	17462414	17462414	G	A	26	0.46	*PCSK2*	NM_002594	Missense	p.R539H	-4.56	Deleterious	0	Damaging	1	probably damaging
C12	1	236148750	236148750	G	A	60	0.47	*NID1*	NM_002508	Missense	p.T995M	-5.26	Deleterious	0	Damaging	1	probably damaging
C12	9	134312068	134312074	GTCTCCA	G	60	0.48	*PRRC2B*	NM_013318	In_Frame_Del	p.119_121VSN>D	-9.94	Deleterious	NA	NA	NA	NA
C13	7	5781220	5781220	G	GAGATTA	207	0.13	*RNF216*	NM_207116	In_Frame_Ins	p.85_86insLI	-2.25	Neutral	NA	NA	NA	NA
C13	X	46359511	46359511	C	CT	93	0.26	*ZNF674*	NM_001039891	Frame_Shift_Ins	p.A505fs	NA	NA	NA	NA	NA	NA
C13	11	55418452	55418452	T	G	62	0.27	*OR4S2*	NM_001004059	Missense	p.C25G	-6.36	Deleterious	0.02	Damaging	0.913	possibly damaging
C13	19	50385601	50385601	G	A	90	0.21	*TBC1D17*	NM_024682	Missense	p.D248N	-0.87	Neutral	0.12	Tolerated	0.001	benign
C13	7	127014468	127014468	C	G	92	0.12	*ZNF800*	NM_176814	Missense	p.E308Q	-0.87	Neutral	NA	NA	0.992	probably damaging
C13	5	26988247	26988247	T	A	26	0.27	*CDH9*	NM_016279	Missense	p.E65V	-5.91	Deleterious	NA	NA	1	probably damaging
C13	1	115258744	115258744	C	A	73	0.14	*NRAS*	NM_002524	Missense	p.G13V	-7.65	Deleterious	0	Damaging	0.998	probably damaging
C13	19	45885952	45885952	C	G	41	0.17	*PPP1R13L*	NM_006663	Missense	p.G761R	-7.34	Deleterious	0	Damaging	1	probably damaging
C13	5	140896543	140896543	G	C	85	0.09	*DIAPH1*	NM_005219	Missense	p.L1232V	-0.43	Neutral	0.25	Tolerated	0.001	benign
C13	6	136475299	136475299	C	G	32	0.19	*PDE7B*	NM_018945	Missense	p.L189V	-2.96	Deleterious	0	Damaging	0.934	possibly damaging
C13	2	272145	272145	C	T	87	0.18	*ACP1*	NM_004300	Missense	p.R76W	-7	Deleterious	0.01	Damaging	0.662	possibly damaging
C13	7	80295767	80295767	C	T	32	0.16	*CD36*	NM_001001547	Missense	p.S237F	-4.07	Deleterious	NA	NA	0.96	probably damaging
C13	3	53783437	53783437	G	A	71	0.18	*CACNA1D*	NM_000720	Missense	p.V1173I	-0.71	Neutral	0.18	Tolerated	0.975	probably damaging
C13	1	216595534	216595534	C	A	53	0.53	*USH2A*	NM_206933	Missense	p.V49F	-2.56	Deleterious	0	Damaging	0.79	possibly damaging
C15	6	10586757	10586757	G	A	100	0.10	*GCNT2*	NM_145655	Missense	p.A179T	-1.89	Neutral	0.54	Tolerated	0.004	benign
C15	X	48456391	48456391	G	A	27	0.22	*WDR13*	NM_017883	Missense	p.A3T	0.48	Neutral	1	Tolerated	0.279	benign
C15	4	119661940	119661940	C	T	81	0.14	*SEC24D*	NM_014822	Missense	p.G706S	-5.6	Deleterious	0	Damaging	1	probably damaging
C15	7	140453134	140453134	T	C	28	0.18	*BRAF*	NM_004333	Missense	p.K601E	-3.71	Deleterious	0	Damaging	0.784	possibly damaging
C15	5	176759181	176759181	A	C	55	0.44	*LMAN2*	NM_006816	Missense	p.L326R	-3.93	Deleterious	0.03	Damaging	0.935	possibly damaging
C15	6	29141972	29141972	G	A	120	0.20	*OR2J2*	NM_030905	Missense	p.R187H	-2.85	Deleterious	0.01	Damaging	0.901	possibly damaging
C15	5	160721153	160721153	G	A	98	0.12	*GABRB2*	NM_021911	Missense	p.R492C	-6.88	Deleterious	0	Damaging	1	probably damaging
C15	1	227174287	227174287	G	A	127	0.43	*ADCK3*	NM_020247	Missense	p.R598H	-4.88	Deleterious	0.02	Damaging	1	probably damaging
C15	7	5342472	5342472	T	C	13	0.31	*SLC29A4*	NM_153247	Missense	p.S499P	-4.24	Deleterious	0.01	Damaging	1	probably damaging
C15	7	43484367	43484367	C	A	80	0.51	*HECW1*	NM_015052	Missense	p.S532R	-1.35	Neutral	0.15	Tolerated	0.09	benign
C17	19	45912353	45912353	C	T	113	0.51	*CD3EAP*	NM_012099	Missense	p.A376V	-2.26	Neutral	0.02	Damaging	0.253	benign
C17	4	103720611	103720611	G	T	70	0.29	*UBE2D3*	NM_181893	Missense	p.D119E	-3.56	Deleterious	0	Damaging	0.914	possibly damaging
C17	12	25398284	25398284	C	T	64	0.31	*KRAS*	NM_033360	Missense	p.G12D	-5.37	Deleterious	0	Damaging	0.517	possibly damaging

C17	12	79685850	79685851	AG	A	279	0.23	*SYT1*	NM_001135805	Frame_Shift_Del	p.K138fs	NA	NA	NA	NA	NA	NA
C17	17	39671746	39671746	G	C	115	0.33	*KRT15*	NM_002275	Missense	p.L409V	-2.78	Deleterious	0	Damaging	1	probably damaging
C17	6	114181209	114181210	GA	G	33	0.21	*MARCKS*	NM_002356	Frame_Shift_Del	p.P151fs	NA	NA	NA	NA	NA	NA
C17	1	171301908	171301908	C	T	239	0.18	*FMO4*	NM_002022	Missense	p.P230S	-7.79	Deleterious	0.02	Damaging	1	probably damaging
C17	2	179453984	179453984	C	T	492	0.33	*TTN*	NM_001267550	Missense	p.R20823H	-0.58	Neutral	0	Damaging	0.014	benign
C17	14	29237444	29237444	G	A	149	0.32	*FOXG1*	NM_005249	Missense	p.R320H	-0.2	Neutral	0.38	Tolerated	0.999	probably damaging
C17	6	94066648	94066648	G	A	133	0.24	*EPHA7*	NM_004440	Missense	p.R371W	-4.17	Deleterious	0	Damaging	1	probably damaging
C17	21	28338577	28338577	C	G	48	0.38	*ADAMTS5*	NM_007038	Missense	p.R45P	0.68	Neutral	0.29	Tolerated	0.2	benign
C17	2	69709858	69709858	A	T	169	0.31	*AAK1*	NM_014911	Missense	p.S818T	-0.72	Neutral	0.03	Damaging	0.001	benign
C17	2	198636664	198636664	G	A	121	0.18	*BOLL*	NM_197970	Missense	p.T144I	-2.62	Deleterious	0	Damaging	1	probably damaging
C17	21	46021504	46021504	T	A	80	0.29	*KRTAP10-7*	NM_198689	Missense	p.V323E	-4.23	Deleterious	0.27	Tolerated	0.911	possibly damaging
C18	22	39815589	39815589	G	A	45	0.51	*TAB1*	NM_006116	Missense	p.G244R	-7.07	Deleterious	0	Damaging	1	probably damaging
C18	19	22157500	22157500	G	T	182	0.46	*ZNF208*	NM_007153	Missense	p.H112Q	-0.72	Neutral	0.22	Tolerated	0.015	benign
C18	7	100481725	100481725	A	G	83	0.39	*SRRT*	NM_015908	Missense	p.K208E	-2.42	Neutral	0.28	Tolerated	0.58	possibly damaging
C18	8	143816819	143816819	A	T	56	0.34	*THEM6*	NM_016647	Missense	p.M197L	-0.6	Neutral	0.19	Tolerated	0.002	benign
C18	1	197237545	197237545	G	A	157	0.45	*CRB1*	NM_201253	Missense	p.M1I	-0.81	Neutral	0	Damaging	0.745	possibly damaging
C18	3	169846579	169846579	G	C	123	0.41	*PHC3*	NM_024947	Missense	p.P561A	-3.46	Deleterious	0.31	Tolerated	0.999	probably damaging
C18	6	169625297	169625297	G	T	67	0.52	*THBS2*	NM_003247	Missense	p.P906T	-5.11	Deleterious	0.06	Tolerated	1	probably damaging
C18	1	27876993	27876993	C	T	69	0.36	*AHDC1*	NM_001029882	Missense	p.R545H	-2.33	Neutral	0	Damaging	1	probably damaging
C18	X	5811397	5811397	G	A	211	0.38	*NLGN4X*	NM_020742	Missense	p.R638C	-2.88	Deleterious	0.02	Damaging	0.998	probably damaging
C18	11	2189411	2189411	T	A	74	0.45	*TH*	NM_199292	Splice Site	p.V194sp	NA	NA	NA	NA	NA	NA
C19	2	171071239	171071239	G	A	148	0.26	*MYO3B*	NM_138995	Missense	p.G143S	-3.52	Deleterious	NA	NA	1	probably damaging
C19	12	113874593	113874593	C	T	26	0.35	*SDSL*	NM_138432	Missense	p.R237W	-4.63	Deleterious	0.02	Damaging	0.892	possibly damaging
C19	2	183050753	183050753	G	A	77	0.53	*PDE1A*	NM_001258312	Missense	p.T481I	1.02	Neutral	0.32	Tolerated	0	benign
C20	16	85667582	85667582	G	A	65	0.43	*GSE1*	NM_014615	Missense	p.A24T	-1.75	Neutral	0.01	Damaging	1	probably damaging
C20	5	56229220	56229220	C	A	158	0.49	*MIER3*	NM_152622	Nonsense	p.E201_	NA	NA	0.01	Damaging	NA	NA
C20	7	116339898	116339898	G	C	314	0.43	*MET*	NM_001127500	Missense	p.E254Q	-0.33	Neutral	0.26	Tolerated	0.961	probably damaging
C20	16	2125841	2125841	G	A	78	0.36	*TSC2*	NM_000548	Missense	p.E863K	-2.35	Neutral	0.2	Tolerated	0.995	probably damaging
C20	6	129959708	129959708	C	G	114	0.08	*ARHGAP18*	NM_033515	Missense	p.G128A	0.04	Neutral	NA	NA	0.004	benign
C20	9	123313133	123313133	G	C	91	0.55	*CDK5RAP2*	NM_018249	Missense	p.I81M	-2.04	Neutral	0.04	Damaging	1	probably damaging
C20	15	72338088	72338088	G	C	145	0.41	*MYO9A*	NM_006901	Missense	p.L273V	-2.59	Deleterious	0	Damaging	1	probably damaging
C20	2	171239598	171239598	C	T	35	0.20	*MYO3B*	NM_138995	Nonsense	p.Q362_	NA	NA	0.14	Tolerated	NA	NA
C20	8	75927085	75927085	G	A	120	0.34	*CRISPLD1*	NM_031461	Missense	p.R222Q	-1.65	Neutral	0.41	Tolerated	0.007	benign

C20	12	81751968	81751968	G	A	44	0.34	*PPFIA2*	NM_003625	Missense	p.R556W	-6.2	Deleterious	0.01	Damaging	1	probably damaging
C20	2	173362731	173362731	C	CGG	138	0.14	*ITGA6*	NM_001079818	Frame_Shift_Ins	p.T1006fs	NA	NA	NA	NA	NA	NA
C21	3	193007675	193007675	T	TCCC	53	0.36	*ATP13A5*	NM_198505	In_Frame_Ins	p.1007_1008insG	-4.51	Deleterious	NA	NA	NA	NA
C21	2	168107600	168107600	A	G	213	0.39	*XIRP2*	NM_152381	Missense	p.D3233G	-2.28	Neutral	0.03	Damaging	0.971	probably damaging
C21	7	117864897	117864897	T	C	35	0.51	*ANKRD7*	NM_019644	Missense	p.F5L	-3.35	Deleterious	0.09	Tolerated	0.064	benign
C21	1	115258748	115258748	C	T	82	0.52	*NRAS*	NM_002524	Missense	p.G12S	-4.44	Deleterious	0.04	Damaging	0.329	benign
C21	14	95080781	95080781	G	A	79	0.43	*SERPINA3*	NM_001085	Missense	p.M1I	-0.26	Neutral	0	Damaging	0.029	benign
C21	4	184240941	184240941	G	A	69	0.52	*CLDN22*	NM_001111319	Missense	p.T144M	-2.51	Deleterious	0	Damaging	0.99	probably damaging
C22	19	21910750	21910750	C	T	63	0.35	*ZNF100*	NM_173531	Missense	p.D122N	0.18	Neutral	0.6	Tolerated	0.001	benign
C22	1	115258747	115258747	C	T	61	0.13	*NRAS*	NM_002524	Missense	p.G12D	-5.35	Deleterious	0	Damaging	0.372	benign
C22	8	110450677	110450677	C	A	19	0.47	*PKHD1L1*	NM_177531	Missense	p.T1251K	-0.99	Neutral	0.5	Tolerated	0.757	possibly damaging
C23	5	180486332	180486332	G	A	23	0.35	*BTNL9*	NM_152547	Missense	p.A360T	-0.74	Neutral	0.21	Tolerated	0.249	benign
C23	19	7927007	7927007	G	A	64	0.55	*EVI5L*	NM_145245	Splice Site	p.A538sp	NA	NA	NA	NA	NA	NA
C23	8	110986176	110986176	C	T	41	0.78	*KCNV1*	NM_014379	Missense	p.D148N	-2.38	Neutral	0.09	Tolerated	0.982	probably damaging
C23	3	167761190	167761191	TC	T	181	0.53	*GOLIM4*	NM_014498	Frame_Shift_Del	p.E165fs	NA	NA	NA	NA	NA	NA
C23	7	98586392	98586392	G	A	83	0.31	*TRRAP*	NM_001244580	Missense	p.E3136K	-2.77	Deleterious	0.01	Damaging	1	probably damaging
C23	10	49658431	49658431	C	T	32	0.38	*ARHGAP22*	NM_001256024	Missense	p.E597K	-1.89	Neutral	0.84	Tolerated	0.999	probably damaging
C23	4	82355875	82355875	A	T	137	0.28	*RASGEF1B*	NM_152545	Missense	p.F373Y	-2.54	Deleterious	0.14	Tolerated	0.95	possibly damaging
C23	9	13150542	13150542	C	T	114	0.50	*MPDZ*	NM_003829	Missense	p.G1200R	-4.13	Deleterious	0.05	Damaging	1	probably damaging
C23	2	189927933	189927933	C	T	80	0.20	*COL5A2*	NM_000393	Missense	p.G612R	-7.32	Deleterious	NA	NA	1	probably damaging
C23	12	12022844	12022844	A	AACTC	68	0.37	*ETV6*	NM_001987	Frame_Shift_Ins	p.H317fs	NA	NA	NA	NA	NA	NA
C23	6	101077007	101077007	T	A	54	0.39	*ASCC3*	NM_006828	Missense	p.K1420M	-2.04	Neutral	0.02	Damaging	0.281	benign
C23	10	135020804	135020804	G	A	135	0.27	*KNDC1*	NM_152643	Missense	p.R1248H	-3.08	Deleterious	0.13	Tolerated	0.999	probably damaging
C23	2	237489593	237489593	G	A	203	0.52	*CXCR7*	NM_020311	Missense	p.R162H	-3.52	Deleterious	0.04	Damaging	0.995	probably damaging
C23	16	23718096	23718096	G	A	55	0.56	*ERN2*	NM_033266	Missense	p.R204C	0.95	Neutral	0.05	Damaging	0.975	probably damaging
C23	18	6977821	6977821	G	A	140	0.29	*LAMA1*	NM_005559	Missense	p.R2084W	-5.63	Deleterious	0	Damaging	1	probably damaging
C23	X	96140069	96140069	C	T	92	0.43	*RPA4*	NM_013347	Missense	p.R254W	-2.09	Neutral	0	Damaging	0.001	benign
C23	9	140123227	140123227	C	T	21	0.29	*RNF224*	NM_001190228	Missense	p.R54W	-5.99	Deleterious	0	Damaging	NA	NA
C23	6	16306669	16306669	C	T	188	0.35	*ATXN1*	NM_001128164	Missense	p.R780H	-1.39	Neutral	0.02	Damaging	1	probably damaging
C23	6	71236340	71236340	T	A	327	0.39	*FAM135A*	NM_001162529	Missense	p.S1185T	-1.42	Neutral	0.65	Tolerated	0.868	possibly damaging
C23	7	82997263	82997264	GT	CG	96	0.34	*SEMA3E*	NM_012431	Missense	p.T656R	-2.04	Neutral	NA	NA	NA	NA
C23	16	88691140	88691140	A	AC	37	0.46	*ZC3H18*	NM_144604	Frame_Shift_Ins	p.T677fs	NA	NA	NA	NA	NA	NA

C23	7	5427882	5427882	C	T	131	0.44	*TNRC18*	NM_001080495	Missense	p.V525M	-1.35	Neutral	0.06	Tolerated	0.999	probably damaging
C23	17	74382478	74382478	T	TGA	88	0.38	*SPHK1*	NM_001142602	Frame_Shift_Ins	p.V88fs	NA	NA	NA	NA	NA	NA
C23	5	38482753	38482753	A	G	45	0.49	*LIFR*	NM_001127671	Missense	p.Y870H	-3.64	Deleterious	0.04	Damaging	1	probably damaging
C24	13	99907742	99907742	C	T	126	0.34	*GPR18*	NM_001098200	Missense	p.A129T	-0.44	Neutral	NA	NA	0.004	benign
C24	19	39334496	39334496	T	C	63	0.43	*HNRNPL*	NM_001533	Missense	p.N289S	-0.78	Neutral	0.66	Tolerated	0.002	benign
C24	12	100466453	100466453	G	C	59	0.20	*UHRF1BP1L*	NM_015054	Missense	p.P516A	-7.17	Deleterious	0	Damaging	1	probably damaging
C24	6	27101163	27101163	C	T	55	0.25	*HIST1H2AG*	NM_021064	Nonsense	p.Q105*	NA	NA	0	Damaging	NA	NA
C25	21	46596127	46596127	G	A	225	0.18	*ADARB1*	NM_015833	Missense	p.D171N	-2.94	Deleterious	0	Damaging	0.997	probably damaging
C25	6	17131032	17131032	G	C	216	0.24	*STMND1*	NM_001190766	Missense	p.D251H	-3.68	Deleterious	NA	NA	NA	NA
C25	7	107258901	107258901	G	T	73	0.26	*BCAP29*	NM_001008405	Missense	p.D300Y	-0.59	Neutral	0	Damaging	0.815	possibly damaging
C25	5	93807373	93807373	C	T	106	0.12	*KIAA0825*	NM_001145678	Missense	p.D507N	-0.77	Neutral	0.22	Tolerated	0.493	possibly damaging
C25	19	22000744	22000744	C	G	223	0.25	*ZNF43*	NM_001256653	Missense	p.E68Q	-0.4	Neutral	0.05	Damaging	0.072	benign
C25	12	112888210	112888210	G	A	107	0.16	*PTPN11*	NM_002834	Missense	p.E76K	-3.45	Deleterious	0	Damaging	0.998	probably damaging
C25	1	111891232	111891232	G	A	399	0.41	*PIFO*	NM_181643	Missense	p.R118Q	-3.71	Deleterious	0.01	Damaging	0.993	probably damaging
C25	11	6816047	6816047	C	T	203	0.25	*OR6A2*	NM_003696	Missense	p.R298H	-4.09	Deleterious	0	Damaging	1	probably damaging
C25	11	62746961	62746961	G	A	67	0.13	*SLC22A6*	NM_004790	Missense	p.R454W	-7.74	Deleterious	0	Damaging	1	probably damaging
C25	6	90354840	90354840	C	T	135	0.10	*MDN1*	NM_014611	Missense	p.R5499Q	-3.39	Deleterious	0.13	Tolerated	1	probably damaging
C25	4	186361839	186361839	C	G	77	0.23	*C4orf47*	NM_001114357	Nonsense	p.S227_	NA	NA	NA	NA	NA	NA
C25	14	53098885	53098885	C	G	110	0.23	*GPR137C*	NM_001099652	Missense	p.S242C	-3.23	Deleterious	0.01	Damaging	1	probably damaging
C26	18	63547790	63547790	A	C	321	0.12	*CDH7*	NM_033646	Missense	p.N673T	-4.27	Deleterious	0.08	Tolerated	0.98	probably damaging
C27	19	43382182	43382182	C	A	64	0.23	*PSG1*	NM_006905	Missense	p.A105S	-1.87	Neutral	0.01	Damaging	0.986	probably damaging
C27	2	60773366	60773366	T	TC	54	0.24	*BCL11A*	NM_022893	Frame_Shift_Ins	p.D42fs	NA	NA	NA	NA	NA	NA
C27	20	1162219	1162222	GGCC	GA	43	0.53	*TMEM74B*	NM_018354	Frame_Shift_Del	p.G14fs	NA	NA	NA	NA	NA	NA
C27	14	24707823	24707823	C	A	105	0.25	*GMPR2*	NM_016576	Missense	p.P314T	-5.93	Deleterious	0	Damaging	0.999	probably damaging
C27	8	110476977	110476977	C	A	122	0.25	*PKHD1L1*	NM_177531	Missense	p.T2639K	-1.12	Neutral	0.92	Tolerated	0.332	benign
C27	X	47086410	47086410	A	T	81	0.30	*CDK16*	NM_001170460	Missense	p.T459S	-2.36	Neutral	0.11	Tolerated	0.132	benign
C28	5	76335536	76335536	G	A	41	0.24	*AGGF1*	NM_018046	Missense	p.E288K	-1.18	Neutral	0.42	Tolerated	0.877	possibly damaging
C28	6	26413657	26413657	G	C	80	0.24	*BTN3A1*	NM_007048	Missense	p.E427Q	-0.54	Neutral	0.79	Tolerated	0.077	benign
C28	7	113518362	113518362	C	T	65	0.14	*PPP1R3A*	NM_002711	Missense	p.E929K	-0.82	Neutral	0.18	Tolerated	0.002	benign
C28	X	107407857	107407857	C	T	43	0.88	*COL4A6*	NM_001847	Missense	p.G1349R	-5.87	Deleterious	0	Damaging	1	probably damaging
C28	12	81655796	81655796	A	T	69	0.23	*PPFIA2*	NM_003625	Missense	p.L1247I	-0.8	Neutral	0.02	Damaging	0.982	probably damaging
C28	19	45912243	45912243	G	A	76	0.22	*CD3EAP*	NM_012099	Missense	p.M339I	-1.32	Neutral	0.13	Tolerated	0.292	benign

C28	7	133682303	133682303	G	C	150	0.11	*EXOC4*	NM_021807	Missense	p.Q755H	-0.59	Neutral	0.12	Tolerated	0.904	possibly damaging
C28	20	50769100	50769100	C	T	83	0.18	*ZFP64*	NM_018197	Missense	p.R544H	-0.12	Neutral	0.01	Damaging	0.008	benign
C28	6	127765336	127765336	C	G	64	0.45	*KIAA0408*	NM_014702	Missense	p.R668T	-3.05	Deleterious	0	Damaging	1	probably damaging
C28	11	106558438	106558438	C	T	90	0.48	*GUCY1A2*	NM_001256424	Missense	p.R710H	-3.67	Deleterious	0.09	Tolerated	0.667	possibly damaging
C28	19	17735637	17735637	C	T	21	0.43	*UNC13A*	NM_001080421	Missense	p.V1400M	NA	NA	NA	NA	NA	NA
C29	19	55284962	55284962	C	A	80	0.35	*KIR2DL1*	NM_014218	Missense	p.A83D	-3.3	Deleterious	0	Damaging	0.992	probably damaging
C29	7	80387773	80387773	A	C	45	0.18	*SEMA3C*	NM_006379	Missense	p.V506G	-6.2	Deleterious	0	Damaging	0.925	possibly damaging
C30	13	48947605	48947605	G	C	44	0.64	*RB1*	NM_000321	Missense	p.E398Q	-1.4	Neutral	0.25	Tolerated	0.544	possibly damaging
C30	6	169632235	169632235	T	G	94	0.49	*THBS2*	NM_003247	Missense	p.E664A	-2.97	Deleterious	0.23	Tolerated	0.997	probably damaging
C30	22	39448661	39448662	TC	T	82	0.44	*APOBEC3F*	NM_145298	Frame_Shift_Del	p.F361fs	NA	NA	NA	NA	NA	NA
C30	19	46417600	46417600	C	T	59	0.42	*NANOS2*	NM_001029861	Missense	p.G118S	-0.27	Neutral	0.87	Tolerated	0.326	benign
C30	12	104124023	104124023	G	A	63	0.22	*STAB2*	NM_017564	Missense	p.G1738R	-1.66	Neutral	0.54	Tolerated	0.99	probably damaging
C30	1	94016536	94016536	G	C	80	0.41	*FNBP1L*	NM_001164473	Missense	p.G562R	-6.7	Deleterious	0	Damaging	1	probably damaging
C30	2	39082371	39082371	G	A	99	0.09	*DHX57*	NM_198963	Missense	p.P578L	-8.5	Deleterious	0.01	Damaging	1	probably damaging
C30	7	13940403	13940403	C	T	76	0.24	*ETV1*	NM_004956	Missense	p.R391H	-4.77	Deleterious	0.01	Damaging	1	probably damaging
C30	6	27101172	27101172	G	GA	100	0.58	*HIST1H2AG*	NM_021064	Frame_Shift_Ins	p.V108fs	NA	NA	NA	NA	NA	NA
C30	4	73981617	73981617	A	G	37	0.38	*ANKRD17*	NM_032217	Missense	p.V1402A	-3.28	Deleterious	0.08	Tolerated	0.997	probably damaging
C31	6	169632236	169632236	C	T	125	0.32	*THBS2*	NM_003247	Missense	p.E664K	-1.27	Neutral	0.63	Tolerated	0.997	probably damaging
C31	9	123163162	123163162	C	A	37	0.27	*CDK5RAP2*	NM_018249	Missense	p.G1770V	-2.85	Deleterious	0.22	Tolerated	0.994	probably damaging
C31	12	80899904	80899904	A	T	51	0.57	*PTPRQ*	NM_001145026	Nonsense	p.K620_	NA	NA	NA	NA	NA	NA
C31	10	69281671	69281671	G	A	148	0.22	*CTNNA3*	NM_001127384	Missense	p.L170F	-2.81	Deleterious	0	Damaging	0.999	probably damaging
C31	3	78717047	78717047	G	T	68	0.56	*ROBO1*	NM_002941	Missense	p.P651Q	-6.33	Deleterious	NA	NA	0.999	probably damaging
C31	22	41923389	41923389	G	A	27	0.41	*ACO2*	NM_001098	Missense	p.R684Q	-2	Neutral	0.13	Tolerated	0.533	possibly damaging
C31	16	88691668	88691668	C	T	67	0.39	*ZC3H18*	NM_144604	Nonsense	p.R701_	NA	NA	1	Tolerated	NA	NA
C31	X	30577847	30577847	A	G	115	0.46	*CXorf21*	NM_025159	Missense	p.V209A	-1.62	Neutral	0.16	Tolerated	0.005	benign
C31	11	119182869	119182869	C	T	182	0.45	*MCAM*	NM_006500	Missense	p.V346I	0.03	Neutral	0.91	Tolerated	0.012	benign
C31	7	122303456	122303456	A	T	246	0.48	*CADPS2*	NM_001167940	Nonsense	p.Y207_	NA	NA	0.3	Tolerated	NA	NA
C32	16	26147078	26147078	G	A	82	0.45	*HS3ST4*	NM_006040	Missense	p.A294T	-3.56	Deleterious	0.01	Damaging	1	probably damaging
C32	15	55516147	55516147	T	A	325	0.50	*RAB27A*	NM_183234	Missense	p.D136V	-8.69	Deleterious	0	Damaging	1	probably damaging
C32	11	8118835	8118835	G	A	40	0.28	*TUB*	NM_003320	Missense	p.D305N	-0.39	Neutral	0.41	Tolerated	0.045	benign
C32	2	33534563	33534563	G	T	101	0.57	*LTBP1*	NM_206943	Missense	p.G1182W	-7.54	Deleterious	0	Damaging	1	probably damaging
C32	17	10542681	10542681	T	G	71	0.55	*MYH3*	NM_002470	Missense	p.Q1012H	-3.51	Deleterious	0.1	Tolerated	1	probably damaging
C32	3	52740168	52740168	A	G	14	0.36	*SPCS1*	NM_014041	Missense	p.Q36R	0.12	Neutral	1	Tolerated	0	benign

C32	16	57552146	57552146	C	T	116	0.42	*CCDC102A*	NM_033212	Missense	p.R361Q	-3.99	Deleterious	0.05	Damaging	0.999	probably damaging
C32	20	44006195	44006195	C	T	27	0.41	*TP53TG5*	NM_014477	Missense	p.R36Q	-2.63	Deleterious	0.08	Tolerated	0.95	possibly damaging
C32	14	73735278	73735278	G	A	61	0.46	*PAPLN*	NM_173462	Missense	p.V1145M	-1.63	Neutral	0.09	Tolerated	0.876	possibly damaging
C33	20	42788847	42788847	C	T	20	0.40	*JPH2*	NM_020433	Missense	p.A194T	-0.91	Neutral	0.41	Tolerated	0.003	benign
C33	2	68873139	68873139	G	T	163	0.42	*PROKR1*	NM_138964	Missense	p.K62N	-2.37	Neutral	0.18	Tolerated	0.155	benign
C33	19	40902993	40902993	C	A	98	0.40	*PRX*	NM_181882	Missense	p.M422I	-2	Neutral	0.4	Tolerated	0.004	benign
C33	19	51013587	51013587	C	G	68	0.34	*JOSD2*	NM_138334	Missense	p.Q34H	-4.81	Deleterious	0	Damaging	0.996	probably damaging
C33	20	49626374	49626374	G	A	103	0.49	*KCNG1*	NM_002237	Missense	p.R168C	-6.66	Deleterious	NA	NA	1	probably damaging
C33	12	20769201	20769201	G	A	48	0.42	*PDE3A*	NM_000921	Missense	p.R436Q	-3.18	Deleterious	0	Damaging	1	probably damaging
C33	1	115142855	115142855	C	T	176	0.41	*DENND2C*	NM_001256404	Missense	p.R692H	-4.68	Deleterious	0	Damaging	1	probably damaging
C33	19	19656281	19656281	G	A	83	0.47	*CILP2*	NM_153221	Missense	p.R976Q	-2.48	Neutral	0.1	Tolerated	0.947	possibly damaging
C33	16	81241118	81241118	T	G	53	0.47	*PKD1L2*	NM_001076780	Missense	p.T295P	NA	NA	0.01	Damaging	0.993	probably damaging
C34	1	156823691	156823691	C	T	66	0.44	*INSRR*	NM_014215	Missense	p.A164T	0.13	Neutral	0.25	Tolerated	0.001	benign
C34	16	67578666	67578666	C	CCGGGGGG	83	0.29	*FAM65A*	NM_024519	Frame_Shift_Ins	p.A954fs	NA	NA	NA	NA	NA	NA
C34	19	34945455	34945455	C	A	40	0.38	*UBA2*	NM_005499	Nonsense	p.C413_	NA	NA	1	Tolerated	NA	NA
C34	2	211158507	211158507	C	A	163	0.36	*MYL1*	NM_079420	Nonsense	p.E166_	NA	NA	0.02	Damaging	NA	NA
C34	12	63042357	63042357	C	A	56	0.20	*PPM1H*	NM_020700	Missense	p.G486V	-5.97	Deleterious	NA	NA	1	probably damaging
C34	1	55075191	55075191	C	T	51	0.37	*FAM151A*	NM_176782	Missense	p.G503E	-1.82	Neutral	0.52	Tolerated	0.012	benign
C34	19	15839720	15839720	C	G	161	0.24	*OR10H2*	NM_013939	Missense	p.I289M	-0.71	Neutral	0.54	Tolerated	0.998	probably damaging
C34	16	21030965	21030965	G	C	61	0.31	*DNAH3*	NM_017539	Missense	p.N2001K	-1.82	Neutral	0.91	Tolerated	0.881	possibly damaging
C34	10	43089790	43089790	C	T	167	0.40	*ZNF33B*	NM_006955	Missense	p.R203H	0.54	Neutral	0.25	Tolerated	0	benign
C34	7	95439761	95439761	C	T	103	0.20	*DYNC1I1*	NM_004411	Nonsense	p.R56_	NA	NA	1	Tolerated	NA	NA
C34	10	121551093	121551093	C	G	42	0.12	*INPP5F*	NM_014937	Nonsense	p.S127_	NA	NA	0.07	Tolerated	NA	NA
C34	X	153716361	153716361	T	C	113	0.29	*SLC10A3*	NM_001142392	Missense	p.S307G	1.72	Neutral	0.61	Tolerated	0.003	benign
C34	9	115407938	115407938	A	C	54	0.59	*KIAA1958*	NM_133465	Missense	p.T394P	1.13	Neutral	0.25	Tolerated	0.995	probably damaging
C34	14	60977881	60977881	G	A	72	0.13	*SIX6*	NM_007374	Missense	p.V218I	-0.27	Neutral	0.14	Tolerated	0.005	benign
C35	2	141232889	141232890	TC	TTAGG	75	0.57	*LRP1B*	NM_018557	In_Frame_Ins	p.3147_3148insP	-12.41	Deleterious	NA	NA	NA	NA
C35	3	101090891	101090891	C	T	126	0.37	*SENP7*	NM_020654	Missense	p.D253N	-0.38	Neutral	0.14	Tolerated	0.651	possibly damaging
C35	18	19444508	19444508	G	A	152	0.45	*MIB1*	NM_020774	Missense	p.D968N	-3.21	Deleterious	0.01	Damaging	0.963	probably damaging
C35	19	7927119	7927119	G	A	106	0.50	*EVI5L*	NM_001159944	Missense	p.E586K	-3.03	Deleterious	0.07	Tolerated	0.835	possibly damaging
C35	6	152527480	152527480	A	AGGGCT	18	0.33	*SYNE1*	NM_182961	Frame_Shift_Ins	p.F7614fs	NA	NA	NA	NA	NA	NA

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C35	10	76797622	76797622	C	T	27	0.59	*DUPD1*	NM_001003892	Missense	p.G212D	-0.25	Neutral	0.77	Tolerated	0.004	benign
C35	7	92888886	92888886	C	T	125	0.57	*CCDC132*	NM_017667	Nonsense	p.Q201_	NA	NA	0.31	Tolerated	NA	NA
C35	11	33886217	33886217	C	T	72	0.58	*LMO2*	NM_005574	Missense	p.R132Q	-3.67	Deleterious	0.51	Tolerated	0.996	probably damaging
C35	6	80223162	80223162	G	A	128	0.57	*LCA5*	NM_001122769	Missense	p.R163C	-5.23	Deleterious	0	Damaging	1	probably damaging
C35	19	3620125	3620125	C	T	43	0.33	*CACTIN*	NM_001080543	Missense	p.R295H	-4.64	Deleterious	NA	NA	1	probably damaging
C35	5	167824747	167824747	C	A	47	0.64	*WWC1*	NM_001161661	Missense	p.S151Y	-3.88	Deleterious	0.09	Tolerated	0.999	probably damaging
C35	20	18163808	18163808	C	T	140	0.44	*CSRP2BP*	NM_020536	Missense	p.S617L	-1.96	Neutral	0.18	Tolerated	0.014	benign
C35	9	124855504	124855504	C	T	23	0.52	*TTLL11*	NM_001139442	Missense	p.S65N	0.03	Neutral	NA	NA	0.718	possibly damaging
C35	19	15083538	15083538	G	A	100	0.29	*SLC1A6*	NM_005071	Missense	p.T62M	-3.68	Deleterious	0	Damaging	1	probably damaging
C35	10	97194435	97194435	A	G	164	0.48	*SORBS1*	NM_001034954	Missense	p.V39A	-1.65	Neutral	0	Damaging	0.996	probably damaging
C36	19	7918032	7918032	G	A	162	0.31	*EVI5L*	NM_001159944	Missense	p.A350T	-3.36	Deleterious	0	Damaging	0.982	probably damaging
C36	9	133748403	133748403	A	G	48	0.25	*ABL1*	NM_007313	Missense	p.E374G	-6.75	Deleterious	0	Damaging	1	probably damaging
C36	4	1803576	1803576	C	T	32	0.50	*FGFR3*	NM_001163213	Missense	p.R252W	-6.7	Deleterious	0	Damaging	1	probably damaging
C36	20	37257577	37257577	C	T	51	0.47	*ARHGAP40*	NM_001164431	Missense	p.S188L	-1.11	Neutral	0.76	Tolerated	NA	NA
C36	19	17922789	17922789	C	T	185	0.11	*B3GNT3*	NM_014256	Missense	p.S326L	-4.52	Deleterious	0.34	Tolerated	0.963	probably damaging
C36	9	133747523	133747523	C	A	125	0.11	*ABL1*	NM_007313	Missense	p.T296N	-4.74	Deleterious	0	Damaging	0.089	benign
C36	19	9089510	9089510	C	T	121	0.20	*MUC16*	NM_024690	Missense	p.V769I	0.01	Neutral	0	Damaging	0	benign
C37	3	153203810	153203810	G	A	64	0.25	*C3orf79*	NM_001101337	Missense	p.G47S	-3.5	Deleterious	0	Damaging	0.002	benign
C37	2	145147550	145147550	T	C	95	0.29	*ZEB2*	NM_014795	Missense	p.H1038R	-7.28	Deleterious	0.08	Tolerated	0.992	probably damaging
C37	3	111312899	111312902	CTTG	C	107	0.43	*ZBED2*	NM_024508	In_Frame_Del	p.N49del	-2.9	Deleterious	NA	NA	NA	NA
C37	X	24844665	24844665	G	A	103	0.26	*POLA1*	NM_016937	Missense	p.R1222Q	-3.7	Deleterious	0	Damaging	1	probably damaging
C37	3	126226844	126226844	C	T	39	0.41	*UROC1*	NM_001165974	Missense	p.R169H	-1.7	Neutral	0	Damaging	0.879	possibly damaging
C37	X	37948815	37948815	G	A	35	0.23	*SYTL5*	NM_001163334	Missense	p.R269Q	-1.04	Neutral	0.57	Tolerated	0.414	benign
C37	16	78466519	78466519	G	A	199	0.38	*WWOX*	NM_016373	Missense	p.R309H	-3.44	Deleterious	0	Damaging	0.999	probably damaging
C37	X	34148663	34148663	G	T	140	0.41	*FAM47A*	NM_203408	Missense	p.S578Y	-3.61	Deleterious	0.03	Damaging	0.995	probably damaging
C37	6	130363924	130363924	C	T	169	0.22	*L3MBTL3*	NM_032438	Missense	p.T27M	-3.26	Deleterious	0.05	Damaging	1	probably damaging
C37	1	16459788	16459788	G	A	138	0.51	*EPHA2*	NM_004431	Missense	p.T647M	-5.05	Deleterious	0	Damaging	1	probably damaging
C37	18	44104787	44104787	C	T	105	0.40	*LOXHD1*	NM_144612	Missense	p.V1542M	-0.03	Neutral	0.01	Damaging	1	probably damaging
C38	19	49926530	49926533	CCAG	C	73	0.11	*PTH2*	NM_178449	In_Frame_Del	p.L22del	-1.56	Neutral	NA	NA	NA	NA
C38	11	107832848	107832848	G	A	207	0.46	*RAB39A*	NM_017516	Missense	p.R135H	-4.84	Deleterious	0	Damaging	1	probably damaging
C38	15	25223575	25223575	G	A	18	0.28	*SNRPN*	NM_022806	Missense	p.R236H	-0.96	Neutral	0.08	Tolerated	0.006	benign
C38	19	15222526	15222526	C	T	66	0.36	*SYDE1*	NM_033025	Missense	p.R501W	-3.29	Deleterious	0.02	Damaging	0.993	probably damaging

C38	1	154427014	154427018	AGCCT	AACA	81	0.11	*IL6R*	NM_000565	Frame_Shift_Del	p.S373fs	NA	NA	NA	NA	NA	NA
C38	12	49432060	49432060	T	TG	146	0.12	*MLL2*	NM_003482	Frame_Shift_Ins	p.T3027fs	NA	NA	NA	NA	NA	NA
C38	4	55561808	55561808	G	A	220	0.25	*KIT*	NM_000222	Nonsense	p.W66_	NA	NA	1	Tolerated	NA	NA
C39	15	55972314	55972314	C	T	145	0.48	*PRTG*	NM_173814	Missense	p.C304Y	-9.8	Deleterious	0	Damaging	1	probably damaging
C39	14	89629231	89629231	C	T	76	0.22	*FOXN3*	NM_001085471	Missense	p.D334N	-3.12	Deleterious	0.18	Tolerated	1	probably damaging
C39	3	100093866	100093866	C	T	129	0.26	*TOMM70A*	NM_014820	Missense	p.G408E	-5.76	Deleterious	0	Damaging	1	probably damaging
C39	12	49416138	49416138	T	A	32	0.50	*MLL2*	NM_003482	Splice Site	p.N5447sp	NA	NA	NA	NA	NA	NA
C39	7	88963897	88963897	C	T	171	0.13	*ZNF804B*	NM_181646	Missense	p.P534L	1.22	Neutral	1	Tolerated	0	benign
C39	3	101284167	101284167	G	A	203	0.25	*TRMT10C*	NM_017819	Missense	p.R181Q	-2.13	Neutral	0.12	Tolerated	0.399	benign
C39	1	35370276	35370276	G	A	48	0.38	*DLGAP3*	NM_001080418	Missense	p.R237W	-4.31	Deleterious	0	Damaging	0.999	probably damaging
C39	9	129958803	129958803	C	T	141	0.11	*RALGPS1*	NM_014636	Missense	p.S363L	-1.06	Neutral	0.12	Tolerated	0.348	benign
C40	4	54343013	54343013	T	C	94	0.39	*LNX1*	NM_001126328	Missense	p.D600G	-1.73	Neutral	0.42	Tolerated	0.032	benign
C40	12	6700692	6700692	C	T	178	0.15	*CHD4*	NM_001273	Missense	p.E1094K	-3.59	Deleterious	0	Damaging	1	probably damaging
C40	9	21974799	21974799	C	CTT	29	0.79	*CDKN2A*	NM_000077	Frame_Shift_Ins	p.E10fs	NA	NA	NA	NA	NA	NA
C40	1	207225577	207225577	C	A	60	0.40	*YOD1*	NM_001276320	Nonsense	p.E2_	NA	NA	0.88	Tolerated	NA	NA
C40	1	1735942	1735942	C	G	73	0.29	*GNB1*	NM_002074	Missense	p.G116R	-7.06	Deleterious	0	Damaging	0.998	probably damaging
C40	9	138667193	138667193	G	A	50	0.60	*KCNT1*	NM_020822	Missense	p.G761S	-5.76	Deleterious	0	Damaging	1	probably damaging
C40	2	43452637	43452637	C	CG	41	0.12	*ZFP36L2*	NM_006887	Frame_Shift_Ins	p.K102fs	NA	NA	NA	NA	NA	NA
C40	16	4626101	4626101	G	T	57	0.44	*C16orf96*	NM_001145011	Missense	p.K540N	-1.29	Neutral	0.32	Tolerated	0.997	probably damaging
C40	6	157527665	157527675	TGTTTGTTGTT	TAAAGC	79	0.29	*ARID1B*	NM_017519	Frame_Shift_Del	p.L1779fs	NA	NA	NA	NA	NA	NA
C40	19	10084845	10084845	A	G	224	0.34	*COL5A3*	NM_015719	Splice Site	p.M1168sp	NA	NA	NA	NA	NA	NA
C40	7	44805109	44805109	C	A	28	0.32	*ZMIZ2*	NM_031449	Missense	p.P725T	-5.16	Deleterious	0.12	Tolerated	1	probably damaging
C40	17	8791888	8791888	G	A	55	0.40	*PIK3R5*	NM_014308	Missense	p.R406C	-0.12	Neutral	0.06	Tolerated	0.7	possibly damaging
C40	5	63890629	63890629	G	A	30	0.37	*RGS7BP*	NM_001029875	Missense	p.V186I	-0.3	Neutral	0.45	Tolerated	0.001	benign
C40	6	29797631	29797631	G	C	93	0.10	*HLA-G*	NM_002127	Missense	p.V312L	-0.82	Neutral	0	Damaging	0.054	benign
C40	6	34003582	34003582	C	T	122	0.42	*GRM4*	NM_000841	Missense	p.V769M	-2.2	Neutral	0.04	Damaging	0.999	probably damaging
C40	3	50404342	50404342	C	T	100	0.46	*CACNA2D2*	NM_001174051	Missense	p.V844I	-0.16	Neutral	0.53	Tolerated	0.703	possibly damaging
C41	11	120008124	120008124	C	T	44	0.36	*TRIM29*	NM_012101	Missense	p.A206T	-1.57	Neutral	NA	NA	1	probably damaging
C41	1	152777633	152777633	C	T	28	0.32	*LCE1C*	NM_178351	Missense	p.G108R	-2.94	Deleterious	0	Damaging	1	probably damaging
C41	8	77768194	77768194	G	A	164	0.34	*ZFHX4*	NM_024721	Missense	p.G3013R	-5.37	Deleterious	0.03	Damaging	1	probably damaging
C41	11	134239725	134239725	G	A	114	0.40	*GLB1L2*	NM_138342	Missense	p.G352S	-5.63	Deleterious	0	Damaging	1	probably damaging
C41	16	3788596	3788596	A	ACC	80	0.38	*CREBBP*	NM_004380	Frame_Shift_Ins	p.I1453fs	NA	NA	NA	NA	NA	NA
C41	12	120208588	120208588	C	T	128	0.30	*CIT*	NM_001206999	Splice Site	p.L736sp	NA	NA	NA	NA	NA	NA

C41	1	155874261	155874261	C	T	50	0.32	*RIT1*	NM_001256821	Missense	p.M107I	-3.99	Deleterious	0.06	Tolerated	0.999	probably damaging
C41	1	42654583	42654583	C	G	70	0.50	*FOXJ3*	NM_001198851	Missense	p.M490I	-1.23	Neutral	0.01	Damaging	0.067	benign
C41	16	20559743	20559743	C	T	80	0.34	*ACSM2B*	NM_001105069	Missense	p.R316Q	-3.28	Deleterious	0.02	Damaging	0.983	probably damaging
C41	22	40042778	40042778	C	T	83	0.39	*CACNA1I*	NM_021096	Missense	p.R452C	-6.25	Deleterious	0.01	Damaging	1	probably damaging
C41	2	179612384	179612384	G	A	235	0.15	*TTN*	NM_133379	Missense	p.R4915C	-0.81	Neutral	0.07	Tolerated	0.85	possibly damaging
C41	10	129901283	129901283	T	C	68	0.47	*MKI67*	NM_002417	Missense	p.S2941G	-1.25	Neutral	0.38	Tolerated	0.907	possibly damaging
C43	10	118451956	118451956	G	A	77	0.42	*HSPA12A*	NM_025015	Missense	p.S190L	-2.01	Neutral	0.11	Tolerated	0.006	benign
C43	11	134253729	134253729	C	T	71	0.34	*B3GAT1*	NM_054025	Missense	p.G156R	-0.8	Neutral	0.5	Tolerated	0.017	benign
C43	12	64472862	64472862	C	A	48	0.40	*SRGAP1*	NM_020762	Missense	p.A430D	-4.6	Deleterious	NA	NA	0.991	probably damaging
C43	20	20226778	20226778	A	T	172	0.31	*C20orf26*	NM_015585	Missense	p.N693I	-6.6	Deleterious	0.04	Damaging	0.991	probably damaging
C43	4	103498066	103498066	G	T	141	0.33	*NFKB1*	NM_003998	Missense	p.K147N	-4.12	Deleterious	0	Damaging	1	probably damaging
C43	6	147049845	147049845	C	A	90	0.09	*ADGB*	NM_024694	Missense	p.H830N	-0.81	Neutral	0.52	Tolerated	0	benign
C43	6	56426287	56426287	A	T	176	0.35	*DST*	NM_001144769	Missense	p.L2591H	-2.65	Deleterious	0.12	Tolerated	0.996	probably damaging
C43	9	32632278	32632278	C	A	105	0.35	*TAF1L*	NM_153809	Missense	p.E1100D	-2.22	Neutral	0.26	Tolerated	0.044	benign
C43	12	11905512	11905513	G	GC	29	0.31	*ETV6*	NM_001987	Splice Site	p.R55sp	NA	NA	NA	NA	NA	NA
C43	12	92538064	92538067	G	GGTC	67	0.21	*BTG1*	NM_001731	In_Frame_Ins	p.103_103T>RP	-15.62	Deleterious	NA	NA	NA	NA
C44	12	111908474	111908474	C	T	106	0.39	*ATXN2*	NM_002973	Missense	p.G1024D	-4.86	Deleterious	0.12	Tolerated	1	probably damaging
C44	12	112888189	112888189	G	A	95	0.46	*PTPN11*	NM_002834	Missense	p.E69K	-3.44	Deleterious	0	Damaging	0.987	probably damaging
C44	13	37439770	37439770	C	T	46	0.22	*SMAD9*	NM_001127217	Missense	p.D303N	-3.38	Deleterious	0.16	Tolerated	0.811	possibly damaging
C44	16	57702302	57702302	C	A	25	0.24	*GPR97*	NM_170776	Missense	p.L15M	-0.47	Neutral	0.06	Tolerated	0.98	probably damaging
C44	17	4446282	4446282	C	G	124	0.54	*MYBBP1A*	NM_001105538	Missense	p.E940Q	-0.85	Neutral	0.42	Tolerated	0.557	possibly damaging
C44	18	6962054	6962054	C	A	212	0.22	*LAMA1*	NM_005559	Missense	p.G2448C	-4.83	Deleterious	0.06	Tolerated	0.999	probably damaging
C44	19	49116250	49116250	C	T	44	0.11	*FAM83E*	NM_017708	Missense	p.R127Q	-3.94	Deleterious	0	Damaging	0.901	possibly damaging
C44	20	57045782	57045782	C	A	19	0.11	*APCDD1L*	NM_153360	Missense	p.G24V	-2.07	Neutral	0.08	Tolerated	0.893	possibly damaging
C44	3	113866342	113866342	C	T	51	0.20	*DRD3*	NM_000796	Missense	p.R149H	-4.24	Deleterious	0	Damaging	1	probably damaging
C44	3	75714034	75714034	C	G	25	0.12	*FRG2C*	NM_001124759	Missense	p.S81R	-1.4	Neutral	0.2	Tolerated	0.978	probably damaging
C44	6	102376488	102376488	C	A	144	0.28	*GRIK2*	NM_021956	Missense	p.A689E	-2.37	Neutral	0	Damaging	0.995	probably damaging
C44	9	121976256	121976256	T	C	102	0.28	*DBC1*	NM_014618	Missense	p.Y288C	-1.51	Neutral	0.03	Damaging	0.867	possibly damaging
C44	1	152975658	152975658	AGAGCCAGGCTGTACCAAGGTCCCT	A	71	0.38	*SPRR3*	NM_005416	In_Frame_Del	p.EPGCTKVP95del	-9.33	Deleterious	NA	NA	NA	NA
C45	1	115258744	115258744	C	T	36	0.42	*NRAS*	NM_002524	Missense	p.G13D	-5.48	Deleterious	0.03	Damaging	0.434	benign

C45	12	52794403	52794403	C	T	81	0.46	*KRT82*	NM_033033	Missense	p.V229M	-2.73	Deleterious	0	Damaging	1	probably damaging
C45	15	75970059	75970059	G	T	49	0.49	*CSPG4*	NM_001897	Missense	p.L1707I	-0.51	Neutral	0.16	Tolerated	0.996	probably damaging
C45	X	150908126	150908126	G	T	111	0.22	*CNGA2*	NM_005140	Missense	p.R99L	-3.04	Deleterious	0.08	Tolerated	0.546	possibly damaging
C46	1	145293566	145293566	G	A	14	0.14	*NBPF10*	NM_001039703	Missense	p.R54Q	0.82	Neutral	1	Tolerated	NA	NA
C46	17	72889676	72889694	G	GGGCTCCGTAGGTTCCATG	49	0.24	*FADS6*	NM_178128	In_Frame_Ins	p.6_6P>PMEPTEP	0.08	Neutral	NA	NA	NA	NA
C47	11	34140049	34140049	A	C	40	0.60	*NAT10*	NM_024662	Missense	p.Q260P	-5.88	Deleterious	0	Damaging	1	probably damaging
C47	12	112926900	112926900	C	A	50	0.42	*PTPN11*	NM_002834	Missense	p.T507K	-5.22	Deleterious	0	Damaging	0.995	probably damaging
C47	16	1259318	1259318	G	A	129	0.45	*CACNA1H*	NM_021098	Missense	p.R1217H	-0.8	Neutral	0	Damaging	0.964	probably damaging
C47	2	112834830	112834830	A	C	45	0.33	*TMEM87B*	NM_032824	Missense	p.E188A	-1.27	Neutral	0.49	Tolerated	0.459	possibly damaging
C47	21	47417641	47417641	G	A	20	0.50	*COL6A1*	NM_001848	Missense	p.G497R	-5.93	Deleterious	0	Damaging	1	probably damaging
C47	7	148526913	148526913	T	G	34	0.29	*EZH2*	NM_004456	Missense	p.I131L	-1.93	Neutral	0.09	Tolerated	0.045	benign
C47	X	38033523	38033523	G	T	20	0.10	*SRPX*	NM_006307	Missense	p.A80D	-1.18	Neutral	0.26	Tolerated	0.87	possibly damaging
C47	11	62364130	62364136	G	GGGGGCA	84	0.23	*MTA2*	NM_004739	In_Frame_Ins	p.287_288insAP	-9.67	Deleterious	NA	NA	NA	NA
C47	7	148526914	148526914	GTTA	G	34	0.29	*EZH2*	NM_004456	In_Frame_Del	p.N130del	-15.27	Deleterious	NA	NA	NA	NA
C47	Y	15417399	15417399	T	TA	20	0.80	*UTY*	NM_001258249	Frame_Shift_Ins	p.T1051fs	NA	NA	NA	NA	NA	NA
C48	17	42980123	42980123	G	A	47	0.11	*CCDC103*	NM_213607	Missense	p.G223S	-0.03	Neutral	0.61	Tolerated	0.22	benign
C48	3	195507925	195507925	C	T	20	0.20	*MUC4*	NM_018406	Missense	p.G3509D	0.22	Neutral	NA	NA	0.003	benign
C48	3	50333012	50333012	C	A	15	0.13	*HYAL3*	NM_001200029	Missense	p.A8S	-0.97	Neutral	0.39	Tolerated	0.009	benign
C48	4	184129219	184129219	C	T	66	0.18	*WWC2*	NM_024949	Missense	p.H119Y	-1.71	Neutral	0	Damaging	0.337	benign
C48	9	35547618	35547618	G	A	98	0.18	*RUSC2*	NM_014806	Missense	p.R367H	0.91	Neutral	0.62	Tolerated	0	benign
C48	9	79252335	79252335	G	A	130	0.12	*PRUNE2*	NM_015225	Missense	p.R2988W	-5.45	Deleterious	0	Damaging	1	probably damaging
C49	12	109698323	109698323	G	A	60	0.38	*ACACB*	NM_001093	Missense	p.V2179M	-2.79	Deleterious	0	Damaging	1	probably damaging
C49	12	112186172	112186172	C	A	44	0.09	*ACAD10*	NM_001136538	Missense	p.P877Q	-3.56	Deleterious	0.1	Tolerated	0.999	probably damaging
C49	12	49087925	49087925	T	C	195	0.43	*CCNT1*	NM_001240	Missense	p.T358A	0.12	Neutral	0.76	Tolerated	0.001	benign
C49	19	55237768	55237768	C	T	69	0.36	*KIR3DL3*	NM_153443	Missense	p.S107L	-3.91	Deleterious	0.03	Damaging	0.955	possibly damaging
C49	2	120197712	120197712	C	T	24	0.08	*SCTR*	NM_002980	Missense	p.C435Y	-1.22	Neutral	1	Tolerated	0	benign
C49	4	77691818	77691818	C	A	41	0.39	*SHROOM3*	NM_020859	Missense	p.L1797I	-1.95	Neutral	0	Damaging	1	probably damaging
C49	7	16649289	16649289	T	C	60	0.42	*ANKMY2*	NM_020319	Missense	p.Q283R	-1.83	Neutral	0.56	Tolerated	0.145	benign
C49	8	22105765	22105765	A	G	44	0.23	*POLR3D*	NM_001722	Missense	p.I154V	-0.55	Neutral	0.52	Tolerated	0.802	possibly damaging
C49	14	35742652	35742653	C	CA	62	0.37	*KIAA0391*	NM_014672	Frame_Shift_Ins	p.S544fs	NA	NA	NA	NA	NA	NA

C49	14	35742656	35742656	GACACA	G	46	0.20	*KIAA0391*	NM_014672	Frame_Shift_Del	p.D546fs	NA	NA	NA	NA	NA	NA
C51	1	115258748	115258748	C	T	48	0.10	*NRAS*	NM_002524	Missense	p.G12S	-4.44	Deleterious	0.04	Damaging	0.329	benign
C51	5	16781904	16781904	C	T	146	0.14	*MYO10*	NM_012334	Missense	p.V213M	-2.43	Neutral	0	Damaging	1	probably damaging
C51	9	139272464	139272464	CCCAGGTCCAGGGCCCCCTTCTCAGGCCCAGGCTGGGGTAGGGGCGGCTTCT	C	18	0.33	*SNAPC4*	NM_003086	In_Frame_Del	p.EKPPLPQPGPEKGALDL1255del	-3.72	Deleterious	NA	NA	NA	NA
C54	1	209961775	209961775	G	A	24	0.42	*IRF6*	NM_006147	Missense	p.P465L	-0.45	Neutral	0.18	Tolerated	0.08	benign
C54	11	121030929	121030929	C	A	144	0.53	*TECTA*	NM_005422	Missense	p.T1592N	-3.37	Deleterious	0.01	Damaging	0.939	possibly damaging
C54	10	70968723	70968723	G	GA	34	0.41	*SUPV3L1*	NM_003171	Frame_Shift_Ins	p.E765fs	NA	NA	NA	NA	NA	NA
C54	2	43452511	43452511	G	GC	134	0.32	*ZFP36L2*	NM_006887	Frame_Shift_Ins	p.G144fs	NA	NA	NA	NA	NA	NA
C54	20	62705521	62705521	GTAGT	G	122	0.13	*RGS19*	NM_005873	Frame_Shift_Del	p.Y146fs	NA	NA	NA	NA	NA	NA
C55	12	25378647	25378647	T	A	48	0.48	*KRAS*	NM_033360	Missense	p.K117N	-4.56	Deleterious	0.01	Damaging	1	probably damaging
C55	3	49162595	49162595	C	A	80	0.43	*LAMB2*	NM_002292	Missense	p.A910S	0.35	Neutral	0.6	Tolerated	0.412	benign
C55	7	128486205	128486205	G	A	64	0.30	*FLNC*	NM_001458	Missense	p.A1318T	-0.8	Neutral	0	Damaging	0.95	possibly damaging
C56	1	115258747	115258747	C	T	41	0.46	*NRAS*	NM_002524	Missense	p.G12D	-5.35	Deleterious	0	Damaging	0.372	benign
C56	1	247875276	247875276	C	T	103	0.37	*OR6F1*	NM_001005286	Missense	p.R261H	-3.74	Deleterious	0	Damaging	1	probably damaging
C56	10	118661351	118661351	G	A	131	0.31	*KIAA1598*	NM_001127211	Missense	p.P533L	-0.55	Neutral	0.04	Damaging	0.007	benign
C56	10	49444566	49444566	C	A	29	0.10	*FRMPD2*	NM_001018071	nonsense	p.G318_	NA	NA	0.56	Tolerated	NA	NA
C56	11	45928199	45928199	C	T	56	0.43	*C11orf94*	NM_001080446	Missense	p.R73Q	-0.63	Neutral	0.08	Tolerated	0.786	possibly damaging
C56	11	4790354	4790354	C	T	80	0.38	*OR51F1*	NM_001004752	Missense	p.R265H	-4.36	Deleterious	0.01	Damaging	0.865	possibly damaging
C56	19	2216563	2216563	C	A	24	0.08	*DOT1L*	NM_032482	Missense	p.P736H	-2.54	Deleterious	0	Damaging	0.999	probably damaging
C56	2	116572427	116572427	G	A	86	0.49	*DPP10*	NM_001178034	Missense	p.V591I	-0.77	Neutral	0.05	Damaging	0.995	probably damaging
C56	22	23523656	23523656	C	T	69	0.33	*BCR*	NM_004327	Missense	p.A170V	-1.18	Neutral	0.09	Tolerated	0.254	benign
C56	4	436233	436233	C	T	101	0.29	*ZNF721*	NM_133474	Missense	p.G675S	-3.93	Deleterious	0.03	Damaging	0.994	probably damaging
C56	5	172560650	172560650	C	A	98	0.27	*CREBRF*	NM_153607	Missense	p.Q608K	-1.18	Neutral	0.11	Tolerated	0.865	possibly damaging
C56	7	140453153	140453153	A	C	24	0.29	*BRAF*	NM_004333	Missense	p.D594E	-3.59	Deleterious	0	Damaging	1	probably damaging
C56	7	63673527	63673527	C	G	120	0.40	*ZNF735*	NM_001159524	Missense	p.L33V	NA	NA	NA	NA	NA	NA
C56	1	50884699	50884699	C	A	21	0.10	*DMRTA2*	NM_032110	Missense	p.A423S	-0.45	Neutral	0.07	Tolerated	0.953	possibly damaging
C56	2	31560683	31560683	C	A	24	0.08	*XDH*	NM_000379	Missense	p.A1259S	-2.35	Neutral	0.03	Damaging	0.989	probably damaging
C57	11	120686132	120686132	C	G	29	0.48	*GRIK4*	NM_014619	Missense	p.S98W	-4.01	Deleterious	0	Damaging	1	probably damaging

C57	12	25398284	25398284	C	A	64	0.28	*KRAS*	NM_033360	Missense	p.G12V	-7.11	Deleterious	0.01	Damaging	0.999	probably damaging
C57	19	14261828	14261828	G	T	21	0.10	*LPHN1*	NM_001008701	Missense	p.P1428T	-0.32	Neutral	0.06	Tolerated	0.994	probably damaging
C57	19	3760231	3760231	G	A	48	0.50	*APBA3*	NM_004886	Missense	p.S11L	-1.98	Neutral	0.09	Tolerated	0	benign
C57	20	46307420	46307420	C	A	23	0.09	*SULF2*	NM_018837	Missense	p.R398L	-4.22	Deleterious	NA	NA	1	probably damaging
C57	21	39795341	39795341	C	T	27	0.37	*ERG*	NM_001243428	Missense	p.V134M	-1.74	Neutral	0	Damaging	1	probably damaging
C57	3	97720503	97720503	G	T	92	0.35	*GABRR3*	NM_001105580	nonsense	p.S288_	NA	NA	NA	NA	NA	NA
C57	4	114177072	114177072	C	T	41	0.32	*ANK2*	NM_001148	Missense	p.P391L	-9.1	Deleterious	0.05	Damaging	0.971	probably damaging
C57	4	146073788	146073788	C	A	45	0.09	*OTUD4*	NM_001102653	Splice Site	p.V227sp	NA	NA	NA	NA	NA	NA
C57	4	1806171	1806171	G	A	47	0.34	*FGFR3*	NM_001163213	Missense	p.R399H	-3.16	Deleterious	0.2	Tolerated	0.925	possibly damaging
C57	4	71824700	71824700	C	T	102	0.09	*MOB1B*	NM_001244766	Missense	p.R47W	-6.39	Deleterious	0	Damaging	1	probably damaging
C57	6	55198589	55198589	G	T	60	0.42	*GFRAL*	NM_207410	Missense	p.G55C	-2.18	Neutral	0.12	Tolerated	0.502	possibly damaging
C57	X	7890140	7890140	C	A	22	0.18	*PNPLA4*	NM_004650	Splice Site	p.E61sp	NA	NA	NA	NA	NA	NA
C58	1	15689212	15689212	G	A	30	0.53	*FHAD1*	NM_052929	Missense	p.E991K	-1.86	Neutral	0.47	Tolerated	0.882	possibly damaging
C58	12	15811502	15811502	G	A	125	0.45	*EPS8*	NM_004447	Missense	p.R319W	-7.55	Deleterious	0	Damaging	1	probably damaging
C58	12	25398285	25398285	C	T	94	0.10	*KRAS*	NM_033360	Missense	p.G12S	-4.44	Deleterious	0.01	Damaging	0.682	possibly damaging
C58	12	43769864	43769864	A	C	91	0.43	*ADAMTS20*	NM_025003	Missense	p.F1770V	-1.97	Neutral	0.44	Tolerated	0.005	benign
C58	14	64518809	64518809	G	C	252	0.47	*SYNE2*	NM_182914	Missense	p.Q2726H	-0.8	Neutral	0.18	Tolerated	0.958	probably damaging
C58	15	71184341	71184341	G	A	63	0.41	*THAP10*	NM_020147	Missense	p.R91W	-1.23	Neutral	0.18	Tolerated	0.999	probably damaging
C58	16	2215893	2215893	C	T	114	0.43	*TRAF7*	NM_032271	Missense	p.T32M	-0.91	Neutral	0.03	Damaging	0.997	probably damaging
C58	16	84690558	84690558	G	C	110	0.38	*KLHL36*	NM_024731	Missense	p.V49L	-1.51	Neutral	0.16	Tolerated	0.792	possibly damaging
C58	17	53398155	53398155	G	A	45	0.11	*HLF*	NM_002126	Missense	p.R268H	-3.6	Deleterious	0.09	Tolerated	1	probably damaging
C58	19	41800563	41800563	G	C	73	0.45	*HNRNPUL1*	NM_007040	Missense	p.R497P	-5.32	Deleterious	0	Damaging	1	probably damaging
C58	2	207631709	207631709	C	G	88	0.31	*FASTKD2*	NM_001136194	Missense	p.L98V	0.09	Neutral	1	Tolerated	0.001	benign
C58	20	45354636	45354636	G	A	58	0.55	*SLC2A10*	NM_030777	Missense	p.V321M	-0.51	Neutral	0.2	Tolerated	0.586	possibly damaging
C58	22	35947882	35947882	C	T	100	0.52	*RASD2*	NM_014310	Missense	p.R202C	-6.2	Deleterious	0.01	Damaging	0.916	possibly damaging
C58	3	155210550	155210550	G	T	46	0.15	*PLCH1*	NM_001130960	Missense	p.P747T	-7.43	Deleterious	0.02	Damaging	1	probably damaging
C58	5	162898274	162898274	G	A	92	0.39	*HMMR*	NM_001142556	Missense	p.M182I	-1	Neutral	0.21	Tolerated	0.865	possibly damaging
C58	7	13935705	13935705	C	T	36	0.42	*ETV1*	NM_004956	Missense	p.G407E	-7.63	Deleterious	0	Damaging	1	probably damaging
C58	8	77763763	77763763	G	A	171	0.45	*ZFHX4*	NM_024721	Missense	p.D1536N	-4.68	Deleterious	0.01	Damaging	1	probably damaging
C58	9	21971186	21971186	G	A	22	0.36	*CDKN2A*	NM_001195132	nonsense	p.R58_	-4.7	Deleterious	0.01	Damaging	0.824	possibly damaging
C59	1	115258748	115258748	C	A	47	0.40	*NRAS*	NM_002524	Missense	p.G12C	-7.09	Deleterious	0.01	Damaging	0.675	possibly damaging
C59	1	177911176	177911176	C	T	39	0.36	*SEC16B*	NM_033127	Splice Site	p.V183sp	NA	NA	NA	NA	NA	NA
C59	11	100922187	100922187	C	T	35	0.37	*PGR*	NM_000926	Missense	p.M775I	-2.77	Deleterious	0.47	Tolerated	0.885	possibly damaging

C59	11	55111475	55111475	A	C	33	0.52	*OR4A16*	NM_001005274	Missense	p.K267Q	-3.69	Deleterious	0	Damaging	1	probably damaging
C59	12	49439958	49439958	C	A	101	0.47	*MLL2*	NM_003482	Splice Site	p.R1528sp	NA	NA	NA	NA	NA	NA
C59	14	57268607	57268607	G	T	88	0.30	*OTX2*	NM_001270525	Missense	p.S247Y	-2.8	Deleterious	0.01	Damaging	0.911	possibly damaging
C59	14	60213121	60213121	G	T	88	0.26	*RTN1*	NM_021136	Missense	p.S107Y	-2.31	Neutral	0.18	Tolerated	0.89	possibly damaging
C59	16	22826263	22826263	C	T	93	0.42	*HS3ST2*	NM_006043	Missense	p.T111I	-2.72	Deleterious	0.1	Tolerated	0.157	benign
C59	19	5832454	5832454	G	A	184	0.47	*FUT6*	NM_001040701	Missense	p.T42I	-1	Neutral	0.06	Tolerated	0.216	benign
C59	4	103718593	103718593	C	T	33	0.33	*UBE2D3*	NM_181893	nonsense	p.W143_	NA	NA	1	Tolerated	NA	NA
C59	4	148463742	148463742	G	A	97	0.27	*EDNRA*	NM_001957	Missense	p.R419Q	-1.59	Neutral	0.05	Damaging	0.614	possibly damaging
C59	4	6051548	6051548	C	T	178	0.20	*JAKMIP1*	NM_001099433	Missense	p.G654R	-3.09	Deleterious	0.45	Tolerated	0.999	probably damaging
C59	6	32497918	32497918	C	G	27	0.15	*HLA-DRB5*	NM_002125	Missense	p.L28F	-1.12	Neutral	0.04	Damaging	0.999	probably damaging
C59	7	91794338	91794338	G	A	96	0.57	*LRRD1*	NM_001161528	Missense	p.P60L	-2.06	Neutral	0.01	Damaging	0.829	possibly damaging
C59	8	77763349	77763349	C	T	184	0.40	*ZFHX4*	NM_024721	Missense	p.R1398C	-7.21	Deleterious	0.05	Damaging	1	probably damaging
C61	13	28592639	28592639	T	G	58	0.52	*FLT3*	NM_004119	Missense	p.I836L	-1.83	Neutral	0.01	Damaging	0.13	benign
C61	1	2160695	2160695	A	T	44	0.43	*SKI*	NM_003036	Missense	p.M164L	-0.58	Neutral	0.81	Tolerated	0	benign
C61	10	29776183	29776183	G	A	49	0.57	*SVIL*	NM_021738	Missense	p.A1465V	-2.93	Deleterious	0	Damaging	0	benign
C61	13	28592641	28592641	T	G	55	0.55	*FLT3*	NM_004119	Missense	p.D835A	-7.25	Deleterious	0	Damaging	1	probably damaging
C61	2	25965112	25965112	G	A	77	0.43	*ASXL2*	NM_018263	Missense	p.T1365I	-2.16	Neutral	0.13	Tolerated	1	probably damaging
C61	3	195509747	195509747	G	A	24	0.21	*MUC4*	NM_018406	Missense	p.L2902F	-0.53	Neutral	NA	NA	0.949	possibly damaging
C61	3	196664445	196664445	C	T	51	0.29	*NCBP2*	NM_007362	Missense	p.R112H	-4.23	Deleterious	0.11	Tolerated	1	probably damaging
C61	7	100491715	100491715	G	A	26	0.50	*ACHE*	NM_015831	Missense	p.R47W	-3.61	Deleterious	0.04	Damaging	0.999	probably damaging
C61	6	10410369	10410369	A	ACC	59	0.25	*TFAP2A*	NM_003220	Frame_Shift_Ins	p.L82fs	NA	NA	NA	NA	NA	NA
C63	1	115258744	115258744	C	T	55	0.33	*NRAS*	NM_002524	Missense	p.G13D	-5.48	Deleterious	0.03	Damaging	0.434	benign
C63	16	20476893	20476893	G	T	64	0.25	*ACSM2A*	NM_001010845	nonsense	p.E78_	NA	NA	0.03	Damaging	NA	NA
C63	17	263253	263253	C	A	22	0.09	*C17orf97*	NM_001013672	Missense	p.P207T	-1.97	Neutral	0.47	Tolerated	0.001	benign
C63	9	33385815	33385815	T	C	15	0.13	*AQP7*	NM_001170	Missense	p.Q192R	-0.66	Neutral	0.58	Tolerated	0.009	benign
C63	15	52017161	52017161	G	GA	77	0.47	*LYSMD2*	NM_153374	Frame_Shift_Ins	p.F143fs	NA	NA	NA	NA	NA	NA
C63	2	228563910	228563934	A	ACTGCCACCCTCTGAAGGACCCCGC	123	0.14	*SLC19A3*	NM_025243	In_Frame_Ins	p.173_174insGGVLQRVA	-15.58	Deleterious	NA	NA	NA	NA
C64	11	77907300	77907300	G	C	77	0.10	*USP35*	NM_020798	Missense	p.K3N	-2.12	Neutral	0	Damaging	1	probably damaging
C64	17	6023811	6023811	G	A	97	0.38	*WSCD1*	NM_015253	Missense	p.V520M	-2.22	Neutral	0	Damaging	1	probably damaging
C64	18	58039300	58039300	C	T	229	0.12	*MC4R*	NM_005912	Missense	p.V95I	-0.39	Neutral	0.2	Tolerated	0.873	possibly damaging

C64	3	195512734	195512734	T	G	21	0.10	*MUC4*	NM_018406	Missense	p.H1906P	-0.4	Neutral	NA	NA	0	benign
C64	6	144843201	144843201	T	G	23	0.48	*UTRN*	NM_007124	Missense	p.I1876S	-2.6	Deleterious	0.07	Tolerated	0.995	probably damaging
C64	7	158621950	158621950	C	A	16	0.13	*ESYT2*	NM_020728	Missense	p.G102C	-7.68	Deleterious	0	Damaging	1	probably damaging
C64	8	13948115	13948115	C	A	16	0.13	*SGCZ*	NM_139167	Missense	p.G259V	-0.81	Neutral	0.16	Tolerated	1	probably damaging
C64	9	14789063	14789063	T	C	56	0.30	*FREM1*	NM_144966	Missense	p.E1344G	-3.92	Deleterious	0.13	Tolerated	0.002	benign
C64	5	26881534	26881534	G	T	181	0.39	*CDH9*	NM_016279	Missense	p.P694H	-7.49	Deleterious	NA	NA	1	probably damaging
C65	1	1225756	1225756	C	T	76	0.42	*SCNN1D*	NM_001130413	Missense	p.H590Y	-4.58	Deleterious	0.33	Tolerated	0.967	probably damaging
C65	1	145296448	145296448	T	A	12	0.25	*NBPF10*	NM_001039703	Missense	p.Y124N	1.63	Neutral	1	Tolerated	NA	NA
C65	1	184787942	184787942	C	T	36	0.47	*FAM129A*	NM_052966	Missense	p.A335T	-3.28	Deleterious	0.18	Tolerated	0.999	probably damaging
C65	1	196398790	196398790	C	T	147	0.42	*KCNT2*	NM_198503	Missense	p.G246R	-7.82	Deleterious	0	Damaging	1	probably damaging
C65	10	73056447	73056447	G	A	53	0.38	*UNC5B*	NM_170744	Missense	p.R813Q	-2.37	Neutral	0.3	Tolerated	1	probably damaging
C65	12	113624621	113624621	G	T	108	0.32	*C12orf52*	NM_032848	Missense	p.G24C	-3.16	Deleterious	0.06	Tolerated	0.921	possibly damaging
C65	12	25398281	25398281	C	T	139	0.31	*KRAS*	NM_033360	Missense	p.G13D	-5.4	Deleterious	0	Damaging	0.803	possibly damaging
C65	17	6909219	6909219	C	T	66	0.68	*ALOX12*	NM_000697	Missense	p.R431W	-6.67	Deleterious	0	Damaging	0.997	probably damaging
C65	2	105858490	105858490	G	A	178	0.11	*GPR45*	NM_007227	Missense	p.V59M	-1.81	Neutral	0	Damaging	1	probably damaging
C65	2	188349537	188349537	C	T	62	0.31	*TFPI*	NM_006287	Splice Site	p.P179sp	NA	NA	NA	NA	NA	NA
C65	7	88965742	88965742	C	A	123	0.35	*ZNF804B*	NM_181646	Missense	p.T1149K	-3.46	Deleterious	0.04	Damaging	1	probably damaging
C65	X	100297055	100297055	G	T	82	0.20	*TRMT2B*	NM_024917	Missense	p.P75Q	-1.7	Neutral	0.61	Tolerated	0.994	probably damaging
C65	X	54319385	54319385	C	T	285	0.22	*WNK3*	NM_020922	Missense	p.G658E	-1.35	Neutral	0.27	Tolerated	0.917	possibly damaging
C65	4	88537504	88537504	CAGCAATGAA	C	87	0.09	*DSPP*	NM_014208	In_Frame_Del	p.SNE1231del	-1.19	Neutral	NA	NA	NA	NA
C66	22	19967317	19967317	C	T	105	0.30	*ARVCF*	NM_001670	Missense	p.V449M	-2.04	Neutral	NA	NA	0.998	probably damaging
C66	7	148080827	148080827	G	A	99	0.23	*CNTNAP2*	NM_014141	Missense	p.A1188T	-1.99	Neutral	0.49	Tolerated	0.954	possibly damaging
C66	13	37678523	37678523	G	C	87	0.24	*CSNK1A1L*	NM_145203	Missense	p.Q291E	-1.76	Neutral	0.06	Tolerated	0.035	benign
C66	19	47856948	47856948	G	A	36	0.08	*DHX34*	NM_014681	Missense	p.A221T	-2.4	Neutral	0	Damaging	1	probably damaging
C66	9	91727516	91727516	C	T	98	0.44	*SHC3*	NM_016848	Missense	p.R167H	-2.85	Deleterious	0.02	Damaging	1	probably damaging
C66	19	7685860	7685860	C	T	36	0.31	*XAB2*	NM_020196	Missense	p.V615M	-2.63	Deleterious	0	Damaging	1	probably damaging
C66	9	37002647	37002647	T	TG	81	0.48	*PAX5*	NM_016734	Frame_Shift_Ins	p.E201fs	NA	NA	NA	NA	NA	NA
C67	2	71058242	71058242	G	A	63	0.19	*CD207*	NM_015717	Missense	p.A309V	0.51	Neutral	0.57	Tolerated	0.149	benign
C67	9	99797098	99797098	C	T	108	0.52	*CTSL2*	NM_001333	Missense	p.S272N	-1.47	Neutral	NA	NA	0.087	benign
C67	10	134981802	134981802	G	A	144	0.40	*KNDC1*	NM_152643	Missense	p.G116R	-6.32	Deleterious	0	Damaging	1	probably damaging
C67	5	140176747	140176747	C	T	89	0.34	*PCDHA2*	NM_018905	Missense	p.A733V	-2.37	Neutral	0.53	Tolerated	0.021	benign
C67	17	27284161	27284161	G	A	116	0.28	*SEZ6*	NM_178860	Missense	p.S865L	-0.99	Neutral	0.4	Tolerated	1	probably damaging
C67	19	51220001	51220001	C	T	109	0.42	*SHANK1*	NM_016148	Missense	p.G59D	-1.36	Neutral	0.08	Tolerated	0.08	benign

C67	3	140785272	140785272	G	A	63	0.56	*SPSB4*	NM_080862	Missense	p.R109H	-4.96	Deleterious	0.45	Tolerated	1	probably damaging
C67	10	123989930	123989930	C	A	106	0.22	*TACC2*	NM_206862	Missense	p.A2701D	-1.4	Neutral	0.63	Tolerated	0.999	probably damaging
C67	2	234680928	234680928	G	A	63	0.48	*UGT1A5*	NM_019078	Missense	p.R443H	-2.83	Deleterious	0.08	Tolerated	0.235	benign
C68	1	77627075	77627075	C	T	40	0.30	*PIGK*	NM_005482	Missense	p.A240T	-1.24	Neutral	0.17	Tolerated	0.051	benign
C68	4	87724960	87724960	C	T	133	0.09	*PTPN13*	NM_080685	nonsense	p.R2207_	NA	NA	1	Tolerated	NA	NA
C68	X	84363866	84363866	C	G	118	0.33	*SATL1*	NM_001012980	Missense	p.G37R	0.84	Neutral	NA	NA	0	benign
C69	1	118539004	118539004	T	C	122	0.52	*SPAG17*	NM_206996	Missense	p.Q1681R	-1.46	Neutral	0.46	Tolerated	0.873	possibly damaging
C69	1	154026844	154026844	G	A	123	0.47	*NUP210L*	NM_207308	Missense	p.H1115Y	-1.02	Neutral	1	Tolerated	0.993	probably damaging
C69	1	177901659	177901659	G	A	82	0.51	*SEC16B*	NM_033127	Missense	p.A993V	-1.39	Neutral	0.26	Tolerated	0.196	benign
C69	1	215953355	215953355	G	A	40	0.43	*USH2A*	NM_206933	Missense	p.P3590L	-6.84	Deleterious	0	Damaging	0.445	benign
C69	1	228468338	228468338	C	T	69	0.36	*OBSCN*	NM_001271223	Missense	p.R3109C	-3.19	Deleterious	0.18	Tolerated	0.511	possibly damaging
C69	10	5791976	5791976	T	G	69	0.45	*FAM208B*	NM_017782	Missense	p.F2198V	-3.33	Deleterious	0.03	Damaging	0.972	probably damaging
C69	11	59860317	59860317	A	G	47	0.51	*MS4A2*	NM_000139	Missense	p.Y125C	-2.3	Neutral	0.53	Tolerated	0.243	benign
C69	12	123344702	123344702	G	A	53	0.47	*HIP1R*	NM_003959	Missense	p.R835Q	-1.31	Neutral	0.53	Tolerated	0.865	possibly damaging
C69	12	6715464	6715464	T	C	26	0.62	*CHD4*	NM_001273	Missense	p.N26D	0.39	Neutral	0.13	Tolerated	0.593	possibly damaging
C69	12	98926903	98926903	A	G	209	0.46	*TMPO*	NM_003276	Missense	p.K290E	0.18	Neutral	0.47	Tolerated	0	benign
C69	14	64484470	64484470	T	C	37	0.43	*SYNE2*	NM_182914	Missense	p.L1682P	-4.26	Deleterious	0.01	Damaging	1	probably damaging
C69	15	55516177	55516177	G	A	117	0.46	*RAB27A*	NM_183234	Missense	p.P126L	-8.04	Deleterious	0.03	Damaging	1	probably damaging
C69	17	18058025	18058025	T	C	27	0.37	*MYO15A*	NM_016239	Missense	p.L2727P	-5.22	Deleterious	0.03	Damaging	0.989	probably damaging
C69	2	11751118	11751118	G	A	30	0.30	*GREB1*	NM_014668	Missense	p.V991I	0.73	Neutral	0.9	Tolerated	0	benign
C69	2	171225863	171225863	A	T	156	0.40	*MYO3B*	NM_138995	Missense	p.H316L	-2.4	Neutral	0.42	Tolerated	0.017	benign
C69	22	42473944	42473944	C	G	53	0.42	*FAM109B*	NM_001002034	Missense	p.P216R	-5.18	Deleterious	0.05	Damaging	1	probably damaging
C69	3	160138627	160138627	G	C	64	0.41	*SMC4*	NM_001002800	Missense	p.E653Q	-0.11	Neutral	0.6	Tolerated	0.013	benign
C69	3	195474138	195474138	A	G	156	0.22	*MUC4*	NM_018406	Missense	p.L5383P	-3.64	Deleterious	0	Damaging	1	probably damaging
C69	3	47163971	47163971	T	G	171	0.48	*SETD2*	NM_014159	Missense	p.N719H	-1.45	Neutral	NA	NA	0.998	probably damaging
C69	4	119649805	119649805	T	C	65	0.45	*SEC24D*	NM_014822	Missense	p.T957A	-1.94	Neutral	0.48	Tolerated	0.156	benign
C69	4	48371900	48371900	A	G	125	0.44	*SLAIN2*	NM_020846	Missense	p.M142V	-0.96	Neutral	0.69	Tolerated	0	benign
C69	6	109480306	109480306	G	A	21	0.95	*CEP57L1*	NM_001083535	Splice Site	p.K274sp	0.24	Neutral	NA	NA	NA	NA
C69	6	5368934	5368934	A	G	104	0.47	*FARS2*	NM_006567	Missense	p.Q44R	-0.59	Neutral	0.32	Tolerated	0	benign
C69	6	56765367	56765367	G	A	87	0.44	*DST*	NM_001144769	Missense	p.A90V	-0.28	Neutral	0.05	Damaging	0.001	benign
C69	7	128492992	128492992	G	A	54	0.52	*FLNC*	NM_001458	Missense	p.G2039R	-7.52	Deleterious	0	Damaging	1	probably damaging
C69	7	157370775	157370775	C	T	50	0.36	*PTPRN2*	NM_002847	Missense	p.G852S	-5.74	Deleterious	0.07	Tolerated	1	probably damaging
C69	9	127088681	127088681	G	A	130	0.44	*NEK6*	NM_001145001	Missense	p.V194M	-0.05	Neutral	0.05	Damaging	0.992	probably damaging

C69	9	96070829	96070829	C	T	36	0.69	*WNK2*	NM_006648	Missense	p.A2160V	-1.1	Neutral	0.07	Tolerated	0.975	probably damaging
C69	16	85689982	85689982	G	GGAGCGCGAGCGCGAGCGC	57	0.19	*GSE1*	NM_014615	In_Frame_Ins	p.342_342E>ERERERE	5.86	Neutral	NA	NA	NA	NA
C69	2	97790243	97790243	ATTC	A	63	0.54	*ANKRD36*	NM_001164315	In_Frame_Del	p.L217del	-1.26	Neutral	NA	NA	NA	NA
C69	4	9784517	9784517	CAAG	C	22	0.45	*DRD5*	NM_000798	In_Frame_Del	p.K290del	-11.02	Deleterious	NA	NA	NA	NA
C69	9	123476542	123476542	ACGGCGG	A	77	0.94	*MEGF9*	NM_001080497	In_Frame_Del	p.AA30del	0.62	Neutral	NA	NA	NA	NA
C70	1	11009766	11009766	G	C	24	0.54	*C1orf127*	NM_001170754	Missense	p.AATTPS1161del	-2.16	Neutral	0.08	Tolerated	0.997	probably damaging
C70	1	237205840	237205840	G	A	41	0.39	*RYR2*	NM_001035	Missense	p.G7S	-2.14	Neutral	0.48	Tolerated	0.779	possibly damaging
C70	1	55080445	55080445	C	T	48	0.50	*FAM151A*	NM_176782	Missense	p.R168Q	-2.22	Neutral	0.4	Tolerated	0.145	benign
C70	1	97700514	97700514	G	T	99	0.47	*DPYD*	NM_000110	Missense	p.T779N	-0.47	Neutral	0	Damaging	0.144	benign
C70	10	129906577	129906577	G	A	115	0.43	*MKI67*	NM_002417	Missense	p.T1176M	-3.4	Deleterious	0.07	Tolerated	1	probably damaging
C70	11	113285144	113285144	C	T	53	0.34	*DRD2*	NM_000795	Missense	p.V255I	-0.16	Neutral	0.49	Tolerated	0.012	benign
C70	11	16077359	16077359	G	A	67	0.46	*SOX6*	NM_001145819	Missense	p.T410M	-0.68	Neutral	0.05	Damaging	0.653	possibly damaging
C70	11	58206931	58206931	G	A	134	0.49	*OR5B12*	NM_001004733	Missense	p.R232C	-3.98	Deleterious	0.02	Damaging	0.009	benign
C70	11	64594617	64594617	C	G	59	0.41	*CDC42BPG*	NM_017525	Missense	p.V1432L	0.18	Neutral	1	Tolerated	0.01	benign
C70	11	6561178	6561178	C	T	114	0.46	*DNHD1*	NM_144666	Missense	p.R1165C	-2.24	Neutral	0.1	Tolerated	0.952	possibly damaging
C70	11	92088309	92088309	C	T	141	0.48	*FAT3*	NM_001008781	Missense	p.R1011W	-0.05	Neutral	0.08	Tolerated	1	probably damaging
C70	13	53422307	53422307	C	G	152	0.43	*PCDH8*	NM_002590	Missense	p.G89R	0.22	Neutral	1	Tolerated	1	probably damaging
C70	14	73976161	73976161	G	T	36	0.47	*HEATR4*	NM_001220484	Missense	p.D525E	0.12	Neutral	0.41	Tolerated	0.005	benign
C70	16	15178499	15178499	G	A	113	0.12	*RRN3*	NM_018427	Missense	p.S199L	-0.5	Neutral	NA	NA	0.496	possibly damaging
C70	17	11597273	11597273	A	C	81	0.37	*DNAH9*	NM_001372	Missense	p.N1568T	-4.59	Deleterious	0.31	Tolerated	0.455	possibly damaging
C70	17	76464713	76464713	G	A	57	0.47	*DNAH17*	NM_173628	Missense	p.R2922C	-7.06	Deleterious	0	Damaging	NA	NA
C70	17	76567792	76567792	G	C	62	0.42	*DNAH17*	NM_173628	Missense	p.I204M	-2.24	Neutral	0.11	Tolerated	NA	NA
C70	18	24628464	24628464	C	T	81	0.48	*CHST9*	NM_031422	Missense	p.R42K	-0.05	Neutral	1	Tolerated	0.001	benign
C70	2	102956678	102956678	T	G	40	0.53	*IL1RL1*	NM_016232	Missense	p.I131M	-2.23	Neutral	0.05	Damaging	1	probably damaging
C70	2	128389922	128389922	G	A	64	0.44	*MYO7B*	NM_001080527	Missense	p.R1758Q	-3.24	Deleterious	0.09	Tolerated	1	probably damaging
C70	2	158971625	158971625	G	A	60	0.37	*UPP2*	NM_001135098	Missense	p.G122S	-5.48	Deleterious	0.03	Damaging	1	probably damaging
C70	2	167992437	167992437	A	G	79	0.46	*XIRP2*	NM_152381	Missense	p.S143G	-0.69	Neutral	0.28	Tolerated	0.037	benign
C70	2	74273972	74273972	C	T	72	0.51	*TET3*	NM_144993	Missense	p.P175S	-1.17	Neutral	0.44	Tolerated	0	benign
C70	20	60887279	60887279	C	T	78	0.45	*LAMA5*	NM_005560	Missense	p.G3152S	-1.86	Neutral	0.3	Tolerated	0.991	probably damaging

C70	3	156742576	156742576	G	A	48	0.44	*LEKR1*	NM_001004316	Missense	p.A411T	-0.78	Neutral	0.54	Tolerated	0.996	probably damaging
C70	4	123108615	123108615	C	G	39	0.38	*KIAA1109*	NM_015312	Missense	p.P192R	-1.22	Neutral	0.72	Tolerated	0.535	possibly damaging
C70	5	73236833	73236833	C	T	127	0.50	*ARHGEF28*	NM_001080479	Missense	p.L1731F	0.09	Neutral	0	Damaging	1	probably damaging
C70	6	132030966	132030966	G	C	24	1.00	*CTAGE9*	NM_001145659	Missense	p.L398V	-2.48	Neutral	0	Damaging	0.999	probably damaging
C70	6	169642053	169642053	G	A	51	0.53	*THBS2*	NM_003247	Missense	p.A232V	-0.4	Neutral	0.62	Tolerated	0	benign
C70	6	37139063	37139063	G	A	150	0.50	*PIM1*	NM_001243186	Missense	p.E226K	-3.87	Deleterious	0.01	Damaging	0.08	benign
C70	7	116339770	116339770	T	G	181	0.48	*MET*	NM_001127500	Missense	p.L211W	-1.86	Neutral	0.03	Damaging	1	probably damaging
C70	7	91774219	91774219	G	A	48	0.44	*LRRD1*	NM_001161528	Missense	p.R856C	-1.57	Neutral	0.12	Tolerated	0.001	benign
C70	7	91793095	91793095	G	T	43	0.37	*LRRD1*	NM_001161528	Missense	p.N474K	-5.14	Deleterious	0.01	Damaging	1	probably damaging
C70	8	9610060	9610060	G	T	31	0.55	*TNKS*	NM_003747	Missense	p.G1026V	-1.01	Neutral	0.06	Tolerated	0.001	benign
C70	9	115336773	115336773	A	T	162	0.46	*KIAA1958*	NM_133465	Missense	p.Y138F	-0.46	Neutral	0.25	Tolerated	0.997	probably damaging
C70	9	14816816	14816816	G	A	144	0.80	*FREM1*	NM_144966	Missense	p.T867I	-4.35	Deleterious	0	Damaging	1	probably damaging
C70	9	34977120	34977120	G	A	57	0.53	*KIAA1045*	NM_015297	Missense	p.R297Q	-1.63	Neutral	0.02	Damaging	1	probably damaging
C70	X	3241940	3241940	T	C	32	0.97	*MXRA5*	NM_015419	Missense	p.T596A	-1.18	Neutral	0.82	Tolerated	0.002	benign
C70	11	6662745	6662745	C	CCAG	28	0.21	*DCHS1*	NM_003737	In_Frame_Ins	p.33_34insL	-0.08	Neutral	NA	NA	NA	NA
C70	12	50749738	50749738	CAT	C	132	0.38	*FAM186A*	NM_001145475	Frame_Shift_Del	p.H292fs	NA	NA	NA	NA	NA	NA
C70	9	100092968	100092968	A	AGAGGAG	36	0.25	*CCDC180*	NM_020893	In_Frame_Ins	p.915_915E>EEE	0.28	Neutral	NA	NA	NA	NA
C70	X	41204685	41204685	A	ACC	21	0.90	*DDX3X*	NM_001356	Frame_Shift_Ins	p.I401fs	NA	NA	NA	NA	NA	NA
C71	1	176998832	176998832	G	A	62	0.48	*ASTN1*	NM_004319	Missense	p.A353V	-1.33	Neutral	0.02	Damaging	0.073	benign
C71	1	181701989	181701989	C	T	100	0.41	*CACNA1E*	NM_001205293	Missense	p.H923Y	-2.58	Deleterious	0.23	Tolerated	0.957	probably damaging
C71	1	215990508	215990508	C	T	80	0.53	*USH2A*	NM_206933	Missense	p.R3134Q	-0.9	Neutral	0.59	Tolerated	0.453	possibly damaging
C71	1	39788353	39788353	G	A	45	0.51	*MACF1*	NM_012090	Missense	p.R1373H	-4.38	Deleterious	0.01	Damaging	1	probably damaging
C71	10	29779847	29779847	A	C	154	0.14	*SVIL*	NM_021738	Missense	p.L1374R	-4.99	Deleterious	0	Damaging	0.991	probably damaging
C71	10	64968527	64968527	G	A	68	0.63	*JMJD1C*	NM_032776	Missense	p.R968W	-2.58	Deleterious	0	Damaging	1	probably damaging
C71	10	79581223	79581223	C	T	88	0.66	*DLG5*	NM_004747	Missense	p.A1007T	0.52	Neutral	0.43	Tolerated	0.026	benign
C71	11	22284493	22284493	G	T	148	0.44	*ANO5*	NM_213599	Missense	p.C601F	-10.68	Deleterious	0.03	Damaging	1	probably damaging
C71	11	60696170	60696170	C	T	29	0.59	*TMEM132A*	NM_017870	Missense	p.R202W	-3.15	Deleterious	0	Damaging	1	probably damaging
C71	11	92623734	92623734	C	T	16	0.38	*FAT3*	NM_001008781	nonsense	p.Q4377_	NA	NA	0.07	Tolerated	NA	NA
C71	11	9286541	9286541	T	C	32	0.50	*DENND5A*	NM_015213	Missense	p.T26A	-0.48	Neutral	0.77	Tolerated	0	benign
C71	11	94759620	94759620	A	T	72	0.44	*KDM4E*	NM_001161630	Missense	p.Y300F	-3.87	Deleterious	0.13	Tolerated	0.998	probably damaging
C71	12	133067343	133067343	A	G	29	1.00	*FBRSL1*	NM_001142641	Missense	p.T63A	0.5	Neutral	1	Tolerated	0	benign
C71	12	6680061	6680061	G	A	43	0.44	*CHD4*	NM_001273	Missense	p.R1899W	-4.51	Deleterious	0	Damaging	1	probably damaging

