Whole-genome profiling of primary cutaneous anaplastic large cell lymphoma

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Supplementary information

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SUPPLEMENTARY METHODS

Sequencing

For WGS, 1.2 ng of high-molecular weight genomic DNA was used to generate DNA linked-read libraries using the Chromium Genome Library & Gel Bead kit v2 (10x Genomics) according to the manufacturer's protocol. Libraries were sequenced on the Illumina HiSeq X-Ten platform using paired-end 150bp reads. For WES, genomic DNA was fragmented, 3'-adenylated and subjected to whole-exome capture using SureSelect Exome Target Enrichment kit (Agilent). Captured exome DNA was converted into single-stranded circle DNA libraries, nanoball amplified and sequenced on the BGISEQ-500 platform. For RNA-seq, transcripts were enriched with Oligo(dT) Dynabeads (Invitrogen), and libraries were prepared using reverse transcribed cDNA using TruSeq library preparation kit (Illumina) according to the manufacturer's protocol. Libraries were sequenced on the Illumina HiSeq 4000 platform. All datasets (WGS, WES, RNA-seq) have been deposited in the European Genome-Phenome Archive (EGA) under study number EGAS00001004429.

Sequence data processing

For WGS, raw data were processed using the Long Ranger pipeline (10X Genomics). Raw files were demultiplexed and converted into FastQ files with Long Ranger mkfastq (v2.1.3) function. FastQ files were aligned to reference genome GRCh38 using Long Ranger's 'Lariat' aligner (Table S2). For WES, raw reads were processed using FastQC (v0.11.7), SeqTK (v1.0-r63) and Cutadapt (v2.4). Clean reads were aligned to the human reference genome GRCh38 using BWA-MEM (v0.7.17-r1188) (Table S3). For RNA-seq, raw reads were processed with FastQC (v0.11.7) and Cutadapt (v2.4). Clean reads were aligned to human reference genome GRCh38 using STAR (v2.6.0c). Fragment counts were obtained with HTSeq-count (v0.9.1) using Ensembl gene annotations (v94). Custom scripts used for data processing can be found on GitHub (https://github.com/cagaser/pcALCL).

DNA sequencing analyses

Detection of structural genomic variants (SV) was performed using the integrated structural variant caller of 10X Genomics Long Ranger pipeline. Events detected in a healthy control (granulocytes) processed with the same pipeline were regarded as mapping artefacts and filtered out accordingly. Copy number alterations (CNAs) were identified with Control-FREEC (v8.7)[1] and GISTIC2.0[2] (Figure S2, Table S4). Non-cancer structural variants were identified using the Database of Genomic Variants[3] and filtered out accordingly. SV and CNAs were visually verified/curated using the Integrative Genomic Viewer (IGV, v2.3.78)[4] (Table S5-S6). Gene ontology annotation of rearranged genes was performed with DAVID (v6.8)[5] (Table S7). Structurally altered genes implicated in cancer were identified using the Network of Cancer Genes 6.0 (NGC 6.0)[6] and literature search (Table S8). Detection of indels/SNVs in patients with matched tumor/germline samples (i.e. cAL2-5/9-11) was performed with Mutect2 using WES data. Only variants that passed Mutect2's somatic variant filter were used for downstream analyses (Table S9-S10). Mutational signatures were detected with MuSiCa software.[7] Thirty Sézary syndrome patients with previously characterized mutational signatures[8] were included in the analysis as a technical control group. For variant analysis, exonic variants were further investigated whereas intronic/intergenic variants were excluded. Minimum sequencing depth of ≥20, variant allele frequency of ≥0.1 and ≤0.9 and variant read coverage of ≥8 were applied. To verify the somatic nature and veracity of the WES calls, aligned reads of 20 somatic mutations per patient selected at random were visually inspected in matched tumor/germline WES datasets using IGV. Cancer genes affected by indels/SNVs were identified using NGC 6.0 (Table S11). Enrichment analysis of mutated genes (indels/SNVs) was performed with Panther (v14.0)[9] (Table S12). Pathogenicity prediction of splice site mutations in *PIK3R1* was assessed with MutationTaster.[10] Indels/SNVs of special interest (i.e. PI-3-K/AKT, MAPK and G-protein pathways) detected by WES and highlighted in the manuscript were cross-verified using the WGS data. The absence of pathogenic mutations in JAK-STAT genes (i.e. *JAK1*, *JAK2*, *JAK3*, *TYK2*, *STAT1*, *STAT2*, *STAT3*, *STAT4*, *STAT5A*, *STAT5B*, *STAT6*) was confirmed by cross-examining the WGS and RNA-seq data. Detection of indels/SNVs in patients without germline samples (i.e. cAL1/6-8/12) was performed with GATK (v4.1.2) using the WGS data. Minimum sequencing depth of ≥10, variant allele frequency of ≥0.1 and ≤0.9 and variant read coverage of ≥5 were applied. Non-cancer indels/SNVs were eliminated by filtering out polymorphisms in dbSNP, variants with >5% minor allele frequency in ExAC and variants detected in exomes of an in-house cohort formed by eleven healthy volunteers. Exonic sequences of 759 genes found to be genetically altered in patients with matched tumor/germline samples (Table S13) were screened for deleterious indels/SNVs. Indels/SNVs predicted as benign/tolerated (SIFT and PolyPhen-2) and not flagged on COSMIC/ClinVar were excluded. Indels/SNVs predicted as deleterious and/or flagged as pathogenic on COSMIC/ClinVar were further investigated on Varsome and literature (Table S14). Custom scripts used for the DNA analyses can be found on GitHub (https://github.com/cagaser/pcALCL).

RNA sequencing analyses

Differential expression (DE) analysis was performed using Limma-Voom (v3.40.6) with TMM-normalized data. pcALCL samples were compared to a control group formed by seven CD4+ T-cell subsets ($T_{\text{naïve}}$, T_{H1}, T_{H2}, T_{H17}, T_{reg}, T_{EM}, T_{CM}; 5 samples per subset) generated by Bonnal et al.[11] and downloaded from EBI (https://www.ebi.ac.uk/). Genes with FDR <0.01 were considered differentially expressed (Table S15). t-SNE dimensionality reduction cluster analysis of normalized count data was performed with Rtsne package (v0.15) to assess similarities among expression profiles of sample groups (Figure S3). Fusion transcripts were investigated using an in-house pipeline that included FusionCatcher (v0.99.6a) and Star Fusion (v0.8.0). Fusion transcript calls were contrasted with genomic SV data and visually verified at DNA level using IGV (Table 1, Table S16). Gene set pathway analysis of DE genes was performed with GeneAnalytics[12] using default settings (Table S17). Activation of JAK-STAT signaling was evaluated with Broad Institute's gene set enrichment analysis software (GSEA, v2.2.4)[13] using KEGG's gene set JAK-STAT signaling from the Molecular Signatures Database (MSigDB). FDR *q* value threshold of ≤0.25, recommended by the developer, was used (Figure S4). Additional characterization of the transcriptome (ARCHS4 database)[14] as performed with Enrichr[15] (Table S18). Custom scripts used for the RNA analyses can be found on GitHub (https://github.com/cagaser/pcALCL).

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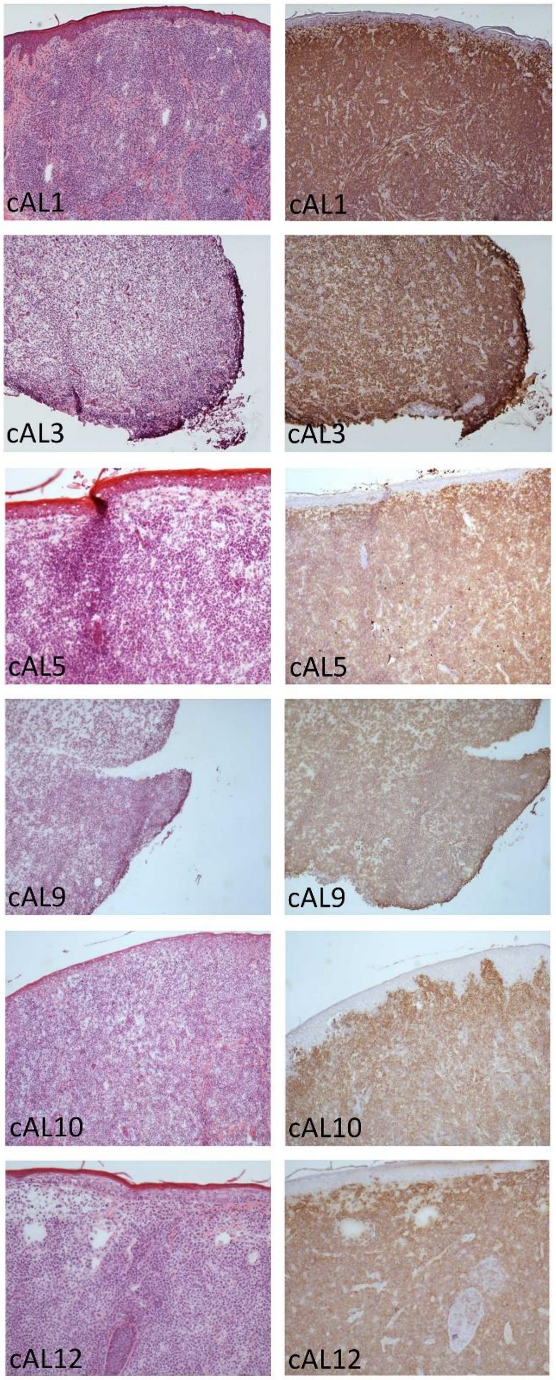
SUPPLEMENTARY FIGURES

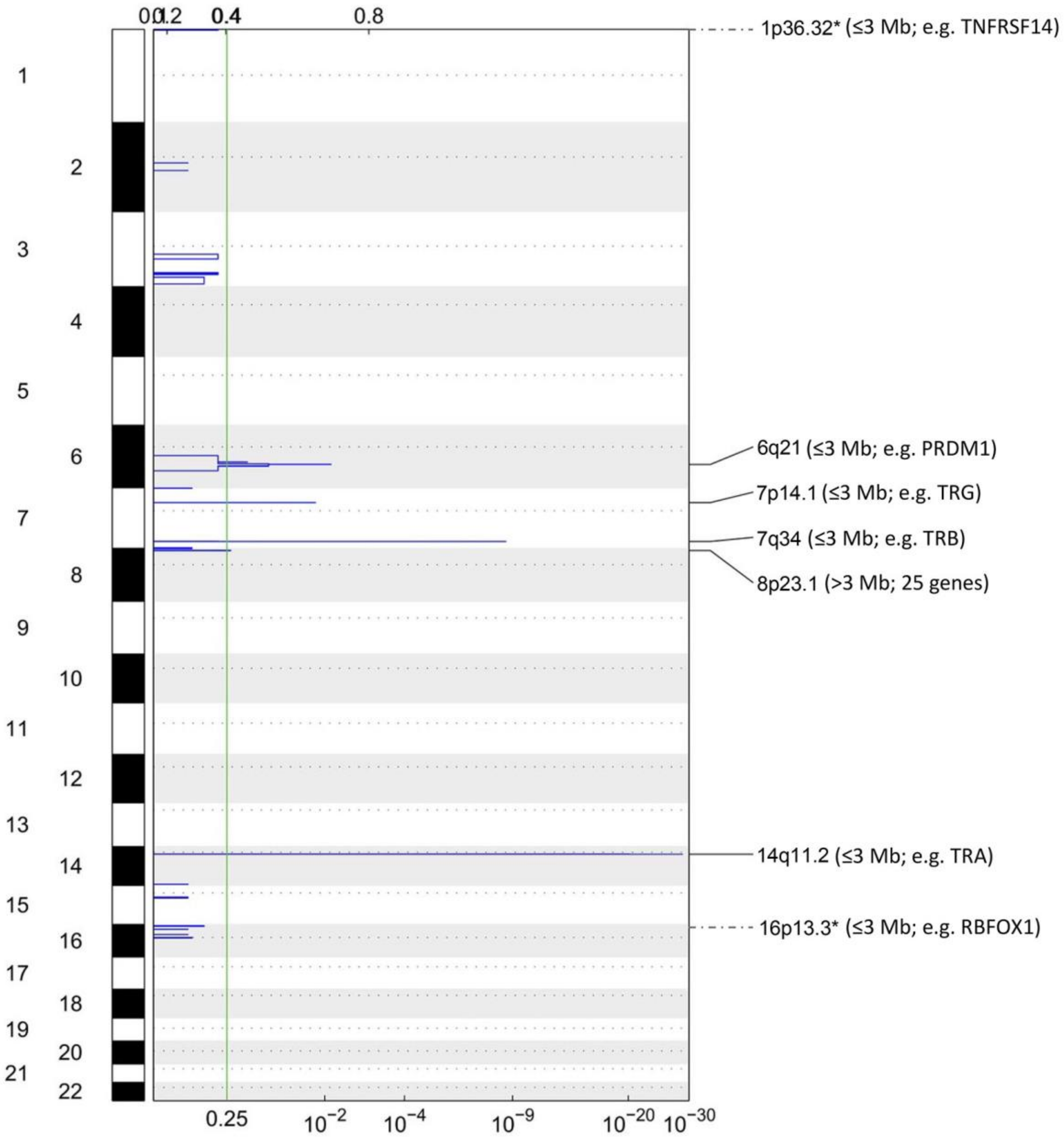
Supplementary Figure S1. Microscopy images of H&E- and CD30-stained tumor tissue from representative pcALCL patients included in the study.