C71	13	28608285	28608285	A	C	58	0.36	*FLT3*	NM_004119	Missense	p.Y591D	-8.42	Deleterious	0.04	Damaging	1	probably damaging
C71	14	104642408	104642408	C	G	158	0.47	*KIF26A*	NM_015656	Missense	p.P1095A	-1.55	Neutral	0.58	Tolerated	0.001	benign
C71	14	105353935	105353935	C	G	78	0.49	*CEP170B*	NM_001112726	Missense	p.P1120R	-7.96	Deleterious	0	Damaging	0.999	probably damaging
C71	14	105413921	105413921	C	T	100	0.51	*AHNAK2*	NM_138420	Missense	p.A2623T	-1.55	Neutral	0.29	Tolerated	0.718	possibly damaging
C71	15	77329487	77329487	C	A	37	0.46	*PSTPIP1*	NM_003978	Missense	p.F407L	-0.28	Neutral	1	Tolerated	0.013	benign
C71	16	20944655	20944655	T	C	39	0.46	*DNAH3*	NM_017539	Missense	p.M4058V	-0.6	Neutral	0.14	Tolerated	0.003	benign
C71	16	71007809	71007809	C	T	118	0.29	*HYDIN*	NM_001270974	Missense	p.V1718M	-2.05	Neutral	0.02	Damaging	0.383	benign
C71	16	87748173	87748173	T	G	39	0.51	*KLHDC4*	NM_017566	Missense	p.K256Q	-3.52	Deleterious	0.16	Tolerated	0.995	probably damaging
C71	17	53398202	53398202	A	G	22	0.55	*HLF*	NM_002126	Missense	p.I284V	-0.14	Neutral	0.55	Tolerated	0.01	benign
C71	18	19057136	19057136	G	C	78	0.59	*GREB1L*	NM_001142966	Missense	p.G792A	-2.01	Neutral	0.13	Tolerated	0.357	benign
C71	2	170094614	170094614	G	A	73	0.51	*LRP2*	NM_004525	Missense	p.T1498M	-3.61	Deleterious	0.19	Tolerated	1	probably damaging
C71	2	186661506	186661506	G	A	118	0.51	*FSIP2*	NM_173651	Missense	p.E3304K	-3	Deleterious	0.17	Tolerated	NA	NA
C71	2	32750579	32750579	C	T	47	0.30	*BIRC6*	NM_016252	Missense	p.P3935L	-4.15	Deleterious	0	Damaging	1	probably damaging
C71	22	32992709	32992709	T	G	47	0.51	*SYN3*	NM_003490	Missense	p.H242P	-0.83	Neutral	0.25	Tolerated	0.025	benign
C71	22	46785367	46785367	C	G	63	0.41	*CELSR1*	NM_014246	Missense	p.Q2125H	-1.6	Neutral	0.12	Tolerated	0.941	possibly damaging
C71	3	194081166	194081166	G	A	108	0.47	*LRRC15*	NM_001135057	Missense	p.R209W	-2.08	Neutral	0.18	Tolerated	1	probably damaging
C71	3	37360684	37360684	T	C	70	0.47	*GOLGA4*	NM_001172713	Missense	p.L537P	-4.07	Deleterious	0.28	Tolerated	1	probably damaging
C71	4	954436	954436	G	A	57	0.65	*DGKQ*	NM_001347	Missense	p.A934V	0.17	Neutral	0.73	Tolerated	0.001	benign
C71	6	38545467	38545467	T	C	90	0.51	*BTBD9*	NM_052893	Missense	p.M355V	-1.92	Neutral	0.67	Tolerated	0.843	possibly damaging
C71	6	38913338	38913338	C	T	94	0.51	*DNAH8*	NM_001206927	Missense	p.P4035S	-3.36	Deleterious	0.29	Tolerated	0.099	benign
C71	7	73646449	73646449	G	A	42	0.45	*RFC2*	NM_181471	Missense	p.P351L	-2.07	Neutral	0.33	Tolerated	0.333	benign
C71	7	82785661	82785661	G	A	102	0.58	*PCLO*	NM_033026	Missense	p.P99L	-3.8	Deleterious	0	Damaging	0.069	benign
C71	8	145106273	145106273	T	A	53	0.62	*OPLAH*	NM_017570	Missense	p.E1274V	NA	NA	0.24	Tolerated	0.981	probably damaging
C71	8	77766676	77766676	C	T	81	0.54	*ZFHX4*	NM_024721	Missense	p.L2507F	-2.28	Neutral	0.06	Tolerated	0.997	probably damaging
C71	9	133943614	133943614	C	T	28	0.61	*LAMC3*	NM_006059	Missense	p.R915W	-2.71	Deleterious	0.01	Damaging	0.994	probably damaging
C71	X	153595109	153595109	G	T	209	0.45	*FLNA*	NM_001110556	Missense	p.H326Q	-4.24	Deleterious	0.11	Tolerated	0.06	benign
C71	4	76797511	76797511	A	AG	30	0.80	*PPEF2*	NM_006239	Frame_Shift_Ins	p.S417fs	NA	NA	NA	NA	NA	NA
C71	6	34857302	34857302	G	GGGCGGC	21	0.29	*ANKS1A*	NM_015245	In_Frame_Ins	p.42_42G>GGG	-0.63	Neutral	NA	NA	NA	NA
C71	X	84362472	84362472	C	CA	179	0.69	*SATL1*	NM_001012980	Frame_Shift_Ins	p.L314fs	NA	NA	NA	NA	NA	NA
C72	4	177067156	177067156	G	T	147	0.24	*WDR17*	NM_170710	Missense	p.A538S	-2.15	Neutral	0	Damaging	1	probably damaging
C72	4	187541622	187541622	C	T	56	0.34	*FAT1*	NM_005245	Missense	p.D2040N	-4.91	Deleterious	0.03	Damaging	1	probably damaging
C72	2	50170907	50170907	G	T	36	0.47	*NRXN1*	NM_001135659	Missense	p.A1424D	-2.9	Deleterious	0.03	Damaging	1	probably damaging

C72	12	69103871	69103871	T	A	23	0.09	*NUP107*	NM_020401	nonsense	p.Y296_	NA	NA	NA	NA	NA	NA
C72	1	214171319	214171319	C	T	51	0.37	*PROX1*	NM_001270616	Missense	p.R481C	-2.18	Neutral	0.03	Damaging	1	probably damaging
C72	19	47944662	47944662	T	C	22	0.27	*SLC8A2*	NM_015063	Missense	p.E600G	-4.82	Deleterious	0	Damaging	0.999	probably damaging
C72	5	101593662	101593662	C	T	18	0.28	*SLCO4C1*	NM_180991	Missense	p.A420T	-3.25	Deleterious	0.03	Damaging	0.974	probably damaging
C72	2	241991826	241991826	G	A	34	0.44	*SNED1*	NM_001080437	Missense	p.R675Q	-0.1	Neutral	0.59	Tolerated	0.785	possibly damaging
C72	1	202573665	202573665	C	T	46	0.48	*SYT2*	NM_001136504	Missense	p.C88Y	-1.78	Neutral	0.74	Tolerated	0.995	probably damaging
C73	1	180853153	180853153	G	T	224	0.65	*XPR1*	NM_004736	Missense	p.R681L	-0.72	Neutral	0.11	Tolerated	0.004	benign
C73	17	39240795	39240795	A	T	23	0.17	*KRTAP4-7*	NM_033061	Missense	p.S113C	-3.33	Deleterious	0.05	Damaging	0.002	benign
C73	17	45663749	45663749	G	A	71	0.10	*NPEPPS*	NM_006310	Missense	p.G322D	-6.19	Deleterious	0	Damaging	0.998	probably damaging
C73	19	45404331	45404331	C	A	37	0.08	*TOMM40*	NM_001128917	Missense	p.H271Q	-7.04	Deleterious	0.03	Damaging	0.808	possibly damaging
C74	10	61868693	61868693	C	T	88	0.23	*ANK3*	NM_020987	Missense	p.R1023H	-4.83	Deleterious	0	Damaging	1	probably damaging
C74	20	42814983	42814983	C	A	45	0.09	*JPH2*	NM_020433	Missense	p.E121D	-2.57	Deleterious	0.11	Tolerated	1	probably damaging
C74	X	24024195	24024195	G	A	83	0.23	*KLHL15*	NM_030624	Missense	p.R206W	-2.32	Neutral	0	Damaging	0.999	probably damaging
C74	17	18023904	18023904	C	T	72	0.26	*MYO15A*	NM_016239	Missense	p.A597V	-0.84	Neutral	0.24	Tolerated	0.001	benign
C74	15	56435072	56435072	C	T	100	0.45	*RFX7*	NM_022841	Missense	p.R102Q	-1.91	Neutral	0.01	Damaging	1	probably damaging
C74	1	1007475	1007475	C	T	64	0.42	*RNF223*	NM_001205252	Missense	p.V158I	0	Neutral	0.45	Tolerated	NA	NA
C75	19	20727673	20727673	T	C	65	0.11	*ZNF737*	NM_001159293	Missense	p.I446V	-0.81	Neutral	0.07	Tolerated	0.325	benign
C75	19	13873847	13873847	C	A	16	0.25	*CCDC130*	NM_030818	Missense	p.L386I	-0.92	Neutral	0.01	Damaging	1	probably damaging
C75	16	75327887	75327887	A	G	123	0.13	*CFDP1*	NM_006324	Missense	p.I288T	-3.08	Deleterious	0.58	Tolerated	0.955	possibly damaging
C75	7	27170313	27170313	C	T	93	0.24	*HOXA4*	NM_002141	Missense	p.E14K	-2.58	Deleterious	0.01	Damaging	0.999	probably damaging
C75	X	86773055	86773055	G	C	44	0.14	*KLHL4*	NM_057162	Missense	p.K53N	-0.56	Neutral	0.08	Tolerated	0	benign
C75	18	21338406	21338406	C	A	22	0.18	*LAMA3*	NM_198129	Missense	p.R332S	-3.63	Deleterious	0.05	Damaging	0.937	possibly damaging
C75	15	66274815	66274815	C	A	22	0.18	*MEGF11*	NM_032445	Missense	p.D136Y	-2.63	Deleterious	0.01	Damaging	0.999	probably damaging
C75	X	110406143	110406143	A	G	49	0.35	*PAK3*	NM_001128168	Missense	p.S193G	-1.04	Neutral	NA	NA	0	benign
C75	22	33402569	33402569	G	A	52	0.25	*SYN3*	NM_003490	Missense	p.R27C	-4.49	Deleterious	0	Damaging	1	probably damaging
C75	12	109490560	109490560	C	A	16	0.19	*USP30*	NM_032663	Missense	p.A26D	-0.82	Neutral	0.26	Tolerated	0.079	benign
C76	2	242757730	242757730	G	A	48	0.35	*NEU4*	NM_001167599	Missense	p.E284K	-4	Deleterious	0.01	Damaging	1	probably damaging
C76	6	72892042	72892042	C	T	45	0.16	*RIMS1*	NM_014989	Missense	p.R290W	-3.83	Deleterious	0.01	Damaging	1	probably damaging
C76	14	21359943	21359943	C	T	113	0.22	*RNASE3*	NM_002935	Missense	p.T33M	-4.33	Deleterious	0	Damaging	1	probably damaging
C76	4	77662502	77662502	G	A	57	0.37	*SHROOM3*	NM_020859	Missense	p.R1059H	-2.86	Deleterious	0.01	Damaging	1	probably damaging
C76	11	44958419	44958419	G	A	20	0.25	*TP53I11*	NM_001258320	Missense	p.A90V	-0.85	Neutral	0.93	Tolerated	0.001	benign
C76	4	68506879	68506879	T	C	63	0.10	*UBA6*	NM_018227	Missense	p.H515R	-2.67	Deleterious	0.52	Tolerated	0	benign
C76	19	11833222	11833222	C	T	105	0.15	*ZNF823*	NM_001080493	Missense	p.R376Q	-1.38	Neutral	0.72	Tolerated	0.987	probably damaging

C77	13	25021323	25021323	A	G	19	0.21	*PARP4*	NM_006437	Missense	p.I1039T	-3.94	Deleterious	0.01	Damaging	0.856	possibly damaging
C77	7	140453987	140453987	T	A	102	0.52	*BRAF*	NM_004333	Missense	p.N581Y	-6.88	Deleterious	NA	NA	1	probably damaging
C77	4	74702556	74702556	C	T	70	0.23	*CXCL6*	NM_002993	Missense	p.P30L	-1.23	Neutral	0.5	Tolerated	0.007	benign
C77	6	50011374	50011374	C	A	117	0.25	*DEFB112*	NM_001037498	nonsense	p.E86_	NA	NA	0.11	Tolerated	NA	NA
C77	3	57616442	57616442	C	T	73	0.40	*DENND6A*	NM_152678	Missense	p.R506Q	-3.1	Deleterious	NA	NA	0.999	probably damaging
C77	16	26147117	26147117	G	A	93	0.46	*HS3ST4*	NM_006040	Missense	p.E307K	-2.67	Deleterious	0.21	Tolerated	0.998	probably damaging
C77	16	71103195	71103195	C	T	160	0.21	*HYDIN*	NM_001270974	Missense	p.R650H	-2.48	Neutral	0.13	Tolerated	1	probably damaging
C77	5	78610246	78610246	G	A	98	0.53	*JMY*	NM_152405	Missense	p.R744H	-0.16	Neutral	0.17	Tolerated	0.688	possibly damaging
C77	12	21799857	21799857	T	A	80	0.09	*LDHB*	NM_001174097	Missense	p.T75S	-2.09	Neutral	0.24	Tolerated	0.79	possibly damaging
C77	20	33570341	33570341	G	A	75	0.28	*MYH7B*	NM_020884	Missense	p.G245R	0.47	Neutral	0.58	Tolerated	0.91	possibly damaging
C77	17	29664869	29664869	G	A	106	0.27	*NF1*	NM_001042492	nonsense	p.W2225_	NA	NA	0.02	Damaging	NA	NA
C77	11	4566923	4566923	G	A	108	0.22	*OR52M1*	NM_001004137	Missense	p.R168Q	-1.86	Neutral	0.08	Tolerated	0.692	possibly damaging
C77	13	46287368	46287368	C	T	116	0.49	*SPERT*	NM_152719	Missense	p.R70C	-1.58	Neutral	0	Damaging	0.999	probably damaging
C77	19	41081429	41081429	C	A	38	0.58	*SPTBN4*	NM_020971	Missense	p.P2550H	-2.67	Deleterious	0.01	Damaging	0.952	possibly damaging
C77	12	58120415	58120415	TGCTGGGCGTGGTGGCCGC	T	31	0.29	*AGAP2*	NM_001122772	In_Frame_Del	p.AATTPS1161del	-1.69	Neutral	NA	NA	NA	NA
C77	17	54672052	54672052	C	CG	148	0.43	*NOG*	NM_005450	Frame_Shift_Ins	p.P156fs	NA	NA	NA	NA	NA	NA
C77	5	98228230	98228230	T	TCCCCCACAACCA	99	0.30	*CHD1*	NM_001270	Splice Site	p.726_727YK>YWLWGK	-11.97	Deleterious	NA	NA	NA	NA
C78	3	75715099	75715099	T	A	17	0.24	*FRG2C*	NM_001124759	Missense	p.D252E	-0.31	Neutral	1	Tolerated	0	benign
C78	17	42152054	42152054	C	T	64	0.17	*G6PC3*	NM_138387	Missense	p.P111L	-9.53	Deleterious	0	Damaging	1	probably damaging
C78	18	14542791	14542791	C	T	22	0.27	*POTEC*	NM_001137671	Missense	p.A119T	-0.93	Neutral	0.4	Tolerated	0.005	benign
C78	8	113668566	113668566	G	A	60	0.15	*CSMD3*	NM_198123	nonsense	p.Q941_	NA	NA	0.78	Tolerated	NA	NA
C78	7	55210046	55210046	G	C	112	0.11	*EGFR*	NM_005228	Missense	p.Q52H	-1.23	Neutral	0.07	Tolerated	0.998	probably damaging
C78	5	73931322	73931322	C	G	84	0.12	*ENC1*	NM_003633	Missense	p.R330T	-0.77	Neutral	0	Damaging	0.987	probably damaging
C78	17	42155773	42155773	C	A	40	0.13	*HDAC5*	NM_001015053	nonsense	p.E1115_	NA	NA	0	Damaging	NA	NA
C78	9	138903486	138903486	G	A	79	0.48	*NACC2*	NM_144653	Missense	p.P547L	-0.9	Neutral	0	Damaging	0.001	benign
C78	8	69002888	69002888	G	C	71	0.14	*PREX2*	NM_024870	Missense	p.E730Q	-1.14	Neutral	0.13	Tolerated	0.964	probably damaging
C78	7	148949838	148949838	G	A	48	0.25	*ZNF212*	NM_012256	Missense	p.E195K	-0.92	Neutral	0.31	Tolerated	0.455	possibly damaging
C79	22	30772543	30772543	C	T	22	0.14	*CCDC157*	NM_001017437	Missense	p.P690S	0.49	Neutral	0.17	Tolerated	0.007	benign
C79	20	44803387	44803387	C	A	96	0.09	*CDH22*	NM_021248	Missense	p.D749Y	-5.01	Deleterious	0	Damaging	0.995	probably damaging
C79	X	14862069	14862069	G	C	18	0.17	*FANCB*	NM_001018113	Missense	p.L734V	-2.32	Neutral	0.01	Damaging	0.998	probably damaging

C79	X	14863022	14863022	G	A	23	0.09	*FANCB*	NM_001018113	Missense	p.S628L	-2.28	Neutral	1	Tolerated	0.021	benign
C79	4	46930510	46930510	C	T	110	0.31	*GABRA4*	NM_000809	Missense	p.R466Q	0.25	Neutral	0.24	Tolerated	0	benign
C80	10	13702524	13702524	G	T	22	0.09	*FRMD4A*	NM_018027	Missense	p.P564T	-0.85	Neutral	0.15	Tolerated	0.756	possibly damaging
C80	1	115256528	115256528	T	A	86	0.30	*NRAS*	NM_002524	Missense	p.Q61H	-4.43	Deleterious	0.01	Damaging	0.294	benign
C81	10	70509310	70509310	C	T	130	0.24	*CCAR1*	NM_018237	Missense	p.S329L	-2.51	Deleterious	0.29	Tolerated	0.999	probably damaging
C81	2	111691094	111691094	G	A	41	0.22	*ACOXL*	NM_001142807	Missense	p.V312I	0.04	Neutral	0.38	Tolerated	0.001	benign
C81	2	175986221	175986221	C	G	69	0.14	*ATF2*	NM_001880	Missense	p.E50D	-1.27	Neutral	0.21	Tolerated	0.518	possibly damaging
C81	14	31355028	31355028	C	G	84	0.18	*COCH*	NM_001135058	Missense	p.F329L	-3.52	Deleterious	0.2	Tolerated	0.997	probably damaging
C81	1	46870746	46870746	C	G	119	0.16	*FAAH*	NM_001441	Missense	p.Q124E	-1.99	Neutral	0.26	Tolerated	0.035	benign
C81	X	150884610	150884610	A	G	18	0.22	*FATE1*	NM_033085	Missense	p.N7D	-2	Neutral	0.19	Tolerated	0.411	benign
C81	9	130155466	130155466	C	T	46	0.43	*GARNL3*	NM_032293	Missense	p.P992L	-0.93	Neutral	NA	NA	0.063	benign
C81	2	109109062	109109062	G	C	85	0.20	*GCC2*	NM_181453	Missense	p.M1421I	-0.66	Neutral	0.56	Tolerated	0.022	benign
C81	2	75900583	75900583	G	T	57	0.37	*GCFC2*	NM_003203	Missense	p.L626M	-1.47	Neutral	0.07	Tolerated	1	probably damaging
C81	4	62599088	62599088	T	A	221	0.10	*LPHN3*	NM_015236	Missense	p.N337K	-3.25	Deleterious	0	Damaging	0.999	probably damaging
C81	11	67800437	67800437	G	C	61	0.44	*NDUFS8*	NM_002496	Missense	p.D53H	-4.48	Deleterious	0	Damaging	1	probably damaging
C81	16	50759416	50759416	C	T	53	0.25	*NOD2*	NM_022162	Missense	p.L967F	-2.16	Neutral	0.01	Damaging	0.954	possibly damaging
C81	10	74890477	74890477	G	C	39	0.18	*NUDT13*	NM_015901	Missense	p.R292T	0.15	Neutral	0.01	Damaging	0.017	benign
C81	17	36895095	36895095	C	G	33	0.18	*PCGF2*	NM_007144	Missense	p.E112D	-2.21	Neutral	0.21	Tolerated	0.031	benign
C81	20	37121726	37121726	C	G	22	0.27	*RALGAPB*	NM_020336	Missense	p.Q114E	-0.54	Neutral	0.37	Tolerated	0.001	benign
C81	4	39291553	39291553	G	A	152	0.39	*RFC1*	NM_001204747	Missense	p.S1093L	-2.67	Deleterious	0.23	Tolerated	0.009	benign
C81	6	72962492	72962492	C	G	66	0.15	*RIMS1*	NM_014989	Missense	p.I909M	-1.95	Neutral	0.02	Damaging	0.992	probably damaging
C81	2	180008387	180008387	A	G	82	0.40	*SESTD1*	NM_178123	Missense	p.Y261H	-2.16	Neutral	NA	NA	0.995	probably damaging
C81	5	128351735	128351735	G	A	44	0.16	*SLC27A6*	NM_014031	Missense	p.R376K	2.38	Neutral	NA	NA	0	benign
C81	5	101572570	101572570	C	G	59	0.37	*SLCO4C1*	NM_180991	Missense	p.E723Q	-0.43	Neutral	0.31	Tolerated	0.849	possibly damaging
C81	1	118574321	118574321	C	G	73	0.12	*SPAG17*	NM_206996	Missense	p.E1201D	-0.81	Neutral	0.19	Tolerated	0.999	probably damaging
C81	7	89854811	89854811	G	C	159	0.21	*STEAP2*	NM_152999	Missense	p.D139H	-1.56	Neutral	0.08	Tolerated	0.95	possibly damaging
C81	19	48848467	48848467	C	A	48	0.08	*TMEM143*	NM_018273	Missense	p.D172Y	-4.15	Deleterious	0.01	Damaging	1	probably damaging
C81	9	73457992	73457992	C	G	100	0.11	*TRPM3*	NM_001007471	Missense	p.R243P	-3.2	Deleterious	0.07	Tolerated	1	probably damaging
C81	2	179594275	179594275	C	T	87	0.32	*TTN*	NM_001267550	Missense	p.R6203K	-1.19	Neutral	0	Damaging	0.022	benign
C81	19	34945425	34945425	G	T	65	0.22	*UBA2*	NM_005499	Missense	p.L403F	-0.68	Neutral	0.75	Tolerated	0.309	benign
C81	17	56058057	56058057	G	A	29	0.21	*VEZF1*	NM_007146	Missense	p.L295F	-0.05	Neutral	0.08	Tolerated	0.932	possibly damaging
C82	1	207758146	207758146	C	T	196	0.22	*CR1*	NM_000651	Missense	p.R1819C	-2.58	Deleterious	0.17	Tolerated	1	probably damaging
C82	9	14776191	14776191	T	G	151	0.25	*FREM1*	NM_144966	Missense	p.S1485R	-3.86	Deleterious	0	Damaging	1	probably damaging

C82	5	90070067	90070067	G	A	145	0.23	*GPR98*	NM_032119	Missense	p.R4117H	-0.78	Neutral	0.68	Tolerated	0.006	benign
C83	6	32712999	32712999	C	G	102	0.10	*HLA-DQA2*	NM_020056	Missense	p.T49S	-1.64	Neutral	0.12	Tolerated	0.016	benign
C83	17	19861720	19861720	G	A	204	0.41	*AKAP10*	NM_007202	Missense	p.H162Y	-1.18	Neutral	0.1	Tolerated	0.003	benign
C83	X	63411614	63411614	G	C	92	0.29	*AMER1*	NM_152424	Missense	p.S518C	-1.66	Neutral	0.1	Tolerated	1	probably damaging
C83	X	129148865	129148865	C	G	188	0.47	*BCORL1*	NM_021946	nonsense	p.S706_	NA	NA	0.28	Tolerated	NA	NA
C83	13	103492093	103492093	C	T	108	0.42	*BIVM-ERCC5*	NM_001204425	Missense	p.R464C	-2.3	Neutral	0	Damaging	1	probably damaging
C83	11	14991611	14991611	C	A	31	0.29	*CALCA*	NM_001741	nonsense	p.E33_	NA	NA	0	Damaging	NA	NA
C83	15	49054815	49054815	G	C	152	0.44	*CEP152*	NM_001194998	Missense	p.Q779E	0.27	Neutral	1	Tolerated	0.046	benign
C83	9	101784374	101784374	G	A	136	0.43	*COL15A1*	NM_001855	Missense	p.G568D	-3.34	Deleterious	0.03	Damaging	0.001	benign
C83	3	121591540	121591540	C	G	115	0.40	*EAF2*	NM_018456	nonsense	p.S214_	NA	NA	0.32	Tolerated	NA	NA
C83	4	72649719	72649719	A	T	144	0.40	*GC*	NM_001204307	Missense	p.V25E	-2.04	Neutral	0	Damaging	0.818	possibly damaging
C83	3	37323516	37323516	G	A	107	0.53	*GOLGA4*	NM_001172713	Missense	p.R99Q	-1.91	Neutral	0.04	Damaging	1	probably damaging
C83	15	33023118	33023118	C	G	54	0.54	*GREM1*	NM_013372	Missense	p.S76C	-4.15	Deleterious	0.01	Damaging	1	probably damaging
C83	8	145066727	145066727	G	A	261	0.43	*GRINA*	NM_000837	Missense	p.R306H	-2.25	Neutral	0.16	Tolerated	0.999	probably damaging
C83	6	43589830	43589830	G	C	61	0.39	*GTPBP2*	NM_019096	Missense	p.F514L	-3.79	Deleterious	0.16	Tolerated	0.981	probably damaging
C83	10	124896669	124896669	G	C	104	0.09	*HMX3*	NM_001105574	Missense	p.E166Q	-1.04	Neutral	0.2	Tolerated	0.9	possibly damaging
C83	8	103664601	103664601	C	G	74	0.46	*KLF10*	NM_005655	Missense	p.E21Q	-1.93	Neutral	0	Damaging	0.883	possibly damaging
C83	2	141242919	141242919	G	C	103	0.46	*LRP1B*	NM_018557	Missense	p.Q3140E	-1.21	Neutral	1	Tolerated	0.006	benign
C83	6	90384205	90384205	G	A	41	0.49	*MDN1*	NM_014611	Missense	p.R4289C	-4.84	Deleterious	0.05	Damaging	0.999	probably damaging
C83	8	89209517	89209517	C	T	34	0.44	*MMP16*	NM_005941	Missense	p.G51S	-4.67	Deleterious	0.04	Damaging	1	probably damaging
C83	14	105936422	105936422	C	G	93	0.48	*MTA1*	NM_004689	nonsense	p.S673_	NA	NA	0.01	Damaging	NA	NA
C83	16	86565986	86565986	G	T	61	0.41	*MTHFSD*	NM_001159378	Missense	p.H261Q	-0.32	Neutral	0.33	Tolerated	0.207	benign
C83	15	48435137	48435137	C	G	238	0.50	*MYEF2*	NM_016132	Missense	p.E591Q	-1.45	Neutral	0.24	Tolerated	0.999	probably damaging
C83	11	7079555	7079555	C	G	117	0.53	*NLRP14*	NM_176822	Missense	p.S836C	-2.61	Deleterious	0.01	Damaging	1	probably damaging
C83	5	68805051	68805051	C	G	148	0.52	*OCLN*	NM_002538	Missense	p.S45C	-4.2	Deleterious	0	Damaging	1	probably damaging
C83	11	58207423	58207423	C	A	68	0.54	*OR5B12*	NM_001004733	Missense	p.D68Y	-8.96	Deleterious	0	Damaging	1	probably damaging
C83	13	25021323	25021323	A	G	38	0.18	*PARP4*	NM_006437	Missense	p.I1039T	-3.94	Deleterious	0.01	Damaging	0.856	possibly damaging
C83	10	56128882	56128882	C	G	56	0.45	*PCDH15*	NM_001142763	Missense	p.E163Q	-2.5	Deleterious	0	Damaging	1	probably damaging
C83	13	53418719	53418719	C	G	26	0.38	*PCDH8*	NM_002590	Missense	p.K1063N	-0.32	Neutral	0.03	Damaging	0.302	benign
C83	6	41705498	41705498	G	T	34	0.74	*PGC*	NM_002630	Missense	p.F328L	-4.44	Deleterious	0.09	Tolerated	0.268	benign
C83	X	54012212	54012212	G	A	43	0.37	*PHF8*	NM_001184898	nonsense	p.Q682_	NA	NA	0.56	Tolerated	NA	NA
C83	3	64085170	64085170	C	T	86	0.43	*PRICKLE2*	NM_198859	Missense	p.A698T	-1.92	Neutral	0	Damaging	1	probably damaging

C83	1	57169915	57169915	G	C	137	0.51	*PRKAA2*	NM_006252	Missense	p.D354H	-0.6	Neutral	0.21	Tolerated	0.228	benign
C83	10	120354242	120354242	G	A	131	0.49	*PRLHR*	NM_004248	Missense	p.S172L	-2.87	Deleterious	0	Damaging	1	probably damaging
C83	X	48433668	48433668	G	A	155	0.50	*RBM3*	NM_006743	Missense	p.E34K	-2.03	Neutral	0.11	Tolerated	0.379	benign
C83	1	167663379	167663379	C	T	74	0.24	*RCSD1*	NM_052862	Missense	p.S105L	-3.39	Deleterious	0.09	Tolerated	1	probably damaging
C83	16	53721803	53721803	C	G	39	0.44	*RPGRIP1L*	NM_015272	Missense	p.E202Q	-1.67	Neutral	0.12	Tolerated	0.143	benign
C83	17	38787032	38787032	C	G	88	0.51	*SMARCE1*	NM_003079	Missense	p.E321Q	-0.38	Neutral	0.39	Tolerated	0.596	possibly damaging
C83	17	35937489	35937489	A	C	162	0.47	*SYNRG*	NM_007247	Missense	p.I271S	-0.33	Neutral	0.08	Tolerated	0.012	benign
C83	11	64896053	64896053	C	T	60	0.48	*SYVN1*	NM_172230	Missense	p.E577K	0	Neutral	0.86	Tolerated	0.215	benign
C83	22	22599370	22599370	A	G	28	0.82	*VPREB1*	NM_007128	Missense	p.Q20R	-3.61	Deleterious	0.03	Damaging	0.974	probably damaging
C83	4	1962801	1962801	G	A	94	0.46	*WHSC1*	NM_001042424	Missense	p.E1099K	-3.29	Deleterious	0.01	Damaging	1	probably damaging
C83	9	104170480	104170480	G	A	140	0.45	*ZNF189*	NM_003452	Missense	p.E144K	-0.29	Neutral	0.05	Damaging	0.167	benign
C83	19	44739542	44739542	G	C	145	0.46	*ZNF227*	NM_182490	Missense	p.G320A	-2.68	Deleterious	0.01	Damaging	0.99	probably damaging
C83	10	61083760	61083760	C	T	83	0.51	*FAM13C*	NM_198215	Missense	p.R144Q	-0.95	Neutral	0.08	Tolerated	0.055	benign
C83	X	2779579	2779579	T	TG	39	0.41	*GYG2*	NM_003918	Frame_Shift_Ins	p.V316fs	NA	NA	NA	NA	NA	NA
C84	4	1017706	1017706	C	T	75	0.12	*FGFRL1*	NM_001004356	Missense	p.R179W	-4.53	Deleterious	0.02	Damaging	0.999	probably damaging
C84	14	65239614	65239614	C	T	107	0.15	*SPTB*	NM_001024858	Missense	p.R1746Q	-3.56	Deleterious	0	Damaging	1	probably damaging
C84	4	79229294	79229294	G	A	66	0.38	*FRAS1*	NM_025074	Missense	p.V537M	-1.18	Neutral	0.09	Tolerated	0.879	possibly damaging
C84	9	131721149	131721149	C	A	18	0.11	*NUP188*	NM_015354	Missense	p.F147L	-2.76	Deleterious	0.03	Damaging	0.963	probably damaging
C84	3	77684173	77684173	C	T	98	0.37	*ROBO2*	NM_002942	nonsense	p.R1305_	NA	NA	1	Tolerated	NA	NA
C84	5	32385747	32385747	G	T	26	0.38	*ZFR*	NM_016107	Missense	p.S836R	-2.51	Deleterious	0.01	Damaging	0.846	possibly damaging
C85	4	967182	967182	C	A	22	0.09	*DGKQ*	NM_001347	Missense	p.G30V	-0.98	Neutral	0.05	Damaging	0.901	possibly damaging
C85	12	25398285	25398285	C	T	89	0.25	*KRAS*	NM_033360	Missense	p.G12S	-4.44	Deleterious	0.01	Damaging	0.682	possibly damaging
C85	4	141074043	141074043	C	A	21	0.10	*MAML3*	NM_018717	Missense	p.A147S	-0.13	Neutral	0.63	Tolerated	0.002	benign
C86	10	102822384	102822384	C	T	13	0.15	*KAZALD1*	NM_030929	Missense	p.A12V	-0.41	Neutral	0.18	Tolerated	0.001	benign
C86	11	60540905	60540905	C	T	20	0.10	*MS4A15*	NM_001098835	Missense	p.A149V	-1.32	Neutral	0.64	Tolerated	0.011	benign
C86	17	43907524	43907524	G	A	63	0.37	*CRHR1*	NM_001145146	Missense	p.A196T	-1.02	Neutral	0.01	Damaging	0.253	benign
C86	2	84771536	84771536	C	A	54	0.50	*DNAH6*	NM_001370	Missense	p.A281D	-4.04	Deleterious	NA	NA	0.848	possibly damaging
C86	11	126134396	126134396	C	T	22	0.09	*SRPR*	NM_003139	Missense	p.A522T	-3.95	Deleterious	0.05	Damaging	0.998	probably damaging
C86	1	55089061	55089061	C	A	39	0.59	*FAM151A*	NM_176782	Missense	p.C3F	-2.37	Neutral	0.03	Damaging	0.001	benign
C86	18	24497291	24497291	C	A	109	0.45	*CHST9*	NM_031422	Missense	p.E88D	-0.82	Neutral	0.28	Tolerated	0.156	benign
C86	4	52861843	52861843	G	T	120	0.41	*LRRC66*	NM_001024611	Missense	p.L449I	-0.57	Neutral	0.23	Tolerated	0.51	possibly damaging
C86	7	50680520	50680520	T	C	12	1.00	*GRB10*	NM_005311	Missense	p.N371S	-0.46	Neutral	0.95	Tolerated	0.002	benign
C86	3	77657037	77657037	TC	T	44	0.36	*ROBO2*	NM_002942	Frame_Shift_Del	p.P1078fs	NA	NA	NA	NA	NA	NA

C86	1	150460440	150460440	C	A	20	0.10	*TARS2*	NM_025150	Missense	p.P58H	-2.27	Neutral	0.1	Tolerated	0.001	benign
C86	7	150839561	150839561	C	CT	57	0.35	*AGAP3*	NM_031946	Frame_Shift_Ins	p.R374fs	NA	NA	NA	NA	NA	NA
C86	3	119190272	119190272	G	T	45	0.42	*POGLUT1*	NM_152305	Missense	p.R98L	-6.87	Deleterious	0.5	Tolerated	0.998	probably damaging
C86	5	82835698	82835698	T	A	85	0.44	*VCAN*	NM_004385	Missense	p.S2292R	-0.88	Neutral	0.07	Tolerated	0.047	benign
C86	4	62849222	62849222	C	A	66	0.41	*LPHN3*	NM_015236	nonsense	p.S978_	NA	NA	1	Tolerated	NA	NA
C86	7	122337939	122337939	G	T	82	0.41	*RNF133*	NM_139175	Missense	p.T345N	-0.06	Neutral	0.52	Tolerated	0.04	benign
C86	19	15989730	15989730	T	C	26	0.19	*CYP4F2*	NM_001082	Missense	p.T472A	-2.06	Neutral	0.47	Tolerated	0	benign
C86	12	15095465	15095465	C	A	30	0.27	*ARHGDIB*	NM_001175	Missense	p.W199C	-11.73	Deleterious	0	Damaging	1	probably damaging
C87	7	48316074	48316074	T	G	43	0.51	*ABCA13*	NM_152701	Missense	p.F2271V	-1.83	Neutral	NA	NA	0.018	benign
C87	11	125864193	125864193	C	A	28	0.14	*CDON*	NM_001243597	Missense	p.R879M	-3.27	Deleterious	0	Damaging	1	probably damaging
C87	1	79392673	79392673	C	A	18	0.28	*ELTD1*	NM_022159	Missense	p.E327D	-0.06	Neutral	NA	NA	0.27	benign
C87	9	131019537	131019537	C	A	24	0.08	*GOLGA2*	NM_004486	Missense	p.G940C	-1.77	Neutral	0.01	Damaging	0.999	probably damaging
C87	1	150676820	150676820	C	A	20	0.10	*HORMAD1*	NM_032132	Splice Site	p.D269sp		NA	NA	NA	NA	NA
C87	5	133914430	133914430	G	A	62	0.47	*PHF15*	NM_015288	Missense	p.R599H	-1.67	Neutral	0.24	Tolerated	1	probably damaging
C87	20	50408582	50408582	G	A	77	0.52	*SALL4*	NM_020436	Missense	p.P147L	-0.25	Neutral	0.34	Tolerated	0	benign
C87	20	35491480	35491480	C	A	34	0.09	*SOGA1*	NM_080627	Missense	p.G90W	-1.16	Neutral	0	Damaging	NA	NA
C87	2	171573367	171573367	C	T	30	0.30	*SP5*	NM_001003845	Missense	p.P217L	-1.58	Neutral	0.36	Tolerated	0	benign
C88	1	55603221	55603221	A	ACTG	111	0.36	*USP24*	NM_015306	In_Frame_Ins	p.1056_1056S>SS	-1.56	Neutral	NA	NA	NA	NA
C88	16	84476125	84476125	G	T	79	0.27	*ATP2C2*	NM_014861	Missense	p.V441F	-3.91	Deleterious	0.02	Damaging	0.984	probably damaging
C88	9	117038025	117038025	C	T	76	0.14	*COL27A1*	NM_032888	Missense	p.P1232S	-1.35	Neutral	0.67	Tolerated	0.872	possibly damaging
C88	11	102819876	102819876	C	T	77	0.35	*MMP13*	NM_002427	Missense	p.R310H	-4.52	Deleterious	0	Damaging	1	probably damaging
C89	6	26637796	26637796	C	A	20	0.20	*ZNF322*	NM_001242798	Missense	p.G329V	-0.1	Neutral	0.05	Damaging	0.149	benign
C89	9	100092968	100092968	A	AGAGGAG	44	0.32	*CCDC180*	NM_020893	In_Frame_Ins	p.915_915E>EEE	0.28	Neutral	NA	NA	NA	NA
C89	9	2039776	2039776	A	ACAG	51	0.43	*SMARCA2*	NM_003070	In_Frame_Ins	p.223_223Q>QQ	-0.09	Neutral	NA	NA	NA	NA
C89	9	124855337	124855337	C	T	26	0.12	*TTLL11*	NM_001139442	Missense	p.E121K	-0.91	Neutral	NA	NA	0.514	possibly damaging
C89	9	112811015	112811015	TCCCCCGGAGTCTCCTGGA	T	22	0.41	*AKAP2*	NM_001198656	In_Frame_Del	p.PPESPG19del	-0.22	Neutral	NA	NA	NA	NA
C90	11	89447517	89447517	T	C	58	0.47	*TRIM77*	NM_001146162	Missense	p.M222T	NA	NA	NA	NA	NA	NA
C90	13	28608281	28608281	A	T	63	0.65	*FLT3*	NM_004119	Missense	p.V592D	-6.04	Deleterious	0	Damaging	0.881	possibly damaging
C90	4	2172860	2172860	G	A	85	0.40	*POLN*	NM_181808	Missense	p.R475W	-3.3	Deleterious	0	Damaging	0.996	probably damaging

C90	6	18218070	18218070	A	T	38	0.32	*KDM1B*	NM_153042	Missense	p.D548V	-7.73	Deleterious	0	Damaging	1	probably damaging
C90	7	148454139	148454139	G	A	30	0.43	*CUL1*	NM_003592	Missense	p.R127Q	1.21	Neutral	0.48	Tolerated	0.009	benign
C90	8	38297866	38297866	C	T	27	0.33	*FGFR1*	NM_001174064	Missense	p.G9S	0.49	Neutral	0.91	Tolerated	0.004	benign
C90	9	139741265	139741265	C	T	26	0.50	*C9orf172*	NM_001080482	Missense	p.A800V	0.45	Neutral	0.76	Tolerated	0.951	possibly damaging
C90	1	152975658	152975658	AGAGCCAGGCTGTACCAAGGTCCCT	A	15	0.40	*SPRR3*	NM_005416	In_Frame_Del	p.EPGCTKVP95del	-9.33	Deleterious	NA	NA	NA	NA
C90	12	49942953	49942953	G	GGCA	33	0.39	*KCNH3*	NM_012284	In_Frame_Ins	p.489_490insS	-9.53	Deleterious	NA	NA	NA	NA
C90	2	27324253	27324253	GGCCTCTGCCTGGCCCCCAGCTTCCCCTCTGGGCCCGGGGGCATCTCCTTCA	G	34	0.24	*CGREF1*	NM_001166239	In_Frame_Del	p.EGDAPGPRGEAGGQAEA248del	1.04	Neutral	NA	NA	NA	NA
C91	19	14037500	14037500	G	A	140	0.35	*CC2D1A*	NM_017721	Missense	p.D679N	-4.98	Deleterious	0.14	Tolerated	1	probably damaging
C91	14	92537353	92537353	C	CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	40	0.20	*ATXN3*	NM_004993	In_Frame_Ins	p.306_306G>EQQQQQQQQQQR	-1.38	Neutral	NA	NA	NA	NA
C91	3	100170625	100170625	C	CCAGGAATTCCGATGCCG	93	0.59	*LNP1*	NM_001085451	Frame_Shift_Ins	p.R79fs	NA	NA	NA	NA	NA	NA
C92	1	45241721	45241721	A	G	71	0.45	*RPS8*	NM_001012	Missense	p.N7S	0.16	Neutral	1	Tolerated	0	benign
C92	13	103346742	103346742	T	A	43	0.44	*METTL21C*	NM_001010977	Missense	p.D36V	-1.27	Neutral	0.33	Tolerated	0.745	possibly damaging
C92	16	66436747	66436747	C	T	87	0.37	*CDH5*	NM_001795	Missense	p.A677V	-0.5	Neutral	0.14	Tolerated	0.726	possibly damaging
C93	1	22915717	22915717	G	A	58	0.36	*EPHA8*	NM_001006943	Missense	p.V445I	-0.01	Neutral	NA	NA	0.164	benign
C93	1	26139220	26139220	G	A	28	0.54	*SEPN1*	NM_020451	Missense	p.A442T	-1.7	Neutral	0.03	Damaging	0.647	possibly damaging
C93	11	17408533	17408533	C	T	45	0.42	*KCNJ11*	NM_000525	Missense	p.R369H	-1.26	Neutral	0.02	Damaging	1	probably damaging
C93	15	59510118	59510118	T	A	41	0.46	*MYO1E*	NM_004998	Missense	p.H360L	-5.01	Deleterious	0	Damaging	0.019	benign
C93	2	103068619	103068619	G	A	55	0.45	*IL18RAP*	NM_003853	Missense	p.S593N	-0.95	Neutral	0.36	Tolerated	0.006	benign
C93	5	35072820	35072820	C	A	69	0.43	*PRLR*	NM_000949	Missense	p.A134S	0.8	Neutral	0.18	Tolerated	0	benign

C93	5	78379100	78379100	G	A	40	0.25	*BHMT2*	NM_017614	nonsense	p.W228_	NA	NA	0.19	Tolerated	NA	NA
C93	6	51619602	51619602	C	T	62	0.34	*PKHD1*	NM_138694	Missense	p.R2926Q	-0.91	Neutral	0.11	Tolerated	0.988	probably damaging
C93	7	6080788	6080788	G	A	55	0.42	*EIF2AK1*	NM_014413	Missense	p.T285I	-2.04	Neutral	0.18	Tolerated	0.067	benign
C93	3	100170607	100170607	A	AAGGCATTCTCATGAGGACCAGGAATTCCGATGCCG	115	0.25	*LNP1*	NM_001085451	Frame_Shift_Ins	p.R68fs	NA	NA	NA	NA	NA	NA
C94	18	29848289	29848289	G	C	53	0.30	*GAREM*	NM_001242409	Missense	p.P726A	-2.15	Neutral	0.02	Damaging	1	probably damaging
C94	19	875264	875264	C	T	14	0.43	*MED16*	NM_005481	Missense	p.C584Y	-5.25	Deleterious	0.46	Tolerated	0.997	probably damaging
C94	22	30772543	30772543	C	T	16	0.13	*CCDC157*	NM_001017437	Missense	p.P690S	0.49	Neutral	0.17	Tolerated	0.007	benign
C94	14	92537353	92537353	C	CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	24	0.38	*ATXN3*	NM_004993	In_Frame_Ins	p.306_306G>EQQQQQQQQQQQQQR	-1.77	Neutral	NA	NA	NA	NA
C94	3	100170600	100170600	A	ATCCTAGAAGGCATTCTCATGAGGACCAGGAATTCCGATGCCG	44	0.91	*LNP1*	NM_001085451	In_Frame_Ins	p.66_67insRRHSHEDQEFRCRP	-4.77	Deleterious	NA	NA	NA	NA
C95	1	181058201	181058201	C	T	11	0.27	*IER5*	NM_016545	Missense	p.L55F	-2.68	Deleterious	0.02	Damaging	0.375	benign
C95	19	34955037	34955037	G	T	22	0.14	*UBA2*	NM_005499	Splice Site	p.S535sp	NA	NA	NA	NA	NA	NA
C95	2	27324371	27324371	C	T	16	0.25	*CGREF1*	NM_001166239	Missense	p.G243E	-0.08	Neutral	0.34	Tolerated	0.36	benign
C95	X	154194714	154194714	C	T	39	0.69	*F8*	NM_000132	Missense	p.A420T	-0.13	Neutral	0.87	Tolerated	0.002	benign
C96	10	128193128	128193128	G	T	143	0.56	*C10orf90*	NM_001004298	Missense	p.T214N	-0.44	Neutral	0.13	Tolerated	0.804	possibly damaging
C96	11	88029392	88029392	C	T	73	0.29	*CTSC*	NM_001814	Missense	p.M266I	-2.95	Deleterious	NA	NA	0.969	probably damaging
C96	12	112888198	112888198	G	A	91	0.25	*PTPN11*	NM_002834	Missense	p.A72T	-3.45	Deleterious	0.05	Damaging	0.996	probably damaging

C96	12	40704362	40704362	C	T	94	0.30	*LRRK2*	NM_198578	nonsense	p.R1483_	NA	NA	1	Tolerated	NA	NA
C96	17	44055759	44055759	G	T	181	0.22	*MAPT*	NM_001123066	Missense	p.G109V	-2.94	Deleterious	0.03	Damaging	1	probably damaging
C96	2	238280593	238280593	G	A	54	0.31	*COL6A3*	NM_004369	Missense	p.A1356V	-3.79	Deleterious	0.27	Tolerated	1	probably damaging
C96	20	25470611	25470611	C	T	104	0.36	*NINL*	NM_025176	Missense	p.R499H	-4.38	Deleterious	0.04	Damaging	1	probably damaging
C96	20	35060602	35060602	C	T	92	0.30	*DLGAP4*	NM_014902	Missense	p.A161V	-1.36	Neutral	0.04	Damaging	0.001	benign
C96	22	31285535	31285535	G	A	91	0.37	*OSBP2*	NM_030758	Missense	p.R512H	-3.28	Deleterious	0.1	Tolerated	0.444	benign
C96	4	1962801	1962801	G	A	85	0.22	*WHSC1*	NM_001042424	Missense	p.E1099K	-3.29	Deleterious	0.01	Damaging	1	probably damaging
C96	7	4259800	4259800	C	T	49	0.29	*SDK1*	NM_152744	Missense	p.R1867W	-5	Deleterious	0	Damaging	1	probably damaging
C97	1	11136933	11136933	C	A	48	0.10	*EXOSC10*	NM_001001998	Missense	p.C651F	-1.76	Neutral	0.22	Tolerated	0	benign
C97	1	148009349	148009349	A	G	16	0.19	*NBPF14*	NM_015383	Missense	p.M653T	-1.04	Neutral	0.28	Tolerated	0.629	possibly damaging
C97	10	104182677	104182677	C	A	46	0.39	*FBXL15*	NM_024326	Missense	p.P277Q	-1.74	Neutral	0.52	Tolerated	0.999	probably damaging
C97	10	78708910	78708910	G	A	126	0.31	*KCNMA1*	NM_001161352	Missense	p.S900F	-2.67	Deleterious	0.63	Tolerated	0.019	benign
C97	11	65792857	65792857	G	A	96	0.35	*CATSPER1*	NM_053054	Missense	p.R332W	0.45	Neutral	0.23	Tolerated	0	benign
C97	15	48054484	48054484	G	A	67	0.39	*SEMA6D*	NM_153618	Missense	p.R209H	-4.64	Deleterious	0	Damaging	1	probably damaging
C97	15	65959810	65959810	C	A	96	0.11	*DENND4A*	NM_001144823	nonsense	p.E1739_	NA	NA	0.44	Tolerated	NA	NA
C97	18	18619484	18619484	G	A	116	0.17	*ROCK1*	NM_005406	nonsense	p.R334_	NA	NA	0.65	Tolerated	NA	NA
C97	2	160982966	160982966	C	A	51	0.10	*ITGB6*	NM_000888	Missense	p.V603F	-1.71	Neutral	0.03	Damaging	0.526	possibly damaging
C97	2	166221681	166221681	G	A	76	0.33	*SCN2A*	NM_001040142	Missense	p.G1143D	-5.69	Deleterious	0	Damaging	1	probably damaging
C97	4	186253770	186253770	G	C	32	0.19	*SNX25*	NM_031953	Missense	p.E427Q	-1.36	Neutral	0.37	Tolerated	0.972	probably damaging
C97	5	168310330	168310330	T	C	62	0.35	*SLIT3*	NM_001271946	Missense	p.E142G	-4.04	Deleterious	0.08	Tolerated	0.986	probably damaging
C97	X	11781041	11781041	C	A	18	0.28	*MSL3*	NM_078629	Missense	p.A225D	-1.31	Neutral	0.51	Tolerated	1	probably damaging
C97	11	1651585	1651585	CCTGCTGCCAGTCCAGCTGCTGTAAGCCTTA	C	29	0.34	*KRTAP5-5*	NM_001001480	In_Frame_Del	p.CCQSSCCKPY183del	-34.05	Deleterious	NA	NA	NA	NA
C97	17	18918510	18918510	A	ACGGTACGGGGGTGGGGGC	23	0.35	*SLC5A10*	NM_152351	In_Frame_Ins	p.414_414R>RYGGGGR	-13.77	Deleterious	NA	NA	NA	NA
C98	1	115258744	115258744	C	T	42	0.10	*NRAS*	NM_002524	Missense	p.G13D	-5.48	Deleterious	0.03	Damaging	0.434	benign
C98	1	34677971	34677971	G	A	74	0.32	*C1orf94*	NM_001134734	Missense	p.G562E	-5.89	Deleterious	0.01	Damaging	1	probably damaging
C98	1	6155658	6155658	C	G	89	0.38	*KCNAB2*	NM_001199862	Missense	p.P308A	-6.73	Deleterious	0	Damaging	0.898	possibly damaging
C98	1	955673	955673	G	A	13	0.15	*AGRN*	NM_198576	Missense	p.E41K	-1.13	Neutral	0.03	Damaging	0.975	probably damaging
C98	11	88300578	88300578	G	A	147	0.46	*GRM5*	NM_001143831	Missense	p.A758V	-3.71	Deleterious	NA	NA	1	probably damaging

C98	12	25398284	25398284	C	G	56	0.21	*KRAS*	NM_033360	Missense	p.G12A	-4.62	Deleterious	0	Damaging	0.956	possibly damaging
C98	14	33147613	33147613	C	T	137	0.28	*AKAP6*	NM_004274	nonsense	p.R943_	NA	NA	1	Tolerated	NA	NA
C98	14	65271736	65271736	C	T	102	0.28	*SPTB*	NM_001024858	Missense	p.R74H	-4.4	Deleterious	0.11	Tolerated	0.445	benign
C98	14	93730193	93730193	C	T	115	0.41	*BTBD7*	NM_001002860	Missense	p.D437N	-0.97	Neutral	0.14	Tolerated	0.985	probably damaging
C98	17	1962014	1962014	A	C	93	0.18	*HIC1*	NM_001098202	Missense	p.K696T	-2.49	Neutral	0.57	Tolerated	0.384	benign
C98	19	38385469	38385469	G	A	109	0.47	*WDR87*	NM_031951	nonsense	p.R253_	NA	NA	1	Tolerated	NA	NA
C98	19	39371484	39371484	C	A	33	0.09	*SIRT2*	NM_012237	Missense	p.Q267H	-3.73	Deleterious	0.12	Tolerated	0.062	benign
C98	20	43851853	43851853	C	G	101	0.39	*SEMG2*	NM_003008	Missense	p.S527C	-2.08	Neutral	0.08	Tolerated	0.989	probably damaging
C98	3	125690929	125690929	C	T	34	0.50	*ROPN1B*	NM_001012337	Missense	p.P11L	-8.83	Deleterious	0	Damaging	1	probably damaging
C98	3	195512671	195512671	G	T	17	0.53	*MUC4*	NM_018406	Missense	p.S1927Y	-0.4	Neutral	NA	NA	0.486	possibly damaging
C98	7	122768933	122768933	C	T	85	0.39	*SLC13A1*	NM_022444	Missense	p.G367R	-7.19	Deleterious	0.02	Damaging	1	probably damaging
C98	15	40648365	40648365	ACCATGGTCCAGGGCCCTGCGGGCCACCCCCTGG	A	57	0.47	*PHGR1*	NM_001145643	In_Frame_Del	p.HGPGPCGPPPG38del	-48.33	Deleterious	NA	NA	NA	NA
C98	16	27238138	27238138	A	AAGG	34	0.26	*NSMCE1*	NM_145080	In_Frame_Ins	p.167_168insP	-8.86	Deleterious	NA	NA	NA	NA
C99	1	85506823	85506823	G	A	75	0.27	*MCOLN3*	NM_018298	Missense	p.A89V	-1.35	Neutral	0.23	Tolerated	0.44	benign
C99	11	85396974	85396974	C	T	50	0.16	*CCDC89*	NM_152723	Missense	p.R67H	-3.05	Deleterious	NA	NA	0.038	benign
C99	12	27127133	27127133	A	G	109	0.19	*TM7SF3*	NM_016551	Missense	p.M493T	-1.83	Neutral	0.15	Tolerated	0.955	possibly damaging
C99	13	33344667	33344667	C	T	85	0.27	*PDS5B*	NM_015032	nonsense	p.Q1345_	NA	NA	0.93	Tolerated	NA	NA
C99	16	90095620	90095620	A	G	55	0.13	*C16orf3*	NM_001214	Missense	p.V44A	-2.67	Deleterious	NA	NA	NA	NA
C99	19	45731431	45731431	C	T	56	0.20	*EXOC3L2*	NM_138568	Missense	p.V62M	-2.28	Neutral	0.11	Tolerated	1	probably damaging
C99	3	52829640	52829640	G	A	38	0.13	*ITIH3*	NM_002217	Splice Site	p.G38sp	NA	NA	NA	NA	NA	NA
C99	8	73848252	73848252	C	T	125	0.24	*KCNB2*	NM_004770	Missense	p.T221M	-0.36	Neutral	0.13	Tolerated	0.002	benign
C99	X	136112552	136112552	C	T	97	0.22	*GPR101*	NM_054021	Missense	p.E428K	-0.44	Neutral	0.76	Tolerated	0.048	benign
C100	17	1563731	1563731	A	G	26	0.12	*PRPF8*	NM_006445	Missense	p.C1594R	-10.07	Deleterious	0.01	Damaging	0.966	probably damaging
C100	1	115258744	115258744	C	T	51	0.47	*NRAS*	NM_002524	Missense	p.G13D	-5.48	Deleterious	0.03	Damaging	0.434	benign
C100	11	133802018	133802018	G	A	58	0.43	*IGSF9B*	NM_001277285	Missense	p.P353L	-9.06	Deleterious	0.15	Tolerated	1	probably damaging
C100	13	26620656	26620656	C	A	22	0.18	*SHISA2*	NM_001007538	Missense	p.V295L	-0.15	Neutral	0.02	Damaging	0.984	probably damaging
C100	19	3816809	3816809	C	T	57	0.25	*ZFR2*	NM_015174	Missense	p.V656I	-0.92	Neutral	0.02	Damaging	1	probably damaging
C100	2	61719472	61719472	C	T	83	0.37	*XPO1*	NM_003400	Missense	p.E571K	-3.82	Deleterious	0.02	Damaging	1	probably damaging
C100	22	21346030	21346030	C	T	31	0.52	*LZTR1*	NM_006767	Missense	p.A302V	-2.92	Deleterious	0.5	Tolerated	0.901	possibly damaging
C100	3	130281956	130281956	C	T	175	0.42	*COL6A6*	NM_001102608	Missense	p.R37C	-1.39	Neutral	0.13	Tolerated	0.662	possibly damaging

C100	7	1478631	1478631	G	A	27	0.19	*MICALL2*	NM_182924	Missense	p.A656V	-1.07	Neutral	0.53	Tolerated	0.791	possibly damaging
C101	11	88241905	88241905	G	T	128	0.34	*GRM5*	NM_001143831	Missense	p.P1165Q	-4.1	Deleterious	NA	NA	1	probably damaging
C101	13	28608329	28608329	A	T	46	0.35	*FLT3*	NM_004119	Missense	p.L576Q	-2.28	Neutral	0	Damaging	0.867	possibly damaging
C101	15	40648365	40648365	ACCATGGTCCAGGGCCCTGCGGGCCACCCCCTGG	A	55	0.31	*PHGR1*	NM_001145643	In_Frame_Del	p.HGPGPCGPPPG38del	-48.33	Deleterious	NA	NA	NA	NA
C102	1	115258747	115258747	C	T	48	0.42	*NRAS*	NM_002524	Missense	p.G12D	-5.35	Deleterious	0	Damaging	0.372	benign
C102	10	61028336	61028336	A	T	45	0.11	*FAM13C*	NM_198215	Missense	p.F307I	-5.73	Deleterious	0	Damaging	1	probably damaging
C102	13	28609758	28609758	C	A	171	0.12	*FLT3*	NM_004119	Missense	p.V491L	-0.39	Neutral	0.87	Tolerated	0.792	possibly damaging
C102	2	29450475	29450475	C	A	34	0.12	*ALK*	NM_004304	Missense	p.S960I	-2.84	Deleterious	NA	NA	0.708	possibly damaging
C102	20	62705890	62705890	G	A	32	0.34	*RGS19*	NM_005873	nonsense	p.Q53_	NA	NA	0.42	Tolerated	NA	NA
C102	4	110897177	110897177	C	A	31	0.10	*EGF*	NM_001963	Missense	p.F613L	-4.83	Deleterious	0	Damaging	0.759	possibly damaging
C102	7	1539133	1539133	G	A	40	0.28	*INTS1*	NM_001080453	Missense	p.R274C	-2.66	Deleterious	0.05	Damaging	0.998	probably damaging
C102	9	119976922	119976922	C	T	76	0.11	*ASTN2*	NM_014010	Missense	p.A244T	-1.98	Neutral	NA	NA	1	probably damaging
C102	1	27741446	27741446	TTTC	T	60	0.27	*WASF2*	NM_006990	In_Frame_Del	p.K182del	-4.53	Deleterious	NA	NA	NA	NA
CA69	X	132091229	132091229	G	A	136	0.42	*HS6ST2*	NM_001077188	Missense	p.A185V	-0.7	Neutral	0.2	Tolerated	0.999	probably damaging
CA69	3	134884864	134884864	C	T	146	0.40	*EPHB1*	NM_004441	Missense	p.A547V	-0.49	Neutral	1	Tolerated	0.011	benign
CA69	X	44703391	44703391	G	A	43	0.47	*DUSP21*	NM_022076	Missense	p.A5T	-0.1	Neutral	0.54	Tolerated	0.024	benign
CA69	8	9588469	9588469	G	A	89	0.40	*TNKS*	NM_003747	Missense	p.A691T	-3.39	Deleterious	0.04	Damaging	0.964	probably damaging
CA69	10	5789068	5789068	C	G	140	0.46	*FAM208B*	NM_017782	Missense	p.C1228W	-1.78	Neutral	0.05	Damaging	0.657	possibly damaging
CA69	3	195508406	195508406	C	T	16	0.19	*MUC4*	NM_018406	Missense	p.D3349N	-1.07	Neutral	NA	NA	0.842	possibly damaging
CA69	21	30927384	30927384	C	T	125	0.51	*GRIK1*	NM_000830	Missense	p.D866N	-1.32	Neutral	0.15	Tolerated	0.001	benign
CA69	22	26849318	26849318	A	G	44	0.34	*HPS4*	NM_022081	Missense	p.F670L	-4.53	Deleterious	0	Damaging	1	probably damaging
CA69	6	26225762	26225762	T	G	131	0.46	*HIST1H3E*	NM_003532	Missense	p.L127R	-4.05	Deleterious	0	Damaging	NA	NA
CA69	13	28608329	28608329	A	T	51	0.57	*FLT3*	NM_004119	Missense	p.L576Q	-2.28	Neutral	0	Damaging	0.867	possibly damaging
CA69	12	49448427	49448427	G	GGGCCC	84	0.14	*MLL2*	NM_003482	Frame_Shift_Ins	p.P95fs	NA	NA	NA	NA	NA	NA
CA69	9	117108158	117108158	G	C	27	0.37	*AKNA*	NM_030767	Missense	p.R1216G	-3.66	Deleterious	0.06	Tolerated	0.949	possibly damaging
CA69	4	156835562	156835562	C	T	74	0.32	*TDO2*	NM_005651	Missense	p.R272C	-2.16	Neutral	0.09	Tolerated	0.998	probably damaging
CA92	19	12874555	12874555	G	A	64	0.39	*HOOK2*	NM_013312	Missense	p.A622V	-0.7	Neutral	0.11	Tolerated	0	benign
CA92	4	78650155	78650155	C	T	80	0.09	*CNOT6L*	NM_144571	Missense	p.D369N	-4.66	Deleterious	0	Damaging	1	probably damaging
CA92	8	119209973	119209973	T	C	97	0.41	*SAMD12*	NM_001101676	Splice Site	p.D634sp	NA	NA	NA	NA	NA	NA
CA92	1	214557043	214557043	C	T	104	0.18	*PTPN14*	NM_005401	Missense	p.E719K	-0.61	Neutral	0.69	Tolerated	0	benign

CA92	20	57288994	57288994	C	A	32	0.09	*NPEPL1*	NM_024663	Missense	p.H383N	-6.13	Deleterious	0.12	Tolerated	1	probably damaging
CA92	1	1737942	1737942	A	T	50	0.14	*GNB1*	NM_002074	Missense	p.I80N	-5.87	Deleterious	0.04	Damaging	1	probably damaging
CA92	12	20858892	20858892	T	C	67	0.25	*SLCO1C1*	NM_001145946	Missense	p.L94S	-5.2	Deleterious	0.05	Damaging	1	probably damaging
CA92	X	53231109	53231109	G	A	40	0.30	*KDM5C*	NM_004187	Missense	p.P598L	-8.75	Deleterious	0	Damaging	0.996	probably damaging
CA92	9	14313482	14313482	T	G	124	0.21	*NFIB*	NM_001190737	Missense	p.Q10P	-3.64	Deleterious	0.06	Tolerated	0.968	probably damaging
CA92	1	44395863	44395863	C	T	21	0.52	*ST3GAL3*	NM_174965	Missense	p.R168C	0	Neutral	0	Damaging	0	benign
CA92	20	45170427	45170427	C	T	25	0.20	*OCSTAMP*	NM_080721	Missense	p.R396H	-0.88	Neutral	0.26	Tolerated	0.141	benign
CA92	17	7748879	7748879	C	T	45	0.16	*KDM6B*	NM_001080424	Missense	p.R3W	-1.39	Neutral	0	Damaging	1	probably damaging
CA92	X	15584479	15584479	G	A	51	0.29	*ACE2*	NM_021804	nonsense	p.R671_	NA	NA	0.92	Tolerated	NA	NA
CA92	14	103430965	103430965	C	T	78	0.31	*CDC42BPB*	NM_006035	Missense	p.R867H	-4.4	Deleterious	0.03	Damaging	1	probably damaging
CA92	6	132031946	132031946	T	C	21	0.19	*CTAGE9*	NM_001145659	Missense	p.Y71C	-7.62	Deleterious	0	Damaging	1	probably damaging
CA97	1	228481245	228481245	G	A	30	0.33	*OBSCN*	NM_001271223	Missense	p.V4116M	-0.54	Neutral	0.1	Tolerated	0.981	probably damaging
CA97	11	105775972	105775972	G	A	24	0.29	*GRIA4*	NM_000829	Missense	p.R368H	-1.97	Neutral	0.11	Tolerated	1	probably damaging
CA97	16	89652131	89652131	G	A	17	0.47	*CPNE7*	NM_014427	Missense	p.D315N	-4.86	Deleterious	0	Damaging	1	probably damaging
CA97	3	156570749	156570749	G	A	24	0.25	*LEKR1*	NM_001004316	Missense	p.D81N	-0.69	Neutral	NA	NA	0.005	benign
CA97	4	17488829	17488829	G	T	17	0.12	*QDPR*	NM_000320	Missense	p.N220K	-0.8	Neutral	0.44	Tolerated	0.005	benign
CA97	4	48384816	48384816	G	A	19	0.32	*SLAIN2*	NM_020846	Missense	p.R365Q	-0.12	Neutral	0.48	Tolerated	1	probably damaging
CA97	9	133730371	133730371	A	G	23	0.57	*ABL1*	NM_007313	Missense	p.N165S	-4.66	Deleterious	0	Damaging	0.763	possibly damaging

Table S3. Recurrent gene mutations identified by whole exome sequencing and whole genome sequencing

#Genes labeled in black have been found mutated in B-ALL, in blue found mutated in other cancers or leukemia, in red not found mutated in cancer or leukemia

*Numbers in the parentheses indicate the recurrent times of 2 or more than 2.

Mutation count	**Gene#**	**Chromosome**	**Transcription ID**	**Strand**	**Amino Acid Change***	**Patients with mutations***
27	*NRAS*	1	NM_002524	-	p.G12A(2),p.G12C(2),p.G12D(6),p.G12S(4),p.G12V,p.G13D(6),p.G13V(2), p.Q61H(2),p.Q61K,p.Q61L	A24,A27,A42,A50,A55,A68,A71,A72,A85,AC04,AC14(2),B02,B15, C03,C100,C102,C13,C21,C22,C45,C51,C56,C59,C63,C80,C98
15	*KRAS*	12	NM_033360	-	p.A146T,p.A59E,p.G12A,p.G12D(2),p.G12R,p.G12S(3),p.G12V(2), p.G13D(2),p.I36M,p.K117N	A04,A41,A52,A88,A90,AC06,AC10,C02,C17,C55,C57,C58,C65,C85,C98
15	*PAX5*	9	NM_016734	-	p.E201fs,p.E205_,p.L58F(3),p.N29K,p.P80R(3),p.R140Q,p.V26fs, p.V26G(3),p.Y7C	A01,A11,A27(2),A32,A51,A52,A53,A78,AC14,B12,B13,B15,B16,C66

15	*SETD2*	3	NM_014159	-	p.A2357fs,p.F1454fs,p.F1664Y,p.K2123fs,p.K2511fs,p.K2511Q, p.KKDSV1711fs,p.N719H,p.Q1734_,p.S1531del,p.S1572_,p.S1838fs, p.T2101fs,p.Y1472_,p.Y2523fs	A01,A17,A24(3),A39,A53,A64(2),A65(2),AC10(2),B06,C69
14	*MLL2*	12	NM_003482	-	p.5494_5495insL,p.E3214fs,p.G2715fs,p.G3465fs,p.N5447fs,p.P480fs,p.P95fs,p.Q3961fs,p.Q836fs,p.R1528fs,p.R2789fs,p.R2801_,p.T1496fs,p.T3027fs	A06,A07,A08,A09,A19,A32,A33,A37,A54,A88,C38,C39,C59,CA69
14	*MUC4*	3	NM_018406	-	p.A1929V,p.A3481V,p.D3349N,p.G3509D(2),p.G4421D,p.H1906P,p.L2899V,p.L2902F,p.L5383P,p.P1680S(2),p.S1653I,p.S1927Y	A46,A51,A53(3),A62,A65,A68,C48,C61,C64,C69,C98,CA69
13	*FLT3*	13	NM_004119	-	p.D593_F594delinsEC,p.D835A,p.D835Y,p.D839G,p.I836L,p.L576P,p.L576Q(2),p.V491L(2),p.V592D,p.Y591D,p.Y842C	A14,A17,A25,A36,A43,A52,C101,C102,C61(2),C71,C90,CA69
10	*TTN*	2	NM_001267550	-	p.E13766G,p.G8481R,p.K13332fs,p.R17618C,p.R20823H,p.R24742H,p.R4915C,p.R6203K,p.S5306del,p.T3743M	A08,A11,A21,A27,A50,A83,B16,C17,C41,C81
9	*PTPN11*	12	NM_002834	+	p.A72T,p.A72V,p.D61G,p.E69K,p.E76K,p.G503R,p.S502A,p.T507K,p.T73I	A20,A27,A52,A93,C02,C25,C44,C47,C96
6	*EZH2*	7	NM_004456	-	p.G155R,p.G738fs,p.I131L,p.K568E,p.N130del,p.S695A	A08(2),A20,A83,C47(2)
6	*RUNX1*	21	NM_001754	-	p.I337fs,p.L71fs,p.R166_(2),p.R201_,p.S114fs	A05,A12,A34,A60,A62,AC11
6	*ZFHX4*	8	NM_024721	+	p.D1536N,p.G3013R,p.L2507F,p.M2936K,p.Q2331E,p.R1398C	A29,A76,C41,C58,C59,C71
5	*ABL1*	9	NM_007313	+	p.E30D,p.E374G,p.E472G,p.N165S,p.T296N	A52,AC11,C36(2),CA97
5	*BRAF*	7	NM_004333	-	p.D594E,p.K601E(2),p.N581Y,p.V600E	A73,A93,C15,C56,C77
5	*CHD4*	12	NM_001273	-	p.E1094K,p.I989T,p.N26D,p.R1162P,p.R1899W	A66,A89,C40,C69,C71
5	*CREBBP*	16	NM_004380	-	p.C1421F,p.I1084fs,p.I1453fs,p.Q1209fs,p.Y1539D	A06,A32,A37,C08,C41
5	*NF1*	17	NM_001042492	+	p.G2334D,p.L626fs,p.T676fs,p.V1019fs,p.W2225_	A01,A07,A08,A81,C77
5	*USH2A*	1	NM_206933	-	p.D1788G,p.F1110V,p.P3590L,p.R3134Q,p.V49F	A08,A32,C13,C69,C71
4	*ANO5*	11	NM_213599	+	p.C601F,p.L610F,p.R160H,p.R484H	A08,A50,B15,C71
4	*ASXL1*	20	NM_015338	+	p.G642fs,p.L765fs,p.Q512_,p.W1037_	A05,A20,A23(2)
4	*CDKN2A*	9	NM_001195132	-	p.D153fs,p.E10fs,p.M1K,p.R58_	A54,A71,C40,C58
4	*CGREF1*	2	NM_001166239	-	p.EGDAPGPRGEAGGQAEA248del,p.G243E(3)	A67,A96,C90,C95
4	*DCHS1*	11	NM_003737	-	p.33_34insL,p.A2095E,p.P500R,p.T1733M	A32,A82,B06,C70
4	*DST*	6	NM_001144769	-	p.A5251V,p.A90V,p.L2591H,p.R4599H	A27,A32,C43,C69
4	*EPHA6*	3	NM_001080448	+	p.D546E,p.G108A,p.L582P,p.P822L	A30,A38,A85,A96
4	*ETV6*	12	NM_001987	+	p.C338Y,p.H317fs,p.R359_,p.R55fs	A05,A96,C23,C43
4	*FAT3*	11	NM_001008781	+	p.A3911V,p.Q4377_,p.R1011W,p.R1658C	A16,A76,C70,C71
4	*GNB1*	1	NM_002074	-	p.G116R,p.I80N(2),p.I80S	A29,A73,C40,CA92
4	*GRM5*	11	NM_001143831	-	p.A758V,p.F137L,p.G964D,p.P1165Q	A08,A77,C101,C98
4	*IKZF1*	7	NM_006060	+	p.E16fs,p.M459fs,p.R143Q,p.S17fs	A01,A56,A70,A87

4	*MXRA5*	X	NM_015419	-	p.E893K,p.P1841H,p.T2430M,p.T596A	A32,A43,B18,C70
4	*PCLO*	7	NM_033026	-	p.P3595H,p.P99L,p.R5085Q,p.S78_	A32,A78,A87,C71
4	*SVIL*	10	NM_021738	-	p.A1465V,p.E1835V,p.L1374R,p.S620L	A57,AC10,C61,C71
4	*THBS2*	6	NM_003247	-	p.A232V,p.E664A,p.E664K,p.P906T	C18,C30,C31,C70
4	*UBA2*	19	NM_005499	+	p.C413_,p.L403F,p.R122Q,p.S535fs	B04,C34,C81,C95
4	*ZC3H18*	16	NM_144604	+	p.K823_,p.R436_,p.R701_,p.T677fs	A85,A93,C23,C31
4	*ZEB2*	2	NM_014795	-	p.H1038R(4)	A50,A51,AC09,C37
3	*ADCY8*	8	NM_001115	-	p.L89M,p.R611W,p.R930_	A30,A95,AC16
3	*ANK3*	10	NM_020987	-	p.R1023H,p.S919L,p.T109K	A35,A95,C74
3	*ASTN2*	9	NM_014010	-	p.A244T,p.R1279_,p.R285W	A24,B17,C102
3	*ATXN3*	14	NM_004993	-	p.306_306G>EQQQQQQQQQQQQQR,p.306_306G>EQQQQQQQQQQQQR,p.T136A	A95,C91,C94
3	*BCORL1*	X	NM_021946	+	p.Q565_,p.S706_,p.V1049fs	A12,A77,C83
3	*BCR*	22	NM_004327	+	p.A170V,p.A249G,p.A677T	A32,A64,C56
3	*C3*	19	NM_000064	-	p.A1239D,p.P292T,p.R1548Q	A33,A52,B01
3	*CACNA1E*	1	NM_001205293	+	p.H923Y,p.R2077H,p.R2157W	A05,A32,C71
3	*CELSR1*	22	NM_014246	-	p.A1233V,p.A2137V,p.Q2125H	A62,A83,C71
3	*DNAH17*	17	NM_173628	-	p.D2053G,p.I204M,p.R2922C	A94,C70(2)
3	*DNAH3*	16	NM_017539	-	p.A1612D,p.M4058V,p.N2001K	A61,C34,C71
3	*ERBB4*	2	NM_005235	-	p.E141_,p.N504K,p.R1045K	A11,A29,C08
3	*EVI5L*	19	NM_001159944	+	p.A350T,p.A538fs,p.E586K	C23,C35,C36
3	*FAM151A*	1	NM_176782	-	p.C3F,p.G503E,p.R168Q	C34,C70,C86
3	*FAM208B*	10	NM_017782	+	p.C1228W,p.F2198V,p.M638I	A01,C69,CA69
3	*FLNC*	7	NM_001458	+	p.A1318T,p.G2039R,p.R420W	A77,C55,C69
3	*FREM1*	9	NM_144966	-	p.E1344G,p.S1485R,p.T867I	C64,C70,C82
3	*FRG2C*	3	NM_001124759	+	p.D252E,p.S81R,p.T30S	A55,C44,C78
3	*GREB1*	2	NM_014668	+	p.I861T,p.S1214L,p.V991I	A32,A95,C69
3	*HMCN1*	1	NM_031935	+	p.E3443D,p.R3795Q,p.S928L	A08,A27,B15
3	*JAK2*	9	NM_004972	+	p.R683G,p.R683S,p.T875N	A46(2),A66
3	*KDM5C*	X	NM_004187	-	p.I648fs,p.L526R,p.P598L	A14(2),CA92
3	*LAMA1*	18	NM_005559	-	p.G2448C,p.R162H,p.R2084W	A21,C23,C44
3	*LNP1*	3	NM_001085451	+	p.66_67insRRHSHEDQEFRCRP,p.R68fs,p.R79fs	C91,C93,C94
3	*LPHN2*	1	NM_012302	+	p.G787E,p.T67M,p.V320A	A07,A43,C01

3	*LRRD1*	7	NM_001161528	-	p.N474K,p.P60L,p.R856C	C59,C70(2)
3	*MET*	7	NM_001127500	+	p.E254Q,p.G1183fs,p.L211W	A17,C20,C70
3	*MPDZ*	9	NM_003829	-	p.A1787V,p.G1200R,p.T1942M	A46,A90,C23
3	*MUC16*	19	NM_024690	-	p.G1254R,p.V4948L,p.V769I	A23,A66,C36
3	*MYC*	8	NM_002467	+	p.P74Q,p.T73I,p.T73N	A32,A33,A54
3	*MYO3B*	2	NM_138995	+	p.G143S,p.H316L,p.Q362_	C19,C20,C69
3	*NBPF10*	1	NM_001039703	+	p.R54Q(2),p.Y124N	A71,C46,C65
3	*OBSCN*	1	NM_001271223	+	p.G7622S,p.R3109C,p.V4116M	A68,C69,CA97
3	*PIM1*	6	NM_001243186	+	p.E226K,p.G119D,p.N109D	A32(2),C70
3	*PKHD1*	6	NM_138694	-	p.G2224_,p.R2926Q,p.W2383L	A01,A08,C93
3	*PRICKLE2*	3	NM_198859	-	p.A698T,p.F645S,p.Q613P	A25,A56,C83
3	*RIMS1*	6	NM_014989	+	p.I909M,p.R290W,p.R903Q	A52,C76,C81
3	*RIT1*	1	NM_001256821	-	p.F99L,p.M107I,p.M107V	A36,A85,C41
3	*RP1L1*	8	NM_178857	-	p.1341_1342insKTEEGLQEEGVQLEGT,p.E1340G,p.M1670L	A81,A95,AC14
3	*RYR2*	1	NM_001035	+	p.G7S,p.R296_,p.V203M	A36,A40,C70
3	*SPEF2*	5	NM_024867	+	p.D634fs,p.E965_,p.K195fs	A79,B06,C02
3	*SPRR3*	1	NM_005416	+	p.EPGCTKVP95del(3)	A90,C44,C90
3	*SYNE1*	6	NM_182961	-	p.F7614fs,p.N4560H,p.R1537_	A40,A94,C35
3	*TMTC2*	12	NM_152588	+	p.I33del,p.L110H,p.T390M	A08,A59,A87
3	*TP53*	17	NM_001126112	-	p.282_283insG,p.R175H,p.R342_	A08,A39,AC16
3	*UPP2*	2	NM_001135098	+	p.G122S,p.K258E,p.R369W	A85,A90,C70
3	*XBP1*	22	NM_001079539	-	p.G160fs,p.L169fs(2)	A15,A17,A26
3	*XDH*	2	NM_000379	-	p.A1259S,p.A432V,p.W994_	A72,B15,C56
3	*ZNF804B*	7	NM_181646	+	p.P458S,p.P534L,p.T1149K	A43,C39,C65
3	*DSPP*	4	NM_014208	+	p.NSSDSS1029del,p.SDSSNS1025del,p.SNE1231del	A58,A59,C65
2	*ABCA13*	7	NM_152701	+	p.F2271V,p.K513T	A75,C87
2	*ADAM29*	4	NM_001130704	+	p.N645H,p.R696_	A40,A84
2	*ADARB1*	21	NM_015833	+	p.D171N,p.E733K	AC09,C25
2	*AFAP1*	4	NM_001134647	-	p.A670V,p.T204M	A09,A54
2	*AGAP3*	7	NM_031946	+	p.E391G,p.R374fs	A53,C86
2	*AHNAK2*	14	NM_138420	-	p.A2623T,p.R5502Q	B17,C71
2	*ANKRD36*	2	NM_001164315	+	p.I368T,p.L217del	A88,C69
2	*ANKS1A*	6	NM_015245	+	p.42_42G>GGG,p.S661L	A78,C71

2	*APC2*	19	NM_005883	+	p.A556T,p.S929N	A20,B17
2	*ARHGEF28*	5	NM_001080479	+	p.L1731F,p.R634Q	A75,C70
2	*ARHGEF37*	5	NM_001001669	+	p.P560L,p.R547C	A01,A06
2	*ASTN1*	1	NM_004319	-	p.A353V,p.R880Q	A50,C71
2	*ASXL2*	2	NM_018263	-	p.Q635_,p.T1365I	A27,C61
2	*ATP2C2*	16	NM_014861	+	p.E224K,p.V441F	A09,C88
2	*ATRX*	X	NM_000489	-	p.Q1105_,p.Y1667fs	A83,A90
2	*BAHCC1*	17	NM_001080519	+	p.P626L,p.T2545M	A33,A68
2	*BAI3*	6	NM_001704	+	p.G323R,p.L396I	A32,A65
2	*BIRC6*	2	NM_016252	+	p.L3396R,p.P3935L	A42,C71
2	*BMPR2*	2	NM_001204	+	p.S350I,p.T740A	A33,A75
2	*BTBD9*	6	NM_052893	-	p.G321D,p.M355V	A32,C71
2	*BTG1*	12	NM_001731	-	p.103_103T>RP,p.E101fs	AC04,C43
2	*C16orf3*	16	NM_001214	-	p.51_52insAACPVGCP,p.V44A	A55,C99
2	*C1orf127*	1	NM_001170754	-	p.AATTPS1161del,p.N301S	A18,C70
2	*CACNA1H*	16	NM_021098	+	p.R1217H,p.R2257Q	A59,C47
2	*CACNA1I*	22	NM_021096	+	p.R1456H,p.R452C	A47,C41
2	*CCDC157*	22	NM_001017437	+	p.P690S(2)	C79,C94
2	*CCDC180*	9	NM_020893	+	p.915_915E>EEE(2)	C70,C89
2	*CD3EAP*	19	NM_012099	+	p.A376V,p.M339I	C17,C28
2	*CDC42BPB*	14	NM_006035	-	p.R1203K,p.R867H	B15,CA92
2	*CDC42BPG*	11	NM_017525	-	p.R977C,p.V1432L	A41,C70
2	*CDH13*	16	NM_001220488	+	p.A643V,p.T393M	A56,A64
2	*CDH9*	5	NM_016279	-	p.E65V,p.P694H	C13,C64
2	*CDK16*	X	NM_001170460	+	p.G135C,p.T459S	A70,C27
2	*CDK5RAP2*	9	NM_018249	-	p.G1770V,p.I81M	C20,C31
2	*CEP170B*	14	NM_001112726	+	p.P1120R,p.P214S	A79,C71
2	*CEP57L1*	6	NM_001083535	+	p.K274fs,p.K417R	A56,C69
2	*CHD2*	15	NM_001271	+	p.K1389fs,p.M1388fs	A40,A89
2	*CHST9*	18	NM_031422	-	p.E88D,p.R42K	C70,C86
2	*CILP2*	19	NM_153221	+	p.R1111_,p.R976Q	A93,C33
2	*CLDN22*	4	NM_001111319	-	p.T144M(2)	A37,C21
2	*CNTN4*	3	NM_175607	+	p.R564Q,p.V530M	A50,A90

2	*CNTNAP5*	2	NM_130773	+	p.E331K,p.V793I	A95,A96
2	*COL4A2*	13	NM_001846	+	p.G1332R,p.P1479L	A20,A90
2	*COL5A2*	2	NM_000393	-	p.G612R,p.R1136_	C01,C23
2	*COL6A3*	2	NM_004369	-	p.A1356V,p.P2748S	A78,C96
2	*CRISPLD1*	8	NM_031461	+	p.A393S,p.R222Q	A44,C20
2	*CSMD3*	8	NM_198123	-	p.Q941_,p.S2192I	A13,C78
2	*CSNK1A1L*	13	NM_145203	-	p.Q291E,p.T299M	A39,C66
2	*CTAGE9*	6	NM_001145659	-	p.L398V,p.Y71C	C70,CA92
2	*CTNNA3*	10	NM_001127384	-	p.H881Q,p.L170F	A82,C31
2	*CXCR7*	2	NM_020311	+	p.R162H,p.S242F	A36,C23
2	*DDC*	7	NM_000790	-	p.A106V,p.G96R	A23,A72
2	*DDX3X*	X	NM_001356	+	p.D354N,p.I401fs	A24,C70
2	*DENND2A*	7	NM_015689	-	p.P697S,p.R688_	A11,A90
2	*DENND5A*	11	NM_015213	-	p.C383W,p.T26A	A77,C71
2	*DGKQ*	4	NM_001347	-	p.A934V,p.G30V	C71,C85
2	*DLG5*	10	NM_004747	-	p.A1007T,p.R1501H	A20,C71
2	*DMD*	X	NM_004006	-	p.C1267Y,p.M975L	A07,A40
2	*DNAH5*	5	NM_001369	-	p.R4199H,p.V3399I	A03,A15
2	*DNAH6*	2	NM_001370	+	p.A281D,p.G795S	AC14,C86
2	*DNAH8*	6	NM_001206927	+	p.P4035S,p.S2819L	A28,C71
2	*DNAH9*	17	NM_001372	+	p.L836F,p.N1568T	A01,C70
2	*DNHD1*	11	NM_144666	+	p.P271H,p.R1165C	A46,C70
2	*DOCK5*	8	NM_024940	+	p.E1387K,p.R1121W	A19,B15
2	*DPYD*	1	NM_000110	-	p.58_59insGI,p.T779N	A65,C70
2	*DRD2*	11	NM_000795	-	p.V154I,p.V255I	B04,C70
2	*DRD5*	4	NM_000798	+	p.K290del,p.P330L	A57,C69
2	*EDNRA*	4	NM_001957	+	p.R419Q,p.T39I	A74,C59
2	*EPHA10*	1	NM_001099439	-	p.R205H,p.V965M	A53,AC16
2	*EPHA7*	6	NM_004440	-	p.A848T,p.R371W	A77,C17
2	*EPHA8*	1	NM_020526	+	p.G220E,p.V445I	A61,C93
2	*ETV1*	7	NM_004956	-	p.G407E,p.R391H	C30,C58
2	*FAM109B*	22	NM_001002034	+	p.P216R,p.R239Q	AC10,C69
2	*FAM13C*	10	NM_198215	-	p.F307I,p.R144Q	C102,C83

2	*FAM186A*	12	NM_001145475	-	p.H292fs,p.K985N	A44,C70
2	*FARS2*	6	NM_006567	+	p.E219fs,p.Q44R	A16,C69
2	*FBRSL1*	12	NM_001142641	+	p.P686L,p.T63A	A78,C71
2	*FGFR3*	4	NM_001163213	+	p.R252W,p.R399H	C36,C57
2	*FLNA*	X	NM_001110556	-	p.H326Q,p.V2007M	A84,C71
2	*FOXB2*	9	NM_001013735	+	p.R51C,p.S242F	A18,A50
2	*FRAS1*	4	NM_025074	+	p.R3768C,p.V537M	A96,C84
2	*FSIP2*	2	NM_173651	+	p.E3304K,p.T1981M	A38,C71
2	*GAB3*	X	NM_001081573	-	p.S218_,p.S574R	A54,C02
2	*GOLGA4*	3	NM_001172713	+	p.L537P,p.R99Q	C71,C83
2	*GPC5*	13	NM_004466	+	p.A283V,p.M215N	A40,A90
2	*GPR137C*	14	NM_001099652	+	p.L331fs,p.S242C	A21,C25
2	*GPR162*	12	NM_019858	+	p.R496W,p.R559H	A14,A53
2	*GPR45*	2	NM_007227	+	p.V210I,p.V59M	A36,C65
2	*GREB1L*	18	NM_001142966	+	p.G792A,p.M95fs	A33,C71
2	*GRM7*	3	NM_181874	+	p.G64R,p.R191H	A32,A84
2	*GRXCR1*	4	NM_001080476	+	p.A21V,p.R14W	A66,C02
2	*GSE1*	16	NM_014615	+	p.342_342E>ERERERE,p.A24T	C20,C69
2	*HCN2*	19	NM_001194	+	p.M425I,p.R659S	A25,A93
2	*HDAC5*	17	NM_001015053	-	p.E1115_,p.V449M	A65,C78
2	*HEATR4*	14	NM_001220484	-	p.D525E,p.P964L	A46,C70
2	*HIP1R*	12	NM_003959	+	p.H59R,p.R835Q	A03,C69
2	*HIST1H2AG*	6	NM_021064	+	p.Q105*,p.V108fs	C24,C30
2	*HLF*	17	NM_002126	+	p.I284V,p.R268H	C58,C71
2	*HS3ST4*	16	NM_006040	+	p.A294T,p.E307K	C32,C77
2	*HYDIN*	16	NM_001270974	-	p.R650H,p.V1718M	C71,C77
2	*IDH1*	2	NM_005896	-	p.R132C(2)	A44,A88
2	*IGFN1*	1	NM_001164586	+	p.R2891W,p.T3222I	A40,A95
2	*IGSF9B*	11	NM_001277285	-	p.A1389D,p.P353L	A32,C100
2	*IL1RAPL1*	X	NM_014271	+	p.D399N,p.R297Q	A06,B03
2	*IL1RL1*	2	NM_016232	+	p.I131M,p.T195M	A90,C70
2	*INSRR*	1	NM_014215	-	p.A164T,p.V27A	A01,C34
2	*JAK3*	19	NM_000215	-	p.M511I,p.V836M	A05,A47

2	*JMJD1C*	10	NM_032776	-	p.I862V,p.R968W	A25,C71
2	*JMY*	5	NM_152405	+	p.G466D,p.R744H	A06,C77
2	*JPH2*	20	NM_020433	-	p.A194T,p.E121D	C33,C74
2	*KCNH3*	12	NM_012284	+	p.489_490insS,p.T304I	A76,C90
2	*KCNMA1*	10	NM_001161352	-	p.L902F,p.S900F	A05,C97
2	*KCNT2*	1	NM_198503	-	p.G246R,p.R190H	A32,C65
2	*KCNV1*	8	NM_014379	-	p.D148N,p.S180I	A32,C23
2	*KDM4E*	11	NM_001161630	+	p.G134D,p.Y300F	A51,C71
2	*KIAA1045*	9	NM_015297	+	p.R225H,p.R297Q	A63,C70
2	*KIAA1109*	4	NM_015312	+	p.N3353D,p.P192R	A09,C70
2	*KIAA1958*	9	NM_133465	+	p.T394P,p.Y138F	C34,C70
2	*KIF26A*	14	NM_015656	+	p.P1095A,p.R1222fs	A51,C71
2	*KLHDC4*	16	NM_017566	-	p.K256Q,p.L69H	A53,C71
2	*KNDC1*	10	NM_152643	+	p.G116R,p.R1248H	C23,C67
2	*LAMA5*	20	NM_005560	-	p.E2291K,p.G3152S	A96,C70
2	*LAMB2*	3	NM_002292	-	p.A910S,p.T1221M	A18,C55
2	*LAMC3*	9	NM_006059	+	p.A854T,p.R915W	A62,C71
2	*LEKR1*	3	NM_001004316	+	p.A411T,p.D81N	C70,CA97
2	*LPHN3*	4	NM_015236	+	p.N337K,p.S978_	C81,C86
2	*LRP1B*	2	NM_018557	-	p.3147_3148insP,p.Q3140E	C35,C83
2	*LRP2*	2	NM_004525	-	p.G2351S,p.T1498M	A34,C71
2	*LRRC15*	3	NM_001135057	-	p.R209W,p.R382H	A84,C71
2	*LY75-CD302*	2	NM_001198759	-	p.D783G,p.R772S	A04,A40
2	*MACF1*	1	NM_012090	+	p.R1373H,p.V3109I	B01,C71
2	*MAPT*	17	NM_001123066	+	p.G109V,p.V371I	A02,C96
2	*MCAM*	11	NM_006500	-	p.T71M,p.V346I	A68,C31
2	*MDN1*	6	NM_014611	-	p.R4289C,p.R5499Q	C25,C83
2	*MEGF9*	9	NM_001080497	-	p.AA30del,p.E435G	AC16,C69
2	*MGA*	15	NM_001080541	+	p.D536fs,p.R903fs	A17,B04
2	*MKI67*	10	NM_002417	-	p.S2941G,p.T1176M	C41,C70
2	*MMP13*	11	NM_002427	-	p.P447H,p.R310H	A09,C88
2	*MS4A2*	11	NM_000139	+	p.R217H,p.Y125C	AC11,C69
2	*MTOR*	1	NM_004958	-	p.A1459P,p.W1449R	A88,B15

2	*MUC17*	7	NM_001040105	+	p.E4270K,p.T4115M	A53,B01
2	*MYH7B*	20	NM_020884	+	p.A250fs,p.G245R	A81,C77
2	*MYO15A*	17	NM_016239	+	p.A597V,p.L2727P	C69,C74
2	*MYO7B*	2	NM_001080527	+	p.R1758Q,p.R367Q	A01,C70
2	*NAALADL2*	3	NM_207015	+	p.A683T,p.E618_	A08,A32
2	*NCBP2*	3	NM_007362	-	p.R112H(2)	B13,C61
2	*NCKAP5*	2	NM_207363	-	p.G569D,p.L872I	A32,A66
2	*NEK6*	9	NM_001145001	+	p.G226A,p.V194M	A46,C69
2	*NFIB*	9	NM_001190737	-	p.Q10P,p.S264P	A32,CA92
2	*NRXN1*	2	NM_001135659	-	p.A1424D,p.A165T	A77,C72
2	*NUP107*	12	NM_020401	+	p.S108R,p.Y296_	A46,C72
2	*NUP210L*	1	NM_207308	-	p.A976T,p.H1115Y	B15,C69
2	*OPLAH*	8	NM_017570	-	p.E1274V,p.P1248T	A90,C71
2	*OR5B12*	11	NM_001004733	-	p.D68Y,p.R232C	C70,C83
2	*P4HA2*	5	NM_001017973	-	p.R448S,p.S207L	A25,B15
2	*PABPC3*	13	NM_030979	+	p.K156_,p.T379S	A14,A33
2	*PARP4*	13	NM_006437	-	p.I1039T(2)	C77,C83
2	*PCDH15*	10	NM_001142763	-	p.D542V,p.E163Q	A90,C83
2	*PCDH8*	13	NM_002590	-	p.G89R,p.K1063N	C70,C83
2	*PCDHA8*	5	NM_018911	+	p.R65W,p.V374M	A84,C05
2	*PCK1*	20	NM_002591	+	p.R518W,p.T178M	A08,A86
2	*PCSK2*	20	NM_002594	+	p.R539H,p.R80K	A49,C12
2	*PDE1A*	2	NM_001003683	-	p.M358fs,p.T481I	A06,C19
2	*PHF6*	X	NM_001015877	+	p.C305R,p.R274_	A05,A49
2	*PHGR1*	15	NM_001145643	+	p.HGPGPCGPPPG38del(2)	C101,C98
2	*PKHD1L1*	8	NM_177531	+	p.T1251K,p.T2639K	C22,C27
2	*PLCH1*	3	NM_001130960	-	p.P747T,p.T1658M	B17,C58
2	*PLXNA4*	7	NM_020911	-	p.N1421fs,p.R483W	A30,A87
2	*PPEF2*	4	NM_006239	-	p.S113T,p.S417fs	A03,C71
2	*PPFIA2*	12	NM_003625	-	p.L1247I,p.R556W	C20,C28
2	*PPP1R26*	9	NM_014811	+	p.F724Y,p.V129M	A08,A27
2	*PROKR1*	2	NM_138964	+	p.A298V,p.K62N	A05,C33
2	*PSG1*	19	NM_006905	-	p.A105S,p.R137C	A54,C27

2	*PSTPIP1*	15	NM_003978	+	p.F407L,p.Q83_	A22,C71
2	*PTPN13*	4	NM_080685	+	p.R2207_,p.T590I	A40,C68
2	*PTPRN2*	7	NM_002847	-	p.A468T,p.G852S	C05,C69
2	*RAB27A*	15	NM_183234	-	p.D136V,p.P126L	C32,C69
2	*RB1*	13	NM_000321	+	p.E398Q,p.S807_	C08,C30
2	*RFC2*	7	NM_181471	-	p.166_167insRGC,p.P351L	A31,C71
2	*RGS19*	20	NM_005873	-	p.Q53_,p.Y146fs	C102,C54
2	*RNASE3*	14	NM_002935	+	p.D139E,p.T33M	A46,C76
2	*ROBO2*	3	NM_002942	+	p.P1078fs,p.R1305_	C84,C86
2	*RPL5*	1	NM_000969	+	p.Y86fs,p.YAAA95del	A41,A52
2	*RRN3*	16	NM_018427	-	p.S199L(2)	B12,C70
2	*SACS*	13	NM_014363	-	p.P4278S,p.R2214H	A05,A54
2	*SATL1*	X	NM_001012980	-	p.G37R,p.L314fs	C68,C71
2	*SEC16B*	1	NM_033127	-	p.A993V,p.V183fs	C59,C69
2	*SEC24D*	4	NM_014822	-	p.G706S,p.T957A	C15,C69
2	*SHROOM3*	4	NM_020859	+	p.L1797I,p.R1059H	C49,C76
2	*SLAIN2*	4	NM_020846	+	p.M142V,p.R365Q	C69,CA97
2	*SLC1A6*	19	NM_005071	-	p.T200M,p.T62M	A81,C35
2	*SLC22A6*	11	NM_004790	-	p.R454W,p.T22I	A14,C25
2	*SLC29A4*	7	NM_153247	+	p.R324C,p.S499P	A46,C15
2	*SLCO4C1*	5	NM_180991	-	p.A420T,p.E723Q	C72,C81
2	*SLITRK3*	3	NM_014926	-	p.P251L,p.R777C	A27,B04
2	*SMC4*	3	NM_001002800	+	p.E653Q,p.S781L	A21,C69
2	*SOGA3*	6	NM_001012279	-	p.R422H,p.R866W	A37,B15
2	*SOX5*	12	NM_006940	-	p.A436V,p.E703_	A34,A50
2	*SOX6*	11	NM_001145819	-	p.P444A,p.T410M	A30,C70
2	*SPAG17*	1	NM_206996	-	p.E1201D,p.Q1681R	C69,C81
2	*SPTB*	14	NM_001024858	-	p.R1746Q,p.R74H	C84,C98
2	*SPTBN4*	19	NM_020971	+	p.M930K,p.P2550H	A13,C77
2	*ST6GAL2*	2	NM_001142351	-	p.P164L,p.R398H	A33,AC11
2	*SYN3*	22	NM_003490	-	p.H242P,p.R27C	C71,C75
2	*SYNE2*	14	NM_182914	+	p.L1682P,p.Q2726H	C58,C69
2	*TDO2*	4	NM_005651	+	p.L209M,p.R272C	A02,CA69

2	*TENM1*	X	NM_014253	-	p.A755fs,p.N2551S	A31,A90
2	*TET3*	2	NM_144993	+	p.L871P,p.P175S	A81,C70
2	*TMEM132A*	11	NM_017870	+	p.R202W,p.R499C	A36,C71
2	*TMPO*	12	NM_003276	+	p.K290E,p.S282T	A25,C69
2	*TNKS*	8	NM_003747	+	p.A691T,p.G1026V	C70,CA69
2	*TRAF7*	16	NM_032271	+	p.T32M,p.T425A	A88,C58
2	*TRPC7*	5	NM_020389	-	p.P519L,p.V549M	A18,A56
2	*TRPM3*	9	NM_001007471	-	p.M1263V,p.R243P	A43,C81
2	*TSC2*	16	NM_000548	+	p.E863K,p.R611W	A90,C20
2	*TTLL11*	9	NM_001139442	-	p.E121K,p.S65N	C35,C89
2	*UBE2D3*	4	NM_181893	-	p.D119E,p.W143_	C17,C59
2	*UHRF1BP1L*	12	NM_015054	-	p.P516A,p.S99N	A73,C24
2	*USP24*	1	NM_015306	-	p.1056_1056S>SS,p.S882_	A04,C88
2	*USP35*	11	NM_020798	+	p.K3N,p.R323W	A91,C64
2	*USP9X*	X	NM_001039590	+	p.E1444fs,p.G1619fs	A16,A87
2	*VCAN*	5	NM_004385	+	p.E2299_,p.S2292R	A55,C86
2	*VPS13B*	8	NM_017890	+	p.L1166F,p.V2414M	A35,B02
2	*WDR17*	4	NM_170710	+	p.A538S,p.R1144H	AC04,C72
2	*WDR87*	19	NM_031951	-	p.K2692N,p.R253_	A65,C98
2	*WHSC1*	4	NM_001042424	+	p.E1099K(2)	C83,C96
2	*WNK2*	9	NM_006648	+	p.A2160V,p.V1507I	A17,C69
2	*XAB2*	19	NM_020196	-	p.V615M,p.V798M	A38,C66
2	*XIRP2*	2	NM_152381	+	p.D3233G,p.S143G	C21,C70
2	*ZFP36L2*	2	NM_006887	-	p.G144fs,p.K102fs	C40,C54
2	*ASNA1*	19	NM_004317	+	p.262_263insG,p.I262V	A68(2)
2	*BCL2*	18	NM_000633	-	p.A60T,p.T7A	A32(2)
2	*CASK*	X	NM_003688	-	p.D280H,p.R279Q	A75(2)
2	*DNAH10*	12	NM_207437	+	p.R2563_,p.S3189F	A90(2)
2	*FANCB*	X	NM_001018113	-	p.L734V,p.S628L	C79(2)
2	*KIAA0391*	14	NM_014672	+	p.D546fs,p.S544fs	C49(2)
2	*MUC6*	11	NM_005961	-	p.P823L,p.V105I	A32(2)
2	*PER3*	1	NM_016831	+	p.K998E,p.M997R	A68(2)

Table S4. Somatic CNVs identified by high-density SNP arrays

*Based on UCSC hg19 reference

Age group	Cytoband	Start*	End*	Gene length*	Gene	Gains	Losses
adult	1q24	174128551	174927327	9910	*RABGAP1L*	1.22	0
adult	1q24-q25	174968570	174981163	27101	*CACYBP*	1.2567	0
adult	1q25.1	174982093	174992591	63931	*MRPS14*	1.2567	0
adult	1q23-q24	175036993	175117202	63923	*TNN*	1.2567	0
adult	1q25.1	175126122	175161949	9674	*KIAA0040*	1.2567	0
adult	1q24	175291934	175712752	7143	*TNR*	1.2567	0
adult	1q25.1-q25.2	175913961	176176380	64326	*RFWD2*	1.2567	0
adult	1q25.1	175937532	175937676	677679	*SCARNA3*	1.2567	0
adult	1q25.2	176432306	176660341	60676	*PAPPA2*	1.2567	0
adult	1q25.2	176830199	177134040	460	*ASTN1*	1.2567	0
adult	1q25.2	176998498	176998581	574441	*MIR488*	1.2567	0
adult	1q25.2	177898241	177939050	89866	*SEC16B*	1.2567	0
adult	1q25.2	177975274	178007142	730102	*LOC730102*	1.2567	0
adult	1q24	178062863	178448648	9462	*RASAL2*	1.2567	0
adult	1q25.2	178482211	178490946	84066	*TEX35*	1.2567	0
adult	1q25.2	178511930	178518024	400798	*C1orf220*	1.2567	0
adult	1q25.2	178694281	178890977	55103	*RALGPS2*	1.2547	0
adult	1q25.2	178818669	178840215	9068	*ANGPTL1*	1.2547	0
adult	1q25	178995073	179045702	9917	*FAM20B*	1.2547	0
adult	1q25.2	179051111	179065129	64222	*TOR3A*	1.2547	0
adult	1q25.2	179068461	179112224	27	*ABL2*	1.2547	0
adult	1q25	179262848	179327814	6646	*SOAT1*	1.2547	0
adult	1q25.2	179334854	179523870	126859	*AXDND1*	1.2547	0
adult	1q25.2	179560747	179660407	163589	*TDRD5*	1.24295	0
adult	1q25.2	179712297	179785333	148753	*FAM163A*	1.4434	0
adult	1q25.2	179809101	179846941	163590	*TOR1AIP2*	1.4434	0
adult	1q24.2	179851176	179889212	26092	*TOR1AIP1*	1.4434	0
adult	1q25.2	179923907	180084015	9857	*CEP350*	1.4434	0
adult	1q24	180123967	180167169	5768	*QSOX1*	1.4434	0

adult	1q25.2	180167143	180169859	200058	*FLJ23867*	1.4434	0
adult	1q25.2	180199432	180244188	89884	*LHX4*	1.4434	0
adult	1q25.3	180257351	180472022	84320	*ACBD6*	1.4434	0
adult	1q25.1	180601145	180859415	9213	*XPR1*	1.4434	0
adult	1q25.3	180882312	180915239	57710	*KIAA1614*	1.4434	0
adult	1q25.3	180941849	180992257	10228	*STX6*	1.4434	0
adult	1q25.3	181002560	181031074	3140	*MR1*	1.4434	0
adult	1q25.3	181057637	181059979	51278	*IER5*	1.4434	0
adult	1q25.3	181205523	181207740	100287948	*GM140*	1.4434	0
adult	1q25.3	181452685	181775921	777	*CACNA1E*	1.4434	0
adult	1q25.3	182023704	182030847	127665	*ZNF648*	1.4434	0
adult	1q31	182347227	182360539	2752	*GLUL*	1.4434	0
adult	1q25.3	182367251	182369751	127670	*TEDDM1*	1.6767	0
adult	1q25.3	182376755	182383948	388719	*LINC00272*	1.6767	0
adult	1q25	182419255	182529732	353299	*RGSL1*	1.6767	0
adult	1q25	182542768	182558394	6041	*RNASEL*	1.6767	0
adult	1q25-q31	182567757	182573548	6004	*RGS16*	1.6767	0
adult	1q25.3	182584274	182585764	284648	*LOC284648*	1.6767	0
adult	1q25	182615791	182642067	85397	*RGS8*	1.6767	0
adult	1q25	182758583	182799519	80896	*NPL*	1.6767	0
adult	1q25	182808438	182857117	1660	*DHX9*	1.6767	0
adult	1q25.3	182868999	182922553	81626	*SHCBP1L*	1.6767	0
adult	1q31	182992594	183114727	3915	*LAMC1*	1.6767	0
adult	1q25-q31	183155173	183210406	3918	*LAMC2*	1.6767	0
adult	1q25	183217371	183274009	23057	*NMNAT2*	1.6767	0
adult	1q25.3	183430010	183441117	284649	*SMG7-AS1*	1.6767	0
adult	1q25	183441505	183523328	9887	*SMG7*	1.6767	0
adult	1q25	183524696	183559739	4688	*NCF2*	1.6767	0
adult	1q25.3	183595327	183605076	10092	*ARPC5*	1.6767	0
adult	1q25.3	183605181	183897685	23179	*RGL1*	1.6767	0
adult	1q25.3	183615410	183622448	403314	*APOBEC4*	1.6767	0
adult	1q25	183904965	184006904	23127	*COLGALT2*	1.6767	0
adult	1q25	184020784	184043344	116461	*TSEN15*	1.6767	0

adult	1q25	184356149	184598155	81563	*C1orf21*	1.6767	0
adult	1q25	184659624	184724041	80267	*EDEM3*	1.6767	0
adult	1q25	184760158	184943718	116496	*FAM129A*	1.6767	0
adult	1q25.3	185014550	185071740	6045	*RNF2*	1.9423	0
adult	1q25.2	185087217	185126116	81627	*TRMT1L*	1.9423	0
adult	1q25	185126191	185260913	54823	*SWT1*	1.9423	0
adult	1q25.1-q31.1	185265521	185286461	10625	*IVNS1ABP*	2.15	0
adult	1q25.3-q31.1	185703682	186160085	83872	*HMCN1*	2.15	0
adult	10q21.1	186029866	186446655	100302192	*MIR548F1*	2.15	0
adult	1q25-q31	186265404	186283694	10216	*PRG4*	2.15	0
adult	1q25	186280785	186344457	7175	*TPR*	2.15	0
adult	1q25	186344889	186390503	54953	*C1orf27*	2.15	0
adult	1q25	186369703	186370587	10896	*OCLM*	2.15	0
adult	1q25.2	186412697	186417856	5132	*PDC*	2.15	0
adult	1q25.2-q25.3	186640943	186649559	5743	*PTGS2*	2.15	0
adult	1q25	186798031	186958113	5321	*PLA2G4A*	2.15	0
adult	1q31.1-q31.2	190594019	190770788	440704	*LOC440704*	2.54235	0
adult	1q31.2	192127591	192154945	64407	*RGS18*	2.4033	0
adult	1q31.2	192286121	192336414	431704	*RGS21*	2.4033	0
adult	1q31	192544856	192549159	5996	*RGS1*	2.4033	0
adult	1q31.2	192605267	192629440	6003	*RGS13*	2.4033	0
adult	1q31	192778168	192781407	5997	*RGS2*	2.4033	0
adult	1q32	192981495	193028523	51377	*UCHL5*	2.4033	0
adult	1q31	193028551	193055115	6738	*TROVE2*	2.4033	0
adult	1q31.2	193065594	193074608	51022	*GLRX2*	2.4033	0
adult	1q25	193091087	193223942	79577	*CDC73*	2.4033	0
adult	1q31	193147859	193155743	8707	*B3GALT2*	2.4033	0
adult	1q31.3	196194909	196577561	343450	*KCNT2*	2.6728	0
adult	1q32	196621007	196670695	3075	*CFH*	2.6728	0
adult	1q32	196743929	196763203	10878	*CFHR3*	2.6728	0
adult	1q32	196788860	196801319	3078	*CFHR1*	2.4522	0
adult	1q32	196857143	196887843	10877	*CFHR4*	2.6649	0
adult	1q31.3	196912897	196928356	3080	*CFHR2*	2.6649	0

adult	1q31.3	196946666	196978803	81494	*CFHR5*	2.6649	0
adult	1q31-q32.1	197008320	197036397	2165	*F13B*	2.6649	0
adult	1q31	197053256	197115824	259266	*ASPM*	2.6649	0
adult	1q31.3	197122813	197169672	360023	*ZBTB41*	2.6649	0
adult	1q31.3	197170591	197447585	23418	*CRB1*	2.6649	0
adult	1q31.3	197473878	197744623	163486	*DENND1B*	2.6649	0
adult	1q31.3	197871681	197876497	388722	*C1orf53*	2.6649	0
adult	1q31.1	197881634	197899273	56956	*LHX9*	2.6649	0
adult	1q31.3	198126107	198291548	140609	*NEK7*	2.6649	0
adult	1q31.3	198492351	198510075	127124	*ATP6V1G3*	2.4018	0
adult	1q31-q32	198608097	198664300	5788	*PTPRC*	2.4018	0
adult	1q32.1	198777131	198906558	100131234	*MIR181A1HG*	1.9622	-0.4867
adult	1q32.1	198828001	198828111	406955	*MIR181B1*	1.9622	-0.4867
adult	1q32.1	198828172	198828282	406995	*MIR181A1*	1.9622	-0.4867
adult	1q32.1	199996729	200146550	2494	*NR5A2*	1.9622	0
adult	1q32.1	200311671	200342920	554279	*LINC00862*	1.9622	0
adult	1q32.1	200374074	200379186	23528	*ZNF281*	1.9622	0
adult	1q32.1	200520624	200589862	9928	*KIF14*	1.9622	0
adult	1q32.1	200613164	200639126	83479	*DDX59*	1.9622	0
adult	1q32.1	200708685	200829835	23271	*CAMSAP2*	1.9622	0
adult	1q32.1	200842082	200843306	2848	*GPR25*	1.9622	0
adult	1q32.1	200860626	200884864	55765	*C1orf106*	1.9622	0
adult	1q32.1	200938513	200992828	23046	*KIF21B*	1.9622	0
adult	1q32	201008639	201081694	779	*CACNA1S*	1.9622	0
adult	1q32.1	201083080	201084500	647219	*ASCL5*	1.9622	0
adult	1q32.1	201159952	201198080	91156	*IGFN1*	1.4566	0
adult	1q32	201252579	201302121	5317	*PKP1*	1.4566	0
adult	1q32	201328135	201346828	7139	*TNNT2*	1.4566	0
adult	1q25.1-q32.3	201349965	201368669	3898	*LAD1*	1.4566	0
adult	1q31.3	201372894	201390874	7135	*TNNI1*	1.4566	0
adult	1q31	201433411	201438299	23612	*PHLDA3*	1.4566	0
adult	1q32	201452657	201465701	1465	*CSRP1*	1.4566	0
adult	1q32.1	201489031	201489720	376693	*RPS10P7*	1.4566	0

adult	1q32.3	201617449	201796102	89796	*NAV1*	1.4566	0
adult	1q32.1	201798287	201853422	55705	*IPO9*	1.4566	0
adult	1q32.1	201857796	201861715	149345	*SHISA4*	1.4566	0
adult	1q32	201865583	201915716	25802	*LMOD1*	1.4566	0
adult	1q32.1	201924618	201939789	10440	*TIMM17A*	1.4566	0
adult	1q32	201951765	201975275	6051	*RNPEP*	1.4566	0
adult	1q32.2	201979689	201986315	1999	*ELF3*	1.4566	0
adult	1q32.1	202092028	202098634	9283	*GPR37L1*	1.4566	0
adult	1q32.1	202102531	202113871	127829	*ARL8A*	1.4566	0
adult	1q32.1	202116140	202129119	5778	*PTPN7*	1.4566	0
adult	1q32.1	202137178	202158577	148713	*PTPRVP*	1.4566	0
adult	1q32.1	202163117	202288889	59352	*LGR6*	1.4566	0
adult	1q32.1	202300784	202311094	29089	*UBE2T*	1.4566	0
adult	1q32.1	202317829	202407370	4660	*PPP1R12B*	1.4566	0
adult	1q32.1	202559724	202612581	127833	*SYT2*	1.4566	0
adult	1q32.1	202694312	202778598	10765	*KDM5B*	1.4566	0
adult	1q32.1	202830881	202844369	148709	*LOC148709*	1.4566	0
adult	1q32.1	202847409	202858385	5877	*RABIF*	1.4566	0
adult	1q32.1	202860223	202896400	59349	*KLHL12*	1.4566	0
adult	1q32.1	202909952	202927524	51094	*ADIPOR1*	1.4566	0
adult	1q32.1	202931000	202936404	51706	*CYB5R1*	1.4566	0
adult	1q32.1	202976533	202993197	92703	*TMEM183A*	1.4566	0
adult	1q31-q41	203052256	203055166	4656	*MYOG*	1.4566	0
adult	1q32.1	203096835	203136533	134	*ADORA1*	1.4566	0
adult	1q32.1	203136938	203144942	4608	*MYBPH*	1.4566	0
adult	1q32.1	203148058	203155922	1116	*CHI3L1*	1.4566	0
adult	1q32.1	203185206	203198860	1118	*CHIT1*	1.4566	0
adult	1q32	203274663	203278729	7832	*BTG2*	1.4566	0
adult	1q32	203309748	203320557	2331	*FMOD*	1.4566	0
adult	1q32	203444882	203460479	5549	*PRELP*	1.4566	0
adult	1q32.1	203463270	203478077	26254	*OPTC*	1.4566	0
adult	1q32.1	203595914	203713209	493	*ATP2B4*	1.4368	0
adult	1q32.1	203698708	203698833	677843	*SNORA77*	1.2228	0

adult	1q32.1	203699704	203700979	84719	*LINC00260*	1.2228	0
adult	1q32.1	203734283	203745480	54900	*LAX1*	1.2228	0
adult	1q32.1	203764750	203823256	9877	*ZC3H11A*	1.2228	0
adult	1q32.1	203766650	203769590	100381270	*ZBED6*	1.2228	0
adult	1q32	203830712	203840280	6635	*SNRPE*	1.2228	0
adult	1q32.1	204001574	204010392	284573	*LINC00303*	1.2228	0
adult	1q32	204042245	204096871	9580	*SOX13*	1.2228	0
adult	1q32.1	204100188	204121310	55224	*ETNK2*	1.2228	0
adult	1q32	204123943	204135465	5972	*REN*	1.2228	0
adult	1q32	204159468	204165619	3814	*KISS1*	1.2228	0
adult	1q32.1	204167287	204183220	127845	*GOLT1A*	1.2228	0
adult	1q32.1	204187978	204329057	22874	*PLEKHA6*	1.2228	0
adult	1q32.1	204337557	204338847	127841	*LINC00628*	1.2228	0
adult	1q32.1	204372491	204380945	84919	*PPP1R15B*	1.2228	0
adult	1q32	204391757	204459474	5287	*PIK3C2B*	1.2228	0
adult	1q32	204485506	204527248	4194	*MDM4*	1.2228	0
adult	1q32.1	204586302	204654481	10446	*LRRN2*	1.2228	0
adult	1q32.1	204797781	204946274	23114	*NFASC*	1.2228	0
adult	1q32.1	205012339	205047171	6900	*CNTN2*	1.2228	0
adult	1q32.1	205052256	205053588	388730	*TMEM81*	1.2228	0
adult	1q32	205055269	205091150	5929	*RBBP5*	1.2228	0
adult	1q32.1	205111630	205180727	25778	*DSTYK*	1.2228	0
adult	1q32.1	205197037	205242471	9911	*TMCC2*	1.2228	0
adult	1q32.1	205271190	205290919	81788	*NUAK2*	1.2228	0
adult	1q32.1	205305192	205326128	55220	*KLHDC8A*	1.2228	0
adult	1q32.1	205342379	205356568	284576	*LEMD1-AS1*	1.2228	0
adult	1q32.1	205350505	205391214	93273	*LEMD1*	1.2228	0
adult	1q32.1	205417429	205417526	442891	*MIR135B*	1.2228	0
adult	1q31-q32	205473683	205501921	5129	*CDK18*	1.2228	0
adult	1q32.1	205523400	205525763	284578	*LOC284578*	1.2228	0
adult	1q32.1	205538111	205572046	148808	*MFSD4*	1.2228	0
adult	1q32	205577070	205602000	2005	*ELK4*	1.2228	0
adult	1q32.1	205626980	205649630	85414	*SLC45A3*	1.2228	0

adult	1q32.1	205681946	205719372	64710	*NUCKS1*	1.2228	0
adult	1q32.1	205758220	205782324	254428	*SLC41A1*	1.2228	0
adult	1q32.1	205797149	205819276	148811	*PM20D1*	1.2228	0
adult	1q32.1	205831206	205865215	284581	*LOC284581*	1.2228	0
adult	1q32.1	205882176	205912588	115019	*SLC26A9*	1.2228	0
adult	1q32.1	206138454	206155151	729533	*FAM72A*	1.2228	0
adult	1q32	206224282	206231482	553	*AVPR1B*	1.2228	0
adult	1q32.1	206238871	206288647	440712	*C1orf186*	1.2228	0
adult	1q31	206317458	206332104	1510	*CTSE*	1.2228	0
adult	1p11.2	206516199	206581301	653464	*SRGAP2C*	1.2228	0
adult	1q32.1	206516199	206637783	23380	*SRGAP2*	1.2228	0
adult	1q32.1	206643585	206670223	9641	*IKBKE*	1.2228	0
adult	1q32.1	206680862	206762616	83593	*RASSF5*	1.2228	0
adult	1q32.1	206764973	206785904	1939	*EIF2D*	1.2228	0
adult	1q32.1	206808880	206822542	8444	*DYRK3*	1.2228	0
adult	1q32	206858364	206907630	9261	*MAPKAPK2*	1.2228	0
adult	1q31-q32	206940947	206945839	3586	*IL10*	1.2228	0
adult	1q32.2	206972214	207016326	29949	*IL19*	1.2228	0
adult	1q32	207039153	207042568	50604	*IL20*	1.2228	0
adult	1q32	207070787	207077484	11009	*IL24*	1.2228	0
adult	1q32.1	207076630	207095235	9214	*FAIM3*	1.2228	0
adult	1q31-q41	207101866	207119811	5284	*PIGR*	1.2228	0
adult	1q32.1	207131311	207143970	83953	*FCAMR*	1.2228	0
adult	1q32.1	207191865	207206101	79098	*C1orf116*	1.2228	0
adult	1q32.2	207217193	207224422	55432	*YOD1*	1.2228	0
adult	1q31	207226619	207251162	5208	*PFKFB2*	1.2228	0
adult	1q32	207262186	207273337	725	*C4BPB*	1.2228	0
adult	1q32	207277606	207318317	722	*C4BPA*	1.2103	0
adult	1q32	207494816	207534311	1604	*CD55*	1.3989	0
adult	1q32	207627644	207663240	1380	*CR2*	1.8156	0
adult	1q32	207669472	207815110	1378	*CR1*	1.8156	0
adult	1q32.1	207818457	207897036	1379	*CR1L*	1.8156	0
adult	1q32	207925382	207968861	4179	*CD46*	1.8156	0

adult	1q32.2	207975787	207975868	407026	*MIR29C*	1.8156	0
adult	1q32.2	207991723	207995941	148696	*LOC148696*	1.8156	0
adult	1q32	208059882	208084683	947	*CD34*	1.8156	0
adult	1q32.2	208195587	208417665	5362	*PLXNA2*	1.8156	0
adult	1q32.2	209602167	209605892	642587	*MIR205HG*	1.8156	0
adult	1q32.2	209605477	209605587	406988	*MIR205*	1.8156	0
adult	1q32.2	209757044	209787284	57172	*CAMK1G*	1.8156	0
adult	1q32	209788217	209824679	3914	*LAMB3*	1.8156	0
adult	1q32.2	209848669	209849735	50486	*G0S2*	1.8156	0
adult	1q32-q41	209859524	209908295	3290	*HSD11B1*	1.8156	0
adult	1q32	209929376	209955668	80342	*TRAF3IP3*	1.8156	0
adult	1q32.2	209952552	209958075	148304	*C1orf74*	1.8156	0
adult	1q32.3-q41	209958967	209979520	3664	*IRF6*	1.8156	0
adult	1q32.2	210001311	210030910	27042	*DIEXF*	1.8156	0
adult	1q32.2	210111518	210337633	255928	*SYT14*	1.8617	0
adult	1q32.2	210404803	210407466	574036	*SERTAD4-AS1*	1.8617	0
adult	1q32.1-q41	210406194	210416440	56256	*SERTAD4*	1.8617	0
adult	1q32	210501595	210849638	55733	*HHAT*	1.8656	0
adult	1q32.2	210851656	211307457	3756	*KCNH1*	2.08075	0
adult	1q32.2	211432707	211486655	55758	*RCOR3*	2.0876	0
adult	1q32	211499956	211548286	7188	*TRAF5*	2.0876	0
adult	1q32.3	211556096	211605877	84791	*LINC00467*	2.0876	0
adult	1q32.3	211649863	211666259	343035	*RD3*	2.0876	0
adult	1q32.3	211748380	211752099	7779	*SLC30A1*	2.0876	0
adult	1q32.3	211831598	211848972	4751	*NEK2*	2.0876	0
adult	1q32	211916798	212004114	9926	*LPGAT1*	2.0876	0
adult	1q32.3	212113740	212209002	25896	*INTS7*	2.0876	0
adult	1q32	212208894	212278348	51514	*DTL*	2.0876	0
adult	1q32.2-q32.3	212458878	212535205	5525	*PPP2R5A*	2.096	0
adult	1q32.3	212526159	212526292	692157	*SNORA16B*	2.096	0
adult	1q32.3	212537815	212588243	55248	*TMEM206*	2.096	0
adult	1q32.3	212606228	212619721	29937	*NENF*	2.096	0
adult	1q32.3	212738675	212794119	467	*ATF3*	2.096	0

adult	1q32.3	212797788	212800120	149647	*FAM71A*	2.096	0
adult	1q32.3	212859758	212873327	55509	*BATF3*	2.096	0
adult	1q41	212899494	212965139	25936	*NSL1*	2.096	0
adult	1q32.3	212965169	212990167	128387	*TATDN3*	2.096	0
adult	1q32.3	213029945	213031480	642946	*FLVCR1-AS1*	2.096	0
adult	1q32.3	213031596	213072705	28982	*FLVCR1*	2.096	0
adult	1q32.3	213123861	213164927	79805	*VASH2*	2.096	0
adult	1q32.3	213165523	213189217	90806	*ANGEL2*	2.096	0
adult	1q41	213224574	213446808	26750	*RPS6KC1*	2.096	0
adult	1q32.3	214098091	214099996	100861504	*LINC00538*	2.096	0
adult	1q41	214161277	214214847	5629	*PROX1*	2.096	0
adult	1q32.3	214454564	214510477	56950	*SMYD2*	2.096	0
adult	1q32.2	214522038	214725024	5784	*PTPN14*	2.096	0
adult	1q41	214776531	214837914	1063	*CENPF*	2.096	0
adult	1q41	215178884	215410436	3776	*KCNK2*	2.096	0
adult	1q41	215740734	215795149	51133	*KCTD3*	2.09	0
adult	1q41	215796235	216596738	7399	*USH2A*	2.09	0
adult	1q41	216676587	216896814	2104	*ESRRG*	2.09	0
adult	1q41	217600334	217804444	55105	*GPATCH2*	2.09	0
adult	1q41	217804665	218041495	128153	*SPATA17*	2.09	0
adult	1q41	218066241	218094146	100885798	*LINC00210*	2.09	0
adult	1q41	218458628	218511325	51018	*RRP15*	2.09	0
adult	1q41	218518675	218617961	7042	*TGFB2*	2.09	0
adult	1q41	219347172	219386207	127018	*LYPLAL1*	2.09	0
adult	1p34.1	220046618	220292777	26828	*RNU5F-1*	2.09	0
adult	1q41	220087605	220101993	55532	*SLC30A10*	2.09	0
adult	1q41	220141941	220220000	2058	*EPRS*	2.09	0
adult	1q41	220230823	220263195	10380	*BPNT1*	2.09	0
adult	1q41	220267454	220321383	55699	*IARS2*	2.09	0
adult	1q41	220291194	220291304	406997	*MIR215*	2.09	0
adult	1q41	220291498	220291583	406969	*MIR194-1*	2.09	0
adult	1q41	220321609	220445843	25782	*RAB3GAP2*	2.09	0
adult	1q41	220373887	220374018	677818	*SNORA36B*	2.09	0

adult	1q41	220439520	220441057	6791	*AURKAPS1*	2.09	0
adult	1q41	220701524	220837799	4139	*MARK1*	1.8804	0
adult	1q41	220863627	220872499	79762	*C1orf115*	1.8804	0
adult	1q41	220921587	220958157	54996	*2-Mar*	1.8804	0
adult	1q41	220960038	220987741	64757	*1-Mar*	1.8804	0
adult	1q41	221052742	221058400	3142	*HLX*	1.8804	0
adult	1q41	221503269	221509638	400804	*C1orf140*	1.8804	0
adult	1q41	221874761	221915518	11221	*DUSP10*	1.8881	0
adult	1q41	222695601	222721444	79802	*HHIPL2*	1.8634	0
adult	1q42	222731243	222763275	9015	*TAF1A*	1.8634	0
adult	1q41	222791443	222841354	375056	*MIA3*	1.8634	0
adult	1q41	222841354	222885864	64853	*AIDA*	1.8634	0
adult	1q41	222885894	222908538	148362	*BROX*	1.8634	0
adult	1q41	222910557	222924002	400823	*FAM177B*	1.8634	0
adult	1q41	222988430	223179337	84976	*DISP1*	1.8634	0
adult	1q41-q42	223282747	223316624	7100	*TLR5*	1.8634	0
adult	1q41	223394160	223537544	55061	*SUSD4*	1.8634	0
adult	1q41	223714971	223853436	388743	*CAPN8*	1.8634	0
adult	1q41-q42	223889294	223963720	824	*CAPN2*	1.8634	0
adult	1q41	223967594	224033674	7159	*TP53BP2*	1.8634	0
adult	1q42.11	224301788	224349749	23219	*FBXO28*	1.8634	0
adult	1q42.11	224370909	224381142	8560	*DEGS1*	1.6543	0
adult	1q41-q42.2	224415035	224517891	4931	*NVL*	1.8699	0
adult	1q42.11	224444705	224444843	100313769	*MIR320B2*	1.8699	0
adult	1q42.11	224544512	224564586	29097	*CNIH4*	1.8699	0
adult	1q42.13	224572844	224622001	80232	*WDR26*	1.8699	0
adult	1q42.12	224804178	224928249	149111	*CNIH3*	1.8699	0
adult	1q42.12	225117355	225211991	127602	*DNAH14*	1.8699	0
adult	1q42.1	225589203	225615815	3930	*LBR*	1.8699	0
adult	1q42.12	225674533	225840845	55740	*ENAH*	1.8699	0
adult	1q42.12	225965514	225978168	6726	*SRP9*	1.8699	0
adult	1q42.1	225997775	226033262	2052	*EPHX1*	1.8699	0
adult	1q42.12	226033232	226070420	9725	*TMEM63A*	1.8699	0

adult	1q42.1	226073981	226076846	10637	*LEFTY1*	1.8699	0
adult	1q42.12	226107576	226112040	29920	*PYCR2*	1.8699	0
adult	1q42.1	226124297	226129083	7044	*LEFTY2*	1.8699	0
adult	1q42.12	226170402	226187066	163859	*SDE2*	1.8699	0
adult	1q42.12	226332379	226374423	64746	*ACBD3*	1.8699	0
adult	1q42.12	226411318	226414756	83881	*MIXL1*	1.8699	0
adult	1q42.12	226418849	226497204	286826	*LIN9*	1.8699	0
adult	1q41-q42	226548391	226595801	142	*PARP1*	1.8699	0
adult	1q42.12	226736500	226796915	375057	*C1orf95*	1.8699	0
adult	1q42.13	226819390	226926876	3707	*ITPKB*	1.8699	0
adult	1q42.13	227058272	227083804	5664	*PSEN2*	1.8699	0
adult	1q42.13	227127937	227175246	56997	*ADCK3*	1.8699	0
adult	1q42.11	227177565	227505826	8476	*CDC42BPA*	1.8699	0
adult	1q42.13	227751219	227850164	339500	*ZNF678*	1.8699	0
adult	1q42.13	227884732	227885408	401983	*ZNF847P*	1.8699	0
adult	1q42.13	227916239	227922055	100130093	*LOC100130093*	1.8699	0
adult	1q42.13	227918889	227923112	65094	*JMJD4*	1.8699	0
adult	1q42.13	227922696	227968932	116841	*SNAP47*	1.8699	0
adult	1q42.13	228003417	228034171	339501	*PRSS38*	1.6543	0
adult	1q42	228109164	228135676	7483	*WNT9A*	1.6543	0
adult	1q42	228194722	228248972	89780	*WNT3A*	1.6543	0
adult	1q42	228270360	228286913	375	*ARF1*	1.6543	0
adult	1q42.13	228288427	228291163	79169	*C1orf35*	1.6543	0
adult	1q42.13	228294379	228297013	128308	*MRPL55*	1.6543	0
adult	1q32-q41	228327784	228336655	2987	*GUK1*	1.6543	0
adult	1q42.13	228337414	228347527	57165	*GJC2*	1.6543	0
adult	1q42.13	228353508	228369958	200205	*IBA57*	1.6543	0
adult	1q42.13	228391206	228401356	574407	*C1orf145*	1.6543	0
adult	1q42.13	228395830	228548951	84033	*OBSCN*	1.6543	0
adult	1q42.13	228581376	228594517	81559	*TRIM11*	1.6543	0
adult	1q42	228595635	228604583	51127	*TRIM17*	1.6543	0
adult	1q42	228612545	228613026	8290	*HIST3H3*	1.6543	0
adult	1q42.13	228645064	228645560	92815	*HIST3H2A*	1.6543	0

adult	1q42.13	228645807	228646259	128312	*HIST3H2BB*	1.6543	0
adult	1q42.13	228675067	228683889	149603	*RNF187*	1.6543	0
adult	1q42.11-q42.3	228780393	228882416	58480	*RHOU*	1.4238	0
adult	1q42.13	228780656	228788159	574029	*DUSP5P1*	1.1273	0
adult	4q32.2	229310429	229310548	100616234	*MIR4454*	1.4238	0
adult	1q42-q43	229406808	229441640	5867	*RAB4A*	1.4238	0
adult	1q42.13	229440128	229441250	10638	*SPHAR*	1.4238	0
adult	1q42.13	229456751	229478688	126731	*CCSAP*	1.4238	0
adult	1q42.13	229566992	229569843	58	*ACTA1*	1.4238	0
adult	1q42.13	229577043	229644088	55746	*NUP133*	1.4238	0
adult	1q42.13	229652328	229694442	23456	*ABCB10*	1.4238	0
adult	1q42.13	229728865	229761794	27097	*TAF5L*	1.4238	0
adult	1q42.13	229761962	229795947	9816	*URB2*	1.4238	0
adult	1q41-q42	230202941	230417876	2590	*GALNT2*	1.4853	0
adult	1q42.13	230457391	230561674	79605	*PGBD5*	1.4853	0
adult	1q42.2	230778201	230829731	22796	*COG2*	1.4853	0
adult	1q42.2	230838271	230850336	183	*AGT*	1.4853	0
adult	1q42.11-q42.3	230883129	230937518	10753	*CAPN9*	1.4853	0
adult	1q42.2	230972864	230991782	84886	*C1orf198*	1.4853	0
adult	1q42.2	231041986	231114618	79573	*TTC13*	1.4853	0
adult	1q42.2	231114822	231136479	64801	*ARV1*	1.4853	0
adult	1q42.2	231154703	231175995	375061	*FAM89A*	1.4853	0
adult	1q42.2	231155573	231155670	100302132	*MIR1182*	1.4853	0
adult	1q42.2	231298673	231357314	440730	*TRIM67*	1.4853	0
adult	1q42.2	231319844	231323373	149373	*LOC149373*	1.4853	0
adult	1q42.2	231359508	231376933	128061	*C1orf131*	1.4853	0
adult	1q42	231376918	231413719	8443	*GNPAT*	1.4853	0
adult	1q42.2	231468476	231473618	149371	*EXOC8*	1.4853	0
adult	1q42.12-q43	231473681	231490773	83932	*SPRTN*	1.4853	0
adult	1q42.1	231499496	231560790	54583	*EGLN1*	1.4853	0
adult	1q42.2	231611509	231612271	645339	*SNRPD2P2*	1.4853	0
adult	1q42.1	231664398	231702269	7257	*TSNAX*	1.4853	0
adult	1q42.2	231727037	231747836	100287814	*LINC00582*	1.4853	0

adult	1q42.1	231762560	231859820	27185	*DISC1*	1.4853	0
adult	1q42.1	231950371	231954263	27184	*DISC2*	1.4853	0
adult	1q42.2	232533711	232651354	57568	*SIPA1L2*	1.4853	0
adult	1q42.2	232940637	232946092	54627	*MAP10*	1.4853	0
adult	1q42.2	233086369	233114219	84284	*NTPCR*	1.4853	0
adult	1q42.2	233119881	233431459	80003	*PCNXL2*	1.4853	0
adult	1q42	233463513	233520894	84451	*KIAA1804*	1.4853	0
adult	1q42-q43	233749749	233808258	3775	*KCNK1*	1.4853	0
adult	1q42.2	234040457	234460264	148641	*SLC35F3*	1.7084	0
adult	1q42.2	234509182	234519795	388753	*COA6*	1.7413	0
adult	1q42.3	234527058	234614849	6894	*TARBP1*	1.7413	0
adult	1q42.3	234740014	234745271	359948	*IRF2BP2*	1.2229	0
adult	1q42.3	234765056	234770526	100302691	*LINC00184*	1.4536	0
adult	1q42	235272657	235292256	9804	*TOMM20*	1.4536	0
adult	1q42.3	235291117	235291252	677802	*SNORA14B*	1.4536	0
adult	1q42.3	235294497	235324571	23029	*RBM34*	1.4536	0
adult	1q42.3	235330209	235490802	51742	*ARID4B*	1.4536	0
adult	1q43	235491752	235507844	9453	*GGPS1*	1.4536	0
adult	1q42.3	235530674	235612283	6905	*TBCE*	1.4536	0
adult	1q42.3	235610504	235667781	148789	*B3GALNT2*	1.4536	0
adult	1q42.3	235710984	235813293	2786	*GNG4*	1.4536	0
adult	1q42.1-q42.2	235824330	236030227	1130	*LYST*	1.4536	0
adult	1q43	236139131	236228481	4811	*NID1*	1.4536	0
adult	1q42-q43	236305831	236372209	7107	*GPR137B*	1.4536	0
adult	1q42.2-q43	236378421	236445339	56605	*ERO1LB*	1.4536	0
adult	1q42.3	236557679	236648008	128178	*EDARADD*	1.70445	0
adult	1q43	236681513	236716279	3964	*LGALS8*	1.759	0
adult	1q43	236686368	236687808	100287902	*LGALS8-AS1*	1.759	0
adult	1q43	236712304	236767841	55127	*HEATR1*	1.759	0
adult	1q42-q43	236849753	236927927	88	*ACTN2*	1.786	0
adult	1q43	236958580	237067281	4548	*MTR*	1.813	0
adult	1q43	237167402	237167718	645745	*MT1HL1*	1.813	0
adult	1q43	237205701	237997288	6262	*RYR2*	1.5996	0

adult	1q43	238025474	238091619	100130331	*LOC100130331*	1.5996	0
adult	1q43	238041163	238054222	57829	*ZP4*	1.5996	0
adult	1q43	239792372	240072717	1131	*CHRM3*	1.5996	0
adult	1q43	240170823	240176560	645884	*RPS7P5*	1.5996	0
adult	1q43	240255184	240638489	56776	*FMN2*	1.5719	0
adult	1q43	240652872	240775462	64388	*GREM2*	1.3514	0
adult	1q43	240938813	241520530	6000	*RGS7*	1.3514	0
adult	1q42.1	241660856	241683085	2271	*FH*	1.3514	0
adult	1q42-q44	241695433	241758949	8564	*KMO*	1.3514	0
adult	1q43	241756451	241803701	23596	*OPN3*	1.3514	0
adult	1q43	241792166	241799232	1122	*CHML*	1.3514	0
adult	1q43	241815579	241965434	128025	*WDR64*	1.3514	0
adult	1q43	242011492	242053241	9156	*EXO1*	1.3514	0
adult	1q43	242158791	242162385	440738	*MAP1LC3C*	1.3514	0
adult	1q43	242251688	242612784	200150	*PLD5*	1.3514	0
adult	1q44	243287729	243418708	9859	*CEP170*	1.3514	0
adult	1q43	243419306	243663393	10806	*SDCCAG8*	1.3514	0
adult	1q44	243651534	244006584	10000	*AKT3*	1.33005	-0.3109
adult	1q44	244080703	244210619	339529	*LOC339529*	1.3087	-0.3109
adult	1q44	244212240	244220780	10472	*ZBTB18*	1.3087	-0.3109
adult	1q44	244515936	244552388	200159	*C1orf100*	1.081	0
adult	1q44	244571793	244615436	159	*ADSS*	1.081	0
adult	1q44	244624672	244803662	257044	*C1orf101*	1.081	0
adult	1q44	244816349	244872336	51029	*DESI2*	1.081	0
adult	1q44	244998630	245008365	116228	*COX20*	1.081	0
adult	1q44	245013601	245027827	3192	*HNRNPU*	1.081	0
adult	1q44	245133170	245251148	84288	*EFCAB2*	1.081	0
adult	1q44	245318286	245866428	55083	*KIF26B*	1.081	0
adult	1q44	245912641	246580714	64754	*SMYD3*	1.081	0
adult	1q44	246679340	246687589	255654	*LOC255654*	1.081	0
adult	1q44	246703862	246729565	64216	*TFB2M*	1.0963	0
adult	1q44	246729638	246811544	163882	*CNST*	1.0963	0
adult	1q44	246887377	246931440	51097	*SCCPDH*	1.0963	0

adult	1q44	247002401	247094726	25909	*AHCTF1*	1.0963	0
adult	1q44	247108848	247171395	57116	*ZNF695*	1.0963	0
adult	1q	247108848	247242115	100533111	*ZNF670-ZNF695*	1.0963	0
adult	1q44	247197939	247242115	93474	*ZNF670*	1.0963	0
adult	1q44	247263263	247267674	79862	*ZNF669*	1.0963	0
adult	1q44	247273461	247275719	388759	*C1orf229*	1.0963	0
adult	1q44	247285276	247335319	7678	*ZNF124*	1.1104	0
adult	1q44	247419373	247420447	317705	*VN1R5*	1.1104	0
adult	1q44	247463621	247495045	84838	*ZNF496*	1.1104	0
adult	1q44	247579457	247612406	114548	*NLRP3*	1.3244	0
adult	1q44	247614330	247615284	127623	*OR2B11*	1.3244	0
adult	1q44	247654369	247655711	441932	*OR2W5*	1.3244	0
adult	1q44	247687980	247694106	148824	*GCSAML-AS1*	1.3244	0
adult	1q44	247693433	247697141	81472	*OR2C3*	1.3244	0
adult	1q44	247712346	247740992	148823	*GCSAML*	1.3244	0
adult	1q44	247751661	247752615	81470	*OR2G2*	1.3244	0
adult	1q44	247768887	247769817	81469	*OR2G3*	1.3244	0
adult	1q44	247835419	247836343	441933	*OR13G1*	1.3244	0
adult	1q44	247875130	247876057	343169	*OR6F1*	1.3244	0
adult	1q44	247920763	247921708	26188	*OR1C1*	1.3244	0
adult	1q44	247978101	247979031	284532	*OR14A16*	1.3244	0
adult	1q44	248004229	248005198	391189	*OR11L1*	1.3244	0
adult	1q44	248020500	248043438	25893	*TRIM58*	1.3244	0
adult	1q44	248084319	248085258	343172	*OR2T8*	1.3244	0
adult	1q44	248100330	248264224	284521	*OR2L13*	1.1135	0
adult	1q44	248112159	248113098	391190	*OR2L8*	1.3244	0
adult	1q44	248128633	248129641	391191	*OR2AK2*	1.3244	0
adult	1q44	248153568	248154493	26247	*OR2L1P*	1.3244	0
adult	1q44	248185249	248186188	81466	*OR2L5*	1.1135	0
adult	1q44	248201473	248202607	26246	*OR2L2*	1.1135	0
adult	1q44	248223983	248224922	391192	*OR2L3*	1.1135	0
adult	1q44	248285437	248286082	388762	*OR2M1P*	1.1135	0
adult	1q44	248308449	248309388	127059	*OR2M5*	1.1135	0

adult	1q44	248343287	248344331	391194	*OR2M2*	1.1135	0
adult	1q44	248366369	248367308	127062	*OR2M3*	1.1135	0
adult	1q44	248402230	248403166	26245	*OR2M4*	1.1135	0
adult	1q44	248436153	248437116	391195	*OR2T33*	1.1135	0
adult	1q44	248457917	248458880	127064	*OR2T12*	1.1135	0
adult	1q44	248486931	248487870	391196	*OR2M7*	1.1135	0
adult	1q44	248512076	248513015	127066	*OR14C36*	1.1135	0
adult	1q44	248524882	248525929	127074	*OR2T4*	1.1135	0
adult	1q44	248550909	248551836	254879	*OR2T6*	1.1135	0
adult	1q44	248569295	248570405	26696	*OR2T1*	1.1135	0
adult	1q44	248616098	248617073	401992	*OR2T2*	1.0877	0
adult	1q44	248636651	248637608	343173	*OR2T3*	1.0877	0
adult	1q44	248651889	248652837	401993	*OR2T5*	1.0877	0
adult	1q44	248684947	248685898	391211	*OR2G6*	1.0877	0
adult	1q44	248721844	248722792	343563	*OR2T29*	1.0877	0
adult	1q44	248737101	248738058	127068	*OR2T34*	1.0877	0
adult	1q44	248756130	248757069	127069	*OR2T10*	1.0877	0
adult	1q44	248789478	248790429	127077	*OR2T11*	1.0877	0
adult	1q44	248801587	248802559	403244	*OR2T35*	1.0877	0
adult	1q44	248813231	248814185	403239	*OR2T27*	1.0877	0
adult	1q44	248844669	248845605	401994	*OR14I1*	1.0877	0
adult	1q44	248902716	248903151	646627	*LYPD8*	1.0877	0
adult	1q44	249104650	249120154	80851	*SH3BP5L*	1.0877	0
adult	1q44	249132376	249143716	79894	*ZNF672*	1.0877	0
adult	1q44	249144202	249153125	55657	*ZNF692*	1.0877	0
adult	12p13-p12	10004967	10022458	9976	*CLEC2B*	0.2932	-1.5326
adult	12p13	10034087	10048432	100431172	*KLRF2*	0.2932	-1.5326
adult	12p13.31	10065825	10084980	387836	*CLEC2A*	0.2932	-1.5326
adult	12p13.2	10103914	10138194	160364	*CLEC12A*	0.2932	-1.5326
adult	12p13.2	10145661	10151899	51266	*CLEC1B*	0.2932	-1.5326
adult	12p13.2	10163230	10170548	387837	*CLEC12B*	0.2932	-1.5326
adult	12p13.2	10183275	10218629	283420	*CLEC9A*	0.2932	-1.5326
adult	12p13.2	10222152	10251664	51267	*CLEC1A*	0.2932	-1.5326

adult	12p13.2	10269375	10282868	64581	*CLEC7A*	0.2932	-1.5326
adult	12p13.2-p12.3	10310898	10324790	4973	*OLR1*	0.2932	-1.5326
adult	12p13.2	10331556	10344403	120939	*TMEM52B*	0.2932	-1.5326
adult	12p13.2	10365488	10375724	23710	*GABARAPL1*	0.2932	-1.5326
adult	12p13	10457049	10469850	3824	*KLRD1*	0.2932	-1.5326
adult	12p13.2-p12.3	10524951	10542653	22914	*KLRK1*	0.2932	-1.5326
adult	12p	10524951	10562745	100528032	*KLRC4-KLRK1*	0.2932	-1.5326
adult	12p13.2-p12.3	10559982	10562356	8302	*KLRC4*	0.2932	-1.5326
adult	12p13	10564913	10573194	3823	*KLRC3*	0.2932	-1.5326
adult	12p13.2	10741076	10752434	10748	*KLRAP1*	0.2932	-1.5459
adult	12p13.2	10756363	10766208	55110	*MAGOHB*	0.2932	-1.5459
adult	12p13.2	10771537	10826891	55359	*STYK1*	0.2932	-1.5459
adult	12p13.1	10851675	10875953	8531	*YBX3*	0.2932	-1.5459
adult	12p13	10954130	10955226	50837	*TAS2R7*	0.2932	-1.5459
adult	12p13	10958649	10959579	50836	*TAS2R8*	0.2932	-1.8088
adult	12p13	10961692	10962767	50835	*TAS2R9*	0.2932	-1.8088
adult	12p13	10977944	10978868	50839	*TAS2R10*	0.2932	-1.8088
adult	12p13	10998447	11002075	11272	*PRR4*	0.2932	-1.8088
adult	12p	10998447	11324224	100533464	*PRH1-PRR4*	0.2932	-1.8317
adult	12p13	11060524	11062161	50838	*TAS2R13*	0.2932	-1.8088
adult	12p13.2	11081834	11087444	5555	*PRH2*	0.2932	-1.8088
adult	12p13	11090852	11091806	50840	*TAS2R14*	0.2932	-1.8088
adult	12p13.2	11138511	11139511	259296	*TAS2R50*	0.2932	-1.8088
adult	12p13.2	11148560	11150474	259295	*TAS2R20*	0.2932	-1.8088
adult	12p13.2	11174217	11175219	259294	*TAS2R19*	0.2932	-2.1407
adult	12p13.2	11182985	11184006	259290	*TAS2R31*	0.2932	-2.1407
adult	12p13.2	11213963	11214893	259292	*TAS2R46*	0.2932	-1.8738
adult	12p13.2	11243885	11244912	259289	*TAS2R43*	0.2932	-1.8738
adult	12p13.2	11285883	11286843	259293	*TAS2R30*	0.2932	-2.1865
adult	12p13	11338598	11339543	353164	*TAS2R42*	0.2932	-2.1865
adult	12p13.2	11418846	11422641	5544	*PRB3*	0.2932	-2.1865
adult	12p13.2	11460014	11463369	5545	*PRB4*	0.2932	-2.1865
adult	12p13.2	11504756	11508524	5542	*PRB1*	0.2932	-2.1865

adult	12p13.2	11544473	11548498	653247	*PRB2*	0.2932	-2.1865
adult	12p13	11802787	12048325	2120	*ETV6*	0.2932	-2.1065
adult	12p13-p12	12223877	12252627	79370	*BCL2L14*	0.2932	-2.3481
adult	12p13.2	12268960	12419811	4040	*LRP6*	0.2932	-2.3811
adult	12p13.2	12482217	12503169	54682	*MANSC1*	0.2932	-2.3811
adult	12p13.2	12508341	12510001	503693	*LOH12CR2*	0.2932	-2.3811
adult	12p12	12510012	12619838	118426	*LOH12CR1*	0.2932	-2.3811
adult	12p13	12626215	12715448	80824	*DUSP16*	0.2932	-2.3811
adult	12p13	12764766	12798042	1389	*CREBL2*	0.2932	-2.3811
adult	12p12.3	12813994	12849121	2842	*GPR19*	0.2932	-2.3811
adult	12p13.1-p12	12870203	12875316	1027	*CDKN1B*	0.2932	-2.3811
adult	12p13.1	12878850	12944399	81575	*APOLD1*	0.2932	-2.3811
adult	12p13.1	12917582	12917677	693198	*MIR613*	0.2932	-2.3811
adult	12p13.1	12966279	12982915	51202	*DDX47*	0.2932	-2.3811
adult	12p13.1	13028410	13029070	387841	*RPL13AP20*	0.2932	-2.3811
adult	12p13.1	13043955	13066600	9052	*GPRC5A*	0.2932	-2.3811
adult	12p13.1	13068762	13068852	693199	*MIR614*	0.2932	-2.3811
adult	12p13.3	13093708	13103318	55507	*GPRC5D*	0.2932	-2.3811
adult	12p13.1	13127798	13153243	50865	*HEBP1*	0.2932	-2.3811
adult	12p13.1	13153375	13157764	93164	*HTR7P1*	0.2932	-2.3811
adult	12p13.1	13197314	13236383	57613	*KIAA1467*	0.2932	-2.3811
adult	12p13.1	13236470	13248740	83445	*GSG1*	0.2932	-2.3811
adult	12p12.3	13349601	13369708	2012	*EMP1*	0.2932	-2.3811
adult	12p12	13714409	14133022	2904	*GRIN2B*	0.2932	-2.3811
adult	12p13.1	14518565	14655869	55729	*ATF7IP*	0.2932	-2.0833
adult	12p13.1	14656596	14720791	79887	*PLBD1*	0.2932	-2.1174
adult	12p12	14765567	14849519	2984	*GUCY2C*	0.2932	-2.1174
adult	12p12.3	14923653	14924065	121504	*HIST4H4*	0.2932	-2.1174
adult	12p12.3	14927269	14930936	55766	*H2AFJ*	0.2932	-2.1174
adult	12p12.3	14939411	14956401	51729	*WBP11*	0.2932	-2.1174
adult	12p12.3	14956505	14976791	144608	*C12orf60*	0.2932	-2.1174
adult	12p12.3	14957583	14967116	440087	*SMCO3*	0.2932	-2.1174
adult	12p13-p12	14982244	14996413	420	*ART4*	0.2932	-2.1174

adult	12p12.3	15034114	15038853	4256	*MGP*	0.2932	-2.1174
adult	12p12.3	15066960	15091483	121506	*ERP27*	0.2932	-2.1174
adult	12p12.3	15094949	15114562	397	*ARHGDIB*	0.2932	-2.1174
adult	12p13	15125955	15134799	5149	*PDE6H*	0.2932	-2.1174
adult	12p12.3	15260715	15374411	85004	*RERG*	0.2932	-2.1174
adult	12p13.3-p13.2	15475190	15751265	5800	*PTPRO*	0.2932	-2.1174
adult	12p12.3	15773074	15942510	2059	*EPS8*	0.2932	-2.1174
adult	12p12.3	16035287	16056410	11171	*STRAP*	0.2932	-1.7948
adult	12p12.3	16064105	16190315	51071	*DERA*	0.2932	-1.7948
adult	12p12.3	16341418	16430619	729025	*SLC15A5*	0.2932	-1.8728
adult	12p12.3-p12.1	16500075	16517344	4257	*MGST1*	0.5126	-1.9508
adult	12p12.3	16701305	16758313	55885	*LMO3*	0.5126	-1.9508
adult	12p12.3	17141680	17143562	728622	*SKP1P2*	0.5126	-1.9508
adult	12p12.3	18233802	18243127	79785	*RERGL*	0.2384	-2.0312
adult	12p12	18414473	18801352	5288	*PIK3C2G*	0.2384	-2.0312
adult	12p12.3	18836109	18890993	89869	*PLCZ1*	0.2384	-2.0312
adult	12p12.3	18891044	18892122	93661	*CAPZA3*	0.2384	-2.0312
adult	12p12	19282625	19354937	54477	*PLEKHA5*	0.2384	-2.0312
adult	12p12.3	19592607	19675173	121536	*AEBP2*	0.2384	-2.0312
adult	12p12	20167618	20251802	100506393	*LOC100506393*	0.2384	-1.6492
adult	12p12	20522178	20837041	5139	*PDE3A*	0.2384	-1.6492
adult	12p12.2	20848288	20906320	53919	*SLCO1C1*	0.2384	-1.6492
adult	12p12	20963637	21069843	28234	*SLCO1B3*	0.2384	-1.6492
adult	12p12.2	21168629	21243040	338821	*SLCO1B7*	0.2384	-1.6492
adult	12p	21284127	21392730	10599	*SLCO1B1*	0.2384	-1.6492
adult	12p12	21417533	21487832	6579	*SLCO1A2*	0.2384	-1.6492
adult	12p12.1	21525801	21532914	3375	*IAPP*	0.2384	-1.6492
adult	12p12.1	21590537	21624182	79912	*PYROXD1*	0.2384	-1.6492
adult	12p12	21621843	21654603	5965	*RECQL*	0.2384	-1.6492
adult	12p12.1	21654698	21671337	51026	*GOLT1B*	0.2384	-1.6492
adult	12p12.2	21689122	21757781	2998	*GYS2*	0.2384	-1.6492
adult	12p12.2-p12.1	21788275	21810728	3945	*LDHB*	0.2384	-1.6492
adult	12p11.23	21917888	21927755	3764	*KCNJ8*	0.4637	-1.5628

adult	12p12.1	21950323	22089628	10060	*ABCC9*	0.4637	-1.5628
adult	12p12.1	22199109	22218606	55907	*CMAS*	0.4637	-1.5628
adult	12p12.1-p11.2	22346324	22487648	6489	*ST8SIA1*	0.4637	-1.5628
adult	12p12.1	22601479	22697480	9847	*C2CD5*	0.4396	-1.5767
adult	12p12.1	22778075	22797349	55500	*ETNK1*	0.4396	-1.5767
adult	12p12.1	23685230	23737546	6660	*SOX5*	0.4396	-1.5767
adult	12p12.1	24365354	24365429	100126320	*MIR920*	0.4396	-1.5767
adult	12p12.1	24719897	24737102	144360	*LINC00477*	0.4396	-1.5767
adult	12p12.1	24962957	25055322	586	*BCAT1*	0.4396	-1.5767
adult	12p12.1	25146364	25150373	196415	*C12orf77*	0.4396	-1.5767
adult	12p12.1	25205180	25261269	4033	*LRMP*	0.4396	-1.5767
adult	12p12.1	25261222	25348094	55259	*CASC1*	0.4396	-1.5767
adult	12p12.1	25348149	25357949	144363	*LYRM5*	0.4396	-1.5767
adult	12p12.1	25357722	25403865	3845	*KRAS*	0.4396	-1.5767
adult	12p12.3	26111963	26225807	11228	*RASSF8*	0.4396	-1.5018
adult	12p12.1	26272958	26278003	79365	*BHLHE41*	0.4396	-1.5018
adult	12p11.2	26348268	26387708	8082	*SSPN*	0.4396	-1.5018
adult	12p11	26488269	26986131	3709	*ITPR2*	0.4396	-1.5018
adult	12p11.23	27058111	27091254	55726	*ASUN*	0.4396	-1.5018
adult	12p11.23	27091304	27113679	26127	*FGFR1OP2*	0.4396	-1.5018
adult	12q11-q12	27124505	27167339	51768	*TM7SF3*	0.4396	-1.5018
adult	12p11.23	27175454	27183606	9412	*MED21*	0.4396	-1.5018
adult	12p11.23	27233989	27235455	728858	*C12orf71*	0.4396	-1.5018
adult	12p11.23	27397077	27478890	23012	*STK38L*	0.4396	-1.5018
adult	12p12.2-p11.2	27485786	27578746	56938	*ARNTL2*	0.4396	-1.5018
adult	12p11.23	27619742	27655118	341346	*SMCO2*	0.4396	-1.5018
adult	12p12.1	27677044	27848497	8496	*PPFIBP1*	0.4396	-1.5018
adult	12p11.22	27849427	27850566	387849	*REP15*	0.4396	-1.5018
adult	12p11	27863705	27909237	60488	*MRPS35*	0.4396	-1.5018
adult	12p11.22	27915598	27924209	100287284	*MANSC4*	0.4396	-1.5018
adult	12p11.22	27933186	27955973	57542	*KLHL42*	0.2253	-1.5018
adult	12p12.1-p11.2	28111016	28122894	5744	*PTHLH*	0.2253	-1.5018
adult	12p11.22	28410132	28703099	55297	*CCDC91*	0.2253	-1.5031

adult	12p11.22	29301935	29488549	55711	*FAR2*	0.2253	-1.5043
adult	12p11.22	29493578	29534143	51290	*ERGIC2*	0.2253	-1.5043
adult	12p	29542226	29617863	101055625	*OVCH1-AS1*	0.27885	-1.4948
adult	12p11.22	29580488	29650619	341350	*OVCH1*	0.3324	-1.4853
adult	12p11.22	29653745	29936743	83857	*TMTC1*	0.30385	-1.4668
adult	12p11.21	30781914	30830178	10526	*IPO8*	0.2753	-1.4135
adult	12p11	30862485	30907448	65981	*CAPRIN2*	0.2753	-1.4135
adult	12p11.21	30948614	30955645	100287314	*LINC00941*	0.2753	-1.4135
adult	12p11.21	31079837	31149537	441631	*TSPAN11*	0.2753	-1.4135
adult	12p11	31226778	31257725	1663	*DDX11*	0.2753	-1.4135
adult	12p11	31433519	31479121	58516	*FAM60A*	0.2753	-1.4135
adult	12p11.21	31477249	31478879	79857	*FLJ13224*	0.2753	-1.4135
adult	12p11.21	31535156	31743952	160518	*DENND5B*	0.2753	-1.4135
adult	12p11.21	31800093	31822016	254013	*METTL20*	0.2753	-1.4135
adult	12p11.21	31824070	31882108	196394	*AMN1*	0.2753	-1.4135
adult	12p11.21	31944118	31945175	440093	*H3F3C*	0.2753	-1.4135
adult	12p11.21	32112352	32146043	55196	*KIAA1551*	0.2449	-1.792
adult	12p11.2-p11.1	32260184	32531141	636	*BICD1*	0.2449	-1.5319
adult	12p11.21	32654976	32798984	121512	*FGD4*	0.2449	-1.5319
adult	12p13	8608590	8630926	93978	*CLEC6A*	0.2932	-1.4639
adult	12p13.31	8666135	8674960	338339	*CLEC4D*	0.2932	-1.4639
adult	12p13.31	8685900	8693558	26253	*CLEC4E*	0.2932	-1.4639
adult	12p13	8754761	8765442	57379	*AICDA*	0.2932	-1.4639
adult	12p13.1-p12.3	8798538	8815484	8076	*MFAP5*	0.2932	-1.4639
adult	12p13.31	8852380	8929787	57494	*RIMKLB*	0.2932	-1.4639
adult	12p13.31	8975067	9029377	144568	*A2ML1*	0.2932	-1.4639
adult	12p13	9067315	9094060	1911	*PHC1*	0.2932	-1.4639
adult	12p13	9092956	9102357	4074	*M6PR*	0.2932	-1.4639
adult	12p13.31	9142220	9163340	10219	*KLRG1*	0.2932	-1.4639
adult	12p13.31	9208184	9217666	253128	*LINC00612*	0.2932	-1.4639
adult	12p13.31	9217772	9220651	144571	*A2M-AS1*	0.2932	-1.4639
adult	12p13.31	9220303	9268558	2	*A2M*	0.2932	-1.4639
adult	12q22	92534053	92539673	694	*BTG1*	0.5185	-1.7676

adult	12p13-p12.2	9301435	9360966	5858	*PZP*	0.2932	-1.4639
adult	12p13.31	9381128	9386803	3	*A2MP1*	0.2932	-1.4639
adult	12p13.31	9436252	9466684	642846	*LOC642846*	0.2932	-1.4639
adult	12p13.31	9570286	9600768	440081	*DDX12P*	0.2932	-1.4639
adult	12p13	9747869	9760497	3820	*KLRB1*	0.2932	-1.5326
adult	12p13.31	9769879	9811010	374443	*LOC374443*	0.2932	-1.5326
adult	12p13	9822303	9852151	29121	*CLEC2D*	0.2932	-1.5326
adult	12p13.31	9868455	9885895	160365	*CLECL1*	0.2932	-1.5326
adult	12p13	9905081	9913497	969	*CD69*	0.2932	-1.5326
adult	12p13.31	9980076	9997603	51348	*KLRF1*	0.2932	-1.5326
adult	13q21.31	64311567	64316701	283491	*OR7E156P*	0.657	-1.3758
adult	13q21.32	66876965	67804468	5101	*PCDH9*	0.657	-1.3758
adult	13q21.33	69435416	69459457	338862	*LINC00550*	0.657	-1.3758
adult	13q31.1	79173229	79177695	5457	*POU4F1*	1.27025	-1.0716
adult	13q31.1	79188420	79233314	79596	*RNF219*	1.7848	-1.319
adult	13q31.1	79893002	79980356	64062	*RBM26*	1.7848	-1.319
adult	13q31.1	80055258	80130212	54602	*NDFIP2*	1.7848	-1.319
adult	13q31.1	80910111	80915086	10253	*SPRY2*	1.7848	-1.319
adult	13q31.1	84451339	84456528	114798	*SLITRK1*	1.8122	-1.363
adult	13q31.1	86366921	86373483	84189	*SLITRK6*	1.8122	-1.363
adult	13q31.2	88096241	88323218	642345	*MIR4500HG*	1.8122	-1.363
adult	13q31.2	88270919	88270995	100616182	*MIR4500*	1.8122	-1.363
adult	13q31.2	88324869	88331870	26050	*SLITRK5*	1.8122	-1.363
adult	13q31.3	90883435	90883531	693207	*MIR622*	1.8112	-0.7462
adult	13q31.3	91543207	91578851	144776	*LINC00410*	1.8112	-0.7462
adult	18q22.1	65173818	65183967	92126	*DSEL*	1.1089	-0.5644
adult	18q22.1	65183782	65566856	643542	*LOC643542*	1.12305	-0.3551
adult	18q22	66340924	66382353	54495	*TMX3*	1.1372	0
adult	18q22.1	66382490	66722426	79839	*CCDC102B*	1.1372	0
adult	21p11	10906186	10990943	7179	*TPTE*	1.5813	-0.2818
adult	21p11.2	11020841	11098925	85318	*BAGE3*	1.5813	-0.2818
adult	21p11.1 not on reference assembly	11057795	11098937	574	*BAGE*	1.5813	-0.2818
adult	21q11.2	14410486	14490571	149992	*ANKRD30BP2*	1.06	-0.2818

adult	21q11.2	14982497	15013906	317754	*POTED*	1.06	-0.2818
adult	21q11.2	15316095	15352765	391267	*ANKRD20A11P*	1.06	-0.2818
adult	21q11.2	15481134	15579270	149998	*LIPI*	1.06	-0.2818
adult	21q11	15588465	15600693	54033	*RBM11*	1.06	-0.2818
adult	21q11.2	15646119	15663706	150000	*ABCC13*	1.06	-0.2818
adult	21q11	15743436	15755509	6782	*HSPA13*	1.06	-0.2818
adult	21q11	15857548	15918681	64092	*SAMSN1*	1.06	-0.2818
adult	21q11.2	15963712	16015428	388813	*LOC388813*	1.06	-0.2818
adult	21q11.2	16333555	16437126	8204	*NRIP1*	1.06	-0.2818
adult	21q11.2	17102343	17252390	29761	*USP25*	1.6741	-0.2818
adult	21q21.1	17911408	17911489	407055	*MIR99A*	1.6741	-0.2818
adult	21q21.1	17912147	17912231	406885	*MIRLET7C*	1.6741	-0.2818
adult	21q21.1	17962556	17962645	406912	*MIR125B2*	1.6741	-0.2818
adult	21q21.1	18885223	18942429	1525	*CXADR*	1.6741	-0.2818
adult	21q21.1	18965967	18985268	10950	*BTG3*	1.6741	-0.2818
adult	21q21.1	19149720	19164826	246312	*C21orf91-OT1*	1.6741	-0.2818
adult	21q21.1	19161283	19191703	54149	*C21orf91*	1.6741	-0.2818
adult	21q21.1	19207988	19257925	54075	*CHODL-AS1*	1.6741	-0.2818
adult	21q11.2	19289656	19639687	140578	*CHODL*	1.742	-0.2818
adult	21q21.1	19641432	19775970	5651	*TMPRSS15*	1.8099	-0.2818
adult	21q21.1	22114907	22175426	387486	*LINC00320*	1.8154	-0.2818
adult	21q21.1	22370632	22912517	4685	*NCAM2*	1.8154	-0.2818
adult	21q21.1	23095612	23109639	378828	*LINC00317*	1.7208	-0.2818
adult	21q21.1	23470935	23488847	54143	*LINC00308*	1.7208	-0.2818
adult	21q21.1-q21.2	26212863	26430056	339622	*LOC339622*	1.6036	0
adult	21q21.3	26758132	26804013	54072	*LINC00158*	1.6036	0
adult	21q21.3	26946291	26946356	406947	*MIR155*	1.6036	0
adult	21q21.3	26955086	26955536	282566	*LINC00515*	1.6036	0
adult	21q21.3	26957967	26979801	54148	*MRPL39*	1.6036	0
adult	21q21.2	27011593	27086885	58494	*JAM2*	1.6036	0
adult	21q21.1	27096790	27107965	522	*ATP5J*	1.6036	0
adult	21q21.3	27107257	27144771	2551	*GABPA*	1.6036	0
adult	21q21.3	27252860	27512708	351	*APP*	1.6036	0

adult	21q21.2	27838527	27945581	116159	*CYYR1*	1.6036	0
adult	21q21.2	28208605	28217728	9510	*ADAMTS1*	1.6036	0
adult	21q21.3	28290230	28339439	11096	*ADAMTS5*	1.6036	0
adult	21q21.3	29094697	29123552	54088	*LINC00113*	1.6036	0
adult	21q21.3	29385681	29395528	246705	*LINC00314*	1.6036	0
adult	21q21.3	29911639	29912677	118421	*LINC00161*	1.6036	0
adult	21q21.3	30248385	30257695	29104	*N6AMT1*	1.6036	0
adult	21q22.11	30300465	30365277	26046	*LTN1*	1.6036	0
adult	21q22.11	30378079	30391685	10069	*RWDD2B*	1.6036	0
adult	21q22.11	30396937	30426807	10600	*USP16*	1.6036	0
adult	21q22.11	30428642	30446118	10694	*CCT8*	1.6036	0
adult	21q22.3	30449791	30548210	56911	*MAP3K7CL*	1.6036	0
adult	21q22.11	30565814	30660526	193629	*LINC00189*	1.6036	0
adult	21q22.11	30671115	30718469	571	*BACH1*	1.6036	0
adult	21q22.11	30909253	31312282	2897	*GRIK1*	1.6036	0
adult	21q22.11	30968359	31003067	100379661	*GRIK1-AS2*	1.6036	0
adult	21q22.11	31120493	31136325	642976	*GRIK1-AS1*	1.6036	0
adult	21q22.11	31538240	31538971	26285	*CLDN17*	1.6036	0
adult	21q22.11	31581468	31584101	266919	*LINC00307*	1.6036	0
adult	21q22.11	31586323	31588469	9073	*CLDN8*	1.6036	0
adult	21q22.11	31653626	31655276	643803	*KRTAP24-1*	1.6036	0
adult	21q22.11	31661462	31661832	100131902	*KRTAP25-1*	1.6036	0
adult	21q22.11	31691449	31692607	388818	*KRTAP26-1*	1.6036	0
adult	21q22.11	31709330	31710012	643812	*KRTAP27-1*	1.6036	0
adult	21q22.1	31720716	31720924	337963	*KRTAP23-1*	1.6036	0
adult	21q22.1	31743708	31744557	337959	*KRTAP13-2*	1.6036	0
adult	21q22.1	31768391	31769138	140258	*KRTAP13-1*	1.6036	0
adult	21q22.1	31797710	31798230	337960	*KRTAP13-3*	1.6036	0
adult	21q22.1	31802593	31803076	284827	*KRTAP13-4*	1.6036	0
adult	21q22.1	31812645	31813098	254950	*KRTAP15-1*	1.6036	0
adult	21q22.1	31852363	31852636	337882	*KRTAP19-1*	1.6036	0
adult	21q22.1	31859508	31859667	337969	*KRTAP19-2*	1.6036	0
adult	21q22.1	31863781	31864275	337970	*KRTAP19-3*	1.6036	0

adult	21q22.1	31869173	31869428	337971	*KRTAP19-4*	1.6036	0
adult	21q22.1	31874189	31874408	337972	*KRTAP19-5*	1.6036	0
adult	21q22.1	31913853	31914183	337973	*KRTAP19-6*	1.6036	0
adult	21q22.1	31933416	31933608	337974	*KRTAP19-7*	1.6036	0
adult	21q22.11	31962423	31962716	100288287	*KRTAP22-2*	1.6036	0
adult	21q22.1	31964758	31965374	337968	*KRTAP6-3*	1.6036	0
adult	21q22.1	31971004	31971193	337967	*KRTAP6-2*	1.6036	0
adult	21q22.1	31973439	31973586	337979	*KRTAP22-1*	1.6036	0
adult	21q22.1	31986004	31986223	337966	*KRTAP6-1*	1.6036	0
adult	21q22.1	31988773	31988944	337975	*KRTAP20-1*	1.6036	0
adult	21q22.11	31992945	31993169	100151643	*KRTAP20-4*	1.6036	0
adult	21q22.1	32007582	32007780	337976	*KRTAP20-2*	1.6036	0
adult	21q22.11	32015182	32015455	337985	*KRTAP20-3*	1.6036	0
adult	21q22.11	32090842	32091095	100288323	*KRTAP21-3*	1.6036	0
adult	21q22.1	32119268	32119520	337978	*KRTAP21-2*	1.6036	0
adult	21q22.1	32127456	32127696	337977	*KRTAP21-1*	1.6036	0
adult	21q22.1	32185014	32185570	337879	*KRTAP8-1*	1.6036	0
adult	21q22.11	32201357	32202051	337878	*KRTAP7-1*	1.6036	0
adult	21q22.1	32252963	32253874	337880	*KRTAP11-1*	1.6036	0
adult	21q22.11	32410477	32410795	728299	*KRTAP19-8*	1.6036	0
adult	21q22.11	32490735	32931290	7074	*TIAM1*	1.6036	0
adult	21q22.11	33031934	33041243	6647	*SOD1*	1.6036	0
adult	21q22.1	33043312	33104431	57466	*SCAF4*	1.6036	0
adult	21q22.1	33245627	33376377	30811	*HUNK*	1.6036	0
adult	21q22.11	33452793	33458608	100551499	*LINC00159*	1.6036	0
adult	21q22.11	33640529	33651376	54069	*MIS18A*	1.6036	0
adult	21q22.1	33664123	33684599	56246	*MRAP*	1.6036	0
adult	21q22.11	33683329	33765312	9875	*URB1*	1.6036	0
adult	21q22.11	33784744	33887710	59271	*EVA1C*	1.6036	0
adult	21q22.1	33973983	33984913	56683	*C21orf59*	1.6036	0
adult	21q22.2	34001068	34100250	8867	*SYNJ1*	1.6036	0
adult	21q21.3	34106209	34144169	94104	*PAXBP1*	1.6036	0
adult	21q22.11	34162983	34186053	56245	*C21orf62*	1.6036	0

adult	21q22.11	34398215	34401503	10215	*OLIG2*	1.4879	0
adult	21q22.11	34442449	34444728	116448	*OLIG1*	1.4879	0
adult	21q22.11	34602199	34635062	3455	*IFNAR2*	1.4879	0
adult	21q22.11	34637936	34638565	100288432	*IL10RB-AS1*	1.4879	0
adult	21q22.11	34638664	34669539	3588	*IL10RB*	1.4879	0
adult	21q22.11	34697213	34732128	3454	*IFNAR1*	1.4879	0
adult	21q22.11	34775201	34809828	3460	*IFNGR2*	1.4879	0
adult	21q22.11	34821447	34852316	757	*TMEM50B*	1.4879	0
adult	21q22.11	34860361	34863790	54943	*DNAJC28*	1.4879	0
adult	21q22.11	34876237	34914464	2618	*GART*	1.4879	0
adult	21q22.11	34915343	34932973	6651	*SON*	1.4879	0
adult	21q22.1	34949858	34961014	29980	*DONSON*	1.4879	0
adult	21q21.3	34961647	35014160	9946	*CRYZL1*	1.4879	0
adult	21q22.1-q22.2	35014783	35210802	6453	*ITSN1*	1.4879	0
adult	21q22.11	35275756	35288158	539	*ATP5O*	1.4879	0
adult	21q22.3	36160097	36421595	861	*RUNX1*	1.09225	0
adult	21q22.12	36410232	36411723	80215	*RUNX1-IT1*	1.1042	0
adult	21q22.12	37093012	37093106	768219	*MIR802*	1.1042	0
adult	21q22.13	37406838	37433116	54093	*SETD4*	1.1042	0
adult	21q22.12	37441939	37498938	100133286	*LOC100133286*	1.1042	0
adult	21q22.13	37442221	37445475	873	*CBR1*	1.1042	0
adult	21q22.2	37507262	37518860	874	*CBR3*	1.1042	0
adult	21q22.2	37536838	37666572	9980	*DOPEY2*	1.1042	0
adult	21q22.13	37692486	37748944	23515	*MORC3*	1.1042	0
adult	21q22.13	37757688	37789125	8208	*CHAF1B*	1.1042	0
adult	21q22.3	37832919	37838739	23562	*CLDN14*	1.1042	0
adult	21q22.13	38071432	38118219	6493	*SIM2*	1.1042	0
adult	21q22.13	38123188	38338956	3141	*HLCS*	1.1042	0
adult	21q22.2	38378862	38391958	53820	*RIPPLY3*	1.1042	0
adult	21q22.2	38437663	38445103	51227	*PIGP*	1.1042	0
adult	21q22.2	38445570	38575408	7267	*TTC3*	1.1042	0
adult	21q22.13	38580803	38594037	257203	*DSCR9*	1.1042	0
adult	21q22.2	38595725	38639833	10311	*DSCR3*	1.1042	0

adult	21q22.13	38739858	38887679	1859	*DYRK1A*	1.1042	0
adult	21q22.1	38996524	39288741	3763	*KCNJ6*	1.1042	0
adult	21q22.2	39426312	39493454	10281	*DSCR4*	1.1042	0
adult	21q22.2	39493544	39528605	84677	*DSCR8*	1.1042	0
adult	21q22.13	39578249	39580738	259234	*DSCR10*	1.1042	0
adult	21q22.2	39601836	39673746	3772	*KCNJ15*	1.1042	0
adult	21q22.3	39739182	40033704	2078	*ERG*	1.1042	0
adult	21q22.2	40110878	40124181	400866	*LINC00114*	1.1042	0
adult	21q22.2	40177230	40196878	2114	*ETS2*	1.1042	0
adult	21q22.3	40547371	40555440	8624	*PSMG1*	1.1042	0
adult	21q22.2	40557403	40685712	54014	*BRWD1*	1.1042	0
adult	21q22.2	40714240	40721047	3150	*HMGN1*	1.1042	0
adult	21q22.3	40752212	40769815	7485	*WRB*	1.1042	0
adult	21q22.2	40777769	40816128	150082	*LCA5L*	1.1042	0
adult	21q22.3	40817796	40887433	6450	*SH3BGR*	1.1042	0
adult	21q22.3	41029246	41034816	10317	*B3GALT5*	1.1042	0
adult	21q22.2	41117333	41174023	150084	*IGSF5*	1.1042	0
adult	21q22.2	41239346	41301322	5121	*PCP4*	1.08065	0
adult	21p11.2	9907188	9968594	100132288	*TEKT4P2*	1.5813	-0.2818
adult	22q11.22	22599191	22599927	7441	*VPREB1*	0.6387	-1.5219
adult	4q32.1	160188997	160281301	9693	*RAPGEF2*	1.1753	-0.667
adult	4q22	89011415	89080011	9429	*ABCG2*	1.1809	-0.2421
adult	4q22.1	89178760	89205983	152926	*PPM1K*	1.1809	-0.2421
adult	4q22.1	89299890	89364249	55008	*HERC6*	1.1809	-0.2421
adult	4q22.1	89378267	89427319	51191	*HERC5*	1.1809	-0.2421
adult	4q	89442128	89444952	100996939	*PYURF*	1.1809	-0.2421
adult	4q22.1	89442128	89444952	84992	*PIGY*	1.1809	-0.2421
adult	4q21	89513573	89629693	8916	*HERC3*	1.1809	-0.2421
adult	4q22.1	89617063	89619386	266812	*NAP1L5*	1.1809	-0.2421
adult	4q22.1	89630939	89651254	285512	*FAM13A-AS1*	1.1809	-0.2421
adult	4q22.1	89647104	89744512	10144	*FAM13A*	1.1809	-0.2421
adult	4q22.1	90033967	90036052	166815	*TIGD2*	1.1809	-0.2421
adult	4q22.1	90165428	90229161	285513	*GPRIN3*	1.1809	-0.2421

adult	4q21	90645249	90758127	6622	*SNCA*	1.1809	-0.2421
adult	4q22	90816051	90875780	22915	*MMRN1*	1.1809	-0.2421
adult	4q22.1	91048683	92523370	401145	*CCSER1*	1.13705	-0.2421
adult	6q16.2	100054649	100063454	59336	*PRDM13*	0.2477	-1.8758
adult	6q16	100367785	100442099	84539	*MCHR2*	0.2477	-1.8758
adult	6q16.3	100836749	100911551	6492	*SIM1*	0.2477	-1.8758
adult	6q16	100956070	101329248	10973	*ASCC3*	0.2477	-1.8758
adult	6q16.3	101846860	102517958	2898	*GRIK2*	0.2477	-1.9288
adult	6q16.3	105175967	105307794	57531	*HACE1*	0.261	-1.9189
adult	6q21	105384168	105388402	100113403	*LINC00577*	0.261	-1.5242
adult	6q21	105404922	105531207	389421	*LIN28B*	0.261	-1.5242
adult	6q21	105544698	105584221	11149	*BVES*	0.261	-1.5242
adult	6q21	105585561	105617819	154442	*BVES-AS1*	0.261	-1.5242
adult	6q21	105605774	105624130	64208	*POPDC3*	0.261	-1.5242
adult	6q22	105725441	105850999	5550	*PREP*	0.261	-1.5242
adult	6q21	106534194	106557814	639	*PRDM1*	0.261	-1.5242
adult	6q21	106632351	106773695	9474	*ATG5*	0.261	-1.5242
adult	6q15	89966839	90025018	2570	*GABRR2*	0.4183	-1.5105
adult	6q15	90036343	90062619	51465	*UBE2J1*	0.4183	-1.5105
adult	6q15	90074334	90121995	58528	*RRAGD*	0.4183	-1.5105
adult	6q15	90142896	90343553	22881	*ANKRD6*	0.4183	-1.5105
adult	6q15	90341942	90348216	57226	*LYRM2*	0.4183	-1.5105
adult	6q15	90352493	90529513	23195	*MDN1*	0.4183	-1.5105
adult	6q15	90539618	90584155	9994	*CASP8AP2*	0.4183	-1.5105
adult	6q15	90604187	90605819	84694	*GJA10*	0.4183	-1.5105
adult	6q15	90636246	91006627	60468	*BACH2*	0.4183	-1.5105
adult	6q15	91223291	91297020	6885	*MAP3K7*	0.6465	-2.0851
adult	6q16.1	93949739	94129300	2045	*EPHA7*	0.6465	-2.0851
adult	6q16.1	94416800	94486199	643432	*TSG1*	0.6465	-2.0851
adult	6q16.1	96025372	96057328	79694	*MANEA*	0.9176	-2.4058
adult	6q16	96463844	96663488	10690	*FUT9*	0.6272	-1.9927
adult	6q16.1	96969701	97003151	23376	*UFL1*	0.6272	-1.9927
adult	6q16.1-q16.3	97010423	97064512	9457	*FHL5*	0.6272	-1.9927

adult	6q16.1-q16.3	97241997	97285353	81491	*GPR63*	0.6272	-1.9927
adult	6q16.1	97337186	97345767	29078	*NDUFAF4*	0.6272	-1.9927
adult	6q16.1	97372495	97588630	114792	*KLHL32*	0.6272	-1.9927
adult	6q16.1	97590036	97731052	253714	*MMS22L*	0.6272	-1.9927
adult	6q16	99282579	99286666	5454	*POU3F2*	0.6272	-1.7924
adult	6q16.1-q16.3	99321600	99395882	26235	*FBXL4*	0.6272	-1.7924
adult	6q16.2	99720792	99797531	84553	*FAXC*	0.6272	-1.7924
adult	6q16.2	99817347	99842082	51805	*COQ3*	0.6272	-1.7924
adult	6q16.3	99847840	99873207	25957	*PNISR*	0.6272	-1.7924
adult	6q16.2	99880183	99963252	85015	*USP45*	0.6272	-1.7924
adult	6q16.2	99968869	99981059	100130890	*TSTD3*	0.6272	-1.7924
adult	6q21	99990262	100016690	892	*CCNC*	0.6272	-1.7924
adult	7q22.1	100026412	100031749	56257	*MEPCE*	0.2794	-2.5063
adult	7q22.1	100032911	100034094	221908	*PPP1R35*	0.2794	-2.5063
adult	7q22.1	100054237	100061894	402573	*C7orf61*	0.2794	-2.5063
adult	7p21-p15	100064141	100076902	81628	*TSC22D4*	0.2794	-2.5063
adult	7q22.1	100081549	100092424	222950	*NYAP1*	0.2794	-2.5063
adult	7q22.1	100136833	100165843	3268	*AGFG2*	0.2794	-2.5063
adult	7q22.1	100169852	100171270	100316904	*SAP25*	0.2794	-2.5063
adult	7q22	100171633	100183811	4034	*LRCH4*	0.2794	-2.5063
adult	7q22	100183955	100198740	26261	*FBXO24*	0.2794	-2.5063
adult	7q22.1	100187023	100201661	100129845	*PCOLCE-AS1*	0.2794	-2.5063
adult	7q22	100199881	100205798	5118	*PCOLCE*	0.2794	-2.5063
adult	7q22	100209724	100213000	64598	*MOSPD3*	0.2794	-2.5063
adult	7q22	100218038	100231273	7036	*TFR2*	0.2794	-2.5063
adult	7q22	100240725	100254084	51412	*ACTL6B*	0.2794	-2.5063
adult	7q22	100271362	100276792	2783	*GNB2*	0.2794	-2.5063
adult	7q22	100277129	100286870	64599	*GIGYF1*	0.2794	-2.5063
adult	7q22	100303675	100305123	10248	*POP7*	0.2794	-2.5063
adult	7q22	100318422	100321323	2056	*EPO*	0.2794	-2.5063
adult	7q22	100331248	100395419	7455	*ZAN*	0.2794	-2.5063
adult	7q22	100400186	100425143	2050	*EPHB4*	0.2794	-2.5063
adult	7p22.3	1004485	1015235	90639	*COX19*	0	-1.8331

adult	7q22	100450340	100463160	56996	*SLC12A9*	0.2794	-2.5063
adult	7q22	100464949	100471076	7205	*TRIP6*	0.2794	-2.5063
adult	7q21	100472700	100486285	51593	*SRRT*	0.2794	-2.5063
adult	7q22.1	100486343	100487339	402682	*UFSP1*	0.2794	-2.5063
adult	7q22	100487614	100493541	43	*ACHE*	0.2794	-2.5063
adult	7q22	100612903	100662230	10071	*MUC12*	0.2794	-2.5063
adult	7q22.1	100663363	100702140	140453	*MUC17*	0.2794	-2.5063
adult	7q22.1	100728719	100735019	81844	*TRIM56*	0.2794	-2.5063
adult	7q22.1	100770369	100782547	5054	*SERPINE1*	0.2794	-2.5063
adult	7q22.1	100797685	100804557	1174	*AP1S1*	0.2794	-2.5063
adult	7q22.1	100805789	100808852	7425	*VGF*	0.2794	-2.5063
adult	7q22.1	100813773	100823557	375607	*NAT16*	0.2794	-2.5063
adult	7q22.1	100839011	100844302	346606	*MOGAT3*	0.2794	-2.5063
adult	7q22	100849257	100861011	8985	*PLOD3*	0.2794	-2.5063
adult	7q22.1	100860984	100867471	10467	*ZNHIT1*	0.2794	-2.5063
adult	7q11.22	100875372	100881227	24146	*CLDN15*	0.2794	-2.5063
adult	7q22.1	100882892	100888371	51024	*FIS1*	0.2794	-2.5063
adult	7q22.1	101006100	101202304	136227	*COL26A1*	0.2794	-2.5063
adult	7q22.1	101256604	101272576	93408	*MYL10*	0.2794	-2.5063
adult	7q22.1	101459183	101901513	1523	*CUX1*	0.2794	-2.5063
adult	7q22	101928352	101962178	10603	*SH2B2*	0.2794	-2.5063
adult	7q22.1	101986191	101996889	729597	*SPDYE6*	0.2794	-2.5063
adult	7q22.1	102073976	102097268	80228	*ORAI2*	0.2794	-2.5063
adult	7q22.1	102096666	102105321	54784	*ALKBH4*	0.2794	-2.5063
adult	7q22.1	102105329	102113615	222229	*LRWD1*	0.2794	-2.5063
adult	7q22.1	102113547	102119381	5439	*POLR2J*	0.2794	-2.5063
adult	7q22.1	102178365	102213068	548644	*POLR2J3*	0.2794	-2.5063
adult	7q22.1	102191678	102202757	100310812	*SPDYE2B*	0.2794	-2.5063
adult	7q22.1	102277194	102312176	246721	*POLR2J2*	0.2794	-2.5063
adult	7p22.3	1022834	1029276	54905	*CYP2W1*	0	-1.8331
adult	7q22.1	102389398	102449672	222234	*FAM185A*	0.2794	-2.5063
adult	7q22.1	102453307	102715015	222235	*FBXL13*	0.2794	-2.5063
adult	7q22.1	102553343	102585556	10234	*LRRC17*	0.2794	-2.5063