Supplementary Figure S1. Microscopy images (magnification, 100X) of H&E-stained (left) and CD30-stained (right) tumor tissue from patients with pcALCL subjected to NGS.

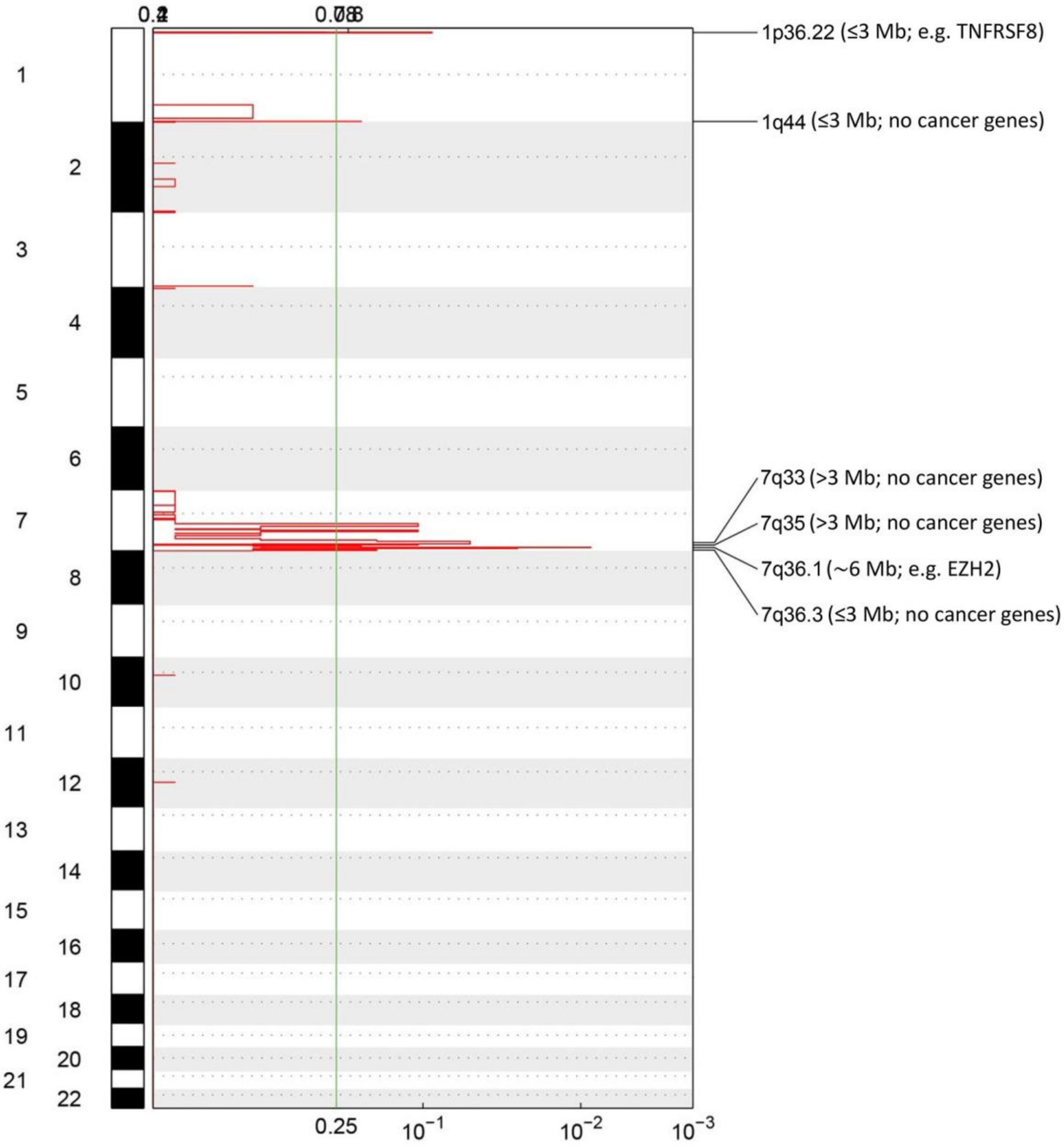
Supplementary Figure S2. Common CNAs in pcALCL detected by GISTIC2.0. analysis.

A)



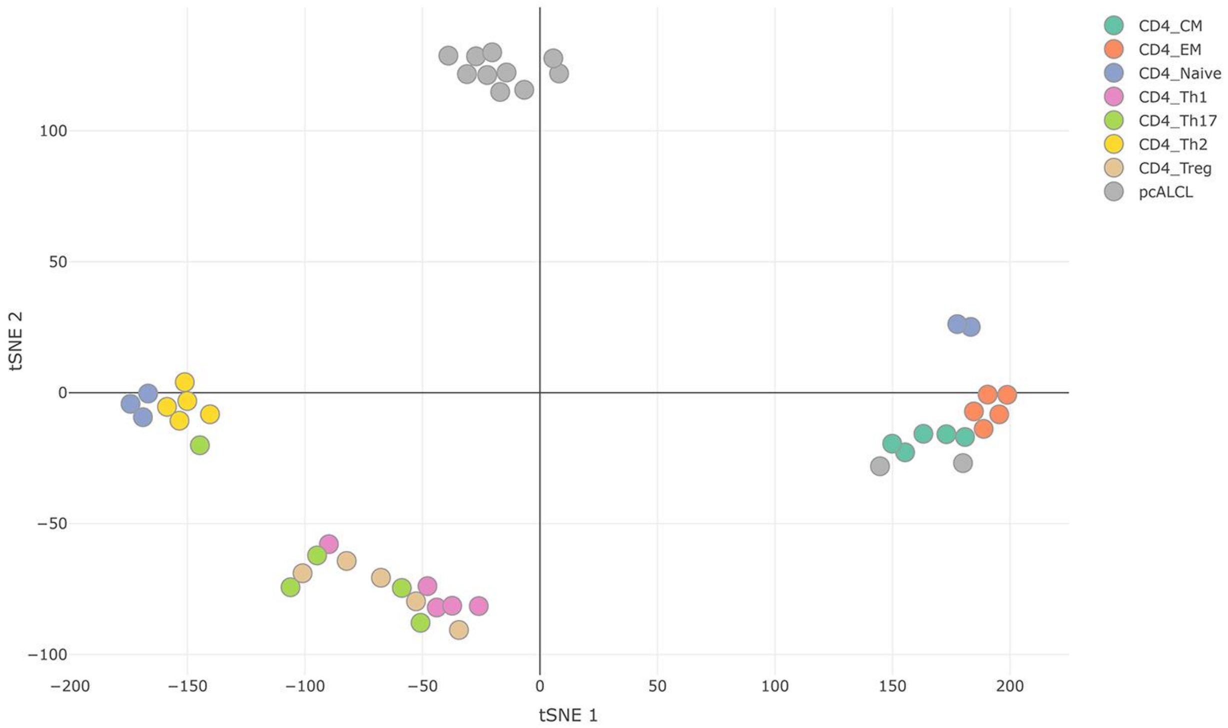
Common losses in pcALCL detected by GISTIC2.0 analysis. GISTIC2.0 detected high confidence common losses (q value ≤0.25) shared by pcALCL patients within chromosomes 6, 7, 8 and 14. Peaks at 6q21, 7p14.1, 7q34 and 14q11.2 were all ≤ 3Mb long (as verified with IGV). The peak at 6q21 enclosed tumor suppressor *PRDM1* (*BLIMP1*). Peaks at 7p14.1, 7q34 and 14q11.2 contained loci encoding the γ (TRG), β (TRB) and α (TRA) chains of the T-cell receptor (TCR), which are rearranged during T-cell development. Loss of the exact same region within *TRA*, *TRB* and *TRG* in tumor DNA from patients suggests that pcALCL is a clonal disease. Losses at lower confidence peaks (*q value >0.25) 1p36.32 and 16p13.3 were verified in patients by inspection of WGS data with IGV. These peaks contained cancer genes *TNFRSF14* and *RBFOX1*, respectively.

B)



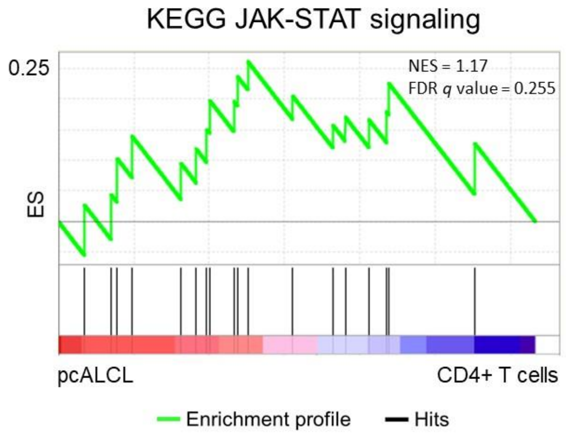
Common gains in pcALCL detected by GISTIC2.0 analysis. GISTIC2.0 detected high confidence common gains (q value ≤0.25) shared by pcALCL patients within chromosomes 1 and 7. The peak at 1p36.22 contained *TNFRSF8* (CD30), whose overexpression is a hallmark of pcALCL. Except for 7q36.1, which enclosed *EZH2*, peaks within chromosome 7 were either > 3Mb long or devoid of (putative) cancer genes, and consequently, excluded.

Supplementary Figure S3. Dimensionality reduction cluster analysis (t-SNE) of pcALCL and CD4+ T cells.



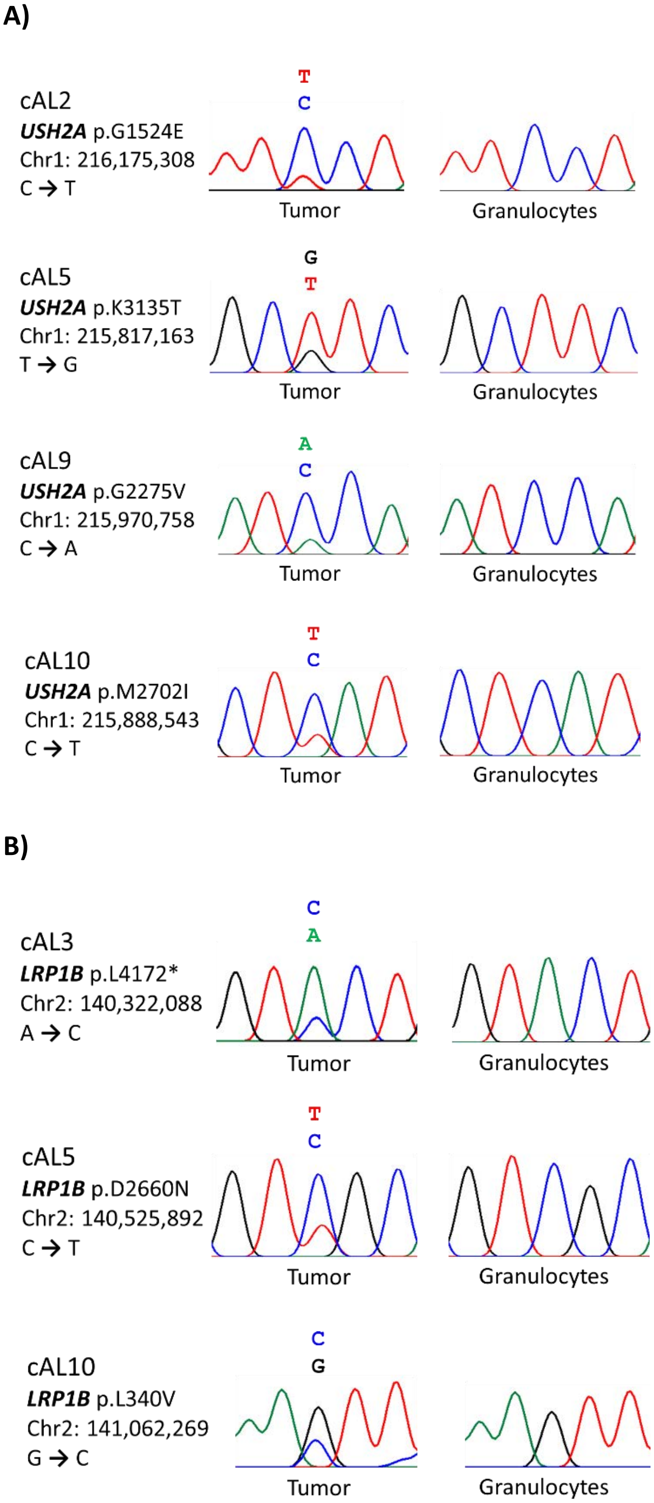
Supplementary Figure S3. t-SNE analysis of RNA-seq data did not reveal any clear preferential proximity of pcALCL towards a particular subset of normal CD4+ T cells.