adult	7q22.1	102715327	102740210	83787	*ARMC10*	0.2794	-2.5063
adult	7q22.1	102740022	102789569	222236	*NAPEPLD*	0.2794	-2.5063
adult	7q22.1	102781716	102782850	100129424	*RPL19P12*	0.2794	-2.5063
adult	7q22.1	102815461	102920759	349152	*DPY19L2P2*	0.2794	-2.5063
adult	7q22.1	102937872	102955133	9512	*PMPCB*	0.2794	-2.5063
adult	7q22	102952920	102985320	27000	*DNAJC2*	0.2794	-2.5063
adult	7q22.1-q22.3	102987970	103002914	5701	*PSMC2*	0.2794	-2.5063
adult	7q22.1	102993176	103086624	375611	*SLC26A5*	0.2794	-2.5063
adult	7q22	103112230	103629963	5649	*RELN*	0.2794	-2.5063
adult	7p22.3	1036622	1177893	84310	*C7orf50*	0	-1.8331
adult	7q22.1	103766787	103848495	5001	*ORC5*	0.2794	-2.5063
adult	7q22.2	103969103	104549003	375612	*LHFPL3*	0.2794	-2.5063
adult	7q22.1	104436953	104444539	645591	*LHFPL3-AS1*	0.2794	-2.5063
adult	7q22.1	104654636	104754532	55904	*KMT2E*	0.2794	-2.5063
adult	7q22-q31.1	104756820	104909524	6733	*SRPK2*	0.2794	-2.5063
adult	7q22.3	105096959	105162685	54517	*PUS7*	0.2794	-2.5063
adult	7q22.3	105172531	105208124	60561	*RINT1*	0.2794	-2.5063
adult	7q22.3	105205579	105221976	100130771	*EFCAB10*	0.2794	-2.5063
adult	7q22.3	105245220	105319609	222255	*ATXN7L1*	0.2794	-2.5063
adult	7q22.3	105603656	105676877	222256	*CDHR3*	0.2794	-2.5063
adult	7q22.3	105730813	105752791	6856	*SYPL1*	0.2794	-2.5063
adult	7q22.3	105888731	105925638	10135	*NAMPT*	0.2794	-2.5063
adult	7p22.3	1062568	1062662	442907	*MIR339*	0	-1.8331
adult	7q22.3	106297210	106301634	168455	*CCDC71L*	0.2794	-2.5063
adult	7q22.3	106505923	106549423	5294	*PIK3CG*	0.2794	-2.5063
adult	7q22	106685177	106802256	5577	*PRKAR2B*	0.2794	-2.5063
adult	7q22.3	106809405	106842974	26959	*HBP1*	0.2794	-2.5063
adult	7q31	106842188	107204959	10466	*COG5*	0.2794	-2.5063
adult	7q22-q31.1	107110501	107116125	2845	*GPR22*	0.2794	-2.5063
adult	7q22-q31	107204401	107218968	11062	*DUS4L*	0.2794	-2.5063
adult	7q22.3	107220421	107263762	55973	*BCAP29*	0.2794	-2.5063
adult	7q22.3	107296960	107302243	286002	*SLC26A4-AS1*	0.2794	-2.5063
adult	7q31	107301079	107358252	5172	*SLC26A4*	0.2794	-2.5063

adult	7q22.3	107384141	107402112	79872	*CBLL1*	0.2794	-2.5063
adult	7q31	107405911	107443678	1811	*SLC26A3*	0.2794	-2.5063
adult	7q31-q32	107531551	107561643	1738	*DLD*	0.2794	-2.5063
adult	7q22	107564245	107643804	3912	*LAMB1*	0.2794	-2.5063
adult	7q31	107663995	107770801	22798	*LAMB4*	0.2794	-2.5063
adult	7q31	107788070	107880614	4897	*NRCAM*	0.2794	-2.5063
adult	7q31	108110865	108166762	50640	*PNPLA8*	0.2794	-2.5063
adult	7q31.1	108202587	108209897	168451	*THAP5*	0.2794	-2.5063
adult	7q31	108210188	108215294	4189	*DNAJB9*	0.2794	-2.5063
adult	7q31.1	108524031	108524644	154907	*C7orf66*	0.2794	-2.5247
adult	7p22.3	1094910	1098905	115330	*GPR146*	0	-1.8331
adult	7q31.1	109599283	109600270	442720	*EIF3IP1*	0.5528	-2.6228
adult	7p21.3	10971579	10979813	4697	*NDUFA4*	0.2466	-2.947
adult	7p21.3	11013498	11147376	9678	*PHF14*	0.2466	-2.947
adult	7q31	110303105	111202347	83943	*IMMP2L*	0.2734	-2.6228
adult	7q31.1	110731061	110765509	54674	*LRRN3*	0.2734	-2.6228
adult	7q31.1	111366163	111846462	9732	*DOCK4*	0.2734	-2.6228
adult	7q31.1	111846642	111983989	11179	*ZNF277*	0.2734	-2.6228
adult	7q31.1	112063198	112117258	3475	*IFRD1*	0.2734	-2.6228
adult	7q31.1	112120907	112130943	286006	*LSMEM1*	0.2734	-2.6228
adult	7q31.32	112402436	112430478	64418	*TMEM168*	0.2734	-2.6228
adult	7q31.1	112459201	112579932	154743	*C7orf60*	0.2734	-2.6228
adult	7q31	112720467	112726393	54329	*GPR85*	0.2734	-2.6228
adult	7q31.1	113516881	113559082	5506	*PPP1R3A*	0.2734	-2.6228
adult	7q31	113726364	114333827	93986	*FOXP2*	0.2734	-2.678
adult	7p21.3	11410061	11871824	221981	*THSD7A*	0.2162	-2.947
adult	7q31.1-q31.2	114562208	114563720	29969	*MDFIC*	0.2734	-2.7331
adult	7q31.2	115575201	115608367	22797	*TFEC*	0.2734	-2.7331
adult	7q31.2	115850546	115898837	26136	*TES*	0.2734	-2.7331
adult	7q31.1	116139654	116148595	858	*CAV2*	0.2734	-2.6812
adult	7q31.1	116164838	116201239	857	*CAV1*	0.2734	-2.6812
adult	7q31	116312458	116438440	4233	*MET*	0.2734	-2.6812
adult	7q31.2-q31.3	116502562	116559313	830	*CAPZA2*	0.2734	-2.6812

adult	7q31.2	116592500	116594388	93653	*ST7-AS1*	0.2734	-2.6812
adult	7q31.2	116593380	116863961	7982	*ST7*	0.2734	-2.6812
adult	7q31.2	116593952	116599867	338069	*ST7-OT4*	0.2734	-2.6812
adult	7q31.2	116752345	116785646	93654	*ST7-AS2*	0.2734	-2.6812
adult	7q31.3	116822734	116849991	93655	*ST7-OT3*	0.2734	-2.6812
adult	7q31.2	116916685	116963343	7472	*WNT2*	0.2734	-2.6812
adult	7q31.2	117003275	117067577	136991	*ASZ1*	0.2734	-2.6812
adult	7q31.2	117120016	117308718	1080	*CFTR*	0.2734	-2.6296
adult	7q31	117350705	117513561	83992	*CTTNBP2*	0.2734	-2.5779
adult	17p13.1	117824085	117844093	84316	*NAA38*	0.2734	-2.5779
adult	7q31	117864711	117882784	56311	*ANKRD7*	0.2734	-2.5779
adult	7p22.3	1192542	1199855	90637	*ZFAND2A*	0	-1.8331
adult	7q31	119913721	120390387	3751	*KCND2*	0.2734	-2.7668
adult	7q31.31	120427373	120498177	23554	*TSPAN12*	0.2734	-2.7668
adult	7q31	120590816	120597034	54556	*ING3*	0.2734	-2.7668
adult	7q31.31	120628750	120937498	79974	*CPED1*	0.2734	-2.7668
adult	7q31	120965420	120981158	51384	*WNT16*	0.2734	-2.7668
adult	7q31	120988904	121036422	10447	*FAM3C*	0.2734	-2.7668
adult	7q31.3	121513158	121702090	5803	*PTPRZ1*	0.2734	-2.7668
adult	7q31.3	121713597	121784344	10157	*AASS*	0.2734	-2.7668
adult	7q31.32	121941362	121944565	389549	*FEZF1*	0.2734	-2.7668
adult	7q31.32	121943711	121950131	154860	*FEZF1-AS1*	0.2734	-2.7668
adult	7q31.3	121958477	122526813	93664	*CADPS2*	0.2734	-2.7668
adult	7q31.32	122337765	122339208	168433	*RNF133*	0.2734	-2.7668
adult	7q31.33	122341719	122343021	378925	*RNF148*	0.2734	-2.7668
adult	7p21.3	12250847	12276890	54664	*TMEM106B*	0	-3.0829
adult	7q31.1-q31.3	122634758	122635754	50833	*TAS2R16*	0.2734	-2.7668
adult	7q31.32	122753587	122840025	6561	*SLC13A1*	0.2734	-2.7668
adult	7q31.32	123092235	123174718	154865	*IQUB*	0.2734	-2.7668
adult	7q31.33	123177051	123197958	4698	*NDUFA5*	0.2734	-2.7668
adult	7q31.31	123249076	123277934	142685	*ASB15*	0.2734	-2.7668
adult	7q31.32	123295860	123304147	442721	*LMOD2*	0.2734	-2.7668
adult	7q31.3	123321980	123389125	8976	*WASL*	0.2734	-2.7668

adult	7q31.3	123454192	123459484	26062	*HYALP1*	0.2734	-2.7668
adult	7q31.3	123485222	123517531	23553	*HYAL4*	0.2734	-2.7668
adult	7q31.3	123565285	123600100	6677	*SPAM1*	0.2734	-2.7668
adult	7q31.32	123670969	123673523	730130	*TMEM229A*	0.2734	-2.7668
adult	7p21.3	12370508	12443852	221806	*VWDE*	0	-3.0856
adult	7q31	124385654	124406079	2861	*GPR37*	0.2734	-2.7668
adult	7q31.33	124417345	124430864	154872	*LOC154872*	0.2734	-2.7668
adult	7q31.33	124462439	124570037	25913	*POT1*	0.2734	-2.7668
adult	7q31.3-q32.1	126078651	126883569	2918	*GRM8*	0.5373	-2.5166
adult	7p21.3	12610202	12693228	85477	*SCIN*	0	-3.3629
adult	7q31.33	126698141	126698238	693177	*MIR592*	0.5373	-2.8215
adult	7q31.33	127010096	127032778	168850	*ZNF800*	0.5373	-2.8215
adult	7q32.1	127220681	127225654	79571	*GCC1*	0.3008	-2.3982
adult	7q31.3	127228405	127231759	381	*ARF5*	0.3008	-2.3982
adult	7q31.3	127233688	127241851	29999	*FSCN3*	0.3008	-2.3982
adult	7q32	127250345	127255780	5078	*PAX4*	0.3008	-2.3982
adult	7p21.3	12726451	12730558	10124	*ARL4A*	0	-3.3629
adult	7p22.3	1272653	1276613	340260	*UNCX*	0	-1.8331
adult	7q31.3	127292201	127732659	27044	*SND1*	0.3008	-2.3982
adult	7q31	127637561	127640130	27099	*SND1-IT1*	0.3008	-2.3982
adult	7q31.3	127667123	127671002	64101	*LRRC4*	0.3008	-2.3982
adult	7q32.1	127721912	127722012	693178	*MIR593*	0.3008	-2.3982
adult	7q32.1	127847924	127847996	406917	*MIR129-1*	0.3008	-2.3982
adult	7q31.3	127881330	127897682	3952	*LEP*	0.3008	-2.3982
adult	7q32.1	127937737	127947816	157247	*MGC27345*	0.3008	-2.3982
adult	7q32.1	127950435	127983962	55131	*RBM28*	0.3008	-2.3982
adult	7q32.1	127990378	128001739	401399	*PRRT4*	0.3008	-2.3982
adult	7q31.3-q32	128032330	128046024	3614	*IMPDH1*	0.3008	-2.3982
adult	7q32.1	128095883	128098472	29923	*HILPDA*	0.3008	-2.3982
adult	7q32.1	128116782	128142978	55798	*METTL2B*	0.3008	-2.3982
adult	7q32.1	128312319	128327926	346653	*FAM71F2*	0.3008	-2.3982
adult	7q32.1	128355395	128371797	84691	*FAM71F1*	0.3008	-2.3982
adult	7q32.1	128379345	128413477	813	*CALU*	0.3008	-2.3982

adult	7q32.1	128412542	128415844	611	*OPN1SW*	0.3008	-2.3982
adult	7q33	128431463	128462187	64753	*CCDC136*	0.3008	-2.3982
adult	7q32-q35	128470482	128499328	2318	*FLNC*	0.3008	-2.3982
adult	7q32	128502856	128505903	9296	*ATP6V1F*	0.3008	-2.3982
adult	7q32.1	128506463	128512101	100130705	*LOC100130705*	0.3008	-2.3982
adult	7q32.1	128516918	128550773	375616	*KCP*	0.3008	-2.3982
adult	7q32	128577990	128590096	3663	*IRF5*	0.3008	-2.3982
adult	7q32.1	128594233	128695227	23534	*TNPO3*	0.3008	-2.3982
adult	7q32.1	128695276	128697293	286016	*TPI1P2*	0.3008	-2.3982
adult	7q32.3	128766324	128768050	407835	*LOC407835*	0.3008	-2.3982
adult	7q32.1	128784711	128809535	340348	*TSPAN33*	0.3008	-2.3982
adult	7q32.3	128828712	128853385	6608	*SMO*	0.3008	-2.3982
adult	7q32.1	128864854	129070052	23382	*AHCYL2*	0.3008	-2.3982
adult	7q32.1	129074273	129123475	57464	*STRIP2*	0.3008	-2.3982
adult	7q32.1	129142319	129152773	100287482	*SMKR1*	0.3008	-2.3982
adult	7q32	129251542	129396922	4899	*NRF1*	0.3008	-2.3982
adult	7q32.2	129410222	129410332	406958	*MIR182*	0.3008	-2.3982
adult	7q32.2	129414532	129414609	407053	*MIR96*	0.3008	-2.3982
adult	7q32.2	129414744	129414854	406959	*MIR183*	0.3008	-2.3982
adult	7q32	129470572	129592783	7328	*UBE2H*	0.3008	-2.3982
adult	7q32.2	129658125	129691291	51530	*ZC3HC1*	0.3008	-2.3982
adult	7q32.2	129710348	129775560	23008	*KLHDC10*	0.3008	-2.3982
adult	7q32.2	129804554	129845338	84928	*TMEM209*	0.3008	-2.3982
adult	7q32.2	129847703	129856684	136263	*SSMEM1*	0.3008	-2.3982
adult	7q32	129906702	129929637	1358	*CPA2*	0.3008	-2.3982
adult	7q32	129932973	129964020	51200	*CPA4*	0.3008	-2.3982
adult	7q32	129984629	130008569	93979	*CPA5*	0.3008	-2.3982
adult	7q32	130020211	130027949	1357	*CPA1*	0.3008	-2.3982
adult	7q32	130033611	130081051	95681	*CEP41*	0.3008	-2.3982
adult	7q32	130126015	130146138	4232	*MEST*	0.3008	-2.3982
adult	7q32.2	130126897	130131013	317751	*MESTIT1*	0.3008	-2.3982
adult	7q32.2	130135951	130136045	442904	*MIR335*	0.3008	-2.3982
adult	7q32	130146079	130353598	26958	*COPG2*	0.3008	-2.3982

adult	7q32	130353485	130371406	114960	*TSGA13*	0.3008	-2.3982
adult	7q32.3	130417381	130418860	136259	*KLF14*	0.3008	-2.3982
adult	7q32.3	130561505	130561569	407021	*MIR29A*	0.3008	-2.3982
adult	7q32.3	130562217	130562298	407024	*MIR29B1*	0.3008	-2.3982
adult	7q32	130794854	131181398	4289	*MKLN1*	0.3008	-2.3982
adult	7q32-q33	131185020	131241376	5420	*PODXL*	0.3008	-2.3982
adult	7q32.3	131808090	132261323	91584	*PLXNA4*	0.3008	-2.3982
adult	7q32.3	132333552	132413528	286023	*FLJ40288*	0.5034	-2.3982
adult	7q33	132469622	132766918	54927	*CHCHD3*	0.5034	-2.3982
adult	7q31	132937822	133168946	60412	*EXOC4*	0.5034	-2.3982
adult	7q33	133812104	133948933	136332	*LRGUK*	0.5034	-2.4144
adult	7q33	133974089	134001827	84912	*SLC35B4*	0.5034	-2.4144
adult	7q35	134127106	134143888	231	*AKR1B1*	0.5034	-2.4144
adult	7q33	134212343	134226166	57016	*AKR1B10*	0.5034	-2.4144
adult	7q33	134233848	134264592	441282	*AKR1B15*	0.5034	-2.4144
adult	7q33	134331530	134364567	669	*BPGM*	0.5034	-2.4144
adult	7q33	134464163	134655480	800	*CALD1*	0.5034	-2.4144
adult	7q33	134671258	134820530	340351	*AGBL3*	0.5034	-2.4144
adult	7q33	134832765	134850967	55281	*TMEM140*	0.5034	-2.4144
adult	7q33	134850531	134854226	78996	*C7orf49*	0.5034	-2.4144
adult	7q33	134868589	134896316	29062	*WDR91*	0.5034	-2.4144
adult	7q33	134916730	134943244	346673	*STRA8*	0.5034	-2.4144
adult	7q33	135046546	135194875	4850	*CNOT4*	0.5034	-2.4286
adult	7q33	135242661	135333499	23165	*NUP205*	0.5034	-2.4428
adult	7q33	135347220	135361160	647087	*C7orf73*	0.5034	-2.4428
adult	7q33	135365986	135412933	26266	*SLC13A4*	0.5034	-2.4428
adult	7q33	135414345	135433594	389558	*FAM180A*	0.5034	-2.4428
adult	7q33	135611502	135662204	767558	*LUZP6*	0.5034	-2.4428
adult	7q31-q35	136553398	136701771	1129	*CHRM2*	0.5034	-2.4428
adult	7q34	136583519	136849088	349160	*LOC349160*	0.5034	-2.4428
adult	7q33	136587913	136588041	574443	*MIR490*	0.5034	-2.4428
adult	7q33	136912091	137028546	5764	*PTN*	0.5034	-2.4428
adult	7q32.3-q33	137074384	137531609	9162	*DGKI*	0.5034	-2.4428

adult	7q34	137559724	137686847	64764	*CREB3L2*	0.5034	-2.4428
adult	7q33	137638093	137642712	100130880	*LOC100130880*	0.5034	-2.4428
adult	7q32-q33	137761177	137803050	6718	*AKR1D1*	0.5034	-2.4428
adult	7q32-q34	138145078	138270332	8805	*TRIM24*	0.5034	-2.4428
adult	7q34	138279029	138348969	136306	*SVOPL*	0.5034	-2.4428
adult	7q34	138391038	138458782	50617	*ATP6V0A4*	0.5034	-2.4428
adult	7q34	138482738	138490769	155006	*TMEM213*	0.5034	-2.4428
adult	7q34	138516126	138666064	57670	*KIAA1549*	0.5034	-2.4428
adult	7q34	138710451	138720775	92092	*ZC3HAV1L*	0.5034	-2.4428
adult	7q34	138728265	138794465	56829	*ZC3HAV1*	0.5034	-2.4428
adult	7q34	138818489	138876732	79989	*TTC26*	0.5034	-2.4428
adult	7q34	138916230	138992982	254048	*UBN2*	0.5034	-2.4428
adult	7q34	139025104	139108203	51631	*LUC7L2*	0.5034	-2.4428
adult	7q34	139025877	139031065	154791	*C7orf55*	0.5034	-2.4428
adult	7q	139025877	139108203	100996928	*C7orf55-LUC7L2*	0.5034	-2.4428
adult	7q34	139102208	139112272	100129148	*LOC100129148*	0.5034	-2.4428
adult	7q34	139138087	139168457	346689	*KLRG2*	0.5034	-2.4428
adult	7q34	139208673	139229731	154790	*CLEC2L*	0.5034	-2.4428
adult	7q34	139246315	139477693	28996	*HIPK2*	0.5034	-2.4428
adult	7p21.3	13930855	14026139	2115	*ETV1*	0	-3.5222
adult	7q34-q35	139478046	139720125	6916	*TBXAS1*	0.5034	-2.4428
adult	7q34	139723543	139763521	64761	*PARP12*	0.5034	-2.4428
adult	7q34	140033551	140098350	84255	*SLC37A3*	0.5034	-2.4428
adult	7q34	140103842	140126050	401409	*RAB19*	0.5034	-2.4428
adult	7q34	140152839	140179369	23608	*MKRN1*	0.5034	-2.4428
adult	7q34	140218219	140302342	27147	*DENND2A*	0.5034	-2.4428
adult	7q34	140372952	140394908	90956	*ADCK2*	0.5034	-2.4428
adult	7q34	140395135	140396877	100134713	*NDUFB2-AS1*	0.5034	-2.4428
adult	7q34	140396480	140406446	4708	*NDUFB2*	0.5034	-2.4428
adult	7q34	140433812	140624564	673	*BRAF*	0.5034	-2.4428
adult	7q34	140705960	140714479	51650	*MRPS33*	0.5034	-2.4428
adult	7q34	140774031	141180179	100507421	*TMEM178B*	0.5034	-2.4428
adult	7q34	141251077	141354209	55750	*AGK*	0.5034	-2.4428

adult	7q34	141356527	141401953	57189	*KIAA1147*	0.5034	-2.4428
adult	7q34	141404137	141438030	285962	*WEE2-AS1*	0.5034	-2.4428
adult	7q32	141408152	141431071	494551	*WEE2*	0.5034	-2.4428
adult	7q34	141438120	141450288	6742	*SSBP1*	0.5034	-2.4428
adult	7q31.3-q32	141463896	141464997	50831	*TAS2R3*	0.5034	-2.4428
adult	7q31.3-q32	141478288	141479188	50832	*TAS2R4*	0.5034	-2.4428
adult	7q31.3-q32	141490016	141491166	54429	*TAS2R5*	0.5034	-2.4428
adult	7q34	141536077	141541221	136242	*PRSS37*	0.5034	-2.4428
adult	7q34	141618675	141619620	130075	*OR9A4*	0.5034	-2.4428
adult	7q33	141627156	141646783	23601	*CLEC5A*	0.5034	-2.4428
adult	7q34	141672430	141673573	5726	*TAS2R38*	0.5034	-2.4428
adult	7q34	141695678	141806547	8972	*MGAM*	0.5034	-2.3783
adult	7p21.2	14184673	14881075	1607	*DGKB*	0	-3.5081
adult	7q34	141940555	141946886	100289017	*MOXD2P*	0.5034	-2.3138
adult	7q34	141951957	141957878	136541	*PRSS58*	0.5034	-2.3138
adult	7q34	142374130	142375525	100463482	*MTRNR2L6*	0.3008	-2.3138
adult	7q34	142457318	142460927	5644	*PRSS1*	0.3008	-1.6321
adult	7q33-q35	142560513	142568847	2051	*EPHB6*	0.3008	-2.1912
adult	7q34	142568955	142583490	55503	*TRPV6*	0.3008	-2.1912
adult	7q35	142605266	142630820	56302	*TRPV5*	0.3008	-2.1912
adult	7q34	142636602	142637957	135927	*C7orf34*	0.3008	-2.1912
adult	7q33	142638200	142659503	3792	*KEL*	0.3008	-2.1912
adult	7q34	142723286	142724219	135924	*OR9A2*	0.3008	-2.1912
adult	7q34	142749437	142750379	346517	*OR6V1*	0.3008	-2.1912
adult	7q34	142759380	142760882	89883	*OR6W1P*	0.3008	-2.1912
adult	7q34	142829173	142836834	5304	*PIP*	0.3008	-2.1912
adult	7q34	142880511	142881528	259285	*TAS2R39*	0.3008	-2.1912
adult	7q34	142919171	142920143	259286	*TAS2R40*	0.3008	-2.1912
adult	7q34	142960521	142966222	373156	*GSTK1*	0.3008	-2.1912
adult	7q34	142981991	142985142	135932	*TMEM139*	0.3008	-2.1912
adult	7q34-q35	142985307	143004789	835	*CASP2*	0.3008	-2.1912
adult	7q35	143013218	143049097	1180	*CLCN1*	0.3008	-2.1912
adult	7q34	143050492	143059173	9715	*FAM131B*	0.3008	-2.1912

adult	7q32	143078359	143088206	7791	*ZYX*	0.3008	-2.1912
adult	7q34	143088204	143105985	2041	*EPHA1*	0.3008	-2.1912
adult	7q35	143104905	143220540	285965	*EPHA1-AS1*	0.3008	-2.1912
adult	7q35	143140545	143141502	338398	*TAS2R60*	0.3008	-2.1912
adult	7q35	143174965	143175889	259287	*TAS2R41*	0.3008	-2.1912
adult	7q35	143268893	143271480	441294	*CTAGE15*	0.3008	-2.1912
adult	7q35	143452181	143454843	340307	*CTAGE6*	0.3008	-1.929
adult	7q35	143509060	143533810	154761	*LOC154761*	0.3008	-1.929
adult	7q35	143632325	143633279	135948	*OR2F2*	0.3008	-2.1747
adult	7q35	143657019	143658108	26211	*OR2F1*	0.3008	-2.1747
adult	7q35	143701089	143702025	135946	*OR6B1*	0.3008	-2.1747
adult	7q35	143747494	143748430	393046	*OR2A5*	0	-2.1331
adult	7q35	143771312	143772245	392138	*OR2A25*	0	-2.1331
adult	7q35	143792200	143793133	346525	*OR2A12*	0	-2.1331
adult	7q35	143806675	143807632	442361	*OR2A2*	0	-2.1331
adult	7q35	143826205	143827138	135941	*OR2A14*	0	-2.1331
adult	7q35	143880547	143883173	100128553	*CTAGE4*	0	-2.1331
adult	7q35	143883175	143892791	445328	*ARHGEF35*	0	-2.1331
adult	7q35	143929003	143929936	346528	*OR2A1*	0.3858	-2.1331
adult	7q35	143947563	143948548	441295	*OR2A9P*	0.3858	-2.1331
adult	7q35	143955788	143956721	401427	*OR2A7*	0.3858	-2.1331
adult	7q35	143956088	143983096	728377	*ARHGEF34P*	0.3858	-2.1331
adult	7q35	144052488	144077725	7984	*ARHGEF5*	0.3858	-2.2606
adult	7q35	144094332	144107320	135935	*NOBOX*	0.3858	-2.2606
adult	7q34-q35	144149033	144533146	27010	*TPK1*	0.3858	-2.2606
adult	7q35	145813452	148118088	26047	*CNTNAP2*	0.3858	-2.2722
adult	7q35	147075108	147075213	100313895	*MIR548F4*	0.2999	-2.5048
adult	7p22.3	1473994	1499109	79778	*MICALL2*	0	-2.055
adult	7q36.1	148287656	148312952	202865	*C7orf33*	0.3385	-1.8463
adult	7q36.1	148395932	148498202	8454	*CUL1*	0.3385	-1.7713
adult	7q35-q36	148504463	148580601	2146	*EZH2*	0.3385	-1.6963
adult	7q35	148700153	148725782	9601	*PDIA4*	0.3385	-1.6963
adult	7q36.1	148766732	148787869	136051	*ZNF786*	0.3385	-1.3896

adult	7q36.1	148799877	148823438	155054	*ZNF425*	0.3385	-1.3896
adult	7q36.1	148823507	148880118	57541	*ZNF398*	0.3385	-1.3896
adult	7q36.1	148892553	148923339	8427	*ZNF282*	0.3385	-1.3896
adult	7q36.1	148936741	148952700	7988	*ZNF212*	0.3385	-1.3896
adult	7q36.1	148982371	148994403	155060	*LOC155060*	0.3385	-1.3896
adult	7q36.1	149128453	149158053	27153	*ZNF777*	0.3385	-1.3896
adult	7q36.1	149169883	149194898	155061	*ZNF746*	0.3385	-1.3896
adult	7q36	149412101	149431664	84626	*KRBA1*	0.3385	-1.3896
adult	7q36.1	149461452	149470295	168544	*ZNF467*	0.3385	-1.3896
adult	7q36.1	149473130	149531053	23145	*SSPO*	0.3385	-1.3896
adult	7q36.1	149535508	149564568	643641	*ZNF862*	0.3385	-1.3896
adult	7q36.1	149564782	149570951	401431	*ATP6V0E2-AS1*	0.3385	-1.3896
adult	7q36.1	149570056	149577801	155066	*ATP6V0E2*	0.3385	-1.3896
adult	7q36.1	149944300	150020758	653857	*ACTR3C*	0.3385	-1.3896
adult	7q36.1	150020295	150035245	65999	*LRRC61*	0.3385	-1.3896
adult	7q36.1	150026937	150029811	113763	*ZBED6CL*	0.3385	-1.3896
adult	7q36.1	150035406	150038763	5919	*RARRES2*	0.3385	-1.3896
adult	7q36.1	150065878	150071133	29803	*REPIN1*	0.3385	-1.3896
adult	7q36.1	150076405	150095719	285971	*ZNF775*	0.3385	-1.3896
adult	7q36.1	150102839	150109558	728743	*LOC728743*	0.3385	-1.3896
adult	7q36.1	150147717	150176483	155038	*GIMAP8*	0.3385	-1.3896
adult	7q36.1	150211944	150218161	168537	*GIMAP7*	0.3385	-1.3896
adult	7q36.1	150264457	150271041	55303	*GIMAP4*	0.3385	-1.3896
adult	7q36.1	150382793	150390728	26157	*GIMAP2*	0.3385	-1.3896
adult	7q36.1	150413644	150421368	170575	*GIMAP1*	0.3385	-1.3896
adult	7q	150413644	150440737	100527949	*GIMAP1-GIMAP5*	0.3385	-1.3896
adult	7q36.1	150434435	150440737	55340	*GIMAP5*	0.3385	-1.3896
adult	7q36.1	150488375	150497621	28959	*TMEM176B*	0.3385	-1.3896
adult	7q36.1	150497853	150502208	55365	*TMEM176A*	0.3385	-1.3896
adult	7p22.3	1509912	1544018	26173	*INTS1*	0	-2.055
adult	7q36.1	151832009	152133090	58508	*KMT2C*	0.3385	-1.3225
adult	7p21.2	15239942	15601640	392636	*AGMO*	0	-3.4939
adult	7q36.2	153584181	154686000	1804	*DPP6*	0.30765	-1.6464

adult	7q36	154735399	154794682	22976	*PAXIP1*	0.2768	-1.5379
adult	7q36.1	154862033	154879102	3361	*HTR5A*	0.2768	-1.5379
adult	7q36	155089485	155101945	3638	*INSIG1*	0.2768	-1.5379
adult	7q36	155250823	155257526	2020	*EN2*	0.2768	-1.5379
adult	7q36.3	155293952	155326539	285888	*CNPY1*	0.2768	-1.5379
adult	7q36.3	155437202	155574179	155435	*RBM33*	0.2768	-1.5379
adult	7q36	155594933	155604967	6469	*SHH*	0.2768	-1.5379
adult	7q36.3	156230482	156238282	285889	*LOC285889*	0.2768	-1.5379
adult	7q36	156333184	156333795	64433	*LINC00244*	0.2768	-1.5379
adult	7q36.3	156431059	156433348	129790	*C7orf13*	0.2768	-1.5379
adult	7q36	156433352	156469820	140545	*RNF32*	0.2768	-1.5379
adult	7q36	156473569	156685902	64327	*LMBR1*	0.2768	-1.5379
adult	7p22.1-p21.3	15650836	15726308	4223	*MEOX2*	0	-3.4831
adult	7q36.3	156742416	156765876	64434	*NOM1*	0.2768	-1.5379
adult	7q36	156797546	156802129	3110	*MNX1*	0.2768	-1.5379
adult	7q36.3	156931654	157062066	9690	*UBE3C*	0.2768	-1.5379
adult	7p22.3	1570367	1582679	7975	*MAFK*	0.425	-2.055
adult	7q36.3	157129709	157179018	10049	*DNAJB6*	0.2768	-1.5379
adult	7q36	157331745	158380494	5799	*PTPRN2*	0.38745	-1.511
adult	7q36.3	157367027	157367114	406945	*MIR153-2*	0.2768	-1.5379
adult	7p22.3	1581870	1596066	202915	*TMEM184A*	0.425	-2.055
adult	7q36.3	158325409	158325505	693180	*MIR595*	0.4981	-1.3773
adult	7q36.3	158423860	158497522	54892	*NCAPG2*	0.4981	-1.3773
adult	7p22.3	1606969	1609629	84262	*PSMG3*	0.425	-2.055
adult	7p22.3	1609708	1629261	114796	*PSMG3-AS1*	0.425	-2.055
adult	7p21.2	16127151	16460947	729920	*ISPD*	0	-3.4113
adult	7p21.1	16501105	16505474	25928	*SOSTDC1*	0	-3.3395
adult	7p22.3	1654105	1656328	260341	*TFAMP1*	0.425	-2.055
adult	7p21.1	16566504	16621114	100506049	*LRRC72*	0	-3.3395
adult	7p21	16639400	16685442	57037	*ANKMY2*	0	-3.3395
adult	7p21.1	16685758	16746148	28969	*BZW2*	0	-3.3395
adult	7p21.1	16793350	16824161	27075	*TSPAN13*	0	-3.3395
adult	7p21.3	16832263	16844738	10551	*AGR2*	0	-3.3395

adult	7p21.1	16899029	16921613	155465	*AGR3*	0	-3.3395
adult	7p15	17338275	17385775	196	*AHR*	0	-3.0542
adult	7p22.3	1748797	1787590	392617	*ELFN1*	0.425	-2.044
adult	7p21.1	17830384	17980131	23161	*SNX13*	0	-3.0542
adult	7p21.1	18066399	18067486	221823	*PRPS1L1*	0	-3.0542
adult	7p21.1	18126571	18708466	9734	*HDAC9*	0	-3.0542
adult	7p22	1855427	2272583	8379	*MAD1L1*	0.425	-2.044
adult	7p21.2	19155090	19157295	7291	*TWIST1*	0	-3.0542
adult	7p21.1	19184404	19185044	222894	*FERD3L*	0	-3.0542
adult	7p22.3	192968	300740	56975	*FAM20C*	0	-1.82
adult	7p21.1	19735084	19748660	221830	*TWISTNB*	0	-3.0662
adult	7p21.1	19758937	19812404	256130	*TMEM196*	0	-3.0662
adult	7p21.1	20174278	20257013	346389	*MACC1*	0	-3.0662
adult	7p21.1	20370724	20455382	3696	*ITGB8*	0	-3.0662
adult	7p21.1	20655244	20796637	340273	*ABCB5*	0.2268	-3.0397
adult	7p21.2	20821893	20826508	221833	*SP8*	0.2859	-3.0132
adult	7p21.1	20866916	20867439	222901	*RPL23P8*	0.2859	-3.0132
adult	7p15.3	21467688	21554151	6671	*SP4*	0.2859	-3.0132
adult	7p21	21582832	21941186	8701	*DNAH11*	0.2859	-2.8798
adult	7p15.3	21940516	21985542	55536	*CDCA7L*	0.2859	-2.7463
adult	7p15.3	22157907	22396533	9771	*RAPGEF5*	0.2859	-2.7463
adult	7p15.3	22459062	22539901	256227	*STEAP1B*	0.252	-2.4832
adult	7p22	2273925	2281833	29960	*FTSJ2*	0.425	-2.044
adult	7p21	22766765	22771621	3569	*IL6*	0.252	-2.7718
adult	7p22	2281856	2290780	4521	*NUDT1*	0.425	-2.044
adult	7p15.3	22852250	22862471	54543	*TOMM7*	0.252	-2.7718
adult	7p15.3	22896231	22896305	692210	*SNORD93*	0.252	-2.7718
adult	7p22.3	2291404	2354110	29886	*SNX8*	0.425	-2.044
adult	7p15.3	22980877	23053770	84668	*FAM126A*	0.252	-2.7718
adult	7p15.3	23140846	23145322	100775104	*KLHL7-AS1*	0.252	-2.7718
adult	7p15.3	23145352	23165669	55975	*KLHL7*	0.252	-2.7718
adult	7p15	23221445	23240630	11097	*NUPL2*	0.252	-2.7718
adult	7p15	23286315	23314729	10457	*GPNMB*	0.252	-2.7718

adult	7p15.3	23338939	23349180	115416	*MALSU1*	0.252	-2.7718
adult	7p11	23349827	23509995	10643	*IGF2BP3*	0.252	-2.7718
adult	7p15.3	23530006	23531031	256355	*RPS2P32*	0.252	-2.7718
adult	7p15.3	23544400	23571660	29896	*TRA2A*	0.252	-2.7718
adult	7p15.3	23636997	23684327	90693	*CCDC126*	0.252	-2.7718
adult	7p15.3	23719732	23742269	340277	*FAM221A*	0.252	-2.7718
adult	7p15.3	23749785	23872130	56164	*STK31*	0.252	-2.7718
adult	7p22.3	2394473	2420377	8662	*EIF3B*	0.425	-2.044
adult	7p15.1	24323806	24331484	4852	*NPY*	0.3051	-2.3955
adult	7p22	2443194	2474216	55501	*CHST12*	0.425	-2.044
adult	7p15	24612964	24733322	51678	*MPP6*	0.3051	-2.3819
adult	7p15	24737973	24797083	1687	*DFNA5*	0.3051	-2.3683
adult	7p15	24836155	24932240	26031	*OSBPL3*	0.3051	-2.3683
adult	7p15.3	25158269	25164980	54205	*CYCS*	0.3051	-2.3683
adult	7p15.3	25174315	25219817	136895	*C7orf31*	0.3051	-2.3683
adult	7p15.3	25264190	25268105	64111	*NPVF*	0.3051	-2.3683
adult	7p22.2	2552162	2568063	3955	*LFNG*	0.425	-2.044
adult	7p22.3	2577443	2595392	221927	*BRAT1*	0.425	-2.044
adult	7p22.3	2598605	2654368	23288	*IQCE*	0.425	-2.044
adult	7p15.2	25989538	25989606	406940	*MIR148A*	0.3051	-2.3683
adult	7p15.2	26191846	26226756	9603	*NFE2L3*	0.3051	-2.3743
adult	7p15	26229555	26240413	3181	*HNRNPA2B1*	0.3051	-2.3743
adult	7p15.2	26240830	26253227	11335	*CBX3*	0.3051	-2.3743
adult	7p15.2	26331514	26413949	29887	*SNX10*	0.3051	-2.3743
adult	7p15.2	26443107	26535986	441204	*LOC441204*	0.3051	-2.3743
adult	7p15.2	26572739	26578444	9808	*KIAA0087*	0.3051	-2.3743
adult	7p15.2	26677489	26686889	285941	*C7orf71*	0.3051	-2.3743
adult	7p15.2	26706680	26904362	8935	*SKAP2*	0.3051	-2.3743
adult	7p22	2671602	2704436	80727	*TTYH3*	0.425	-2.044
adult	7p15.3	27132613	27135625	3198	*HOXA1*	0.3051	-2.3743
adult	7p15.2	27135712	27139877	100506311	*HOTAIRM1*	0.3051	-2.3743
adult	7p15.2	27139972	27142394	3199	*HOXA2*	0.3051	-2.3743
adult	7p15.2	27145808	27159214	3200	*HOXA3*	0.3051	-2.3743

adult	7p15.2	27168125	27170399	3201	*HOXA4*	0.3051	-2.3743
adult	7p15.2	27179982	27195547	100133311	*HOXA-AS3*	0.3051	-2.3743
adult	7p15.2	27180670	27183287	3202	*HOXA5*	0.3051	-2.3743
adult	7p15.2	27185201	27187393	3203	*HOXA6*	0.3051	-2.3743
adult	7p22.3	2719155	2755070	155185	*AMZ1*	0.425	-2.044
adult	7p15.2	27193337	27196296	3204	*HOXA7*	0.3051	-2.3743
adult	7p15.2	27202056	27205149	3205	*HOXA9*	0.3051	-2.3743
adult	7p15.2	27202056	27219880	100534589	*HOXA10-HOXA9*	0.3051	-2.3743
adult	7p15.2	27209098	27209182	442920	*MIR196B*	0.3051	-2.3743
adult	7p15.2	27210209	27213955	3206	*HOXA10*	0.3051	-2.3743
adult	7p15.2	27220775	27224835	3207	*HOXA11*	0.3051	-2.3743
adult	7p15.2	27225026	27228912	221883	*HOXA11-AS*	0.3051	-2.3743
adult	7p15.2	27236498	27239725	3209	*HOXA13*	0.3051	-2.3743
adult	7p15.2	27240039	27246878	100316868	*HOTTIP*	0.3051	-2.3743
adult	7p15.2	27282163	27287438	2128	*EVX1*	0.3051	-2.3743
adult	7p15.2	27565058	27702620	11112	*HIBADH*	0.3051	-2.3743
adult	7p22.2	2767740	2883959	2768	*GNA12*	0.425	-2.044
adult	7p15	27778991	27869386	8887	*TAX1BP1*	0.3051	-2.3743
adult	7p15.2-p15.1	27870192	28220437	221895	*JAZF1*	0.3051	-2.3743
adult	7p15.1	28220075	28280996	100128081	*JAZF1-AS1*	0.3051	-2.3743
adult	7p15.1	28338939	28865511	9586	*CREB5*	0.3051	-2.3753
adult	7p14.3	28992973	28998029	9865	*TRIL*	0.3051	-2.3762
adult	7p15.1	29035246	29186153	54504	*CPVL*	0.3051	-2.3762
adult	7p15.3	29234120	29553951	1124	*CHN2*	0.3051	-2.3762
adult	7p22	2945709	3083579	84433	*CARD11*	0.425	-2.044
adult	7p14.3	29603426	29606911	222171	*PRR15*	0.3051	-2.3762
adult	7p14.3	29685537	29724754	646762	*LOC646762*	0.3051	-2.3753
adult	7p15.1	29724769	29727859	442524	*DPY19L2P3*	0.3051	-2.3753
adult	7p14.3	29846169	29956682	644150	*WIPF3*	0.3051	-2.3753
adult	7p14.3	29959718	30029425	9805	*SCRN1*	0.3051	-2.3753
adult	7p14.3	30050198	30066417	55033	*FKBP14*	0.3051	-2.3753
adult	7p14.3	30067976	30124278	84725	*PLEKHA8*	0.3051	-2.3753
adult	7p14.3	30323922	30407308	223082	*ZNRF2*	0.3051	-2.3753

adult	7p14.3	30329409	30329506	693133	*MIR550A1*	0.3051	-2.3753
adult	7p14.3	30409665	30412410	222161	*DKFZP586I1420*	0.3051	-2.3753
adult	7p14.3	30464142	30518393	10392	*NOD1*	0.3051	-2.3753
adult	7p15-p14	30536236	30544457	79017	*GGCT*	0.3051	-2.3753
adult	7p15.1	30587972	30617395	401320	*LOC401320*	0.3051	-2.3753
adult	7p15	30634508	30673648	2617	*GARS*	0.3051	-2.3753
adult	7p14.3	30691558	30722141	1395	*CRHR2*	0.3051	-2.3753
adult	7p14.3	30791750	30797218	11185	*INMT*	0.3051	-2.3753
adult	7p14	30951414	30965131	358	*AQP1*	0.3051	-2.3753
adult	7p14	31003635	31019146	2692	*GHRHR*	0.3051	-2.3753
adult	7p14	31092075	31151093	117	*ADCYAP1R1*	0.3051	-2.3753
adult	7p14.3	31377074	31380538	63974	*NEUROD6*	0.3051	-2.0015
adult	7p14.3	31553684	31693303	223075	*CCDC129*	0.3051	-2.4505
adult	7p15	31726630	31748069	10842	*PPP1R17*	0.3051	-2.4993
adult	7p14.3	31790792	32110474	5137	*PDE1C*	0.3051	-2.4993
adult	7p14.3	32496509	32498106	100130673	*LOC100130673*	0.3051	-2.4697
adult	7p14.3	32524944	32530023	23658	*LSM5*	0.3051	-2.4697
adult	7p14.3	32535037	32628353	23080	*AVL9*	0.3051	-2.4697
adult	7p14.3	32620552	32758780	100129460	*DPY19L1P1*	0.3051	-2.1971
adult	7p14.3	32767561	32769595	441208	*ZNRF2P1*	0.3051	-2.1971
adult	7p14.3	32772592	32772689	693134	*MIR550A2*	0.3051	-2.1971
adult	7p14.3	32907777	32931468	25948	*KBTBD2*	0	-2.2178
adult	7p14.3	32956426	32982782	441212	*RP9P*	0	-2.2178
adult	7p11.1	32997015	33046543	11328	*FKBP9*	0	-2.2178
adult	7p14.3	33053724	33080777	51251	*NT5C3A*	0	-2.2178
adult	7p14.3	33134409	33149002	6100	*RP9*	0	-2.2178
adult	7p14	33169151	33645680	27241	*BBS9*	0.2172	-2.4853
adult	7p22.2	3341079	4308631	221935	*SDK1*	0.3358	-2.0693
adult	7p14.3	33944522	34195484	168667	*BMPER*	0.2172	-2.4843
adult	7p14.3	34386123	34797884	404744	*NPSR1-AS1*	0.2172	-2.4843
adult	7p14.3	34697896	34889590	387129	*NPSR1*	0.2172	-2.4843
adult	7p14.3-p14.2	34968492	35077653	23333	*DPY19L1*	0.2172	-2.0721
adult	7p14.2	35120898	35225774	554236	*DPY19L2P1*	0.2172	-2.4278

adult	7p14.3	35242041	35293711	57057	*TBX20*	0.2172	-2.4278
adult	7p14.2	35353465	35416086	401324	*LOC401324*	0.2172	-2.4278
adult	7p14.2	35672269	35734772	64224	*HERPUD2*	0.2172	-2.4278
adult	7p14.2	35840595	35946715	989	*7-Sep*	0.2172	-2.4278
adult	7p14.2	36192835	36341152	80820	*EEPD1*	0.2172	-2.4278
adult	7p14.2	36363758	36406782	23366	*KIAA0895*	0.2172	-2.4278
adult	7p15-p14	36429411	36493401	54443	*ANLN*	0.2172	-2.4278
adult	7p14.2	36552548	36764154	313	*AOAH*	0.2172	-2.4421
adult	7p14.1	36892510	37024717	9844	*ELMO1*	0.2172	-2.4564
adult	7p14.2	36958961	36959037	100302113	*MIR1200*	0.2172	-2.4564
adult	7p14.1	37779995	37780913	353345	*GPR141*	0.2172	-2.4564
adult	7p14.1	37888198	37940002	51314	*NME8*	0.2172	-2.4564
adult	7p14.1	37945534	37956525	6424	*SFRP4*	0.2172	-2.4564
adult	7p14.1	37960162	37991542	54749	*EPDR1*	0.2172	-2.4564
adult	7p14-p13	38217807	38270272	83930	*STARD3NL*	0.2172	-2.4564
adult	7p14-p13	38423296	38671167	273	*AMPH*	0.2172	-2.58
adult	7p14.1	38724945	38726689	340286	*FAM183B*	0.2172	-2.58
adult	7p14-p13	38763542	38948800	27072	*VPS41*	0.2172	-2.58
adult	7p14.1	39017608	39504390	11281	*POU6F2*	0.2172	-2.7818
adult	7p14.1	39444197	39445945	100861520	*POU6F2-AS1*	0.2172	-2.7818
adult	7p14.1	39605974	39612480	57002	*YAE1D1*	0.2172	-2.58
adult	7p15-p13	39663151	39747723	5898	*RALA*	0.2172	-2.58
adult	7p14.1	39773166	39834222	349114	*LINC00265*	0.2172	-2.5561
adult	7p13	39989958	40136733	8621	*CDK13*	0.2172	-2.5095
adult	7p14.1	40172341	40174251	136647	*MPLKIP*	0.2172	-2.5095
adult	7p15-p13	41728600	41742706	3624	*INHBA*	0.2172	-2.5095
adult	7p14.1	41733513	41818976	285954	*INHBA-AS1*	0.2172	-2.5095
adult	7p22	419390	422845	442497	*LOC442497*	0	-1.82
adult	7p13	42000547	42276618	2737	*GLI3*	0.2172	-2.5095
adult	7p14.1	42948871	42951689	79020	*C7orf25*	0.2172	-2.5095
adult	7p13	42956461	42971805	5683	*PSMA2*	0.2172	-2.5095
adult	7p14	42971938	42977453	64983	*MRPL32*	0.2172	-2.5095
adult	7p13	43152197	43602938	23072	*HECW1*	0.2172	-2.5095

adult	7p13	43622691	43666978	9263	*STK17A*	0.2172	-2.5095
adult	7p13	43670750	43769140	55744	*COA1*	0.2172	-2.5095
adult	7p13	43798271	43846941	644	*BLVRA*	0.2172	-2.5095
adult	7p14	43906156	43909145	64951	*MRPS24*	0.2172	-2.5095
adult	7p13	43906156	43946231	100534592	*URGCP-MRPS24*	0.2172	-2.5095
adult	7p13	43915492	43946668	55665	*URGCP*	0.2172	-2.5095
adult	7p13	43966034	43995735	51619	*UBE2D4*	0.2172	-2.5095
adult	7p13	43980493	44058793	84820	*POLR2J4*	0.2172	-2.5095
adult	7p13	44040488	44049723	285955	*SPDYE1*	0.2172	-2.1529
adult	7p13	44078647	44082082	255031	*LINC00957*	0.2172	-2.1529
adult	7p13	44084238	44101315	28988	*DBNL*	0.2172	-2.4287
adult	7p13-p12	44102325	44105186	5224	*PGAM2*	0.2172	-2.4287
adult	7p13	44111660	44122139	27434	*POLM*	0.2172	-2.4287
adult	7p13	44143959	44154164	165	*AEBP1*	0.2172	-2.4287
adult	7p13	44154278	44163107	5425	*POLD2*	0.2172	-2.4287
adult	7p21-p11.2	44178462	44180916	58498	*MYL7*	0.2172	-2.4287
adult	7p15.3-p15.1	44183869	44198887	2645	*GCK*	0.2172	-2.4287
adult	7p15.1	44240577	44253893	10652	*YKT6*	0.2172	-2.4287
adult	7p14.3-p14.1	44256748	44365230	816	*CAMK2B*	0.2172	-2.3852
adult	7p13-p12	44421964	44530385	23386	*NUDCD3*	0.2172	-2.3416
adult	7p13	44552134	44580914	29881	*NPC1L1*	0.2172	-2.3416
adult	7p13	44605015	44614137	54606	*DDX56*	0.2172	-2.3416
adult	7p13	44617493	44621894	222068	*TMED4*	0.2172	-2.3416
adult	7p14-p13	44646120	44716195	4967	*OGDH*	0.2172	-2.3416
adult	7p13	44788529	44809479	83637	*ZMIZ2*	0.2172	-2.3416
adult	7p13	44836234	44842722	5478	*PPIA*	0.2172	-2.3416
adult	7p13	44866487	44887725	94239	*H2AFV*	0.2172	-2.3416
adult	7p13	44915891	44924984	5814	*PURB*	0.2172	-2.3416
adult	7p13	45002259	45018704	64005	*MYO1G*	0.2172	-2.3416
adult	7p13	45022626	45026259	285958	*SNHG15*	0.2172	-2.3416
adult	7p13	45024976	45025109	677798	*SNORA9*	0.2172	-2.3416
adult	7p13	45039344	45116069	83605	*CCM2*	0.2172	-2.3416
adult	7p13	45120035	45128493	23148	*NACAD*	0.2172	-2.3416

adult	7p13	45139698	45151346	9238	*TBRG4*	0.2172	-2.3416
adult	7p13	45144504	45144641	677796	*SNORA5C*	0.2172	-2.3416
adult	7p13	45145566	45145698	677795	*SNORA5B*	0.2172	-2.3416
adult	7p13-p12	45197366	45223850	10268	*RAMP3*	0.2172	-2.3416
adult	7p12.3	45614124	45762714	107	*ADCY1*	0.2172	-2.3416
adult	7p12.3	45763385	45808617	641977	*SEPT7P2*	0.2172	-2.3416
adult	7p12.3	45927958	45933267	3484	*IGFBP1*	0.2172	-2.4137
adult	7p12.3	45951843	45960871	3486	*IGFBP3*	0.2172	-2.4137
adult	7p22.1	4721929	4811074	221937	*FOXK1*	0.2466	-2.2983
adult	7p12.3	47314751	47621742	64759	*TNS3*	0.2172	-2.3863
adult	7p12.3	47694841	47701246	401335	*C7orf65*	0.2172	-2.3863
adult	7p12.3	47801073	47806370	84847	*LINC00525*	0.2172	-2.4135
adult	7p12.3	47814249	47988071	168507	*PKD1L1*	0.2172	-2.4135
adult	7p12.3	47834888	47859444	80099	*C7orf69*	0.2172	-2.4135
adult	7p13-p12	48002884	48019222	3364	*HUS1*	0.2172	-2.4135
adult	7p12.3	48026745	48068716	256979	*SUN3*	0.2172	-2.4135
adult	7p12.3	48075107	48100894	136288	*C7orf57*	0.2172	-2.4135
adult	7p12.3	48128808	48148330	7378	*UPP1*	0.2172	-2.4135
adult	7p22.2	4815261	4834026	9907	*AP5Z1*	0.2466	-2.2983
adult	7p12.3	48211056	48687091	154664	*ABCA13*	0.2172	-2.4274
adult	7p22.1	4838739	4923335	55698	*RADIL*	0.2466	-2.2983
adult	7p12.3	48964156	48967049	168448	*CDC14C*	0.2172	-2.4413
adult	7p22.1	4897368	4901625	56903	*PAPOLB*	0.2466	-2.2983
adult	7p22.1	4931875	4998844	221938	*MMD2*	0.2466	-2.2983
adult	7p12.2	49813256	49952138	375567	*VWC2*	0.2172	-2.5524
adult	7p14.3	49977023	50132860	11055	*ZPBP*	0.2172	-2.5524
adult	7p12.2	50135681	50198852	100130988	*C7orf72*	0.2172	-2.5524
adult	7p22.1	5013615	5037800	441191	*RNF216P1*	0.2466	-2.2983
adult	7p12.2	50344264	50472798	10320	*IKZF1*	0.2172	-2.4597
adult	7p12.1	50511826	50518088	63979	*FIGNL1*	0.2172	-2.4214
adult	7p12.2	50526133	50628768	1644	*DDC*	0.2172	-2.4214
adult	7p12.2	50657759	50772998	2887	*GRB10*	0.2172	-2.4214
adult	7p22.1	5085451	5109119	57786	*RBAK*	0.2466	-2.2983

adult	7p12.1	51083908	51384515	23242	*COBL*	0.2172	-2.4214
adult	7p22.1	5111690	5112854	389458	*RBAKDN*	0.2466	-2.2983
adult	7p22.1	5160940	5184177	645700	*ZNF890P*	0.2466	-2.2983
adult	7p22.1	5229834	5273486	26100	*WIPI2*	0.2466	-2.2983
adult	7p12.1	53103348	53104618	285877	*POM121L12*	0	-2.9565
adult	7p22.1	5322560	5343704	222962	*SLC29A4*	0.2466	-2.2983
adult	7p22.1	5346422	5463177	84629	*TNRC18*	0.2466	-2.2983
adult	7p22	536896	559481	5154	*PDGFA*	0	-1.82
adult	7p11.2	54268916	54270114	3262	*HPVC1*	0	-2.9565
adult	7p11.2	54610017	54638773	222008	*VSTM2A*	0	-2.2525
adult	7p11.2	54819939	54826939	23480	*SEC61G*	0	-2.2525
adult	7p12	55086724	55224644	1956	*EGFR*	0	-2.2525
adult	7p22.2	5515427	5553399	80028	*FBXL18*	0.2466	-2.2983
adult	7p22.1	5535449	5535548	693174	*MIR589*	0.2466	-2.2983
adult	7q31.1-q31.33	55433140	55501435	55915	*LANCL2*	0	-2.1838
adult	7p11.2	55538305	55640200	81552	*VOPP1*	0	-2.1838
adult	7p22	5566778	5570232	60	*ACTB*	0.2466	-2.2983
adult	7p22.3	560027	564869	441307	*FLJ44511*	0	-1.82
adult	7p22	5632435	5646287	6624	*FSCN1*	0.2466	-2.2983
adult	7p22.1	5659671	5821361	54476	*RNF216*	0.2466	-2.2983
adult	7p22.1	5862790	5894066	401303	*ZNF815P*	0.2466	-2.2983
adult	7p22	588833	752161	5575	*PRKAR1B*	0	-1.82
adult	7p22.1	5920428	5925994	654231	*OCM*	0.2466	-2.2983
adult	7p22.1	5938340	5965603	51622	*CCZ1*	0.2466	-2.2983
adult	7p22.1	5965776	6010314	728194	*RSPH10B2*	0.2466	-2.2983
adult	7p22.2	6012869	6048737	5395	*PMS2*	0.2466	-2.2983
adult	7p22	6048881	6063465	7965	*AIMP2*	0.2466	-2.2983
adult	7p22	6061877	6098860	27102	*EIF2AK1*	0.2466	-2.2983
adult	7p22	6071006	6076183	100310846	*ANKRD61*	0.2466	-2.2983
adult	7p22.1	6144549	6201195	84132	*USP42*	0.2466	-2.2983
adult	7p22.1	6201411	6312242	9265	*CYTH3*	0.2466	-2.2983
adult	7q11.21	62751669	62764434	643955	*ZNF733P*	0.2525	-1.4205
adult	7q11.21	62809447	62812152	100287834	*LOC100287834*	0.2525	-1.4205

adult	7q11.21	63505820	63538927	442319	*ZNF727*	0.2525	-1.4321
adult	7q11.21	63667580	63680668	730291	*ZNF735*	0.2525	-1.4321
adult	7q11.21	63688851	63727309	168417	*ZNF679*	0.2525	-1.4321
adult	7p22.1	6369039	6388590	84792	*FAM220A*	0.2466	-2.2983
adult	7q11.21	63774250	63817012	728927	*ZNF736*	0.2525	-1.4321
adult	7q11.21	63980254	64023505	340252	*ZNF680*	0.2525	-1.4321
adult	7q11.21	64035072	64078967	100128885	*LOC100128885*	0.2525	-1.4321
adult	7q11.21	64042987	64044129	641746	*LOC641746*	0.2525	-1.4321
adult	7q11.2	64126460	64171960	51427	*ZNF107*	0.2525	-1.4321
adult	7p22	6414125	6443598	5879	*RAC1*	0.2466	-2.2983
adult	7q11.21	64254765	64294059	7697	*ZNF138*	0.2525	-1.4321
adult	7q11.21	64363619	64391955	10793	*ZNF273*	0.2525	-1.5927
adult	7q11.21	64434829	64451414	51351	*ZNF117*	0.2525	-1.5927
adult	7q11.2	64450732	64467124	2086	*ERV3-1*	0.2525	-1.5927
adult	7p22.1	6448746	6487643	221955	*DAGLB*	0.2466	-2.2983
adult	7q11.21	64498731	64535091	643180	*CCT6P3*	0.2525	-1.5927
adult	7q11.21	64838711	64866048	168374	*ZNF92*	0.2559	-1.5658
adult	7p22.1	6500711	6523849	11014	*KDELR2*	0.2466	-2.2983
adult	7q11.21	65111923	65235797	441242	*LOC441242*	0.2559	-1.7764
adult	7q11.21	65216091	65228662	643253	*CCT6P1*	0.2559	-1.7764
adult	7q11.21	65220512	65220646	677807	*SNORA22*	0.2559	-1.7764
adult	7q11.21	65338256	65424550	154807	*VKORC1L1*	0.2559	-1.7764
adult	7p22.1	6536408	6591067	392862	*GRID2IP*	0.2466	-2.2983
adult	7q21.11	65425672	65447301	2990	*GUSB*	0.2559	-1.7764
adult	7q11.21	65540775	65558329	435	*ASL*	0.2559	-1.7764
adult	7q11.21	65579804	65619553	27297	*CRCP*	0.2559	-1.7764
adult	7q11.21	65670258	65825438	8460	*TPST1*	0.2559	-1.7764
adult	7q11.21	65841030	65865395	285908	*LINC00174*	0.2559	-1.7764
adult	7q11.21	66093867	66108216	154881	*KCTD7*	0.2559	-1.7764
adult	7p22.1	6617064	6628610	55146	*ZDHHC4*	0.2466	-2.2983
adult	7q11.21	66205642	66276448	27342	*RABGEF1*	0.2559	-1.7764
adult	7q11.21	66274979	66309813	729156	*GTF2IRD1P1*	0.2559	-1.7764
adult	7p22.1	6629651	6648357	79034	*C7orf26*	0.2466	-2.2983

adult	7q11.21	66386202	66423538	55069	*TMEM248*	0.2559	-1.7764
adult	7q11.21	66452689	66460588	51119	*SBDS*	0.2559	-1.7764
adult	7q11.21	66461791	66704507	55253	*TYW1*	0.2559	-1.7764
adult	7p22.1	6655526	6663921	54753	*ZNF853*	0.2466	-2.2983
adult	7q11.22	66741117	66767429	5382	*PMS2P4*	0.2559	-1.7764
adult	7p11.2-q11.2	66767624	66786513	64940	*STAG3L4*	0.2559	-1.7764
adult	7p22.1	6728063	6746566	7559	*ZNF12*	0.2466	-2.8743
adult	7p22.1	6774935	6791232	441194	*PMS2CL*	0.2466	-2.8743
adult	7p22.1	6838565	6865926	221960	*CCZ1B*	0.2466	-2.8743
adult	7q11.22	69063904	69755772	26053	*AUTS2*	0.2559	-1.7764
adult	7q11.23	70597522	71178586	64409	*WBSCR17*	0.2559	-1.8061
adult	7p22.1	7115400	7136417	100131257	*LOC100131257*	0.2466	-2.8743
adult	7q11	71244475	71802208	83698	*CALN1*	0.2559	-1.8061
adult	7q11.23	72039491	72298813	441250	*TYW1B*	0.2559	-1.5499
adult	7p21.3	7222245	7288280	56913	*C1GALT1*	0.2466	-2.8743
adult	7q11.23	72299951	72304586	155370	*SBDSP1*	0.2559	-1.5043
adult	7q11.23	72333320	72339656	441251	*SPDYE7P*	0.2559	-1.5043
adult	7q11.23	72349905	72421979	9883	*POM121*	0.2559	-1.5043
adult	7q11.23	72418831	72425302	260294	*NSUN5P2*	0.2559	-1.5043
adult	7q11.23	72440164	72443674	541473	*LOC541473*	0.2559	-1.5043
adult	7q11.23	72467817	72476466	442578	*STAG3L3*	0.2559	-1.5043
adult	7q11.23	72476618	72520245	5383	*PMS2P5*	0.2559	-1.5043
adult	7q11.23	72490259	72500309	728524	*SPDYE8P*	0.2559	-1.5043
adult	7q11.23	72569011	72621336	100093631	*LOC100093631*	0.2559	-1.5043
adult	7q11.23	72634673	72649979	654816	*NCF1B*	0.2559	-1.5043
adult	7q11.23	72716512	72722864	55695	*NSUN5*	0.2559	-1.5043
adult	7q11.23	72726531	72742085	135892	*TRIM50*	0.2559	-1.5043
adult	7q11.23	72742154	72772646	8468	*FKBP6*	0.2559	-1.5043
adult	7q11.23	72848108	72850450	8326	*FZD9*	0.2559	-1.5043
adult	7q11.23	72854727	72936615	9031	*BAZ1B*	0.2559	-1.5043
adult	7q11.23	72950682	72971602	9275	*BCL7B*	0.2559	-1.5043
adult	7q11.23	72983276	72993013	26608	*TBL2*	0.2559	-1.5043
adult	7q11.23	73007523	73038870	51085	*MLXIPL*	0.2559	-1.5043

adult	7q11.23	73082173	73086440	155382	*VPS37D*	0.2559	-1.5043
adult	7q11.23	73095247	73097781	84277	*DNAJC30*	0.2559	-1.5043
adult	7q11.23	73097897	73112551	114049	*WBSCR22*	0.2559	-1.5043
adult	7q11.23	73113534	73134017	6804	*STX1A*	0.2559	-1.5043
adult	7q11.23	73150424	73153184	83451	*ABHD11*	0.2559	-1.5043
adult	7q11.23	73183326	73184600	1365	*CLDN3*	0.2559	-1.5043
adult	7q11.23	73245192	73247023	1364	*CLDN4*	0.2559	-1.5043
adult	7q11.23	73248920	73256855	155368	*WBSCR27*	0.2559	-1.5043
adult	7q11.23	73275488	73280223	135886	*WBSCR28*	0.2559	-1.5043
adult	7q11.23	73442118	73484236	2006	*ELN*	0.2559	-1.5043
adult	7q11.23	73498106	73536855	3984	*LIMK1*	0.2559	-1.5043
adult	7q11.23	73588705	73611429	7458	*EIF4H*	0.2559	-1.5043
adult	7q11.23	73605527	73605624	693175	*MIR590*	0.2559	-1.5043
adult	7q11.23	73624086	73644164	7462	*LAT2*	0.2559	-1.5043
adult	7q11.23	73645831	73668788	5982	*RFC2*	0.2559	-1.5043
adult	7q11.23	73703804	73820273	7461	*CLIP2*	0.2559	-1.5043
adult	7q11.23	73868119	74016920	9569	*GTF2IRD1*	0.2559	-1.5318
adult	7p21.3	7398243	7575460	340267	*COL28A1*	0.2466	-2.8743
adult	7q11.23	74071990	74175022	2969	*GTF2I*	0.2559	-1.5318
adult	7q11.23	74188308	74203720	653361	*NCF1*	0.2559	-1.5318
adult	7q11.23	74298091	74306731	442582	*STAG3L2*	0.2559	-1.5318
adult	7q11.23	74456269	74489717	81554	*WBSCR16*	0.2559	-1.7576
adult	7q11.23	74508346	74565623	389524	*GTF2IRD2B*	0.2559	-1.7576
adult	7q11.23	74572383	74587802	654817	*NCF1C*	0.2559	-1.7576
adult	7q11.23	74800771	74867509	729438	*GATSL2*	0.2559	-1.7576
adult	7q11.23	75024902	75034896	375593	*TRIM73*	0.2559	-2.0764
adult	7q11.2	75046059	75115565	100101267	*POM121C*	0.2559	-2.0764
adult	7q11.23	75137068	75157453	5387	*PMS2P3*	0.2559	-2.0764
adult	7q11.23	75162618	75368290	3092	*HIP1*	0.2559	-2.0764
adult	7q11.23	75398841	75419064	10344	*CCL26*	0.2559	-2.0764
adult	7q11.23	75441113	75443033	6369	*CCL24*	0.2559	-2.0764
adult	7q11.23	75508316	75518244	57414	*RHBDD2*	0.2559	-2.3931
adult	7q11.2	75544419	75616173	5447	*POR*	0.2559	-2.3931

adult	7q11.23	75573100	75573234	677801	*SNORA14A*	0.2559	-2.3931
adult	7q11.23	75616154	75623992	83862	*TMEM120A*	0.2559	-2.3931
adult	7q11.23	75625654	75677321	51657	*STYXL1*	0.2559	-2.3931
adult	7cen-q22	75677336	75696827	4191	*MDH2*	0.2559	-2.3931
adult	7q11.23	75831210	75916609	222183	*SRRM3*	0.2559	-2.3931
adult	7q11.23	75931874	75933614	3315	*HSPB1*	0.2559	-2.3931
adult	7q11.23	75956107	75988342	7532	*YWHAG*	0.2559	-2.3931
adult	7q11.23	76026840	76071388	7784	*ZP3*	0.2559	-2.3931
adult	7p21.3	7606615	7647110	54468	*MIOS*	0.2466	-2.8743
adult	7q11.23	76090971	76135312	113878	*DTX2*	0.2559	-2.3931
adult	7q11.23	76099336	76104317	619190	*FDPSP2*	0.2559	-2.3931
adult	7q11.2	76139739	76157199	80761	*UPK3B*	0	-2.6206
adult	7q11.23	76178657	76257299	100133091	*LOC100133091*	0	-2.6509
adult	7q11.23	76239302	76256620	22932	*POMZP3*	0	-2.6509
adult	7q11.23	76610138	76653076	441263	*DTX2P1-UPK3BP1-PMS2P11*	0	-2.6509
adult	7q11.23	76751933	76924521	57639	*CCDC146*	0	-2.6509
adult	7p22	7676193	7758238	6119	*RPA3*	0.2466	-2.9239
adult	7q11.23	76822687	76829150	10875	*FGL2*	0	-2.6509
adult	7q11.23	76940067	77045717	54103	*GSAP*	0	-2.6509
adult	7q11.23	77166772	77269388	5782	*PTPN12*	0	-2.6509
adult	7q11.23	77325742	77409120	222194	*RSBN1L*	0	-2.6509
adult	7q11.23	77423044	77427747	85025	*TMEM60*	0	-2.6509
adult	7q11.23-q21	77428108	77553500	57157	*PHTF2*	0	-2.6509
adult	7q21	77646373	79082890	9863	*MAGI2*	0	-2.6509
adult	7q21.11	77976558	77988770	399670	*RPL13AP17*	0	-2.6509
adult	7q21	79764139	79848725	2770	*GNAI1*	0	-2.9669
adult	7p21.3	8008373	8128709	113263	*GLCCI1*	0.2466	-2.6908
adult	7q21.11	80087950	80141325	346562	*GNAT3*	0	-2.9669
adult	7q11.2	80231503	80303734	948	*CD36*	0	-2.9669
adult	7q21-q31	80371853	80548667	10512	*SEMA3C*	0	-2.9669
adult	7q21.1	81331443	81399452	3082	*HGF*	0	-2.9669
adult	7p22	8152814	8301682	3382	*ICA1*	0.2466	-2.6908
adult	7q21-q22	81575759	82073122	781	*CACNA2D1*	0	-2.7892

adult	7q21.11	82383320	82792197	27445	*PCLO*	0	-2.5499
adult	7q21.11	82993221	83270747	9723	*SEMA3E*	0	-2.5499
adult	7p12.1	83587658	83824217	10371	*SEMA3A*	0	-2.5499
adult	7q21.11	84624871	84751247	223117	*SEMA3D*	0	-2.5499
adult	7p22	8473584	8792593	30010	*NXPH1*	0.2466	-2.6908
adult	7p22.3	855193	883509	23353	*SUN1*	0	-1.82
adult	7q21.1-q21.2	86273229	86494192	2913	*GRM3*	0	-2.5496
adult	7q21.12	86506222	86595291	222223	*KIAA1324L*	0	-2.5496
adult	7q21	86781676	86825648	9988	*DMTF1*	0	-2.5496
adult	7q21.12	86825477	86849031	79161	*TMEM243*	0	-2.5496
adult	7q21.1	86954663	86974808	11257	*TP53TG1*	0	-2.5496
adult	7q21.1	86974950	86989425	54677	*CROT*	0	-2.5496
adult	7q21.1	87031360	87105019	5244	*ABCB4*	0	-2.5496
adult	7q21.12	87133178	87342639	5243	*ABCB1*	0	-2.5496
adult	7q21.12	87257728	87461613	154661	*RUNDC3B*	0	-2.5496
adult	7q21.12	87463813	87505692	55972	*SLC25A40*	0	-2.5496
adult	7q21.3	87505543	87538856	10926	*DBF4*	0	-2.5496
adult	7q21	87563565	87811428	53616	*ADAM22*	0	-2.5496
adult	7q21.1	87834431	87849399	6717	*SRI*	0	-2.5496
adult	7q21.12	87905743	87936228	79689	*STEAP4*	0	-2.5496
adult	7q21.13	88388681	88966371	219578	*ZNF804B*	0	-2.5496
adult	7q21.13	88423419	88425031	219557	*C7orf62*	0	-2.5496
adult	7q21.13	89748713	89754914	442523	*DPY19L2P4*	0	-2.5496
adult	7q21	89783688	89794141	26872	*STEAP1*	0	-2.5496
adult	7q21.13	89840999	89866992	261729	*STEAP2*	0.2381	-2.5151
adult	7q21.13	89975978	90020769	85865	*GTPBP10*	0.2381	-2.5151
adult	7q21	90025605	90027550	101409256	*LOC101409256*	0.2381	-2.5151
adult	7q21	90032647	90045268	9069	*CLDN12*	0.2381	-2.5151
adult	7q21-q22	90338711	90839905	5218	*CDK14*	0.2381	-2.5151
adult	7q21	90893782	90898132	8321	*FZD1*	0.2381	-2.5151
adult	7q21-q22	91570188	91739987	10142	*AKAP9*	0.2381	-2.4718
adult	7p22.3	916190	936071	51608	*GET4*	0	-1.82
adult	7q21.2	91741462	91763840	1595	*CYP51A1*	0.2381	-2.4718

adult	7q21.2	91774197	91794590	401387	*LRRD1*	0.2381	-2.4718
adult	7q21.2	91828282	91875212	889	*KRIT1*	0.2381	-2.4718
adult	7q21.2	91875547	92030698	54467	*ANKIB1*	0.2381	-2.4718
adult	7q21-q22	92076761	92089381	57798	*GATAD1*	0.2381	-2.4718
adult	7q21.2	92116336	92157845	5189	*PEX1*	0.2381	-2.4718
adult	7q21.2	92158086	92169795	84060	*RBM48*	0.2381	-2.4718
adult	7q21.2	92167788	92169079	84849	*MGC16142*	0.2381	-2.4718
adult	7q21.2	92190071	92219708	257415	*FAM133B*	0.2381	-2.4718
adult	7q21-q22	92234234	92463231	1021	*CDK6*	0.2381	-2.4718
adult	7q21.2	92728825	92747336	54809	*SAMD9*	0.2381	-2.7396
adult	7q21.2	92759366	92777701	219285	*SAMD9L*	0.2381	-2.7396
adult	7q21.3	92817898	92848908	253012	*HEPACAM2*	0.2381	-2.7396
adult	7q21.3	92861652	92905737	55610	*CCDC132*	0.2381	-2.7396
adult	7q21.3	93053798	93189122	799	*CALCR*	0.2381	-2.7396
adult	7q21.3	93112071	93112167	724023	*MIR653*	0.2381	-2.7396
adult	7q21.3	93113247	93113331	574442	*MIR489*	0.2381	-2.7396
adult	7q22	93514708	93520303	7980	*TFPI2*	0.2381	-2.7396
adult	7q21.3	93535819	93540485	2792	*GNGT1*	0.2381	-2.7396
adult	7q21	93551015	93555826	2791	*GNG11*	0.2794	-2.6462
adult	7q21.1-q22	93622553	93633694	10282	*BET1*	0.2794	-2.6462
adult	7p22.3	937536	994319	11033	*ADAP1*	0	-2.0298
adult	7q22.1	94023872	94060544	1278	*COL1A2*	0.2794	-2.6462
adult	7q21.3	94139169	94186328	64921	*CASD1*	0.2794	-2.6462
adult	7q21.3	94214535	94285521	8910	*SGCE*	0.2794	-2.6462
adult	7q21	94285636	94299006	23089	*PEG10*	0.2794	-2.6462
adult	7q21.3	94536948	94925727	55607	*PPP1R9A*	0.2794	-2.6462
adult	7q21.3	94927668	94953884	5444	*PON1*	0.2794	-2.6462
adult	7q21.3	94989183	95025687	5446	*PON3*	0.2794	-2.6462
adult	7q21.3	95034173	95064384	5445	*PON2*	0.2794	-2.6462
adult	7q21-q22	95115212	95158113	51666	*ASB4*	0.2794	-2.6462
adult	7q21.3	95212808	95225925	5166	*PDK4*	0.2794	-2.6462
adult	7q21.3	95401817	95727736	1780	*DYNC1I1*	0.2794	-2.6462
adult	7q21.3	95749531	95951459	10165	*SLC25A13*	0.2794	-2.6462

adult	7q21.3	95848973	95849068	693176	*MIR591*	0.2794	-2.6462
adult	7q21.3	96110937	96132835	401388	*C7orf76*	0.2794	-2.6462
adult	7q21.3	96318078	96339203	7979	*SHFM1*	0.2794	-2.6462
adult	7q21.3	96597826	96643377	285987	*DLX6-AS1*	0.2794	-2.6023
adult	7q22	96635289	96640352	1750	*DLX6*	0.2794	-2.6023
adult	7q22	96649701	96654143	1749	*DLX5*	0.2794	-2.6023
adult	7p21.3	9673899	9675447	168741	*PER4*	0.2466	-2.947
adult	7q21-q22	97361270	97369784	6863	*TAC1*	0.2794	-2.6023
adult	7q21.3	97481428	97501477	440	*ASNS*	0.2794	-2.066
adult	7q21.3	97595907	97601638	389538	*MGC72080*	0.2794	-2.5063
adult	7q21.2	97614012	97619416	4951	*OCM2*	0.2794	-2.5063
adult	7q21.3	97736196	97838944	22853	*LMTK2*	0.2794	-2.5063
adult	7q21.3	97841565	97842271	168620	*BHLHA15*	0.2794	-2.5063
adult	7q21.3	97844754	97881563	25851	*TECPR1*	0.2794	-2.5063
adult	7q21.3	97910978	97920839	25798	*BRI3*	0.2794	-2.5063
adult	7q22.1	97920961	98030427	55971	*BAIAP2L1*	0.2794	-2.5063
adult	7q21.3-q22.1	98246596	98259181	4885	*NPTX2*	0.2794	-2.5063
adult	7q22.1	98444110	98467673	222865	*TMEM130*	0.2794	-2.5063
adult	7q21.2-q22.1	98476112	98610866	8295	*TRRAP*	0.2794	-2.5063
adult	7q21.2-q22.1	98479272	98479352	100500819	*MIR3609*	0.2794	-2.5063
adult	7q22.1	98625057	98741743	57154	*SMURF1*	0.2794	-2.5063
adult	7q22.1	98771196	98805089	402569	*KPNA7*	0.2794	-2.5063
adult	7q22.1	98870923	98895594	84176	*MYH16*	0.2794	-2.5063
adult	7q22.1	98923495	98963885	10552	*ARPC1A*	0.2794	-2.5063
adult	7q22.1	98972297	98992404	10095	*ARPC1B*	0.2794	-2.5063
adult	7q22.1	98992297	99006305	11333	*PDAP1*	0.2794	-2.5063
adult	7q22.1	99006600	99017239	8896	*BUD31*	0.2794	-2.5063
adult	7q22.1	99014361	99036462	26024	*PTCD1*	0.2794	-2.5063
adult	7q	99014361	99063824	100526740	*ATP5J2-PTCD1*	0.2794	-2.5063
adult	7q22.1	99036562	99054996	10898	*CPSF4*	0.2794	-2.5063
adult	7q22.1	99055783	99063824	9551	*ATP5J2*	0.2794	-2.5063
adult	7q22.1	99070514	99079948	285989	*ZNF789*	0.2794	-2.5063
adult	7q22.1	99090853	99097877	84124	*ZNF394*	0.2794	-2.5063

adult	7q22	99102272	99131445	23660	*ZKSCAN5*	0.2794	-2.5063
adult	7q22.1	99143922	99149757	221786	*FAM200A*	0.2794	-2.5063
adult	7q22.1	99156044	99162328	79027	*ZNF655*	0.2794	-2.5063
adult	7q22.1	99214570	99230030	221785	*ZSCAN25*	0.2794	-2.5063
adult	7q21.1	99245811	99277649	1577	*CYP3A5*	0.2794	-2.5063
adult	7q22.1	99302659	99332823	1551	*CYP3A7*	0.2794	-2.5063
adult	7q21.1	99354582	99381811	1576	*CYP3A4*	0.2794	-2.5063
adult	7q21.1	99425635	99463727	64816	*CYP3A43*	0.2794	-2.5063
adult	7q22.1	99473684	99474656	81392	*OR2AE1*	0.2794	-2.5063
adult	7q22-q31.1	99488029	99517223	89122	*TRIM4*	0.2794	-2.5063
adult	7q22.1	99520891	99527243	349149	*GJC3*	0.2794	-2.5063
adult	7q22.1	99564349	99573735	563	*AZGP1*	0.2794	-2.5063
adult	7q22.1	99578384	99581860	646282	*AZGP1P1*	0.2794	-2.5063
adult	7q22	99613194	99639312	7586	*ZKSCAN1*	0.2794	-2.5063
adult	7q22.1	99647416	99662663	7589	*ZSCAN21*	0.2794	-2.5063
adult	7q22.1	99661469	99679387	7551	*ZNF3*	0.2794	-2.5063
adult	7q22.1	99686582	99689822	10980	*COPS6*	0.2794	-2.5063
adult	7q21.3-q22.1	99690350	99698403	4176	*MCM7*	0.2794	-2.5063
adult	7q22.1	99691182	99691266	407014	*MIR25*	0.2794	-2.5063
adult	7q22.1	99691390	99691470	407050	*MIR93*	0.2794	-2.5063
adult	7q22.1	99691615	99691697	406900	*MIR106B*	0.2794	-2.5063
adult	7q22.1	99699129	99704803	9179	*AP4M1*	0.2794	-2.5063
adult	7q22.1	99704692	99716995	6878	*TAF6*	0.2794	-2.5063
adult	7q22.1	99717264	99723128	245812	*CNPY4*	0.2794	-2.5063
adult	7q22.1	99724316	99726121	255374	*MBLAC1*	0.2794	-2.5063
adult	7q22.1	99746529	99751833	389541	*LAMTOR4*	0.2794	-2.5063
adult	7q22.1	99752042	99756344	55262	*C7orf43*	0.2794	-2.5063
adult	7q22.1	99756864	99766373	79690	*GAL3ST4*	0.2794	-2.5063
adult	7q22.1	99767228	99775049	221914	*GPC2*	0.2794	-2.5063
adult	7q22.1	99775365	99812010	10734	*STAG3*	0.2794	-2.5063
adult	7q22.1	99798277	99869855	352954	*GATS*	0.2794	-2.5063
adult	7q22.1	99816870	99819111	79037	*PVRIG*	0.2794	-2.5063
adult	7q22.1	99905324	99919819	441272	*SPDYE3*	0.2794	-2.5063

adult	7q22.1	99918262	99933930	5379	*PMS2P1*	0.2794	-2.5063
adult	7q22.1	99955625	99965454	29990	*PILRB*	0.2794	-2.5063
adult	7q22.1	99971067	99997722	29992	*PILRA*	0.2794	-2.5063
adult	7q22.1	99998494	100026431	55063	*ZCWPW1*	0.2794	-2.5063
adult	8q22.2	100025493	100133987	157680	*VPS13B*	1.0372	0
adult	8q22.2	100548863	100548958	693184	*MIR599*	1.0372	0
adult	8q22.2	100549013	100549089	100126309	*MIR875*	1.0372	0
adult	8q22.2	100890222	100906242	1345	*COX6C*	1.0372	0
adult	8q22.2	100973165	101118344	26166	*RGS22*	1.0372	0
adult	8q22.2	101145587	101158099	286151	*FBXO43*	1.0372	0
adult	8q22.2	101162838	101166230	5440	*POLR2K*	1.0372	0
adult	8q22.2	101170262	101254132	6674	*SPAG1*	1.0372	0
adult	8q22	101269286	101315487	25897	*RNF19A*	1.0372	0
adult	8q22.2	101521979	101572014	157567	*ANKRD46*	1.0372	0
adult	8q22.3	101585111	101661893	169166	*SNX31*	1.0372	0
adult	8q22.2-q23	101715143	101734315	26986	*PABPC1*	1.0372	0
adult	8q23.1	101930803	101962799	7534	*YWHAZ*	1.0372	0
adult	8q22.3	102064281	102088479	441374	*FLJ42969*	1.0372	0
adult	8q22.3	102209265	102217960	51123	*ZNF706*	1.0372	0
adult	8q22.3	102381120	102381823	83955	*NACAP1*	1.0372	0
adult	8q22.3	102504667	102681952	79977	*GRHL2*	1.0372	0
adult	8q22.2	102698769	102803439	83988	*NCALD*	1.0372	0
adult	8q23.1	103216728	103251059	50484	*RRM2B*	1.0372	0
adult	8q22	103264501	103424917	51366	*UBR5*	1.0372	0
adult	8q22.3	103563847	103573245	4956	*ODF1*	1.0372	0
adult	8q22.2	103661004	103666192	7071	*KLF10*	1.0372	0
adult	8q22.3	103838529	103876428	51582	*AZIN1*	1.0372	0
adult	8q24.12	116420723	116681255	7227	*TRPS1*	1.0486	-0.3737
adult	8q23.3	116962735	117337297	100859921	*LINC00536*	1.0486	-0.3737
adult	8q24.11	117657054	117768062	8667	*EIF3H*	1.0486	-0.3737
adult	8q24.11	117778741	117786921	84294	*UTP23*	1.0486	-0.3737
adult	8q24	117858172	117887105	5885	*RAD21*	1.0486	-0.3737
adult	8q24.11	117886662	117889107	644660	*RAD21-AS1*	1.0486	-0.3737

adult	8q24.11	117950463	117956239	441376	*AARD*	1.0486	-0.3737
adult	8q24.11	117962511	118188953	169026	*SLC30A8*	1.0486	-0.3737
adult	8q24.11	118532951	118552501	90390	*MED30*	1.0486	-0.3737
adult	8q24.11	118811601	119124058	2131	*EXT1*	1.0486	0
adult	8q24.12	119201694	119634184	401474	*SAMD12*	1.0486	0
adult	8q24.12	119633239	119738306	552860	*SAMD12-AS1*	1.0486	0
adult	8q24	119935795	119964383	4982	*TNFRSF11B*	1.0486	0
adult	8q23-q24.1	120079423	120119202	10584	*COLEC10*	1.0486	0
adult	8q23	120220609	120257914	114569	*MAL2*	1.0486	0
adult	8q24.1	120428551	120436678	4856	*NOV*	1.0486	0
adult	8q24.1	120569316	120651106	5168	*ENPP2*	1.0486	0
adult	8q24.12	120743013	120845074	6873	*TAF2*	1.0486	0
adult	8q24.12	120846180	120868170	79075	*DSCC1*	1.0486	0
adult	8q24.12	120885894	121063157	64798	*DEPTOR*	1.0486	0
adult	8q23	121137346	121384273	7373	*COL14A1*	1.0486	0
adult	8q22.1-q22.3	121408082	121457647	28998	*MRPL13*	1.0486	0
adult	8q24.12	121457637	121535875	27085	*MTBP*	1.0486	0
adult	8q23-q24	121547984	121824309	6641	*SNTB1*	1.0486	0
adult	8p22	13424351	13425797	157773	*C8orf48*	1.1814	0
adult	8p22	13947372	15095792	137868	*SGCZ*	1.1814	-0.246
adult	8p22	14710946	14711019	494332	*MIR383*	1.1814	-0.705
adult	8p22	15397595	15624158	7991	*TUSC3*	1.1814	-0.4728
adult	8p22	15965386	16050300	4481	*MSR1*	1.1814	-0.6762
adult	8p22	16850333	16859674	26281	*FGF20*	1.2037	-0.6762
adult	8p22	16884746	16980148	286097	*MICU3*	1.2037	-0.6762
adult	8p22	17013835	17080241	51201	*ZDHHC2*	1.2037	-0.6762
adult	8p22-p21.3	17086739	17104387	29883	*CNOT7*	1.2037	-0.6762
adult	8p22	17104400	17155533	137492	*VPS37A*	1.2037	-0.2268
adult	8p22	17154305	17271040	9108	*MTMR7*	1.2037	-0.2268
adult	8p22	17354596	17428077	6542	*SLC7A2*	1.2037	-0.2268
adult	8p22-p21.3	17433941	17500642	5157	*PDGFRL*	1.2037	-0.2268
adult	8p22	17501302	17555246	57509	*MTUS1*	1.2037	-0.2268
adult	8p22	17721899	17752913	2267	*FGL1*	1.2037	-0.2268

adult	8p22-p21.3	17780365	17887457	5108	*PCM1*	1.2037	0
adult	8p22	17913807	17941879	427	*ASAH1*	1.2037	0
adult	8p22	18027970	18081198	9	*NAT1*	1.2037	0
adult	8p22	18248754	18258723	10	*NAT2*	1.2037	0
adult	8p21.3	18384812	18666405	23362	*PSD3*	1.2037	0
adult	8p21.3	19041185	19103032	100128993	*LOC100128993*	1.2037	0
adult	8p21.2	19171080	19253729	63898	*SH2D4A*	1.2037	0
adult	8p21.3	19261671	19460056	55790	*CSGALNACT1*	1.19595	0
adult	8p21.3	19674917	19709586	55174	*INTS10*	1.1882	0
adult	8p22	19796581	19824770	4023	*LPL*	1.1882	0
adult	8p21.3	20002365	20040717	6570	*SLC18A1*	1.1882	0
adult	8p21.3	20054703	20079207	526	*ATP6V1B2*	1.1882	0
adult	8p22	20103675	20112803	11178	*LZTS1*	1.1882	0
adult	8p21.3	20831496	20852630	286114	*LOC286114*	1.1882	0
adult	8p21.3	21549529	21646346	2675	*GFRA2*	1.1882	0
adult	8p23.2	2792874	4852328	64478	*CSMD1*	1.30375	0
adult	8p12	33228343	33330664	84750	*FUT10*	1.0326	0
adult	8p12	33342684	33358778	84549	*MAK16*	1.0326	0
adult	8p12	33356026	33370703	80185	*TTI2*	1.0326	0
adult	8p12	33405271	33424646	79845	*RNF122*	1.0326	0
adult	8p12	33448847	33457624	78986	*DUSP26*	1.0326	0
adult	8p12	35092974	35652181	137970	*UNC5D*	1.0326	0
adult	8p11.23	36641841	36793643	157855	*KCNU1*	1.0326	0
adult	8p11.23	37553268	37557539	80139	*ZNF703*	1.0326	-0.2191
adult	8p11.2	37594096	37604071	11160	*ERLIN2*	1.0326	-0.2191
adult	8p11.23	37604073	37605564	728024	*LOC728024*	1.0326	-0.2191
adult	8p11.2	37620100	37637286	11212	*PROSC*	1.0326	-0.2191
adult	8p11.23	37701397	37707431	55290	*BRF2*	1.0326	-0.2191
adult	8p11.22	37716464	37757015	80223	*RAB11FIP1*	1.0326	-0.2191
adult	8p11.23	37791799	37797647	137362	*GOT1L1*	1.0326	-0.2191
adult	8p12	37820513	37824184	155	*ADRB3*	1.0326	-0.2191
adult	8p12	37888019	37917883	1978	*EIF4EBP1*	1.0326	-0.2191
adult	8p11.2	37963010	37997598	9070	*ASH2L*	1.0326	-0.2191

adult	8p11.2	38000217	38008600	6770	*STAR*	1.0326	-0.2191
adult	8p11.2	38020838	38034248	27257	*LSM1*	1.0326	-0.2191
adult	8p11.23	38034105	38070819	9530	*BAG4*	1.0326	-0.2191
adult	8p11.23	38089008	38096610	23259	*DDHD2*	1.0326	-0.2191
adult	8p11.23	38120649	38126738	84513	*PPAPDC1B*	1.0326	-0.2191
adult	8p11.2	38132560	38239790	54904	*WHSC1L1*	1.0326	-0.2191
adult	8p11.23	38243958	38267042	137994	*LETM2*	1.0326	-0.2191
adult	8p11.23-p11.22	38268655	38325363	2260	*FGFR1*	1.0326	-0.2191
adult	8p11.22	38368351	38386180	389649	*C8orf86*	1.0326	-0.2191
adult	8p11.22	38457692	38458775	286140	*RNF5P1*	1.0326	-0.2191
adult	8p11.22	38585703	38710546	6867	*TACC1*	1.0326	-0.2191
adult	8p11.22	38758752	38831430	59339	*PLEKHA2*	1.0326	-0.2191
adult	8p11.22	38831667	38846181	203100	*HTRA4*	1.0326	-0.2191
adult	8p11.22	38846326	38854041	83877	*TM2D2*	1.0326	-0.2191
adult	8p11.22	38854504	38962779	8754	*ADAM9*	1.0326	-0.2191
adult	8p11.22	38965047	39142436	203102	*ADAM32*	1.0326	-0.2191
adult	8p11.22	39172181	39260375	255926	*ADAM5*	1.0326	-0.2191
adult	8p11.23	39308563	39380508	1587	*ADAM3A*	1.0734	-0.2191
adult	8p11.22	39420630	39437653	100130964	*LOC100130964*	1.0734	-0.2191
adult	8p11.22	39442086	39469094	8749	*ADAM18*	1.0734	-0.2191
adult	8p11.2	39601254	39695808	2515	*ADAM2*	1.0734	-0.2191
adult	8p12-p11	39771327	39786309	3620	*IDO1*	1.0734	-0.2191
adult	8p11.21	39792473	39873910	169355	*IDO2*	1.0734	-0.2191
adult	8p11.2	40010986	40012827	56892	*C8orf4*	1.0734	-0.2191
adult	8p11.21	40388110	40755343	79698	*ZMAT4*	1.0734	0
adult	8p11.21	41119475	41166990	6422	*SFRP1*	1.0947	0
adult	8p11.21	41348080	41368499	51125	*GOLGA7*	1.0947	0
adult	8p11.21	41386724	41402565	84296	*GINS4*	1.0947	0
adult	8p11.21	41435706	41482520	137964	*AGPAT6*	1.0947	0
adult	8p11.21	41503828	41504878	157848	*NKX6-3*	1.0947	0
adult	8p11.1	41510743	41522804	286	*ANK1*	1.0947	0
adult	8p11	41786996	41909544	7994	*KAT6A*	1.0947	0
adult	8p11.2	42010463	42028701	10947	*AP3M2*	1.0947	0

adult	8p12	42032235	42065194	5327	*PLAT*	1.0947	0
adult	8p11.2	42128819	42190171	3551	*IKBKB*	1.0947	0
adult	8q11.1	47752507	47765929	497634	*LINC00293*	1.0876	0
adult	8q11.21	48100929	48104439	100287846	*LOC100287846*	1.0876	0
adult	8p11.2-p11.1	48649475	48650726	1052	*CEBPD*	1.0876	0
adult	8q11	48685668	48872743	5591	*PRKDC*	1.0876	0
adult	8q11.2	48872762	48890719	4173	*MCM4*	1.0876	0
adult	8q11.21	48920994	48974454	7336	*UBE2V2*	1.0876	0
adult	8q11.21	49627473	49647870	79645	*EFCAB1*	1.0876	0
adult	8q11	49830238	49833999	6591	*SNAI2*	1.0876	0
adult	8q11	49966894	49988642	492307	*C8orf22*	1.0876	0
adult	8q11.21	50824338	51706678	54212	*SNTG1*	1.1157	0
adult	8q11.22-q11.23	52232136	52722005	137902	*PXDNL*	1.1438	0
adult	8q11.23	52730134	52811746	115294	*PCMTD1*	1.1438	0
adult	8q11.23	53023391	53322439	9705	*ST18*	1.1438	0
adult	8q11.23	53446596	53478021	389658	*FAM150A*	1.1438	0
adult	8q11	53535017	53627026	9821	*RB1CC1*	1.1438	0
adult	8p22-q21.13	53852467	53853454	2831	*NPBWR1*	1.1438	0
adult	8q11.2	54138275	54164194	4986	*OPRK1*	1.1438	0
adult	8q11.2	54628102	54755602	51606	*ATP6V1H*	1.1438	0
adult	8q11.23	54764367	54871864	8601	*RGS20*	1.1438	0
adult	8q11.2	54879113	54935016	6917	*TCEA1*	1.1438	0
adult	8q11.23	54958926	55014577	10434	*LYPLA1*	1.1438	0
adult	8q11.2-q13	55047780	55061074	29088	*MRPL15*	1.1438	0
adult	8q11.23	55370494	55373456	64321	*SOX17*	1.1438	0
adult	8q12.1	55528626	55543394	6101	*RP1*	1.1438	0
adult	8q12.1	56015016	56438710	114786	*XKR4*	1.0463	0
adult	8q12.1	56361756	56367881	100133234	*SBF1P1*	1.0463	0
adult	8q12.1	56651302	56685966	137695	*TMEM68*	1.0463	0
adult	8q11	56685790	56739004	96764	*TGS1*	1.0463	0
adult	8q13	56792385	56925006	4067	*LYN*	1.0463	0
adult	8q12	56980738	56987140	6224	*RPS20*	1.0463	0
adult	8q12	56986397	56986460	26795	*SNORD54*	1.0463	0