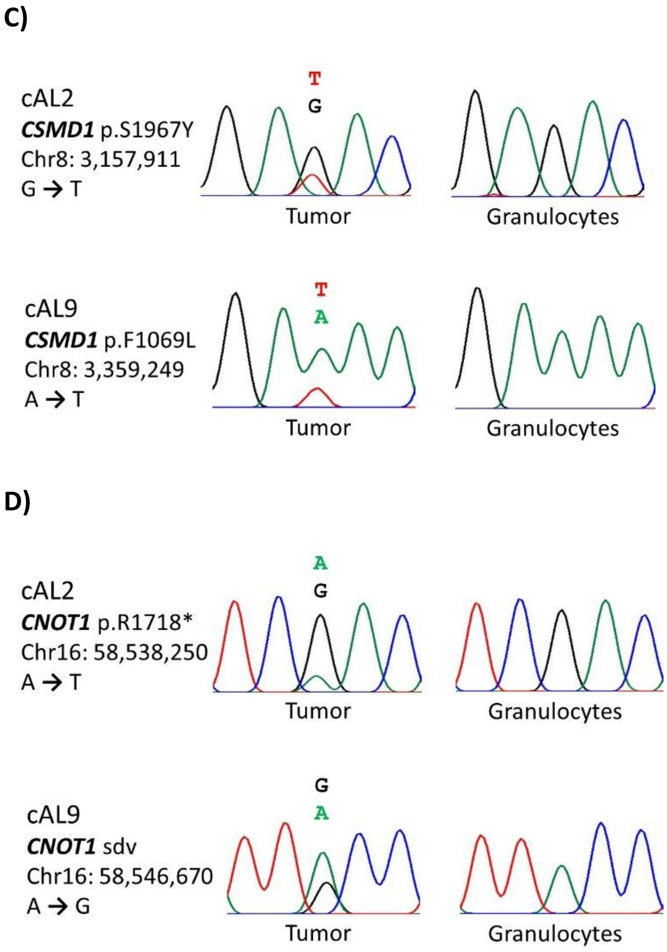
Supplementary Figure S4. GSEA of JAK-STAT signaling in pcALCL (KEGG).



Supplementary Figure S4. Gene set enrichment analysis (GSEA) of DE genes using KEGG's gene set JAK-STAT signaling produced a signature suggestive of pathway activation in pcALCL (*q*-value just outside the recommended significance cutoff point, FDR *q* value ≤ 0.25). The activation of the JAK-STAT pathway (via STAT3) was subsequently confirmed in 3 out of 8 sequenced patients with available tumor tissue by immunohistochemistry.

Supplementary Figure S5. Sanger sequencing validation of select SNVs.

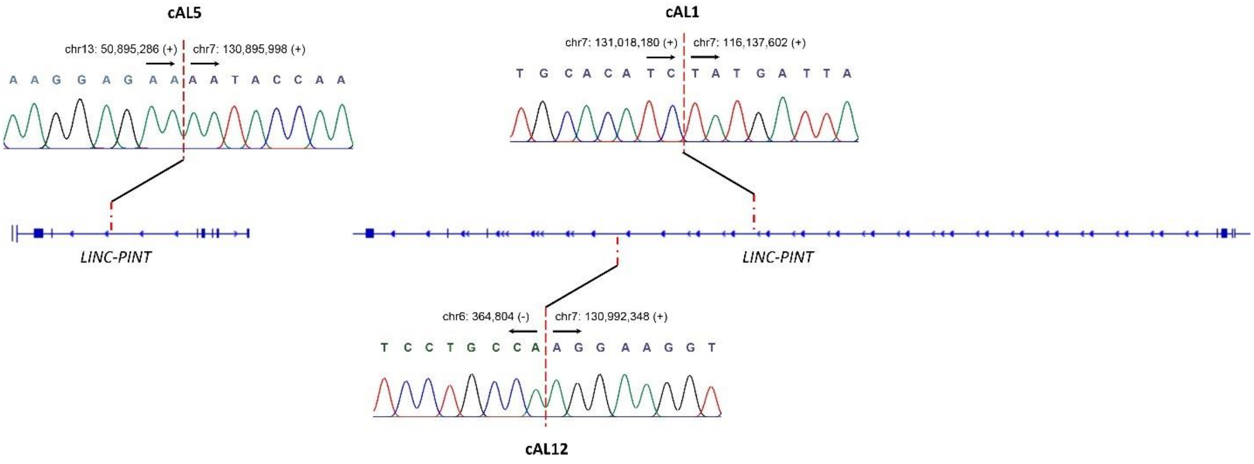




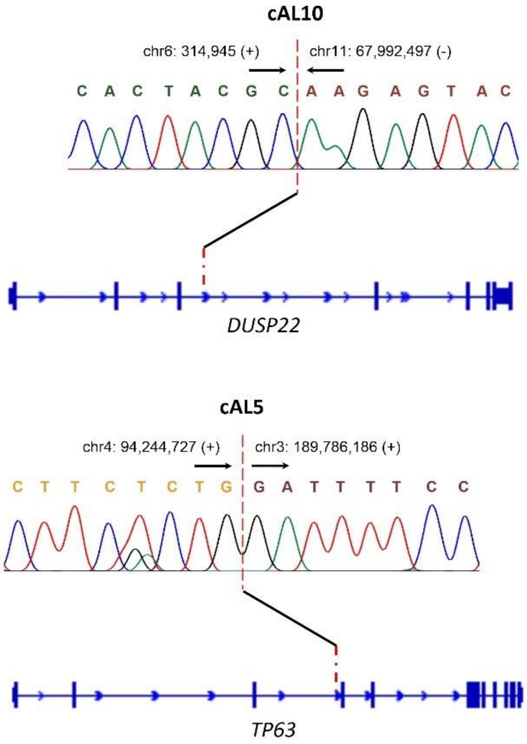
Supplementary Figure S5. Sanger chromatograms showing somatic point mutations in (A) *USH2A*, (B) *LRP1B*, (C) *CSMD1* and (D) *CNOT1* detected in pcALCL tumors by WES. These cancer-associated genes were recurrently mutated in pcALCL. Genomic coordinates according to reference genome GRCh38.

Supplementary Figure S6. Sanger sequencing validation of select genomic rearrangements.

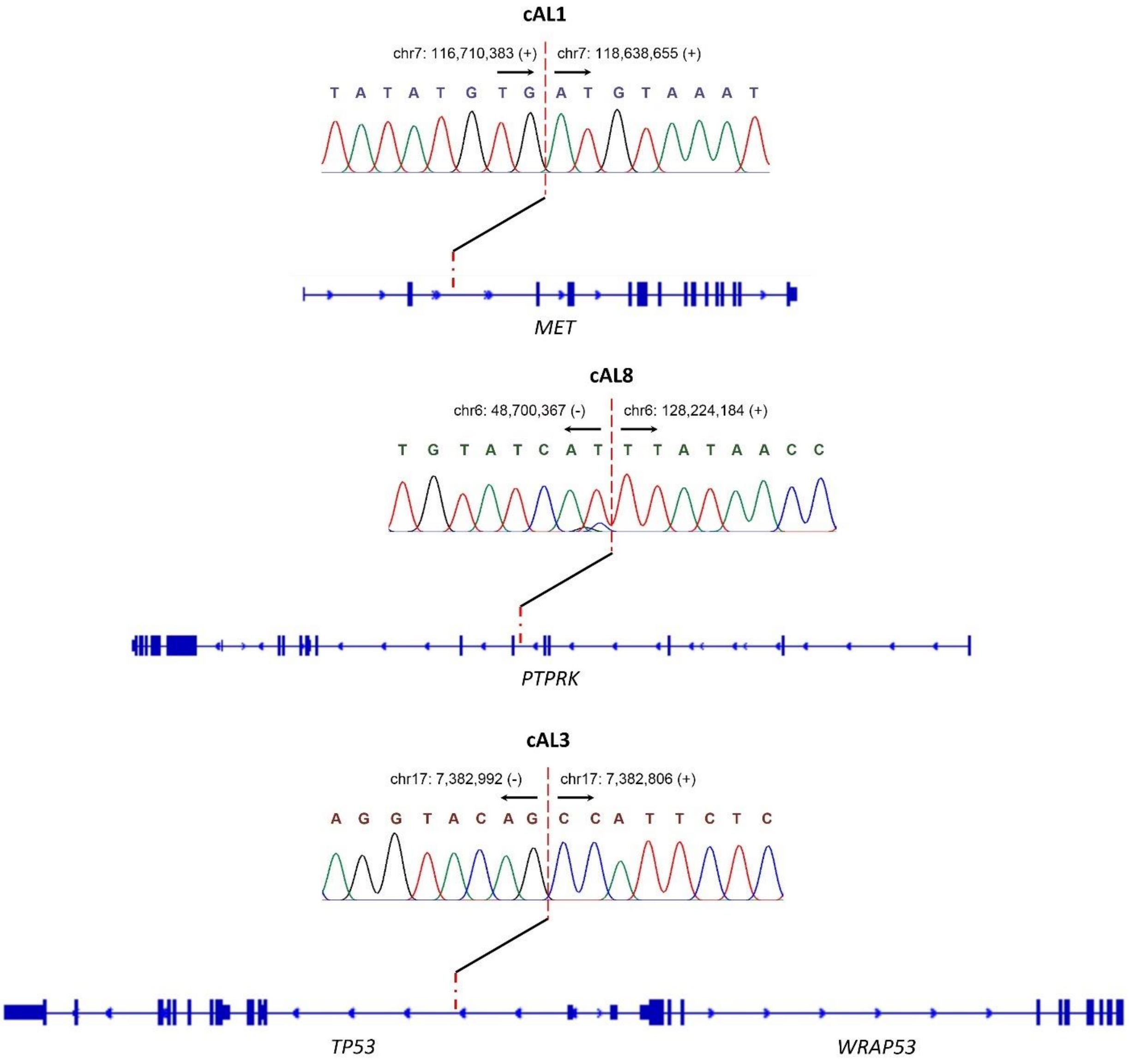
A)



B)

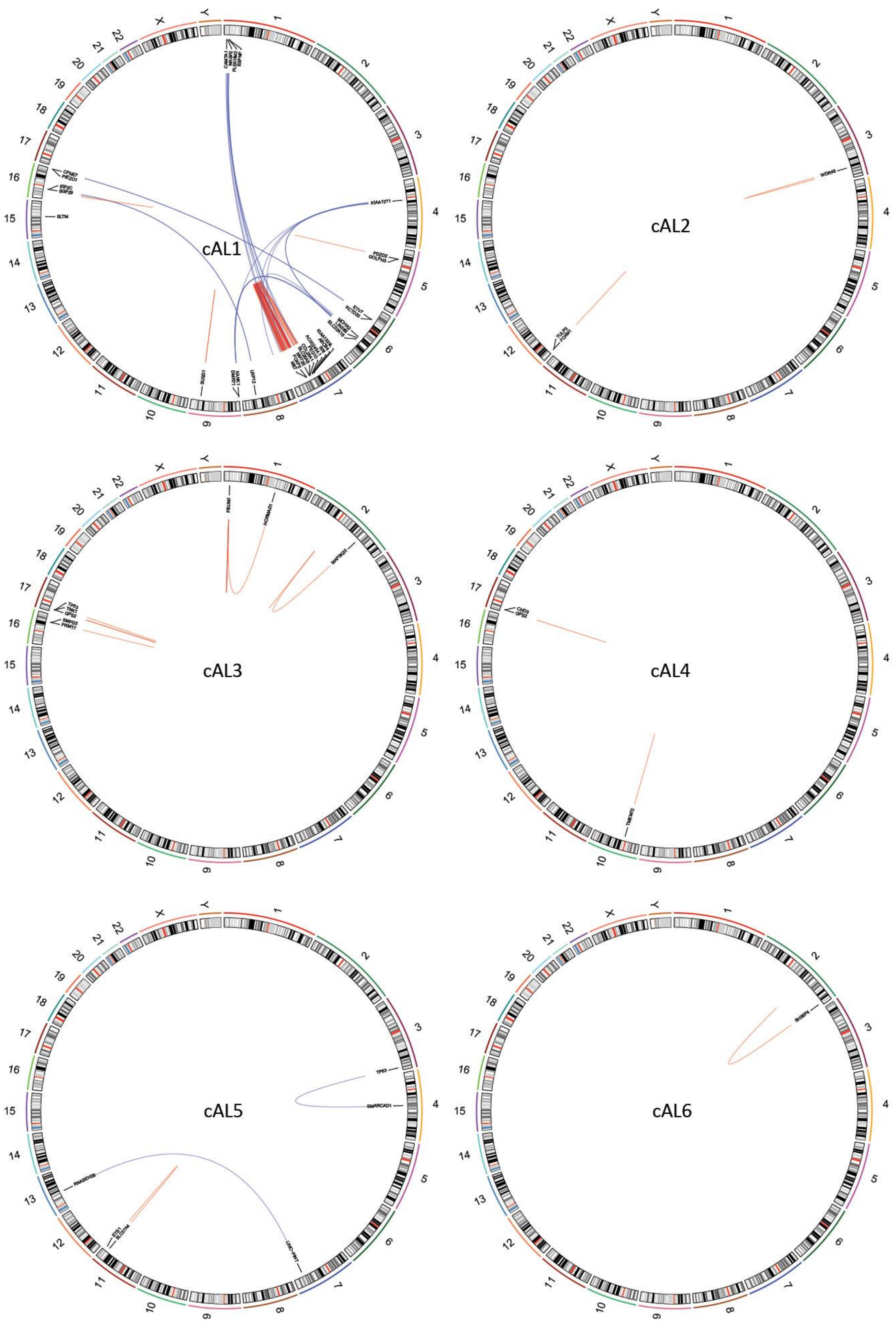


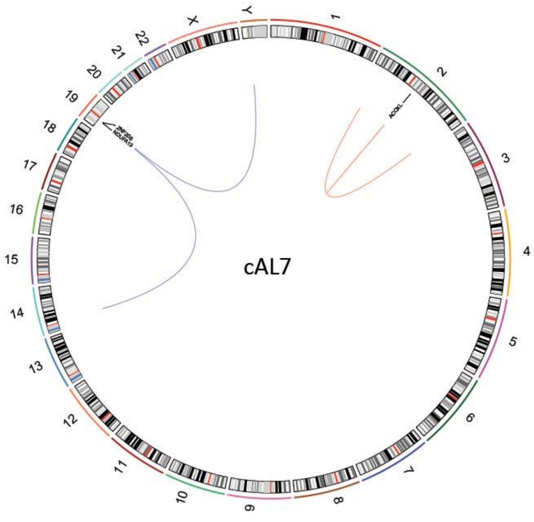
C)

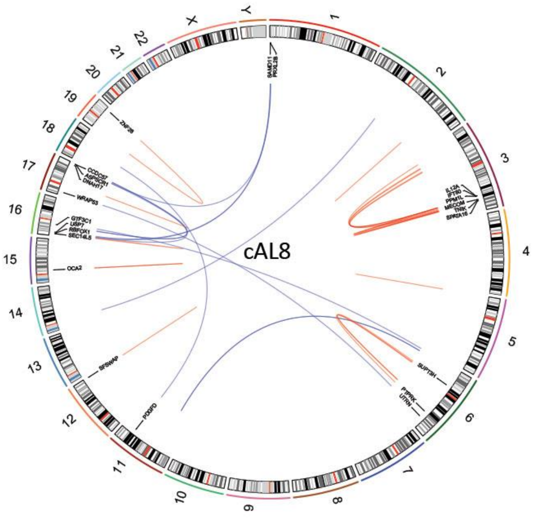


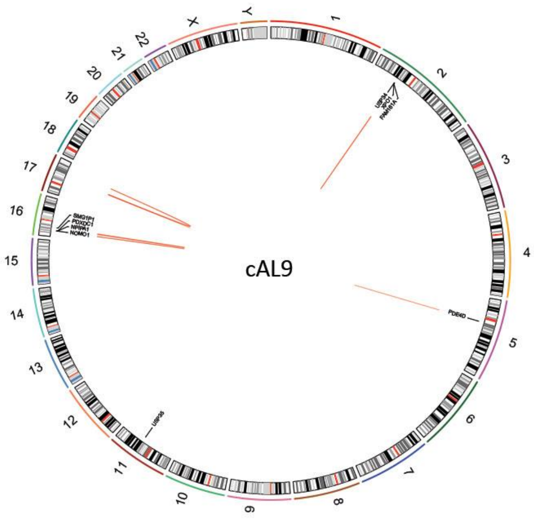
Supplementary Figure S6. Sanger chromatograms showing breakpoints of genomic rearrangements affecting cancer genes identified in pcALCL tumors by WGS. (A) Events involving *LINC-PINT* (3 of 12 patients), were the most recurrent rearrangements in pcALCL. (B) Rearrangements at *DUSP22* and *TP63* were observed in solitary cases. These events are known to occur at low frequencies in pcALCL. C) Numerous *bona fide* cancer genes (e.g. *MET*, *PTPRK*, *TP53*) were found to be impacted by rearrangements in pcALCL (See Supplementary Table S8 for a complete list of rearranged genes). Genomic coordinates according to reference genome GRCh38.

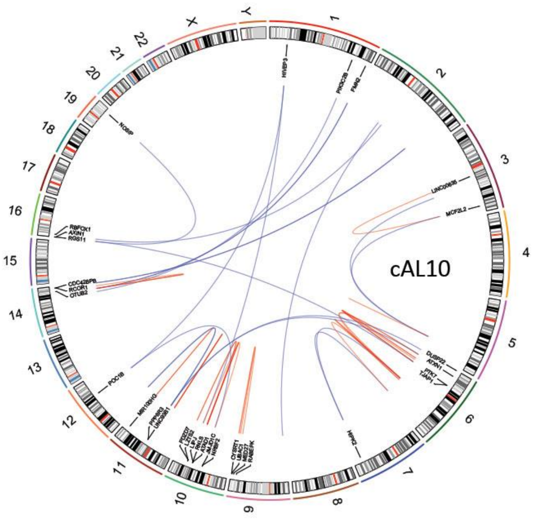
Supplementary Figure S7. Circos plots displaying genomic rearrangements per patient.

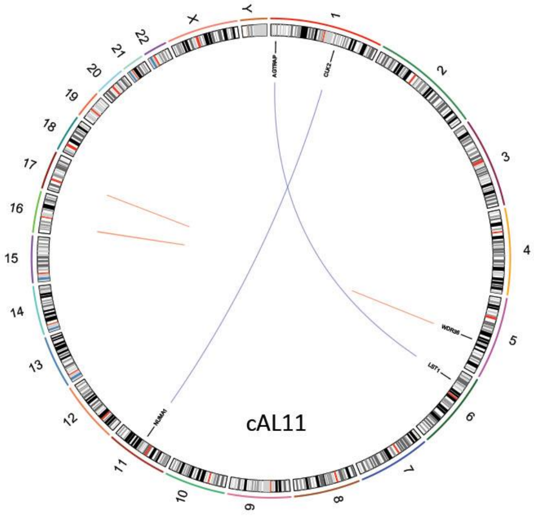


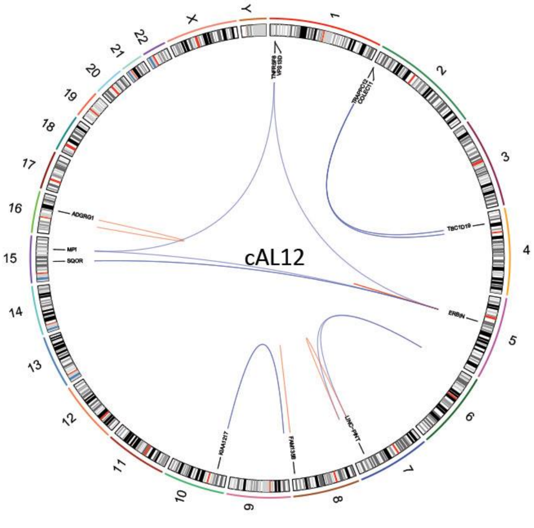












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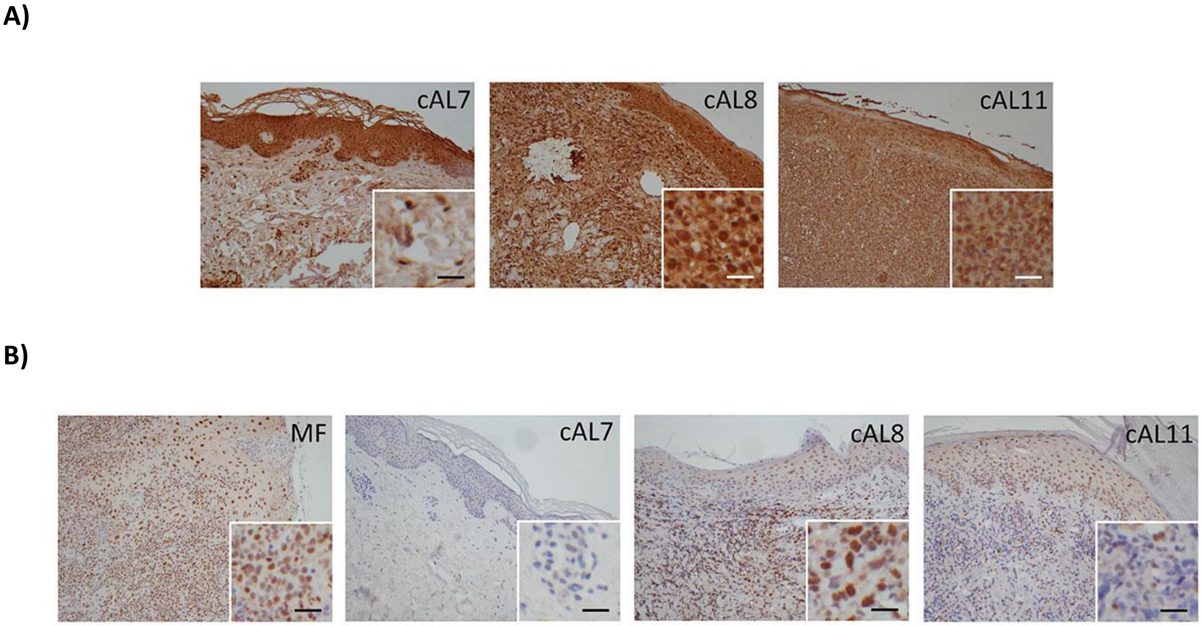
Supplementary Figure S7. Tumors from patients with pcALCL were genetically heterogeneous and contained diverse inter- and intrachromosomal rearrangements. The number of events ranged from 1 (patient cAL6) to 51 (patient cAL1) in the analyzed cohort. Rearrangements involving long noncoding RNA *LINC-PINT* (patients cAL1, cAL5, cAL12) and negative regulators of RAS-MAPK signaling: *GPS2* (patients cAL3, cAL4) and *TNK1* (patients cAL3, cAL4) were the most prominent events in pcALCL.

Supplementary Figure S8. Evaluation of AKT and STAT3 activation by immunohistochemistry on tissue of sequenced pcALCL tumors.



Supplementary Figure S8. A) Activation of P-I-3K/AKT signaling (pAKT) was positive in patients cAL8 and cAL11 and largely negative in patient cAL7. Tumor cells exhibited activated AKT in the nucleus and the cytoplasm. B) Activation of STAT3 signaling (pSTAT3) was positive in the positive control (tumor-stage mycosis fungoides, MF) and patient cAL8, negative in patient cAL7 and largely negative in patient cAL11. Tumor cells exhibited activated STAT3 in the nucleus. Scale bar, 50 µm.

SUPPLEMENTARY TABLES

Supplementary Table S1. Clinical information of samples used in the study.

Patient	Sex (M/F)	Age at diagnosis (y)	Clinical presentation	Received therapy	Result therapy	Relapse	Follow-up (months)	Tumor cell % (biopsy)
cAL1	M	62	Tumour leg	Radiotherapy	CR	No	Do (157)	75%
cAL2	M	56	Tumour elbow	Radiotherapy	CR	Skin	A+ (48)	85%
cAL3	F	30	Tumour lower leg	Radiotherapy	CR	No	Ao (42)	90%
cAL4	F	17	Tumour back	Radiotherapy	CR	No	Ao (42)	80%
cAL5	M	62	Tumour upper leg	Radiotherapy	CR	No	Ao (39)	90%
cAL6	M	80	Tumour foot	Radiotherapy	CR	Skin	Ao (78)	90%
cAL7	M	45	Multiple lesions lower leg/back	Methotrexate	PD	Skin, lymph node, pulmonary, renal	D+ (20)	90%
cAL8	M	70	Tumour back	Excision	CR	Skin, inguinal and clavicular lymph node, pulmonary	D+ (116)	90%
cAL9	M	64	Two papules flank	Radiotherapy	CR	Lymph node	Do (97)	75%
cAL10	M	68	Tumour hip	Radiotherapy	CR	No	Ao (21)	90%
cAL11	M	86	Tumour elbow	Radiotherapy	CR	No	Do (47)	80%
cAL12	M	78	Tumour forehead	Radiotherapy	CR	No	Do (39)	75%

CR, Complete remission, PD = Progressive disease, Ao = Alive without disease, A+ = Alive with disease, Do = Dead of unrelated condition, D+ = Dead of lymphoma

Supplementary Table S2. Mapping and Coverage metrics of samples subjected to WGS.