adult	8q11	57025500	57026541	4342	*MOS*	1.0463	0
adult	8q12	57073467	57123859	5324	*PLAG1*	1.0463	0
adult	8q12.1	57124196	57131357	79145	*CHCHD7*	1.0463	0
adult	8q12.1	57212569	57233241	195814	*SDR16C5*	1.0463	0
adult	8q23-q24	57353512	57359293	5179	*PENK*	1.0463	0
adult	8q12.1	57870487	57906430	54928	*IMPAD1*	1.0463	0
adult	8q12.1	58173784	58179170	286177	*LOC286177*	1.0463	0
adult	8q12.1	58192101	58197290	26138	*LINC00588*	1.0463	0
adult	8q12.1	58907112	59062277	90362	*FAM110B*	1.0463	0
adult	8q12.1	59323822	59364060	137886	*UBXN2B*	1.0463	0
adult	8q11-q12	59402736	59412720	1581	*CYP7A1*	1.0463	0
adult	8q12	59465727	59495419	6386	*SDCBP*	1.0463	0
adult	8q12-q13	59496063	59571966	8439	*NSMAF*	1.0463	0
adult	8q12.1	59717976	60031767	9760	*TOX*	1.0463	0
adult	8q12.1	61101422	61193954	767	*CA8*	1.0463	0
adult	8q12.1	61429468	61536203	5862	*RAB2A*	1.0463	0
adult	8q12.2	61591323	61780586	55636	*CHD7*	1.0463	0
adult	8q12.2	61878679	61880307	100130298	*LOC100130298*	1.0463	0
adult	8q12.3	62200524	62414204	157807	*CLVS1*	1.0463	0
adult	8q12.1	62413114	62602408	444	*ASPH*	1.0463	0
adult	8q12.3	63890419	63897460	643763	*UG0898H09*	1.0463	0
adult	8q12.3	63927638	63951610	8836	*GGH*	1.0463	0
adult	8q12.3	63972047	63998612	7274	*TTPA*	1.0463	0
adult	8q12.3	64081111	64125346	253943	*YTHDF3*	1.0463	0
adult	8q12.3	65291705	65291814	406908	*MIR124-2*	1.0463	0
adult	8q12.3	65486865	65489820	401463	*LOC401463*	1.0463	0
adult	8q13	65492794	65496191	27319	*BHLHE22*	1.0463	0
adult	8q21.3	65508528	65711348	9420	*CYP7B1*	1.0463	0
adult	8q13.1	66073379	66092575	552859	*LINC00251*	1.0463	0
adult	8q13.1	66514690	66546452	55156	*ARMC1*	1.0463	0
adult	8q13.1	66556887	66620573	9650	*MTFR1*	1.0463	0
adult	8q13	66626568	66701329	5150	*PDE7A*	1.0463	0
adult	8q13.1	66933790	67012755	85479	*DNAJC5B*	1.0463	0

adult	8q13.1	67039277	67087718	84675	*TRIM55*	1.0463	0
adult	8q13	67088611	67090880	1392	*CRH*	1.0463	0
adult	8q13.1	67341262	67342968	23212	*RRS1*	1.0463	0
adult	8q13.1	67344717	67381044	137872	*ADHFE1*	1.0463	0
adult	8q13.1	67405490	67430759	254778	*C8orf46*	1.0463	0
adult	8q13.1	67474409	67525484	4603	*MYBL1*	1.0463	0
adult	8q13	67542487	67579452	80124	*VCPIP1*	1.0463	0
adult	8q13.1	67579786	67593377	56260	*C8orf44*	1.0463	0
adult	8q12	67624652	67774257	23678	*SGK3*	1.0463	0
adult	8q13.1	67679631	67680240	26255	*PTTG3P*	1.0463	0
adult	8q13.1	67782983	67814014	157777	*MCMDC2*	1.0463	0
adult	8q13	67834164	67837777	641638	*SNHG6*	1.0463	0
adult	8q13.1	67834708	67834784	641648	*SNORD87*	1.0463	0
adult	8q13.1	67858735	67874825	100129654	*TCF24*	1.0463	0
adult	8q13.1	67900366	67940786	286187	*PPP1R42*	1.0463	0
adult	8q13.1	67955314	67974562	10987	*COPS5*	1.0463	0
adult	8q13.2	67976602	68108849	79848	*CSPP1*	1.0463	0
adult	8q13	68109883	68255912	10565	*ARFGEF1*	1.0463	0
adult	8q13.2	68334404	68658620	57094	*CPA6*	1.0463	0
adult	8q13.2	68864602	69017654	80243	*PREX2*	1.0463	0
adult	8q13	69242956	69448062	116328	*C8orf34*	1.0463	0
adult	8q13.2	70378858	70573147	23213	*SULF1*	1.0463	0
adult	8q13.3	70584567	70745404	81796	*SLCO5A1*	1.0463	0
adult	8q13.3	70963885	70983562	63978	*PRDM14*	1.0463	0
adult	8q13.3	71024266	71316020	10499	*NCOA2*	1.0463	0
adult	8q13.3	71485452	71520694	23471	*TRAM1*	1.0463	0
adult	8q13.3	71549500	71581447	51110	*LACTB2*	1.0463	0
adult	8q13.3	71581599	71648177	389668	*XKR9*	1.0463	0
adult	8q13.3	72109667	72268746	2138	*EYA1*	1.0463	0
adult	8q21	72753776	72756731	9242	*MSC*	1.0463	0
adult	8q13	72933485	72987819	8989	*TRPA1*	1.0463	0
adult	8q13.3	73114986	73163869	392232	*LOC392232*	1.0463	0
adult	8q13.2	73449625	73850584	9312	*KCNB2*	1.0463	0

adult	8q21.11	73921096	73959987	7013	*TERF1*	1.0463	0
adult	8q21.11	73976777	74005507	157869	*SBSPON*	1.0463	0
adult	8q21.11	74202873	74205869	6129	*RPL7*	1.0463	0
adult	8q21.11	74206836	74237520	157506	*RDH10*	1.0463	0
adult	8q21.11	74332308	74353753	100128126	*STAU2-AS1*	1.0463	0
adult	8q21.11	74332603	74659162	27067	*STAU2*	1.0463	0
adult	8q21.11	74692331	74791145	55284	*UBE2W*	1.0463	0
adult	8q21.11	74857372	74884143	6921	*TCEB1*	1.0463	0
adult	8q21.11	74888376	74895018	54968	*TMEM70*	1.0463	0
adult	8q21.11	74903563	74941307	23643	*LY96*	1.0463	0
adult	8q21	75146934	75233596	56704	*JPH1*	1.0463	0
adult	8q21.11	75262617	75279335	54332	*GDAP1*	1.0463	0
adult	8q21.11	75736771	75767264	51050	*PI15*	1.1037	0
adult	8q21.11	75896707	75946793	83690	*CRISPLD1*	1.1037	0
adult	8q21.11	76452202	76479061	3174	*HNF4G*	1.1037	0
adult	8q21.11	77523113	77595510	100192378	*ZFHX4-AS1*	1.1002	0
adult	8q21.11	77593514	77779521	79776	*ZFHX4*	1.0967	0
adult	8q21.1	77892493	77912524	5828	*PEX2*	1.0967	0
adult	8q21.12	79428335	79517502	5569	*PKIA*	1.0967	0
adult	8q21.12	79578281	79631997	51101	*ZC2HC1A*	1.0967	0
adult	8q21	79635082	79636609	101241902	*LOC101241902*	1.0967	0
adult	8q12-q13	79645006	79717758	3574	*IL7*	1.0967	0
adult	8q21.13	80523048	80578410	11075	*STMN2*	1.0967	0
adult	8q21	80676244	80680098	23462	*HEY1*	1.0967	0
adult	8q21.1-q21.2	80831094	80942506	28957	*MRPS28*	1.0967	0
adult	8q21.13	80947102	80993066	7163	*TPD52*	1.0967	0
adult	8q13-q21.1	81397853	81438500	65986	*ZBTB10*	1.0967	0
adult	8q21.13	81540685	81787016	619279	*ZNF704*	1.0967	0
adult	8q21.13	81880045	82024303	55824	*PAG1*	1.0967	0
adult	8q21.13	82192717	82197012	2171	*FABP5*	1.0967	0
adult	8q21.3-q22.1	82352563	82359719	5375	*PMP2*	1.0967	0
adult	8q21.13	82370617	82373758	646480	*FABP9*	1.0967	0
adult	8q21	82390731	82395473	2167	*FABP4*	1.0967	0

adult	8q21.13	82437280	82443550	646486	*FABP12*	1.0967	0
adult	8q21.13-q21.3	82569150	82598589	3612	*IMPA1*	1.0967	0
adult	8q21.13	82605890	82607207	347051	*SLC10A5*	1.0967	0
adult	8q21.13	82613565	82633539	79752	*ZFAND1*	1.3018	0
adult	8q21.13	82644687	82671748	92421	*CHMP4C*	1.3274	0
adult	8q21.13	82711817	82754521	64089	*SNX16*	1.3274	0
adult	8q21.2	85095452	85834078	138046	*RALYL*	1.3274	0
adult	8q21.2	86019322	86058314	85444	*LRRCC1*	1.3274	0
adult	8q21.2	86089618	86126753	1875	*E2F5*	1.3274	0
adult	8q21.2	86126287	86132651	401466	*C8orf59*	1.3274	0
adult	8q21.2	86157715	86196302	377677	*CA13*	1.3274	0
adult	8q21.2	86240457	86253943	759	*CA1*	1.3274	0
adult	8q21.2	86351055	86361267	761	*CA3*	1.3274	0
adult	8q22	86376130	86393721	760	*CA2*	1.3274	0
adult	8q21.3	87060690	87081851	85481	*PSKH2*	1.2747	0
adult	8q21.3	87226287	87242604	157724	*SLC7A13*	1.2747	0
adult	8q21	87354993	87480178	11059	*WWP1*	1.2747	0
adult	8q21.3	87484577	87521009	51115	*RMDN1*	1.2747	0
adult	8q21.3	87526655	87573726	8895	*CPNE3*	1.2747	0
adult	8q21.3	87586162	87755903	54714	*CNGB3*	1.2747	0
adult	8q21.3	87878675	88394955	168975	*CNBD1*	1.2747	0
adult	8q21.3	88882970	88886296	138009	*DCAF4L2*	1.2747	0
adult	8q21.3	89049459	89339717	4325	*MMP16*	1.2747	0
adult	8q21	90769974	90803292	8767	*RIPK2*	1.2747	0
adult	8q21	90914095	90940095	734	*OSGIN2*	1.2747	0
adult	8q21	90945563	90996899	4683	*NBN*	1.2747	0
adult	8q21.3	91013579	91064227	1666	*DECR1*	1.2747	0
adult	8q21.3	91070835	91095109	793	*CALB1*	1.2747	0
adult	8q21.3	91634222	91658133	169200	*TMEM64*	1.2747	0
adult	8q21.3	91803920	91971630	64168	*NECAB1*	1.2747	0
adult	8q21.3	92006501	92053203	55529	*TMEM55A*	1.2747	0
adult	8q21.3	92082423	92099323	51633	*OTUD6B*	1.2747	0
adult	8q21.3	92114846	92231464	100130742	*LRRC69*	1.2747	0

adult	8q23	92261515	92406946	115111	*SLC26A7*	1.2747	0
adult	8q22	92967194	93029908	862	*RUNX1T1*	1.2747	0
adult	8q22.1	93725189	93798288	441369	*FLJ46284*	1.2747	0
adult	8q22.1	93895757	93977817	286144	*TRIQK*	1.2747	0
adult	8q22.1	94146323	94179079	389676	*C8orf87*	1.2747	0
adult	8q22.1	94358694	94712661	642924	*LINC00535*	1.2747	0
adult	8q22.1	94712734	94741478	137392	*FAM92A1*	1.2747	0
adult	8q22.1	94743730	94753224	389677	*RBM12B*	1.2747	0
adult	8q22.1	94752338	94753047	55472	*RBM12B-AS1*	1.2747	0
adult	8q22.1	94767071	94830347	91147	*TMEM67*	1.2747	0
adult	8q22.1	94929082	94938296	54704	*PDP1*	1.2747	0
adult	8q22.1	95139393	95220815	1015	*CDH17*	1.2747	0
adult	8q13-q21	95261484	95274547	2669	*GEM*	1.2747	0
adult	8q22.1	95384187	95449180	25788	*RAD54B*	1.2747	0
adult	8q	95439939	95449180	100861412	*FSBP*	1.2747	0
adult	8q22.1	95500004	95565746	25962	*KIAA1429*	1.044	0
adult	8q22.1	95649512	95651695	100288748	*LOC100288748*	1.044	0
adult	8q22.1	95653363	95719694	54845	*ESRP1*	1.044	0
adult	8q22.1	95732102	95806076	286148	*DPY19L4*	1.0372	0
adult	8q22.1	95835517	95892721	55656	*INTS8*	1.0372	0
adult	8q22.1	95892452	95907482	9134	*CCNE2*	1.0372	0
adult	8q22	95938199	95961615	94241	*TP53INP1*	1.0372	0
adult	8q22.1	96037213	96070944	137682	*NDUFAF6*	1.0372	0
adult	8q22.1	96145948	96168913	79666	*PLEKHF2*	1.0372	0
adult	8q22.1	96257140	96281462	157657	*C8orf37*	1.0372	0
adult	8q22.1	97154557	97173020	392255	*GDF6*	1.0372	0
adult	8q22	97238903	97247862	7381	*UQCRB*	1.0372	0
adult	8q22	97274113	97346779	9791	*PTDSS1*	1.0372	0
adult	8q22-q23	97505881	97624037	6383	*SDC2*	1.0372	0
adult	8q22.2	97657454	98155731	10404	*CPQ*	1.0372	0
adult	8q22.1	98285713	98290176	85453	*TSPYL5*	1.0372	0
adult	8q22.1	98656406	98742488	92140	*MTDH*	1.0372	0
adult	8q22.1	98787808	98864830	55353	*LAPTM4B*	1.0372	0

adult	8q22	98881248	99048946	4147	*MATN2*	1.0372	0
adult	8q22	99053937	99057818	6156	*RPL30*	1.0372	0
adult	8q22	99054313	99054445	26775	*SNORA72*	1.0372	0
adult	8q22	99114566	99129418	10247	*HRSP12*	1.0372	0
adult	8q22.1	99129520	99172069	10940	*POP1*	1.0372	0
adult	8q22.2	99204386	99306621	79815	*NIPAL2*	1.0372	0
adult	8q22	99439249	99443023	3788	*KCNS2*	1.0372	0
adult	8q22.2	99466858	99837899	6788	*STK3*	1.0372	0
adult	8q22.2	99956630	99964332	116039	*OSR2*	1.0372	0
adult	9p24.3	1050345	1057554	10655	*DMRT2*	0.2975	-2.1972
adult	9p24.3	116230	118417	2298	*FOXD4*	0.2975	-1.5045
adult	9p24.3	11986	14525	100287596	*DDX11L5*	0.2975	-1.5045
adult	9p24.3	121037	179075	55871	*CBWD1*	0.2975	-1.8201
adult	9p23	12693385	12710266	7306	*TYRP1*	0	-3.9262
adult	9p23	12775011	12823059	286343	*LURAP1L*	0	-3.9262
adult	9p23	13105702	13279563	8777	*MPDZ*	0	-3.9262
adult	9p23	13927969	13945606	100113404	*LINC00583*	0	-2.9486
adult	9p24.1	14081841	14314045	4781	*NFIB*	0.307	-2.515
adult	9p24.3	14510	29739	100287171	*WASH1*	0.2975	-1.5045
adult	9p22.3	14611068	14693480	340481	*ZDHHC21*	0.5104	-2.0471
adult	9p23-p22	14719731	14722715	9350	*CER1*	0.5742	-2.0129
adult	9p22.3	14734663	14779531	158326	*FREM1*	0.5742	-2.0129
adult	9p22.3	14993324	15019722	389705	*LOC389705*	0.5742	-2.0129
adult	9p22.3	15170841	15250198	158219	*TTC39B*	0.5742	-1.9521
adult	9p22.3	15422781	15461627	6619	*SNAPC3*	0.5742	-1.9521
adult	9p22.3	15464064	15511017	11168	*PSIP1*	0.5742	-1.9521
adult	9p22.3	15553096	15971897	203238	*CCDC171*	0.56865	-1.9521
adult	9p22.3	16203932	16253105	100129385	*C9orf92*	0.5631	-2.3461
adult	9p22.2	16409500	16870786	54796	*BNC2*	0.5631	-2.3461
adult	9p22.2	17134988	17302049	54875	*CNTLN*	0.5631	-2.0323
adult	9p22	17578951	17797126	6456	*SH3GL2*	0.5631	-2.2579
adult	9p21.3	18474078	18684952	92949	*ADAMTSL1*	0.4773	-2.4291
adult	9p22.1	19049371	19051021	10670	*RRAGA*	0.4773	-2.4015

adult	9p22.1	19053134	19102940	54801	*HAUS6*	0.4773	-2.4015
adult	9p22.1	19063653	19063784	677776	*SCARNA8*	0.4773	-2.4015
adult	9p22.1	19115758	19127604	123	*PLIN2*	0.4773	-2.4015
adult	9p22.1	19230762	19374266	55667	*DENND4C*	0.4773	-2.4015
adult	9p21	19376253	19380235	6194	*RPS6*	0.4773	-2.4015
adult	9p22.1	19408924	19452500	340485	*ACER2*	0.4773	-4.4015
adult	9p22.1	19507449	19787017	25769	*SLC24A2*	0.2299	-8.2125
adult	9p22.3	2015218	2193623	6595	*SMARCA2*	0.2975	-2.1972
adult	9p22	20341662	20622542	4300	*MLLT3*	0.2299	-9.5844
adult	9p21	20658307	20995954	54914	*FOCAD*	0.2299	-12.111
adult	9p21.3	20716103	20716187	574444	*MIR491*	0.2299	-11.892
adult	9p21	21077103	21077962	3456	*IFNB1*	0.2299	-13.691
adult	9p22	21140630	21141900	3467	*IFNW1*	0.2299	-15.324
adult	9p22	21165635	21166659	3452	*IFNA21*	0.2299	-15.324
adult	9p22	21186617	21187598	3441	*IFNA4*	0.2299	-15.324
adult	9p22	21201467	21202204	3444	*IFNA7*	0.2299	-15.324
adult	9p22	21206179	21207142	3446	*IFNA10*	0.2299	-15.324
adult	9p22	21216371	21217310	3449	*IFNA16*	0.2299	-15.324
adult	9p22	21227241	21228221	3451	*IFNA17*	0.2299	-15.324
adult	9p22	21239200	21239978	3448	*IFNA14*	0.2299	-15.324
adult	9p22	21277686	21278562	3453	*IFNA22P*	0.2299	-16.947
adult	9p22	21304612	21305312	3442	*IFNA5*	0.2299	-16.947
adult	9p24.3	213107	215893	157983	*C9orf66*	0.2975	-1.8201
adult	9p22	21331017	21335429	55958	*KLHL9*	0.2299	-16.947
adult	9p22	21350316	21350886	3443	*IFNA6*	0.2299	-16.947
adult	9p22	21367370	21368075	3447	*IFNA13*	0.2299	-16.947
adult	9p22	21384253	21385396	3440	*IFNA2*	0.2299	-16.947
adult	9p22	21409145	21410184	3445	*IFNA8*	0.2299	-16.947
adult	9p22	21440452	21441315	3439	*IFNA1*	0.2299	-16.947
adult	9p21.3	21454266	21559697	554202	*MIR31HG*	0.2299	-16.947
adult	9p21.3	21480838	21482312	338376	*IFNE*	0.2299	-16.947
adult	9p24.3	214864	465259	81704	*DOCK8*	0.2975	-2.1795
adult	9p21.3	21512113	21512184	407035	*MIR31*	0.2299	-16.947

adult	9p21	21802634	21865969	4507	*MTAP*	0.2299	-17.962
adult	9p21	21967750	21974826	1029	*CDKN2A*	0.2299	-20.459
adult	9p21.3	21994789	22077889	100048912	*CDKN2B-AS1*	0.2299	-25.947
adult	9p21	22002901	22009312	1030	*CDKN2B*	0.2299	-24.375
adult	9p21.3	22446839	22452472	63951	*DMRTA1*	0.2299	-19.838
adult	9p21	23690102	23821478	1993	*ELAVL2*	0.3033	-11.03
adult	9p21.3	24543212	24545674	100129669	*IZUMO3*	0.3056	-9.5736
adult	9p21.2	25676386	25678856	286319	*TUSC1*	0.3056	-6.5622
adult	9p21.2	26066672	26118406	100506422	*LOC100506422*	0.3056	-6.5622
adult	9p24	2621792	2654485	7436	*VLDLR*	0.2975	-2.1972
adult	9p21.2	26840682	26892826	79886	*CAAP1*	0.3056	-6.5235
adult	9p21	26903367	26947468	9373	*PLAA*	0.3056	-6.5235
adult	9p21.2	26947036	27062931	80173	*IFT74*	0.3056	-6.2916
adult	9p21.2	26993134	27005691	64922	*LRRC19*	0.3056	-6.2916
adult	9p21	27109138	27230176	7010	*TEK*	0.3056	-4.7229
adult	9p24.2	2717525	2730037	169522	*KCNV2*	0.2975	-2.1972
adult	9p21	27245681	27282791	158035	*LINC00032*	0.3056	-4.7229
adult	9p21	27284653	27297137	54586	*EQTN*	0.3056	-4.7229
adult	9p21.2	27325206	27529850	79817	*MOB3B*	0.3056	-4.7229
adult	9p21.2	27546543	27573491	203228	*C9orf72*	0.3056	-4.2916
adult	9p21.2	27948083	28719303	158038	*LINGO2*	0.55805	-4.7706
adult	9p24.2	2804154	2844130	9933	*KIAA0020*	0.2975	-2.1972
adult	9p21.1	28863623	28863704	100126310	*MIR876*	0.2094	-5.2351
adult	9p21.1	28888876	28888953	100126316	*MIR873*	0.2094	-5.2351
adult	9p24.2	3218296	3526001	5991	*RFX3*	0.2975	-2.1972
adult	9p21.1	32384600	32450832	48	*ACO1*	0.2415	-4.2035
adult	9p12	32455299	32526322	23586	*DDX58*	0.2415	-3.9621
adult	9p21	32540541	32552626	10210	*TOPORS*	0.2415	-3.7308
adult	9p21.1	32551141	32553015	100129250	*TOPORS-AS1*	0.2415	-3.7308
adult	9p21.1	32553523	32573182	4712	*NDUFB6*	0.2415	-3.7308
adult	9p21.1	32629451	32635667	138474	*TAF1L*	0.2415	-3.7308
adult	9p21.1	32783496	32789199	401498	*TMEM215*	0.2415	-3.7308
adult	9p13.3	32972603	33001574	54840	*APTX*	0.2415	-3.7308

adult	9p13.3	33025200	33039906	3301	*DNAJA1*	0.2415	-3.7308
adult	9p12	33041849	33076714	55234	*SMU1*	0.2415	-3.7308
adult	9p13	33110638	33167356	2683	*B4GALT1*	0.2415	-3.7308
adult	9p13.3	33240195	33248565	27290	*SPINK4*	0.2415	-3.7308
adult	9p12	33252469	33264759	573	*BAG1*	0.2415	-3.7308
adult	9p13.3	33264876	33282067	51510	*CHMP5*	0.2415	-3.7308
adult	9p13.3	33290417	33348721	4799	*NFX1*	0.2415	-3.7308
adult	9p13	33384947	33402517	364	*AQP7*	0.2415	-3.7308
adult	9p13	33441151	33447631	360	*AQP3*	0.2415	-3.7308
adult	9p13.3	33461350	33473941	65083	*NOL6*	0.2415	-3.7308
adult	9p13.3	33504534	33511164	441394	*SUGT1P1*	0.2415	-3.7308
adult	9p13.3	33524410	33573001	441459	*ANKRD18B*	0.2415	-3.7308
adult	9p13.3	33673501	33677418	11191	*PTENP1*	0.2415	-3.7308
adult	9p11.2	33750463	33799229	5646	*PRSS3*	0.2415	-3.7308
adult	9p13.3	33817181	33920401	54926	*UBE2R2*	0.2415	-3.6133
adult	9p13.3	33921690	34048947	55833	*UBAP2*	0.2415	-3.6133
adult	9p13.3	33934294	33934373	101340252	*SNORD121B*	0.2415	-3.6133
adult	9p13.3	33952761	33952852	100113379	*SNORD121A*	0.2415	-3.6133
adult	9p13.3	34086380	34126771	25853	*DCAF12*	0.2415	-3.6133
adult	9p13.3	34179002	34252521	51271	*UBAP1*	0.2415	-3.6133
adult	9p13.3	34252377	34329198	347240	*KIF24*	0.2415	-3.6133
adult	9p13	34329503	34343711	318	*NUDT2*	0.2415	-3.6133
adult	9p13.3	34366663	34376894	57462	*KIAA1161*	0.2415	-3.6133
adult	9p13.3	34379016	34381598	84688	*C9orf24*	0.2415	-3.6133
adult	9p24.3	34393	35864	654835	*FAM138C*	0.2975	-1.5045
adult	9p13.3	34398181	34458568	203259	*FAM219A*	0.2415	-3.6133
adult	9p13.3	34458749	34520987	27019	*DNAI1*	0.2415	-3.6133
adult	9p13.3	34521039	34523037	375704	*ENHO*	0.2415	-3.6133
adult	9p13	34551429	34589735	1271	*CNTFR*	0.2415	-3.6133
adult	9p13.3	34610481	34612110	138716	*RPP25L*	0.2415	-3.6133
adult	9p13	34613541	34620520	11258	*DCTN3*	0.2415	-3.6133
adult	9p13.3	34621454	34628011	138715	*ARID3C*	0.2415	-3.6133
adult	9p13.3	34634718	34637823	10280	*SIGMAR1*	0.2415	-3.6133

adult	9p13	34646585	34650595	2592	*GALT*	0.2415	-3.6133
adult	9p13	34652181	34661898	3590	*IL11RA*	0.2415	-3.6133
adult	9p13	34661879	34662689	10850	*CCL27*	0.2415	-3.6133
adult	9p13	34689566	34691274	6363	*CCL19*	0.2415	-3.6133
adult	9p13	34709001	34710164	6366	*CCL21*	0.2415	-3.6133
adult	9p12	34723049	34729535	259308	*FAM205A*	0.2415	-3.6133
adult	9p13.3	34958191	34982541	23349	*KIAA1045*	0.2415	-3.507
adult	9p13.3	34989637	34998430	25822	*DNAJB5*	0.2415	-3.507
adult	9p13.3	35041091	35045988	138724	*C9orf131*	0.2415	-3.507
adult	9p13.3	35056064	35072739	7415	*VCP*	0.2415	-3.507
adult	9p13	35073834	35080013	2189	*FANCG*	0.2415	-3.507
adult	9p13.3	35088684	35096546	84720	*PIGO*	0.2415	-3.507
adult	9p13.1	35099772	35103192	30968	*STOML2*	0.2415	-3.507
adult	9p13.3	35104117	35115908	80256	*FAM214B*	0.2415	-3.507
adult	9p13.3	35161988	35405332	10497	*UNC13B*	0.2415	-3.507
adult	9p13.3	35406751	35451105	158381	*ATP8B5P*	0.2415	-3.507
adult	9p13.3	35489948	35561895	9853	*RUSC2*	0.2415	-3.507
adult	9p13.3	35561826	35563896	730112	*FAM166B*	0.2415	-3.507
adult	9p13	35605280	35610038	7016	*TESK1*	0.2415	-3.1517
adult	9p13.3	35609975	35618424	971	*CD72*	0.2415	-3.1517
adult	9p13-p12	35649296	35650947	27240	*SIT1*	0.2415	-3.4513
adult	9p13.3	35657747	35658015	6023	*RMRP*	0.2415	-3.4513
adult	9p13.3	35658286	35661500	203260	*CCDC107*	0.2415	-3.4513
adult	9p13.3	35659340	35665278	84904	*ARHGEF39*	0.2415	-3.4513
adult	9p13.3	35673914	35681154	768	*CA9*	0.2415	-3.4513
adult	9p13	35681989	35690053	7169	*TPM2*	0.2415	-3.4513
adult	9p13	35697333	35732392	7094	*TLN1*	0.2415	-3.4513
adult	9p13.3	35732316	35737005	10488	*CREB3*	0.2415	-3.4513
adult	9p13.3	35736862	35749225	57704	*GBA2*	0.2415	-3.4513
adult	9p13.3	35749276	35753264	9827	*RGP1*	0.2415	-3.4513
adult	9p13.3	35752987	35754274	692094	*MSMP*	0.2415	-3.4513
adult	9p21-p12	35792405	35809728	4882	*NPR2*	0.2415	-3.4513
adult	9p13.3	35807781	35812259	26206	*SPAG8*	0.2415	-3.4513

adult	9p13.3	35812956	35815042	84681	*HINT2*	0.2415	-3.4513
adult	9p13.3	35817013	35828744	392307	*FAM221B*	0.2415	-3.4513
adult	9p13.3	35829221	35847232	51754	*TMEM8B*	0.2415	-3.4513
adult	9p13.3	35860270	35865515	92973	*LINC00950*	0.2415	-3.4513
adult	9p13.3	35869459	35870398	392309	*OR13J1*	0.2415	-3.4513
adult	9p13.3	35906188	35907138	646962	*HRCT1*	0.2415	-3.4513
adult	9p13.3	35957104	35958151	56656	*OR2S2*	0.2415	-3.3689
adult	9p13.3	36036909	36124452	8434	*RECK*	0.2415	-3.3328
adult	9p13.3	36136532	36163910	152007	*GLIPR2*	0.2415	-3.3328
adult	9p13.3	36169388	36171331	881	*CCIN*	0.2415	-3.3328
adult	9p13	36190852	36212059	1211	*CLTA*	0.2415	-3.3328
adult	9p13.3	36214438	36258496	10020	*GNE*	0.2415	-3.3328
adult	9p13	36336398	36400296	152006	*RNF38*	0.27615	-3.2785
adult	9p13.2	36572858	36677680	9833	*MELK*	0.3108	-3.1289
adult	9p13	36833271	37034476	5079	*PAX5*	0.3108	-2.7055
adult	9p13.2	36864250	36864305	100616278	*MIR4540*	0.3108	-3.1289
adult	9p13.2	37120468	37358145	84186	*ZCCHC7*	0.3108	-2.3249
adult	9q12	37422706	37436986	9380	*GRHPR*	0.3108	-2.6061
adult	9p13.2	37438099	37465407	9925	*ZBTB5*	0.3108	-2.6061
adult	9p13.2	37485931	37503694	64425	*POLR1E*	0.3108	-2.6061
adult	9p13.2	37510888	37576250	26267	*FBXO10*	0.3108	-2.6061
adult	9p13.2	37588411	37592636	401505	*TOMM5*	0.3108	-2.6061
adult	9p13.2	37651051	37746901	22844	*FRMPD1*	0.3108	-2.6061
adult	9p13.2	37753799	37778969	158234	*TRMT10B*	0.3108	-2.6061
adult	9p11	37779710	37785089	51010	*EXOSC3*	0.3108	-2.6061
adult	9p13.2	37800782	37867665	79269	*DCAF10*	0.3108	-2.6061
adult	9p13.3-p12	37877571	37904350	92014	*SLC25A51*	0.3108	-2.3249
adult	9p13.2	37915894	38069210	6461	*SHB*	0.3108	-2.081
adult	9p24.2	3824127	4152183	169792	*GLIS3*	0.2975	-2.1972
adult	9p11.1	38392660	38398662	219	*ALDH1B1*	0.3108	-2.4556
adult	9p13.1	38406524	38424444	347252	*IGFBPL1*	0.3108	-2.4556
adult	9p13.1	38571360	38620360	253650	*ANKRD18A*	0.3108	-2.4556
adult	9p13.1	38621084	38623277	158228	*FAM201A*	0.3108	-2.2544

adult	9p24.2	3898645	3901248	84850	*GLIS3-AS1*	0.2975	-2.1972
adult	9p24	4490426	4587469	6505	*SLC1A1*	0.2975	-2.2422
adult	9p24.2	4598315	4666674	55064	*SPATA6L*	0.2975	-2.2352
adult	9p24.1	4662293	4665272	403313	*PPAPDC2*	0.2975	-2.2319
adult	9p24.1	4679552	4708398	55664	*CDC37L1*	0.2975	-2.2319
adult	9p24.3	470293	746106	23189	*KANK1*	0.2975	-2.1972
adult	9p24.1	4709556	4726227	50808	*AK3*	0.2975	-2.2319
adult	9p24.1-p23	4792833	4861077	10171	*RCL1*	0.2975	-2.2319
adult	9p24.1	4850296	4850375	406894	*MIR101-2*	0.2975	-2.2319
adult	9p24	4985244	5128183	3717	*JAK2*	0.2975	-2.2319
adult	9p24	5163862	5185618	11172	*INSL6*	0.2975	-2.2319
adult	9p24	5231418	5233967	3641	*INSL4*	0.2975	-2.2319
adult	9p24.1	5299865	5304611	6019	*RLN2*	0.2975	-2.2319
adult	9p24.1	5334931	5339873	6013	*RLN1*	0.2975	-2.2319
adult	9p24.1	5357966	5437937	55848	*PLGRKT*	0.2975	-2.2319
adult	9p24	5450502	5470567	29126	*CD274*	0.2975	-2.2319
adult	9p24.2	5510544	5571282	80380	*PDCD1LG2*	0.2975	-2.2319
adult	9p24	5784571	5833081	79956	*ERMP1*	0.2975	-2.2335
adult	9p24.1	5890908	5909822	2315	*MLANA*	0.2975	-2.2335
adult	9p24.1	5919007	6008003	158358	*KIAA2026*	0.2975	-2.2599
adult	9p24.1	6011018	6015640	26953	*RANBP6*	0.2975	-2.2763
adult	9p24.1	6215785	6257983	90865	*IL33*	0.2975	-2.2663
adult	9p24.1	6328348	6330918	89882	*TPD52L3*	0.2975	-2.2663
adult	9p24.1	6413150	6507051	115426	*UHRF2*	0.2975	-2.2663
adult	9p22	6532463	6645692	2731	*GLDC*	0.2975	-2.2663
adult	9p24.1	6720862	7077264	23081	*KDM4C*	0.2975	-2.3212
adult	9p23-p24.3	8314245	10612723	5789	*PTPRD*	0.21855	-2.4888
adult	9p24.3	841689	969090	1761	*DMRT1*	0.2975	-2.1972
adult	9p24.3	976967	991732	58524	*DMRT3*	0.2975	-2.1972
children	1q31.1-q31.2	190594019	190770788	440704	*LOC440704*	1.9155	-0.2573
children	1q31.2	192127591	192154945	64407	*RGS18*	1.8336	-0.2573
children	1q31.2	192286121	192336414	431704	*RGS21*	1.8336	-0.2573
children	1q31	192544856	192549159	5996	*RGS1*	1.8336	-0.2573

children	1q31.2	192605267	192629440	6003	*RGS13*	1.8336	-0.2573
children	1q31	192778168	192781407	5997	*RGS2*	1.8336	-0.2573
children	1q32	192981495	193028523	51377	*UCHL5*	1.8336	-0.2573
children	1q31	193028551	193055115	6738	*TROVE2*	1.8336	-0.2573
children	1q31.2	193065594	193074608	51022	*GLRX2*	1.8336	-0.2573
children	1q25	193091087	193223942	79577	*CDC73*	1.8336	-0.2573
children	1q31	193147859	193155743	8707	*B3GALT2*	1.8336	-0.2573
children	1q31.3	196194909	196577561	343450	*KCNT2*	1.8269	-0.2573
children	1q32	196621007	196670695	3075	*CFH*	1.8269	-0.2573
children	1q32	196743929	196763203	10878	*CFHR3*	1.8269	-0.2573
children	1q32	196788860	196801319	3078	*CFHR1*	1.8269	-0.2573
children	1q32	196857143	196887843	10877	*CFHR4*	1.5673	-0.2573
children	1q31.3	196912897	196928356	3080	*CFHR2*	1.7968	-0.2573
children	1q31.3	196946666	196978803	81494	*CFHR5*	1.7968	-0.2573
children	1q31-q32.1	197008320	197036397	2165	*F13B*	1.7968	-0.2573
children	1q31	197053256	197115824	259266	*ASPM*	1.7968	-0.2573
children	1q31.3	197122813	197169672	360023	*ZBTB41*	1.7968	-0.2573
children	1q31.3	197170591	197447585	23418	*CRB1*	1.7968	-0.2573
children	1q31.3	197473878	197744623	163486	*DENND1B*	1.7968	-0.2573
children	1q31.3	197871681	197876497	388722	*C1orf53*	1.7968	-0.2573
children	1q31.1	197881634	197899273	56956	*LHX9*	1.7968	-0.2573
children	1q31.3	198126107	198291548	140609	*NEK7*	1.7968	-0.2573
children	1q32.2	210851656	211307457	3756	*KCNH1*	1.3856	0
children	1q32.2	211432707	211486655	55758	*RCOR3*	1.3856	0
children	1q32	211499956	211548286	7188	*TRAF5*	1.3856	0
children	1q32.3	211556096	211605877	84791	*LINC00467*	1.3856	0
children	1q32.3	211649863	211666259	343035	*RD3*	1.3856	0
children	1q32.3	211748380	211752099	7779	*SLC30A1*	1.3856	0
children	1q32.3	211831598	211848972	4751	*NEK2*	1.6051	0
children	1q32	211916798	212004114	9926	*LPGAT1*	1.6051	0
children	1q32.3	212113740	212209002	25896	*INTS7*	1.6051	0
children	1q32	212208894	212278348	51514	*DTL*	1.6051	0
children	1q32.2-q32.3	212458878	212535205	5525	*PPP2R5A*	1.3856	0

children	1q32.3	212526159	212526292	692157	*SNORA16B*	1.3856	0
children	1q32.3	212537815	212588243	55248	*TMEM206*	1.3856	0
children	1q32.3	212606228	212619721	29937	*NENF*	1.3856	0
children	1q32.3	212738675	212794119	467	*ATF3*	1.3856	0
children	1q32.3	212797788	212800120	149647	*FAM71A*	1.3856	0
children	1q32.3	212859758	212873327	55509	*BATF3*	1.3856	0
children	1q41	212899494	212965139	25936	*NSL1*	1.3856	0
children	1q32.3	212965169	212990167	128387	*TATDN3*	1.3856	0
children	1q32.3	213029945	213031480	642946	*FLVCR1-AS1*	1.3856	0
children	1q32.3	213031596	213072705	28982	*FLVCR1*	1.3856	0
children	1q32.3	213123861	213164927	79805	*VASH2*	1.3856	0
children	1q32.3	213165523	213189217	90806	*ANGEL2*	1.3856	0
children	1q41	213224574	213446808	26750	*RPS6KC1*	1.3856	0
children	1q32.3	214098091	214099996	100861504	*LINC00538*	1.3856	0
children	1q41	214161277	214214847	5629	*PROX1*	1.3856	0
children	1q32.3	214454564	214510477	56950	*SMYD2*	1.3856	0
children	1q32.2	214522038	214725024	5784	*PTPN14*	1.3856	0
children	1q41	214776531	214837914	1063	*CENPF*	1.3856	0
children	1q41	215178884	215410436	3776	*KCNK2*	1.3856	0
children	1q41	215740734	215795149	51133	*KCTD3*	1.3856	0
children	1q41	215796235	216596738	7399	*USH2A*	1.3856	0
children	1q41	216676587	216896814	2104	*ESRRG*	1.3856	-0.2856
children	1q41	217600334	217804444	55105	*GPATCH2*	1.3856	-0.2856
children	1q41	217804665	218041495	128153	*SPATA17*	1.3856	-0.2856
children	1q41	218066241	218094146	100885798	*LINC00210*	1.3856	0
children	1q41	218458628	218511325	51018	*RRP15*	1.3856	0
children	1q41	218518675	218617961	7042	*TGFB2*	1.3856	0
children	1q41	219347172	219386207	127018	*LYPLAL1*	1.3856	0
children	1p34.1	220046618	220292777	26828	*RNU5F-1*	1.3856	0
children	1q41	220087605	220101993	55532	*SLC30A10*	1.3856	0
children	1q41	220141941	220220000	2058	*EPRS*	1.3856	0
children	1q41	220230823	220263195	10380	*BPNT1*	1.3856	0
children	1q41	220267454	220321383	55699	*IARS2*	1.3856	0

children	1q41	220291194	220291304	406997	*MIR215*	1.3856	0
children	1q41	220291498	220291583	406969	*MIR194-1*	1.3856	0
children	1q41	220321609	220445843	25782	*RAB3GAP2*	1.3856	0
children	1q41	220373887	220374018	677818	*SNORA36B*	1.3856	0
children	1q41	220439520	220441057	6791	*AURKAPS1*	1.3856	0
children	1q42.2	232533711	232651354	57568	*SIPA1L2*	1.3649	0
children	1q42.2	232940637	232946092	54627	*MAP10*	1.3649	0
children	1q42.2	233086369	233114219	84284	*NTPCR*	1.3649	0
children	1q42.2	233119881	233431459	80003	*PCNXL2*	1.3649	0
children	1q42	233463513	233520894	84451	*KIAA1804*	1.3649	0
children	1q42-q43	233749749	233808258	3775	*KCNK1*	1.3649	-0.3122
children	1q42.2	234040457	234460264	148641	*SLC35F3*	1.56375	-0.3194
children	1q42.2	234509182	234519795	388753	*COA6*	1.5686	-0.3265
children	1q42.3	234527058	234614849	6894	*TARBP1*	1.5681	-0.3265
children	1q42.3	234740014	234745271	359948	*IRF2BP2*	1.5676	-0.3265
children	1q42.3	234765056	234770526	100302691	*LINC00184*	1.5676	-0.3265
children	1q42	235272657	235292256	9804	*TOMM20*	1.5676	-0.3258
children	1q42.3	235291117	235291252	677802	*SNORA14B*	1.5676	-0.3258
children	1q42.3	235294497	235324571	23029	*RBM34*	1.5676	-0.3258
children	1q42.3	235330209	235490802	51742	*ARID4B*	1.5676	-0.3258
children	1q43	235491752	235507844	9453	*GGPS1*	1.5676	-0.3258
children	1q42.3	235530674	235612283	6905	*TBCE*	1.5676	-0.3258
children	1q42.3	235610504	235667781	148789	*B3GALNT2*	1.5676	-0.3258
children	1q42.3	235710984	235813293	2786	*GNG4*	1.5676	-0.3258
children	1q42.1-q42.2	235824330	236030227	1130	*LYST*	1.5676	-0.3258
children	1q43	236139131	236228481	4811	*NID1*	1.5676	-0.3258
children	1q42-q43	236305831	236372209	7107	*GPR137B*	1.5676	-0.3258
children	1q42.2-q43	236378421	236445339	56605	*ERO1LB*	1.5676	-0.3258
children	1q42.3	236557679	236648008	128178	*EDARADD*	1.5676	-0.3311
children	1q43	236681513	236716279	3964	*LGALS8*	1.5676	-0.3311
children	1q43	236686368	236687808	100287902	*LGALS8-AS1*	1.5676	-0.3311
children	1q43	236712304	236767841	55127	*HEATR1*	1.5676	-0.3311
children	1q42-q43	236849753	236927927	88	*ACTN2*	1.5676	-0.3311

children	1q43	236958580	237067281	4548	*MTR*	1.5676	-0.3311
children	1q43	237167402	237167718	645745	*MT1HL1*	1.5676	-0.3311
children	1q43	237205701	237997288	6262	*RYR2*	1.5676	-0.3311
children	1q43	238025474	238091619	100130331	*LOC100130331*	1.5676	-0.3311
children	1q43	238041163	238054222	57829	*ZP4*	1.5676	-0.3311
children	1q43	239792372	240072717	1131	*CHRM3*	1.5676	-0.3311
children	1q43	240170823	240176560	645884	*RPS7P5*	1.5676	-0.3311
children	1q43	240255184	240638489	56776	*FMN2*	1.5622	-0.3311
children	1q43	240652872	240775462	64388	*GREM2*	1.5568	-0.3311
children	1q43	240938813	241520530	6000	*RGS7*	1.3548	0
children	1q42.1	241660856	241683085	2271	*FH*	1.3548	0
children	1q42-q44	241695433	241758949	8564	*KMO*	1.3548	0
children	1q43	241756451	241803701	23596	*OPN3*	1.3548	0
children	1q43	241792166	241799232	1122	*CHML*	1.3548	0
children	1q43	241815579	241965434	128025	*WDR64*	1.3548	0
children	1q43	242011492	242053241	9156	*EXO1*	1.3548	0
children	1q43	242158791	242162385	440738	*MAP1LC3C*	1.3548	0
children	1q43	242251688	242612784	200150	*PLD5*	1.3548	0
children	1q44	243287729	243418708	9859	*CEP170*	1.3548	0
children	1q43	243419306	243663393	10806	*SDCCAG8*	1.3548	0
children	1q44	243651534	244006584	10000	*AKT3*	1.3548	0
children	1q44	244080703	244210619	339529	*LOC339529*	1.3548	0
children	1q44	244212240	244220780	10472	*ZBTB18*	1.3548	0
children	1q44	244515936	244552388	200159	*C1orf100*	1.3548	0
children	1q44	244571793	244615436	159	*ADSS*	1.3548	0
children	1q44	244624672	244803662	257044	*C1orf101*	1.3548	0
children	1q44	244816349	244872336	51029	*DESI2*	1.3548	0
children	1q44	244998630	245008365	116228	*COX20*	1.3548	0
children	1q44	245013601	245027827	3192	*HNRNPU*	1.3548	0
children	1q44	245133170	245251148	84288	*EFCAB2*	1.3548	0
children	1q44	245318286	245866428	55083	*KIF26B*	1.3548	0
children	1q44	245912641	246580714	64754	*SMYD3*	1.3548	0
children	1q44	246679340	246687589	255654	*LOC255654*	1.3548	0

children	1q44	246703862	246729565	64216	*TFB2M*	1.3548	0
children	1q44	246729638	246811544	163882	*CNST*	1.3548	0
children	1q44	246887377	246931440	51097	*SCCPDH*	1.3548	0
children	1q44	247002401	247094726	25909	*AHCTF1*	1.3548	0
children	1q44	247108848	247171395	57116	*ZNF695*	1.3548	0
children	1q	247108848	247242115	100533111	*ZNF670-ZNF695*	1.3548	0
children	1q44	247197939	247242115	93474	*ZNF670*	1.3548	0
children	1q44	247263263	247267674	79862	*ZNF669*	1.3548	0
children	1q44	247273461	247275719	388759	*C1orf229*	1.3548	0
children	1q44	247285276	247335319	7678	*ZNF124*	1.3548	0
children	1q44	247419373	247420447	317705	*VN1R5*	1.3548	0
children	1q44	247463621	247495045	84838	*ZNF496*	1.3548	0
children	1q44	247579457	247612406	114548	*NLRP3*	1.3548	0
children	1q44	247614330	247615284	127623	*OR2B11*	1.3548	0
children	1q44	247654369	247655711	441932	*OR2W5*	1.3548	0
children	1q44	247687980	247694106	148824	*GCSAML-AS1*	1.3548	0
children	1q44	247693433	247697141	81472	*OR2C3*	1.3548	0
children	1q44	247712346	247740992	148823	*GCSAML*	1.3548	0
children	1q44	247751661	247752615	81470	*OR2G2*	1.3548	0
children	1q44	247768887	247769817	81469	*OR2G3*	1.3548	0
children	1q44	247835419	247836343	441933	*OR13G1*	1.3548	0
children	1q44	247875130	247876057	343169	*OR6F1*	1.3548	0
children	1q44	247920763	247921708	26188	*OR1C1*	1.3548	0
children	1q44	247978101	247979031	284532	*OR14A16*	1.3548	0
children	1q44	248004229	248005198	391189	*OR11L1*	1.3548	0
children	1q44	248020500	248043438	25893	*TRIM58*	1.3548	0
children	1q44	248084319	248085258	343172	*OR2T8*	1.3548	0
children	1q44	248100330	248264224	284521	*OR2L13*	1.3548	0
children	1q44	248112159	248113098	391190	*OR2L8*	1.3548	0
children	1q44	248128633	248129641	391191	*OR2AK2*	1.3548	0
children	1q44	248153568	248154493	26247	*OR2L1P*	1.3548	0
children	1q44	248185249	248186188	81466	*OR2L5*	1.3548	0
children	1q44	248201473	248202607	26246	*OR2L2*	1.3548	0

children	1q44	248223983	248224922	391192	*OR2L3*	1.3548	0
children	1q44	248285437	248286082	388762	*OR2M1P*	1.3548	0
children	1q44	248308449	248309388	127059	*OR2M5*	1.3548	0
children	1q44	248343287	248344331	391194	*OR2M2*	1.3548	0
children	1q44	248366369	248367308	127062	*OR2M3*	1.3548	0
children	1q44	248402230	248403166	26245	*OR2M4*	1.3548	0
children	1q44	248436153	248437116	391195	*OR2T33*	1.3548	0
children	1q44	248457917	248458880	127064	*OR2T12*	1.3548	0
children	1q44	248486931	248487870	391196	*OR2M7*	1.3548	0
children	1q44	248512076	248513015	127066	*OR14C36*	1.3548	0
children	1q44	248524882	248525929	127074	*OR2T4*	1.3548	0
children	1q44	248550909	248551836	254879	*OR2T6*	1.3548	0
children	1q44	248569295	248570405	26696	*OR2T1*	1.3548	0
children	1q44	248616098	248617073	401992	*OR2T2*	1.3548	0
children	12p13-p12	10004967	10022458	9976	*CLEC2B*	0	-2.3863
children	12p13	10034087	10048432	100431172	*KLRF2*	0	-2.3863
children	12p13.31	10065825	10084980	387836	*CLEC2A*	0	-2.3863
children	12p13.2	10103914	10138194	160364	*CLEC12A*	0	-2.3863
children	12p13.2	10145661	10151899	51266	*CLEC1B*	0	-2.3863
children	12p13.2	10163230	10170548	387837	*CLEC12B*	0	-2.3863
children	12p13.2	10183275	10218629	283420	*CLEC9A*	0	-2.3863
children	12p13.2	10222152	10251664	51267	*CLEC1A*	0	-2.3863
children	12p13.2	10269375	10282868	64581	*CLEC7A*	0	-2.3863
children	12p13.2-p12.3	10310898	10324790	4973	*OLR1*	0	-2.3863
children	12p13.2	10331556	10344403	120939	*TMEM52B*	0	-2.3863
children	12p13.2	10365488	10375724	23710	*GABARAPL1*	0	-2.3863
children	12p13	10457049	10469850	3824	*KLRD1*	0	-2.3863
children	12p13.2-p12.3	10524951	10542653	22914	*KLRK1*	0	-2.3863
children	12p	10524951	10562745	100528032	*KLRC4-KLRK1*	0	-2.3863
children	12p13.2-p12.3	10559982	10562356	8302	*KLRC4*	0	-2.3863
children	12p13	10564913	10573194	3823	*KLRC3*	0	-2.3863
children	12p13	10583205	10588592	3822	*KLRC2*	0	-2.3863
children	12p13	10598637	10605979	3821	*KLRC1*	0	-2.3863

children	12p13.2	10741076	10752434	10748	*KLRAP1*	0	-2.3863
children	12p13.2	10756363	10766208	55110	*MAGOHB*	0	-2.3863
children	12p13.2	10771537	10826891	55359	*STYK1*	0	-2.3863
children	12p13.1	10851675	10875953	8531	*YBX3*	0	-2.3863
children	12p13	10954130	10955226	50837	*TAS2R7*	0	-2.3863
children	12p13	10958649	10959579	50836	*TAS2R8*	0	-2.3863
children	12p13	10961692	10962767	50835	*TAS2R9*	0	-2.3863
children	12p13	10977944	10978868	50839	*TAS2R10*	0	-2.3863
children	12p13	10998447	11002075	11272	*PRR4*	0	-2.3863
children	12p	10998447	11324224	100533464	*PRH1-PRR4*	0	-2.3936
children	12p13.3	1100373	1605099	23085	*ERC1*	0	-1.0903
children	12p13	11060524	11062161	50838	*TAS2R13*	0	-2.3863
children	12p13.2	11081834	11087444	5555	*PRH2*	0	-2.3863
children	12p13	11090852	11091806	50840	*TAS2R14*	0	-2.3863
children	12p13.2	11138511	11139511	259296	*TAS2R50*	0	-2.3863
children	12p13.2	11148560	11150474	259295	*TAS2R20*	0	-2.3863
children	12p13.2	11174217	11175219	259294	*TAS2R19*	0	-2.3863
children	12p13.2	11182985	11184006	259290	*TAS2R31*	0	-2.3863
children	12p13.2	11213963	11214893	259292	*TAS2R46*	0	-2.091
children	12p13.2	11243885	11244912	259289	*TAS2R43*	0	-2.091
children	12p13.2	11285883	11286843	259293	*TAS2R30*	0	-2.4008
children	12p13	11338598	11339543	353164	*TAS2R42*	0	-2.4008
children	12p13.2	11418846	11422641	5544	*PRB3*	0	-2.4008
children	12p13.2	11460014	11463369	5545	*PRB4*	0	-2.4008
children	12p13.2	11504756	11508524	5542	*PRB1*	0	-2.4008
children	12p13.2	11544473	11548498	653247	*PRB2*	0	-2.4008
children	12p13	11802787	12048325	2120	*ETV6*	0	-2.8575
children	12p13-p12	12223877	12252627	79370	*BCL2L14*	0	-2.2088
children	12p13.2	12268960	12419811	4040	*LRP6*	0	-2.2088
children	12p13.2	12482217	12503169	54682	*MANSC1*	0	-2.2088
children	12p13.2	12508341	12510001	503693	*LOH12CR2*	0	-2.2088
children	12p12	12510012	12619838	118426	*LOH12CR1*	0	-2.2088
children	12p13	12626215	12715448	80824	*DUSP16*	0	-2.2088

children	12p13	12764766	12798042	1389	*CREBL2*	0	-2.2088
children	12p12.3	12813994	12849121	2842	*GPR19*	0	-2.2088
children	12p13.1-p12	12870203	12875316	1027	*CDKN1B*	0	-2.2088
children	12p13.1	12878850	12944399	81575	*APOLD1*	0	-2.2088
children	12p13.1	12917582	12917677	693198	*MIR613*	0	-2.2088
children	12p13.1	12966279	12982915	51202	*DDX47*	0	-2.2088
children	12p13.1	13028410	13029070	387841	*RPL13AP20*	0	-2.2088
children	12p13.1	13043955	13066600	9052	*GPRC5A*	0	-2.2088
children	12p13.1	13068762	13068852	693199	*MIR614*	0	-2.2088
children	12p13.3	13093708	13103318	55507	*GPRC5D*	0	-2.2088
children	12p13.1	13127798	13153243	50865	*HEBP1*	0	-2.2088
children	12p13.1	13153375	13157764	93164	*HTR7P1*	0	-2.2088
children	12p13.1	13197314	13236383	57613	*KIAA1467*	0	-2.2088
children	12p13.1	13236470	13248740	83445	*GSG1*	0	-2.2088
children	12p12.3	13349601	13369708	2012	*EMP1*	0	-2.2088
children	12p12	13714409	14133022	2904	*GRIN2B*	0	-2.2088
children	12p13.1	14518565	14655869	55729	*ATF7IP*	0	-2.6086
children	12p13.1	14656596	14720791	79887	*PLBD1*	0	-2.6086
children	12p12	14765567	14849519	2984	*GUCY2C*	0	-2.6086
children	12p12.3	14923653	14924065	121504	*HIST4H4*	0	-2.6086
children	12p12.3	14927269	14930936	55766	*H2AFJ*	0	-2.6086
children	12p12.3	14939411	14956401	51729	*WBP11*	0	-2.6086
children	12p12.3	14956505	14976791	144608	*C12orf60*	0	-2.6086
children	12p12.3	14957583	14967116	440087	*SMCO3*	0	-2.6086
children	12p13-p12	14982244	14996413	420	*ART4*	0	-2.6086
children	12p12.3	15034114	15038853	4256	*MGP*	0	-2.6086
children	12p12.3	15066960	15091483	121506	*ERP27*	0	-2.6086
children	12p12.3	15094949	15114562	397	*ARHGDIB*	0	-2.6086
children	12p13	15125955	15134799	5149	*PDE6H*	0	-2.6086
children	12p12.3	15260715	15374411	85004	*RERG*	0	-2.175
children	12p13.3-p13.2	15475190	15751265	5800	*PTPRO*	0	-1.7809
children	12p12.3	15773074	15942510	2059	*EPS8*	0	-1.7809
children	12p12.3	16035287	16056410	11171	*STRAP*	0	-1.7809

children	12p12.3	16064105	16190315	51071	*DERA*	0	-1.7809
children	12p13	1609656	1613590	100292680	*LINC00942*	0	-1.1266
children	12p12.3	16341418	16430619	729025	*SLC15A5*	0	-1.5383
children	12p12.3-p12.1	16500075	16517344	4257	*MGST1*	0	-1.5628
children	12p12.3	16701305	16758313	55885	*LMO3*	0	-1.5628
children	12p12.3	17141680	17143562	728622	*SKP1P2*	0	-1.5628
children	12p13.31	1800246	1897845	79602	*ADIPOR2*	0	-1.121
children	12p12.3	18233802	18243127	79785	*RERGL*	0	-1.5838
children	12p12	18414473	18801352	5288	*PIK3C2G*	0	-1.5838
children	12p12.3	18836109	18890993	89869	*PLCZ1*	0	-1.5838
children	12p12.3	18891044	18892122	93661	*CAPZA3*	0	-1.5838
children	12p13.33	1901122	2027870	93589	*CACNA2D4*	0	-1.121
children	12p12	19282625	19354937	54477	*PLEKHA5*	0	-1.5838
children	12p13.33	1929432	1945918	654429	*LRTM2*	0	-1.121
children	12p12.3	19592607	19675173	121536	*AEBP2*	0	-1.5838
children	12p12	20167618	20251802	100506393	*LOC100506393*	0	-1.5838
children	12p12	20522178	20837041	5139	*PDE3A*	0	-1.5838
children	12p13.33	2055213	2113677	196513	*DCP1B*	0	-1.121
children	12p12.2	20848288	20906320	53919	*SLCO1C1*	0	-1.5838
children	12p12	20963637	21069843	28234	*SLCO1B3*	0	-1.5838
children	12p12.2	21168629	21243040	338821	*SLCO1B7*	0	-1.1957
children	12p	21284127	21392730	10599	*SLCO1B1*	0	-1.1957
children	12p12	21417533	21487832	6579	*SLCO1A2*	0	-1.1957
children	12p12.1	21525801	21532914	3375	*IAPP*	0	-1.1957
children	12p12.1	21590537	21624182	79912	*PYROXD1*	0	-1.1957
children	12p12	21621843	21654603	5965	*RECQL*	0	-1.1957
children	12p13.3	2162415	2807115	775	*CACNA1C*	0	-1.1104
children	12p12.1	21654698	21671337	51026	*GOLT1B*	0	-1.1957
children	12p12.2	21689122	21757781	2998	*GYS2*	0	-1.1957
children	12p12.2-p12.1	21788275	21810728	3945	*LDHB*	0	-1.1957
children	12p11.23	21917888	21927755	3764	*KCNJ8*	0	-1.1957
children	12p12.1	21950323	22089628	10060	*ABCC9*	0	-1.1957
children	12p12.1	22199109	22218606	55907	*CMAS*	0	-1.1957

children	12p12.1-p11.2	22346324	22487648	6489	*ST8SIA1*	0	-1.1957
children	12p12.1	22601479	22697480	9847	*C2CD5*	0	-1.1957
children	12p12.1	22778075	22797349	55500	*ETNK1*	0	-1.1957
children	12p12.1	23685230	23737546	6660	*SOX5*	0	-1.1318
children	12p12.1	24365354	24365429	100126320	*MIR920*	0	-1.2974
children	12p12.1	24719897	24737102	144360	*LINC00477*	0	-1.2974
children	12p12.1	24962957	25055322	586	*BCAT1*	0	-1.2974
children	12p12.1	25146364	25150373	196415	*C12orf77*	0	-1.2974
children	12p12.1	25205180	25261269	4033	*LRMP*	0	-1.0678
children	12p12.1	25261222	25348094	55259	*CASC1*	0	-1.0678
children	12p12.1	25348149	25357949	144363	*LYRM5*	0	-1.0678
children	12p12.1	25357722	25403865	3845	*KRAS*	0	-1.0678
children	12p12.3	26111963	26225807	11228	*RASSF8*	0	-1.0678
children	12p12.1	26272958	26278003	79365	*BHLHE41*	0	-1.0678
children	12p11.2	26348268	26387708	8082	*SSPN*	0	-1.0678
children	12p11	26488269	26986131	3709	*ITPR2*	0	-1.0678
children	12p11.23	27058111	27091254	55726	*ASUN*	0	-1.0678
children	12p11.23	27091304	27113679	26127	*FGFR1OP2*	0	-1.0678
children	12q11-q12	27124505	27167339	51768	*TM7SF3*	0	-1.0678
children	12p11.23	27175454	27183606	9412	*MED21*	0	-1.0678
children	12p11.23	27233989	27235455	728858	*C12orf71*	0	-1.0678
children	12p11.23	27397077	27478890	23012	*STK38L*	0	-1.0678
children	12p12.2-p11.2	27485786	27578746	56938	*ARNTL2*	0	-1.0678
children	12p11.23	27619742	27655118	341346	*SMCO2*	0	-1.0678
children	12p12.1	27677044	27848497	8496	*PPFIBP1*	0	-1.0678
children	12p11.22	27849427	27850566	387849	*REP15*	0	-1.0678
children	12p11	27863705	27909237	60488	*MRPS35*	0	-1.0678
children	12p11.22	27915598	27924209	100287284	*MANSC4*	0	-1.0678
children	12p13.33	2870365	2880835	283440	*LOC283440*	0	-1.0998
children	12p13.33	2904107	2914587	2288	*FKBP4*	0	-1.0998
children	12p13.33	2921786	2934237	55846	*ITFG2*	0	-1.0998
children	12p13.33	2934513	2944221	83714	*NRIP2*	0	-1.0998
children	12p13	2966846	2986321	2305	*FOXM1*	0	-1.0998

children	12p13.33	2986364	2998691	83695	*RHNO1*	0	-1.0998
children	12p13.3	3000032	3050306	7289	*TULP3*	0	-1.0998
children	12p13.3-p13.2	3068477	3149842	7004	*TEAD4*	0	-1.0998
children	12p13.33-p13.32	3186520	3395730	10867	*TSPAN9*	0	-1.114
children	12p13.3	3490514	3703138	56341	*PRMT8*	0	-1.1281
children	12p13.3	3918026	3982614	57097	*PARP11*	0	-1.1281
children	12p13	4382901	4414522	894	*CCND2*	0	-1.3585
children	12p13.3	4430358	4469190	57103	*C12orf5*	0	-1.3585
children	12p13.3	4477392	4488894	8074	*FGF23*	0	-1.3585
children	12p13	4543307	4554780	2251	*FGF6*	0	-1.3585
children	12p13.3	4596895	4647674	57102	*C12orf4*	0	-1.3585
children	12p13.2-p13.1	4647949	4669213	10635	*RAD51AP1*	0	-1.3585
children	12p13.32	4699237	4723054	8798	*DYRK4*	0	-1.3585
children	12p13.3	4724673	4758213	10566	*AKAP3*	0	-1.3585
children	12p13.3	4758263	4796720	4704	*NDUFA9*	0	-1.3585
children	12p13.3	4829751	4881892	26290	*GALNT8*	0	-1.3585
children	12p13	4918341	4960278	3742	*KCNA6*	0	-1.3585
children	12p13.32	5019072	5027422	3736	*KCNA1*	0	-1.3585
children	12p13	5153084	5155954	3741	*KCNA5*	0	-1.3585
children	12p13	5541279	5604465	4908	*NTF3*	0	-1.3585
children	12p13.3	6058039	6233836	7450	*VWF*	0	-1.3386
children	12p13.3	6309481	6347437	928	*CD9*	0	-1.3416
children	12p13.31	6419601	6437672	55200	*PLEKHG6*	0	-1.3416
children	12p13.2	6437922	6451283	7132	*TNFRSF1A*	0	-1.3416
children	12p13	6456008	6484390	6337	*SCNN1A*	0	-1.3416
children	12p13	6484533	6500737	4055	*LTBR*	0	-1.3416
children	12p13.31	6548166	6560683	678655	*CD27-AS1*	0	-1.3416
children	12p13	6554050	6560884	939	*CD27*	0	-1.3416
children	12p13.31	6561176	6571488	55080	*TAPBPL*	0	-1.3416
children	12p	6571403	6580065	6843	*VAMP1*	0	-1.3416
children	12p13.3-p13.1	6601315	6602471	51258	*MRPL51*	0	-1.3416
children	12p13.3	6603297	6641132	9918	*NCAPD2*	0	-1.3416
children	12p13.31	6619387	6619717	692148	*SCARNA10*	0	-1.3416

children	12p13	6643570	6647541	2597	*GAPDH*	0	-1.3416
children	12p13.3	6648693	6665249	25900	*IFFO1*	0	-1.3416
children	12p13	6666035	6677498	4839	*NOP2*	0	-1.3416
children	12p13	6679247	6716599	1108	*CHD4*	0	-1.3416
children	12p13.31	6690638	6690775	677780	*SCARNA11*	0	-1.3416
children	12p13.31	6728000	6740815	57121	*LPAR5*	0	-1.3416
children	12p13.31	6747241	6756580	84519	*ACRBP*	0	-1.3416
children	12p13.31	6759703	6772308	51147	*ING4*	0	-1.3416
children	12p12	6775642	6798541	171017	*ZNF384*	0	-1.3416
children	12p13.31	6802956	6809596	196500	*PIANP*	0	-1.3416
children	12p13.31	6833149	6841041	50813	*COPS7A*	0	-1.3416
children	12p13	6857157	6862082	8079	*MLF2*	0	-1.3416
children	12p13	6875540	6880118	5763	*PTMS*	0	-1.3416
children	12p13.32	6881669	6887621	3902	*LAG3*	0	-1.3416
children	12p13.31	6898637	6929976	920	*CD4*	0	-1.3416
children	12p13	6930962	6936583	27239	*GPR162*	0	-1.3416
children	12p13	6950017	6956559	2784	*GNB3*	0	-1.3416
children	12p13	6957971	6961230	83461	*CDCA3*	0	-1.3416
children	12p13	6961284	6975795	8078	*USP5*	0	-1.3416
children	12p13	6976692	6980110	7167	*TPI1*	0	-1.3416
children	12p13.31	6980099	6982449	84727	*SPSB2*	0	-1.3416
children	12p13.31	6993144	6993768	283345	*RPL13P5*	0	-1.3416
children	12p13	6993845	6994950	171220	*DSTNP2*	0	-1.3416
children	12p13	7013896	7023406	10233	*LRRC23*	0	-1.3416
children	12p13	7023613	7032859	2026	*ENO2*	0	-1.3416
children	12p13.31	7033625	7051484	1822	*ATN1*	0	-1.3416
children	12p13.31	7052979	7055166	113246	*C12orf57*	0	-1.3416
children	12p13	7055739	7070479	5777	*PTPN6*	0	-1.3416
children	12p13.31	7072861	7072929	406985	*MIR200C*	0	-1.3416
children	12p13.31	7073259	7073354	406933	*MIR141*	0	-1.3416
children	12p13	7074514	7079916	11331	*PHB2*	0	-1.3416
children	12p13.31	7076499	7076769	677777	*SCARNA12*	0	-1.3416
children	12p13.3	7079943	7085165	10436	*EMG1*	0	-1.3416

children	12p13	7085346	7125842	10162	*LPCAT3*	0	-1.3416
children	12p13	7167979	7178335	716	*C1S*	0	-1.3416
children	12p13	7187514	7245043	715	*C1R*	0	-1.3416
children	12p13.31	7247145	7261874	51279	*C1RL*	0	-1.3416
children	12p13.31	7260903	7274447	283314	*C1RL-AS1*	0	-1.3416
children	12p13.31	7276279	7281466	83758	*RBP5*	0	-1.3416
children	12p13.31	7282966	7311530	9746	*CLSTN3*	0	-1.3416
children	12p13.31	7341758	7371169	5830	*PEX5*	0	-1.3416
children	12p13.31	7456927	7480969	341392	*ACSM4*	0	-1.6087
children	12p13.3	7507555	7596781	283316	*CD163L1*	0	-1.6087
children	12p13.3	7623411	7656414	9332	*CD163*	0	-1.6087
children	12p13.1	7801995	7818499	339	*APOBEC1*	0	-1.4142
children	12p13.1	7842380	7848360	9573	*GDF3*	0	-1.4142
children	12p13.31	7864049	7870152	359787	*DPPA3*	0	-1.4142
children	12p13.2-p12.3	7882010	7902069	170482	*CLEC4C*	0	-1.4142
children	12p13.31	7917811	7926717	360030	*NANOGNB*	0	-1.4142
children	12p13.31	7941991	7948657	79923	*NANOG*	0	-1.4142
children	12p13.31	7965107	8025635	144195	*SLC2A14*	0	-1.4142
children	12p13.3	8071823	8088892	6515	*SLC2A3*	0	-1.4142
children	12p13.31	8185358	8208118	55810	*FOXJ2*	0	-1.4142
children	12p13.31	8210918	8218955	719	*C3AR1*	0	-1.4142
children	12p13.31	8234806	8250373	25977	*NECAP1*	0	-1.4142
children	12p13	8276227	8291203	50856	*CLEC4A*	0	-1.4142
children	12p13	8608590	8630926	93978	*CLEC6A*	0	-1.2745
children	12p13.31	8666135	8674960	338339	*CLEC4D*	0	-1.2745
children	12p13.31	8685900	8693558	26253	*CLEC4E*	0	-1.2745
children	12p13	8754761	8765442	57379	*AICDA*	0	-1.2745
children	12p13.1-p12.3	8798538	8815484	8076	*MFAP5*	0	-1.2745
children	12p13.31	8852380	8929787	57494	*RIMKLB*	0	-1.5649
children	12p13.31	8975067	9029377	144568	*A2ML1*	0	-1.5649
children	12p13	9067315	9094060	1911	*PHC1*	0	-1.5649
children	12p13	9092956	9102357	4074	*M6PR*	0	-1.5649
children	12p13.31	9142220	9163340	10219	*KLRG1*	0	-1.5649

children	12p13.31	9208184	9217666	253128	*LINC00612*	0	-1.5649
children	12p13.31	9217772	9220651	144571	*A2M-AS1*	0	-1.5649
children	12p13.31	9220303	9268558	2	*A2M*	0	-1.5649
children	12q22	92534053	92539673	694	*BTG1*	0	-1.1201
children	12p13-p12.2	9301435	9360966	5858	*PZP*	0	-1.5649
children	12p13.31	9381128	9386803	3	*A2MP1*	0	-1.5649
children	12p13.31	9436252	9466684	642846	*LOC642846*	0	-1.5649
children	12p13.31	9570286	9600768	440081	*DDX12P*	0	-1.088
children	12p13	9747869	9760497	3820	*KLRB1*	0	-2.3863
children	12p13.31	9769879	9811010	374443	*LOC374443*	0	-2.3863
children	12p13	9822303	9852151	29121	*CLEC2D*	0	-2.3863
children	12p13.31	9868455	9885895	160365	*CLECL1*	0	-2.3863
children	12p13	9905081	9913497	969	*CD69*	0	-2.3863
children	12p13.31	9980076	9997603	51348	*KLRF1*	0	-2.3863
children	13q14.2	49550047	49783915	22862	*FNDC3A*	0	-1.1587
children	13q14-q21	49794473	49796513	2862	*MLNR*	0	-1.1587
children	13q14.2	49822046	49867622	81602	*CDADC1*	0	-1.1587
children	13q14.2	49882785	49975674	81617	*CAB39L*	0	-1.1587
children	13q14	50018428	50069139	83852	*SETDB2*	0	-1.1587
children	13q14.2	50069800	50103117	51131	*PHF11*	0	-1.1587
children	13q14	50106081	50159719	55213	*RCBTB1*	0	-1.1587
children	13q14.2	50202434	50208008	115761	*ARL11*	0	-1.1587
children	13q12-q13	50234811	50265623	84650	*EBPL*	0	-1.1587
children	13q14.3	50273442	50367057	3839	*KPNA3*	0	-1.1587
children	13q14.2	50464544	50467516	220429	*CTAGE10P*	0	-1.1587
children	13q14	50486837	50510637	57213	*SPRYD7*	0	-1.1587
children	13q14.3	50556687	50699677	8847	*DLEU2*	0	-1.1587
children	13q14	50571142	50592603	10206	*TRIM13*	0	-1.1587
children	13q14.2	50589389	50595058	283518	*KCNRG*	0	-1.1587
children	13q14.2	50623254	50623337	406950	*MIR16-1*	0	-1.1587
children	13q14.3	50656304	50681354	10301	*DLEU1*	0	-1.1587
children	13q14.3	50746153	50747751	145165	*ST13P4*	0	-1.1587
children	13q14.3	51285161	51418075	220107	*DLEU7*	0	-1.1587

children	13q14.3	51483813	51530901	79621	*RNASEH2B*	0	-1.1587
children	13q14.3	51568646	51640293	2974	*GUCY1B2*	0	-1.1587
children	13q14.3	51656983	51746358	647166	*LINC00371*	0	-1.1587
children	13q14.3	51796469	51858377	220108	*FAM124A*	0	-1.1587
children	13q14.3	51915167	51936239	647174	*SERPINE3*	0	-1.1587
children	13q14.3	51935700	52027275	26512	*INTS6*	0	-1.1587
children	13q14.3	52158483	52336171	115825	*WDFY2*	0	-1.1587
children	13q14.3	52342128	52378298	79758	*DHRS12*	0	-1.1587
children	13q14.3	52387482	52419286	283521	*LINC00282*	0	-1.1587
children	13q14.3	52436116	52440372	83446	*CCDC70*	0	-1.1587
children	13q14.3	52506805	52585630	540	*ATP7B*	0	-1.1587
children	13q14.2	52586522	52603780	9724	*UTP14C*	0	-1.1587
children	13q14.3	52638899	52703228	341676	*NEK5*	0	-1.1587
children	13q14.13	52706778	52733670	4752	*NEK3*	0	-1.1587
children	13q	52741844	52768602	100887750	*MRPS31P5*	0	-1.1587
children	13q14.3	52951302	52980629	55901	*THSD1*	0	-1.1587
children	13q14.3	52986736	53024813	51028	*VPS36*	0	-1.1587
children	13q14	53029494	53050766	26586	*CKAP2*	0	-1.1587
children	13q14.3	53063127	53161225	220115	*TPTE2P3*	0	-1.1587
children	13q14.3	53191604	53217919	144983	*HNRNPA1L2*	0	-1.1587
children	13q14.3	53226830	53262433	10910	*SUGT1*	0	-1.1587
children	13q14.3	53277399	53313947	11061	*LECT1*	0	-1.1587
children	13q21.1	53418108	53422775	5100	*PCDH8*	0	-1.2538
children	13q14.3	53602875	53626196	10562	*OLFM4*	0	-1.6628
children	13q14.3	54389553	54450254	100861552	*LINC00558*	0	-1.6628
children	13q21.1	58205788	58303065	27253	*PCDH17*	0	-1.5837
children	13q21.2	60239720	60738119	81624	*DIAPH3*	0	-1.6522
children	13q21.2	60970590	61148013	81550	*TDRD3*	0	-1.6522
children	13q21	61983818	61989655	64881	*PCDH20*	0	-1.6721
children	13q21.31	64311567	64316701	283491	*OR7E156P*	0	-2.3171
children	13q21.32	66876965	67804468	5101	*PCDH9*	0	-2.3068
children	13q21.33	69435416	69459457	338862	*LINC00550*	0	-2.3068
children	13q21	70274724	70682625	57626	*KLHL1*	0	-2.3068

children	13q21	70681344	70713885	6315	*ATXN8OS*	0	-2.3068
children	13q21.33	71589272	71742549	100885781	*LINC00348*	0	-2.3068
children	13q22	72012097	72441330	1602	*DACH1*	0	-2.2774
children	13q22.1	73282494	73301938	440145	*MZT1*	0	-2.0778
children	13q22.1	73301886	73330336	79866	*BORA*	0	-1.6067
children	13q22.1	73329539	73356266	22894	*DIS3*	0	-1.6067
children	13q22.1	73356229	73590591	10464	*PIBF1*	0	-1.6067
children	13q22.1	73632929	73651680	688	*KLF5*	0	-1.6067
children	13q22	74260148	74708066	11278	*KLF12*	0	-1.6067
children	13q22.1	74993309	75009296	100874151	*LINC00381*	0	-1.6067
children	13q21.33	75126979	75131257	338864	*LINC00347*	0	-1.6067
children	13q22.2	75811888	75814517	647288	*CTAGE11P*	0	-1.6067
children	13q22.2	75858799	76056304	9882	*TBC1D4*	0	-1.6067
children	13q22	76099349	76112008	170622	*COMMD6*	0	-1.6067
children	13q22.2	76123615	76180156	7347	*UCHL3*	0	-1.6067
children	13q22.2	76194569	76434006	4008	*LMO7*	0	-1.3215
children	13q22.3	77454303	77460540	115207	*KCTD12*	0	-1.3215
children	13q22	77502584	77503224	690	*BTF3P11*	0	-1.3268
children	13q22.3	77526623	77532776	730249	*IRG1*	0	-1.3268
children	13q21.1-q32	77566058	77576652	1203	*CLN5*	0	-1.3268
children	13q22	77579388	77601331	26224	*FBXL3*	0	-1.3268
children	13q22	77618791	77901177	23077	*MYCBP2*	0	-1.3268
children	13q22	78109808	78219398	8796	*SCEL*	0	-1.3268
children	13q22.3	78271988	78338377	122060	*SLAIN1*	0	-1.3268
children	13q22	78469615	78492966	1910	*EDNRB*	0	-1.3268
children	13q31.1	79173229	79177695	5457	*POU4F1*	0	-1.3268
children	13q31.1	79188420	79233314	79596	*RNF219*	0	-1.3268
children	13q31.1	79893002	79980356	64062	*RBM26*	0	-1.3268
children	13q31.1	80055258	80130212	54602	*NDFIP2*	0	-1.3268
children	13q31.1	80910111	80915086	10253	*SPRY2*	0	-1.3268
children	13q31.1	84451339	84456528	114798	*SLITRK1*	0	-1.4446
children	13q31.1	86366921	86373483	84189	*SLITRK6*	0	-1.4446
children	13q31.2	88096241	88323218	642345	*MIR4500HG*	0	-1.4446

children	13q31.2	88270919	88270995	100616182	*MIR4500*	0	-1.4446
children	13q31.2	88324869	88331870	26050	*SLITRK5*	0	-1.4446
children	13q31.3	90883435	90883531	693207	*MIR622*	0	-1.4533
children	13q31.3	91543207	91578851	144776	*LINC00410*	0	-1.4533
children	15q14	41952609	42062141	23269	*MGA*	0	-1.204
children	15q15.1	41983782	41983876	693211	*MIR626*	0	-1.4471
children	15q15.1	42066631	42120053	23005	*MAPKBP1*	0	-1.4471
children	15q15.1	42120282	42129785	100137047	*JMJD7*	0	-1.4471
children	15q11.2-q21.3	42120282	42140346	8681	*JMJD7-PLA2G4B*	0	-1.4471
children	15q11.2-q21.3	42131010	42140346	100137049	*PLA2G4B*	0	-1.4471
children	15q21	42140343	42186275	51332	*SPTBN5*	0	-1.4471
children	15q11.1	42191638	42264755	30844	*EHD4*	0	-1.4471
children	15q15.1	42273779	42342901	123745	*PLA2G4E*	0	-1.2132
children	15q15.1	42359880	42386752	283748	*PLA2G4D*	0	-1.2132
children	15q15.1	42433331	42448839	255189	*PLA2G4F*	0	-1.2132
children	15q15.1	42450898	42500524	23339	*VPS39*	0	-1.2132
children	15q15.1	42491767	42491864	693212	*MIR627*	0	-1.2132
children	15q15.1	42502649	42565782	25963	*TMEM87A*	0	-1.2132
children	15q15.2	42566365	42645864	2595	*GANC*	0	-1.2132
children	15q15.1	42651697	42704515	825	*CAPN3*	0	-1.2132
children	15q15.1	42704634	42749765	64397	*ZNF106*	0	-1.2132
children	15q14	42787503	42825259	8773	*SNAP23*	0	-1.2132
children	15q15.2	42834719	42841002	255252	*LRRC57*	0	-1.2132
children	15q15.2	42841010	42862190	55142	*HAUS2*	0	-1.2132
children	18q22.1	65173818	65183967	92126	*DSEL*	1.2279	-1.1123
children	18q22.1	65183782	65566856	643542	*LOC643542*	1.2279	-1.0627
children	19p13.3	1040101	1065570	10347	*ABCA7*	0.7347	-1.6301
children	19p13.3	1065921	1087830	23526	*HMHA1*	0.7347	-1.8712
children	19p13.3	1086577	1095391	5434	*POLR2E*	0.7347	-1.8712
children	19p13.3	1103924	1106788	2879	*GPX4*	0.7347	-1.8712
children	19p13.3	1107632	1132273	22904	*SBNO2*	0.7347	-1.8712
children	19p13.3	1205797	1228434	6794	*STK11*	0.7347	-1.8712
children	19p13.3	1229946	1237990	255057	*C19orf26*	0.7347	-1.8712

children	19p13.3	1241748	1244824	513	*ATP5D*	0.7347	-1.8712
children	19p13.3	1248551	1259142	90007	*MIDN*	0.4264	-1.8712
children	19p13.3	1267469	1270259	148046	*CIRBP-AS1*	0.4264	-1.8712
children	19p13.3	1269266	1273171	1153	*CIRBP*	0.4264	-1.8712
children	19p13.3	1275519	1279243	55009	*C19orf24*	0.4264	-1.8712
children	19p13.3	1286152	1301429	1943	*EFNA2*	0.4264	-1.8712
children	19p13.3	1354975	1378430	84939	*MUM1*	0.4264	-1.8712
children	19p13.3	1383882	1395588	374291	*NDUFS7*	0.4264	-1.8712
children	19p13.3	1397024	1401569	2593	*GAMT*	0.4264	-1.8712
children	19p13.3	1407567	1435686	26528	*DAZAP1*	0.4264	-1.8712
children	19p13.3	1438362	1440496	6209	*RPS15*	0.4264	-1.8712
children	19p13.3	1450147	1473243	10297	*APC2*	0.4264	-1.8712
children	19p13.3	1473199	1479228	148223	*C19orf25*	0.7997	-2.2014
children	19p13.3	1481426	1490449	54760	*PCSK4*	0.7997	-2.2014
children	19p13.3	1491164	1497924	92840	*REEP6*	0.7997	-2.2014
children	19p13.3	1505016	1513188	339366	*ADAMTSL5*	0.7997	-2.2014
children	19p13.3	1524072	1535455	126520	*PLK5*	0.7997	-2.2014
children	19p13.3	1554667	1568057	399664	*MEX3D*	0.7997	-1.9685
children	19p13.3	416582	460996	25759	*SHC2*	0.9926	-1.3618
children	19p13.3	463345	474983	284451	*ODF3L2*	0.9926	-1.3618
children	19p13.3	496489	505343	8174	*MADCAM1*	0.9926	-1.3618
children	19p13.3	507496	519654	91978	*TPGS1*	0.9926	-1.3618
children	19p13.3	531732	542087	997	*CDC34*	1.0596	-1.3618
children	19p13.3	544033	549920	3004	*GZMM*	1.0596	-1.3618
children	19p13.3	589892	617159	610	*HCN2*	1.0596	-1.3926
children	19p13.3	617222	633568	5442	*POLRMT*	1.0596	-1.3926
children	19p13.3	639925	643604	27006	*FGF22*	1.0596	-1.3926
children	19p13.3	647525	663233	55658	*RNF126*	1.0596	-1.3926
children	19p13	676388	683392	10272	*FSTL3*	1.0596	-1.3926
children	19p13.3	685520	695461	400668	*PRSS57*	1.0596	-1.3926
children	19p13.3	708952	748330	5064	*PALM*	1.0596	-1.3926
children	19p13.3	751145	764318	126353	*MISP*	1.0596	-1.3926
children	19p13.3	797391	812327	5725	*PTBP1*	1.0596	-1.3926

children	19p13.3	812487	821952	79948	*LPPR3*	1.0596	-1.3926
children	19p13.3	827825	832018	566	*AZU1*	1.0596	-1.3926
children	19p13.3	840984	848175	5657	*PRTN3*	1.0596	-1.3926
children	19p13.3	852290	856246	1991	*ELANE*	1.0596	-1.3926
children	19p13.3	859658	863569	1675	*CFD*	1.0596	-1.3926
children	19p13.3	867961	893218	10025	*MED16*	1.0596	-1.3926
children	20q11.22	33703159	33735161	55741	*EDEM2*	0	-1.1439
children	20q11.2	33759739	33765165	10544	*PROCR*	0	-1.1439
children	20q11.2	33814538	33864804	10893	*MMP24*	0	-1.1439
children	20q11.22	33864135	33865960	101410538	*MMP24-AS1*	0	-1.1439
children	20q12	33866708	33872520	3692	*EIF6*	0	-1.1439
children	20q11.22	33873533	33880225	128876	*FAM83C*	0	-1.1439
children	20q11.2	34021144	34025970	8200	*GDF5*	0	-1.1439
children	20q11.22	34043222	34099803	11190	*CEP250*	0	-1.1439
children	20q11.22	34114798	34117481	140873	*C20orf173*	0	-1.1439
children	20pter-q12	34129777	34145405	51614	*ERGIC3*	0	-1.1439
children	20q11.21	34203805	34208971	6676	*SPAG4*	0	-1.1439
children	20q11.22	34213952	34241831	8904	*CPNE1*	0	-1.1439
children	20q11.21	34236846	34252878	10137	*RBM12*	0	-1.1439
children	20q11.22	34256609	34287287	9054	*NFS1*	0	-1.1439
children	20q11.22	34287231	34288902	140823	*ROMO1*	0	-1.1439
children	20q11.22	34291530	34330258	9584	*RBM39*	0	-1.1439
children	20q11.22-q11.23	34359922	34538288	51230	*PHF20*	0	-1.1439
children	20q11.1-q11.23	34541538	34542548	51282	*SCAND1*	0	-1.1439
children	20q11.23	34556502	34618622	140894	*CNBD2*	0	-1.1439
children	20q11.23	34633539	34638882	647979	*LINC00657*	0	-1.1439
children	20q11.2-q12	34679425	34820721	2036	*EPB41L1*	0	-1.1439
children	20pter-q12	34824338	34844863	25980	*AAR2*	0	-1.1439
children	20q11.23	34894244	35157040	22839	*DLGAP4*	0	-1.1439
children	20q11.23	35169886	35178226	10398	*MYL9*	0	-1.1439
children	20q11.23	35201875	35222355	60436	*TGIF2*	0	-1.1439
children	20q	35202956	35240960	100527943	*TGIF2-C20orf24*	0	-1.1439
children	20q11.23	35234136	35240960	55969	*C20orf24*	0	-1.1439

children	20q11.23	35240923	35274619	84174	*SLA2*	0	-1.1439
children	20q11.21-q11.23	35280168	35374541	57446	*NDRG3*	0	-1.1439
children	20q11.23	35380193	35402154	79980	*DSN1*	0	-1.1439
children	20q11.23	35405844	35488276	140710	*SOGA1*	0	-1.1439
children	20q11.23	35504523	35522634	140711	*TLDC2*	0	-1.1439
children	20pter-q12	35520226	35580246	25939	*SAMHD1*	0	-1.1439
children	20q11.2	35624754	35724403	5933	*RBL1*	0	-1.1439
children	20q11.22	35729628	35807991	140699	*MROH8*	0	-1.1439
children	20q12-q13.1	35807455	35870025	6185	*RPN2*	0	-1.1439
children	20q11.2	35879489	35885299	2691	*GHRH*	0	-1.1439
children	20q11.23	35918050	35945663	63905	*MANBAL*	0	-1.1439
children	20q12-q13	35973087	36033835	6714	*SRC*	0	-1.1439
children	20q11.23	36145818	36152953	10904	*BLCAP*	0	-1.1439
children	20q11.2-q12	36149606	36152090	4826	*NNAT*	0	-1.1439
children	20q11.23	36247699	36251521	100861522	*LINC00489*	0	-1.1439
children	20q11.23	36305311	36311636	100287792	*LOC100287792*	0	-1.1439
children	20q11.23-q12	36322356	36500531	56259	*CTNNBL1*	0	-1.1439
children	20q11.23	36531498	36573747	128434	*VSTM2L*	0	-1.1439
children	20q11.23	36611408	36661870	9675	*TTI1*	0	-1.1439
children	20q11.23	36661947	36720766	58490	*RPRD1B*	0	-1.1439
children	20q12	36756863	36793700	7052	*TGM2*	0	-1.1439
children	20q11.23	36838906	36889174	85449	*KIAA1755*	0	-1.1439
children	20q11.23	36932551	36965905	671	*BPI*	0	-1.1439
children	20q11.23	36974813	37005653	3929	*LBP*	0	-1.1439
children	20q11.23	37049238	37064018	388796	*SNHG17*	0	-1.1818
children	20q11.23	37053842	37053978	26776	*SNORA71B*	0	-1.1818
children	20q11.23	37055948	37056086	26777	*SNORA71A*	0	-1.1818
children	20q11.23	37058309	37058447	677839	*SNORA71C*	0	-1.1818
children	20q11.23	37062504	37062642	677840	*SNORA71D*	0	-1.1818
children	20q11.23	37075296	37079564	128439	*SNHG11*	0	-1.1818
children	20q11.23	37101448	37207504	57148	*RALGAPB*	0	-1.1818
children	20q11.23	37209837	37217106	149685	*ADIG*	0	-1.1818
children	20q11.23	37230576	37279295	343578	*ARHGAP40*	0	-1.1818

children	20q11.23	37353104	37358015	140679	*SLC32A1*	0	-1.1818
children	20q11.23	37377096	37401089	79913	*ACTR5*	0	-1.1818
children	20q11.23	37434335	37551667	26051	*PPP1R16B*	0	-1.1818
children	20q11.23	37554954	37581703	81610	*FAM83D*	0	-1.1818
children	20q11.22-q12	37590980	37668366	60625	*DHX35*	0	-1.1818
children	20q12	37842423	37853391	339568	*LOC339568*	0	-1.1818
children	20q12	39314487	39317880	9935	*MAFB*	0	-1.1818
children	20q12-q13.1	39657461	39753126	7150	*TOP1*	0	-1.1818
children	20q12-q13.1	39766160	39804357	5335	*PLCG1*	0	-1.1818
children	20q12	39807088	39928739	23051	*ZHX3*	0	-1.2202
children	20q12	39988605	39995498	90187	*EMILIN3*	0	-1.2586
children	20q12	40030742	40247133	84181	*CHD6*	0	-1.2586
children	20q12-q13	40701391	41818557	11122	*PTPRT*	0	-1.2487
children	20q12-q13.1	42086503	42092244	6431	*SRSF6*	0	-1.2387
children	20q13.12	42136319	42170535	26013	*L3MBTL1*	0	-1.2387
children	20q13.2	42187634	42214273	10110	*SGK2*	0	-1.2387
children	20q13.12	42543491	42698254	84969	*TOX2*	0	-1.0972
children	20q13.12	42740336	42816218	57158	*JPH2*	0	-1.0972
children	20q13.11	42824580	42839546	51526	*OSER1*	0	-1.0972
children	20q12	42875738	42909557	78997	*GDAP1L1*	0	-1.0972
children	20q13.12	42935196	42939889	128486	*FITM2*	0	-1.0972
children	20q13.12	42965797	42979432	140902	*R3HDML*	0	-1.0972
children	20q13.12	42984440	43053276	3172	*HNF4A*	0	-1.0972
children	20q13.12	43104525	43123244	79183	*TTPAL*	0	-1.0972
children	20q13.12	43124863	43150726	10955	*SERINC3*	0	-1.0972
children	20q12-q13.1	43160421	43247678	11142	*PKIG*	0	-1.0972
children	20q13.12	43248162	43280376	100	*ADA*	0	-1.0972
children	20q13.12	43343884	43356452	8839	*WISP2*	0	-1.0953
children	20q13.12	43374487	43380954	60598	*KCNK15*	0	-1.0953
children	20q13.12	43380444	43438979	140730	*RIMS4*	0	-1.0953
children	20q13.1	43514239	43537175	7529	*YWHAB*	0	-1.0953
children	20q11.2-q13.2	43595119	43708593	6789	*STK4*	0	-1.0953
children	20q12	43720949	43729753	3787	*KCNS1*	0	-1.0953