Sample	Mean depth of coverage (X)	Zero coverage (%)	Mapped reads (%)	PCR duplication (%)
cAL1	35.4	0.26	98.10	17.70
cAL2	39.5	0.25	97.80	17.50
cAL3	31.6	0.98	96.70	14.20
cAL4	33.6	0.94	95.00	15.90
cAL5	11.8	12.20	89.00	14.50
cAL6	37.7	0.28	95.20	23.00
cAL7	37.5	0.30	98.30	18.00
cAL8	38.8	0.38	98.90	6.07
cAL9	36.5	0.21	95.70	5.25
cAL10	36.7	0.50	96.50	10.10
cAL11	36.8	0.22	98.40	9.74
cAL12	34.9	0.57	98.20	7.62

Supplementary Table S3. Mapping and Coverage metrics of samples subjected to WES.

Sample	Type	Number of reads before QC	Number of reads after QC	Mapped reads (%)	Mean depth of coverage (X)
cAL2-t	Tumor	63523013	62861978	99.92%	72.1
cAL3-t	Tumor	65903884	65069310	99.92%	69.4
cAL4-t	Tumor	64797546	64033119	99.92%	71.1
cAL5-t	Tumor	64566353	63928541	99.92%	68.1
cAL9-t	Tumor	63120978	62352226	99.92%	73.3
cAL10-t	Tumor	64335450	63529715	99.89%	75.2
cAL11-t	Tumor	64436296	63721391	99.89%	71.3
cAL2-g	Germline	64397581	63622775	99.96%	74.3
cAL3-g	Germline	65176035	64433861	99.89%	73.0
cAL4-g	Germline	64896737	64105963	99.90%	75.9
cAL5-g	Germline	64016167	63204083	99.89%	71.2
cAL9-g	Germline	64154688	63474392	99.88%	68.2
cAL10-g	Germline	65635688	64899877	99.96%	73.6
cAL11-g	Germline	64404333	63709808	99.96%	73.3

Supplementary Table S4. Common CNAs in pcALCL as estimated by GISTIC2.0 algorithm.

Cytoband	Event type	# of genes in peak	*q* value	Wide peak boundaries	Focal (≤3 Mb) (IGV)
14q11.2	Loss	1	1.73E-29	chr14:22180001-22509999	YES
7q34	Loss	2	2.63E-09	chr7:142680001-142809999	YES
6q21	Loss	6	0.007514	chr6:106380498-106859999	YES
7p14.1	Loss	3	0.014838	chr7:38230001-38359999	YES
8p23.1	Loss	25	0.22798	chr8:7130001-8159999	NO
7q36.1	Gain	14	0.008311	chr7:150389993-150900009	NO
7q33	Gain	73	0.055224	chr7:130980001-141509999	NO
1p36.22	Gain	34	0.089479	chr1:11230001-12759999	YES
7q35	Gain	9	0.10552	chr7:143839992-144159779	NO
7q36.3	Gain	6	0.16699	chr7:157230001-158459954	NO
1q44	Gain	5	0.19582	chr1:248780001-248956422	YES

Supplementary Table S5. Genomic rearrangements in pcALCL detected by WGS.

Sample	Left Chr	Left Position	Right Chr	Right Position	Left Gene	Right Gene	Event Type
cAL1	chr5	32106097	chr5	32167670	PDZD2	GOLPH3	ITX
cAL1	chr7	138014393	chr6	99984660		MCHR2	CTX
cAL1	chr7	87031958	chr1	12779799	KIAA1324L		CTX
cAL1	chr7	149262928	chr1	10809783	ZNF783		CTX
cAL1	chr7	124065965	chr7	145699660			ITX
cAL1	chr7	146692041	chr7	153477686	CNTNAP2		ITX
cAL1	chr7	113060705	chr1	16614477			CTX
cAL1	chr7	113705857	chr1	16713444		ESPNP	CTX
cAL1	chr7	134491594	chr7	119257028			ITX
cAL1	chr7	125440339	chr7	119461899			ITX
cAL1	chr7	127058582	chr1	15684940	GRM8	PLEKHM2	CTX
cAL1	chr7	133589672	chr7	141902382	EXOC4		ITX
cAL1	chr7	146707703	chr7	94656441	CNTNAP2	PEG10	ITX
cAL1	chr7	143978651	chr7	149238284			ITX
cAL1	chr7	86998426	chr7	87012500	KIAA1324L	KIAA1324L	ITX
cAL1	chr7	87010194	chr7	87420478	KIAA1324L	ABCB4	ITX
cAL1	chr7	118638655	chr7	116710383		MET	ITX
cAL1	chr7	117127705	chr7	118610173	ST7		ITX
cAL1	chr7	92194866	chr7	114568254		FOXP2	ITX
cAL1	chr7	144273531	chr7	144376057	ARHGEF34P	ARHGEF5	ITX
cAL1	chr7	144186614	chr7	144266256	ARHGEF35	ARHGEF34P	ITX
cAL1	chr7	117823622	chr7	114572277	CTTNBP2	FOXP2	ITX
cAL1	chr7	88223490	chr7	101385479	SRI	COL26A1	ITX
cAL1	chr7	121376471	chr7	145388516	FAM3C		ITX
cAL1	chr7	98577958	chr7	123077802			ITX
cAL1	chr7	138013947	chr4	54915362			CTX
cAL1	chr7	141453533	chr7	137558351	TEM178B	DGKI	ITX
cAL1	chr7	92904141	chr1	11045732	AC002454.1	MASP2	CTX
cAL1	chr7	115773910	chr7	135171347			ITX
cAL1	chr7	116137602	chr7	131018180		LINC-PINT	ITX
cAL1	chr7	139349589	chr7	141496371	LUC7L2		ITX
cAL1	chr7	157017892	chr1	6989106		CAMTA1	CTX
cAL1	chr7	120759276	chr7	134934498		CALD1	ITX
cAL1	chr7	103442919	chr7	105111530	SLC26A5	KMT2E	ITX
cAL1	chr7	131451083	chr7	86984843	MKLN1	KIAA1324L	ITX
cAL1	chr7	151674628	chr7	134981342	PRKAG2		ITX
cAL1	chr6	104998570	chr9	615674	LIN28B	KANK1	CTX
cAL1	chr6	107132693	chr9	937851		DMRT1	CTX
cAL1	chr6	107150681	chr9	615940		KANK1	CTX
cAL1	chr6	110462782	chr4	56268330	SLC22A16	KIAA1211	CTX
cAL1	chr6	36358006	chr16	88736973	ETV7	PIEZO1	CTX
cAL1	chr6	36463801	chr16	89581845	KCTD20	CPNE7	CTX
cAL1	chr8	16843468	chr4	52099365			CTX
cAL1	chr8	100383106	chr16	28553937		CCDC101	CTX
cAL1	chr8	100360890	chr16	28390021		EIF3C	CTX
cAL1	chr4	54838881	chr9	895422		DMRT1	CTX
cAL1	chr4	56266912	chr6	110482684	KIAA1211		CTX
cAL1	chr9	112085252	chr9	112005919	SUSD1		ITX

cAL1	chr9	112085076	chr9	111892105	SUSD1		ITX
cAL1	chr16	21583121	chr16	22699430			ITX
cAL1	chr16	89306818	chr16	89713470	ANKRD11	VPS9D1	ITX
cAL2	chr3	173393661	chr3	167633620		WDR49	ITX
cAL2	chr12	2865243	chr12	2926965	FOXM1	TULP3	ITX
cAL3	chr2	95869386	chr2	173170376		ZAK	ITX
cAL3	chr2	95869249	chr2	95867724			ITX
cAL3	chr1	150708276	chr1	15815482	HORMAD1		ITX
cAL3	chr1	15818607	chr1	15821919			ITX
cAL3	chr1	15821256	chr1	15779885		FBLIM1	ITX
cAL3	chr1	15783253	chr1	15821188	FBLIM1		ITX
cAL3	chr1	15818583	chr1	15780117		FBLIM1	ITX
cAL3	chr16	68341805	chr16	68379554	PRMT7	SMPD3	ITX
cAL3	chr17	7386883	chr17	7315061	TNK1	GPS2	ITX
cAL3	chr17	7382806	chr17	7682463	TNK1	TP53	ITX
cAL3	chr17	17404996	chr17	17445799			ITX
cAL4	chr10	44713186	chr10	44864432		TMEM72	ITX
cAL4	chr17	7886522	chr17	7314379	CHD3	GPS2	ITX
cAL4	chr17	7387361	chr17	7361756	TNK1		ITX
cAL4	chr17	7314284	chr17	7367247	GPS2		ITX
cAL4	chr17	7309134	chr17	7367398	EIF5A		ITX
cAL4	chr17	7309294	chr17	7361671	EIF5A		ITX
cAL5	chr3	189786223	chr4	94244727	TP63	SMARCAD1	CTX
cAL5	chr11	128520859	chr11	119027083	ETS1	SLC37A4	ITX
cAL5	chr7	130895998	chr13	50895286	LINC-PINT	RNASEH2B	CTX
cAL6	chr2	235007265	chr2	153307659	SH3BP4		ITX
cAL7	chr14	19493572	chr19	19521332		NDUFA13	CTX
cAL7	chr19	21991301	chrY	15410075	ZNF208		CTX
cAL7	chr2	21714475	chr2	228188534			ITX
cAL7	chr2	110772179	chr2	111086000	ACOXL	ACOXL	ITX
cAL7	chr11	217595	chr10	102401366	SIRT3	NFKB2	CTX
cAL7	chr11	217564	chr10	102401164	SIRT3	NFKB2	CTX
cAL7	chr6	42232607	chr6	43623524	TRERF1	GTPBP2	ITX
cAL8	chr1	2590108	chr16	11611269	FAM213B		CTX
cAL8	chr1	1375843	chr17	78266463		RP11-219G17.4	CTX
cAL8	chr1	942313	chr16	8943214	SAMD11	USP7	CTX
cAL8	chr16	6707663	chr16	4969866	RBFOX1	SEC14L5	ITX
cAL8	chr16	27546658	chr17	78530684	GTF3C1	DNAH17	CTX
cAL8	chr16	27061505	chr17	82206728		CCDC57	CTX
cAL8	chr16	8506669	chr17	81978834		ASPSCR1	CTX
cAL8	chr16	33626063	chr6	382461			CTX
cAL8	chr17	7688038	chr6	144546428	WRAP53	UTRN	CTX
cAL8	chr17	36109418	chr17	36187341			ITX
cAL8	chr2	78641318	chr14	16123722			CTX
cAL8	chr2	185576951	chr2	185711999			ITX
cAL8	chr3	18016288	chr3	171084870	LOC339862	TNIK	ITX
cAL8	chr3	171085452	chr3	172950080	TNIK	SPATA16	ITX
cAL8	chr3	172956120	chr3	171035447	SPATA16		ITX
cAL8	chr3	167059422	chr3	33487086			ITX
cAL8	chr3	160469383	chr3	31448799			ITX