children	20q13.12	43738092	43743813	149708	*WFDC5*	0	-1.0953
children	20q13.12	43752066	43753106	128488	*WFDC12*	0	-1.0953
children	20q13.12	43803539	43805185	5266	*PI3*	0	-1.0953
children	20q12-q13.2	43835637	43838414	6406	*SEMG1*	0	-1.0953
children	20q12-q13.1	43850009	43853099	6407	*SEMG2*	0	-1.0953
children	20q12	43880879	43883205	6590	*SLPI*	0	-1.0953
children	20q13.12	43922085	43936937	8785	*MATN4*	0	-1.0953
children	20q13.12	43935482	43946464	11317	*RBPJL*	0	-1.0953
children	20q12	43953928	43977064	6385	*SDC4*	0	-1.0953
children	20q13.12	43990576	43997862	90196	*SYS1*	0	-1.0953
children	20q13.12	44002519	44006957	27296	*TP53TG5*	0	-1.0953
children	20q13.12	44034632	44039250	55861	*DBNDD2*	0	-1.0953
children	20q13.12	44044706	44054885	51604	*PIGT*	0	-1.0953
children	20q13.12	44098393	44110172	10406	*WFDC2*	0	-1.0953
children	20q13.12	44141100	44144264	10816	*SPINT3*	0	-1.0953
children	20q13.12	44162835	44168134	140870	*WFDC6*	0	-1.0953
children	20q	44164918	44176065	100526773	*EPPIN-WFDC6*	0	-1.0953
children	20q13.12	44169264	44176065	57119	*EPPIN*	0	-1.0953
children	20q13.12	44179790	44207965	90199	*WFDC8*	0	-1.0695
children	20q13.12	44236577	44259907	259240	*WFDC9*	0	-1.0695
children	20q13.12	44258384	44259831	140832	*WFDC10A*	0	-1.0695
children	20q13.12	44277201	44298878	259239	*WFDC11*	0	-1.0695
children	20q13.12	44313289	44333658	280664	*WFDC10B*	0	-1.0695
children	20q13.12	44330654	44337456	164237	*WFDC13*	0	-1.0695
children	20q13.12	44350987	44354335	391253	*SPINT4*	0	-1.0695
children	20q13.12	44402846	44420547	140686	*WFDC3*	0	-1.0695
children	20q13.12	44420575	44440066	116092	*DNTTIP1*	0	-1.0695
children	20q13.12	44441214	44445596	11065	*UBE2C*	0	-1.0695
children	20q12-q13.11	44451854	44455953	7125	*TNNC2*	0	-1.0695
children	20q13.12	44462469	44471914	90203	*SNX21*	0	-1.0695
children	20q13.12	44470359	44486048	10005	*ACOT8*	0	-1.0695
children	20q13.12	44486219	44507769	140831	*ZSWIM3*	0	-1.0695
children	20q13.12	44509847	44513905	90204	*ZSWIM1*	0	-1.0695

children	20q13.12	44515129	44516238	128497	*SPATA25*	0	-1.0695
children	20q13.1	44518782	44527458	5476	*CTSA*	0	-1.0695
children	20q13.12	44527258	44539633	5360	*PLTP*	0	-1.0695
children	20q13.12	44563316	44576662	63935	*PCIF1*	0	-1.0695
children	20q13.12	44577291	44600833	63925	*ZNF335*	0	-1.0695
children	20q13.12	44637546	44645200	4318	*MMP9*	0	-1.3158
children	20q13.12	44650328	44688789	57468	*SLC12A5*	0	-1.3158
children	20q13.12	44689625	44718580	57727	*NCOA5*	0	-1.3158
children	20q12-q13.2	44746892	44758384	958	*CD40*	0	-1.3158
children	20q13.1	44802371	44937137	64405	*CDH22*	0	-1.3158
children	20q13.12	44978166	44993097	51006	*SLC35C2*	0	-1.3158
children	20q13	44994689	45035271	63916	*ELMO2*	0	-1.3158
children	20q13.12	45092298	45093931	7686	*MKRN7P*	0	-1.3158
children	20q13.12	45128268	45142198	55713	*ZNF334*	0	-1.3158
children	20q13.12	45169669	45179213	128506	*OCSTAMP*	0	-1.3158
children	20q13.12	45186461	45280100	64849	*SLC13A3*	0	-1.3158
children	20q13.2	45313003	45318276	112858	*TP53RK*	0	-1.3158
children	20q13.1	45338278	45364985	81031	*SLC2A10*	0	-1.3158
children	20q13.1	45523262	45817492	2139	*EYA2*	0	-1.3158
children	20q13.12	45837858	45985633	23613	*ZMYND8*	0	-1.3158
children	20q13.12	45947245	45949498	100131496	*LOC100131496*	0	-1.3158
children	20q12	46130600	46285621	8202	*NCOA3*	0	-1.3158
children	20q13.12	46286149	46414808	55959	*SULF2*	0	-1.3158
children	20q13.13	46988653	46999381	284749	*LINC00494*	0	-1.3023
children	20q13.13	47240792	47444420	57580	*PREX1*	0	-1.2755
children	20q13	47662782	47713497	1434	*CSE1L*	0	-1.0695
children	20q13.1	47729875	47804904	6780	*STAU1*	0	-1.314
children	20q13.13	47835831	47860614	55661	*DDX27*	0	-1.314
children	20q13.13	47862438	47894756	57169	*ZNFX1*	0	-1.314
children	20q13.13	47894714	47905795	441951	*ZFAS1*	0	-1.314
children	20q13.13	47895481	47895560	26765	*SNORD12C*	0	-1.314
children	20q13.13	47896849	47896952	100113393	*SNORD12B*	0	-1.314
children	20q13.13	47897219	47897309	692057	*SNORD12*	0	-1.314

children	20q13.2	47988504	48099181	3745	*KCNB1*	0	-1.314
children	20q13.13	48120410	48184707	5740	*PTGIS*	0	-1.314
children	20q13.1-q13.2	48249482	48330421	9334	*B4GALT5*	0	-1.314
children	20q13.13	48429249	48508779	23315	*SLC9A8*	0	-1.314
children	20q13.13	48519928	48530276	9825	*SPATA2*	0	-1.314
children	20q13.13	48552913	48570422	55905	*RNF114*	0	-1.314
children	20q13.2	48599512	48605420	6615	*SNAI1*	0	-1.314
children	20q13.2	48697660	48729735	7335	*UBE2V1*	0	-1.314
children	20q13.2	48697660	48770335	387522	*TMEM189-UBE2V1*	0	-1.314
children	20q13.2	48740273	48770335	387521	*TMEM189*	0	-1.314
children	20q13.1	48807119	48809227	1051	*CEBPB*	0	-1.314
children	20q13.1-q13.2	49126857	49201300	5770	*PTPN1*	0	-1.314
children	20q13.13	49202322	49202416	693230	*MIR645*	0	-1.314
children	20q13.13	49202644	49253455	140876	*FAM65C*	0	-1.314
children	20q13.13	49348080	49370278	84612	*PARD6B*	0	-1.314
children	20q13.13	49411430	49493714	55653	*BCAS4*	0	-1.314
children	20q13.13	49505454	49547527	23394	*ADNP*	0	-1.314
children	20q13.13	49551391	49575101	8813	*DPM1*	0	-1.314
children	20q13.13	49575350	49578399	27304	*MOCS3*	0	-1.314
children	20q13	49620192	49639675	3755	*KCNG1*	0	-1.314
children	20q13.2	50003493	50159258	4773	*NFATC2*	0	-1.314
children	20q13.2	50213313	50384950	10079	*ATP9A*	0	-1.314
children	20q13.2	50400582	50419048	57167	*SALL4*	0	-1.314
children	20q13.2	50700549	50808524	55734	*ZFP64*	0	-1.4405
children	20q13.2	51588945	52111869	128553	*TSHZ2*	0	-1.4968
children	20q13.2	52183609	52199636	7764	*ZNF217*	0	-1.4968
children	20q13.2	52491039	52492248	391257	*SUMO1P1*	0	-1.4997
children	20q13.2	52560078	52687304	8537	*BCAS1*	0	-1.4997
children	20q13	52769987	52790516	1591	*CYP24A1*	0	-1.4997
children	20q13.2	52824501	52836492	5203	*PFDN4*	0	-1.4997
children	20q13.2	53092010	53267710	55816	*DOK5*	0	-1.4997
children	20q13	54572412	54580528	140689	*CBLN4*	0	-1.4997
children	20q13.2-q13.3	54823787	54824871	4159	*MC3R*	0	-1.4997

children	20q13.2	54933982	54943718	116151	*FAM210B*	0	-1.483
children	20q13	54944444	54967351	6790	*AURKA*	0	-1.483
children	20q13.2	54967426	54979582	1477	*CSTF1*	0	-1.483
children	20q13.31	54987167	55034396	57091	*CASS4*	0	-1.483
children	20q13.31	55043640	55093942	51507	*RTFDC1*	0	-1.483
children	20q13.2	55066547	55100981	140687	*GCNT7*	0	-1.483
children	20q13.31	55099784	55101208	200232	*FAM209A*	0	-1.483
children	20q13.31	55108301	55111574	388799	*FAM209B*	0	-1.483
children	20q13.2	55204357	55214338	7022	*TFAP2C*	0	-1.483
children	20q13	55743808	55841707	655	*BMP7*	0	-1.4115
children	20q13.31	55904830	55919049	23626	*SPO11*	0	-1.4115
children	20q13.31	55926144	55953519	8480	*RAE1*	0	-1.4115
children	20q13.31	55933495	55934878	100462983	*MTRNR2L3*	0	-1.4115
children	20q13.31	55966453	55984386	55544	*RBM38*	0	-1.4115
children	20q13.31	56071020	56100183	140690	*CTCFL*	0	-1.4115
children	20q13.31	56136136	56141513	5105	*PCK1*	0	-1.4115
children	20q13.31	56178901	56195632	81030	*ZBP1*	0	-1.4115
children	20q13.31-q13.33	56223447	56265680	56937	*PMEPA1*	0	-1.4115
children	20q13.32	56725982	56736183	128602	*C20orf85*	0.2792	-1.4115
children	20q13.32	56807832	56884495	55370	*PPP4R1L*	0.2792	-1.4115
children	20q13.32	56884770	56942563	57403	*RAB22A*	0.2792	-1.4115
children	20q13.33	56964174	57026156	9217	*VAPB*	0.2792	-1.4115
children	20q13.32	57034159	57089994	164284	*APCDD1L*	0.2792	-1.4115
children	20q13.32	57090434	57194948	149773	*APCDD1L-AS1*	0.2792	-1.4115
children	20q13.32	57226308	57254582	8675	*STX16*	0.2792	-1.4115
children	20q13.32	57264186	57290900	79716	*NPEPL1*	0.2792	-1.4115
children	20q13.32	57392669	57392749	407022	*MIR296*	0.2792	-1.4115
children	20q13.32	57393280	57393368	100126296	*MIR298*	0.2792	-1.4115
children	20q13.32	57393972	57425958	149775	*GNAS-AS1*	0.2792	-1.4115
children	20q13.3	57414772	57486251	2778	*GNAS*	0.24575	-1.4115
children	20q13	57556262	57570188	51497	*NELFCD*	0.2123	-1.4115
children	20q13.32	57570241	57582309	1522	*CTSZ*	0.2123	-1.4115
children	20q13.32	57594308	57601709	81027	*TUBB1*	0.2123	-1.4115

children	20q13.32	57603732	57607422	514	*ATP5E*	0.2123	-1.4115
children	20q13.32	57608199	57617901	51012	*SLMO2*	0.2123	-1.4115
children	20q13.32	57766074	57834167	128611	*ZNF831*	0.2123	-1.4115
children	20q13.2-q13.3	57875481	57901047	1908	*EDN3*	0.2123	-1.4115
children	20q13.32-q13.33	58152563	58422766	116154	*PHACTR3*	0.2123	-1.4115
children	20q13.33	58438611	58508718	10388	*SYCP2*	0.2123	-1.4115
children	20q13.33	58508818	58523702	63939	*FAM217B*	0.2123	-1.4115
children	20q13.3	58511886	58515352	5509	*PPP1R3D*	0.2123	-1.4115
children	20q13.33	58533470	58588168	60437	*CDH26*	0.2123	-1.4115
children	20q13.33	58630979	58648008	284756	*C20orf197*	0.2123	-1.4115
children	20q13.3	59827481	60515673	1002	*CDH4*	0.3115	-1.3833
children	20q13.33	60528601	60528718	100302168	*MIR1257*	0.3115	-1.355
children	20q13.33	60549853	60640866	6874	*TAF4*	0.3115	-1.3497
children	20q13.3	60718775	60757566	26039	*SS18L1*	0.563	-1.2837
children	20q13.33	60758080	60777810	26164	*MTG2*	0.563	-1.2837
children	20q13.33	60790016	60795323	11255	*HRH3*	0.563	-1.2837
children	20q13.33	60813540	60871269	9885	*OSBPL2*	0.563	-1.2837
children	20q13.33	60877951	60883918	11047	*ADRM1*	0.563	-1.2837
children	20q13.2-q13.3	60884115	60942368	3911	*LAMA5*	0.563	-1.2837
children	20q13.3	60962120	60963576	6227	*RPS21*	0.563	-1.2837
children	20q13.33	60963685	60982339	81928	*CABLES2*	0.563	-1.2837
children	20q13.33	60985292	61002629	140893	*RBBP8NL*	0.563	-1.2837
children	20q13.33	61038552	61051026	140628	*GATA5*	0.563	-1.2837
children	20q13.33	61141437	61148768	253868	*C20orf166-AS1*	0.563	-1.2837
children	20q13.33	61151512	61151583	406904	*MIR1-1*	0.563	-1.2837
children	20q13.33	61162118	61162220	406923	*MIR133A2*	0.563	-1.2837
children	20q13.33	61273796	61303647	28231	*SLCO4A1*	0.563	-1.2837
children	20q13	61340188	61394123	4923	*NTSR1*	0.563	-1.2748
children	20q13.33	61427804	61431945	55257	*MRGBP*	0.563	-1.268
children	20q13.33	61431978	61436939	101409261	*OGFR-AS1*	0.563	-1.268
children	20q13.3	61436176	61445352	11054	*OGFR*	0.563	-1.268
children	20q13.3	61448413	61472511	1299	*COL9A3*	0.563	-1.268
children	20q13.33	61472365	61493115	10732	*TCFL5*	0.563	-1.268

children	20q13.33	61475917	61477543	100132911	*DPH3P1*	0.563	-1.268
children	20q13.33	61509089	61557903	11083	*DIDO1*	0.563	-1.268
children	20q13.33	61569440	61579827	54994	*GID8*	0.563	-1.268
children	20q13.33	61583998	61599949	63910	*SLC17A9*	0.563	-1.268
children	20q13.33	61637330	61638387	128408	*BHLHE23*	0.563	-1.268
children	20q13.33	61640734	61716423	63930	*LOC63930*	0.563	-1.268
children	20q13.33	61665568	61668380	100144596	*LINC00029*	0.563	-1.268
children	21p11	10906186	10990943	7179	*TPTE*	5.1376	-0.53
children	21p11.2	11020841	11098925	85318	*BAGE3*	5.1376	-0.53
children	21p11.1 not on reference assembly	11057795	11098937	574	*BAGE*	5.1376	-0.53
children	21q11.2	14410486	14490571	149992	*ANKRD30BP2*	5.1376	-0.53
children	21q11.2	14982497	15013906	317754	*POTED*	5.1376	-0.53
children	21q11.2	15316095	15352765	391267	*ANKRD20A11P*	5.1376	-0.53
children	21q11.2	15481134	15579270	149998	*LIPI*	5.1376	-0.53
children	21q11	15588465	15600693	54033	*RBM11*	5.1376	-0.53
children	21q11.2	15646119	15663706	150000	*ABCC13*	5.1376	-0.53
children	21q11	15743436	15755509	6782	*HSPA13*	5.5068	-0.53
children	21q11	15857548	15918681	64092	*SAMSN1*	5.5068	-0.53
children	21q11.2	15963712	16015428	388813	*LOC388813*	5.5068	-0.53
children	21q11.2	16333555	16437126	8204	*NRIP1*	5.5068	-0.53
children	21q11.2	17102343	17252390	29761	*USP25*	5.6067	-0.53
children	21q21.1	17911408	17911489	407055	*MIR99A*	5.6067	-0.53
children	21q21.1	17912147	17912231	406885	*MIRLET7C*	5.6067	-0.53
children	21q21.1	17962556	17962645	406912	*MIR125B2*	5.6067	-0.53
children	21q21.1	18885223	18942429	1525	*CXADR*	5.6067	-0.53
children	21q21.1	18965967	18985268	10950	*BTG3*	5.6067	-0.53
children	21q21.1	19149720	19164826	246312	*C21orf91-OT1*	5.6067	-0.53
children	21q21.1	19161283	19191703	54149	*C21orf91*	5.6067	-0.53
children	21q21.1	19207988	19257925	54075	*CHODL-AS1*	5.6067	-0.53
children	21q11.2	19289656	19639687	140578	*CHODL*	5.9925	-0.53
children	21q21.1	19641432	19775970	5651	*TMPRSS15*	6.2192	-0.53
children	21q21.1	22114907	22175426	387486	*LINC00320*	5.936	-0.8737
children	21q21.1	22370632	22912517	4685	*NCAM2*	5.936	-0.8737

children	21q21.1	23095612	23109639	378828	*LINC00317*	5.936	-0.8737
children	21q21.1	23470935	23488847	54143	*LINC00308*	5.936	-0.8737
children	21q21.1-q21.2	26212863	26430056	339622	*LOC339622*	6.1652	-0.53
children	21q21.3	26758132	26804013	54072	*LINC00158*	6.1652	-0.53
children	21q21.3	26946291	26946356	406947	*MIR155*	6.1652	-0.53
children	21q21.3	26955086	26955536	282566	*LINC00515*	6.1652	-0.53
children	21q21.3	26957967	26979801	54148	*MRPL39*	6.1652	-0.53
children	21q21.2	27011593	27086885	58494	*JAM2*	6.1652	-0.53
children	21q21.1	27096790	27107965	522	*ATP5J*	6.1652	-0.53
children	21q21.3	27107257	27144771	2551	*GABPA*	6.1652	-0.53
children	21q21.3	27252860	27512708	351	*APP*	6.1652	-0.53
children	21q21.2	27838527	27945581	116159	*CYYR1*	6.1652	-0.53
children	21q21.2	28208605	28217728	9510	*ADAMTS1*	6.0015	-0.4803
children	21q21.3	28290230	28339439	11096	*ADAMTS5*	6.0015	-0.4803
children	21q21.3	29094697	29123552	54088	*LINC00113*	6.0015	-0.4803
children	21q21.3	29385681	29395528	246705	*LINC00314*	5.8286	-0.4803
children	21q21.3	29911639	29912677	118421	*LINC00161*	5.8286	-0.4803
children	21q21.3	30248385	30257695	29104	*N6AMT1*	5.8286	-0.4803
children	21q22.11	30300465	30365277	26046	*LTN1*	5.8286	-0.4803
children	21q22.11	30378079	30391685	10069	*RWDD2B*	5.8286	-0.4803
children	21q22.11	30396937	30426807	10600	*USP16*	5.8286	-0.4803
children	21q22.11	30428642	30446118	10694	*CCT8*	5.8286	-0.4803
children	21q22.3	30449791	30548210	56911	*MAP3K7CL*	5.8286	-0.4803
children	21q22.11	30565814	30660526	193629	*LINC00189*	5.8286	-0.4803
children	21q22.11	30671115	30718469	571	*BACH1*	5.8286	-0.4803
children	21q22.11	30909253	31312282	2897	*GRIK1*	5.8286	-0.4803
children	21q22.11	30968359	31003067	100379661	*GRIK1-AS2*	5.8286	-0.4803
children	21q22.11	31120493	31136325	642976	*GRIK1-AS1*	5.8286	-0.4803
children	21q22.11	31538240	31538971	26285	*CLDN17*	5.8286	-0.4803
children	21q22.11	31581468	31584101	266919	*LINC00307*	5.8286	-0.4803
children	21q22.11	31586323	31588469	9073	*CLDN8*	5.8286	-0.4803
children	21q22.11	31653626	31655276	643803	*KRTAP24-1*	5.8286	-0.4803
children	21q22.11	31661462	31661832	100131902	*KRTAP25-1*	5.8286	-0.4803

children	21q22.11	31691449	31692607	388818	*KRTAP26-1*	5.8286	-0.4803
children	21q22.11	31709330	31710012	643812	*KRTAP27-1*	5.8286	-0.4803
children	21q22.1	31720716	31720924	337963	*KRTAP23-1*	5.8286	-0.4803
children	21q22.1	31743708	31744557	337959	*KRTAP13-2*	5.8286	-0.4803
children	21q22.1	31768391	31769138	140258	*KRTAP13-1*	5.8286	-0.4803
children	21q22.1	31797710	31798230	337960	*KRTAP13-3*	5.8286	-0.4803
children	21q22.1	31802593	31803076	284827	*KRTAP13-4*	5.8286	-0.4803
children	21q22.1	31812645	31813098	254950	*KRTAP15-1*	5.8286	-0.4803
children	21q22.1	31852363	31852636	337882	*KRTAP19-1*	5.8286	-0.4803
children	21q22.1	31859508	31859667	337969	*KRTAP19-2*	5.8286	-0.4803
children	21q22.1	31863781	31864275	337970	*KRTAP19-3*	5.8286	-0.4803
children	21q22.1	31869173	31869428	337971	*KRTAP19-4*	5.8286	-0.4803
children	21q22.1	31874189	31874408	337972	*KRTAP19-5*	5.8286	-0.4803
children	21q22.1	31913853	31914183	337973	*KRTAP19-6*	5.8286	-0.4803
children	21q22.1	31933416	31933608	337974	*KRTAP19-7*	5.8286	-0.4803
children	21q22.11	31962423	31962716	100288287	*KRTAP22-2*	5.8286	-0.4803
children	21q22.1	31964758	31965374	337968	*KRTAP6-3*	5.8286	-0.4803
children	21q22.1	31971004	31971193	337967	*KRTAP6-2*	5.8286	-0.4803
children	21q22.1	31973439	31973586	337979	*KRTAP22-1*	5.8286	-0.4803
children	21q22.1	31986004	31986223	337966	*KRTAP6-1*	5.8286	-0.4803
children	21q22.1	31988773	31988944	337975	*KRTAP20-1*	5.8286	-0.4803
children	21q22.11	31992945	31993169	100151643	*KRTAP20-4*	5.8286	-0.4803
children	21q22.1	32007582	32007780	337976	*KRTAP20-2*	5.8286	-0.4803
children	21q22.11	32015182	32015455	337985	*KRTAP20-3*	5.8286	-0.4803
children	21q22.11	32090842	32091095	100288323	*KRTAP21-3*	5.8286	-0.4803
children	21q22.1	32119268	32119520	337978	*KRTAP21-2*	5.8286	-0.4803
children	21q22.1	32127456	32127696	337977	*KRTAP21-1*	5.8286	-0.4803
children	21q22.1	32185014	32185570	337879	*KRTAP8-1*	5.8286	-0.4803
children	21q22.11	32201357	32202051	337878	*KRTAP7-1*	5.8286	-0.4803
children	21q22.1	32252963	32253874	337880	*KRTAP11-1*	5.8286	-0.4803
children	21q22.11	32410477	32410795	728299	*KRTAP19-8*	5.8286	-0.4803
children	21q22.11	32490735	32931290	7074	*TIAM1*	5.8286	-0.4803
children	21q22.11	33031934	33041243	6647	*SOD1*	5.8286	-0.4803

children	21q22.1	33043312	33104431	57466	*SCAF4*	5.8286	-0.4803
children	21q22.1	33245627	33376377	30811	*HUNK*	5.8286	-0.4803
children	21q22.11	33452793	33458608	100551499	*LINC00159*	5.8286	-0.4803
children	21q22.11	33640529	33651376	54069	*MIS18A*	5.8286	-0.4803
children	21q22.1	33664123	33684599	56246	*MRAP*	5.8286	-0.4803
children	21q22.11	33683329	33765312	9875	*URB1*	5.8286	-0.4803
children	21q22.11	33784744	33887710	59271	*EVA1C*	5.8286	-0.4803
children	21q22.1	33973983	33984913	56683	*C21orf59*	5.8286	-0.4803
children	21q22.2	34001068	34100250	8867	*SYNJ1*	5.8286	-0.4803
children	21q21.3	34106209	34144169	94104	*PAXBP1*	5.8286	-0.4803
children	21q22.11	34162983	34186053	56245	*C21orf62*	5.8286	-0.4803
children	21q22.11	34398215	34401503	10215	*OLIG2*	5.3103	-0.4803
children	21q22.11	34442449	34444728	116448	*OLIG1*	5.3103	-0.4803
children	21q22.11	34602199	34635062	3455	*IFNAR2*	5.3185	-0.4803
children	21q22.11	34637936	34638565	100288432	*IL10RB-AS1*	5.3185	-0.4803
children	21q22.11	34638664	34669539	3588	*IL10RB*	5.3185	-0.4803
children	21q22.11	34697213	34732128	3454	*IFNAR1*	5.2651	-0.2279
children	21q22.11	34775201	34809828	3460	*IFNGR2*	5.2651	-0.2279
children	21q22.11	34821447	34852316	757	*TMEM50B*	5.2651	-0.2279
children	21q22.11	34860361	34863790	54943	*DNAJC28*	5.2651	-0.2279
children	21q22.11	34876237	34914464	2618	*GART*	5.2651	-0.2279
children	21q22.11	34915343	34932973	6651	*SON*	5.2651	-0.2279
children	21q22.1	34949858	34961014	29980	*DONSON*	5.2651	-0.2279
children	21q21.3	34961647	35014160	9946	*CRYZL1*	5.2651	-0.2279
children	21q22.1-q22.2	35014783	35210802	6453	*ITSN1*	5.2651	-0.2279
children	21q22.11	35275756	35288158	539	*ATP5O*	5.2651	-0.2279
children	21q22.12	35445822	35478561	6526	*SLC5A3*	5.3778	-0.2279
children	21q22.11	35445822	35515334	64968	*MRPS6*	5.3778	-0.2279
children	21q22.11	35552977	35555546	114036	*LINC00310*	5.3778	-0.2279
children	21q22.12	35736322	35743440	9992	*KCNE2*	5.3778	-0.2279
children	21q22.12	35747748	35761452	54065	*SMIM11*	5.3778	-0.2279
children	21q22.12	35818985	35828107	3753	*KCNE1*	5.3778	-0.2279
children	21q22.12	35888739	35899308	1827	*RCAN1*	5.3778	-0.2279

children	21q22.12	36041461	36090525	54102	*CLIC6*	5.3778	-0.2279
children	21q22.12	36096104	36109479	54064	*LINC00160*	5.3778	-0.2279
children	21q22.3	36160097	36260987	861	*RUNX1*	5.3778	-0.2279
children	21q22.12	36410232	36411723	80215	*RUNX1-IT1*	4.8258	-0.2279
children	21q22.12	37093012	37093106	768219	*MIR802*	4.8258	-0.2279
children	21q22.13	37406838	37433116	54093	*SETD4*	4.8258	-0.2279
children	21q22.12	37441939	37498938	100133286	*LOC100133286*	4.8258	-0.2279
children	21q22.13	37442221	37445475	873	*CBR1*	4.8258	-0.2279
children	21q22.2	37507262	37518860	874	*CBR3*	4.8258	-0.2279
children	21q22.2	37536838	37666572	9980	*DOPEY2*	4.8258	-0.2279
children	21q22.13	37692486	37748944	23515	*MORC3*	4.8258	-0.2279
children	21q22.13	37757688	37789125	8208	*CHAF1B*	4.8258	-0.2279
children	21q22.3	37832919	37838739	23562	*CLDN14*	4.8258	-0.2279
children	21q22.13	38071432	38118219	6493	*SIM2*	4.8258	-0.2279
children	21q22.13	38123188	38338956	3141	*HLCS*	4.8258	-0.2279
children	21q22.2	38378862	38391958	53820	*RIPPLY3*	4.8258	-0.2279
children	21q22.2	38437663	38445103	51227	*PIGP*	4.8258	-0.2279
children	21q22.2	38445570	38575408	7267	*TTC3*	4.8258	-0.2279
children	21q22.13	38580803	38594037	257203	*DSCR9*	4.8258	-0.2279
children	21q22.2	38595725	38639833	10311	*DSCR3*	4.8258	-0.2279
children	21q22.13	38739858	38887679	1859	*DYRK1A*	4.8258	-0.2279
children	21q22.1	38996524	39288741	3763	*KCNJ6*	4.8258	-0.2279
children	21q22.2	39426312	39493454	10281	*DSCR4*	4.8258	-0.2279
children	21q22.2	39493544	39528605	84677	*DSCR8*	4.8258	-0.2279
children	21q22.13	39578249	39580738	259234	*DSCR10*	4.8258	-0.2279
children	21q22.2	39601836	39673746	3772	*KCNJ15*	4.8258	-0.2279
children	21q22.3	39739182	40033704	2078	*ERG*	4.8258	-0.2279
children	21q22.2	40110878	40124181	400866	*LINC00114*	4.8258	-0.2279
children	21q22.2	40177230	40196878	2114	*ETS2*	4.8258	-0.2279
children	21q22.3	40547371	40555440	8624	*PSMG1*	4.8258	-0.2279
children	21q22.2	40557403	40685712	54014	*BRWD1*	4.8258	-0.2279
children	21q22.2	40714240	40721047	3150	*HMGN1*	4.8258	-0.2279
children	21q22.3	40752212	40769815	7485	*WRB*	4.8258	-0.2279

children	21q22.2	40777769	40816128	150082	*LCA5L*	4.8258	-0.2279
children	21q22.3	40817796	40887433	6450	*SH3BGR*	4.8258	-0.2279
children	21q22.3	41029246	41034816	10317	*B3GALT5*	4.8258	-0.2279
children	21q22.2	41117333	41174023	150084	*IGSF5*	4.4885	-0.2279
children	21q22.2	41239346	41301322	5121	*PCP4*	4.45	-0.5017
children	21q22.2	41384342	42219039	1826	*DSCAM*	4.2202	-0.5017
children	21q22.2	42513426	42519991	284835	*LINC00323*	4.2202	-0.4566
children	21q22.3	42539727	42654461	25825	*BACE2*	4.2202	-0.2279
children	21q22.2	42547157	42557166	191585	*PLAC4*	4.2202	-0.4566
children	21q22.3	42688660	42729654	54097	*FAM3B*	4.5156	-0.2279
children	21q22.3	42733949	42780869	4600	*MX2*	4.5156	-0.2279
children	21q22.3	42792484	42831141	4599	*MX1*	4.5156	-0.2279
children	21q22.3	42836477	42879992	7113	*TMPRSS2*	4.2718	-0.2279
children	21q22.3	43099461	43117496	54090	*LINC00111*	3.6935	-0.2279
children	21q22.3	43131679	43135935	150135	*LINC00479*	3.6935	-0.2279
children	21q22.3	43136595	43137742	54089	*LINC00112*	3.6935	-0.2279
children	21q22.3	43159528	43187249	54101	*RIPK4*	3.4311	-0.2279
children	21q22.3	43218384	43299591	63977	*PRDM15*	3.4311	-0.4749
children	21q22.3	43305218	43346799	25966	*C2CD2*	3.4311	-0.4749
children	21q22.3	43406939	43430496	49854	*ZBTB21*	3.4311	-0.4749
children	21q22.3	43442377	43445029	150142	*ZNF295-AS1*	3.4311	-0.4749
children	21q22.3	43483067	43563105	89766	*UMODL1*	3.4311	-0.4749
children	21q22.3	43619798	43717354	9619	*ABCG1*	3.2148	-0.4749
children	21q22.3	43731776	43735706	7033	*TFF3*	3.2148	-0.4749
children	21q22.3	43766466	43771208	7032	*TFF2*	3.2148	-0.4749
children	21q22.3	43782390	43786644	7031	*TFF1*	3.2148	-0.4749
children	21q22.3	43791995	43809258	64699	*TMPRSS3*	3.2148	-0.4749
children	21q22.3	43823970	43867790	53347	*UBASH3A*	3.2148	-0.4749
children	21q22.3	43892596	43916464	89765	*RSPH1*	3.2148	-0.4749
children	21q22.3	43919741	44001550	54020	*SLC37A1*	3.12805	-0.4658
children	21q22.3	44073861	44195618	5152	*PDE9A*	3.1298	-0.4658
children	21q22.3	44263189	44299693	10785	*WDR4*	3.1298	-0.2279
children	21q22.3	44313377	44329773	4731	*NDUFV3*	3.4661	-0.2279

children	21q22.3	44394619	44454041	5316	*PKNOX1*	3.4661	-0.2279
children	21q22.3	44473300	44496040	875	*CBS*	3.4661	-0.2279
children	21q22.3	44513065	44527688	7307	*U2AF1*	3.4661	-0.2279
children	21q22.3	44589117	44592920	1409	*CRYAA*	3.4661	-0.2279
children	21q22.3	44834397	44847002	150094	*SIK1*	3.1298	-0.498
children	21q22.3	44869903	44873771	284836	*LINC00319*	3.1915	-0.498
children	21q22.3	44881973	44898103	114038	*LINC00313*	3.1915	-0.498
children	21q22.3	44949071	45079374	11077	*HSF2BP*	2.90345	-0.4852
children	21q22.3	45079431	45115960	23076	*RRP1B*	2.4669	-0.4723
children	21q22.3	45138977	45182188	8566	*PDXK*	2.4669	-0.4723
children	21q22.3	45193545	45196256	1476	*CSTB*	2.4669	-0.4723
children	21q22.3	45209417	45223983	8568	*RRP1*	2.4669	-0.4723
children	21q22.3	45285115	45407475	56894	*AGPAT3*	2.4498	-0.4723
children	21q22.3	45432205	45526432	7109	*TRAPPC10*	2.4498	-0.4723
children	21q22.3	45527207	45551063	5822	*PWP2*	2.4498	-0.4723
children	21q22.3	45553493	45565605	8209	*C21orf33*	2.4498	-0.4723
children	21q22.3	45646709	45660887	23308	*ICOSLG*	2.4498	-0.4491
children	21q22.3	45666221	45682099	29947	*DNMT3L*	2.4498	-0.4491
children	21q22.3	45705720	45718102	326	*AIRE*	2.4498	-0.4491
children	21q22.3	45719916	45747264	5211	*PFKL*	2.3568	-0.426
children	21q22.3	45748826	45758221	755	*C21orf2*	1.9969	-0.2212
children	21q22.3	45773483	45862964	7226	*TRPM2*	2.2118	-0.2212
children	21q22.3	45870868	45875167	100861510	*LRRC3-AS1*	2.2118	-0.2212
children	21q22.3	45875368	45878739	81543	*LRRC3*	2.2118	-0.2212
children	21q22.3	45917774	46131495	54084	*TSPEAR*	2.5588	-0.2212
children	21q22.3	45959067	45960078	386677	*KRTAP10-1*	2.5588	-0.2212
children	21q22.3	45970239	45971388	386679	*KRTAP10-2*	2.5588	-0.2212
children	21q22.3	45977905	45978643	386682	*KRTAP10-3*	2.5588	-0.2212
children	21q22.3	45993605	45995248	386672	*KRTAP10-4*	2.5588	-0.2212
children	21q22.3	45999331	46000481	386680	*KRTAP10-5*	2.5588	-0.2212
children	21q22.3	46011148	46012386	386674	*KRTAP10-6*	2.5588	-0.2212
children	21q22.3	46020496	46022091	386675	*KRTAP10-7*	2.5588	-0.2212
children	21q22.3	46031995	46032871	386681	*KRTAP10-8*	2.5588	-0.2212

children	21q22.3	46047039	46048295	386676	*KRTAP10-9*	2.5588	-0.2212
children	21q22.3	46057272	46058372	353333	*KRTAP10-10*	2.5588	-0.2212
children	21q22.3	46066330	46067566	386678	*KRTAP10-11*	2.5588	-0.2212
children	21q22.3	46074129	46074576	386684	*KRTAP12-4*	2.5588	-0.2212
children	21q22.3	46077848	46078258	386683	*KRTAP12-3*	2.5588	-0.2212
children	21q22.3	46086105	46086844	353323	*KRTAP12-2*	2.5588	-0.2212
children	21q22.3	46101490	46102078	353332	*KRTAP12-1*	2.5588	-0.2212
children	21q22.3	46117086	46117959	386685	*KRTAP10-12*	2.5588	-0.2212
children	21q22.3	46188494	46221751	7327	*UBE2G2*	2.5588	-0.2212
children	21q22.3	46225531	46238044	6612	*SUMO3*	2.5588	-0.2212
children	21q22.3	46269499	46293818	754	*PTTG1IP*	2.5588	-0.2212
children	21q22.3	46305868	46340965	3689	*ITGB2*	2.5588	-0.2212
children	21q22.3	46359911	46396904	85395	*FAM207A*	2.5588	-0.2212
children	21q22.3	46409778	46414001	727699	*LINC00163*	2.5588	-0.2212
children	21q22.3	46419121	46424642	378825	*LINC00162*	2.5588	-0.2212
children	21q22.3	46490869	46493126	728039	*SSR4P1*	2.5588	-0.2212
children	21q22.3	46494492	46646478	104	*ADARB1*	2.5588	-0.2212
children	21q22.3	46683842	46707811	23275	*POFUT2*	2.5588	-0.2212
children	21q22.3	46707966	46717269	642852	*LOC642852*	2.5588	-0.2212
children	21q22.3	46825051	46933634	80781	*COL18A1*	2.281	-0.2212
children	21q22.3	46839630	46844955	378832	*COL18A1-AS1*	1.9969	-0.2212
children	21q22.3	46934628	46954542	6573	*SLC19A1*	2.281	-0.2212
children	21q22.3	47247754	47256333	100129027	*LOC100129027*	2.281	-0.2212
children	21q22.3	47269874	47362368	54039	*PCBP3*	2.281	-0.2212
children	21q22.3	47401662	47424963	1291	*COL6A1*	1.7077	-0.2212
children	21q22.3	47518032	47549719	1292	*COL6A2*	2.0126	-0.2212
children	21q22.3	47556175	47575481	10841	*FTCD*	2.0126	-0.2212
children	21q22.3	47581061	47604373	84221	*SPATC1L*	1.7077	-0.2212
children	21q22.3	47608359	47648738	4047	*LSS*	1.9987	-0.2212
children	21q22.3	47649144	47671615	114044	*MCM3AP-AS1*	1.9987	-0.2212
children	21q22.3	47655038	47705308	8888	*MCM3AP*	1.9987	-0.2212
children	21q22.3	47706243	47712435	54059	*YBEY*	1.9987	-0.2212
children	21q22.3	47721043	47743813	54058	*C21orf58*	1.9987	-0.2212

children	21q22.3	47744035	47865682	5116	*PCNT*	1.9987	-0.2212
children	21q22.3	47878861	47966219	23181	*DIP2A*	1.9987	-0.2212
children	21q22.3	47882383	47889218	100862692	*DIP2A-IT1*	1.9987	-0.2212
children	21q22.3	48018530	48025035	6285	*S100B*	1.9987	-0.2212
children	21q22.3	48055506	48075009	3275	*PRMT2*	1.9987	-0.2212
children	21p11.2	9907188	9968594	100132288	*TEKT4P2*	4.9153	-0.53
children	22q11.22	22599191	22599927	7441	*VPREB1*	0.2102	-1.0744
children	22q11.22	22838770	22863505	140883	*ZNF280B*	0.2102	-1.6948
children	22q11.22	22868060	22874624	129025	*ZNF280A*	0.2102	-1.6948
children	22q11.22	22890117	22901768	23532	*PRAME*	0.21105	-1.6948
children	3q12.2	100053561	100074478	56954	*NIT2*	0	-1.0674
children	3q12.2	100082302	100120242	9868	*TOMM70A*	0	-1.0674
children	3q12.2	100120036	100175170	348801	*LNP1*	0	-1.0674
children	3q12.2	100211462	100296296	55076	*TMEM45A*	0	-1.0674
children	3q12.2	100428133	100467811	10342	*TFG*	0	-1.0674
children	3q12	100468178	100712334	25890	*ABI3BP*	0	-1.0674
children	3q12.2-q12.3	100941389	101039419	50939	*IMPG2*	0	-1.0674
children	3q12	101043032	101232085	57337	*SENP7*	0	-1.0674
children	3q12.3	101237710	101242731	131909	*FAM172BP*	0	-1.0674
children	3q12.3	101280679	101285290	54931	*TRMT10C*	0	-1.0674
children	3q12.3	101293041	101313281	57092	*PCNP*	0	-1.0674
children	3q12.3	101368282	101395988	27107	*ZBTB11*	0	-1.0657
children	3q12.3	101395273	101398057	100009676	*ZBTB11-AS1*	0	-1.0657
children	3q12	101399933	101405563	6152	*RPL24*	0	-1.0657
children	3q12.3	101431277	101432260	285359	*PDCL3P4*	0	-1.0657
children	3q12.3	101443436	101489406	79598	*CEP97*	0	-1.0657
children	3q12.3	101498028	101547075	91775	*NXPE3*	0	-1.0657
children	3p12-q12	101546833	101579869	64332	*NFKBIZ*	0	-1.0657
children	3q12.3	101659702	101716770	152225	*LOC152225*	0	-1.0657
children	3q12.3	102153858	102198685	131368	*ZPLD1*	0	-1.0657
children	3q13.1	105085556	105244230	214	*ALCAM*	0	-1.579
children	3q13.11	105377108	105587887	868	*CBLB*	0	-1.579
children	3q13.12	106828636	106959485	100302640	*LINC00882*	0	-1.579

children	3q13.12	106959538	106967719	344595	*LINC00883*	0	-1.579
children	3q13.12	107096187	107097481	84692	*CCDC54*	0	-1.5103
children	3q13.1	107241782	107530176	56987	*BBX*	0	-1.5103
children	3q13.12	107560508	107596915	151658	*LINC00635*	0	-1.5103
children	3q13.12	107602051	107647753	285205	*LINC00636*	0	-1.5103
children	3q13.1-q13.2	107761940	107809935	961	*CD47*	0	-1.5103
children	3q13.13	107879658	107941417	55081	*IFT57*	0	-1.5103
children	3q13.13	108021331	108097131	11148	*HHLA2*	0	-1.5103
children	3q13.13	108099215	108248169	22989	*MYH15*	0	-1.5103
children	3q13.13	108268717	108308491	57650	*KIAA1524*	0	-1.5103
children	3q13.13	108308336	108413693	9666	*DZIP3*	0	-1.5103
children	3q13.1	108474485	108476130	84666	*RETNLB*	0	-1.5103
children	3q13	108541544	108573852	50852	*TRAT1*	0	-1.5103
children	3q13.1	108626641	108672677	9626	*GUCA1C*	0	-1.5103
children	3q13	108677086	108836993	27136	*MORC1*	0	-1.5103
children	3q13.13	108855560	108868951	401081	*FLJ22763*	0	-1.5103
children	3q13.13	108897011	108904108	677779	*LINC00488*	0	-1.5103
children	3q13.13	109012634	109035364	151871	*DPPA2*	0	-1.5103
children	3q13.13	109044987	109056419	55211	*DPPA4*	0	-1.5103
children	3q13.13	110764162	110788806	100506555	*PVRL3-AS1*	0	-1.5103
children	3q13	110790605	110856407	25945	*PVRL3*	0	-1.5103
children	3q13.13-q13.2	111260925	111371206	10225	*CD96*	0	-1.478
children	3q13.2	111311746	111314182	79413	*ZBED2*	0	-1.478
children	3q13.2	111393522	111565294	257068	*PLCXD2*	0	-1.478
children	3q13.2	111451326	111695364	90102	*PHLDB2*	0	-1.478
children	3q13.2	111697722	111712215	55347	*ABHD10*	0	-1.478
children	3q13.2	111717585	111732735	29114	*TAGLN3*	0	-1.478
children	3q13.2	111758464	111800116	344805	*TMPRSS7*	0	-1.478
children	3q13.2	111805181	111837044	79669	*C3orf52*	0	-1.478
children	3q13.2	111831647	111831745	693152	*MIR567*	0	-1.478
children	3q13.2	111839687	111852152	257144	*GCSAM*	0	-1.478
children	3q13.2	111859751	112013074	285335	*SLC9C1*	0	-1.478
children	3q13.2	112051915	112081658	4345	*CD200*	0	-1.478

children	3q13.2	112182812	112218408	151888	*BTLA*	0	-1.478
children	3q13.2	112280856	112303284	55032	*SLC35A5*	0	-1.2628
children	3q13.2	112323232	112359990	151887	*CCDC80*	0	-1.2628
children	3q13.2	112534555	112564797	344807	*CD200R1L*	0	-1.2628
children	3q13.2	112641531	112693937	131450	*CD200R1*	0	-1.2628
children	3q13.2	112709799	112720221	29083	*GTPBP8*	0	-1.2628
children	3q13.2	112721291	112738555	25871	*C3orf17*	0	-1.2628
children	3q13.2	112930311	113006310	91653	*BOC*	0	-1.2628
children	3q13.2	113161564	113234034	152185	*SPICE1*	0	-1.2628
children	3q13.2	113251217	113348422	54847	*SIDT1*	0	-1.2628
children	3q13.2	113367232	113415493	205717	*KIAA2018*	0	-1.2628
children	3q13.2	113435306	113465146	80218	*NAA50*	0	-1.2628
children	3q13.31	113465865	113530905	523	*ATP6V1A*	0	-1.2628
children	3q13.31	113557680	113666021	54762	*GRAMD1C*	0	-1.2628
children	3q25	153742189	153838999	100507524	*ARHGEF26-AS1*	0	-1.0719
children	3q25.2	153838791	153975616	26084	*ARHGEF26*	0	-1.0719
children	3q25.2	153993456	154042286	170506	*DHX36*	0	-1.0719
children	3q25.2	154055460	154147504	344758	*GPR149*	0	-1.0719
children	3q25.2	154797435	154901518	4311	*MME*	0	-1.0719
children	3q25	155008020	155011489	100507537	*LOC100507537*	0	-1.0719
children	3q25.31	155197670	155394105	23007	*PLCH1*	0	-1.0719
children	3q25.31	155480400	155524076	285315	*C3orf33*	0	-1.0719
children	3q25.31	155544300	155572248	9197	*SLC33A1*	0	-1.0719
children	3q24	155588324	155655520	8833	*GMPS*	0	-1.0719
children	3q26.1	155838336	156256927	7881	*KCNAB1*	0	-1.0719
children	3q25.31	156257341	156272989	6747	*SSR3*	0	-1.0719
children	3q25.31	156390959	156393502	100287227	*TIPARP-AS1*	0	-1.0719
children	3q25.31	156392204	156424557	25976	*TIPARP*	0	-1.0719
children	3q25.31	156465131	156534851	730091	*LINC00886*	0	-1.0719
children	3q25.31	156527059	156529810	647033	*PA2G4P4*	0	-1.0719
children	3q25.31	156544095	156763918	389170	*LEKR1*	0	-1.0719
children	3q25.31	156799455	156840791	339894	*LINC00880*	0	-1.0719
children	3q25.31	156807669	156818924	100498859	*LINC00881*	0	-1.0719

children	3q25.31	156865344	156878549	57018	*CCNL1*	0	-1.0719
children	3q24-q25	156977531	157217445	79674	*VEPH1*	0	-1.0719
children	3q25	157154579	157161417	5806	*PTX3*	0	-1.0719
children	3q25.32	157813799	157823952	6474	*SHOX2*	0	-1.0719
children	3q25.32	157827840	158262624	51319	*RSRC1*	0	-1.0719
children	3q25.1	158288952	158324249	4291	*MLF1*	0	-1.0719
children	3q25	158362316	158410360	85476	*GFM1*	0	-1.0719
children	3q25.32	158384202	158390482	56925	*LXN*	0	-1.0719
children	3q25.32	158414896	158450275	5918	*RARRES1*	0	-1.0719
children	3q25.32	158519714	158547508	64747	*MFSD1*	0	-1.0719
children	3q25.32	158787040	158981535	654502	*IQCJ*	0	-1.0719
children	3q26.31	171757417	172118492	64778	*FNDC3B*	0	-1.2507
children	3q26.31	172161080	172166246	2693	*GHSR*	0	-1.2507
children	3q26	172223297	172241297	8743	*TNFSF10*	0	-1.2507
children	3q26.31	172348434	172429008	57552	*NCEH1*	0	-1.2507
children	3q26.1-q26.2	172468474	172539264	1894	*ECT2*	0	-1.2507
children	3q26.31	172607146	172859058	83893	*SPATA16*	0	-1.2507
children	3q26.31	173116237	174001139	22871	*NLGN1*	0	-1.2507
children	3q26.31	174577110	175523428	254827	*NAALADL2*	0	-1.1607
children	3q26.3	174797101	174833032	100862679	*NAALADL2-AS3*	0	-1.2851
children	3q12.1	98451079	98514689	10402	*ST3GAL6*	0	-1.0804
children	3q12.1	98514813	98620533	131566	*DCBLD2*	0	-1.0804
children	3q12.3	99357439	99515577	1295	*COL8A1*	0	-1.0757
children	3q12.1	99536677	99897476	84319	*CMSS1*	0	-1.0757
children	3q12.1	99551987	99833357	11259	*FILIP1L*	0	-1.0757
children	3q12.1	99904667	99913030	644444	*TMEM30C*	0	-1.0757
children	3q12.2	99979660	100044096	55773	*TBC1D23*	0	-1.0674
children	4q23	100010007	100222513	100507053	*LOC100507053*	0.2117	-1.2396
children	4q22	100044807	100065449	127	*ADH4*	0.2117	-1.2396
children	4q24	100081750	100082804	359806	*PCNAP1*	0.2117	-1.2396
children	4q23	100123794	100140403	130	*ADH6*	0.2117	-1.2396
children	4q23	100197522	100212185	124	*ADH1A*	0.2117	-1.2396
children	4q23	100227543	100242599	125	*ADH1B*	0.2117	-1.2396

children	4q23	100257648	100274202	126	*ADH1C*	0.2117	-1.2396
children	4q23-q24	100333417	100356291	131	*ADH7*	0.2117	-1.2396
children	4q23	100432160	100463460	84103	*C4orf17*	0.2117	-1.2396
children	4q23	100467863	100484825	93587	*TRMT10A*	0.2117	-1.2396
children	4q24	100485234	100545154	4547	*MTTP*	0.2117	-1.2396
children	4q25-q27	100737980	100791346	27071	*DAPP1*	0.2117	-1.2396
children	4q23	100799494	100815703	8649	*LAMTOR3*	0.2117	-1.2396
children	4q23	100817406	100867883	79982	*DNAJB14*	0.2117	-1.2396
children	4q24	100869243	100871512	3015	*H2AFZ*	0.2117	-1.2396
children	4q24	101107026	101111655	115265	*DDIT4L*	0.2117	-1.2396
children	4q24	101316497	101439250	51705	*EMCN*	0.2117	-1.2396
children	4q24	101944586	102268628	5530	*PPP3CA*	0.42715	-1.2396
children	4q24	102268933	102270040	90024	*FLJ20021*	0.4462	-1.2396
children	4q24	102711763	102995969	55024	*BANK1*	0.4462	-1.2396
children	4q24	103172197	103266410	64116	*SLC39A8*	0.4462	-1.2396
children	4q24	103422485	103538459	4790	*NFKB1*	0.4249	-1.1779
children	4q24	103552642	103682151	4126	*MANBA*	0.4249	-1.1779
children	4q24	103715539	103748340	7323	*UBE2D3*	0.4249	-1.1779
children	4q24	103790134	103813963	493856	*CISD2*	0.4249	-1.1779
children	4q24	103806204	103940896	150159	*SLC9B1*	0.4249	-1.1779
children	4q24	103946647	103997930	133308	*SLC9B2*	0.4249	-1.1779
children	4q24	103998781	104021024	56898	*BDH2*	0.4249	-1.1779
children	4q24-q25	104026962	104119566	1062	*CENPE*	0.4249	-1.1779
children	4q25	104510624	104640973	6870	*TACR3*	0.4249	-1.1779
children	4q24	105389462	105416058	80319	*CXXC4*	0.4249	-1.1779
children	4q31.1	148999914	149363672	4306	*NR3C2*	0.2092	-1.0773
children	4q22.3	95128758	95212443	56916	*SMARCAD1*	0.649	-1.3635
children	4q22.3	95219706	95264027	27306	*HPGDS*	0.649	-1.3635
children	4q22	95373007	95378340	10611	*PDLIM5*	0.649	-1.3635
children	4q22-q24	95679127	96079601	658	*BMPR1B*	0.4122	-1.2396
children	4q21-q23	96083655	96470361	8633	*UNC5C*	0.4122	-1.2396
children	4q22-q23	96761238	96762625	5161	*PDHA2*	0.4122	-1.2396
children	4q22.3	98288076	98411315	101410545	*STPG2-AS1*	0.2117	-1.2396

children	4q22.3-q23	98480024	99064391	285555	*STPG2*	0.2117	-1.2396
children	4q23-q25	99182526	99365012	5910	*RAP1GDS1*	0.2117	-1.2396
children	4q23	99391517	99579812	10098	*TSPAN5*	0.2117	-1.2396
children	4q23	99799606	99850243	1977	*EIF4E*	0.2117	-1.2396
children	4q23	99916787	99983960	23173	*METAP1*	0.2117	-1.2396
children	4q23	99992129	100009939	128	*ADH5*	0.2117	-1.2396
children	6q16.2	100054649	100063454	59336	*PRDM13*	0.4361	-2.2055
children	6q16	100367785	100442099	84539	*MCHR2*	0.4361	-2.2055
children	6q16.3	100836749	100911551	6492	*SIM1*	0.4361	-2.2055
children	6q16	100956070	101329248	10973	*ASCC3*	0.4361	-2.2055
children	6q16.3	101846860	102517958	2898	*GRIK2*	0.4361	-2.3031
children	6q16.3	105175967	105307794	57531	*HACE1*	0.4361	-1.8278
children	6q21	105384168	105388402	100113403	*LINC00577*	0.2021	-1.8126
children	6q21	105404922	105531207	389421	*LIN28B*	0.2021	-1.8126
children	6q21	105544698	105584221	11149	*BVES*	0.2021	-1.8126
children	6q21	105585561	105617819	154442	*BVES-AS1*	0.2021	-1.8126
children	6q21	105605774	105624130	64208	*POPDC3*	0.2021	-1.8126
children	6q22	105725441	105850999	5550	*PREP*	0.2021	-1.7978
children	6q21	106534194	106557814	639	*PRDM1*	0.2021	-1.783
children	6q21	106632351	106773695	9474	*ATG5*	0.2021	-1.783
children	6q21	106959729	107018324	202	*AIM1*	0.2021	-1.783
children	6q21	107018902	107077373	84816	*RTN4IP1*	0.2021	-1.783
children	6q21	107077440	107116292	55278	*QRSL1*	0.2021	-1.783
children	6q21	107349375	107372790	51250	*C6orf203*	0.2021	-1.783
children	6q21	107386384	107435636	57673	*BEND3*	0.2021	-1.783
children	6q21	107473760	107780779	57107	*PDSS2*	0.2021	-1.783
children	6q21	107811316	107982513	55084	*SOBP*	0.2021	-1.783
children	6q21	108023360	108145521	256380	*SCML4*	0.2021	-1.783
children	6q21	108188959	108279482	11231	*SEC63*	0.2021	-1.783
children	6q21	108362612	108395941	28962	*OSTM1*	0.2021	-1.783
children	6q21	108487261	108510013	7101	*NR2E1*	0.2021	-1.783
children	6q21	108532420	108582464	8724	*SNX3*	0.2021	-1.783
children	6q22.1	108616097	108844251	246269	*LACE1*	0.2021	-1.783

children	6q21	108881025	109005971	2309	*FOXO3*	0.2017	-1.783
children	6q21	109072856	109091145	387111	*LINC00222*	0.2013	-1.783
children	6q21	109169618	109295675	84071	*ARMC2*	0.2013	-1.783
children	6q21	109307639	109330191	27244	*SESN1*	0.2013	-1.783
children	6q21	109416355	109485115	285753	*CEP57L1*	0.2013	-1.783
children	6q21	109615505	109629423	221262	*CCDC162P*	0.2013	-1.783
children	6q21	109687716	109703762	8763	*CD164*	0.2013	-1.783
children	6q21	109711417	109762374	285755	*PPIL6*	0.2013	-1.783
children	6q21	109761930	109765122	6610	*SMPD2*	0.2013	-1.783
children	6q21	109765265	109777190	64780	*MICAL1*	0.2013	-1.783
children	6q21	109783718	109804440	9841	*ZBTB24*	0.2013	-1.783
children	6q21	109814058	110012415	221264	*AK9*	0.2013	-1.783
children	6q21	110012423	110146634	9896	*FIG4*	0.2013	-1.783
children	6q21	110299458	110301923	2830	*GPR6*	0.2013	-1.783
children	6q21	110421021	110501207	8936	*WASF1*	0.2013	-1.783
children	6q21	110501623	110553422	51362	*CDC40*	0.2013	-1.783
children	6q21	110567148	110679475	728464	*METTL24*	0.2013	-1.8062
children	6q21	110713382	110736753	8528	*DDO*	0.2013	-1.8293
children	6q22.1	110745891	110797844	85413	*SLC22A16*	0.2013	-1.8293
children	6q21	110931180	111136519	23097	*CDK19*	0.2013	-1.8293
children	6q21	111195986	111216915	262	*AMD1*	0.2013	-1.8293
children	6q21	111279762	111289091	112495	*GTF3C6*	0.2013	-1.8293
children	6q21	111303219	111349466	84154	*RPF2*	0.2013	-1.8293
children	6q21	111367621	111368757	442245	*GSTM2P1*	0.2013	-1.8293
children	6q21-q22	111408780	111544606	117247	*SLC16A10*	0.2013	-1.8293
children	6q22	111580481	111590261	91749	*KIAA1919*	0.2013	-1.8293
children	6q21	111620233	111804918	5980	*REV3L*	0.2013	-1.8293
children	6q21	111804674	111824811	643749	*TRAF3IP2-AS1*	0.2013	-1.8293
children	6q21	111876580	111888563	10758	*TRAF3IP2*	0.2013	-1.8293
children	6q21	111981534	112041265	2534	*FYN*	0.2013	-1.8293
children	6q21	112375277	112390887	8838	*WISP3*	0.2013	-1.8293
children	6q21	112391859	112408751	51175	*TUBE1*	0.2013	-1.8293
children	6q21	112408673	112423993	619208	*FAM229B*	0.2013	-1.8293

children	6q21	112429133	112575917	3910	*LAMA4*	0.2013	-1.8293
children	6q21	112668531	112672498	442247	*RFPL4B*	0.2013	-1.8293
children	6q22.2	114178513	114184652	4082	*MARCKS*	0.2013	-2.0446
children	6q21	114225550	114242806	285759	*FLJ34503*	0.2013	-2.1193
children	6q21	114257319	114292359	3066	*HDAC2*	0.2013	-2.1193
children	6q21	114376749	114384041	222537	*HS3ST5*	0.2013	-2.1193
children	6q21-q22.3	116262692	116381921	2444	*FRK*	0.2013	-1.4605
children	6q22.1	116359893	116361107	728402	*TPI1P3*	0.2013	-1.4605
children	6q22.1	116421998	116566853	221294	*NT5DC1*	0.2013	-1.4605
children	6q21-q22	116440084	116447296	1300	*COL10A1*	0.2013	-1.4605
children	6q22.1	116571130	116575261	23270	*TSPYL4*	0.2013	-1.4605
children	6q22.1	116596021	116601280	7259	*TSPYL1*	0.2013	-1.4605
children	6q22	116601282	116759442	29940	*DSE*	0.2013	-1.4605
children	6q22.1	116782532	116784934	441168	*FAM26F*	0.2013	-1.4605
children	6q22.1	116817650	116866773	100128327	*TRAPPC3L*	0.2013	-1.4605
children	6q22.1	116832807	116839709	254228	*FAM26E*	0.2013	-1.4605
children	6q22.1	116850175	116880031	221301	*FAM26D*	0.2013	-1.4605
children	6q13-q22.33	116892529	116914764	51389	*RWDD1*	0.2013	-1.4605
children	6q22.1	116937641	116954148	345895	*RSPH4A*	0.2013	-1.4605
children	6q22.1	116956780	116989973	221302	*ZUFSP*	0.2013	-1.4605
children	6q22.1	117002366	117063030	3841	*KPNA5*	0.2013	-1.4605
children	6q22.1	117073359	117086886	221303	*FAM162B*	0.2013	-1.4605
children	6q22.1	117113247	117150220	222545	*GPRC6A*	0.2013	-1.4605
children	6q22.1	117198375	117253326	222546	*RFX6*	0.2013	-1.4605
children	6q22.1	117586720	117594728	245806	*VGLL2*	0.2013	-1.4605
children	6q22	117609529	117747018	6098	*ROS1*	0.2013	-1.4605
children	6q22.1	117803766	117891020	285761	*DCBLD1*	0.2013	-1.4605
children	6q21	117881432	117923705	57120	*GOPC*	0.2013	-1.4605
children	6q22.1	117996616	118031886	116150	*NUS1*	0.2013	-1.4605
children	6q22.31	118228688	118638839	222553	*SLC35F1*	0.2013	-1.4605
children	6q22	118781934	118973020	387119	*CEP85L*	0.2013	-1.4605
children	6q22.31	118822535	118824996	23629	*BRD7P3*	0.2013	-1.4605
children	6q22.1	118869441	118881587	5350	*PLN*	0.2013	-1.4605

children	6q22.31	119103870	119104581	100287632	*LOC100287632*	0.2013	-1.4605
children	6q22.31	119134611	119252903	254394	*MCM9*	0.2013	-1.4605
children	6q22.31	119215240	119230335	25842	*ASF1A*	0.2013	-1.4605
children	6q22.31	119280993	119399812	79632	*FAM184A*	0.2013	-1.4605
children	6q22.31	119390211	119390308	693128	*MIR548B*	0.2013	-1.4605
children	6q22	119498365	119670931	4121	*MAN1A1*	0.2013	-1.4605
children	6q22.31	119773711	119812467	285762	*LOC285762*	0.2013	-1.4605
children	6q22.31	121756722	121770890	2697	*GJA1*	0.2013	-1.4605
children	6q22.31	122720695	122741555	3298	*HSF2*	0.2013	-1.4605
children	6q22.31	122764492	122793026	57515	*SERINC1*	0.2013	-1.4605
children	6q22.31	122793061	123047518	5570	*PKIB*	0.2013	-1.4605
children	6q22-q23	123100645	123105218	2173	*FABP7*	0.2013	-1.4605
children	6q22.31	123110193	123130864	10924	*SMPDL3A*	0.2013	-1.4605
children	6q22.31	123317115	123394064	134829	*CLVS2*	0.2013	-1.4605
children	6q22.31	123537483	123958238	10345	*TRDN*	0.2013	-1.4605
children	6q21	124124990	125146786	154215	*NKAIN2*	0.2013	-1.2611
children	6pter-q22.33	84569369	84670146	51167	*CYB5R4*	0.2021	-1.1817
children	6q14.2	84743419	84800605	112609	*MRAP2*	0.2021	-1.1817
children	6q14-q15	85442215	85473954	9096	*TBX18*	0.2021	-1.1817
children	6q14-q15	87647023	87726397	3354	*HTR1E*	0.2021	-1.2664
children	6q12-q21	87795215	87804865	1081	*CGA*	0.2021	-1.2664
children	6q14.3	87865268	87973406	23036	*ZNF292*	0.2021	-1.2664
children	6q15	87992696	88038996	375519	*GJB7*	0.2021	-1.2664
children	6q15	88032305	88052046	57150	*SMIM8*	0.2021	-1.2664
children	6q15	88054570	88075181	206412	*C6orf163*	0.2021	-1.2664
children	6q15	88117689	88174191	154313	*C6orf165*	0.2021	-1.2664
children	6q15	88182642	88222057	10559	*SLC35A1*	0.2021	-1.2664
children	6q16.1	88224095	88299735	57038	*RARS2*	0.2021	-1.2664
children	6q14.3-q16.1	88299784	88377172	23595	*ORC3*	0.2021	-1.2664
children	6q15	88384577	88411985	55122	*AKIRIN2*	0.2021	-1.2664
children	6q15	88757506	88776550	81833	*SPACA1*	0.2021	-1.2664
children	6q14-q15	88849584	88855056	1268	*CNR1*	0.2021	-1.2396
children	6q16	89319615	89673348	8732	*RNGTT*	0.2021	-1.2396

children	6q15	89790428	89794879	10957	*PNRC1*	0.2021	-1.2396
children	6q15	89805677	89827800	135295	*SRSF12*	0.2021	-1.2396
children	6q15	89855768	89875288	135293	*PM20D2*	0.2021	-1.2396
children	6q15	89887222	89927496	2569	*GABRR1*	0.2021	-1.2404
children	6q15	89966839	90025018	2570	*GABRR2*	0.2021	-1.2412
children	6q15	90036343	90062619	51465	*UBE2J1*	0.2021	-1.2412
children	6q15	90074334	90121995	58528	*RRAGD*	0.2021	-1.2412
children	6q15	90142896	90343553	22881	*ANKRD6*	0.2021	-1.2412
children	6q15	90341942	90348216	57226	*LYRM2*	0.2021	-1.2412
children	6q15	90352493	90529513	23195	*MDN1*	0.2021	-1.2412
children	6q15	90539618	90584155	9994	*CASP8AP2*	0.2021	-1.2412
children	6q15	90604187	90605819	84694	*GJA10*	0.2021	-1.3196
children	6q15	90636246	91006627	60468	*BACH2*	0.2021	-1.3196
children	6q15	91223291	91297020	6885	*MAP3K7*	0.4361	-1.3196
children	6q16.1	93949739	94129300	2045	*EPHA7*	0.4361	-1.3196
children	6q16.1	94416800	94486199	643432	*TSG1*	0.4361	-1.3196
children	6q16.1	96025372	96057328	79694	*MANEA*	0.8796	-1.8492
children	6q16	96463844	96663488	10690	*FUT9*	0.4361	-1.7834
children	6q16.1	96969701	97003151	23376	*UFL1*	0.4361	-2.1374
children	6q16.1-q16.3	97010423	97064512	9457	*FHL5*	0.4361	-2.1374
children	6q16.1-q16.3	97241997	97285353	81491	*GPR63*	0.4361	-2.1374
children	6q16.1	97337186	97345767	29078	*NDUFAF4*	0.4361	-2.1374
children	6q16.1	97372495	97588630	114792	*KLHL32*	0.4361	-2.1374
children	6q16.1	97590036	97731052	253714	*MMS22L*	0.4361	-2.1374
children	6q16	99282579	99286666	5454	*POU3F2*	0.4361	-2.1374
children	6q16.1-q16.3	99321600	99395882	26235	*FBXL4*	0.4361	-2.1374
children	6q16.2	99720792	99797531	84553	*FAXC*	0.4361	-2.1374
children	6q16.2	99817347	99842082	51805	*COQ3*	0.4361	-2.1374
children	6q16.3	99847840	99873207	25957	*PNISR*	0.4361	-1.8389
children	6q16.2	99880183	99963252	85015	*USP45*	0.4361	-1.8389
children	6q16.2	99968869	99981059	100130890	*TSTD3*	0.4361	-1.8389
children	6q21	99990262	100016690	892	*CCNC*	0.4361	-1.8389
children	7p21.3	10971579	10979813	4697	*NDUFA4*	0	-2.1625

children	7p21.3	11013498	11147376	9678	*PHF14*	0	-2.1625
children	7p21.3	11410061	11871824	221981	*THSD7A*	0	-2.1625
children	7p21.3	12250847	12276890	54664	*TMEM106B*	0	-2.1625
children	7p21.3	12370508	12443852	221806	*VWDE*	0	-2.1625
children	7p21.3	12610202	12693228	85477	*SCIN*	0	-2.1625
children	7p21.3	12726451	12730558	10124	*ARL4A*	0	-2.1625
children	7p21.3	13930855	14026139	2115	*ETV1*	0	-2.1006
children	7p21.2	14184673	14881075	1607	*DGKB*	0	-2.1049
children	7p21.2	15239942	15601640	392636	*AGMO*	0	-2.1049
children	7p22.1-p21.3	15650836	15726308	4223	*MEOX2*	0	-2.1049
children	7p22.3	1570367	1582679	7975	*MAFK*	0	-1.1621
children	7p22.3	1581870	1596066	202915	*TMEM184A*	0	-1.1621
children	7p22.3	1606969	1609629	84262	*PSMG3*	0	-1.1621
children	7p22.3	1609708	1629261	114796	*PSMG3-AS1*	0	-1.1621
children	7p21.2	16127151	16460947	729920	*ISPD*	0	-2.1228
children	7p21.1	16501105	16505474	25928	*SOSTDC1*	0	-2.1407
children	7p22.3	1654105	1656328	260341	*TFAMP1*	0	-1.1621
children	7p21.1	16566504	16621114	100506049	*LRRC72*	0	-2.1407
children	7p21	16639400	16685442	57037	*ANKMY2*	0	-2.1407
children	7p21.1	16685758	16746148	28969	*BZW2*	0	-2.1407
children	7p21.1	16793350	16824161	27075	*TSPAN13*	0	-2.1407
children	7p21.3	16832263	16844738	10551	*AGR2*	0	-2.1407
children	7p21.1	16899029	16921613	155465	*AGR3*	0	-2.1407
children	7p15	17338275	17385775	196	*AHR*	0	-2.1407
children	7p22.3	1748797	1787590	392617	*ELFN1*	0	-1.1621
children	7p21.1	17830384	17980131	23161	*SNX13*	0	-2.1407
children	7p21.1	18066399	18067486	221823	*PRPS1L1*	0	-2.1407
children	7p21.1	18126571	18708466	9734	*HDAC9*	0	-2.1407
children	7p22	1855427	2272583	8379	*MAD1L1*	0	-1.1621
children	7p21.2	19155090	19157295	7291	*TWIST1*	0	-2.1407
children	7p21.1	19184404	19185044	222894	*FERD3L*	0	-2.1407
children	7p21.1	19735084	19748660	221830	*TWISTNB*	0	-2.1407
children	7p21.1	19758937	19812404	256130	*TMEM196*	0	-2.1407

children	7p21.1	20174278	20257013	346389	*MACC1*	0	-2.1407
children	7p21.1	20370724	20455382	3696	*ITGB8*	0	-2.1407
children	7p21.1	20655244	20796637	340273	*ABCB5*	0	-1.9968
children	7p21.2	20821893	20826508	221833	*SP8*	0	-1.8529
children	7p21.1	20866916	20867439	222901	*RPL23P8*	0	-1.8529
children	7p15.3	21467688	21554151	6671	*SP4*	0	-1.8529
children	7p21	21582832	21941186	8701	*DNAH11*	0	-1.8529
children	7p15.3	21940516	21985542	55536	*CDCA7L*	0	-1.8529
children	7p15.3	22157907	22396533	9771	*RAPGEF5*	0	-1.8529
children	7p15.3	22459062	22539901	256227	*STEAP1B*	0	-1.7384
children	7p22	2273925	2281833	29960	*FTSJ2*	0	-1.1621
children	7p21	22766765	22771621	3569	*IL6*	0	-1.7384
children	7p22	2281856	2290780	4521	*NUDT1*	0	-1.1621
children	7p15.3	22852250	22862471	54543	*TOMM7*	0	-1.7384
children	7p15.3	22896231	22896305	692210	*SNORD93*	0	-1.7384
children	7p22.3	2291404	2354110	29886	*SNX8*	0	-1.1621
children	7p15.3	22980877	23053770	84668	*FAM126A*	0	-1.7384
children	7p15.3	23140846	23145322	100775104	*KLHL7-AS1*	0	-1.7384
children	7p15.3	23145352	23165669	55975	*KLHL7*	0	-1.7384
children	7p15	23221445	23240630	11097	*NUPL2*	0	-1.7384
children	7p15	23286315	23314729	10457	*GPNMB*	0	-1.7384
children	7p15.3	23338939	23349180	115416	*MALSU1*	0	-1.7384
children	7p11	23349827	23509995	10643	*IGF2BP3*	0	-1.7384
children	7p15.3	23530006	23531031	256355	*RPS2P32*	0	-1.7384
children	7p15.3	23544400	23571660	29896	*TRA2A*	0	-1.7384
children	7p15.3	23636997	23684327	90693	*CCDC126*	0	-1.7384
children	7p15.3	23719732	23742269	340277	*FAM221A*	0	-1.7384
children	7p15.3	23749785	23872130	56164	*STK31*	0	-1.7384
children	7p22.3	2394473	2420377	8662	*EIF3B*	0	-1.1621
children	7p15.1	24323806	24331484	4852	*NPY*	0	-1.2061
children	7p22	2443194	2474216	55501	*CHST12*	0	-1.1621
children	7p15	24612964	24733322	51678	*MPP6*	0	-1.2061
children	7p15	24737973	24797083	1687	*DFNA5*	0	-1.2061

children	7p15	24836155	24932240	26031	*OSBPL3*	0	-1.2061
children	7p15.3	25158269	25164980	54205	*CYCS*	0	-1.2061
children	7p15.3	25174315	25219817	136895	*C7orf31*	0	-1.2061
children	7p15.3	25264190	25268105	64111	*NPVF*	0	-1.2061
children	7p22.2	2552162	2568063	3955	*LFNG*	0	-1.1621
children	7p22.3	2577443	2595392	221927	*BRAT1*	0	-1.1621
children	7p22.3	2598605	2654368	23288	*IQCE*	0	-1.1621
children	7p15.2	25989538	25989606	406940	*MIR148A*	0	-1.2061
children	7p15.2	26191846	26226756	9603	*NFE2L3*	0	-1.1706
children	7p15	26229555	26240413	3181	*HNRNPA2B1*	0	-1.1706
children	7p15.2	26240830	26253227	11335	*CBX3*	0	-1.1706
children	7p15.2	26331514	26413949	29887	*SNX10*	0	-1.1706
children	7p15.2	26443107	26535986	441204	*LOC441204*	0	-1.1706
children	7p15.2	26572739	26578444	9808	*KIAA0087*	0	-1.1706
children	7p15.2	26677489	26686889	285941	*C7orf71*	0	-1.1706
children	7p15.2	26706680	26904362	8935	*SKAP2*	0	-1.1706
children	7p22	2671602	2704436	80727	*TTYH3*	0	-1.1621
children	7p15.3	27132613	27135625	3198	*HOXA1*	0	-1.1706
children	7p15.2	27135712	27139877	100506311	*HOTAIRM1*	0	-1.1706
children	7p15.2	27139972	27142394	3199	*HOXA2*	0	-1.1706
children	7p15.2	27145808	27159214	3200	*HOXA3*	0	-1.1706
children	7p15.2	27168125	27170399	3201	*HOXA4*	0	-1.1706
children	7p15.2	27179982	27195547	100133311	*HOXA-AS3*	0	-1.1706
children	7p15.2	27180670	27183287	3202	*HOXA5*	0	-1.1706
children	7p15.2	27185201	27187393	3203	*HOXA6*	0	-1.1706
children	7p22.3	2719155	2755070	155185	*AMZ1*	0	-1.1621
children	7p15.2	27193337	27196296	3204	*HOXA7*	0	-1.1706
children	7p15.2	27202056	27205149	3205	*HOXA9*	0	-1.1706
children	7p15.2	27202056	27219880	100534589	*HOXA10-HOXA9*	0	-1.1706
children	7p15.2	27209098	27209182	442920	*MIR196B*	0	-1.1706
children	7p15.2	27210209	27213955	3206	*HOXA10*	0	-1.1706
children	7p15.2	27220775	27224835	3207	*HOXA11*	0	-1.1706
children	7p15.2	27225026	27228912	221883	*HOXA11-AS*	0	-1.1706

children	7p15.2	27236498	27239725	3209	*HOXA13*	0	-1.1706
children	7p15.2	27240039	27246878	100316868	*HOTTIP*	0	-1.1706
children	7p15.2	27282163	27287438	2128	*EVX1*	0	-1.1706
children	7p15.2	27565058	27702620	11112	*HIBADH*	0	-1.1706
children	7p22.2	2767740	2883959	2768	*GNA12*	0	-1.1621
children	7p15	27778991	27869386	8887	*TAX1BP1*	0	-1.1706
children	7p15.2-p15.1	27870192	28220437	221895	*JAZF1*	0	-1.1706
children	7p15.1	28220075	28280996	100128081	*JAZF1-AS1*	0	-1.1706
children	7p15.1	28338939	28865511	9586	*CREB5*	0	-1.1706
children	7p14.3	28992973	28998029	9865	*TRIL*	0	-1.1706
children	7p15.1	29035246	29186153	54504	*CPVL*	0	-1.1706
children	7p15.3	29234120	29553951	1124	*CHN2*	0	-1.1706
children	7p22	2945709	3083579	84433	*CARD11*	0	-1.1621
children	7p14.3	29603426	29606911	222171	*PRR15*	0	-1.1706
children	7p14.3	29685537	29724754	646762	*LOC646762*	0	-1.1706
children	7p15.1	29724769	29727859	442524	*DPY19L2P3*	0	-1.1706
children	7p14.3	29846169	29956682	644150	*WIPF3*	0	-1.1735
children	7p14.3	29959718	30029425	9805	*SCRN1*	0	-1.1763
children	7p14.3	30050198	30066417	55033	*FKBP14*	0	-1.1763
children	7p14.3	30067976	30124278	84725	*PLEKHA8*	0	-1.1763
children	7p14.3	30323922	30407308	223082	*ZNRF2*	0	-1.1763
children	7p14.3	30329409	30329506	693133	*MIR550A1*	0	-1.1763
children	7p14.3	30409665	30412410	222161	*DKFZP586I1420*	0	-1.1763
children	7p14.3	30464142	30518393	10392	*NOD1*	0	-1.1763
children	7p15-p14	30536236	30544457	79017	*GGCT*	0	-1.1763
children	7p15.1	30587972	30617395	401320	*LOC401320*	0	-1.1763
children	7p15	30634508	30673648	2617	*GARS*	0	-1.1763
children	7p14.3	30691558	30722141	1395	*CRHR2*	0	-1.1763
children	7p14.3	30791750	30797218	11185	*INMT*	0	-1.1763
children	7p14	30951414	30965131	358	*AQP1*	0	-1.1763
children	7p14	31003635	31019146	2692	*GHRHR*	0	-1.1763
children	7p14	31092075	31151093	117	*ADCYAP1R1*	0	-1.1763
children	7p14.3	31377074	31380538	63974	*NEUROD6*	0	-1.1754

children	7p14.3	31553684	31693303	223075	*CCDC129*	0	-1.1844
children	7p15	31726630	31748069	10842	*PPP1R17*	0	-1.1933
children	7p14.3	31790792	32110474	5137	*PDE1C*	0	-1.1933
children	7p14.3	32496509	32498106	100130673	*LOC100130673*	0	-1.1587
children	7p14.3	32524944	32530023	23658	*LSM5*	0	-1.1587
children	7p14.3	32535037	32628353	23080	*AVL9*	0	-1.1587
children	7p14	33169151	33645680	27241	*BBS9*	0	-1.1525
children	7p22.2	3341079	4308631	221935	*SDK1*	0	-1.4151
children	7p14.3	33944522	34195484	168667	*BMPER*	0	-1.1299
children	7p14.3	34386123	34797884	404744	*NPSR1-AS1*	0	-1.1299
children	7p14.3	34697896	34889590	387129	*NPSR1*	0	-1.1299
children	7p14.3-p14.2	34968492	35077653	23333	*DPY19L1*	0	-1.1299
children	7p14.2	35120898	35225774	554236	*DPY19L2P1*	0	-1.1956
children	7p14.3	35242041	35293711	57057	*TBX20*	0	-1.1956
children	7p14.2	35353465	35416086	401324	*LOC401324*	0	-1.1956
children	7p14.2	35672269	35734772	64224	*HERPUD2*	0	-1.1956
children	7p14.2	35840595	35946715	989	*7-Sep*	0	-1.1956
children	7p14.2	36192835	36341152	80820	*EEPD1*	0	-1.4341
children	7p14.2	36363758	36406782	23366	*KIAA0895*	0	-1.6101
children	7p15-p14	36429411	36493401	54443	*ANLN*	0	-1.6101
children	7p14.2	36552548	36764154	313	*AOAH*	0	-1.6101
children	7p14.1	36892510	37024717	9844	*ELMO1*	0	-1.6101
children	7p14.2	36958961	36959037	100302113	*MIR1200*	0	-1.6101
children	7p14.1	37779995	37780913	353345	*GPR141*	0	-1.6101
children	7p14.1	37888198	37940002	51314	*NME8*	0	-1.6101
children	7p14.1	37945534	37956525	6424	*SFRP4*	0	-1.6101
children	7p14.1	37960162	37991542	54749	*EPDR1*	0	-1.6101
children	7p14-p13	38217807	38270272	83930	*STARD3NL*	0	-1.6101
children	7p14-p13	38423296	38671167	273	*AMPH*	0	-1.1873
children	7p14.1	38724945	38726689	340286	*FAM183B*	0	-1.1873
children	7p14-p13	38763542	38948800	27072	*VPS41*	0	-1.1873
children	7p14.1	39017608	39504390	11281	*POU6F2*	0	-1.1873
children	7p14.1	39444197	39445945	100861520	*POU6F2-AS1*	0	-1.1873

children	7p14.1	39605974	39612480	57002	*YAE1D1*	0	-1.1873
children	7p15-p13	39663151	39747723	5898	*RALA*	0	-1.1873
children	7p14.1	39773166	39834222	349114	*LINC00265*	0	-1.1873
children	7p13	39989958	40136733	8621	*CDK13*	0	-1.1743
children	7p15-p13	41728600	41742706	3624	*INHBA*	0	-1.1748
children	7p14.1	41733513	41818976	285954	*INHBA-AS1*	0	-1.1748
children	7p13	42000547	42276618	2737	*GLI3*	0	-1.1748
children	7p14.1	42948871	42951689	79020	*C7orf25*	0	-1.1825
children	7p13	42956461	42971805	5683	*PSMA2*	0	-1.1825
children	7p14	42971938	42977453	64983	*MRPL32*	0	-1.1825
children	7p13	43152197	43602938	23072	*HECW1*	0	-1.5045
children	7p13	43622691	43666978	9263	*STK17A*	0	-1.5045
children	7p13	43670750	43769140	55744	*COA1*	0	-1.5045
children	7p13	43798271	43846941	644	*BLVRA*	0	-1.5045
children	7p14	43906156	43909145	64951	*MRPS24*	0	-1.5045
children	7p13	43906156	43946231	100534592	*URGCP-MRPS24*	0	-1.5045
children	7p13	43915492	43946668	55665	*URGCP*	0	-1.5045
children	7p13	43966034	43995735	51619	*UBE2D4*	0	-1.5045
children	7p13	43980493	44058793	84820	*POLR2J4*	0	-1.5045
children	7p13	44084238	44101315	28988	*DBNL*	0	-1.1245
children	7p13-p12	44102325	44105186	5224	*PGAM2*	0	-1.1245
children	7p13	44111660	44122139	27434	*POLM*	0	-1.421
children	7p13	44143959	44154164	165	*AEBP1*	0	-1.421
children	7p13	44154278	44163107	5425	*POLD2*	0	-1.421
children	7p21-p11.2	44178462	44180916	58498	*MYL7*	0	-1.421
children	7p15.3-p15.1	44183869	44198887	2645	*GCK*	0	-1.421
children	7p15.1	44240577	44253893	10652	*YKT6*	0	-1.421
children	7p14.3-p14.1	44256748	44365230	816	*CAMK2B*	0	-1.4186
children	7p13-p12	44421964	44530385	23386	*NUDCD3*	0	-1.6166
children	7p13	44552134	44580914	29881	*NPC1L1*	0	-1.6166
children	7p13	44605015	44614137	54606	*DDX56*	0	-1.6166
children	7p13	44617493	44621894	222068	*TMED4*	0	-1.6166
children	7p14-p13	44646120	44716195	4967	*OGDH*	0	-1.6166

children	7p13	44788529	44809479	83637	*ZMIZ2*	0	-1.6166
children	7p13	44836234	44842722	5478	*PPIA*	0	-1.6166
children	7p13	44866487	44887725	94239	*H2AFV*	0	-1.6166
children	7p13	44915891	44924984	5814	*PURB*	0	-1.6166
children	7p13	45002259	45018704	64005	*MYO1G*	0	-1.4162
children	7p13	45022626	45026259	285958	*SNHG15*	0	-1.4162
children	7p13	45024976	45025109	677798	*SNORA9*	0	-1.4162
children	7p13	45039344	45116069	83605	*CCM2*	0	-1.4162
children	7p13	45120035	45128493	23148	*NACAD*	0	-1.4162
children	7p13	45139698	45151346	9238	*TBRG4*	0	-1.4162
children	7p13	45144504	45144641	677796	*SNORA5C*	0	-1.4162
children	7p13	45145566	45145698	677795	*SNORA5B*	0	-1.4162
children	7p13-p12	45197366	45223850	10268	*RAMP3*	0	-1.4162
children	7p12.3	45614124	45762714	107	*ADCY1*	0	-1.4162
children	7p12.3	45763385	45808617	641977	*SEPT7P2*	0	-1.4162
children	7p12.3	45927958	45933267	3484	*IGFBP1*	0	-1.4215
children	7p12.3	45951843	45960871	3486	*IGFBP3*	0	-1.4215
children	7p22.1	4721929	4811074	221937	*FOXK1*	0	-1.628
children	7p12.3	47314751	47621742	64759	*TNS3*	0	-1.4215
children	7p12.3	47694841	47701246	401335	*C7orf65*	0	-1.4215
children	7p12.3	47801073	47806370	84847	*LINC00525*	0	-1.7441
children	7p12.3	47814249	47988071	168507	*PKD1L1*	0	-1.7441
children	7p12.3	47834888	47859444	80099	*C7orf69*	0	-1.7441
children	7p13-p12	48002884	48019222	3364	*HUS1*	0	-1.7441
children	7p12.3	48026745	48068716	256979	*SUN3*	0	-1.7441
children	7p12.3	48075107	48100894	136288	*C7orf57*	0	-1.7441
children	7p12.3	48128808	48148330	7378	*UPP1*	0	-1.7441
children	7p22.2	4815261	4834026	9907	*AP5Z1*	0	-1.628
children	7p12.3	48211056	48687091	154664	*ABCA13*	0	-1.7441
children	7p22.1	4838739	4923335	55698	*RADIL*	0	-1.628
children	7p12.3	48964156	48967049	168448	*CDC14C*	0	-1.7441
children	7p22.1	4897368	4901625	56903	*PAPOLB*	0	-1.628
children	7p22.1	4931875	4998844	221938	*MMD2*	0	-1.628

children	7p12.2	49813256	49952138	375567	*VWC2*	0	-1.7441
children	7p14.3	49977023	50132860	11055	*ZPBP*	0	-1.7674
children	7p12.2	50135681	50198852	100130988	*C7orf72*	0	-1.7906
children	7p22.1	5013615	5037800	441191	*RNF216P1*	0	-1.628
children	7p12.2	50344264	50472798	10320	*IKZF1*	0	-1.7906
children	7p12.1	50511826	50518088	63979	*FIGNL1*	0	-1.7906
children	7p12.2	50526133	50628768	1644	*DDC*	0	-1.7906
children	7p12.2	50657759	50772998	2887	*GRB10*	0	-1.7906
children	7p22.1	5085451	5109119	57786	*RBAK*	0	-1.628
children	7p12.1	51083908	51384515	23242	*COBL*	0	-1.7906
children	7p22.1	5111690	5112854	389458	*RBAKDN*	0	-1.628
children	7p22.1	5160940	5184177	645700	*ZNF890P*	0	-1.628
children	7p22.1	5229834	5273486	26100	*WIPI2*	0	-1.628
children	7p12.1	53103348	53104618	285877	*POM121L12*	0	-1.8371
children	7p22.1	5322560	5343704	222962	*SLC29A4*	0	-1.628
children	7p22.1	5346422	5463177	84629	*TNRC18*	0	-1.628
children	7p11.2	54268916	54270114	3262	*HPVC1*	0	-1.8371
children	7p11.2	54610017	54638773	222008	*VSTM2A*	0	-1.2277
children	7p11.2	54819939	54826939	23480	*SEC61G*	0	-1.2277
children	7p12	55086724	55224644	1956	*EGFR*	0	-1.2277
children	7p22.2	5515427	5553399	80028	*FBXL18*	0	-1.628
children	7p22.1	5535449	5535548	693174	*MIR589*	0	-1.628
children	7q31.1-q31.33	55433140	55501435	55915	*LANCL2*	0	-1.1538
children	7p11.2	55538305	55640200	81552	*VOPP1*	0	-1.1538
children	7p22	5566778	5570232	60	*ACTB*	0	-1.628
children	7p11.2	55861236	55930482	346288	*14-Sep*	0	-1.1538
children	7p11.2	55954969	56009918	349075	*ZNF713*	0	-1.1538
children	7p11	56019610	56023033	51373	*MRPS17*	0	-1.1538
children	7p12	56032269	56067875	2631	*GBAS*	0	-1.1538
children	7p11.2	56078743	56119268	5723	*PSPH*	0	-1.1538
children	7p11.2	56119377	56131682	908	*CCT6A*	0	-1.1538
children	7p11.2	56128162	56128295	677803	*SNORA15*	0	-1.1538
children	7q11.1	56131916	56148365	25870	*SUMF2*	0	-1.1538

children	7p11.2	56147975	56160689	5260	*PHKG1*	0	-1.1538
children	7p11.2	56169265	56174187	51142	*CHCHD2*	0	-1.1538
children	7p11.2	56182373	56184090	389493	*NUPR1L*	0	-1.1538
children	7p22	5632435	5646287	6624	*FSCN1*	0	-1.628
children	7p11.2	56491396	56516068	650226	*LOC650226*	0	-1.1538
children	7p11.2	56563915	56564977	222029	*DKFZp434L192*	0	-1.1538
children	7p22.1	5659671	5821361	54476	*RNF216*	0	-1.628
children	7p22.1	5862790	5894066	401303	*ZNF815P*	0	-1.628
children	7p22.1	5920428	5925994	654231	*OCM*	0	-1.628
children	7p22.1	5938340	5965603	51622	*CCZ1*	0	-1.628
children	7p22.1	5965776	6010314	728194	*RSPH10B2*	0	-1.628
children	7p22.2	6012869	6048737	5395	*PMS2*	0	-1.628
children	7p22	6048881	6063465	7965	*AIMP2*	0	-1.628
children	7p22	6061877	6098860	27102	*EIF2AK1*	0	-1.628
children	7p22	6071006	6076183	100310846	*ANKRD61*	0	-1.628
children	7p22.1	6144549	6201195	84132	*USP42*	0	-1.628
children	7p22.1	6201411	6312242	9265	*CYTH3*	0	-1.628
children	7p22.1	6369039	6388590	84792	*FAM220A*	0	-1.628
children	7p22	6414125	6443598	5879	*RAC1*	0	-1.628
children	7p22.1	6448746	6487643	221955	*DAGLB*	0	-1.628
children	7p22.1	6500711	6523849	11014	*KDELR2*	0	-1.628
children	7p22.1	6536408	6591067	392862	*GRID2IP*	0	-1.628
children	7p22.1	6617064	6628610	55146	*ZDHHC4*	0	-1.628
children	7p22.1	6629651	6648357	79034	*C7orf26*	0	-1.628
children	7p22.1	6655526	6663921	54753	*ZNF853*	0	-1.628
children	7p22.1	6728063	6746566	7559	*ZNF12*	0	-1.6493
children	7p22.1	6774935	6791232	441194	*PMS2CL*	0	-1.6493
children	7p22.1	6838565	6865926	221960	*CCZ1B*	0	-1.6493
children	7p22.1	7115400	7136417	100131257	*LOC100131257*	0	-1.6493
children	7p21.3	7222245	7288280	56913	*C1GALT1*	0	-1.6493
children	7p21.3	7398243	7575460	340267	*COL28A1*	0	-1.6493
children	7p21.3	7606615	7647110	54468	*MIOS*	0	-1.6493
children	7p22	7676193	7758238	6119	*RPA3*	0	-1.6493

children	7q21	79764139	79848725	2770	*GNAI1*	0.306	-1.517
children	7p21.3	8008373	8128709	113263	*GLCCI1*	0	-1.6493
children	7q21.11	80087950	80141325	346562	*GNAT3*	0.306	-1.517
children	7q11.2	80231503	80303734	948	*CD36*	0.306	-1.517
children	7q21-q31	80371853	80548667	10512	*SEMA3C*	0.306	-1.517
children	7q21.1	81331443	81399452	3082	*HGF*	0.306	-1.517
children	7p22	8152814	8301682	3382	*ICA1*	0	-1.6493
children	7q21-q22	81575759	82073122	781	*CACNA2D1*	0.306	-1.4022
children	7q21.11	82383320	82792197	27445	*PCLO*	0.306	-1.4022
children	7q21.11	82993221	83270747	9723	*SEMA3E*	0.306	-1.4022
children	7p12.1	83587658	83824217	10371	*SEMA3A*	0.306	-1.4022
children	7q21.11	84624871	84751247	223117	*SEMA3D*	0.306	-1.4022
children	7p22	8473584	8792593	30010	*NXPH1*	0	-1.6493
children	7q21.1-q21.2	86273229	86494192	2913	*GRM3*	0.306	-1.3957
children	7q21.12	86506222	86595291	222223	*KIAA1324L*	0.306	-1.3957
children	7q21	86781676	86825648	9988	*DMTF1*	0.306	-1.3957
children	7q21.12	86825477	86849031	79161	*TMEM243*	0.306	-1.3957
children	7q21.1	86954663	86974808	11257	*TP53TG1*	0.306	-1.3957
children	7q21.1	86974950	86989425	54677	*CROT*	0.306	-1.3957
children	7q21.1	87031360	87105019	5244	*ABCB4*	0.306	-1.3957
children	7q21.12	87133178	87342639	5243	*ABCB1*	0.306	-1.3957
children	7q21.12	87257728	87461613	154661	*RUNDC3B*	0.306	-1.3957
children	7q21.12	87463813	87505692	55972	*SLC25A40*	0.306	-1.3957
children	7q21.3	87505543	87538856	10926	*DBF4*	0.306	-1.3957
children	7q21	87563565	87811428	53616	*ADAM22*	0.306	-1.3957
children	7q21.1	87834431	87849399	6717	*SRI*	0.306	-1.3957
children	7q21.12	87905743	87936228	79689	*STEAP4*	0.306	-1.3957
children	7q21.13	88388681	88966371	219578	*ZNF804B*	0.306	-1.3957
children	7q21.13	88423419	88425031	219557	*C7orf62*	0.306	-1.3957
children	7q21.13	89748713	89754914	442523	*DPY19L2P4*	0.306	-1.3957
children	7q21	89783688	89794141	26872	*STEAP1*	0.306	-1.3957
children	7q21.13	89840999	89866992	261729	*STEAP2*	0.306	-1.3776
children	7q21.13	89975978	90020769	85865	*GTPBP10*	0.306	-1.3776