cAL8	chr3	42976928	chr3	160399024		IFT80	ITX
cAL8	chr3	45249129	chr3	160469273			ITX
cAL8	chr3	160974186	chr3	169337951	PPM1L	MECOM	ITX
cAL8	chr3	164528936	chr3	160055496		IL12A	ITX
cAL8	chr6	128224184	chr6	48700367	PTPRK		ITX
cAL8	chr6	50339510	chr6	117467344			ITX
cAL8	chr6	117826003	chr6	45276925		SUPT3H	ITX
cAL8	chr6	8355231	chr11	31970543			CTX
cAL8	chr6	8355229	chr11	31970603			CTX
cAL8	chr11	104092030	chr18	41811645	PDGFD		CTX
cAL8	chr15	27847986	chr15	27738001	OCA2		ITX
cAL8	chr15	27778807	chr15	27851156	OCA2	OCA2	ITX
cAL8	chr19	74244	chr19	52799301		ZNF28	ITX
cAL8	chr5	67203	chr5	119065			ITX
cAL8	chr12	131640081	chr12	131744725		SFSWAP	ITX
cAL9	chr16	15030407	chr16	14917179	PDXDC1		ITX
cAL9	chr16	14937514	chr16	14894753	NPIPA1	NOMO1	ITX
cAL9	chr16	22699430	chr16	21583121			ITX
cAL9	chr16	21488891	chr16	22450033	SMG1P3	SMG1P1	ITX
cAL9	chr17	64922453	chr17	46291987			ITX
cAL9	chr17	45584897	chr17	64919395			ITX
cAL9	chr17	45573726	chr17	46489459			ITX
cAL9	chr2	61834588	chr2	61486067	FAM161A	XPO1	ITX
cAL9	chr2	61606318	chr2	61352526		USP34	ITX
cAL9	chr5	60414914	chr5	60477374	PDE4D	PDE4D	ITX
cAL9	chr1	11804847	chr1	12367655	MTHFR	VPS13D	ITX
cAL10	chr1	240333278	chr14	86037339	FMN2	NR_110155	CTX
cAL10	chr1	240333287	chr14	85999555	FMN2	NR_110155	CTX
cAL10	chr1	204439024	chr14	76641250	PIK3C2B		CTX
cAL10	chr1	41890425	chr10	100998633	HIVEP3	LZTS2	CTX
cAL10	chr1	41709462	chr12	89049283	HIVEP3		CTX
cAL10	chr14	85999570	chr14	86051561	NR_110155	NR_110155	ITX
cAL10	chr14	94039156	chr14	85988740	OTUB2	NR_110155	ITX
cAL10	chr14	102686208	chr2	203769534	RCOR1		CTX
cAL10	chr14	102967034	chr2	203767756	CDC42BPB		CTX
cAL10	chr14	85995122	chr14	86037385	NR_110155	NR_110155	ITX
cAL10	chr19	49563990	chr16	272341	NOSIP	RGS11	CTX
cAL10	chr16	7342800	chr2	103334151	RBFOX1		CTX
cAL10	chr16	298236	chr6	43497152	AXIN1	TJAP1	CTX
cAL10	chr2	91996405	chr9	5231296			CTX
cAL10	chr12	12564397	chr11	67822146			CTX
cAL10	chr12	12564409	chr11	67822167			CTX
cAL10	chr12	89460615	chr10	63142329	POC1B	NRBF2	CTX
cAL10	chr11	68467151	chr6	16216851	PPP6R3		CTX
cAL10	chr11	67992497	chr6	314945	UNC93B1	DUSP22	CTX
cAL10	chr11	55678392	chr11	55597952			ITX
cAL10	chr11	55664075	chr11	55597413			ITX
cAL10	chr11	55667022	chr11	55596946			ITX
cAL10	chr11	55676540	chr11	55690280			ITX
cAL10	chr11	122302443	chr11	122191118		MIR100HG	ITX
cAL10	chr11	122190911	chr11	122302392	MIR100HG		ITX

cAL10	chr10	101027816	chr10	63174039	PDZD7	JMJD1C	ITX
cAL10	chr10	88480697	chr10	87801982	RNLS	ATAD1	ITX
cAL10	chr10	88101777	chr10	88580002		RNLS	ITX
cAL10	chr10	120980509	chr10	88230386			ITX
cAL10	chr10	88341561	chr10	88228682	RNLS		ITX
cAL10	chr10	121061103	chr10	88587062		LIPJ	ITX
cAL10	chr3	107845831	chr3	183321155	LINC00635	MCF2L2	ITX
cAL10	chr3	183321166	chr5	145256189	MCF2L2		CTX
cAL10	chr3	125690452	chr5	145674620			CTX
cAL10	chr5	145674619	chr5	145256185			ITX
cAL10	chr6	106346335	chr6	110957755			ITX
cAL10	chr6	105427749	chr6	106823932			ITX
cAL10	chr6	105427756	chr6	16216855			ITX
cAL10	chr6	43490565	chr6	30218650	TJAP1		ITX
cAL10	chr6	29906742	chr6	43140714		PTK7	ITX
cAL10	chr6	43497179	chr6	35192075	TJAP1		ITX
cAL10	chr6	111488547	chr6	16628949	NR_034111	ATXN1	ITX
cAL10	chr6	106085735	chr7	139674052		HIPK2	CTX
cAL10	chr6	159146942	chr7	139674052		HIPK2	CTX
cAL10	chr6	159147129	chr6	106085694			ITX
cAL10	chr9	135960125	chr9	125226314	UBAC1	RABEPK	ITX
cAL10	chr9	137225744	chr9	132013050	C9orf169	MED27	ITX
cAL11	chr17	36187341	chr17	36109418			ITX
cAL11	chr5	111081252	chr5	111111534		WDR36	ITX
cAL11	chr16	21583121	chr16	22699430			ITX
cAL11	chr1	11738153	chr6	31588590	AGTRAP	LST1	CTX
cAL11	chr1	155267627	chr11	72044112	CLK2	NUMA1	CTX
cAL11	chr17	18563491	chr17	16752810	CCDC144B	CCDC144A	ITX
cAL11	chr17	20519907	chr17	16848086			ITX
cAL11	chr17	20517243	chr17	18427376		KRT17P2	ITX
cAL11	chr17	46356512	chr17	46087894	ARL17B	KANSL1	ITX
cAL11	chr17	46292177	chr17	64922515			ITX
cAL11	chr17	64919314	chr17	45585010	LRRC37A3		ITX
cAL11	chr17	46489472	chr17	45573472			ITX
cAL11	chr17	46575286	chr17	46357576	ARL17A	ARL17B	ITX
cAL11	chr16	33626063	chr6	382461			CTX
cAL11	chr16	69389942	chr6	256519			CTX
cAL12	chr16	35980088	chr16	57635883		GPR56	ITX
cAL12	chr1	12142510	chr5	65835505	TNFRSF8		CTX
cAL12	chr1	12244971	chr15	74893691	VPS13D	MPI	CTX
cAL12	chr5	65867113	chr5	66051566		ERBB2IP	ITX
cAL12	chr5	66078502	chr15	45654289	ERBB2IP	SQRDL	CTX
cAL12	chr5	65916857	chr15	45650204		SQRDL	CTX
cAL12	chr5	65899966	chr5	65967591		ERBB2IP	ITX
cAL12	chr5	65993316	chr5	66115339	ERBB2IP		ITX
cAL12	chr5	66129638	chr15	74879200			CTX
cAL12	chr10	24080089	chr9	2981658	KIAA1217		CTX
cAL12	chr10	24080278	chr9	2981551	KIAA1217		CTX
cAL12	chr2	3640549	chr4	37689757	COLEC11		CTX
cAL12	chr2	3646528	chr4	26732789		TBC1D19	CTX
cAL12	chr2	3436901	chr4	26193798	TRAPPC12		CTX

cAL12	chr2	3434484	chr4	37690215	TRAPPC12		CTX
cAL12	chr6	364623	chr7	153281576			CTX
cAL12	chr6	364591	chr7	130992348		LINC-PINT	CTX
cAL12	chr8	137683887	chr8	138275697		FAM135B	ITX
cAL12	chr7	130981567	chr7	153281511	LINC-PINT		ITX

CTX, interchromosomal rearrangement; ITX, intrachromosomal rearrangement.

Supplementary Table S6. Verified focal (≤ 3Mb) minimal common regions (MCRs) between copy number alterations.

Cytogenetic band	Copy number alteration	Chromosome Coordinates MCR		Size	Cancer genes (NCG 6.0)	Affected patients (%)
		Start	End			
1p36.32	Loss	1400000	2800000	1.4 Mb	NADK, GNB1, CFAP74, PRKCZ, SKI, PLCH2, TNFRSF14	2 (16)
3q26.1	Loss	164500000	167050000	2.5 Mb	SLITRK3	2 (16)
6q16.3	Loss	100000000	100650000	650 Kb	None	4 (33)
6q21	Loss	106102862	106107455	4.6 Kb	PRDM1	6 (50)
6q21	Loss	110950000	111500000	550 Kb	REV3L	4 (33)
13q21.1	Loss	54550000	54900000	350 Kb	none	3 (25)
13q32.2	Loss	98450000	98700000	250 Kb	STK24	3 (25)
16p13.3	Loss	4950000	6700000	1.75 Mb	RBFOX1	2 (16)
Xp22.31	Loss	6550000	8200000	1.65 Mb	none	2 (16)
1p36.22	Gain	11250000	12900000	1.65 Mb	TNFRSF18, TNFRSF8	2 (16)
2p25.3	Gain	0	1550000	1.55 Mb	TPO	3 (25)
2p15	Gain	61350000	61850000	500 Kb	XPO1	3 (25)
2q13	Gain	110800000	111100000	300 Kb	ACOXL	3 (25)
3q29	Gain	195600000	195750000	150 Kb	None	2 (16)
12q14.2	Gain	63550000	63750000	200 Kb	None	2 (16)

Supplementary Table S7. Gene ontology annotation (biological process) of genes affected by genomic rearrangements in pcALCL (DAVID v.6.8).

GO Identifier	Term	Genes	# of genes
GO:0006351	Transcription, DNA-templated	KMT2E, ZNF208, USP7, SMARCAD1, XPO1, SUPT3H, CAMTA1, ETV7, FOXM1, TP63, NFKB2, KANK1, SFSWAP, PRMT7, MED27, GTF3C1, AXIN1, CHD3, PTPRK, NRBF2, ZNF28, RCOR1, ARHGEF5, MET, TP53, DMRT1, NDUFA13, DUSP22, MECOM, TRERF1, FOXP2, GPS2, ATXN1, ETS1, ZNF783, HIPK2, HIVEP3, JMJD1C	38
GO:0051641	Cellular localization	SRI, XPO1, LZTS2, PLEKHM2, PRKAG2, UNC93B1, TP63, PPP6R3, KANK1, NUMA1, VPS13D, CNTNAP2, AXIN1, ASPSCR1, PTPRK, TNIK, TP53, NDUFA13, PDE4D, DGKI, ATXN1, TRAPPC12, SH3BP4, FMN2, TULP3, GOLPH3, WRAP53	27
GO:0007049	Cell cycle	KMT2E, SMARCAD1, XPO1, PTPRK, LZTS2, ZAK, FOXM1, PRKAG2, TP53, DMRT1, TP63, RNASEH2B, GPS2, TRAPPC12, FMN2, NUMA1, ETS1, IL12A, HORMAD1, SMPD3, CHD3	21
GO:0080134	Regulation of response to stress	TNIK, ZAK, FOXM1, MET, ARHGEF5, UNC93B1, TP63, DUSP22, MECOM, RNASEH2B, KANK1, GPS2, ETS1, HIPK2, IL12A, AXIN1	16
GO:0016569	Covalent chromatin modification	KMT2E, SMARCAD1, SUPT3H, KANSL1, RCOR1, TP53, MECOM, SIRT3, MTHFR, PRMT7, JMJD1C, USP34, CHD3	13
GO:0016569	MAPK cascade	TNIK, ZAK, FOXM1, ARHGEF5, HIPK2, DUSP22, PPM1L, PDGFD, MECOM, GPS2, AXIN1, SIRT3	12
GO:0043254	Regulation of protein complex assembly	TRAPPC12, FMN2, ARHGEF5, TP53, FBLIM1, PIEZO1, KANK1	7
GO:0001666	Response to hypoxia	FMN2, MTHFR, ETS1, HIPK2, TP53, AGTRAP	6
GO:0060326	Cell chemotaxis	ARHGEF5, SLC37A4, MET, IL12A, PDE4D, PDGFD	6
GO:0009612	Response to mechanical stimulus	PDZD7, SLC26A5, ETS1, CNTNAP2, TNFRSF8, FOXP2	6
GO:0007163	Establishment or maintenance of cell polarity	NUMA1, GOLPH3, PTK7, KANK1, CDC42BPB	5
GO:0031532	Actin cytoskeleton reorganization	MKLN1, TNIK, PTK7, CDC42BPB	4
GO:0009411	Response to UV	PTPRK, TP53, IL12A, TP63	4

Supplementary Table S8. Genes affected by genomic rearrangements in pcALCL.