children	7q21	90025605	90027550	101409256	*LOC101409256*	0.306	-1.3776
children	7q21	90032647	90045268	9069	*CLDN12*	0.306	-1.3776
children	7q21-q22	90338711	90839905	5218	*CDK14*	0.306	-1.3776
children	7q21	90893782	90898132	8321	*FZD1*	0.306	-1.3776
children	7p21.3	9673899	9675447	168741	*PER4*	0	-2.0044
children	9p24.3	1050345	1057554	10655	*DMRT2*	0	-3.6888
children	9p24.3	116230	118417	2298	*FOXD4*	0	-2.2468
children	9p24.3	11986	14525	100287596	*DDX11L5*	0	-1.6447
children	9p24.3	121037	179075	55871	*CBWD1*	0	-2.5826
children	9p23	12693385	12710266	7306	*TYRP1*	0	-4.2889
children	9p23	12775011	12823059	286343	*LURAP1L*	0	-4.2889
children	9p23	13105702	13279563	8777	*MPDZ*	0	-4.2889
children	9p23	13927969	13945606	100113404	*LINC00583*	0	-4.2113
children	9p24.1	14081841	14314045	4781	*NFIB*	0	-4.2113
children	9p24.3	14510	29739	100287171	*WASH1*	0	-1.6447
children	9p22.3	14611068	14693480	340481	*ZDHHC21*	0	-4.1734
children	9p23-p22	14719731	14722715	9350	*CER1*	0	-4.1354
children	9p22.3	14734663	14779531	158326	*FREM1*	0	-4.1354
children	9p22.3	14993324	15019722	389705	*LOC389705*	0	-4.1354
children	9p22.3	15170841	15250198	158219	*TTC39B*	0	-3.9407
children	9p22.3	15422781	15461627	6619	*SNAPC3*	0	-4.3397
children	9p22.3	15464064	15511017	11168	*PSIP1*	0	-4.3397
children	9p22.3	15553096	15971897	203238	*CCDC171*	0	-4.3238
children	9p22.3	16203932	16253105	100129385	*C9orf92*	0	-4.3078
children	9p22.2	16409500	16870786	54796	*BNC2*	0	-4.3078
children	9p22.2	17134988	17302049	54875	*CNTLN*	0	-4.3245
children	9p22	17578951	17797126	6456	*SH3GL2*	0	-4.3187
children	9p21.3	18474078	18684952	92949	*ADAMTSL1*	0	-4.8848
children	9p22.1	19049371	19051021	10670	*RRAGA*	0	-4.8848
children	9p22.1	19053134	19102940	54801	*HAUS6*	0	-4.8848
children	9p22.1	19063653	19063784	677776	*SCARNA8*	0	-4.8848
children	9p22.1	19115758	19127604	123	*PLIN2*	0	-4.8848
children	9p22.1	19230762	19374266	55667	*DENND4C*	0	-5.1662

children	9p21	19376253	19380235	6194	*RPS6*	0	-5.3818
children	9p22.1	19408924	19452500	340485	*ACER2*	0	-5.3818
children	9p22.1	19507449	19787017	25769	*SLC24A2*	0	-6.6051
children	9p22.3	2015218	2193623	6595	*SMARCA2*	0	-3.742
children	9p22	20341662	20622542	4300	*MLLT3*	0	-8.4101
children	9p21	20658307	20995954	54914	*FOCAD*	0	-9.4703
children	9p21.3	20716103	20716187	574444	*MIR491*	0	-9.8099
children	9p21	21077103	21077962	3456	*IFNB1*	0	-9.8099
children	9p22	21140630	21141900	3467	*IFNW1*	0	-9.8099
children	9p22	21165635	21166659	3452	*IFNA21*	0	-11.656
children	9p22	21186617	21187598	3441	*IFNA4*	0	-11.656
children	9p22	21201467	21202204	3444	*IFNA7*	0	-11.225
children	9p22	21206179	21207142	3446	*IFNA10*	0	-11.225
children	9p22	21216371	21217310	3449	*IFNA16*	0	-11.225
children	9p22	21227241	21228221	3451	*IFNA17*	0	-11.225
children	9p22	21239200	21239978	3448	*IFNA14*	0	-11.225
children	9p22	21277686	21278562	3453	*IFNA22P*	0	-13.605
children	9p22	21304612	21305312	3442	*IFNA5*	0	-13.605
children	9p24.3	213107	215893	157983	*C9orf66*	0	-3.6251
children	9p22	21331017	21335429	55958	*KLHL9*	0	-13.605
children	9p22	21350316	21350886	3443	*IFNA6*	0	-13.605
children	9p22	21367370	21368075	3447	*IFNA13*	0	-13.605
children	9p22	21384253	21385396	3440	*IFNA2*	0	-13.605
children	9p22	21409145	21410184	3445	*IFNA8*	0	-13.605
children	9p22	21440452	21441315	3439	*IFNA1*	0	-13.605
children	9p21.3	21454266	21559697	554202	*MIR31HG*	0	-13.66
children	9p21.3	21480838	21482312	338376	*IFNE*	0	-13.605
children	9p24.3	214864	465259	81704	*DOCK8*	0	-3.657
children	9p21.3	21512113	21512184	407035	*MIR31*	0	-13.605
children	9p21	21802634	21865969	4507	*MTAP*	0	-15.661
children	9p21	21967750	21974826	1029	*CDKN2A*	0	-14.404
children	9p21.3	21994789	22077889	100048912	*CDKN2B-AS1*	0	-16.681
children	9p21	22002901	22009312	1030	*CDKN2B*	0	-14.337

children	9p21.3	22446839	22452472	63951	*DMRTA1*	0	-15.06
children	9p21	23690102	23821478	1993	*ELAVL2*	0	-9.2432
children	9p21.3	24543212	24545674	100129669	*IZUMO3*	0	-8.6789
children	9p21.2	25676386	25678856	286319	*TUSC1*	0	-5.9124
children	9p21.2	26066672	26118406	100506422	*LOC100506422*	0	-5.9124
children	9p24	2621792	2654485	7436	*VLDLR*	0	-3.742
children	9p21.2	26840682	26892826	79886	*CAAP1*	0	-5.3718
children	9p21	26903367	26947468	9373	*PLAA*	0	-5.3718
children	9p21.2	26947036	27062931	80173	*IFT74*	0	-5.3718
children	9p21.2	26993134	27005691	64922	*LRRC19*	0	-5.3718
children	9p21	27109138	27230176	7010	*TEK*	0	-5.3718
children	9p24.2	2717525	2730037	169522	*KCNV2*	0	-3.742
children	9p21	27245681	27282791	158035	*LINC00032*	0	-5.3718
children	9p21	27284653	27297137	54586	*EQTN*	0	-5.3718
children	9p21.2	27325206	27529850	79817	*MOB3B*	0	-5.3718
children	9p21.2	27546543	27573491	203228	*C9orf72*	0	-5.3718
children	9p21.2	27948083	28719303	158038	*LINGO2*	0.2031	-5.3826
children	9p24.2	2804154	2844130	9933	*KIAA0020*	0	-3.7575
children	9p21.1	28863623	28863704	100126310	*MIR876*	0.2071	-5.3494
children	9p21.1	28888876	28888953	100126316	*MIR873*	0.2071	-5.3494
children	9p24.2	3218296	3526001	5991	*RFX3*	0	-3.7575
children	9p21.1	32384600	32450832	48	*ACO1*	0	-4.0201
children	9p12	32455299	32526322	23586	*DDX58*	0	-4.0201
children	9p21	32540541	32552626	10210	*TOPORS*	0	-4.0201
children	9p21.1	32551141	32553015	100129250	*TOPORS-AS1*	0	-4.0201
children	9p21.1	32553523	32573182	4712	*NDUFB6*	0	-4.0201
children	9p21.1	32629451	32635667	138474	*TAF1L*	0	-4.0201
children	9p21.1	32783496	32789199	401498	*TMEM215*	0	-4.0201
children	9p13.3	32972603	33001574	54840	*APTX*	0	-4.0201
children	9p13.3	33025200	33039906	3301	*DNAJA1*	0	-4.0201
children	9p12	33041849	33076714	55234	*SMU1*	0	-4.0201
children	9p13	33110638	33167356	2683	*B4GALT1*	0	-4.0201
children	9p13.3	33240195	33248565	27290	*SPINK4*	0	-4.0201

children	9p12	33252469	33264759	573	*BAG1*	0	-4.0201
children	9p13.3	33264876	33282067	51510	*CHMP5*	0	-4.0201
children	9p13.3	33290417	33348721	4799	*NFX1*	0	-4.0201
children	9p13	33384947	33402517	364	*AQP7*	0	-4.0201
children	9p13	33441151	33447631	360	*AQP3*	0	-4.0201
children	9p13.3	33461350	33473941	65083	*NOL6*	0	-4.0201
children	9p13.3	33504534	33511164	441394	*SUGT1P1*	0	-4.0201
children	9p13.3	33524410	33573001	441459	*ANKRD18B*	0	-4.0201
children	9p13.3	33673501	33677418	11191	*PTENP1*	0	-4.0201
children	9p11.2	33750463	33799229	5646	*PRSS3*	0	-4.0201
children	9p13.3	33817181	33920401	54926	*UBE2R2*	0	-3.7921
children	9p13.3	33921690	34048947	55833	*UBAP2*	0	-3.7921
children	9p13.3	33934294	33934373	101340252	*SNORD121B*	0	-3.7921
children	9p13.3	33952761	33952852	100113379	*SNORD121A*	0	-3.7921
children	9p13.3	34086380	34126771	25853	*DCAF12*	0	-3.7921
children	9p13.3	34179002	34252521	51271	*UBAP1*	0	-3.7921
children	9p13.3	34252377	34329198	347240	*KIF24*	0	-3.7921
children	9p13	34329503	34343711	318	*NUDT2*	0	-3.7921
children	9p13.3	34366663	34376894	57462	*KIAA1161*	0	-3.7921
children	9p13.3	34379016	34381598	84688	*C9orf24*	0	-3.7921
children	9p24.3	34393	35864	654835	*FAM138C*	0	-1.6447
children	9p13.3	34398181	34458568	203259	*FAM219A*	0	-3.7921
children	9p13.3	34458749	34520987	27019	*DNAI1*	0	-3.7921
children	9p13.3	34521039	34523037	375704	*ENHO*	0	-3.7921
children	9p13	34551429	34589735	1271	*CNTFR*	0	-3.7921
children	9p13.3	34610481	34612110	138716	*RPP25L*	0	-3.7921
children	9p13	34613541	34620520	11258	*DCTN3*	0	-3.7921
children	9p13.3	34621454	34628011	138715	*ARID3C*	0	-3.7921
children	9p13.3	34634718	34637823	10280	*SIGMAR1*	0	-3.7921
children	9p13	34646585	34650595	2592	*GALT*	0	-3.7921
children	9p13	34652181	34661898	3590	*IL11RA*	0	-3.7921
children	9p13	34661879	34662689	10850	*CCL27*	0	-3.7921
children	9p13	34689566	34691274	6363	*CCL19*	0	-3.7921

children	9p13	34709001	34710164	6366	*CCL21*	0	-3.7921
children	9p12	34723049	34729535	259308	*FAM205A*	0	-3.7921
children	9p13.3	34958191	34982541	23349	*KIAA1045*	0.2438	-3.7921
children	9p13.3	34989637	34998430	25822	*DNAJB5*	0.2438	-3.7921
children	9p13.3	35041091	35045988	138724	*C9orf131*	0.2438	-3.7921
children	9p13.3	35056064	35072739	7415	*VCP*	0.2438	-3.7921
children	9p13	35073834	35080013	2189	*FANCG*	0.2438	-3.7921
children	9p13.3	35088684	35096546	84720	*PIGO*	0.2438	-3.7921
children	9p13.1	35099772	35103192	30968	*STOML2*	0.2438	-3.7921
children	9p13.3	35104117	35115908	80256	*FAM214B*	0.2438	-3.7921
children	9p13.3	35161988	35405332	10497	*UNC13B*	0.2438	-3.7921
children	9p13.3	35406751	35451105	158381	*ATP8B5P*	0.2438	-3.4312
children	9p13.3	35489948	35561895	9853	*RUSC2*	0.2438	-3.7507
children	9p13.3	35561826	35563896	730112	*FAM166B*	0.2438	-3.7507
children	9p13	35605280	35610038	7016	*TESK1*	0	-3.731
children	9p13.3	35609975	35618424	971	*CD72*	0	-3.9629
children	9p13-p12	35649296	35650947	27240	*SIT1*	0	-4.2836
children	9p13.3	35657747	35658015	6023	*RMRP*	0	-4.2836
children	9p13.3	35658286	35661500	203260	*CCDC107*	0	-4.2836
children	9p13.3	35659340	35665278	84904	*ARHGEF39*	0	-4.2836
children	9p13.3	35673914	35681154	768	*CA9*	0	-4.2836
children	9p13	35681989	35690053	7169	*TPM2*	0	-4.2836
children	9p13	35697333	35732392	7094	*TLN1*	0	-4.2836
children	9p13.3	35732316	35737005	10488	*CREB3*	0	-4.2836
children	9p13.3	35736862	35749225	57704	*GBA2*	0	-4.2836
children	9p13.3	35749276	35753264	9827	*RGP1*	0	-4.2836
children	9p13.3	35752987	35754274	692094	*MSMP*	0	-4.2836
children	9p21-p12	35792405	35809728	4882	*NPR2*	0	-4.2836
children	9p13.3	35807781	35812259	26206	*SPAG8*	0	-4.2836
children	9p13.3	35812956	35815042	84681	*HINT2*	0	-4.2836
children	9p13.3	35817013	35828744	392307	*FAM221B*	0	-4.2836
children	9p13.3	35829221	35847232	51754	*TMEM8B*	0	-4.2836
children	9p13.3	35860270	35865515	92973	*LINC00950*	0	-4.2836

children	9p13.3	35869459	35870398	392309	*OR13J1*	0	-4.2836
children	9p13.3	35906188	35907138	646962	*HRCT1*	0	-4.2836
children	9p13.3	35957104	35958151	56656	*OR2S2*	0	-4.3511
children	9p13.3	36036909	36124452	8434	*RECK*	0	-4.3511
children	9p13.3	36136532	36163910	152007	*GLIPR2*	0	-4.3511
children	9p13.3	36169388	36171331	881	*CCIN*	0	-4.3511
children	9p13	36190852	36212059	1211	*CLTA*	0	-4.3511
children	9p13.3	36214438	36258496	10020	*GNE*	0	-4.3511
children	9p13	36336398	36400296	152006	*RNF38*	0	-4.272
children	9p13.2	36572858	36677680	9833	*MELK*	0	-3.9343
children	9p13	36833271	37034476	5079	*PAX5*	0	-3.544
children	9p13.2	36864250	36864305	100616278	*MIR4540*	0	-3.9343
children	9p13.2	37120468	37358145	84186	*ZCCHC7*	0	-2.9001
children	9q12	37422706	37436986	9380	*GRHPR*	0.2189	-2.9001
children	9p13.2	37438099	37465407	9925	*ZBTB5*	0.2189	-2.9001
children	9p13.2	37485931	37503694	64425	*POLR1E*	0.2189	-2.9001
children	9p13.2	37510888	37576250	26267	*FBXO10*	0.2189	-2.9001
children	9p13.2	37588411	37592636	401505	*TOMM5*	0.2189	-2.9001
children	9p13.2	37651051	37746901	22844	*FRMPD1*	0.2189	-2.5806
children	9p13.2	37753799	37778969	158234	*TRMT10B*	0.2189	-2.5806
children	9p11	37779710	37785089	51010	*EXOSC3*	0.2189	-2.5806
children	9p13.2	37800782	37867665	79269	*DCAF10*	0	-2.5806
children	9p13.3-p12	37877571	37904350	92014	*SLC25A51*	0	-2.7985
children	9p13.2	37915894	38069210	6461	*SHB*	0	-2.5433
children	9p24.2	3824127	4152183	169792	*GLIS3*	0	-3.7575
children	9p11.1	38392660	38398662	219	*ALDH1B1*	0	-2.0178
children	9p13.1	38406524	38424444	347252	*IGFBPL1*	0	-2.0178
children	9p13.1	38571360	38620360	253650	*ANKRD18A*	0	-2.0178
children	9p13.1	38621084	38623277	158228	*FAM201A*	0	-2.0178
children	9p24.2	3898645	3901248	84850	*GLIS3-AS1*	0	-3.7575
children	9p24	4490426	4587469	6505	*SLC1A1*	0	-3.789
children	9p24.2	4598315	4666674	55064	*SPATA6L*	0	-3.7835
children	9p24.1	4662293	4665272	403313	*PPAPDC2*	0	-3.778

children	9p24.1	4679552	4708398	55664	*CDC37L1*	0	-3.778
children	9p24.3	470293	746106	23189	*KANK1*	0	-3.6888
children	9p24.1	4709556	4726227	50808	*AK3*	0	-3.778
children	9p24.1-p23	4792833	4861077	10171	*RCL1*	0	-3.778
children	9p24.1	4850296	4850375	406894	*MIR101-2*	0	-3.778
children	9p24	4985244	5128183	3717	*JAK2*	0	-3.778
children	9p24	5163862	5185618	11172	*INSL6*	0	-3.778
children	9p24	5231418	5233967	3641	*INSL4*	0	-3.778
children	9p24.1	5299865	5304611	6019	*RLN2*	0	-3.778
children	9p24.1	5334931	5339873	6013	*RLN1*	0	-3.3845
children	9p24.1	5357966	5437937	55848	*PLGRKT*	0	-3.7871
children	9p24	5450502	5470567	29126	*CD274*	0	-3.7871
children	9p24.2	5510544	5571282	80380	*PDCD1LG2*	0	-3.7871
children	9p24	5784571	5833081	79956	*ERMP1*	0	-3.7871
children	9p24.1	5890908	5909822	2315	*MLANA*	0	-4.1511
children	9p24.1	5919007	6008003	158358	*KIAA2026*	0	-4.1511
children	9p24.1	6011018	6015640	26953	*RANBP6*	0	-4.1511
children	9p24.1	6215785	6257983	90865	*IL33*	0	-4.1511
children	9p24.1	6328348	6330918	89882	*TPD52L3*	0	-4.1511
children	9p24.1	6413150	6507051	115426	*UHRF2*	0	-4.1511
children	9p22	6532463	6645692	2731	*GLDC*	0	-4.1511
children	9p24.1	6720862	7077264	23081	*KDM4C*	0	-4.0646
children	9p23-p24.3	8314245	10612723	5789	*PTPRD*	0	-4.1734
children	9p24.3	841689	969090	1761	*DMRT1*	0	-3.6888
children	9p24.3	976967	991732	58524	*DMRT3*	0	-3.6888

Table S5. Fusion genes identified by RNA-seq in 172 patients

Sample ID	Fusion genes	Frame_info	5' gene				3' gene			
			Gene	**Accession**	**Chromosome**	**Cytoband**	**Gene**	**Accession**	**Chromosome**	**Cytoband**
A03	*NUP214-ABL1*	in-frame	*NUP214*	ENSG00000126883	9	q34.13	*ABL1*	ENSG00000097007	9	q34.12
A03	*EMILIN2-PAX5*	in-frame	*EMILIN2*	ENSG00000132205	18	p11.31	*PAX5*	ENSG00000196092	9	p13.2

A03	*YIPF5-NR3C1*	UTR/UTR	*YIPF5*	ENSG00000145817	5	q31.3	*NR3C1*	ENSG00000113580	5	q31.3
A04	*MLL-ARHGEF12*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*ARHGEF12*	ENSG00000196914	11	q23.3
A05	*RB1-WDFY2*	out-of-frame	*RB1*	ENSG00000139687	13	q14.2	*WDFY2*	ENSG00000139668	13	q14.3
A08	*MSL2-TBL1XR1*	CDS(truncated)/UTR	*MSL2*	ENSG00000174579	3	q22.3	*TBL1XR1*	ENSG00000177565	3	q26.32
A10	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A10	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A13	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A13	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A16	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A18	*MLL-MLLT1*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*MLLT1*	ENSG00000130382	19	p13.3
A19	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A19	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A19	*PAX5-MLLT3*	in-frame	*PAX5*	ENSG00000196092	9	p13.2	*MLLT3*	ENSG00000171843	9	p21.3
A20	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
A21	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A21	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A21	*CSNK1G2-MOB3A*	UTR/UTR	*CSNK1G2*	ENSG00000133275	19	p13.3	*MOB3A*	ENSG00000172081	19	p13.3
A21	*NDUFA4-SCIN*	in-frame	*NDUFA4*	ENSG00000189043	7	p21.3	*SCIN*	ENSG00000006747	7	p21.3
A22	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A22	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A23	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A23	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A23	*ETV6-PDGFRB*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*PDGFRB*	ENSG00000113721	5	q32
A26	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A30	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A30	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A31	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A34	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A34	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A35	*CREBBP-TRBV23-1*	CDS(truncated)/CDS	*CREBBP*	ENSG00000005339	16	p13.3	*TRBV23-1*	ENSG00000211749	7	q34
A35	*EWSR1-ZNF384*	in-frame	*EWSR1*	ENSG00000182944	22	q12.2	*ZNF384*	ENSG00000126746	12	p13.31
A35	*ZNF384-EWSR1*	UTR/CDS(truncated)	*ZNF384*	ENSG00000126746	12	p13.31	*EWSR1*	ENSG00000182944	22	q12.2
A36	*CTDP1-PQLC1*	in-frame	*CTDP1*	ENSG00000060069	18	q23	*PQLC1*	ENSG00000122490	18	q23

A36	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
A37	*EGFL7-METRNL*	UTR/CDS(truncated)	*EGFL7*	ENSG00000172889	9	q34.3	*METRNL*	ENSG00000176845	17	q25.3
A37	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
A38	*MLL-AFF1*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*AFF1*	ENSG00000172493	4	q22.1
A39	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A40	*LCOR-HPSE2*	UTR/CDS(truncated)	*LCOR*	ENSG00000196233	10	q24.1	*HPSE2*	ENSG00000172987	10	q24.2
A41	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	*BCL9*	ENSG00000116128	1	q21.2
A41	*RFWD2-TNFSF18*	in-frame	*RFWD2*	ENSG00000143207	1	q25.2	*TNFSF18*	ENSG00000120337	1	q25.1
A42	*AFF1-MLL*	in-frame	*AFF1*	ENSG00000172493	4	q21.3	*MLL*	ENSG00000118058	11	q23.3
A42	*MLL-AFF1*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*AFF1*	ENSG00000172493	4	q22.1
A43	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
A43	*METRNL-SKI*	out-of-frame	*METRNL*	ENSG00000176845	17	q25.3	*SKI*	ENSG00000157933	1	p36.33
A43	*PQLC1-CTDP1*	in-frame	*PQLC1*	ENSG00000122490	18	q23	*CTDP1*	ENSG00000060069	18	q23
A43	*TTYH3-MAD1L1*	in-frame	*TTYH3*	ENSG00000136295	7	p22.3	*MAD1L1*	ENSG00000002822	7	p22.3
A46	*IGH-CRLF2*	intergenic/intergenic	*IGH*	ENSG00000211899	14	q32.33	*CRLF2*	ENSG00000205755	X	p22.33
A47	*CREBBP-ZNF384*	in-frame	*CREBBP*	ENSG00000005339	16	p13.3	*ZNF384*	ENSG00000126746	12	p13.31
A47	*ZNF384-CREBBP*	UTR/CDS(truncated)	*ZNF384*	ENSG00000126746	12	p13.31	*CREBBP*	ENSG00000005339	16	p13.3
A48	*CD24-RBM3*	UTR/UTR	*CD24*	ENSG00000272398	Y	q11.222	*RBM3*	ENSG00000102317	X	p11.23
A48	*COPS2-FAM129C*	intron\intron	*COPS2*	ENSG00000166200	15	q21.1	*FAM129C*	ENSG00000167483	19	p13.11
A48	*FAM129C-COPS2*	intron\intron	*FAM129C*	ENSG00000167483	19	p13.11	*COPS2*	ENSG00000166200	15	q21.1
A49	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A56	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A56	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A57	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A57	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A58	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A59	*ABL1-PRRC2B*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*PRRC2B*	ENSG00000130723	9	q34.13
A59	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A59	*PAX5-ZCCHC7*	in-frame	*PAX5*	ENSG00000196092	9	p13.2	*ZCCHC7*	ENSG00000147905	9	p13.2
A59	*PRRC2B-BCR*	in-frame	*PRRC2B*	ENSG00000130723	9	q34.13	*BCR*	ENSG00000186716	22	q11.23
A59	*ZCCHC7-PAX5*	in-frame	*ZCCHC7*	ENSG00000147905	9	p13.2	*PAX5*	ENSG00000196092	9	p13.2
A60	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A61	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23

A61	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A62	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A62	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A63	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A63	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A64	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A65	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A65	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A70	*AFF1-MLL*	in-frame	*AFF1*	ENSG00000172493	4	q21.3	*MLL*	ENSG00000118058	11	q23.3
A70	*MLL-AFF1*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*AFF1*	ENSG00000172493	4	q22.1
A73	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
A73	*LPAR5-EP300*	UTR/CDS(truncated)	*LPAR5*	ENSG00000184574	12	p13.31	*EP300*	ENSG00000100393	22	q13.2
A74	*DAZAP1-MEF2D*	out-of-frame	*DAZAP1*	ENSG00000071626	19	p13.3	*MEF2D*	ENSG00000116604	1	q22
A74	*MEF2D-DAZAP1*	in-frame	*MEF2D*	ENSG00000116604	1	q22	*DAZAP1*	ENSG00000071626	19	p13.3
A75	*MEF2D-HNRNPUL1*	in-frame	*MEF2D*	ENSG00000116604	1	q22	*HNRNPUL1*	ENSG00000105323	19	q13.2
A76	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A77	*ANKRD11-SPG7*	intronic/UTR	*ANKRD11*	ENSG00000167522	16	q24.3	*SPG7*	ENSG00000197912	16	q24.3
A77	*ANKRD11-SPG7*	UTR/CDS(truncated)	*ANKRD11*	ENSG00000167522	16	q24.3	*SPG7*	ENSG00000197912	16	q24.3
A77	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A77	*PALM-NCLN*	in-frame	*PALM*	ENSG00000099864	19	p13.3	*NCLN*	ENSG00000125912	19	p13.3
A78	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
A78	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A79	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
A82	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A82	*SLC12A7-NKD2*	in-frame	*SLC12A7*	ENSG00000113504	5	p15.33	*NKD2*	ENSG00000145506	5	p15.33
A82	*MFI2-TNK2*	out-of-frame	*MFI2*	ENSG00000163975	3	q29	*TNK2*	ENSG00000061938	3	q29
A82	*TTYH3-MAD1L1*	in-frame	*TTYH3*	ENSG00000136295	7	p22.3	*MAD1L1*	ENSG00000002822	7	p22.3
A82	*FGFRL1-CTBP1*	in-frame	*FGFRL1*	ENSG00000127418	4	p16.3	*CTBP1*	ENSG00000159692	4	p16.3
A82	*MFI2-FYTTD1*	in-frame	*MFI2*	ENSG00000163975	3	q29	*FYTTD1*	ENSG00000122068	3	q29
A83	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
A86	*TAF15-ZNF384*	in-frame	*TAF15*	ENSG00000270647	17	q12	*ZNF384*	ENSG00000126746	12	p13.31
A86	*ING4-C17ORF50*	in-frame	*ING4*	ENSG00000111653	12	p13.31	*C17ORF50*	ENSG00000270806	17	q12
A86	*TPM4-METRNL*	out-of-frame	*TPM4*	ENSG00000167460	19	p13.12	*METRNL*	ENSG00000176845	17	q25.3

A87	*PAX5-JAK2*	in-frame	*PAX5*	ENSG00000196092	9	p13.2	*JAK2*	ENSG00000096968	9	p24.1
A88	*UQCRC1-ANO10*	out-of-frame	*UQCRC1*	ENSG00000010256	3	p21.31	*ANO10*	ENSG00000160746	3	p22.1
A89	*JAK2-SNX29*	in-frame	*JAK2*	ENSG00000096968	9	p24.1	*SNX29*	ENSG00000048471	16	p13.13
A89	*SNX29-JAK2*	in-frame	*SNX29*	ENSG00000048471	16	p13.13	*JAK2*	ENSG00000096968	9	p24.1
A91	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
A91	*UBAP1-DCAF12*	out-of-frame	*UBAP1*	ENSG00000165006	9	p13.3	*DCAF12*	ENSG00000198876	9	p13.3
A93	*LILRA2-CCBE1*	UTR/UTR	*LILRA2*	ENSG00000239998	19	q13.42	*CCBE1*	ENSG00000183287	18	q21.32
A93	*RAP1B-EMR2*	intron\3'UTR	*RAP1B*	ENSG00000127314	12	q15	*EMR2*	ENSG00000127507	19	p13.12
A94	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
AC11	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
AC11	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
B03	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
B03	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
B12	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	*BCL9*	ENSG00000116128	1	q21.2
B15	*MLL-MLLT3*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*MLLT3*	ENSG00000171843	9	p21.3
B15	*ZNF124-PUS3*	CDS(truncated)/UTR	*ZNF124*	ENSG00000196418	1	q44	*PUS3*	ENSG00000110060	11	q24.2
B16	*WSB1-HYPK*	5'UTR/3'UTR	*WSB1*	ENSG00000109046	17	q11.1	*HYPK*	ENSG00000242028	15	q15.3
B17	*P2RY8-CRLF2*	UTR/UTR	*P2RY8*	ENSG00000182162	X	p22.33	*CRLF2*	ENSG00000205755	X	p22.33
B18	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
B18	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
B18	*ZNF124-PUS3*	CDS(truncated)/UTR	*ZNF124*	ENSG00000196418	1	q44	*PUS3*	ENSG00000110060	11	q24.2
C01	*TCF3-ZNF384*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*ZNF384*	ENSG00000126746	12	p13.31
C01	*ZNF384-RNF180*	UTR/CDS(truncated)	*ZNF384*	ENSG00000126746	12	p13.31	*RNF180*	ENSG00000164197	5	q12.3
C08	*MEF2D-HNRNPUL1*	in-frame	*MEF2D*	ENSG00000116604	1	q22	*HNRNPUL1*	ENSG00000105323	19	q13.2
C15	*TCF3-HLF*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*HLF*	ENSG00000108924	17	q22
C18	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C18	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C19	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C20	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C20	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C24	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C25	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C25	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2

C27	*ACIN1-NUTM1*	in-frame	*ACIN1*	ENSG00000100813	14	q11.2	*NUTM1*	ENSG00000184507	15	q14
C28	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C28	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C29	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C29	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C30	*DCAF8-DNM3*	out-of-frame	*DCAF8*	ENSG00000132716	1	q23.2	*DNM3*	ENSG00000197959	1	q24.3
C30	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	*BCL9*	ENSG00000116128	1	q21.2
C32	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C33	*ETV6-ABL1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*ABL1*	ENSG00000097007	9	q34.12
C33	*NIN-TMX1*	UTR/CDS(truncated)	*NIN*	ENSG00000100503	14	q22.1	*TMX1*	ENSG00000139921	14	q22.1
C34	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C35	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C35	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C36	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
C36	*FAM60A-SEPT9*	UTR/CDS(truncated)	*FAM60A*	ENSG00000139146	12	p11.21	*SEPT9*	ENSG00000184640	17	q25.3
C37	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
C37	*ZNF384-EP300*	UTR/CDS(truncated)	*ZNF384*	ENSG00000126746	12	p13.31	*EP300*	ENSG00000100393	22	q13.2
C38	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
C38	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
C38	*RCAN1-SPRY1*	CDS(truncated)/UTR	*RCAN1*	ENSG00000159200	21	q22.12	*SPRY1*	ENSG00000164056	4	q28.1
C39	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C40	*TSC2-ATP6V0C*	out-of-frame	*TSC2*	ENSG00000103197	16	p13.3	*ATP6V0C*	ENSG00000185883	16	p13.3
C41	*SMARCA2-ZNF362*	in-frame	*SMARCA2*	ENSG00000080503	9	p24.3	*ZNF362*	ENSG00000160094	1	p35.1
C41	*ZNF362-SMARCA2*	in-frame	*ZNF362*	ENSG00000160094	1	p35.1	*SMARCA2*	ENSG00000080503	9	p24.3
C43	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C43	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C44	*BRWD1-ETS2*	CDS(truncated)/UTR	*BRWD1*	ENSG00000185658	21	q22.2	*ETS2*	ENSG00000157557	21	q22.2
C44	*HNRNPU-ZBTB18*	in-frame	*HNRNPU*	ENSG00000153187	1	q44	*ZBTB18*	ENSG00000179456	1	q44
C45	*CSNK1D-METRNL*	out-of-frame	*CSNK1D*	ENSG00000141551	17	q25.3	*METRNL*	ENSG00000176845	17	q25.3
C45	*MBP-TGIF1*	in-frame	*MBP*	ENSG00000197971	18	q23	*TGIF1*	ENSG00000177426	18	p11.31
C45	*P2RY8-ZBED1*	UTR/UTR	*P2RY8*	ENSG00000182162	X	p22.33	*ZBED1*	ENSG00000214717	X	p22.33
C45	*P2RY8-ZBED1*	intronic/UTR	*P2RY8*	ENSG00000182162	X	p22.33	*ZBED1*	ENSG00000214717	X	p22.33
C47	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31

C49	*NUP214-ABL1*	in-frame	*NUP214*	ENSG00000126883	9	q34.13	*ABL1*	ENSG00000097007	9	q34.12
C51	*HBA1-CD74*	UTR/UTR	*HBA1*	ENSG00000206172	16	p13.3	*CD74*	ENSG00000019582	5	q32
C57	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C57	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C57	*RTN3-STIP1*	out-of-frame	*RTN3*	ENSG00000133318	11	q13.1	*STIP1*	ENSG00000168439	11	q13.1
C58	*RUNX1-ETV6*	intronic/UTR	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C58	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C61	*ANKRD45-HOOK3*	UTR/UTR	*ANKRD45*	ENSG00000183831	1	q25.1	*HOOK3*	ENSG00000168172	8	p11.21
C63	*PAX5-AUTS2*	in-frame	*PAX5*	ENSG00000196092	9	p13.2	*AUTS2*	ENSG00000158321	7	q11.22
C64	*WDR4-PDE9A*	out-of-frame	*WDR4*	ENSG00000160193	21	q22.3	*PDE9A*	ENSG00000160191	21	q22.3
C64	*SMARCC1-CDK5RAP3*	out-of-frame	*SMARCC1*	ENSG00000173473	3	p21.31	*CDK5RAP3*	ENSG00000108465	17	q21.32
C66	*CD74-PDGFRB*	in-frame	*CD74*	ENSG00000019582	5	q32	*PDGFRB*	ENSG00000113721	5	q32
C67	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
C67	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
C67	*KDM4B-CUL2*	in-frame	*KDM4B*	ENSG00000127663	19	p13.3	*CUL2*	ENSG00000108094	10	p11.21
C68	*FUS-ERG*	in-frame	*FUS*	ENSG00000089280	16	p11.2	*ERG*	ENSG00000157554	21	q22.2
C68	*ERG-FUS*	in-frame	*ERG*	ENSG00000157554	21	q22.2	*FUS*	ENSG00000089280	16	p11.2
C69	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C69	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C69	*UBA2-PPP1R36*	in-frame	*UBA2*	ENSG00000126261	19	q13.11	*PPP1R36*	ENSG00000165807	14	q23.3
C69	*CDK1-DGKH*	in-frame	*CDK1*	ENSG00000170312	10	q21.2	*DGKH*	ENSG00000102780	13	q14.11
C69	*SKP1-AFF4*	UTR/CDS(truncated)	*SKP1*	ENSG00000113558	5	q31.1	*AFF4*	ENSG00000072364	5	q31.1
C72	*CDKN2A-IGK@*	UTR/---	*CDKN2A*	ENSG00000147889	9	p21.3	*IGK@*	ENSG09000000012	2	p11.2
C73	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C75	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C75	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C76	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C76	*BACH2-PNRC1*	UTR/CDS(truncated)	*BACH2*	ENSG00000112182	6	q15	*PNRC1*	ENSG00000146278	6	q15
C79	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C79	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C80	*TCF3-ZNF384*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*ZNF384*	ENSG00000126746	12	p13.31
C80	*PLK5-ATN1*	UTR/CDS(truncated)	*PLK5*	ENSG00000185988	19	p13.3	*ATN1*	ENSG00000111676	12	p13.31
C81	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12

C81	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C82	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C82	*RUNX1-GART*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*GART*	ENSG00000159131	21	q22.11
C83	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C83	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C84	*AFF1-MLL*	UTR/CDS(truncated)	*AFF1*	ENSG00000172493	4	q21.3	*MLL*	ENSG00000118058	11	q23.3
C84	*MLL-AFF1*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*AFF1*	ENSG00000172493	4	q22.1
C84	*AFF1-MLL*	in-frame	*AFF1*	ENSG00000172493	4	q21.3	*MLL*	ENSG00000118058	11	q23.3
C85	*MLL-MLLT1*	in-frame	*MLL*	ENSG00000118058	11	q23.3	*MLLT1*	ENSG00000130382	19	p13.3
C87	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C88	*ABL1-BCR*	in-frame	*ABL1*	ENSG00000097007	9	q34.12	*BCR*	ENSG00000186716	22	q11.23
C88	*BCR-ABL1*	in-frame	*BCR*	ENSG00000186716	22	q11.23	*ABL1*	ENSG00000097007	9	q34.12
C88	*HINT2-NPR2*	in-frame	*HINT2*	ENSG00000137133	9	p13.3	*NPR2*	ENSG00000159899	9	p13.3
C90	*ZNF384-EP300*	UTR/CDS(truncated)	*ZNF384*	ENSG00000126746	12	p13.31	*EP300*	ENSG00000100393	22	q13.2
C90	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	*ZNF384*	ENSG00000126746	12	p13.31
C91	*TCF3-PBX1*	in-frame	*TCF3*	ENSG00000071564	19	p13.3	*PBX1*	ENSG00000185630	1	q23.3
C93	*MEF2D-SS18*	out-of-frame	*MEF2D*	ENSG00000116604	1	q22	*SS18*	ENSG00000141380	18	q11.2
C93	*SS18-MEF2D*	in-frame	*SS18*	ENSG00000141380	18	q11.2	*MEF2D*	ENSG00000116604	1	q22
C93	*FXR1-TBL1XR1*	CDS(truncated)/UTR	*FXR1*	ENSG00000114416	3	q26.33	*TBL1XR1*	ENSG00000177565	3	q26.32
C93	*FXR1-TBL1XR1*	CDS(truncated)/intronic	*FXR1*	ENSG00000114416	3	q26.33	*TBL1XR1*	ENSG00000177565	3	q26.32
C93	*TBL1XR1-FXR1*	UTR/CDS(truncated)	*TBL1XR1*	ENSG00000177565	3	q26.32	*FXR1*	ENSG00000114416	3	q26.33
C93	*MEF2D-SS18*	in-frame	*MEF2D*	ENSG00000116604	1	q22	*SS18*	ENSG00000141380	18	q11.2
C94	*CTDP1-PQLC1*	in-frame	*CTDP1*	ENSG00000060069	18	q23	*PQLC1*	ENSG00000122490	18	q23
C94	*PQLC1-CTDP1*	in-frame	*PQLC1*	ENSG00000122490	18	q23	*CTDP1*	ENSG00000060069	18	q23
C94	*PIM3-METRNL*	in-frame	*PIM3*	ENSG00000198355	22	q13.33	*METRNL*	ENSG00000176845	17	q25.3
C94	*PIM3-SLC7A5*	in-frame	*PIM3*	ENSG00000198355	22	q13.33	*SLC7A5*	ENSG00000103257	16	q24.2
C94	*EWSR1-ZNF384*	in-frame	*EWSR1*	ENSG00000182944	22	q12.2	*ZNF384*	ENSG00000126746	12	p13.31
C94	*ZNF384-EWSR1*	UTR/CDS(truncated)	*ZNF384*	ENSG00000126746	12	p13.31	*EWSR1*	ENSG00000182944	22	q12.2
C94	*CD81-SLC7A5*	out-of-frame	*CD81*	ENSG00000110651	11	p15.5	*SLC7A5*	ENSG00000103257	16	q24.2
C95	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
C95	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C97	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
C97	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12

C102	*PAX5-CBFA2T3*	in-frame	*PAX5*	ENSG00000196092	9	p13.2	*CBFA2T3*	ENSG00000129993	16	q24.3
CA80	*CEBPE-IGH*	out-of-frame	*CEBPE*	ENSG00000092067	14	q11.2	*IGHM*	ENSG00000211899	14	q32.33
CA92	*ETV6-RUNX1*	in-frame	*ETV6*	ENSG00000139083	12	p13.2	*RUNX1*	ENSG00000159216	21	q22.12
CA92	*RUNX1-ETV6*	in-frame	*RUNX1*	ENSG00000159216	21	q22.12	*ETV6*	ENSG00000139083	12	p13.2
CA92	*CTDP1-PQLC1*	in-frame	*CTDP1*	ENSG00000060069	18	q23	*PQLC1*	ENSG00000122490	18	q23
CA92	*PQLC1-CTDP1*	in-frame	*PQLC1*	ENSG00000122490	18	q23	*CTDP1*	ENSG00000060069	18	q23
CA92	*PRC1-KIF7*	in-frame	*PRC1*	ENSG00000198901	15	q26.1	*KIF7*	ENSG00000166813	15	q26.1
CA92	*NOC4L-FBRSL1*	in-frame	*NOC4L*	ENSG00000184967	12	q24.33	*FBRSL1*	ENSG00000112787	12	q24.33
CA92	*ELF1-FOXO1*	out-of-frame	*ELF1*	ENSG00000120690	13	q14.11	*FOXO1*	ENSG00000150907	13	q14.11
CA92	*PIM3-BRD1*	out-of-frame	*PIM3*	ENSG00000198355	22	q13.33	*BRD1*	ENSG00000100425	22	q13.33
CA92	*POLE-FBRSL1*	out-of-frame	*POLE*	ENSG00000177084	12	q24.33	*FBRSL1*	ENSG00000112787	12	q24.33
CA92	*PTBP1-TMEM259*	in-frame	*PTBP1*	ENSG00000011304	19	p13.3	*TMEM259*	ENSG00000182087	19	p13.3
CA97	*EBF1-JAK2*	in-frame	*EBF1*	ENSG00000164330	5	q33.3	*JAK2*	ENSG00000096968	9	p24.1
CA97	*JAK2-EBF1*	in-frame	*JAK2*	ENSG00000096968	9	p24.1	*EBF1*	ENSG00000164330	5	q33.3

Table S6. Information of newly identified in-frame and out-of-frame fusions by RNA-seq in 172 patients

Sample ID	Fusion genes	Frame_info	5' gene						3' gene					
			Gene	**Accession**	**Chromosome**	**Cytoband**	**Breakpoint**	**Exon**	**Gene**	**Accession**	**Chromosome**	**Cytoband**	**Breakpoint**	**Exon**
A03	*EMILIN2-PAX5*	in-frame	*EMILIN2*	ENSG00000132205	18	p11.31	2907083	5	*PAX5*	ENSG00000196092	9	p13.2	36966721	6
A05	*RB1-WDFY2*	out-of-frame	*RB1*	ENSG00000139687	13	q14.2	48955579	17	*WDFY2*	ENSG00000139668	13	q14.3	52301814	6
A05	*RB1-WDFY2*	out-of-frame	*RB1*	ENSG00000139687	13	q14.2	48955579	17	*WDFY2*	ENSG00000139668	13	q14.3	52313185	7
A19	*PAX5-MLLT3*	in-frame	*PAX5*	ENSG00000196092	9	p13.2	36966546	6	*MLLT3*	ENSG00000171843	9	p21.3	20620833	2
A20	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	41527637	6	*ZNF384*	ENSG00000126746	12	p13.31	6797392	2
A21	*NDUFA4-SCIN*	in-frame	*NDUFA4*	ENSG00000189043	7	p21.3	10979643	1	*SCIN*	ENSG00000006747	7	p21.3	12689092	14
A36	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	41527637	6	*ZNF384*	ENSG00000126746	12	p13.31	6788691	3
A37	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	41527637	6	*ZNF384*	ENSG00000126746	12	p13.31	6788691	3
A37	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	41527637	6	*ZNF384*	ENSG00000126746	12	p13.31	6797392	2
A41	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	156449082	6	*BCL9*	ENSG00000116128	1	q21.2	147095643	10
A41	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	156449082	6	*BCL9*	ENSG00000116128	1	q21.2	147095679	10
A41	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	156449082	6	*BCL9*	ENSG00000116128	1	q21.2	147096129	10

A41	*RFWD2-TNFSF18*	in-frame	*RFWD2*	ENSG00000143207	1	q25.2	176012322	14	*TNFSF18*	ENSG00000120337	1	q25.1	173020053	1
A43	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	41527637	6	*ZNF384*	ENSG00000126746	12	p13.31	6788691	3
A47	*CREBBP-ZNF384*	in-frame	*CREBBP*	ENSG00000005339	16	p13.3	3832685	6	*ZNF384*	ENSG00000126746	12	p13.31	6788691	3
A47	*CREBBP-ZNF384*	in-frame	*CREBBP*	ENSG00000005339	16	p13.3	3843387	4	*ZNF384*	ENSG00000126746	12	p13.31	6788691	3
A59	*PRRC2B-BCR*	in-frame	*PRRC2B*	ENSG00000130723	9	q34.13	134346370	13	*BCR*	ENSG00000186716	22	q11.23	23595986	2
A73	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	41527637	6	*ZNF384*	ENSG00000126746	12	p13.31	6788691	3
A75	*MEF2D-HNRNPUL1*	in-frame	*MEF2D*	ENSG00000116604	1	q22	156444900	9	*HNRNPUL1*	ENSG00000105323	19	q13.2	41808570	12
A77	*PALM-NCLN*	in-frame	*PALM*	ENSG00000099864	19	p13.3	736078	7	*NCLN*	ENSG00000125912	19	p13.3	3192468	2
A82	*SLC12A7-NKD2*	in-frame	*SLC12A7*	ENSG00000113504	5	p15.33	1093648	3	*NKD2*	ENSG00000145506	5	p15.33	1032267	4
A82	*MFI2-TNK2*	out-of-frame	*MFI2*	ENSG00000163975	3	q29	196756525	1	*TNK2*	ENSG00000061938	3	q29	195599341	10
A82	*FGFRL1-CTBP1*	in-frame	*FGFRL1*	ENSG00000127418	4	p16.3	1006352	1	*CTBP1*	ENSG00000159692	4	p16.3	1219354	5
A82	*MFI2-FYTTD1*	in-frame	*MFI2*	ENSG00000163975	3	q29	196756525	1	*FYTTD1*	ENSG00000122068	3	q29	197483297	2
A86	*ING4-C17ORF50*	in-frame	*ING4*	ENSG00000111653	12	p13.31	6761828	5	*C17ORF50*	ENSG00000270806	17	q12	34091026	2
A88	*UQCRC1-ANO10*	out-of-frame	*UQCRC1*	ENSG00000010256	3	p21.31	48640997	6	*ANO10*	ENSG00000160746	3	p22.1	43474219	12
A89	*JAK2-SNX29*	in-frame	*JAK2*	ENSG00000096968	9	p24.1	5070052	12	*SNX29*	ENSG00000048471	16	p13.13	12571576	19
A89	*SNX29-JAK2*	in-frame	*SNX29*	ENSG00000048471	16	p13.13	12497386	18	*JAK2*	ENSG00000096968	9	p24.1	5072492	13
A91	*UBAP1-DCAF12*	out-of-frame	*UBAP1*	ENSG00000165006	9	p13.3	34179238	1	*DCAF12*	ENSG00000198876	9	p13.3	34107563	3
B12	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	156449378	5	*BCL9*	ENSG00000116128	1	q21.2	147094072	9
C08	*MEF2D-HNRNPUL1*	in-frame	*MEF2D*	ENSG00000116604	1	q22	156449082	6	*HNRNPUL1*	ENSG00000105323	19	q13.2	41808570	12
C27	*ACIN1-NUTM1*	in-frame	*ACIN1*	ENSG00000100813	14	q11.2	23550957	5	*NUTM1*	ENSG00000184507	15	q14	34638143	2
C30	*MEF2D-BCL9*	in-frame	*MEF2D*	ENSG00000116604	1	q22	156449082	6	*BCL9*	ENSG00000116128	1	q21.2	147094072	9
C30	*DCAF8-DNM3*	out-of-frame	*DCAF8*	ENSG00000132716	1	q23.2	160195381	8	*DNM3*	ENSG00000197959	1	q24.3	171956796	3
C37	*EP300-ZNF384*	in-frame	*EP300*	ENSG00000100393	22	q13.2	41527637	6	*ZNF384*	ENSG00000126746	12	p13.31	6788691	3
C40	*TSC2-ATP6V0C*	out-of-frame	*TSC2*	ENSG00000103197	16	p13.3	2107179	9	*ATP6V0C*	ENSG00000185883	16	p13.3	2569219	2
C41	*SMARCA2-ZNF362*	in-frame	*SMARCA2*	ENSG00000080503	9	p24.3	2039900	4	*ZNF362*	ENSG00000160094	1	p35.1	33745725	5
C41	*ZNF362-SMARCA2*	in-frame	*ZNF362*	ENSG00000160094	1	p35.1	33742195	4	*SMARCA2*	ENSG00000080503	9	p24.3	2047229	5
C44	*HNRNPU-ZBTB18*	in-frame	*HNRNPU*	ENSG00000153187	1	q44	245026976	1	*ZBTB18*	ENSG00000179456	1	q44	244217090	2
C45	*CSNK1D-METRNL*	out-of-frame	*CSNK1D*	ENSG00000141551	17	q25.3	80231182	1	*METRNL*	ENSG00000176845	17	q25.3	81042814	2
C45	*MBP-TGIF1*	in-frame	MBP	ENSG00000197971	18	q23	74778254	3	TGIF1	ENSG00000177426	18	p11.31	3456352	2
C57	*RTN3-STIP1*	out-of-frame	RTN3	ENSG00000133318	11	q13.1	63449250	1	STIP1	ENSG00000168439	11	q13.1	63960550	2
C64	*WDR4-PDE9A*	out-of-frame	WDR4	ENSG00000160193	21	q22.3	44296812	2	PDE9A	ENSG00000160191	21	q22.3	44189137	17
C64	*SMARCC1-CDK5RAP3*	out-of-frame	SMARCC1	ENSG00000173473	3	p21.31	47770515	6	CDK5RAP3	ENSG00000108465	17	q21.32	46047979	1

C64	*WDR4-PDE9A*	out-of-frame	WDR4	ENSG00000160193	21	q22.3	44296812	2	PDE9A	ENSG00000160191	21	q22.3	44188298	16
C66	*CD74-PDGFRB*	in-frame	CD74	ENSG00000019582	5	q32	149784243	6	PDGFRB	ENSG00000113721	5	q32	149506177	11
C67	*KDM4B-CUL2*	in-frame	KDM4B	ENSG00000127663	19	p13.3	5047680	6	CUL2	ENSG00000108094	10	p11.21	35360267	2
C69	*UBA2-PPP1R36*	in-frame	UBA2	ENSG00000126261	19	q13.11	34929671	6	PPP1R36	ENSG00000165807	14	q23.3	65031469	4
C69	*UBA2-PPP1R36*	in-frame	UBA2	ENSG00000126261	19	q13.11	34929671	6	PPP1R36	ENSG00000165807	14	q23.3	65019532	3
C69	*CDK1-DGKH*	in-frame	CDK1	ENSG00000170312	10	q21.2	62545545	4	DGKH	ENSG00000102780	13	q14.11	42803235	30
C82	*RUNX1-GART*	in-frame	RUNX1	ENSG00000159216	21	q22.12	36421139	2	GART	ENSG00000159131	21	q22.11	34911629	2
C82	*RUNX1-GART*	in-frame	RUNX1	ENSG00000159216	21	q22.12	36421139	2	GART	ENSG00000159131	21	q22.11	34907626	3
C82	*RUNX1-GART*	in-frame	RUNX1	ENSG00000159216	21	q22.12	36421139	2	GART	ENSG00000159131	21	q22.11	34911662	2
C88	*HINT2-NPR2*	in-frame	HINT2	ENSG00000137133	9	p13.3	35814896	1	NPR2	ENSG00000159899	9	p13.3	35805508	13
C93	*MEF2D-SS18*	in-frame	MEF2D	ENSG00000116604	1	q22	156444900	9	SS18	ENSG00000141380	18	q11.2	23619420	6
C93	*SS18-MEF2D*	in-frame	SS18	ENSG00000141380	18	q11.2	23632588	5	MEF2D	ENSG00000116604	1	q22	156438812	10
C94	*CD81-SLC7A5*	out-of-frame	CD81	ENSG00000110651	11	p15.5	2398845	1	SLC7A5	ENSG00000103257	16	q24.2	87874761	3
C102	*PAX5-CBFA2T3*	in-frame	PAX5	ENSG00000196092	9	p13.2	37002645	5	CBFA2T3	ENSG00000129993	16	q24.3	88968064	2
CA92	*PRC1-KIF7*	in-frame	*PRC1*	ENSG00000198901	15	q26.1	91522388	8	*KIF7*	ENSG00000166813	15	q26.1	90177114	12
CA92	*POLE-FBRSL1*	out-of-frame	*POLE*	ENSG00000177084	12	q24.33	133263840	1	*FBRSL1*	ENSG00000112787	12	q24.33	133084739	2
CA92	*PTBP1-TMEM259*	in-frame	*PTBP1*	ENSG00000011304	19	p13.3	799443	2	*TMEM259*	ENSG00000182087	19	p13.3	1014472	2

Table S7. Characteristics of patients with *ZNF384* and *MEF2D* related fusions identified by RNA-seq and RT-PCR

*Last follow up date: 2015/12/3

Related gene	**ID**	**Age (yr)**	**Fusion**	**WBC ($\times 10^9$/L)**	**Karyotype**	**Concurrent key fusion**	**Immunophenotype**	**CD13**	**CD33**	**Death* (0=no, 1=yes)**	**Relapse* (0=no, 1=yes)**
ZNF384	A20	44.3	*EP300-ZNF384*	46.4	46,XY	no	Common-B	+	+	0	0
	A36	23.7	*EP300-ZNF384*	13	46,XY	no	Common-B	-	+	0	0
	A37	22.8	*EP300-ZNF384*	10.34	46-47,XX,+M[CP3][3]/46,XX[17]/[20]	no	Pro-B	+	+	0	0
	A43	30.4	*EP300-ZNF384*	3.8	46,XX	no	Common-B	-	+	0	0
	A73	18.6	*EP300-ZNF384*	12.29	NA	no	Pro-B	+	-	0	0
	A83	18.2	*EP300-ZNF384*	77.98	46,XY	no	Pro-B	+	+	0	0
	F305	23.0	*EP300-ZNF384*	11.5	46,XY	no	Pro-B	+	+	0	0
	F328	56.3	*EP300-ZNF384*	4.6	46.XX	no	Pro-B	+	+	1	0

	F345	19.7	*EP300-ZNF384*	2.23	Fail	no	Pro-B	+	+	NA	NA
	C37	13.8	*EP300-ZNF384*	64.8	46,XX, der(1)t(1;14)(q12;q12),-4,+mar[6]/46,XX [6]	no	Pro-B	-	-	0	0
	C47	4.1	*EP300-ZNF384*	96	46,XY	no	Pro-B	-	+	0	0
	C90	5.0	*EP300-ZNF384*	6.2	46,XY,inv(9)(p12,q13)[10]/49,idem,-Y,+8,+13,+20,+22[10]	no	Pro-B	-	+	0	0
	F038	14.6	*EP300-ZNF384*	36.8	46,XX	no	Pro-B	NA	NA	1	1
	F176	7.3	*EP300-ZNF384*	46	46,XY	no	Pro-B	NA	NA	0	0
	A86	24.8	*TAF15-ZNF384*	27.11	43-46，XX,12p+[cp4]/44-45,XX,6q-,12p+[cp3]/46,XX[5]/[18]	no	Pro-B	+	+	0	0
	F308	33.3	*TAF15-ZNF384*	9.4	46,XX	no	Pro-B	+	+	1	1
	A35	18.6	*EWSR1-ZNF384*	4.3	46,XY[6]/[12], 6q- and M chromosome occasionally seen	no	Pro-B	+	+	0	0
	C94	3.0	*EWSR1-ZNF384*	3.6	46,XX ,t(12;22)(p13;q13),i(13)(q10)/46,XX	no	Common-B	-	-	0	0
	C01	2.3	*TCF3-ZNF384*	104	46,XX	no	Pro-B	-	+	0	1
	C80	2.2	*TCF3-ZNF384*	35.1	46,XY	no	Pro-B	-	+	0	1
	A47	38.5	*CREBBP-ZNF384*	56.59	Fail	no	Pro-B	+	+	1	1
MEF2D	A41	59.1	*MEF2D-BCL9*	58.3	47-48,XX,-4,-6,+M1-M5[CP3]/[4]	no	Common-B	-	+	1	0
	F006	33.2	*MEF2D-BCL9*	4.9	44-47,XY,+7,+8,-20[2]/46,XX[1]/[9]	no	Pre-B	NA	NA	1	1
	F279	22.8	*MEF2D-BCL9*	18.25	Fail	no	Pre-B	NA	NA	1	1
	F339	55.1	*MEF2D-BCL9*	10.93	Fail	no	Pre-B	-	-	0	0
	F348	19.3	*MEF2D-BCL9*	203.7	46,XX	no	Pre-B	-	-	0	0
	F039	15.6	*MEF2D-BCL9*	7.1	43-46,XX,2p-,-9,i(17q)[CP11]/46,XX[4]/[18]	no	Pre-B	NA	NA	1	1
	B12	4.7	*MEF2D-BCL9*	20.9	46,XY	no	Pre-B	-	-	1	1
	C30	12.9	*MEF2D-BCL9*	10.3	44-46,X,-4,-5,-8,+M4-M5/46,XY	no	Pre-B	-	-	0	0
	A75	28.0	*MEF2D-HNRNPUL1*	11.97	NA	no	Pre-B	-	+	0	0
	F014	34.4	*MEF2D-HNRNPUL1*	2.2	Fail	no	Pre-B	NA	NA	1	1
	F041	37.0	*MEF2D-HNRNPUL1*	4.9	Fail	no	Pre-B	-	-	1	1
	F280	33.3	*MEF2D-HNRNPUL1*	7	Fail	no	Pre-B	-	-	0	0
	F304	56.5	*MEF2D-HNRNPUL1*	16.2	46;XY;9q+[1]/46;XY[2]/[8]	no	Pre-B	-	-	0	0
	C08	15.1	*MEF2D-HNRNPUL1*	6.82	46,XX	no	Pre-B	-	+	1	1
	F158	12.1	*MEF2D-HNRNPUL1*	49.5	46,XY,-5,add(9)(p22),-17,+2M	*BCR-ABL1*	Pre-B	NA	NA	1	1
	F177	9.0	*MEF2D-HNRNPUL1*	6	47,XX,+8[2]/46,XX,+8,-19[2]/[9]	no	NA	NA	NA	0	0
	F013	27.4	*MEF2D-SS18*	28.1	42-47,XY,1q-,+M1-M2[cp8]/46,XY[1]/[9]	no	Pre-B	-	-	0	0
	C93	4.9	*MEF2D-SS18*	11	46,XX,+X,t(1;18)(q21;q11.2),del(9)(p22),der(9,10)(q10;q10)[15]/45,XX,t(1;18)(q21;q11.2),t(2;5)(q37;q13),der(9)(p22),der(9;11)(q10;q10)[5]	no	Pre-B	-	-	0	0

A74	22.7	*MEF2D-DAZAP1*	14.03	46,XY,t(1;19)(q23;p13)[10]	no	Pre-B	-	-	1	1

Table S8. Presenting clinical characteristics and outcome of patients with two *MEF2D* and *ZNF384* fusions

*12 patients with available data were included in survival analysis.

		***MEF2D* fusions**		***ZNF384* fusions**	
		Adult	**Pediatric**	**Adult**	**Pediatric**
Number		12	7	13	8
Age at diagnosis (year)					
	Median	33.25	12.1	23.7	4.55
	Range	19.3-59.1	4.7-15.6	18.2-56.3	2.2-14.6
Gender, no. (%)					
	Male	6(50.0%)	3(42.9%)	6(46.2%)	4(50.0%)
	Female	6(50.0%)	4(57.1%)	7(53.8%)	4(50.0%)
WBC count at diagnosis ($\times 10^9$/L)					
	Median	13	10.3	11.5	41.4
	Range	2.2-203.7	6.0-49.5	2.23-77.98	3.6-104.0
% 5-year survival (±SE)		15.6±14.2	33.3±19.2	38.6±28.2*	75.0±21.7

Table S9. Top 864 genes used for unsupervised clustering

FSCN1
CD109
ECM1
TSPAN7
EMP1
BAALC
SOCS2
NPR1
CYGB
CD34
KCNK12
NRXN2
CRLF2
LCN10
LCN6
STK32B
BCL6B
PPP2R2C
COL5A1
NOS2
PEAR1
NRXN3
PCLO
BMP2
PRX
TMEM236
MYO1B
DAB2
POU4F1
TSPAN15
CDC42BPB
CAMSAP2
HS6ST2
STC2
ZNF462
SNX7
PDGFA
SLITRK4
BDKRB2
ITPRIPL2
C3orf56
MARCKS
LPCAT2
H2AFY2
TSKS
TRH
NLRP2
RNF165
ASB9
INHBB
NGFR
PLCH1
EPHA7
CREG2
FAM69C
C18orf63
CADPS
CSF3R
ST3GAL6
CLEC4E
PTPRK
PTPRB
BEST3
VWA5B2
NKAIN4
CDH4
RNF217
FBN2
PID1
SLC8A3
PSD2
KIAA1324L
ITGA9
HTRA3
MDGA1
TRDV2
L3MBTL4
NMD3P1
ABHD12B
NPTX1
MPPED2
TGFA
SPATA6
HOXA1
HOXA2
COL24A1
PTPRM
ARHGAP24
CLEC12A
CLEC1B
IL8
CXCL2
CXCL3
SPG20
VNN1
CEBPA
RPH3AL
RGS16
CCNA1
GATA3
AQP9
SERPINB2
PTGS2
G0S2
CYBB
TLR7
CLECL1
SPI1
ROPN1L
MS4A6A
CD248
VWA1
LRRC38
WDR86
PRR15
PAWR
FERM1
TPBG
C1orf115
MFI2
RORB
CRYM
KCNJ12
SYNPO
MYBPH
KIF12
LAMA5
ITGA8
ASIC2
SH3BP4
COL27A1
GPR125
PARD3
ARPP21
RASAL2
HMX2
IGHJ3P
IGHJ5
IGHJ4
ARHGAP29
NXN
ADAM33
DMD
FAM47A
ANKRD30B
SOX11
SORBS2
VWC2
ADAMS7
PRKCZ

S100A16
GIPC3
ITGA6
UACA
CCND2
NPDC1
EGFL7
MAMLD1
PRDM8
SLC45A3
OLFML2A
STAB1
PVRL2
AIF1L
ROBO4
CYTL1
CMM2
KIAA1462
MRC1L1
MRC1
FKBP9
CNN2P6
ANTXR1
STOX2
PDZRN3
LAMB2
GPC6
IL6R
FUT7
RBM47
IL13RA1
FAM101B
CECR6
TPO
DPEP1
SMAD1
PLEKHG1
MARK2P11
MMP17
ZBTB46
TMPRSS15
C1orf226
CDKN2A
TCAM1P
DAPK1
EGF
TXNRD3
MN1
CD33
GPR162
CALN1
EHD2
IFI44L
ZSCAN23
SHANK3
ACR
SCHIP1
EFNA1
MSR1
S100Z
EPHA2
GPR110
BMPR1B
UNC5C
RASSF8
NRP1
SYDE1
FLT4
GNG11
FZD8
STARD13
SPATS2L
THBS1
ENPP2
IL2RA
ZFPM2
VWA2
WNT9A
CA6
CCL17
IGJ
ENAM
MUC4
GLI2
ECEL1
ABCA9
LDB3
GGT5
SLCO2B1
COL6A3
PTPN14
SPSB4
CFH
CYYR1
KLRF2
SCN2A
CELSR1
NPY
BVES
NOV
PACSIN1
ST14
SYNM
PON2
PDK4
CPVL
SH3BP5
KIAA1211L
CD1C
MS4A1
NLGN4X
SPRY4
CHST3
GABRD
UTS2
GTSF1
PAX8
TMEM100
OR7A5
MUS1
EFEMP1
EDNRB
CAV1
SHISA2
ATP8A2
PLD1
PP13439
CAP2
RBM24
IGF2BP2
C3orf65
AREG
LY6H
HDGFRP3
ARHGAP32
ZNF667
TUSC1
IGFBP2
ZNF135
ZNF112
ZNF662
TRO
DCHS1
SEMA3F
IRX1
SLC32A1
TSHZ3
EBF4
GPR17
LOXHD1
DSG2
CLGN
SLITRK5
PRRG1
PCDHB14
PCDHB13
RAG1
BLACE
CTGF
HRK
LGR5
HERC2P4
PEG10
SGCE
TCL1B
CEBPE
DACH1
OR5E1P
OR5P3
OR10AB1P
OR5P1P
OR5P4P
CYB5R2
OVCH2
LMK3
CLIC5
KCNN1
BIRC7
HAP1
ARHGEF4
KIF26B
NKAIN1
RIMBP2
GBA3
MYOCD
TUSC3
ACVR1C
SEMA3D
DSC2
AJAP1
IRX3
LPHN3
DSC3
IGF2BP1
NOVA1
ARHGAP42P5
ARHGAP42P4
KLF15
ANO1
RAB6C
KCNJ16
CREB3L3
PRKCG
BAMBI
NTRK1
BHLHE23
XIRP1
TSPAN3
FTO
SLC39A10
SYK
IKZF1
RFX5
PYCR2
CHRNB4
RANBP3L
MMP14
LCN8
MYBPC2
GSTM1
GSTM5
SCN3A
RBMS3
BTNL9
CACNA1H
HEY2
EVA1A
C1QTNF4
GREM1
CLEC14A
SDC2
XIST
GSTT1
PRSS21
PPAPDC3
DKFZP434E1119
RPL41P1
RPS23P8
MRNR2L9
M1E
M1G
M1X
AGAP1
PTGFRN
OBSL1
RBFOX2
ADAMS1
FAM150B
CCDC80
ID4
EPB41L3
COL4A1
COL4A2
ALDH1A1
GNG12
CHRDL1
LIFR
FSTL1
WLS
LAPTM4B
DOCK1
CDC42BPA
NGFRAP1
IGFBP5
DCN
ADAMS9
PCDH17
IGF2
MAP3K5
PTH1R
PALLD
ANKRD27
RGS9BP
SMAD9
RHOBTB3
HSPD1P11
NMNAT3
SPATA9
MAP7
MEIS1
PLA2G4A
HOXA10
HOXA9
HOXA7
HOXA5
HOXA3
TCTN1
SLC12A8
CAMK2B
SLC6A13
TSGA10
ACSM4
KLRK1
NPTX2
CSPG4
ODF3L1
SPATA12
NPR3
C1orf186
TDRD9
ATP9A
SALL4
CDH11
TTC28
SPP1
TFPI
PCDH10
DOCK6
TPTEP1
PTPRD
ST18
MECOM
C1orf173
XKR3
EDIL3
PDE1A
NR4A1
NR4A2
NR4A3
CXXC11
NEU4
LRRC32
FOSL2
ABHD17C
EGR1
EGR3
HCAR2
LIF
CCL3L1
MYRIP
TIFAB
SLC12A3
RGS18
TFEC
RAB44
SIGLEC12
VCAN
LGALS2
SIGLEC1
HDAC9
CPED1
DCHS2
C12orf77
HECW1
SLC27A2
SPAG6
NCKAP5
PPM1E
DCLK2
ILDR2
IRF4
FGF9
DUSP4
BCL6
FCRLA
C16orf74
VAT1L
LAMP5
RNF152
INSM1
CPNE8
CRISPLD1
ROR1
KCNK9
DFNA5
MYO3A
IKZF3
ABCB4
ZAP70
FCRL1
MYEF2
PTCH1
MYT1L
HAR1A
HAR1B
IRX2
C5orf38
LAMA3
SLIT2
MYO10
CUX2
TRIM72
KSR2
NELL1
NAV2
PROX1
NLGN4Y
HCG22
TEX41
ADAMS18
ASTN1
BRINP2
CAMK4
KCNMA1
SDC1
KCNJ2
LARP6
LDLRAD3
AR
SEMA6D
PCBP3
CSMD1
TCERG1L
TFAP2C
FBLN7
UNC5D
TACC2
EPHA3
EYA4
PRL
BASP1
GLT1D1
AFF2
PLXDC2
KIAA0125
KANK1
PIEZO2
CCDC149
KIAA1211
MS4A2
MERTK
CPAMD8
F2RL3
TMEM63C
LRRC15
CPN2
GP5
FBLN1
CAMK2D
ST6GALNAC3
FAM19A1
TSPYL5
NETO1
PTP4A3
ELFN1
NRN1
DLGAP2
MDGA2
DAB2IP
PTPRG
KLF4
EFNB2
RGMA
CRMP1
SH3RF3
EVC
EVC2
AKAP12
FLT1
KCNS3
CALD1
PRR26
NOTCH3
ROBO1
SLC44A3
DTX1
RASAL1
BACH2
TCL6
LRRC14B
PLEKHG4B
PCDH9
FAM19A5
NUDT11
RHOBTB1
PKIA
FAM110C
CDH2
PLCB4
DAB1
KIAA1456
IGSF3
CACHD1
NINL
ELOVL2
NKAIN3

HGF	*KCNE3*	*EPHB3*	*FGFR1*	*TNR*	*MMP15*	*AKR1C6P*	*COL3A1*	*RNF220*	*DLL1*	*MAP2*	*HPGD*	*PHLDB2*	*VANGL2*
RFX8	*NR3C2*	*KLF11*	*KHDRBS3*	*NTNG1*	*TRNP1*	*F13A1*	*CXCL12*	*SKIDA1*	*ST8SIA5*	*VIPR2*	*ADAM23*	*RAPGEF5*	*FAM171A1*
EMID1	*SPON1*	*SCML1*	*MLLT4*	*NOL4*	*TRPM4*	*XKR4*	*VCAM1*	*GPR85*	*SNAI1*	*FOXO6*	*OSR2*	*PHGDH*	*CECR2*
LHX6	*SEMA6A*	*LDOC1*	*KIRREL*	*ADARB2*	*CCNJL*	*SBF1P1*	*CD5L*	*LPAR3*	*GJB2*	*APBB2*	*MAGI1*	*SLC7A3*	*TCF3*
PALM	*MMP28*	*CDR1*	*SLC16A2*	*THSD7A*	*KCNK3*	*NBPF13P*	*CYP1B1*	*SLC34A2*	*SRGN*	*FAT1*	*CPXM2*	*SOGA2*	*TCL1A*
PRSS57	*ARHGEF17*	*PCDH18*	*JPH1*	*EVPL*	*SDK1*	*HHIP*	*LPL*	*DTNA*	*QPCT*	*NRG3*	*DGKI*	*ITIH3*	*VPREB3*
PLVAP	*NPAP1P6*	*VPREB1*	*NT5E*	*PRAME*	*KIAA1644*	*RASSF10*	*IGFBP3*	*CNN3*	*CEBPB*	*BEND4*	*PTPRZ1*	*KLHL33*	*IGLL1*
FXYD6	*PTGDR*	*UGT3A2*	*NTSR1*	*IGF2BP3*	*UNC79*	*ATP1A3*	*CHL1*	*POMC*	*C19orf59*	*CNR1*	*HUNK*	*SHROOM3*	*PAX5*
ZC3H12C	*B4GALNT4*	*GPR173*	*MDFI*	*FSTL5*	*TP63*	*KCNQ5*	*ENPEP*	*HES1*	*GJB6*	*ADAMS12*	*AADAT*	*TMEM136*	*EBF1*
CCDC26	*GPA33*	*ZNF516*	*MME*	*TBC1D9*	*CPT1C*	*TMEM121*	*PPBP*	*CDYL2*	*MPO*	*IGHM*	*ANKS1B*	*ZNF711*	*SH2D4B*
DDO	*DUSP27*	*DDIT4L*	*ELFN2*	*MRVI1*	*HS3ST4*	*SERINC2*	*PF4*	*AGAP3*	*PADI2*	*IGLL5*	*PHACTR3*	*TMSB15A*	*LRRC3B*
FLT3	*SYNDIG1*	*KCNK17*	*RAI14*	*WDFY3*	*C1orf222*	*NKD2*	*SDPR*	*TMCC3*	*CEACAM6*	*NYNRIN*	*CHST6*	*SGCB*	*COBL*
PCDHGC3	*SCN4A*	*NEGR1*	*DUSP26*	*SIGLEC15*	*LAMB4*	*CLEC11A*	*VLDLR*	*CREB5*	*FCN1*	*NFATC4*	*NLGN1*	*TENM4*	*MYO18B*
CSPG4P13	*FZD6*	*LHFP*	*ID3*	*ACKR3*	*PEG3*	*WT1*	*KLHL13*	*ZBTB16*	*HK3*	*SYT1*	*WNT16*	*C14orf132*	*MKRN3*
LPAR4	*CTHRC1*	*SNAP91*	*RASIP1*	*ALOX5*	*IGSF10*	*GPR176*	*PPM1H*	*F3*	*SERPINA1*	*AFAP1L1*	*CACNG4*	*GJC1*	*GRIN1*
PROM1	*MMRN1*	*P2RY14*	*FRG2C*	*OR13A1*	*ADAMS16*	*LRFN2*	*COL9A3*	*RGS2*	*FPR1*	*LRP4*	*PBX1*	*ATRNL1*	*LRRC26*
EFCC1	*TM4SF1*	*KCNA5*	*FGF6*	*BMP3*	*SEMA5B*	*APBA1*	*FOXL1*	*RGS1*	*IL1RN*	*TEAD4*	*ZNF385D*	*GLI3*	*ESAM*

Table S10. Mutations of the genes identified in validation group by targeted deep sequencing

*Based on UCSC hg19 reference

Gene	Sample	Age	Amino.Acid. Change	Mutation.Type	Chr	Start.	End.	Reference.Allele	Variant.Allele
MLL2	F234	3.1	p.E1072K	Missense	chr12	49444157	49444157	C	T
MLL2	F229	4.6	p.S3708R	Missense	chr12	49427364	49427364	G	C
MLL2	F365	6.8	p.P2502L	Missense	chr12	49434048	49434048	G	A
MLL2	F318	15.4	p.P3291fs	Frame_Shift_Del	chr12	49431256	49431267	TGGCCTGGGCAG	T
MLL2	F215	17.8	p.E4670fs	Frame_Shift_Ins	chr12	49423251	49423251	C	CCAACCCGGCACGCCCTGGGG
MLL2	F326	18.1	p.P2153fs	Frame_Shift_Ins	chr12	49435095	49435095	G	GGGGGA
MLL2	F348	19.3	p.P4031fs	Frame_Shift_Ins	chr12	49426397	49426397	G	GA
MLL2	F298	21.3	p.T1974M	Missense	chr12	49436060	49436060	G	A
MLL2	F366	23.4	p.A963T	Missense	chr12	49444484	49444484	C	T

MLL2	F124	38.7	p.F2739fs	Frame_Shift_Ins	chr12	49433232	49433232	A	AG
MLL2	F343	38.1	p.K2548E	Missense	chr12	49433911	49433911	T	C
MLL2	F088	50	p.L4532fs	Frame_Shift_Ins	chr12	49424751	49424751	C	CAGGA
MLL2	F328	56.3	p.E5484fs	Frame_Shift_Del	chr12	49415887	49415895	GTCACGACT	G
MLL2	F328	56.3	p.I1300fs	Frame_Shift_Ins	chr12	49443472	49443472	A	AT
SETD2	F360	2.8	p.H216D	Missense	chr3	47165480	47165480	G	C
SETD2	F371	2.4	p.C575S	Missense	chr3	47164402	47164402	C	G
SETD2	F230	4.3	p.S820P	Missense	chr3	47163668	47163668	A	G
SETD2	F347	5.1	p.P2057fs	Frame_Shift_Ins	chr3	47103775	47103775	A	ATCCC
SETD2	F126	6.3	p.M45V	Missense	chr3	47165993	47165993	T	C
SETD2	F313	7.3	p.R400Q	Missense	chr3	47164927	47164927	C	T
SETD2	F296	8.8	p.S1572_splice	Splice_Site	chr3	47155363	47155363	T	TAGGCGGGC
SETD2	F017	13.1	p.V2022A	Missense	chr3	47108604	47108604	A	G
SETD2	F187	13.2	p.S676F	Missense	chr3	47164099	47164099	G	A
SETD2	F210	19.5	p.C2524fs	Frame_Shift_Del	chr3	47058703	47058708	CTTACA	C
SETD2	F369	19.7	p.S1350P	Missense	chr3	47162078	47162078	A	G
SETD2	F298	21.3	p.R2077_	Nonsense	chr3	47103717	47103717	G	A
SETD2	F321	26.2	p.N2058fs	Frame_Shift_Ins	chr3	47103774	47103774	T	TG
SETD2	F312	29.7	p.S689fs	Frame_Shift_Ins	chr3	47164060	47164060	G	GACCA
SETD2	F118	49.7	p.N2394K	Missense	chr3	47084107	47084107	G	T
NRAS	F371	2.4	p.G13D	Missense	chr1	115258744	115258744	C	T
NRAS	F273	3.4	p.F156L	Missense	chr1	115251260	115251260	A	G
NRAS	F259	3.4	p.G13D	Missense	chr1	115258744	115258744	C	T
NRAS	F275	4	p.G12D	Missense	chr1	115258747	115258747	C	T
NRAS	F242	4.9	p.G13D	Missense	chr1	115258744	115258744	C	T
NRAS	F303	4.8	p.G12S	Missense	chr1	115258748	115258748	C	T
NRAS	F126	6.3	p.G12S	Missense	chr1	115258748	115258748	C	T
NRAS	F176	7.3	p.G12D	Missense	chr1	115258747	115258747	C	T
NRAS	F313	7.3	p.G12D	Missense	chr1	115258747	115258747	C	T
NRAS	F138	9.4	p.G12C	Missense	chr1	115258748	115258748	C	A
NRAS	F187	13.2	p.G12S	Missense	chr1	115258748	115258748	C	T
NRAS	F010	14.9	p.G12D	Missense	chr1	115258747	115258747	C	T
NRAS	F318	15.4	p.G12C	Missense	chr1	115258748	115258748	C	A

NRAS	F019	18.9	p.G12D	Missense	chr1	115258747	115258747	C	T
NRAS	F345	19.7	p.G13R	Missense	chr1	115258745	115258745	C	G
NRAS	F348	19.3	p.G12C	Missense	chr1	115258748	115258748	C	A
NRAS	F004	20.7	p.G12D	Missense	chr1	115258747	115258747	C	T
NRAS	F013	27.4	p.G12S	Missense	chr1	115258748	115258748	C	T
NRAS	F335	54.4	p.G12D	Missense	chr1	115258747	115258747	C	T
NRAS	F339	55.1	p.G13D	Missense	chr1	115258744	115258744	C	T
NRAS	F339	55.1	p.G12D	Missense	chr1	115258747	115258747	C	T
FLT3	F238	1.3	p.L576P	Missense	chr13	28608329	28608329	A	G
FLT3	F225	1.4	p.T682I	Missense	chr13	28602323	28602323	G	A
FLT3	F226	2.5	p.582_583insPTT	In_Frame_Ins	chr13	28608309	28608309	C	CGGTGGTAGG
FLT3	F226	2.5	p.Y572H	Missense	chr13	28608342	28608342	A	G
FLT3	F236	4.1	p.S941L	Missense	chr13	28588626	28588626	G	A
FLT3	F255	4.8	p.Y842C	Missense	chr13	28592620	28592620	T	C
FLT3	F287	5.8	p.N676K	Missense	chr13	28602340	28602340	G	T
FLT3	F310	11	p.A680V	Missense	chr13	28602329	28602329	G	A
FLT3	F129	10.1	p.I836del	In_Frame_Del	chr13	28592634	28592637	CATG	C
FLT3	F038	14.6	p.576_578LQM>RG	In_Frame_Del	chr13	28608323	28608329	ATCTGTA	CCCC
FLT3	F038	14.6	p.Q577del	In_Frame_Del	chr13	28608325	28608328	CTGT	C
FLT3	F369	19.7	p.V579G	Missense	chr13	28608320	28608320	A	C
FLT3	F211	21.7	p.E573G	Missense	chr13	28608338	28608338	T	C
FLT3	F121	36.7	p.R230W	Missense	chr13	28624286	28624286	T	A
FLT3	F299	46	p.Y842N	Missense	chr13	28592621	28592621	A	T
FLT3	F346	54.7	p.590_591insP	In_Frame_Ins	chr13	28608285	28608285	A	GGGG
FLT3	F346	54.7	p.590_591insP	In_Frame_Ins	chr13	28608285	28608285	A	AGGG
FLT3	F097	57.8	p.Y572C	Missense	chr13	28608341	28608341	T	C
FLT3	F102	61.6	p.T242S	Missense	chr13	28624249	28624249	G	C
PAX5	F283	2.1	p.D2E	Missense	chr9	37034023	37034023	A	T
PAX5	F166	6.4	p.D2E	Missense	chr9	37034023	37034023	A	T
PAX5	F136	7.6	p.K196_	Nonsense	chr9	37002663	37002663	T	A
PAX5	F163	11.8	p.P215fs	Frame_Shift_Ins	chr9	36966682	36966682	G	GC
PAX5	F019	18.9	p.P80R	Missense	chr9	37015165	37015165	G	C
PAX5	F067	19.1	p.R140L	Missense	chr9	37006526	37006526	C	A

PAX5	F067	19.1	p.R38H	Missense	chr9	37020732	37020732	C	T
PAX5	F312	29.7	p.N195fs	Frame_Shift_Ins	chr9	37002666	37002666	T	TA
PAX5	F076	38.1	p.D2E	Missense	chr9	37034023	37034023	A	T
PAX5	F023	44.8	p.R140Q	Missense	chr9	37006526	37006526	C	T
PAX5	F023	44.8	p.P32L	Missense	chr9	37020750	37020750	G	A
PAX5	F118	49.7	p.P80R	Missense	chr9	37015165	37015165	G	C
PAX5	F088	50	p.K222_	Nonsense	chr9	36966662	36966662	T	A
PAX5	F208	56	p.G183S	Missense	chr9	37002702	37002702	C	T
PAX5	F292	59.5	p.D2E	Missense	chr9	37034023	37034023	A	T
CREBBP	F227	2.9	p.R1446H	Missense	chr16	3788617	3788617	C	T
CREBBP	F232	2.2	p.Q1491K	Missense	chr16	3786740	3786740	G	T
CREBBP	F274	4.6	p.S1680del	Missense	chr16	3781323	3781326	AAGG	A
CREBBP	F373	6.1	p.2202_2207QQQQQQ>Q	In_Frame_Del	chr16	3778427	3778442	TTGCTGCTGCTGTTGC	T
CREBBP	F157	11.5	p.1433_1434insP	In_Frame_Ins	chr16	3788653	3788653	A	AGAG
CREBBP	F102	61.6	p.E1040K	Missense	chr16	3817853	3817853	C	T
NF1	F259	3.4	p.R385C	Missense	chr17	29528145	29528145	C	T
NF1	F277	4.8	p.M645V	Missense	chr17	29552200	29552200	A	G
NF1	F177	9	p.M645V	Missense	chr17	29552200	29552200	A	G
NF1	F002	14.6	p.P1548fs	Frame_Shift_Ins	chr17	29588795	29588795	T	TTGAGG
NF1	F318	15.4	p.L2623_splice	Splice_Site	chr17	29684110	29684110	T	G
NF1	F322	19	p.M645V	Missense	chr17	29552200	29552200	A	G
NF1	F109	26.4	p.F154fs	Frame_Shift_Ins	chr17	29490377	29490377	T	TAGACTTCC
NF1	F321	26.2	p.R69_splice	Splice_Site	chr17	29486026	29486032	TTAGAGA	CCTAGGGGG
NF1	F280	33.3	p.M645V	Missense	chr17	29552200	29552200	A	G
NF1	F037	38.9	p.M645V	Missense	chr17	29552200	29552200	A	G
NF1	F297	54.8	p.M645V	Missense	chr17	29552200	29552200	A	G
NF1	F103	61.5	p.V2148fs	Frame_Shift_Del	chr17	29664400	29664401	GT	G
KRAS	F283	2.1	p.G13D	Missense	chr12	25398281	25398281	C	T
KRAS	F232	2.2	p.G12D	Missense	chr12	25398284	25398284	C	T
KRAS	F274	4.6	p.G12V	Missense	chr12	25398284	25398284	C	A
KRAS	F277	4.8	p.G12R	Missense	chr12	25398285	25398285	C	G
KRAS	F174	6.8	p.G13D	Missense	chr12	25398281	25398281	C	T
KRAS	F373	6.1	p.L23R	Missense	chr12	25398251	25398251	A	C

KRAS	F369	19.7	p.G12V	Missense	chr12	25398284	25398284	C	A
KRAS	F067	19.1	p.G12V	Missense	chr12	25398284	25398284	C	A
KRAS	F035	30.5	p.G12D	Missense	chr12	25398284	25398284	C	T
KRAS	F354	34.1	p.65_65S>RPG	In_Frame_Ins	chr12	25380263	25380263	A	ACCCGGC
KRAS	F023	44.8	p.Q61L	Missense	chr12	25380276	25380276	T	A
KRAS	F118	49.7	p.G12V	Missense	chr12	25398284	25398284	C	A
PTPN11	F230	4.3	p.D373E	Missense	chr12	112919904	112919904	T	G
PTPN11	F248	4.2	p.E76K	Missense	chr12	112888210	112888210	G	A
PTPN11	F285	4.7	p.P491H	Missense	chr12	112926852	112926852	C	A
PTPN11	F255	4.8	p.G60R	Missense	chr12	112888162	112888162	G	C
PTPN11	F286	5.4	p.E76G	Missense	chr12	112888211	112888211	A	G
PTPN11	F224	5.3	p.E76A	Missense	chr12	112888211	112888211	A	C
PTPN11	F382	11.7	p.E69K	Missense	chr12	112888189	112888189	G	A
PTPN11	F181	13.8	p.A72D	Missense	chr12	112888199	112888199	C	A
PTPN11	F078	16.9	p.D61H	Missense	chr12	112888165	112888165	G	C
PTPN11	F078	16.9	p.T468M	Missense	chr12	112926270	112926270	C	T
ASXL1	F275	4	p.R1051C	Missense	chr20	31023666	31023666	C	T
ASXL1	F078	16.9	p.E553fs	Frame_Shift_Ins	chr20	31021659	31021659	A	AGGCG
ASXL1	F109	26.4	p.A158V	Missense	chr20	31017142	31017142	C	T
ASXL1	F308	33.3	p.D954fs	Frame_Shift_Ins	chr20	31023376	31023376	A	ACTCC
ASXL1	F308	33.3	p.T600fs	Frame_Shift_Ins	chr20	31022315	31022315	C	CCGGGG
ASXL1	F336	45.8	p.R1224T	Missense	chr20	31024186	31024186	G	C
RUNX1	F247	2.7	p.K90fs	Frame_Shift_Ins	chr21	36259142	36259142	T	TG
RUNX1	F168	6.6	p.M439L	Missense	chr21	36164479	36164479	T	A
RUNX1	F318	15.4	p.R244K	Missense	chr21	36171753	36171753	C	T
RUNX1	F323	26.7	p.G141R	Missense	chr21	36252860	36252860	C	T
RUNX1	F121	36.7	p.R142G	Missense	chr21	36252857	36252857	T	C
RUNX1	F317	48.3	p.S295_	Nonsense	chr21	36171600	36171600	G	C
RUNX1	F115	60.1	p.P398L	Missense	chr21	36164601	36164601	G	A
TP53	F164	12.2	p._394W	Missense	chr17	7572927	7572927	T	C
JAK2	F197	5.6	p.R683S	Missense	chr9	5078362	5078362	A	C
JAK2	F176	7.3	p._1133S	Nonstop_Mutation	chr9	5126790	5126790	G	C
JAK2	F296	8.8	p.V392M	Missense	chr9	5065000	5065000	G	A

JAK2	F310	11	p.V392M	Missense	chr9	5065000	5065000	G	A
JAK2	F290	18.1	p.T875N	Missense	chr9	5089726	5089726	C	A
JAK2	F312	29.7	p.F694L	Missense	chr9	5078395	5078395	C	G
MET	F232	2.2	p.L211W	Missense	chr7	116339770	116339770	T	G
MET	F255	4.8	p.R1148Q	Missense	chr7	116418932	116418932	G	A
MET	F286	5.4	p.V1287I	Missense	chr7	116435769	116435769	G	A
MET	F301	10.1	p.L211W	Missense	chr7	116339770	116339770	T	G
MET	F011	17.8	p.G500S	Missense	chr7	116380109	116380109	G	A
MET	F079	25.2	p.L211W	Missense	chr7	116339770	116339770	T	G
ETV6	F310	11	p.V166M	Missense	chr12	12022390	12022390	G	A
ETV6	F129	10.1	p.R181H	Missense	chr12	12022436	12022436	G	A
ETV6	F010	14.9	p.V166M	Missense	chr12	12022390	12022390	G	A
ETV6	F052	19	p.V166M	Missense	chr12	12022390	12022390	G	A
ETV6	F370	43.6	p.H119fs	Frame_Shift_Del	chr12	12006387	12006404	CATATTCTGAAGCAGAGG	C
GNB1	F242	4.9	p.G53E	Missense	chr1	1747240	1747240	C	T
GNB1	F279	22.8	p.I80T	Missense	chr1	1737942	1737942	A	G
GNB1	F109	26.4	p.118_119insP	In_Frame_Ins	chr1	1735934	1735934	A	AGGG
GNB1	F006	33.2	p.K89N	Missense	chr1	1737914	1737914	C	G
GNB1	F328	56.3	p.K89E	Missense	chr1	1737916	1737916	T	C
IKZF1	F248	4.2	p.C175_	Nonsense	chr7	50450341	50450341	C	A
IKZF1	F308	33.3	p.Q366_	Nonsense	chr7	50467861	50467861	C	T
IKZF1	F037	38.9	p.L117fs	Frame_Shift_Ins	chr7	50444421	50444421	A	ACCCC
IKZF1	F351	42.4	p.D186G	Missense	chr7	50450373	50450373	A	G
MYC	F230	4.3	p.Q10H	Missense	chr8	128748869	128748869	G	C
MYC	F230	4.3	p.E39D	Missense	chr8	128750625	128750625	G	C
MYC	F078	16.9	p.P60L	Missense	chr8	128750687	128750687	C	T
MYC	F309	46.3	p.F138S	Missense	chr8	128750921	128750921	T	C
MYC	F217	60.4	p.G88D	Missense	chr8	128750771	128750771	G	A
ZEB2	F263	5.3	p.1183_1184EE>E	In_Frame_Del	chr2	145147111	145147114	CTCT	C
ZEB2	F224	5.3	p.Q3H	Missense	chr2	145274909	145274909	C	G
ZEB2	F345	19.7	p.H1038R	Missense	chr2	145147550	145147550	T	C
ZEB2	F089	56.4	p.P498S	Missense	chr2	145157262	145157262	G	A
ZEB2	F304	56.5	p.1183_1184EE>E	In_Frame_Del	chr2	145147111	145147114	CTCT	C

EZH2	F067	19.1	p.Y663C	Missense	chr7	148507466	148507466	T	C
EZH2	F086	50.1	p.R690H	Missense	chr7	148506443	148506443	C	T
EZH2	F088	50	p.F290fs	Frame_Shift_Ins	chr7	148523584	148523584	A	ACT
INSRR	F176	7.3	p.A224E	Missense	chr1	156821950	156821950	G	T
INSRR	F195	13.1	p.C246Y	Missense	chr1	156821884	156821884	C	T
INSRR	F006	33.2	p.G677R	Missense	chr1	156815556	156815556	C	T
INSRR	F037	38.9	p.R140H	Missense	chr1	156823762	156823762	C	T
TET2	F148	5.5	p.R550Q	Missense	chr4	106156748	106156748	G	A
ERBB4	F365	6.8	p.R979Q	Missense	chr2	212286760	212286760	C	T
ERBB4	F163	11.8	p.Y53C	Missense	chr2	212989553	212989553	T	C
ERBB4	F072	15.8	p.D1257H	Missense	chr2	212248498	212248498	C	G
JAK1	F236	4.1	p.R506C	Missense	chr1	65321324	65321324	G	A
JAK1	F307	18.4	p.V658I	Missense	chr1	65312347	65312347	C	T
JAK1	F366	23.4	p.V658F	Missense	chr1	65312347	65312347	C	A
P4HA2	F232	2.2	p.R435M	Missense	chr5	131534573	131534573	C	A
P4HA2	F181	13.8	p.Q140R	Missense	chr5	131549659	131549659	T	C
P4HA2	F369	19.7	p.R367H	Missense	chr5	131539826	131539826	C	T
UBA2	F038	14.6	p.W217_	Nonsense	chr19	34935905	34935905	G	A
UBA2	F050	14.6	p.H332fs	Frame_Shift_Ins	chr19	34943008	34943009	CA	GCCTGG
UBA2	F035	30.5	p.I263V	Missense	chr19	34941185	34941185	A	G
XBP1	F228	4	p.A249V	Missense	chr22	29191548	29191548	G	A
XBP1	F263	5.3	p.V127L	Missense	chr22	29193139	29193139	C	A
XBP1	F118	49.7	p.G184S	Missense	chr22	29192058	29192058	C	T
JAK3	F343	38.1	p.M566V	Missense	chr19	17948746	17948746	T	C
JAK3	F311	63.4	p.V722I	Missense	chr19	17945696	17945696	C	T
PROKR1	F010	14.9	p.R89C	Missense	chr2	68873218	68873218	C	T
PROKR1	F079	25.2	p.G77S	Missense	chr2	68873182	68873182	G	A
BTG1	F093	54.8	p.103_103T>MS	In_Frame_Ins	chr12	92538064	92538064	G	GACA
CD3EAP	F103	61.5	p.R59W	Missense	chr19	45911401	45911401	C	T
CLDN22	F292	59.5	p.S110R	Missense	chr4	184241042	184241042	A	C
CXCR7	F296	8.8	p.T79M	Missense	chr2	237489344	237489344	C	T
EBF1	F004	20.7	p.R242Q	Missense	chr5	158250237	158250237	C	T
EVI5L	F323	26.7	p.R629H	Missense	chr19	7927392	7927392	G	A

RB1	F279	22.8	p.I422fs	Frame_Shift_Del	chr13	48951102	48951110	ATAGGATAC	CGGG
SLC22A6	F190	8.6	p.S195L	Missense	chr11	62751053	62751053	G	A

Table S11. Frequencies of key fusions and mutations of genes screened in the large cohort*

*A total of 383 patients (179 adults and 204 children) were investigated.

	Total		Adults		Children		
Gene	**Number**	**Frequency (%)**	**Number**	**Frequency (%)**	**Number**	**Frequency (%)**	***P* value**
BCR-ABL1	73	19.1	49	27.4	24	11.8	<0.001
ETV6-RUNX1	36	9.4	1	0.6	35	17.2	<0.001
TCF3-PBX1	21	5.5	9	5	12	5.9	0.71
MLL rearranged	18	4.7	12	6.7	6	2.9	0.08
MEF2D fusions	19	5.1	12	6.8	7	3.5	0.15
ZNF384 fusions	21	5.6	13	7.3	8	4	0.16
NRAS	46	12	16	8.9	30	14.7	0.08
FLT3	28	7.3	13	7.3	15	7.4	0.97
MLL2	27	7	18	10.1	9	4.4	0.03
KRAS	27	7	11	6.1	16	7.8	0.52
PAX5	27	7	17	9.5	10	4.9	0.08
SETD2	25	6.5	13	7.3	12	5.9	0.59
PTPN11	18	4.7	4	2.2	14	6.9	0.03
NF1	17	4.4	11	6.1	6	2.9	0.13
RUNX1	13	3.4	9	5	4	2	0.1
CREBBP	11	2.9	4	2.2	7	3.4	0.48
GNB1	9	2.3	6	3.4	3	1.5	0.32
MET	9	2.3	2	1.1	7	3.4	0.18
ZEB2	9	2.3	5	2.8	4	2	0.74
ETV6	9	2.3	4	2.2	5	2.5	1
ASXL1	8	2.1	6	3.4	2	1	0.15
JAK2	8	2.1	4	2.2	4	2	1
IKZF1	8	2.1	7	3.9	1	0.5	0.03

EZH2	7	1.8	6	3.4	1	0.5	0.05
MYC	7	1.8	5	2.8	2	1	0.26
UBA2	7	1.8	1	0.6	6	2.9	0.13
INSRR	6	1.6	3	1.7	3	1.5	1
ERBB4	6	1.6	2	1.1	4	2	0.69
XBP1	6	1.6	4	2.2	2	1	0.42
P4HA2	5	1.3	2	1.1	3	1.5	1
JAK3	4	1	4	2.2	0	0	0.047
JAK1	4	1	2	1.1	2	1	1
PROKR1	4	1	2	1.1	2	1	1
EVI5L	4	1	1	0.6	3	1.5	0.63
TP53	4	1	2	1.1	2	1	1
RIT1	3	0.8	2	1.1	1	0.5	0.6
CXCR7	3	0.8	1	0.6	2	1	1
BTG1	3	0.8	1	0.6	2	1	1
RB1	3	0.8	1	0.6	2	1	1
CLDN22	3	0.8	2	1.1	1	0.5	0.6
SLC22A6	3	0.8	1	0.6	2	1	1
CD3EAP	3	0.8	1	0.6	2	1	1
KDM5C	2	0.5	1	0.6	1	0.5	1
TET2	2	0.5	1	0.6	1	0.5	1
HIST1H2AG	2	0.5	0	0	2	1	0.5
GPR137C	2	0.5	1	0.6	1	0.5	1
IL1RAPL1	2	0.5	1	0.6	1	0.5	1
PDE1A	2	0.5	1	0.6	1	0.5	1
EBF1	2	0.5	2	1.1	0	0	0.22
PHF6	2	0.5	2	1.1	0	0	0.22
ST6GAL2	2	0.5	1	0.6	1	0.5	1
KCNV1	2	0.5	1	0.6	1	0.5	1
PABPC3	2	0.5	2	1.1	0	0	0.22
ADARB1	1	0.5	0	0	2	1	0.5

Table S12. Comparisons of outcome between adult and pediatric patients within each gene expression subgroup*

*The survival data was estimated in each gene expression subgroup. Patients without RNA-seq data were assigned to the cluster groups according to the dominant genetic subtypes. Thus, patients with *MEF2D* fusions were assigned to G1, *TCF3-PBX1* to G2, *ETV6-RUNX1* to G3, *ZNF384* fusions to G5, *MLL* rearranged to G7 and *BCR-ABL1* to G8.

Cluster subgroup	Dominant genetic subtype	Adult		Pediatric		*P* value
		No.	% 5-year OS (±SE)	No.	% 5-year OS (±SE)	
G1	*MEF2D* fusions	13	26.7±16.0	7	44.4±22.2	0.102
G2	*TCF3-PBX1*	9	60.0±18.2	12	100±0.0	0.035
G3	*ETV6-RUNX1*	1	-	32	100±0.0	-
G4	*ERG* deletion/*DUX4-IGH*	5	53.3±24.8	6	100±0.0	0.077
G5	*ZNF384* fusions	13	38.6±28.2	10	83.3±15.2	0.334
G6	Hyperdiploidy	1	-	20	100±0.0	-
G7	*MLL* rearranged	28	20.1±15.8	16	54.1±18.0	0.174
G8	*BCR-ABL1*	47	11.2±7.0	23	39.3±13.4	0.071
	BCR-ABL1-like	8	43.8±31.5	5	75.0±21.7	0.73
Overall	-	169	30.5±6.2	193	69.6±4.3	<0.001

Table S13. Comparisons of outcome between adult and pediatric patients within each genetic subtype

	Adult		Pediatric		*P* value
	No.	% 5-year OS (±SE)	No.	% 5-year OS (±SE)	
BCR-ABL1	48	15.2±7.5	23	39.3±13.4	0.114
BCR-ABL1-like	8	43.8±31.5	5	75.0±21.7	0.730
MLL rearranged	12	0±0.0	4	66.7±27.2	0.172
TCF3-PBX1	9	60.0±18.2	12	100±0.0	0.035
ETV6-RUNX1	1	-	31	100±0.0	-
ZNF384 fusions	12	38.6±28.2	8	75.0±21.7	0.552
MEF2D fusions	12	15.6±14.2	6	40.0±21.9	0.064
Hyperdiploidy>50	1	-	14	65.6±16.4	-
Hypodiploidy	12	0±0.0	4	66.7±27.2	0.070
others	54	51.2±8.1	86	67.3±6.5	0.003

Overall	169	30.5±6.2	193	69.6±4.3	<0.001

Table S14. Genes in pathway analysis

Gene	**Pathway**
BTG1	B-cell Development
EBF1	B-cell Development
ETV6	B-cell Development
IKZF1	B-cell Development
PAX5	B-cell Development
RUNX1	B-cell Development
XBP1	B-cell Development
VPREB1	B-cell Development
IRF8	B-cell Development
FOXP1	B-cell Development
TCF3	B-cell Development
IKZF3	B-cell Development
BCL11A	B-cell Development
IKZF2	B-cell Development
BCL2	B-cell Development
RAG1	B-cell Development
RAG2	B-cell Development
LEF1	B-cell Development
RB1	Cell cycle
TP53	Cell cycle
CDKN2A/2B	Cell cycle
ASXL1	Epigenetic
CREBBP	Epigenetic
EZH2	Epigenetic
HIST1H2AG	Epigenetic
KDM5C	Epigenetic
MLL2	Epigenetic

MYC	Epigenetic
PHF6	Epigenetic
SETD2	Epigenetic
TET2	Epigenetic
CHD4	Epigenetic
CHD2	Epigenetic
HDAC5	Epigenetic
NEK6	Epigenetic
PARP4	Epigenetic
PBRM1	Epigenetic
ASXL2	Epigenetic
TET3	Epigenetic
JMJD1C	Epigenetic
ATRX	Epigenetic
H3F3A	Epigenetic
ARID1A	Epigenetic
SMARCA4	Epigenetic
BCR-ABL1	Key fusions
TCF3-PBX1	Key fusions
MLL rearrangement	Key fusions
ETV6-RUNX1	Key fusions
MEF2D fusions	Key fusions
ZNF384 fusions	Key fusions
JAK1	JAK pathway
JAK2	JAK pathway
JAK3	JAK pathway
IL7R	JAK pathway
CXCR7	Other signaling
ERBB4	Other signaling
EVI5L	Other signaling
GNB1	Other signaling
GPR137C	Other signaling
IL1RAPL1	Other signaling

INSRR	Other signaling
MET	Other signaling
PDE1A	Other signaling
PROKR1	Other signaling
RIT1	Other signaling
ADARB1	Others
CD3EAP	Others
CLDN22	Others
KCNV1	Others
P4HA2	Others
PABPC3	Others
SLC22A6	Others
ST6GAL2	Others
UBA2	Others
ZEB2	Others
FLT3	RAS pathway
KRAS	RAS pathway
NF1	RAS pathway
NRAS	RAS pathway
PTPN11	RAS pathway
BRAF	RAS pathway

Table S15. Sequencing coverage metrics

*Patient ID+A:Tumor sample; Patient ID+C: Matched germline sample
†Based on 33 Mb RefSeq coding region

Platform	**Patient ID**[*]	**Reads Number**	**%Reads Mapped**	**Mean Depth of Coverage**[†]	**% Coding Exonic † (Whole Genome) bases covered**						
					≥1X	**≥4X**	**≥8X**	**≥10X**	**≥15X**	**≥20X**	**≥30X**
WES	A01A	99177130	88.6%	94.1	96.13%	91.20%	87.05%	85.25%	81.05%	77.16%	70.38%
WES	A01C	103309028	88.7%	97.2	96.08%	91.09%	86.83%	84.99%	80.70%	76.76%	69.99%
WES	A02A	100000124	88.8%	94.1	96.18%	91.06%	86.69%	84.77%	80.37%	76.41%	69.63%

WES	A02C	99897854	88.0%	92.0	95.56%	90.00%	85.23%	83.15%	78.40%	74.25%	67.34%
WES	A03A	111461616	79.1%	78.0	95.43%	89.59%	84.48%	82.21%	77.04%	72.51%	65.03%
WES	A03C	111772468	84.3%	88.5	95.87%	90.54%	85.95%	83.94%	79.30%	75.14%	68.06%
WES	A04A	100738948	87.0%	71.3	95.88%	89.76%	84.47%	82.13%	76.80%	72.13%	64.24%
WES	A04C	110765852	83.4%	91.4	95.04%	88.95%	83.66%	81.38%	76.36%	72.09%	65.25%
WES	A05A	107202278	72.3%	72.8	94.12%	87.12%	80.98%	78.33%	72.63%	67.95%	60.59%
WES	A05C	93566934	80.3%	72.7	95.26%	89.27%	84.02%	81.68%	76.28%	71.54%	63.64%
WES	A06A	109169678	74.8%	85.8	94.81%	88.66%	83.23%	80.86%	75.55%	71.09%	64.07%
WES	A06C	92974692	78.5%	77.9	95.01%	88.94%	83.51%	81.09%	75.62%	70.92%	63.46%
WES	A07A	104837958	86.7%	112.9	95.23%	89.74%	85.23%	83.28%	78.90%	75.08%	68.81%
WES	A07C	89017714	89.0%	104.6	95.62%	90.91%	86.68%	84.86%	80.61%	76.72%	70.06%
WES	A08A	104151082	87.8%	118.5	95.48%	89.69%	84.52%	82.32%	77.42%	73.25%	66.67%
WES	A08C	105364116	87.5%	124.9	95.57%	90.20%	85.49%	83.47%	78.93%	74.94%	68.53%
WES	A09A	96986036	88.7%	111.4	96.53%	92.17%	88.18%	86.42%	82.19%	78.12%	70.91%
WES	A09C	102807838	85.3%	96.9	93.83%	87.46%	81.72%	79.24%	73.92%	69.59%	62.94%
WES	A10A	79476300	85.1%	85.2	95.32%	90.54%	86.17%	84.24%	79.84%	75.76%	68.44%
WES	A10C	81157330	89.3%	89.4	95.06%	89.71%	84.85%	82.69%	77.70%	73.28%	66.09%
WES	A11A	81488006	86.2%	83.5	95.60%	90.99%	86.71%	84.76%	80.18%	75.80%	67.72%
WES	A11C	81399236	87.2%	83.2	95.68%	90.63%	86.06%	84.03%	79.28%	74.95%	67.38%
WES	A12A	150152088	98.7%	184.8	98.82%	98.20%	97.69%	97.45%	96.86%	96.24%	94.74%
WES	A12C	145226004	98.3%	173.0	98.83%	98.21%	97.72%	97.49%	96.91%	96.29%	94.82%
WES	A13A	62467344	90.1%	70.0	95.85%	90.33%	85.03%	82.63%	76.94%	71.80%	63.26%
WES	A13C	135020902	79.8%	120.6	98.19%	96.43%	94.56%	93.67%	91.32%	88.68%	82.55%
WES	A14A	62153662	88.9%	71.1	98.48%	96.83%	94.60%	93.31%	89.51%	85.05%	75.02%
WES	A14C	76527808	88.8%	80.0	98.53%	96.94%	94.89%	93.73%	90.37%	86.43%	77.53%
WES	A15A	70337612	90.8%	82.4	96.63%	91.17%	86.17%	83.98%	78.86%	74.26%	66.39%
WES	A15C	79819628	89.5%	91.6	96.31%	91.56%	87.20%	85.27%	80.71%	76.41%	68.88%
WES	A16A	137380870	90.8%	151.2	95.87%	92.70%	89.37%	87.94%	84.68%	81.69%	76.18%
WES	A16C	126546910	98.9%	158.4	98.81%	98.11%	97.51%	97.23%	96.49%	95.69%	93.77%
WES	A17A	92164030	88.8%	112.9	98.39%	96.86%	95.15%	94.22%	91.68%	88.89%	82.75%
WES	A17C	87126490	89.9%	109.0	98.40%	96.98%	95.45%	94.63%	92.32%	89.64%	83.57%
WES	A18A	105231710	88.8%	114.7	98.10%	96.38%	94.41%	93.41%	90.84%	88.16%	82.53%
WES	A18C	107518228	87.3%	119.2	98.07%	96.29%	94.31%	93.31%	90.72%	88.03%	82.43%

WES	A19A	102661926	89.7%	116.3	98.33%	96.84%	95.22%	94.39%	92.19%	89.84%	84.65%
WES	A19C	101434906	89.7%	115.5	98.30%	96.75%	95.00%	94.10%	91.77%	89.28%	83.88%
WES	A20A	107417324	97.3%	68.6	99.06%	97.50%	95.93%	95.09%	92.51%	89.18%	80.46%
WES	A20C	103554248	98.5%	127.9	98.71%	97.91%	97.19%	96.84%	95.88%	94.79%	91.97%
WES	A21A	161343512	98.9%	203.7	98.98%	98.41%	97.96%	97.75%	97.22%	96.66%	95.37%
WES	A21C	151568234	97.7%	189.2	98.84%	98.23%	97.72%	97.48%	96.88%	96.24%	94.75%
WES	A22A	96675786	98.6%	113.6	98.58%	97.78%	97.03%	96.66%	95.63%	94.38%	91.04%
WES	A22C	135750602	98.8%	168.8	98.64%	97.97%	97.42%	97.17%	96.53%	95.84%	94.19%
WES	A23A	131917540	98.7%	162.1	98.75%	98.04%	97.41%	97.12%	96.37%	95.54%	93.56%
WES	A23C	132223032	98.6%	160.9	98.71%	97.97%	97.36%	97.08%	96.33%	95.52%	93.55%
WES	A24A	208184384	98.9%	265.4	98.42%	97.09%	95.78%	95.18%	93.80%	92.54%	90.34%
WES	A24C	189493790	99.0%	238.7	98.18%	96.58%	94.97%	94.24%	92.56%	91.07%	88.48%
WES	A25A	205650646	99.0%	249.6	98.06%	96.46%	94.94%	94.25%	92.71%	91.32%	88.91%
WES	A25C	239453414	99.1%	301.5	98.03%	96.54%	95.06%	94.42%	92.96%	91.64%	89.33%
WES	A26A	195115556	98.4%	203.4	99.21%	98.41%	97.87%	97.65%	97.13%	96.58%	95.27%
WES	A26C	174339204	98.1%	167.2	99.07%	98.23%	97.61%	97.34%	96.64%	95.86%	93.91%
WES	A27A	89538798	83.1%	94.7	94.54%	88.34%	82.76%	80.33%	75.01%	70.63%	63.86%
WES	A27C	140491114	98.9%	168.3	98.73%	98.07%	97.51%	97.25%	96.59%	95.88%	94.16%
WES	A28A	179890220	99.0%	227.0	98.81%	98.04%	97.53%	97.31%	96.79%	96.24%	95.07%
WES	A28C	160949104	98.7%	203.8	98.25%	96.98%	95.71%	95.13%	93.76%	92.51%	90.20%
WES	A29A	170230078	98.1%	172.2	97.89%	96.04%	94.01%	93.08%	90.98%	89.09%	85.47%
WES	A29C	104529198	98.9%	126.2	99.14%	98.44%	97.76%	97.41%	96.43%	95.27%	92.26%
WES	A30A	144351412	98.9%	174.9	98.84%	98.14%	97.60%	97.35%	96.73%	96.06%	94.44%
WES	A30C	124489740	95.2%	142.8	98.64%	97.82%	97.12%	96.78%	95.93%	94.96%	92.54%
WES	A31A	161462578	87.9%	148.4	96.98%	93.11%	89.27%	87.65%	83.91%	80.41%	74.05%
WES	A31C	154114046	88.0%	141.3	97.09%	93.16%	89.34%	87.71%	83.97%	80.44%	74.03%
WES	A32A	213738708	99.0%	273.6	98.91%	98.37%	97.99%	97.83%	97.43%	96.98%	95.95%
WES	A32C	204173408	98.9%	249.8	98.88%	98.35%	97.97%	97.81%	97.39%	96.93%	95.85%
WES	A33A	145968264	98.9%	181.3	98.80%	98.11%	97.58%	97.34%	96.73%	96.08%	94.55%
WES	A33C	136711750	98.7%	163.8	98.75%	98.00%	97.40%	97.13%	96.41%	95.63%	93.72%
WES	A34A	167169230	98.9%	200.2	98.91%	98.24%	97.75%	97.53%	97.01%	96.47%	95.23%
WES	A34C	116367112	99.0%	140.5	98.68%	97.91%	97.23%	96.91%	96.06%	95.09%	92.63%
WES	A35A	78616902	97.7%	130.5	98.81%	97.99%	97.21%	96.83%	95.81%	94.62%	91.67%

WES	A35C	83602298	97.3%	138.6	98.87%	98.12%	97.42%	97.08%	96.19%	95.15%	92.58%
WES	A36A	92210728	97.6%	153.8	98.72%	97.96%	97.27%	96.93%	96.07%	95.12%	92.84%
WES	A36C	82752590	97.6%	138.8	98.78%	98.02%	97.33%	96.99%	96.09%	95.05%	92.47%
WES	A37A	78489590	97.5%	128.8	98.68%	97.84%	97.09%	96.72%	95.71%	94.59%	91.79%
WES	A37C	56161204	97.1%	95.8	98.57%	97.62%	96.51%	95.91%	94.22%	92.20%	87.03%
WES	A38A	66015624	97.9%	106.7	98.39%	97.27%	96.16%	95.58%	94.02%	92.20%	87.64%
WES	A38C	59376424	97.4%	94.0	98.17%	96.90%	95.46%	94.72%	92.61%	90.14%	84.02%
WES	A39A	63618282	98.1%	101.9	98.49%	97.42%	96.27%	95.67%	94.02%	92.06%	87.09%
WES	A39C	71464030	98.3%	124.3	98.55%	97.72%	96.91%	96.53%	95.53%	94.39%	91.52%
WES	A40A	83226500	98.2%	142.3	98.71%	97.91%	97.21%	96.85%	95.94%	94.90%	92.34%
WES	A40C	62188496	97.6%	98.9	98.19%	96.93%	95.53%	94.80%	92.76%	90.37%	84.53%
WES	A41A	83013588	97.6%	139.8	98.83%	98.18%	97.56%	97.25%	96.41%	95.46%	93.07%
WES	A41C	89547250	97.1%	129.8	99.06%	98.24%	97.56%	97.23%	96.29%	95.21%	92.44%
WES	A42A	68869260	97.8%	119.4	98.70%	98.00%	97.25%	96.86%	95.83%	94.60%	91.44%
WES	A42C	77862764	96.1%	124.8	98.84%	98.13%	97.45%	97.11%	96.17%	95.07%	92.27%
WES	A43A	65518372	98.2%	113.8	98.37%	97.48%	96.56%	96.11%	94.91%	93.54%	90.03%
WES	A43C	87904502	96.0%	148.4	98.86%	98.27%	97.71%	97.42%	96.67%	95.83%	93.72%
WES	A44A	83833774	97.5%	106.3	98.56%	97.69%	96.77%	96.28%	94.88%	93.11%	88.52%
WES	A44C	77005250	95.9%	89.6	98.53%	97.34%	96.17%	95.56%	93.79%	91.62%	86.06%
WES	A46A	70483656	98.5%	129.5	99.07%	98.53%	97.97%	97.67%	96.79%	95.72%	92.94%
WES	A46C	62768777	96.5%	112.7	98.98%	98.37%	97.66%	97.25%	96.11%	94.77%	91.35%
WES	A47A	67388399	98.6%	124.4	99.07%	98.50%	97.92%	97.60%	96.67%	95.53%	92.54%
WES	A47C	78655755	98.5%	144.7	99.11%	98.58%	98.07%	97.80%	97.06%	96.16%	93.89%
WES	A48A	76950190	98.5%	141.5	99.12%	98.59%	98.09%	97.83%	97.07%	96.17%	93.88%
WES	A48C	71765543	98.4%	132.0	99.08%	98.53%	97.97%	97.67%	96.82%	95.77%	93.06%
WES	A49A	72807485	98.6%	127.9	99.23%	98.59%	97.97%	97.64%	96.66%	95.46%	92.27%
WES	A49C	73564325	98.2%	130.6	99.23%	98.64%	98.09%	97.81%	96.98%	95.98%	93.31%
WES	A50A	73606478	98.6%	132.3	99.14%	98.53%	97.92%	97.60%	96.64%	95.48%	92.51%
WES	A50C	84902170	98.4%	155.5	99.15%	98.60%	98.12%	97.87%	97.18%	96.37%	94.37%
WES	A51A	68549424	98.8%	117.5	99.26%	98.61%	97.95%	97.60%	96.55%	95.26%	91.87%
WES	A51C	66840256	97.2%	120.1	99.12%	98.51%	97.82%	97.44%	96.35%	95.05%	91.83%
WES	A52A	65980086	99.7%	127.8	99.18%	98.62%	98.07%	97.77%	96.90%	95.82%	92.91%
WES	A52C	69804434	99.8%	137.1	99.19%	98.71%	98.26%	98.02%	97.30%	96.43%	94.11%

WES	A53A	54698928	99.8%	107.0	99.07%	98.53%	97.97%	97.65%	96.66%	95.39%	91.84%
WES	A53C	56350855	99.8%	111.3	99.05%	98.56%	98.03%	97.73%	96.82%	95.68%	92.51%
WES	A54A	58567908	99.8%	121.1	98.99%	98.44%	97.87%	97.56%	96.67%	95.58%	92.72%
WES	A54C	76366911	99.8%	153.5	99.11%	98.64%	98.22%	98.01%	97.44%	96.77%	95.03%
WES	A55A	70472274	99.8%	145.4	99.02%	98.47%	97.91%	97.62%	96.81%	95.89%	93.57%
WES	A55C	59211097	99.8%	122.8	98.87%	98.23%	97.45%	97.04%	95.86%	94.51%	91.16%
WES	A56A	54923109	99.8%	109.4	99.16%	98.63%	98.07%	97.75%	96.75%	95.48%	91.97%
WES	A56C	59790467	99.8%	120.3	99.14%	98.66%	98.16%	97.87%	97.04%	96.00%	93.16%
WES	A57A	68193178	99.7%	136.1	99.05%	98.56%	98.11%	97.87%	97.18%	96.34%	94.13%
WES	A57C	58807553	98.6%	115.3	98.97%	98.42%	97.84%	97.51%	96.55%	95.35%	92.22%
WES	A58A	64083319	99.6%	128.0	99.22%	98.73%	98.27%	98.03%	97.29%	96.35%	93.81%
WES	A58C	71460054	99.7%	141.8	99.24%	98.75%	98.33%	98.12%	97.52%	96.78%	94.79%
WES	A59A	70284672	99.7%	140.6	99.23%	98.74%	98.31%	98.09%	97.44%	96.65%	94.56%
WES	A59C	65749046	99.7%	133.4	99.19%	98.71%	98.26%	98.02%	97.34%	96.49%	94.18%
WES	A60A	65249105	99.8%	130.5	99.11%	98.62%	98.18%	97.96%	97.29%	96.45%	94.16%
WES	A60C	68691888	99.8%	136.1	99.09%	98.56%	98.09%	97.84%	97.15%	96.32%	94.17%
WES	A61A	61326459	99.8%	122.8	99.16%	98.62%	98.09%	97.80%	96.93%	95.81%	92.76%
WES	A61C	72223195	99.8%	141.6	99.23%	98.69%	98.23%	98.00%	97.33%	96.51%	94.37%
WES	A62A	56616376	99.8%	109.7	99.19%	98.69%	98.17%	97.87%	96.98%	95.81%	92.60%
WES	A62C	66170446	99.8%	128.2	99.20%	98.68%	98.18%	97.91%	97.11%	96.16%	93.62%
WES	A63A	56999055	99.8%	110.7	99.23%	98.66%	98.13%	97.84%	96.95%	95.79%	92.60%
WES	A63C	57517713	99.8%	108.8	99.21%	98.65%	98.08%	97.77%	96.84%	95.62%	92.26%
WES	A64A	60509101	99.8%	116.9	99.21%	98.70%	98.20%	97.93%	97.12%	96.09%	93.25%
WES	A64C	50086014	99.8%	96.6	99.18%	98.62%	97.99%	97.63%	96.47%	94.97%	90.81%
WES	A65A	55572883	99.8%	110.6	99.14%	98.59%	98.02%	97.70%	96.72%	95.48%	92.05%
WES	A65C	45026171	99.7%	91.6	98.98%	98.27%	97.30%	96.75%	95.09%	93.01%	87.62%
WES	A66A	41345124	99.8%	89.4	98.51%	97.50%	96.06%	95.28%	93.06%	90.53%	84.54%
WES	A66C	50504943	99.6%	107.2	98.72%	97.78%	96.58%	95.94%	94.21%	92.26%	87.64%
WES	A67A	64346857	99.9%	124.9	99.24%	98.76%	98.32%	98.09%	97.41%	96.54%	94.15%
WES	A67C	59228081	98.9%	113.4	99.16%	98.67%	98.15%	97.86%	96.99%	95.87%	92.82%
WES	A68A	47354150	99.8%	96.6	98.94%	98.31%	97.56%	97.14%	95.88%	94.29%	89.97%
WES	A68C	49202400	98.9%	99.8	98.89%	98.27%	97.45%	96.98%	95.60%	93.90%	89.48%
WES	A70A	76691922	99.7%	148.0	99.16%	98.68%	98.28%	98.09%	97.58%	96.94%	95.27%

WES	A70C	64065304	99.7%	123.5	99.11%	98.63%	98.19%	97.93%	97.20%	96.29%	93.83%
WES	A71A	59662344	99.7%	115.8	99.04%	98.53%	97.96%	97.64%	96.68%	95.45%	92.17%
WES	A71C	58504980	99.5%	111.5	99.06%	98.53%	97.95%	97.62%	96.65%	95.44%	92.19%
WES	A72A	58584181	99.9%	113.7	99.21%	98.69%	98.19%	97.92%	97.08%	95.99%	92.96%
WES	A72C	59563810	99.2%	109.4	99.25%	98.73%	98.25%	97.97%	97.13%	96.02%	92.87%
WES	A73A	75739154	99.9%	148.1	99.23%	98.74%	98.31%	98.09%	97.46%	96.70%	94.76%
WES	A73C	74349712	99.4%	143.4	99.23%	98.72%	98.28%	98.04%	97.38%	96.59%	94.53%
WES	A74A	64862618	99.8%	124.2	99.21%	98.71%	98.21%	97.94%	97.17%	96.22%	93.65%
WES	A74C	63918727	99.2%	121.5	99.22%	98.72%	98.25%	98.00%	97.27%	96.34%	93.77%
WES	A75A	69392546	99.8%	135.2	99.23%	98.72%	98.25%	98.02%	97.31%	96.44%	94.18%
WES	A75C	62206397	99.2%	122.3	99.15%	98.68%	98.17%	97.90%	97.07%	96.06%	93.31%
WES	A76A	42264045	100.0%	109.6	98.88%	98.45%	97.91%	97.61%	96.73%	95.61%	92.47%
WES	A76C	41747885	100.0%	106.8	98.90%	98.46%	97.85%	97.52%	96.54%	95.34%	91.97%
WES	A77A	66092712	99.8%	129.6	99.21%	98.70%	98.21%	97.94%	97.15%	96.16%	93.55%
WES	A77C	66071145	99.8%	131.6	99.21%	98.73%	98.29%	98.05%	97.35%	96.47%	94.12%
WES	A78A	61010177	99.9%	120.3	99.04%	98.53%	97.99%	97.71%	96.84%	95.79%	92.98%
WES	A78C	74009182	99.7%	142.0	99.15%	98.71%	98.34%	98.15%	97.62%	96.96%	95.20%
WES	A79A	61977712	99.5%	121.1	99.20%	98.70%	98.22%	97.95%	97.15%	96.15%	93.40%
WES	A79C	68588896	99.8%	135.1	99.20%	98.71%	98.26%	98.03%	97.35%	96.50%	94.26%
WES	A81A	45141847	99.9%	116.2	98.94%	98.51%	97.95%	97.64%	96.73%	95.57%	92.33%
WES	A81C	44227241	99.7%	110.6	98.95%	98.56%	98.04%	97.76%	96.89%	95.81%	92.68%
WES	A82A	54448786	99.8%	106.7	99.13%	98.58%	97.98%	97.65%	96.66%	95.38%	91.88%
WES	A82C	53161767	99.5%	102.1	99.17%	98.66%	98.09%	97.75%	96.64%	95.13%	90.88%
WES	A83A	67957302	99.9%	133.7	99.19%	98.69%	98.20%	97.95%	97.26%	96.41%	94.15%
WES	A83C	55638838	99.3%	105.8	99.21%	98.68%	98.16%	97.87%	96.96%	95.76%	92.41%
WES	A84A	40547080	100.0%	104.2	99.06%	98.61%	98.01%	97.70%	96.73%	95.54%	92.08%
WES	A84C	37227661	99.9%	94.7	99.07%	98.59%	97.94%	97.58%	96.45%	95.00%	90.78%
WES	A85A	42910578	99.9%	108.4	99.03%	98.53%	97.90%	97.54%	96.47%	95.17%	91.59%
WES	A85C	44450305	100.0%	111.5	99.09%	98.61%	98.05%	97.75%	96.86%	95.76%	92.68%
WES	A86A	41575581	99.9%	99.0	98.98%	98.48%	97.86%	97.52%	96.47%	95.17%	91.39%
WES	A86C	46679860	99.9%	121.6	98.96%	98.40%	97.44%	96.89%	95.31%	93.62%	90.00%
WES	A87A	43427610	99.9%	110.6	99.08%	98.62%	98.01%	97.67%	96.65%	95.38%	91.87%
WES	A87C	43388500	99.9%	108.4	99.05%	98.56%	97.90%	97.54%	96.45%	95.12%	91.49%

WES	A88A	48239049	99.9%	124.7	98.97%	98.54%	98.04%	97.77%	96.99%	96.09%	93.58%
WES	A88C	47390298	99.8%	120.9	98.90%	98.45%	97.86%	97.54%	96.63%	95.58%	92.72%
WES	A89A	42599922	99.9%	101.9	98.90%	98.38%	97.68%	97.30%	96.17%	94.78%	90.91%
WES	A89C	43560843	99.8%	103.2	98.94%	98.50%	97.93%	97.62%	96.71%	95.54%	92.16%
WES	A90A	42712081	99.8%	100.3	98.90%	98.36%	97.69%	97.32%	96.23%	94.84%	91.00%
WES	A90C	41354720	99.1%	96.2	98.91%	98.38%	97.71%	97.35%	96.27%	94.86%	90.87%
WES	A91A	64965849	99.8%	128.2	99.14%	98.68%	98.23%	98.01%	97.33%	96.48%	94.10%
WES	A91C	66385263	99.2%	131.5	99.10%	98.63%	98.21%	97.98%	97.31%	96.47%	94.22%
WES	A93A	57664070	99.8%	113.7	99.21%	98.68%	98.14%	97.84%	96.93%	95.75%	92.50%
WES	A93C	66178068	98.4%	128.6	99.22%	98.77%	98.32%	98.09%	97.39%	96.54%	94.17%
WES	A94A	43600553	99.9%	103.7	98.91%	98.38%	97.71%	97.33%	96.20%	94.78%	90.90%
WES	A94C	38904410	99.9%	92.3	98.84%	98.24%	97.40%	96.93%	95.51%	93.75%	88.87%
WES	A95A	47906214	99.9%	111.8	98.89%	98.34%	97.64%	97.26%	96.17%	94.85%	91.29%
WES	A95C	45916190	99.1%	100.3	98.83%	98.25%	97.47%	97.04%	95.79%	94.32%	90.39%
WES	AC04A	89489842	87.9%	95.0	96.41%	91.85%	87.94%	86.27%	82.33%	78.64%	71.93%
WES	AC04C	95559896	89.4%	99.3	96.28%	91.60%	87.58%	85.87%	81.80%	78.02%	71.30%
WES	AC06A	112710490	84.9%	92.2	95.73%	90.29%	85.57%	83.53%	78.87%	74.74%	67.83%
WES	AC06C	127486576	75.6%	85.5	93.30%	85.86%	79.39%	76.72%	71.18%	66.85%	60.33%
WES	AC09A	169972158	87.2%	169.4	97.00%	94.05%	91.09%	89.81%	86.88%	84.07%	78.59%
WES	AC09C	164665216	88.8%	168.8	96.64%	93.26%	89.90%	88.47%	85.20%	82.13%	76.45%
WES	AC10A	73875194	91.4%	95.1	98.34%	96.67%	94.66%	93.57%	90.52%	87.16%	79.78%
WES	AC10C	91204740	89.4%	109.3	98.23%	96.52%	94.47%	93.37%	90.39%	87.17%	80.28%
WES	AC11A	98544760	89.9%	113.8	98.27%	96.71%	95.01%	94.16%	91.92%	89.53%	84.31%
WES	AC11C	100778188	89.8%	110.7	98.31%	96.61%	94.69%	93.72%	91.15%	88.43%	82.59%
WES	AC14A	125606834	99.0%	157.0	98.80%	98.11%	97.53%	97.25%	96.55%	95.78%	93.90%
WES	AC14C	120015730	98.9%	149.6	98.78%	98.07%	97.44%	97.13%	96.34%	95.46%	93.30%
WES	AC16A	65267962	97.6%	104.3	98.48%	97.20%	95.67%	94.87%	92.59%	89.97%	83.83%
WES	AC16C	71541254	98.0%	117.7	98.71%	97.75%	96.78%	96.30%	94.98%	93.43%	89.58%
WES	B01A	135370194	98.9%	138.3	97.75%	94.87%	91.94%	90.66%	87.71%	85.00%	79.94%
WES	B01C	59998202	98.6%	103.4	96.66%	93.81%	90.67%	89.29%	86.09%	82.99%	76.74%
WES	B02A	110504486	99.1%	88.3	96.57%	91.83%	87.21%	85.18%	80.57%	76.36%	68.66%
WES	B02C	91524598	99.2%	144.1	96.23%	94.71%	92.59%	91.62%	89.38%	87.27%	83.11%
WES	B03A	89612668	98.9%	199.3	96.41%	93.19%	90.95%	89.98%	87.72%	85.54%	81.30%

WES	B03C	74649136	98.6%	103.8	96.53%	94.22%	91.40%	90.13%	87.11%	84.14%	78.14%
WES	B04A	107407478	98.8%	109.0	93.83%	88.38%	83.60%	81.49%	76.77%	72.74%	66.10%
WES	B04C	102755050	98.6%	85.3	96.75%	93.76%	90.49%	89.01%	85.37%	81.74%	74.23%
WES	B06A	57622802	99.1%	79.7	97.47%	94.60%	91.42%	89.96%	86.47%	82.98%	75.50%
WES	B06C	58110028	99.1%	99.0	97.15%	94.88%	92.13%	90.89%	87.97%	85.15%	79.32%
WES	B12A	58936250	99.0%	78.6	97.59%	94.28%	90.77%	89.20%	85.44%	81.67%	73.61%
WES	B12C	72517038	99.0%	62.3	96.72%	92.83%	88.66%	86.71%	81.89%	76.92%	66.64%
WES	B13A	92512322	98.8%	64.9	96.85%	93.00%	88.88%	86.99%	82.35%	77.57%	67.79%
WES	B13C	74247214	98.7%	61.6	96.87%	92.67%	88.27%	86.24%	81.18%	76.04%	65.69%
WES	B15A	80637650	98.9%	106.4	96.35%	94.01%	91.25%	90.01%	87.02%	84.10%	78.23%
WES	B15C	82288722	95.6%	111.7	96.25%	93.93%	91.17%	89.95%	86.97%	84.09%	78.40%
WES	B16A	96981670	98.1%	78.1	96.64%	93.46%	89.94%	88.35%	84.47%	80.58%	72.52%
WES	B16C	236382712	74.2%	94.0	96.96%	94.13%	91.07%	89.69%	86.41%	83.17%	76.51%
WES	B17A	134754804	98.3%	97.7	97.21%	94.59%	91.68%	90.37%	87.32%	84.32%	78.14%
WES	B17C	84661746	95.2%	116.1	96.82%	94.72%	92.17%	91.00%	88.27%	85.66%	80.42%
WES	B18A	84448692	98.9%	64.1	97.11%	93.58%	89.70%	87.91%	83.41%	78.68%	68.84%
WES	B18C	128215626	96.1%	145.1	96.42%	94.92%	92.97%	92.04%	89.86%	87.78%	83.68%
WES	C01A	103843616	85.0%	102.4	96.17%	91.52%	87.57%	85.89%	82.00%	78.37%	71.86%
WES	C01C	60482206	92.2%	72.6	96.85%	92.83%	89.13%	87.54%	83.70%	79.81%	71.91%
WES	C02A	102550382	84.5%	87.1	96.05%	91.08%	86.74%	84.84%	80.35%	76.21%	68.93%
WES	C02C	96655356	88.8%	95.3	96.24%	91.56%	87.49%	85.78%	81.72%	77.94%	71.11%
WES	C03A	97405696	89.1%	82.1	96.23%	91.14%	86.62%	84.64%	79.92%	75.55%	67.82%
WES	C03C	88372826	90.3%	82.7	96.03%	90.80%	86.25%	84.25%	79.59%	75.34%	67.99%
WES	C05A	111790356	86.2%	88.6	95.70%	90.40%	85.78%	83.74%	78.99%	74.75%	67.63%
WES	C05C	108239426	86.7%	96.8	95.98%	90.95%	86.49%	84.53%	79.96%	75.79%	68.68%
WES	C07A	111199230	86.7%	124.8	95.59%	90.25%	85.79%	83.88%	79.52%	75.65%	69.33%
WES	C07C	110659646	86.5%	124.4	95.93%	90.73%	86.32%	84.42%	80.06%	76.12%	69.57%
WES	C08A	112573216	81.0%	102.4	94.52%	88.61%	83.24%	80.86%	75.49%	70.99%	64.01%
WES	C08C	108399762	84.7%	100.0	93.78%	87.16%	81.22%	78.69%	73.29%	68.99%	62.44%
WES	C12A	150290740	89.2%	140.9	97.14%	93.38%	89.76%	88.20%	84.52%	80.99%	74.50%
WES	C12C	153265204	89.0%	145.9	97.22%	93.46%	89.84%	88.31%	84.74%	81.37%	75.15%
WES	C13A	166762904	98.6%	207.8	98.16%	96.96%	95.78%	95.24%	93.99%	92.81%	90.61%
WES	C13C	182887238	98.7%	218.9	97.95%	96.33%	94.69%	93.94%	92.24%	90.74%	88.07%

WES	C15A	148543742	99.0%	187.4	98.59%	97.97%	97.42%	97.16%	96.52%	95.84%	94.26%
WES	C15C	117418550	98.5%	151.4	98.79%	98.05%	97.08%	96.50%	94.84%	93.04%	89.50%
WES	C17A	70084932	98.4%	119.7	98.56%	97.60%	96.70%	96.25%	95.03%	93.57%	89.87%
WES	C17C	82607118	98.4%	137.2	98.69%	97.83%	97.08%	96.72%	95.82%	94.81%	92.26%
WES	C18A	71241326	92.9%	108.4	98.50%	97.45%	96.40%	95.87%	94.44%	92.73%	88.45%
WES	C18C	70384054	93.1%	108.8	98.65%	97.66%	96.64%	96.12%	94.72%	93.07%	88.89%
WES	C19A	60944450	93.0%	95.8	98.47%	97.35%	96.10%	95.46%	93.64%	91.49%	86.07%
WES	C19C	63592428	92.9%	100.2	98.44%	97.42%	96.33%	95.76%	94.24%	92.42%	87.71%
WES	C20A	64746198	92.7%	101.1	98.27%	97.10%	95.86%	95.23%	93.50%	91.48%	86.43%
WES	C20C	62010152	92.8%	98.6	98.38%	97.27%	96.15%	95.55%	93.91%	91.98%	87.00%
WES	C21A	76408552	92.5%	119.5	98.48%	97.49%	96.53%	96.05%	94.78%	93.33%	89.69%
WES	C21C	106218570	92.8%	163.7	98.68%	97.86%	97.15%	96.82%	95.99%	95.09%	92.99%
WES	C22A	49472504	99.2%	70.7	98.53%	97.32%	95.85%	95.02%	92.43%	89.08%	80.47%
WES	C22C	53900010	99.2%	78.3	98.52%	97.45%	96.26%	95.61%	93.60%	91.02%	84.06%
WES	C23A	74455672	97.9%	132.9	98.55%	97.69%	96.89%	96.51%	95.51%	94.36%	91.45%
WES	C23C	79457536	98.1%	141.8	98.69%	97.90%	97.23%	96.92%	96.09%	95.17%	92.89%
WES	C24A	83052482	96.3%	120.3	99.11%	98.07%	97.12%	96.65%	95.39%	93.94%	90.34%
WES	C24C	71983646	97.3%	121.2	98.94%	98.12%	97.31%	96.90%	95.78%	94.48%	91.13%
WES	C25A	86073884	98.0%	151.3	98.88%	98.13%	97.47%	97.16%	96.36%	95.47%	93.29%
WES	C25C	79613832	96.9%	141.6	98.82%	98.01%	97.28%	96.93%	96.02%	95.00%	92.45%
WES	C26A	82493900	98.0%	146.7	98.91%	98.16%	97.47%	97.16%	96.30%	95.35%	92.97%
WES	C26C	76538668	98.4%	140.2	98.85%	98.08%	97.40%	97.08%	96.20%	95.22%	92.74%
WES	C27A	67760494	96.8%	111.7	98.76%	97.84%	96.87%	96.36%	95.00%	93.40%	89.37%
WES	C27C	73132540	97.1%	121.9	98.85%	98.02%	97.16%	96.73%	95.59%	94.28%	90.98%
WES	C28A	61974336	97.0%	106.8	98.78%	97.85%	96.81%	96.27%	94.79%	93.01%	88.53%
WES	C28C	82027190	97.4%	141.5	98.97%	98.18%	97.42%	97.05%	96.07%	94.98%	92.30%
WES	C29A	76334858	97.9%	137.0	98.84%	98.15%	97.50%	97.18%	96.30%	95.30%	92.81%
WES	C29C	81727336	98.3%	140.7	98.88%	98.15%	97.50%	97.17%	96.32%	95.35%	92.96%
WES	C30A	71223118	98.2%	123.6	98.85%	98.13%	97.44%	97.10%	96.16%	95.04%	92.11%
WES	C30C	80221558	98.3%	139.9	98.83%	98.10%	97.43%	97.11%	96.25%	95.27%	92.82%
WES	C31A	72475826	98.0%	126.3	98.84%	98.08%	97.34%	96.97%	95.95%	94.73%	91.63%
WES	C31C	68642542	98.3%	119.5	98.85%	98.11%	97.35%	96.94%	95.84%	94.57%	91.22%
WES	C32A	67634680	98.2%	118.0	98.81%	98.16%	97.53%	97.18%	96.21%	95.02%	91.89%

WES	C32C	71443552	98.1%	119.8	98.84%	98.17%	97.50%	97.15%	96.18%	95.02%	91.93%
WES	C33A	69568680	98.1%	119.2	98.92%	98.21%	97.51%	97.14%	96.11%	94.86%	91.61%
WES	C33C	70656512	98.1%	123.3	98.89%	98.22%	97.50%	97.14%	96.12%	94.89%	91.79%
WES	C34A	72424872	97.8%	122.5	98.76%	97.97%	97.22%	96.84%	95.79%	94.56%	91.44%
WES	C34C	79631866	98.2%	136.2	98.82%	98.16%	97.53%	97.19%	96.29%	95.25%	92.68%
WES	C35A	84651776	98.3%	144.2	98.96%	98.26%	97.62%	97.28%	96.39%	95.38%	92.88%
WES	C35C	82386614	98.2%	139.1	98.93%	98.23%	97.55%	97.20%	96.27%	95.20%	92.55%
WES	C36A	74508318	98.3%	126.7	98.88%	98.17%	97.43%	97.04%	95.96%	94.68%	91.45%
WES	C36C	88234634	98.1%	147.5	99.03%	98.39%	97.80%	97.51%	96.69%	95.77%	93.49%
WES	C37A	75460284	98.4%	123.3	98.85%	98.12%	97.37%	96.98%	95.92%	94.68%	91.51%
WES	C37C	83279860	98.2%	143.6	98.88%	98.27%	97.68%	97.38%	96.57%	95.63%	93.35%
WES	C38A	70696198	98.2%	122.3	98.73%	97.94%	97.12%	96.71%	95.56%	94.23%	90.89%
WES	C38C	79907134	97.9%	135.5	98.76%	98.11%	97.47%	97.16%	96.29%	95.27%	92.71%
WES	C39A	78611244	98.1%	133.6	98.62%	97.89%	97.13%	96.75%	95.73%	94.56%	91.65%
WES	C39C	79735722	97.9%	135.2	98.74%	98.07%	97.43%	97.12%	96.29%	95.33%	92.87%
WES	C40A	59189888	98.0%	97.5	98.78%	97.91%	97.01%	96.53%	95.15%	93.42%	88.81%
WES	C40C	72114230	98.2%	123.7	98.89%	98.18%	97.50%	97.15%	96.20%	95.07%	92.15%
WES	C41A	65950414	98.0%	111.7	98.60%	97.82%	97.08%	96.71%	95.65%	94.37%	90.95%
WES	C41C	70782932	98.1%	123.6	98.56%	97.78%	97.02%	96.65%	95.65%	94.50%	91.57%
WES	C43A	73699323	99.6%	142.9	99.23%	98.78%	98.39%	98.19%	97.62%	96.94%	95.09%
WES	C43C	89392912	99.7%	168.9	99.36%	98.91%	98.58%	98.43%	98.04%	97.55%	96.28%
WES	C44A	80395521	99.6%	155.0	99.13%	98.69%	98.33%	98.16%	97.68%	97.11%	95.56%
WES	C44C	71880146	99.6%	135.8	99.18%	98.67%	98.27%	98.06%	97.46%	96.71%	94.70%
WES	C45A	67738987	99.6%	131.6	99.13%	98.67%	98.28%	98.09%	97.51%	96.78%	94.73%
WES	C45C	68661416	99.5%	132.1	99.13%	98.67%	98.29%	98.08%	97.49%	96.74%	94.66%
WES	C46A	75715523	99.6%	146.5	99.17%	98.69%	98.32%	98.14%	97.61%	96.97%	95.27%
WES	C46C	73701702	99.5%	142.0	99.16%	98.70%	98.33%	98.14%	97.61%	96.96%	95.18%
WES	C47A	63187183	99.9%	124.7	99.21%	98.76%	98.35%	98.12%	97.48%	96.68%	94.39%
WES	C47C	73747351	99.9%	144.2	99.27%	98.83%	98.49%	98.31%	97.82%	97.21%	95.57%
WES	C48A	60947659	99.9%	122.8	99.15%	98.70%	98.27%	98.03%	97.33%	96.44%	94.01%
WES	C48C	65316382	99.9%	126.8	99.23%	98.78%	98.41%	98.22%	97.64%	96.90%	94.79%
WES	C49A	62274724	99.9%	123.2	99.23%	98.79%	98.39%	98.17%	97.52%	96.69%	94.35%
WES	C49C	60575129	99.9%	118.6	99.22%	98.76%	98.35%	98.14%	97.45%	96.58%	94.05%

WES	C51A	92100499	99.7%	179.2	99.29%	98.85%	98.52%	98.36%	97.94%	97.42%	96.07%
WES	C51C	65596676	99.9%	126.8	99.25%	98.78%	98.36%	98.15%	97.51%	96.72%	94.48%
WES	C54A	67710125	99.9%	132.8	99.10%	98.67%	98.30%	98.10%	97.52%	96.80%	94.82%
WES	C54C	70932105	99.7%	139.2	99.11%	98.69%	98.33%	98.14%	97.61%	96.96%	95.18%
WES	C55A	69853525	99.9%	136.0	99.10%	98.67%	98.29%	98.09%	97.50%	96.77%	94.70%
WES	C55C	70608517	99.9%	136.6	99.17%	98.68%	98.30%	98.12%	97.57%	96.89%	95.05%
WES	C56A	85028467	99.7%	167.8	99.21%	98.76%	98.35%	98.14%	97.58%	96.89%	95.11%
WES	C56C	67070271	99.9%	128.5	99.24%	98.74%	98.32%	98.10%	97.44%	96.61%	94.29%
WES	C57A	54147237	99.8%	105.2	99.22%	98.73%	98.23%	97.97%	97.15%	96.02%	92.77%
WES	C57C	70304883	99.9%	131.4	99.34%	98.83%	98.45%	98.27%	97.72%	96.99%	94.93%
WES	C58A	62391545	99.8%	117.4	99.14%	98.60%	98.11%	97.84%	97.01%	95.95%	93.07%
WES	C58C	82015214	99.5%	160.9	99.12%	98.70%	98.35%	98.18%	97.70%	97.12%	95.60%
WES	C59A	68707790	99.9%	128.1	99.29%	98.78%	98.33%	98.09%	97.40%	96.53%	94.14%
WES	C59C	63058371	99.9%	124.4	99.24%	98.77%	98.36%	98.14%	97.48%	96.64%	94.29%
WES	C61A	76223610	99.9%	144.8	99.31%	98.82%	98.44%	98.25%	97.71%	97.05%	95.23%
WES	C61C	74350512	99.8%	141.3	99.32%	98.84%	98.50%	98.34%	97.90%	97.32%	95.67%
WES	C63A	66634270	99.9%	129.3	99.27%	98.79%	98.38%	98.17%	97.54%	96.73%	94.44%
WES	C63C	75353669	99.9%	145.8	99.26%	98.80%	98.40%	98.19%	97.61%	96.88%	94.94%
WES	C64A	62545546	99.9%	119.6	99.24%	98.73%	98.25%	97.99%	97.16%	96.12%	93.17%
WES	C64C	90742053	99.7%	176.7	99.32%	98.88%	98.55%	98.40%	97.97%	97.47%	96.17%
WES	C65A	92121215	99.8%	179.3	99.22%	98.77%	98.46%	98.31%	97.90%	97.40%	96.07%
WES	C65C	68671339	99.9%	137.1	99.09%	98.64%	98.28%	98.09%	97.54%	96.87%	95.05%
WES	C66A	78635299	99.8%	154.9	99.26%	98.80%	98.44%	98.27%	97.77%	97.17%	95.61%
WES	C66C	62738268	99.8%	125.2	99.17%	98.67%	98.22%	97.99%	97.29%	96.39%	93.93%
WES	C67A	78514652	99.8%	155.8	99.28%	98.82%	98.47%	98.30%	97.83%	97.25%	95.70%
WES	C67C	64685635	99.7%	125.3	99.23%	98.74%	98.29%	98.06%	97.36%	96.47%	94.04%
WES	C68A	63243322	99.6%	125.0	99.11%	98.64%	98.24%	98.01%	97.36%	96.53%	94.23%
WES	C68C	60949694	99.7%	117.1	99.18%	98.64%	98.17%	97.93%	97.20%	96.25%	93.63%
WES	C69A	65608776	99.8%	129.5	99.22%	98.74%	98.27%	98.02%	97.30%	96.38%	93.95%
WES	C69C	63893862	99.7%	124.7	99.21%	98.73%	98.26%	98.02%	97.30%	96.39%	93.90%
WES	C70A	61529780	99.8%	121.1	99.17%	98.68%	98.18%	97.91%	97.09%	96.05%	93.26%
WES	C70C	57597417	99.6%	113.5	99.06%	98.56%	98.06%	97.79%	96.97%	95.92%	92.99%
WES	C71A	68482426	99.8%	132.3	99.15%	98.67%	98.25%	98.04%	97.40%	96.58%	94.37%

WES	C71C	69230596	99.7%	136.3	99.25%	98.78%	98.36%	98.14%	97.50%	96.71%	94.55%
WES	C72A	54217802	99.7%	106.8	99.06%	98.56%	98.03%	97.73%	96.80%	95.56%	92.06%
WES	C72C	92368756	99.7%	183.1	99.14%	98.73%	98.43%	98.29%	97.90%	97.46%	96.35%
WES	C73A	61497526	99.6%	119.8	99.15%	98.60%	98.05%	97.73%	96.78%	95.62%	92.47%
WES	C73C	52783645	99.7%	104.1	99.15%	98.61%	98.05%	97.74%	96.74%	95.45%	91.79%
WES	C74A	60995138	99.7%	120.0	99.07%	98.57%	98.06%	97.76%	96.86%	95.71%	92.59%
WES	C74C	70954311	99.7%	139.1	99.12%	98.65%	98.25%	98.03%	97.40%	96.63%	94.63%
WES	C75A	42473294	99.6%	83.4	98.96%	98.28%	97.40%	96.87%	95.21%	93.03%	87.01%
WES	C75C	66771749	99.7%	129.5	99.12%	98.64%	98.22%	98.00%	97.38%	96.60%	94.48%
WES	C76A	56942643	99.7%	113.2	99.04%	98.58%	98.10%	97.83%	97.03%	95.96%	93.03%
WES	C76C	68768658	99.9%	133.8	99.13%	98.66%	98.25%	98.04%	97.41%	96.63%	94.57%
WES	C77A	74294786	99.7%	146.5	99.26%	98.80%	98.44%	98.24%	97.70%	97.05%	95.29%
WES	C77C	69990010	99.7%	138.3	99.25%	98.79%	98.40%	98.21%	97.64%	96.93%	95.02%
WES	C78A	55305757	99.7%	107.4	99.23%	98.69%	98.17%	97.86%	96.92%	95.68%	92.24%
WES	C78C	61610692	99.8%	120.8	99.22%	98.70%	98.20%	97.93%	97.14%	96.12%	93.37%
WES	C79A	60180600	99.7%	119.5	99.20%	98.72%	98.23%	97.96%	97.18%	96.16%	93.37%
WES	C79C	70504110	99.8%	142.6	99.21%	98.77%	98.40%	98.21%	97.69%	97.04%	95.29%
WES	C80A	65611854	99.6%	130.4	99.23%	98.74%	98.33%	98.12%	97.50%	96.71%	94.50%
WES	C80C	62297592	99.8%	123.5	99.18%	98.69%	98.24%	97.98%	97.23%	96.29%	93.72%
WES	C81A	59561870	99.8%	118.7	99.14%	98.65%	98.13%	97.86%	97.02%	95.96%	93.07%
WES	C81C	72847279	99.7%	143.3	99.26%	98.81%	98.46%	98.29%	97.81%	97.19%	95.48%
WES	C82A	73048017	99.7%	144.2	99.27%	98.83%	98.47%	98.30%	97.82%	97.20%	95.49%
WES	C82C	58989000	99.8%	117.9	99.16%	98.67%	98.20%	97.95%	97.17%	96.16%	93.39%
WES	C83A	67407818	99.7%	133.6	99.11%	98.66%	98.28%	98.09%	97.52%	96.79%	94.84%
WES	C83C	39642967	99.6%	76.7	99.00%	98.33%	97.45%	96.90%	95.21%	92.94%	86.53%
WES	C84A	64554664	99.8%	128.7	99.22%	98.73%	98.29%	98.06%	97.38%	96.53%	94.27%
WES	C84C	71273851	99.8%	143.7	99.18%	98.72%	98.33%	98.13%	97.54%	96.82%	94.92%
WES	C85A	68403833	99.7%	130.4	99.19%	98.67%	98.21%	97.98%	97.31%	96.51%	94.31%
WES	C85C	58135164	99.7%	115.2	99.09%	98.59%	98.12%	97.86%	97.08%	96.08%	93.30%
WES	C86A	53267091	99.8%	105.5	99.14%	98.63%	98.09%	97.79%	96.88%	95.69%	92.28%
WES	C86C	69605502	99.7%	133.4	99.28%	98.82%	98.43%	98.24%	97.68%	96.96%	94.99%
WES	C87A	59663167	99.6%	120.0	99.07%	98.58%	98.15%	97.90%	97.16%	96.24%	93.65%
WES	C87C	75392107	99.8%	150.5	99.12%	98.67%	98.29%	98.10%	97.56%	96.89%	95.17%

WES	C88A	72862739	99.7%	145.4	99.26%	98.82%	98.46%	98.28%	97.78%	97.14%	95.40%
WES	C88C	73703593	99.7%	145.9	99.25%	98.81%	98.44%	98.26%	97.72%	97.07%	95.33%
WES	C89A	73958187	99.7%	146.4	99.12%	98.68%	98.32%	98.14%	97.64%	97.01%	95.33%
WES	C89C	68444853	99.8%	136.2	99.10%	98.66%	98.30%	98.11%	97.58%	96.89%	94.95%
WES	C90A	43560152	99.8%	106.7	99.01%	98.49%	97.82%	97.48%	96.49%	95.23%	91.84%
WES	C90C	58658806	99.8%	117.2	99.22%	98.77%	98.34%	98.11%	97.39%	96.44%	93.79%
WES	C91A	42091996	99.8%	103.0	99.00%	98.49%	97.87%	97.52%	96.47%	95.14%	91.44%
WES	C91C	62097179	99.8%	125.7	99.13%	98.70%	98.29%	98.07%	97.38%	96.51%	94.15%
WES	C92A	59904637	99.8%	120.4	99.19%	98.71%	98.24%	97.98%	97.19%	96.17%	93.36%
WES	C92C	65771254	99.8%	134.2	99.20%	98.73%	98.26%	98.01%	97.28%	96.41%	94.12%
WES	C93A	43461081	99.8%	106.5	98.87%	98.34%	97.65%	97.28%	96.24%	94.94%	91.43%
WES	C93C	79712263	99.8%	160.7	99.13%	98.71%	98.40%	98.25%	97.83%	97.33%	95.99%
WES	C94A	42611367	99.8%	104.2	98.88%	98.38%	97.73%	97.38%	96.34%	95.04%	91.44%
WES	C94C	58929405	99.8%	118.6	99.05%	98.60%	98.20%	97.99%	97.34%	96.51%	94.14%
WES	C95A	41220507	99.8%	100.1	98.99%	98.48%	97.82%	97.45%	96.34%	94.94%	90.97%
WES	C95C	72480238	99.8%	146.6	99.18%	98.76%	98.40%	98.22%	97.69%	97.05%	95.31%
WES	C96A	49050655	99.8%	119.4	99.07%	98.55%	97.94%	97.63%	96.72%	95.62%	92.69%
WES	C96C	56723519	99.8%	111.6	99.20%	98.74%	98.27%	98.00%	97.18%	96.11%	93.08%
WES	C97A	53687333	99.8%	109.0	99.13%	98.71%	98.26%	98.01%	97.24%	96.21%	93.27%
WES	C97C	74070299	99.9%	151.3	99.21%	98.79%	98.43%	98.25%	97.74%	97.13%	95.49%
WES	C98A	59704841	99.8%	123.4	99.00%	98.59%	98.17%	97.94%	97.25%	96.36%	93.88%
WES	C98C	58165540	99.8%	114.7	99.12%	98.64%	98.21%	97.98%	97.25%	96.29%	93.61%
WES	C99A	63863475	99.8%	131.7	99.05%	98.60%	98.22%	98.02%	97.43%	96.69%	94.71%
WES	C99C	67988137	99.8%	137.3	99.08%	98.67%	98.34%	98.17%	97.67%	97.03%	95.30%
WES	C100A	68436070	99.8%	139.8	99.17%	98.78%	98.41%	98.21%	97.65%	96.93%	94.98%
WES	C100C	70770937	99.9%	143.1	99.25%	98.84%	98.48%	98.30%	97.77%	97.09%	95.25%
WES	C101A	71789490	99.8%	146.4	99.17%	98.76%	98.42%	98.24%	97.74%	97.11%	95.44%
WES	C101C	52953889	99.8%	106.0	99.14%	98.67%	98.18%	97.89%	97.01%	95.83%	92.51%
WES	C102A	56278593	99.8%	114.0	99.13%	98.69%	98.25%	98.01%	97.24%	96.23%	93.35%
WES	C102C	63081686	99.8%	127.9	99.18%	98.74%	98.34%	98.12%	97.48%	96.64%	94.35%
WES	CA69A	73429586	99.8%	141.6	99.13%	98.62%	98.21%	97.99%	97.36%	96.58%	94.60%
WES	CA69C	79259753	99.7%	150.5	99.19%	98.70%	98.32%	98.13%	97.61%	96.99%	95.35%
WES	CA80A	42819659	99.9%	109.4	98.88%	98.40%	97.75%	97.40%	96.38%	95.13%	91.70%

WES	CA80C	44020509	99.9%	112.5	98.93%	98.49%	97.96%	97.67%	96.82%	95.77%	92.83%
WES	CA92A	64823553	99.8%	127.6	99.10%	98.60%	98.17%	97.94%	97.27%	96.42%	94.11%
WES	CA92C	58458151	95.7%	110.5	99.00%	98.51%	97.97%	97.67%	96.77%	95.63%	92.48%
mRNA-seq	A03	40421034	82.7%	55.6	74.54%	66.94%	53.13%	51.18%	46.99%	43.23%	36.56%
mRNA-seq	A04	42712936	88.3%	68.4	66.11%	61.14%	51.45%	49.58%	45.55%	42.05%	36.18%
mRNA-seq	A05	43637252	82.9%	66.1	76.96%	69.15%	54.62%	52.66%	48.58%	45.07%	39.09%
mRNA-seq	A08	51979920	97.0%	12.4	50.07%	39.86%	17.17%	14.25%	9.90%	7.47%	4.96%
mRNA-seq	A09	44527942	97.1%	33.6	66.29%	60.77%	46.38%	43.00%	35.81%	29.99%	21.73%
mRNA-seq	A10	69120423	96.4%	75.5	70.33%	65.63%	56.32%	54.59%	50.98%	47.90%	42.40%
mRNA-seq	A13	50983045	97.3%	45.9	66.63%	61.27%	48.43%	45.50%	39.36%	34.31%	26.42%
mRNA-seq	A14	48031004	96.5%	62.4	71.08%	66.13%	56.02%	54.06%	49.80%	45.96%	39.25%
mRNA-seq	A15	34832751	77.1%	76.0	71.29%	63.55%	50.10%	48.24%	44.20%	40.73%	34.85%
mRNA-seq	A16	64445657	96.8%	62.2	68.02%	63.20%	53.39%	51.43%	47.20%	43.45%	36.89%
mRNA-seq	A17	48214587	96.7%	48.6	65.30%	59.72%	48.29%	45.92%	40.84%	36.52%	29.49%
mRNA-seq	A18	85008860	96.5%	113.9	72.03%	67.52%	58.82%	57.44%	54.77%	52.55%	48.65%
mRNA-seq	A19	100995362	97.1%	114.7	69.51%	64.78%	55.53%	53.93%	50.65%	47.89%	43.14%
mRNA-seq	A20	41290499	78.5%	64.7	61.29%	57.12%	49.01%	47.28%	43.50%	40.31%	35.01%
mRNA-seq	A21	71409114	97.0%	94.7	73.69%	68.47%	57.50%	55.44%	51.10%	47.47%	41.38%
mRNA-seq	A22	51481748	93.3%	57.7	69.98%	65.28%	55.44%	53.53%	49.32%	45.56%	38.75%
mRNA-seq	A23	38149352	97.2%	46.2	65.90%	61.07%	50.07%	47.60%	42.18%	37.54%	29.83%
mRNA-seq	A25	46187213	92.3%	42.9	65.67%	60.39%	47.59%	44.92%	39.27%	34.58%	27.31%
mRNA-seq	A26	49036403	96.9%	51.6	66.35%	61.31%	50.68%	48.41%	43.41%	38.90%	31.27%
mRNA-seq	A27	32858427	82.6%	68.4	72.83%	65.65%	53.14%	51.27%	47.13%	43.39%	36.77%
mRNA-seq	A28	53109630	96.6%	42.2	68.23%	62.31%	48.62%	45.70%	39.49%	34.24%	26.15%
mRNA-seq	A30	44714864	89.1%	64.6	68.99%	64.29%	53.14%	50.84%	45.91%	41.76%	35.11%
mRNA-seq	A31	48862959	93.4%	35.6	67.99%	62.24%	48.16%	45.17%	38.82%	33.60%	25.69%
mRNA-seq	A32	45937235	91.0%	29.1	68.29%	62.81%	48.09%	44.97%	38.31%	32.82%	24.50%
mRNA-seq	A34	49820286	88.0%	57.2	66.10%	61.14%	48.93%	46.37%	41.14%	37.02%	30.74%
mRNA-seq	A35	42062033	97.1%	64.2	70.80%	65.17%	54.20%	52.13%	47.70%	43.77%	36.95%
mRNA-seq	A36	50385955	97.4%	61.7	66.08%	61.01%	51.11%	49.10%	44.59%	40.58%	33.61%
mRNA-seq	A37	55127067	96.5%	88.2	72.38%	67.28%	57.14%	55.56%	52.32%	49.56%	44.50%
mRNA-seq	A38	45748947	97.0%	24.6	63.23%	57.11%	40.60%	36.76%	29.09%	23.43%	15.90%
mRNA-seq	A39	50275582	97.5%	37.6	64.36%	58.88%	46.69%	43.96%	37.92%	32.80%	25.12%

mRNA-seq	A40	42999582	96.3%	49.7	68.83%	63.29%	51.67%	49.32%	44.06%	39.41%	31.45%
mRNA-seq	A41	43689563	96.6%	50.6	64.67%	59.77%	49.62%	47.49%	42.81%	38.65%	31.50%
mRNA-seq	A42	51482648	97.4%	38.1	63.18%	58.41%	48.10%	45.77%	40.41%	35.70%	27.87%
mRNA-seq	A43	48528152	97.1%	58.9	63.59%	57.30%	42.90%	40.23%	35.20%	31.51%	26.21%
mRNA-seq	A44	49948749	97.0%	35.5	64.97%	59.19%	45.68%	42.70%	36.11%	30.57%	22.34%
mRNA-seq	A46	48214573	96.4%	53.6	64.68%	60.00%	50.05%	47.92%	43.25%	39.27%	32.63%
mRNA-seq	A47	55824284	96.6%	30.2	62.53%	56.19%	39.98%	36.67%	30.30%	25.57%	19.00%
mRNA-seq	A48	47076564	97.1%	76.3	67.67%	63.20%	54.20%	52.37%	48.35%	44.71%	38.35%
mRNA-seq	A49	41575165	96.3%	30.7	66.26%	61.13%	48.32%	45.26%	38.36%	32.53%	23.59%
mRNA-seq	A50	47993093	96.7%	39.2	63.25%	58.49%	47.28%	44.61%	38.59%	33.52%	25.53%
mRNA-seq	A51	42171142	97.0%	26.7	60.46%	54.94%	40.21%	36.75%	29.75%	24.48%	17.42%
mRNA-seq	A52	42118837	88.8%	27.7	58.63%	53.70%	38.08%	34.40%	27.03%	21.70%	14.90%
mRNA-seq	A54	46597748	97.0%	35.8	70.86%	64.45%	49.57%	46.39%	39.47%	33.58%	24.72%
mRNA-seq	A56	50117075	97.4%	58.2	66.62%	62.16%	52.53%	50.44%	45.78%	41.64%	34.74%
mRNA-seq	A57	44856928	96.9%	31.2	64.60%	59.44%	46.15%	42.92%	36.02%	30.41%	21.88%
mRNA-seq	A58	41847859	97.6%	62.6	66.18%	61.70%	52.79%	50.97%	46.89%	43.26%	36.94%
mRNA-seq	A59	48514808	97.1%	66.2	66.35%	61.80%	52.34%	50.51%	46.60%	43.20%	37.30%
mRNA-seq	A60	45695921	97.3%	68.1	68.59%	63.25%	52.36%	50.00%	44.86%	40.54%	33.53%
mRNA-seq	A61	43611765	97.2%	63.5	66.97%	62.34%	52.18%	49.87%	44.80%	40.33%	32.97%
mRNA-seq	A62	41192904	97.4%	49.6	67.97%	62.72%	51.47%	49.07%	43.83%	39.22%	31.51%
mRNA-seq	A63	49753563	96.2%	40.4	63.41%	58.87%	47.72%	45.04%	39.09%	34.16%	26.54%
mRNA-seq	A64	43102272	97.4%	63.5	68.21%	63.08%	52.74%	50.71%	46.29%	42.36%	35.66%
mRNA-seq	A65	59985057	97.5%	89.6	70.53%	65.24%	55.29%	53.45%	49.60%	46.32%	40.70%
mRNA-seq	A70	42576390	97.1%	31.7	62.21%	57.23%	45.55%	42.84%	36.76%	31.55%	23.27%
mRNA-seq	A71	48188588	96.6%	54.6	67.80%	62.48%	51.44%	49.19%	44.25%	39.89%	32.65%
mRNA-seq	A72	45334115	96.1%	35.6	70.65%	65.14%	51.47%	48.53%	42.36%	37.21%	28.70%
mRNA-seq	A73	47010882	97.1%	51.5	68.58%	63.61%	53.48%	51.55%	47.24%	43.33%	36.26%
mRNA-seq	A74	45916235	97.3%	55.2	65.61%	60.86%	51.73%	49.85%	45.56%	41.64%	34.57%
mRNA-seq	A75	59345230	97.0%	60.0	69.89%	64.68%	54.45%	52.57%	48.42%	44.72%	37.94%
mRNA-seq	A76	46617834	96.9%	44.5	69.03%	63.78%	51.38%	48.80%	43.13%	38.33%	30.39%
mRNA-seq	A77	52978608	96.6%	30.3	64.89%	59.48%	45.26%	41.87%	34.78%	29.20%	21.14%
mRNA-seq	A78	46979736	97.3%	65.1	66.68%	61.90%	52.90%	51.14%	47.22%	43.69%	37.26%
mRNA-seq	A79	45789809	96.3%	49.8	67.82%	62.12%	51.49%	49.38%	44.84%	40.90%	34.07%

mRNA-seq	A81	54128295	92.0%	49.4	68.72%	63.91%	53.33%	51.09%	46.12%	41.61%	33.85%
mRNA-seq	A82	52734232	92.7%	36.4	63.03%	56.89%	41.06%	37.82%	31.40%	26.62%	20.04%
mRNA-seq	A83	44807974	96.3%	34.5	62.44%	57.74%	46.98%	44.41%	38.53%	33.37%	24.78%
mRNA-seq	A84	58718409	95.3%	62.0	67.39%	62.72%	52.17%	49.93%	45.00%	40.75%	33.75%
mRNA-seq	A85	53322968	94.3%	64.1	67.22%	62.37%	53.36%	51.64%	47.80%	44.37%	38.36%
mRNA-seq	A86	53079798	95.4%	65.3	67.59%	62.28%	51.99%	49.97%	45.45%	41.45%	34.70%
mRNA-seq	A87	44782260	96.4%	49.0	68.75%	63.78%	52.73%	50.21%	44.69%	40.08%	32.48%
mRNA-seq	A88	51451391	95.2%	74.6	68.28%	63.77%	54.62%	52.93%	49.36%	46.26%	40.75%
mRNA-seq	A89	45563271	88.7%	92.0	66.51%	65.15%	56.14%	54.66%	51.58%	48.99%	44.34%
mRNA-seq	A90	46679135	91.9%	61.1	63.26%	58.69%	49.58%	47.61%	43.26%	39.42%	33.12%
mRNA-seq	A91	57522556	91.7%	57.9	76.11%	70.66%	57.67%	55.55%	51.10%	47.22%	40.49%
mRNA-seq	A93	51389811	89.6%	57.1	70.11%	64.43%	53.74%	51.76%	47.54%	43.69%	36.96%
mRNA-seq	A94	47093724	90.4%	48.0	72.39%	67.32%	55.73%	53.26%	47.86%	43.26%	35.30%
mRNA-seq	A95	67068683	91.1%	64.7	67.93%	62.97%	53.06%	51.20%	47.11%	43.44%	36.92%
mRNA-seq	A96	59796727	91.1%	65.2	70.55%	65.85%	55.86%	54.00%	50.08%	46.64%	40.70%
mRNA-seq	AC06	41916821	96.9%	52.9	67.31%	62.21%	52.75%	50.90%	46.67%	42.87%	36.00%
mRNA-seq	AC11	73660948	96.6%	70.0	69.82%	65.06%	55.00%	53.08%	48.98%	45.43%	39.22%
mRNA-seq	AC16	52559092	96.8%	93.0	70.45%	65.59%	55.64%	54.02%	50.59%	47.61%	42.29%
mRNA-seq	B03	45722902	90.0%	67.6	64.75%	62.44%	53.41%	51.75%	48.19%	45.10%	39.73%
mRNA-seq	B12	43266651	87.5%	73.1	69.30%	66.19%	55.76%	53.93%	50.16%	46.92%	41.33%
mRNA-seq	B13	47474445	88.5%	77.9	69.15%	66.55%	56.83%	55.19%	51.81%	48.95%	43.94%
mRNA-seq	B15	48022546	86.9%	70.0	70.20%	66.44%	55.25%	53.31%	49.43%	46.22%	40.74%
mRNA-seq	B16	44462772	95.4%	61.5	72.75%	67.14%	55.52%	53.51%	49.23%	45.44%	38.86%
mRNA-seq	B17	48091465	96.9%	43.9	65.83%	59.98%	46.21%	43.07%	36.59%	31.58%	24.51%
mRNA-seq	B18	40233359	85.8%	72.0	67.17%	63.96%	51.09%	48.44%	43.08%	38.82%	32.31%
mRNA-seq	C01	48640226	97.0%	53.2	68.46%	63.34%	51.99%	49.63%	44.58%	40.35%	33.43%
mRNA-seq	C05	49359215	96.8%	34.8	67.87%	62.46%	49.77%	46.95%	40.70%	35.27%	26.62%
mRNA-seq	C08	44800840	96.7%	60.1	67.58%	63.14%	53.70%	51.82%	47.77%	44.12%	37.63%
mRNA-seq	C15	43057692	97.2%	47.1	66.15%	61.35%	50.38%	47.90%	42.39%	37.63%	29.87%
mRNA-seq	C17	52890175	96.7%	81.4	67.28%	63.07%	55.38%	54.06%	51.20%	48.61%	43.66%
mRNA-seq	C18	43139020	97.0%	58.6	68.53%	63.65%	54.24%	52.39%	48.46%	44.88%	38.28%
mRNA-seq	C19	51596958	97.2%	78.4	66.75%	61.97%	53.85%	52.47%	49.42%	46.72%	41.75%
mRNA-seq	C20	49598991	97.0%	60.0	70.39%	65.00%	54.44%	52.49%	48.23%	44.49%	37.75%

mRNA-seq	C21	44149239	97.1%	53.2	66.23%	60.85%	51.48%	49.65%	45.49%	41.55%	34.45%
mRNA-seq	C22	50663076	97.2%	49.8	66.41%	61.02%	50.21%	48.01%	43.24%	38.92%	31.51%
mRNA-seq	C23	52777376	97.1%	58.1	65.47%	61.02%	52.81%	51.22%	47.63%	44.24%	37.85%
mRNA-seq	C24	42848202	97.0%	56.3	68.47%	63.39%	52.96%	50.90%	46.50%	42.61%	35.67%
mRNA-seq	C25	47384653	96.2%	50.7	71.87%	66.30%	55.17%	53.07%	48.48%	44.19%	36.72%
mRNA-seq	C26	43659567	93.1%	29.1	65.87%	60.32%	48.11%	45.25%	38.75%	33.00%	23.89%
mRNA-seq	C27	43024036	96.8%	47.5	69.56%	64.09%	52.88%	50.71%	45.94%	41.72%	34.37%
mRNA-seq	C28	43346092	96.7%	52.5	69.70%	64.36%	53.94%	52.00%	47.75%	43.91%	37.03%
mRNA-seq	C29	55740530	95.9%	58.8	70.57%	64.86%	54.65%	52.79%	48.81%	45.24%	38.93%
mRNA-seq	C30	43519107	97.1%	49.1	65.68%	60.80%	51.15%	49.13%	44.59%	40.55%	33.20%
mRNA-seq	C31	46942382	96.5%	44.3	66.98%	62.50%	53.56%	51.72%	47.38%	43.21%	35.51%
mRNA-seq	C32	47576881	96.6%	55.9	69.06%	64.12%	54.42%	52.57%	48.54%	44.91%	38.11%
mRNA-seq	C33	53038862	96.6%	48.4	68.60%	63.71%	53.40%	51.22%	46.32%	41.89%	34.25%
mRNA-seq	C34	42612265	97.1%	50.1	69.85%	64.27%	53.31%	51.08%	46.01%	41.49%	33.77%
mRNA-seq	C35	50778335	97.4%	56.6	66.30%	61.75%	52.30%	50.23%	45.52%	41.29%	34.06%
mRNA-seq	C36	45437202	95.6%	41.5	66.56%	61.38%	49.65%	46.98%	41.16%	36.19%	28.38%
mRNA-seq	C37	44507397	97.1%	52.7	64.92%	60.00%	50.96%	49.03%	44.52%	40.34%	32.82%
mRNA-seq	C38	46159283	97.3%	63.8	67.96%	63.37%	54.34%	52.51%	48.42%	44.68%	38.20%
mRNA-seq	C39	44711921	96.6%	55.0	68.35%	63.56%	53.91%	52.01%	47.89%	44.16%	37.18%
mRNA-seq	C40	40981444	97.3%	41.8	63.42%	58.03%	44.13%	40.98%	34.46%	29.42%	22.15%
mRNA-seq	C41	44029949	97.1%	60.5	68.52%	63.81%	54.22%	52.42%	48.42%	44.81%	38.45%
mRNA-seq	C43	64133859	95.2%	31.4	67.96%	56.70%	49.72%	46.94%	40.82%	35.44%	26.61%
mRNA-seq	C44	53520278	89.1%	105.7	70.25%	61.92%	57.67%	56.21%	53.33%	50.95%	46.77%
mRNA-seq	C45	60960969	89.1%	103.9	71.49%	62.35%	57.62%	56.02%	52.84%	50.19%	45.56%
mRNA-seq	C47	46943156	93.0%	86.7	65.10%	57.20%	53.16%	51.79%	48.86%	46.24%	41.43%
mRNA-seq	C48	54803588	94.6%	71.4	71.48%	61.21%	56.27%	54.46%	50.66%	47.35%	41.46%
mRNA-seq	C49	44836333	93.5%	62.7	70.56%	61.52%	56.30%	54.38%	50.28%	46.71%	40.40%
mRNA-seq	C51	53660217	89.4%	67.5	70.77%	61.31%	55.66%	53.59%	49.26%	45.59%	39.28%
mRNA-seq	C54	43985182	92.6%	52.9	67.09%	57.80%	52.85%	50.98%	46.98%	43.37%	36.93%
mRNA-seq	C55	54105154	91.6%	98.1	69.65%	62.34%	58.06%	56.63%	53.74%	51.26%	46.79%
mRNA-seq	C56	52882478	91.7%	79.6	69.60%	62.17%	57.71%	56.11%	52.80%	49.86%	44.56%
mRNA-seq	C57	57294965	90.0%	109.6	73.13%	64.56%	60.05%	58.54%	55.60%	53.18%	48.91%
mRNA-seq	C58	48575153	93.1%	91.2	72.08%	63.77%	59.09%	57.47%	54.19%	51.43%	46.65%

mRNA-seq	C59	50908102	92.8%	93.6	70.84%	62.87%	58.36%	56.79%	53.69%	51.15%	46.77%
mRNA-seq	C61	50492615	88.8%	87.8	67.60%	59.55%	55.56%	54.17%	51.24%	48.66%	44.01%
mRNA-seq	C63	48623617	93.5%	77.7	66.41%	58.92%	54.83%	53.37%	50.25%	47.45%	42.40%
mRNA-seq	C64	56125359	93.6%	96.7	72.57%	63.82%	59.06%	57.46%	54.27%	51.59%	46.74%
mRNA-seq	C65	58279687	89.0%	44.5	66.50%	57.36%	51.82%	49.71%	45.08%	40.92%	33.61%
mRNA-seq	C66	51178448	91.5%	65.2	68.90%	60.50%	55.30%	53.37%	49.31%	45.83%	39.88%
mRNA-seq	C67	46257360	94.7%	79.5	66.73%	58.72%	54.33%	52.66%	49.13%	46.03%	40.48%
mRNA-seq	C68	54243959	88.3%	49.6	67.09%	56.76%	50.48%	48.07%	42.76%	38.05%	30.23%
mRNA-seq	C69	56733676	87.9%	58.7	71.29%	61.33%	55.94%	53.99%	49.89%	46.19%	39.60%
mRNA-seq	C70	64696190	94.3%	74.1	70.26%	60.83%	56.16%	54.51%	51.09%	48.07%	42.46%
mRNA-seq	C71	47422539	93.0%	72.0	69.79%	61.16%	56.69%	55.07%	51.59%	48.46%	42.78%
mRNA-seq	C72	45963188	90.7%	60.9	68.56%	60.27%	55.15%	53.16%	48.76%	44.84%	38.09%
mRNA-seq	C73	63604360	90.2%	99.8	69.74%	61.27%	56.72%	55.13%	51.87%	49.09%	44.28%
mRNA-seq	C74	51184219	91.7%	68.5	69.18%	61.41%	56.74%	55.15%	51.82%	48.79%	43.14%
mRNA-seq	C75	61160951	89.6%	88.0	72.91%	64.89%	59.86%	58.07%	54.41%	51.25%	45.71%
mRNA-seq	C76	55033197	93.6%	97.2	72.08%	63.84%	59.32%	57.75%	54.63%	52.04%	47.51%
mRNA-seq	C77	60543298	90.4%	102.6	70.25%	63.14%	59.03%	57.66%	54.91%	52.66%	48.66%
mRNA-seq	C78	57149898	93.9%	34.3	68.10%	57.56%	51.00%	48.41%	42.66%	37.66%	29.43%
mRNA-seq	C79	57399051	91.9%	87.4	71.63%	62.96%	58.04%	56.23%	52.50%	49.30%	43.62%
mRNA-seq	C80	57296617	94.0%	62.5	70.60%	60.79%	55.64%	53.74%	49.70%	46.19%	40.02%
mRNA-seq	C81	57239144	90.6%	99.2	71.97%	64.34%	59.90%	58.39%	55.39%	52.84%	48.41%
mRNA-seq	C82	55116502	93.0%	88.5	73.23%	64.54%	59.66%	57.96%	54.55%	51.70%	46.65%
mRNA-seq	C83	58242432	92.2%	104.0	71.53%	64.05%	59.28%	57.68%	54.65%	52.17%	47.84%
mRNA-seq	C84	48666563	93.5%	79.0	69.89%	61.50%	56.75%	55.09%	51.64%	48.68%	43.31%
mRNA-seq	C85	53829979	89.6%	68.9	65.78%	57.41%	53.07%	51.51%	48.17%	45.20%	39.78%
mRNA-seq	C86	52866962	91.6%	92.7	69.45%	61.85%	57.41%	55.90%	52.85%	50.23%	45.51%
mRNA-seq	C87	65054132	94.0%	38.8	65.58%	55.37%	49.80%	47.61%	42.77%	38.46%	31.00%
mRNA-seq	C88	50747792	93.6%	85.0	68.99%	60.88%	56.31%	54.75%	51.58%	48.87%	43.90%
mRNA-seq	C89	51473715	93.6%	94.4	69.04%	61.44%	57.23%	55.78%	52.83%	50.30%	45.81%
mRNA-seq	C90	55504963	88.0%	43.5	67.15%	57.62%	52.05%	49.87%	45.09%	40.82%	33.43%
mRNA-seq	C91	56979003	88.3%	98.5	71.24%	62.50%	58.07%	56.57%	53.42%	50.70%	45.89%
mRNA-seq	C93	60407391	87.7%	85.2	70.56%	62.08%	57.62%	56.09%	52.95%	50.30%	45.51%
mRNA-seq	C94	54869306	87.6%	56.5	66.73%	55.05%	48.11%	45.43%	39.82%	35.37%	28.57%

mRNA-seq	C95	46677801	89.1%	50.0	69.52%	59.45%	53.53%	51.29%	46.36%	41.95%	34.25%
mRNA-seq	C97	48165218	88.3%	59.0	70.81%	61.16%	55.39%	53.24%	48.70%	44.71%	37.64%
mRNA-seq	C98	48160864	89.7%	68.2	66.48%	57.69%	52.89%	51.09%	47.21%	43.85%	37.83%
mRNA-seq	C100	46918546	89.6%	49.1	66.30%	57.26%	52.02%	50.04%	45.73%	41.87%	34.88%
mRNA-seq	C101	46686538	88.7%	42.7	63.95%	55.03%	49.86%	47.79%	43.10%	38.79%	31.34%
mRNA-seq	C102	44028769	88.3%	59.9	67.81%	58.83%	53.94%	52.11%	48.05%	44.37%	37.75%
mRNA-seq	CA69	38623424	97.4%	51.5	66.30%	61.18%	50.69%	48.45%	43.45%	38.92%	31.29%
mRNA-seq	CA80	45967502	97.0%	58.6	67.34%	62.33%	52.05%	49.89%	45.15%	41.02%	33.92%
mRNA-seq	CA92	86966506	90.8%	85.5	72.68%	67.18%	54.85%	52.57%	48.07%	44.59%	39.17%
mRNA-seq	CA97	66656727	90.9%	75.4	70.37%	65.61%	56.12%	54.29%	50.37%	47.07%	41.48%
WGS	A20A	557500841	99.4%	25.6	92.37%	92.26%	91.81%	91.14%	87.23%	78.93%	33.03%
WGS	A20C	554660783	99.4%	25.2	92.37%	92.28%	91.79%	91.04%	86.71%	77.43%	30.19%
WGS	A36A	587832023	99.2%	26.6	92.35%	92.24%	91.85%	91.31%	87.82%	80.30%	38.84%
WGS	A36C	564698093	99.3%	25.7	92.36%	92.26%	91.80%	91.11%	87.02%	78.30%	33.18%
WGS	A37A	593459702	99.4%	27.1	91.71%	91.58%	91.40%	91.21%	89.72%	84.13%	41.08%
WGS	A37C	576049088	95.7%	25.3	91.71%	91.60%	91.37%	91.10%	88.88%	80.36%	30.44%
WGS	A41A	707372963	99.3%	16.7	46.77%	46.74%	46.68%	46.62%	46.14%	44.80%	33.61%
WGS	A41C	646790056	99.1%	15.8	49.60%	49.57%	49.50%	49.44%	48.96%	47.11%	29.36%
WGS	A47A	655864732	99.4%	29.9	91.72%	91.59%	91.45%	91.31%	90.39%	87.28%	57.46%
WGS	A47C	641068663	99.3%	29.1	91.72%	91.61%	91.47%	91.34%	90.41%	86.95%	52.99%
WGS	A74A	635137485	99.4%	28.9	92.37%	92.29%	91.99%	91.56%	88.70%	83.02%	51.78%
WGS	A74C	601139599	99.3%	27.3	92.37%	92.28%	91.92%	91.38%	87.92%	80.79%	42.66%
WGS	A96A	577971904	99.5%	26.3	92.36%	92.20%	91.64%	91.05%	87.43%	76.92%	36.16%
WGS	A96C	696071210	99.2%	31.7	92.37%	92.29%	92.06%	91.79%	89.86%	85.67%	64.80%
WGS	C08A	565823199	99.4%	25.6	91.71%	91.56%	91.26%	90.83%	87.44%	76.60%	28.83%
WGS	C08C	584734725	99.4%	26.5	91.73%	91.60%	91.41%	91.20%	89.51%	83.04%	37.27%
WGS	CA97A	594020294	99.3%	26.9	92.37%	92.26%	91.79%	91.10%	86.72%	78.40%	41.37%
WGS	CA97C	724088801	99.5%	33.0	92.37%	92.30%	92.11%	91.89%	90.27%	86.48%	69.03%

Table S16. Primers used for multiplex nested PCR (F1/R1, outside; F2/R2, inside)

Group ZNF384			
EP300-F1	5' CATCTTCTCGACAAATCATTTCACA 3'	EP300-F2	5' CAAAAATGCTGGTGATAAGAGAAAT 3'
CREBBP-F1	5' ATGCTCATAAGTGTCAGAGACGAGA 3'	CREBBP-F2	5' AGCAAACGGAGAGGTTCGGG 3'
EWSR1-F1	5' CAGTTACTCTCAGCAGAACACCTATG 3'	EWSR1-F2	5' TCCAAGTCAATATAGCCAACAGAG 3'
TCF3-F1	5' GTGGGCAGCAGTGGAAGCA 3'	TCF3-F2	5' CCAGCACGAGCGTATGGGCTA 3'
TAF15-F1	5' TGGTGGTTATGAGAATCAAAAGCA 3'	TAF15-F2	5' AGCCAGCAACCATATAATAACCAG 3'
ZNF384-R1	5' GCAGGCACTGTCAGCAAGGTG 3'	ZNF384-R2	5' CATTGTGTTCTCGATCTGACCTGA 3'
Group MEF2D			
MEF2D-F1	5' TGCCCGTGTCCAATCAGAGC 3'	MEF2D-F2	5' AGCAGCCAGCACTACAGAGGAA 3'
BCL9-R1	5' GGCATTTGGAGAGGGCATC 3'	BCL9-R2	5' CTGATTGGAGTGAGAAAGTGGCT 3'
HNRNPUL1-R1	5' TGCAGCTCAATGAACAGAACCT 3'	HNRNPUL1-R2	5' ATCCAGGAAGTCCCCAACATCT 3'
SS18-R1	5' CCTGTTGAGGAGGTCTATAGGGA 3'	SS18-R2	5' GATTGCCTTGGTTAACTTGACC 3'
DAZAP1-R1	5' ACCATAAGACTGTAAACAAAGTGTGG 3'	DAZAP1-R2	5' GAGTGGCTGGTGGAGGAGGAA 3'

Table S17. Gene burden analysis

Notes:

n_nonsilent, number of non-silent mutations in this gene

n_silent, number of silent mutations in this gene

n_noncoding, number of non-coding mutations

P value, calculated by MutSigCV, by testing whether the observed mutations in a gene significantly exceeded the expected counts based on the background model. Genes with P<0.05 are presented.

FDR, false-discovery rates after multiple testing correction.

Gene	**N_nonsilent**	**N_silent**	**N_noncoding**	***P* value**	**FDR**
NRAS	29	0	0	0	0
PAX5	19	0	0	1.57E-14	1.48E-10
KRAS	15	0	0	9.84E-12	6.19E-08
RUNX1	6	0	0	3.39E-07	1.60E-03
FLT3	14	1	0	3.34E-05	1.26E-01

MLL2	14	1	0	4.03E-05	1.27E-01
PTPN11	9	1	0	1.48E-04	3.74E-01
SPRR3	3	0	0	1.58E-04	3.74E-01
UBA2	5	0	0	1.90E-04	3.98E-01
SETD2	15	0	0	2.37E-04	4.47E-01
BTG1	2	0	0	3.30E-04	5.66E-01
CGREF1	4	0	0	4.12E-04	6.48E-01
XBP1	3	0	0	7.19E-04	9.68E-01
ATXN3	3	0	0	7.84E-04	9.85E-01
CDKN2A	4	0	0	1.05E-03	1
IL1RN	2	0	0	1.19E-03	1
EZH2	6	0	0	1.74E-03	1
RPL5	2	0	0	2.56E-03	1
DCTN5	3	0	0	3.02E-03	1
NCBP2	3	0	0	3.07E-03	1
IKZF1	4	0	0	3.23E-03	1
GNB1	4	1	0	3.41E-03	1
RPTN	10	3	0	3.73E-03	1
HIST1H2AG	2	0	0	3.78E-03	1
TP53	3	0	0	4.87E-03	1
BRAF	5	0	0	6.86E-03	1
ETV6	4	0	0	8.29E-03	1
SPEF2	4	0	0	8.44E-03	1
RIT1	3	0	0	8.60E-03	1
RGS19	2	0	0	1.01E-02	1
ZFP36L2	2	0	0	1.12E-02	1
FABP2	2	0	0	1.15E-02	1
ANO5	5	0	0	1.35E-02	1
CISD1	1	0	0	1.91E-02	1
GPR137C	2	0	0	2.02E-02	1
EVI5L	3	0	0	2.11E-02	1
SH3BGRL2	1	0	0	2.20E-02	1
TMEM14E	1	0	0	2.25E-02	1

SATL1	3	0	0	2.33E-02	1
MYC	3	0	0	2.33E-02	1
TMEM92	1	0	0	2.34E-02	1
UPP2	3	0	0	2.36E-02	1
TMEM87B	2	0	0	2.39E-02	1
TAF15	2	1	0	2.69E-02	1
L3MBTL3	3	0	0	2.69E-02	1
PTH2	1	0	0	2.84E-02	1
BATF3	1	0	0	2.90E-02	1
GOLT1B	1	0	0	2.96E-02	1
FARS2	2	0	0	3.01E-02	1
P4HA2	3	0	0	3.15E-02	1
RHOJ	2	0	0	3.22E-02	1
FAM151A	3	0	0	3.26E-02	1
PDE1A	2	0	0	3.43E-02	1
KCNMB4	1	0	0	3.75E-02	1
PLA2G7	2	0	0	3.78E-02	1
GBAS	1	0	0	3.97E-02	1
TPCN2	2	0	0	3.99E-02	1
UBE2D3	2	0	0	3.99E-02	1
RFC2	2	0	0	4.07E-02	1
CREBBP	5	0	0	4.14E-02	1
ITGA6	2	0	0	4.16E-02	1
XDH	4	0	0	4.21E-02	1
AHRR	2	1	0	4.29E-02	1
XRRA1	2	0	0	4.37E-02	1
ASXL1	4	1	0	4.38E-02	1
YOD1	1	0	0	4.46E-02	1
PNPLA4	1	0	0	4.47E-02	1
LYSMD2	1	0	0	4.60E-02	1
CTTNBP2NL	2	0	0	4.72E-02	1
NF1	5	1	0	4.95E-02	1
ALLC	1	0	0	4.97E-02	1

Table S18. List of Ph-like cases and characteristic gene abnormalities.

Sample ID	gene abnormaties
C64	
A89	SNX29-JAK2
CA97	EBF1-JAK2
C49	NUP214-ABL1
A03	NUP214-ABL1, IKZF1 deletion
A81	Ik6 variant of IKZF1
A84	Ik6 variant of IKZF1
A14	IKZF1 deletion, FLT3 p.Y842C
A40	IKZF1 deletion
A87	PAX5-JAK2
B17	P2RY8-CRLF2
C33	ETV6-ABL1
A46	IGH-CRLF2, JAK2 p.R683S/p.T875N