A	C	D	E	F	G	H	I	J	K	L	M
ABCB4	C9orf169	**DGKI**	EIF3C	**FAM135B**	GOLPH3	HIPK2	IFT80	JMJD1C	KANK1	LIN28B	**MAP3K20**
AC002454.1	**CALD1**	DMRT1	EIF5A	FAM161A	GPR56	HIVEP3	IL12A		**KANSL1**	LINC00635	MASP2
ACOXL	**CAMTA1**	DNAH17	**ERBB2IP**	FAM213B	**GPS2***	**HORMAD1**			KCTD20	**LINC-PINT***	MCF2L2
AGTRAP	CCDC101	DUSP22	ESPNP	FAM3C	**GRM8**				**KIAA1211**	LIPJ	**MCHR2**
ANKRD11	CCDC144A		**ETS1**	FBLIM1	GTF3C1				KIAA1217	LOC339862	**MECOM***
ARHGEF34P	CCDC144B		ETV7	**FMN2**	GTPBP2				KIAA1324L	**LRRC37A3**	MED27
ARHGEF35	CCDC57		EXOC4	**FOXM1***					**KMT2E**	LST1	**MET***
ARHGEF5	**CDC42BPB**			FOXP2					KRT17P2	LUC7L2	MIR100HG
ARL17A	**CHD3**									LZTS2	MKLN1
ARL17B	CLK2										MPI
ASPSCR1	**CNTNAP2**										**MTHFR**
ATAD1	COL26A1										
ATXN1	COLEC11										
AXIN1*	CPNE7										
	CTTNBP2										

Genes in **bold** are implicated in cancer according to NCG 6.0 database. Genes in **bold** and with an **asterisk** have strong support from literature as cancer genes.

Supplementary Table S8. Genes affected by genomic rearrangements in pcALCL (continued).

N	O	P	R	S	T	U	V	W	X	Z
NDUFA13	OCA2	PDE4D	RABEPK	SAMD11	TBC1D19	UBAC1	VPS13D	WDR36	**XPO1***	**ZNF208**
NFKB2*	OTUB2	PDGFD	**RBFOX1**	SEC14L5	TJAP1	UNC93B1	VPS9D1	WDR49		**ZNF28**
NOMO1		**PDXDC1**	RCOR1	SFSWAP	TMEM178B	USP34		WRAP53		ZNF783
NOSIP		**PDZD2**	RGS11	SH3BP4	TMEM72	**USP7**				
NPIPA1		PDZD7	RNASEH2B	SIRT3	TNFRSF8	UTRN				
NR_027155		PEG10	RNLS	SLC22A16	TNIK					
NR_034111		PIEZO1	RP11-219G17.4	SLC26A5	**TNK1***					
NR_110155		**PIK3C2B**		SLC37A4	**TP53***					
NRBF2		PLEKHM2		SMARCAD1	**TP63***					
NUMA1*		POC1B		SMG1P1	TRAPPC12					
		PPM1L		SMPD3	**TRERF1**					
		PPP6R3		SPATA16	TULP3					
		PRKAG2		SQRDL						
		PRMT7		SRI						
		PTK7		ST7						
		PTPRK*		SUPT3H						
				SUSD1						

Genes in **bold** are implicated in cancer according to NCG 6.0 database. Genes in **bold** and with an **asterisk** have strong support from literature as cancer genes.

Supplementary Table S9. Small-scale mutations in patients cAL2-5/9-11 (WES).

Gene	Chr	Position	Exon	Type	Nucleotide change	Peptide change	Samples (Depth)	Samples (Reads)	Samples (VAF)
SCNN1D	chr1	1286227	7/18	Del	c.862_873del	p.E288_L291del	cAL4 (477)	cAL4 (106)	cAL4 (0.22)
PRDM16	chr1	3405532	8/17	SNV	c.1070G>A	p.R357H	cAL2 (230)	cAL2 (49)	cAL2 (0.21)
CAMTA1	chr1	7736996	14/23	SNV	c.3329C>T	p.S1110F	cAL5 (104)	cAL5 (54)	cAL5 (0.52)
H6PD	chr1	9264328	5/5	SNV	c.1868C>T	p.A623V	cAL11 (350)	cAL11 (41)	cAL11 (0.12)
HNRNPCL1	chr1	12848012	2/2	SNV	c.278G>A	p.G93E	cAL2 (422)	cAL2 (55)	cAL2 (0.13)
KLHDC7A	chr1	18483077	1/1	SNV	c.2096C>G	p.T699S	cAL9 (415)	cAL9 (123)	cAL9 (0.3)
HSPG2	chr1	21847801	61/97	SNV	c.7913C>T	p.S2638F	cAL2 (268)	cAL2 (74)	cAL2 (0.28)
C1QC	chr1	22644195	2/3	SNV	c.172G>A	p.G58R	cAL2 (63)	cAL2 (18)	cAL2 (0.29)
HTR1D	chr1	23193099	1/1	Del	c.1120del	p.R374Gfs*9	cAL3 (71)	cAL3 (21)	cAL3 (0.3)
OXCT2	chr1	39770493	1/1	SNV	c.763C>T	p.P255S	cAL5 (335)	cAL5 (100)	cAL5 (0.3)
EXO5	chr1	40515082	2/2	SNV	c.538G>A	p.V180M	cAL2 (92)	cAL2 (31)	cAL2 (0.34)
PTCH2	chr1	44830854	6/22	SNV	c.807C>A	p.S269R	cAL5 (71)	cAL5 (27)	cAL5 (0.38)
PRDX1	chr1	45511335	6/6	SNV	c.594G>T	p.Q198H	cAL5 (43)	cAL5 (18)	cAL5 (0.42)
CYP4Z1	chr1	47117766	12/12	SNV	c.1350G>A	p.R450%3D	cAL10 (145)	cAL10 (56)	cAL10 (0.38)
ZFYVE9	chr1	52238622	4/19	SNV	c.1205G>A	p.W402*	cAL2 (77)	cAL2 (16)	cAL2 (0.2)
ROR1	chr1	64177689	9/9	SNV	c.1648A>C	p.M550L	cAL5 (72)	cAL5 (19)	cAL5 (0.27)
RAVER2	chr1	64807201	.	SNV	c.1373-5T>A	.	cAL9 (88)	cAL9 (35)	cAL9 (0.4)
DNAJC6	chr1	65385758	7/19	SNV	c.847C>T	p.P283S	cAL2 (109)	cAL2 (26)	cAL2 (0.24)
DNAJC6	chr1	65386808	.	SNV	c.996-4A>G	.	cAL10 (78)	cAL10 (21)	cAL10 (0.28)
LEPR	chr1	65601547	9/20	SNV	c.1150G>A	p.V384M	cAL10 (85)	cAL10 (42)	cAL10 (0.5)
SGIP1	chr1	66729293	20/25	SNV	c.1772T>G	p.V591G	cAL5 (187)	cAL5 (62)	cAL5 (0.33)
GADD45A	chr1	67686557	3/4	Del	c.359del	p.P120Rfs*8	cAL3 (211)	cAL3 (91)	cAL3 (0.43)
LRRC7	chr1	70038864	22/27	SNV	c.2941G>A	p.G981R	cAL3 (57)	cAL3 (27)	cAL3 (0.48)
ERICH3	chr1	74606849	10/15	SNV	c.1241A>C	p.K414T	cAL5 (124)	cAL5 (37)	cAL5 (0.3)
WDR63	chr1	85093555	9/23	SNV	c.955G>A	p.D319N	cAL3 (110)	cAL3 (48)	cAL3 (0.44)
SLC44A3	chr1	94824529	3/15	SNV	c.172G>A	p.A58T	cAL2 (114)	cAL2 (29)	cAL2 (0.26)
DPYD	chr1	97079019	23/23	SNV	c.3035A>T	p.E1012V	cAL10 (93)	cAL10 (38)	cAL10 (0.41)
MAGI3	chr1	113580584	3/21	SNV	c.476A>G	p.D159G	cAL10 (180)	cAL10 (89)	cAL10 (0.49)
CD58	chr1	116544385	2/6	SNV	c.290C>A	p.S97*	cAL10 (54)	cAL10 (33)	cAL10 (0.61)
SPAG17	chr1	118028288	26/49	SNV	c.3716G>A	p.G1239E	cAL4 (142)	cAL4 (38)	cAL4 (0.27)

AC241952.2	chr1	120512472	28/42	SNV	n.4766C>T	.	cAL3 (85)	cAL3 (23)	cAL3 (0.28)
MRPL9	chr1	151763096	2/7	Ins	c.203dup	p.R69Pfs*13	cAL10 (255)	cAL10 (67)	cAL10 (0.26)
FLG	chr1	152308900	3/3	SNV	c.5986C>G	p.Q1996E	cAL11 (508)	cAL11 (66)	cAL11 (0.13)
LCE5A	chr1	152511619	2/2	SNV	c.85C>T	p.P29S	cAL10 (333)	cAL10 (86)	cAL10 (0.26)
LORICRIN	chr1	153261345	2/2	Del	c.409_423del	p.S137_S141del	cAL3 (59)	cAL3 (21)	cAL3 (0.35)
PAQR6	chr1	156243982	7/7	Del	c.921_934del	p.H307Qfs*14	cAL10 (268)	cAL10 (63)	cAL10 (0.24)
NES	chr1	156671427	4/4	SNV	c.2761G>A	p.E921K	cAL10 (270)	cAL10 (72)	cAL10 (0.27)
FCRL5	chr1	157527645	9/17	SNV	c.1932C>A	p.H644Q	cAL3 (149)	cAL3 (48)	cAL3 (0.33)
FCRL5	chr1	157544427	5/17	SNV	c.679C>T	p.R227C	cAL3 (104)	cAL3 (32)	cAL3 (0.31)
FCRL6	chr1	159814292	8/10	SNV	c.1147G>T	p.A383S	cAL10 (77)	cAL10 (22)	cAL10 (0.29)
ADAMTS4	chr1	161191439	9/9	SNV	c.2213T>C	p.L738P	cAL10 (199)	cAL10 (61)	cAL10 (0.31)
ADAMTS4	chr1	161193299	7/9	SNV	c.1825C>T	p.R609C	cAL11 (120)	cAL11 (15)	cAL11 (0.12)
F5	chr1	169540506	13/25	SNV	c.4584G>T	p.K1528N	cAL9 (93)	cAL9 (31)	cAL9 (0.34)
EEF1AKNMT	chr1	171784023	2/8	SNV	c.437T>A	p.V146D	cAL9 (116)	cAL9 (37)	cAL9 (0.32)
SEC16B	chr1	177961710	6/26	SNV	c.667C>T	p.L223F	cAL5 (49)	cAL5 (16)	cAL5 (0.33)
RGSL1	chr1	182530295	12/22	SNV	c.2177G>A	p.R726H	cAL10 (189)	cAL10 (67)	cAL10 (0.36)
SMG7	chr1	183544411	15/23	Del	c.1771_1782del	p.T591_Q594del	cAL11 (81)	cAL11 (11)	cAL11 (0.13)
HMCN1	chr1	185981044	17/107	SNV	c.2633C>T	p.S878L	cAL10 (124)	cAL10 (37)	cAL10 (0.3)
HMCN1	chr1	186151665	95/107	SNV	c.14818G>A	p.E4940K	cAL5 (97)	cAL5 (23)	cAL5 (0.23)
HMCN1	chr1	186189507	.	SNV	c.16542-5C>T	.	cAL5 (164)	cAL5 (48)	cAL5 (0.29)
PLA2G4A	chr1	186956107	14/18	SNV	c.1342G>A	p.E448K	cAL9 (24)	cAL9 (10)	cAL9 (0.42)
DENND1B	chr1	197553052	16/23	SNV	c.1210G>A	p.E404K	cAL10 (221)	cAL10 (53)	cAL10 (0.24)
CNTN2	chr1	205072567	21/23	SNV	c.2816G>A	p.R939Q	cAL10 (203)	cAL10 (41)	cAL10 (0.2)
KLHDC8A	chr1	205339323	7/9	SNV	c.628T>A	p.Y210N	cAL5 (289)	cAL5 (81)	cAL5 (0.28)
PM20D1	chr1	205832603	11/13	SNV	c.1280C>T	p.A427V	cAL10 (133)	cAL10 (34)	cAL10 (0.26)
C4BPA	chr1	207131732	8/12	SNV	c.1076G>A	p.G359E	cAL9 (67)	cAL9 (20)	cAL9 (0.31)
PLXNA2	chr1	208216763	2/32	SNV	c.1160T>G	p.L387R	cAL9 (243)	cAL9 (68)	cAL9 (0.28)
ATF3	chr1	212618218	3/4	SNV	c.332C>T	p.T111M	cAL10 (84)	cAL10 (20)	cAL10 (0.24)
USH2A	chr1	215675582	63/72	SNV	c.12329A>T	p.Y4110F	cAL10 (132)	cAL10 (52)	cAL10 (0.4)
USH2A	chr1	215817163	48/72	SNV	c.9404A>C	p.K3135T	cAL5 (97)	cAL5 (27)	cAL5 (0.28)
USH2A	chr1	215888543	41/72	SNV	c.8106G>A	p.M2702I	cAL10 (170)	cAL10 (41)	cAL10 (0.24)
USH2A	chr1	215970708	36/72	SNV	c.6874C>A	p.R2292S	cAL10 (109)	cAL10 (24)	cAL10 (0.22)
USH2A	chr1	216175308	21/72	SNV	c.4571G>A	p.G1524E	cAL2 (124)	cAL2 (38)	cAL2 (0.31)
TLR5	chr1	223113021	6/6	SNV	c.11A>C	p.H4P	cAL3 (150)	cAL3 (57)	cAL3 (0.38)

TMEM63A	chr1	225866672	9/25	SNV	c.577C>T	p.L193F	cAL2 (107)	cAL2 (33)	cAL2 (0.31)
LEFTY2	chr1	225939782	2/4	Subs	c.470_471delinsTT	p.S157F	cAL3 (106)	cAL3 (46)	cAL3 (0.44)
SIPA1L2	chr1	232428559	16/22	SNV	c.4262A>C	p.Y1421S	cAL10 (159)	cAL10 (38)	cAL10 (0.24)
MAP10	chr1	232805679	1/1	SNV	c.656C>T	p.A219V	cAL10 (233)	cAL10 (47)	cAL10 (0.2)
LYST	chr1	235702747	45/53	SNV	c.10374G>C	p.P3458%3D	cAL5 (65)	cAL5 (18)	cAL5 (0.28)
ERO1B	chr1	236253484	3/16	SNV	c.244C>T	p.P82S	cAL4 (127)	cAL4 (25)	cAL4 (0.19)
RYR2	chr1	237503320	22/105	SNV	c.2428G>A	p.E810K	cAL3 (159)	cAL3 (51)	cAL3 (0.32)
RYR2	chr1	237550537	.	SNV	c.3067-7C>T	.	cAL5 (86)	cAL5 (30)	cAL5 (0.35)
RGS7	chr1	240801513	.	SNV	c.1360-5G>A	.	cAL2 (45)	cAL2 (9)	cAL2 (0.19)
KIF26B	chr1	245686566	12/15	SNV	c.3583G>A	p.E1195K	cAL10 (171)	cAL10 (99)	cAL10 (0.58)
KIF26B	chr1	245686776	12/15	SNV	c.3793G>A	p.D1265N	cAL11 (480)	cAL11 (52)	cAL11 (0.11)
KIF26B	chr1	245688097	12/15	SNV	c.5114G>A	p.R1705H	cAL2 (81)	cAL2 (20)	cAL2 (0.24)
OR2M2	chr1	248180479	3/3	SNV	c.494C>T	p.S165F	cAL11 (324)	cAL11 (72)	cAL11 (0.22)
OR2G6	chr1	248521972	2/2	SNV	c.326C>T	p.S109L	cAL10 (174)	cAL10 (95)	cAL10 (0.55)
PGBD2	chr1	248916826	3/3	SNV	c.242G>T	p.C81F	cAL9 (145)	cAL9 (38)	cAL9 (0.26)
ZYG11A	chr1	52854487	2/14	SNV	c.113T>C	p.L38S	cAL9 (81)	cAL9 (9)	cAL9 (0.11)
LAMC2	chr1	183232645	.	SNV	c.2015-7C>T	.	cAL11 (52)	cAL4 (9)	cAL11 (0.13)
OBSCN	chr1	228351343	89/116	SNV	c.21313C>A	p.L7105M	cAL11 (25)	cAL11 (9)	cAL11 (0.26)
ROCK2	chr2	11235745	5/33	SNV	c.680A>G	p.H227R	cAL5 (332)	cAL5 (99)	cAL5 (0.3)
GDF7	chr2	20670553	2/2	SNV	c.481G>A	p.V161M	cAL5 (229)	cAL5 (70)	cAL5 (0.31)
APOB	chr2	21002623	29/29	SNV	c.12799T>C	p.S4267P	cAL2 (85)	cAL2 (25)	cAL2 (0.3)
APOB	chr2	21007203	26/29	SNV	c.9665C>T	p.S3222F	cAL10 (91)	cAL10 (32)	cAL10 (0.36)
KLHL29	chr2	23562254	3/14	SNV	c.58G>A	p.E20K	cAL2 (271)	cAL2 (33)	cAL2 (0.12)
BIRC6	chr2	32414960	10/74	SNV	c.1669C>G	p.Q557E	cAL9 (80)	cAL9 (25)	cAL9 (0.31)
CDKL4	chr2	39178551	9/9	SNV	c.1136C>T	p.S379L	cAL3 (60)	cAL3 (21)	cAL3 (0.36)
PPP1R21	chr2	48465598	9/22	SNV	c.853C>T	p.P285S	cAL5 (207)	cAL5 (68)	cAL5 (0.33)
FANCL	chr2	58198632	7/14	SNV	c.502G>A	p.D168N	cAL10 (43)	cAL10 (19)	cAL10 (0.44)
USP34	chr2	61348887	.	SNV	c.1544-1G>A	.	cAL3 (50)	cAL3 (26)	cAL3 (0.52)
CEP68	chr2	65069764	2/7	SNV	c.320T>C	p.M107T	cAL10 (194)	cAL10 (94)	cAL10 (0.48)
PROKR1	chr2	68655427	3/3	SNV	c.1033G>A	p.V345I	cAL3 (189)	cAL3 (98)	cAL3 (0.52)
ANTXR1	chr2	69070650	4/18	SNV	c.300A>T	p.E100D	cAL9 (53)	cAL9 (12)	cAL9 (0.22)
ZNF638	chr2	71368514	7/28	SNV	c.2128C>T	p.P710S	cAL11 (91)	cAL11 (16)	cAL11 (0.18)
EGR4	chr2	73291837	2/2	SNV	c.1390C>T	p.R464C	cAL10 (92)	cAL10 (43)	cAL10 (0.47)
MRPL19	chr2	75647107	2/6	SNV	c.109C>T	p.H37Y	cAL10 (187)	cAL10 (91)	cAL10 (0.49)

TCF7L1	chr2	85309287	12/12	SNV	c.1592C>T	p.S531F	cAL5 (185)	cAL5 (58)	cAL5 (0.32)
IGKV2D-24	chr2	90005319	2/2	SNV	c.50G>A	p.G17E	cAL4 (224)	cAL4 (48)	cAL4 (0.22)
VWA3B	chr2	98290527	23/28	SNV	c.3062G>A	p.G1021E	cAL5 (27)	cAL5 (14)	cAL5 (0.52)
PAX8	chr2	113242029	6/12	SNV	c.580G>T	p.D194Y	cAL11 (97)	cAL11 (18)	cAL11 (0.18)
STEAP3	chr2	119263318	6/6	SNV	c.1477G>A	p.E493K	cAL10 (246)	cAL10 (136)	cAL10 (0.55)
NCKAP5	chr2	132782090	14/20	SNV	c.4721C>A	p.S1574*	cAL4 (104)	cAL4 (22)	cAL4 (0.22)
NCKAP5	chr2	132785264	14/20	SNV	c.1547C>A	p.T516K	cAL4 (134)	cAL4 (31)	cAL4 (0.23)
RAB3GAP1	chr2	135091118	4/25	SNV	c.271G>T	p.E91*	cAL10 (105)	cAL10 (23)	cAL10 (0.22)
LRP1B	chr2	140322088	82/91	SNV	c.12515T>G	p.L4172*	cAL3 (37)	cAL3 (8)	cAL3 (0.2)
LRP1B	chr2	140525892	49/91	SNV	c.7978G>A	p.D2660N	cAL5 (178)	cAL5 (62)	cAL5 (0.35)
LRP1B	chr2	141062269	8/91	SNV	c.1018C>G	p.L340V	cAL10 (95)	cAL10 (23)	cAL10 (0.24)
SLC4A10	chr2	161771013	2/27	SNV	c.89G>A	p.R30H	cAL5 (49)	cAL5 (20)	cAL5 (0.41)
KCNH7	chr2	162836582	2/16	SNV	c.262G>A	p.G88R	cAL10 (216)	cAL10 (62)	cAL10 (0.29)
STK39	chr2	168138085	.	SNV	c.974+3A>G	.	cAL4 (133)	cAL4 (36)	cAL4 (0.27)
LRP2	chr2	169140540	72/79	SNV	c.13114G>A	p.E4372K	cAL11 (91)	cAL11 (13)	cAL11 (0.15)
LRP2	chr2	169216324	35/79	SNV	c.5755G>A	p.E1919K	cAL10 (139)	cAL10 (30)	cAL10 (0.22)
RAPGEF4	chr2	172922299	6/31	SNV	c.536A>G	p.N179S	cAL10 (177)	cAL10 (39)	cAL10 (0.22)
HOXD10	chr2	176117552	1/2	SNV	c.719C>T	p.P240L	cAL4 (84)	cAL4 (21)	cAL4 (0.26)
TTN	chr2	178573881	326/363	SNV	c.72251C>T	p.S24084F	cAL2 (103)	cAL2 (17)	cAL2 (0.16)
TTN	chr2	178734926	51/363	SNV	c.14998C>T	p.R5000C	cAL3 (124)	cAL3 (23)	cAL3 (0.18)
FSIP2	chr2	185796636	16/23	SNV	c.9500T>A	p.F3167Y	cAL3 (52)	cAL3 (13)	cAL3 (0.26)
GULP1	chr2	188529202	.	Ins	c.261+16dup	.	cAL5 (85)	cAL5 (32)	cAL5 (0.38)
COL3A1	chr2	189010724	50/51	SNV	c.4088G>A	p.R1363Q	cAL4 (110)	cAL4 (20)	cAL4 (0.19)
PMS1	chr2	189854758	9/13	SNV	c.1486G>A	p.D496N	cAL2 (84)	cAL2 (22)	cAL2 (0.26)
BOLL	chr2	197777074	4/11	SNV	c.297A>C	p.Q99H	cAL10 (164)	cAL10 (90)	cAL10 (0.55)
ADAM23	chr2	206594762	23/26	SNV	c.2104G>T	p.D702Y	cAL5 (60)	cAL5 (22)	cAL5 (0.37)
UNC80	chr2	209872847	23/64	SNV	c.3723G>A	p.M1241I	cAL11 (270)	cAL11 (38)	cAL11 (0.14)
ERBB4	chr2	211623954	18/28	Subs	c.2169_2170delinsTT	p.L724F	cAL10 (123)	cAL10 (50)	cAL10 (0.41)
RHBDD1	chr2	226995436	9/9	SNV	c.862A>G	p.T288A	cAL5 (94)	cAL5 (22)	cAL5 (0.24)
COL4A3	chr2	227277512	28/52	SNV	c.2084G>A	p.G695E	cAL5 (85)	cAL5 (20)	cAL5 (0.24)
NMUR1	chr2	231525191	3/3	SNV	c.1133A>G	p.H378R	cAL10 (157)	cAL10 (39)	cAL10 (0.25)
DGKD	chr2	233456976	20/30	SNV	c.2453A>T	p.E818V	cAL10 (57)	cAL10 (16)	cAL10 (0.29)
HDAC4	chr2	239126616	12/27	SNV	c.1358T>C	p.I453T	cAL10 (96)	cAL10 (43)	cAL10 (0.45)
PRPF40A	chr2	152676641	10/26	Del	c.774_794del	p.A261_A267del	cAL11 (40)	cAL2 (10)	cAL11 (0.22)

XIRP2	chr2	167247984	9/11	SNV	c.6592G>A	p.D2198N	cAL11 (63)	cAL4 (9)	cAL11 (0.11)
CNTN4	chr3	2903005	11/24	Subs	c.1207_1207+1delinsAA	.	cAL5 (62)	cAL5 (15)	cAL5 (0.23)
TSEN2	chr3	12503429	5/12	SNV	c.476C>T	p.S159F	cAL10 (93)	cAL10 (39)	cAL10 (0.42)
CAND2	chr3	12816997	10/15	SNV	c.2065C>T	p.P689S	cAL10 (127)	cAL10 (56)	cAL10 (0.44)
FGD5	chr3	14907639	.	SNV	c.3265-1G>A	.	cAL9 (221)	cAL9 (63)	cAL9 (0.29)
TGFBR2	chr3	30650353	4/8	SNV	c.422C>T	p.A141V	cAL10 (62)	cAL10 (31)	cAL10 (0.5)
ACAA1	chr3	38129374	6/12	SNV	c.461C>T	p.S154F	cAL10 (82)	cAL10 (40)	cAL10 (0.49)
SCN5A	chr3	38562489	22/28	Subs	c.3888_3889delinsAA	p.M1296_G1297delinsIS	cAL9 (94)	cAL9 (26)	cAL9 (0.28)
SCN11A	chr3	38863203	31/33	Subs	c.4047_4048delinsCT	p.R1350W	cAL9 (55)	cAL9 (14)	cAL9 (0.26)
SCN11A	chr3	38872212	27/33	SNV	c.3476C>T	p.S1159F	cAL10 (107)	cAL10 (37)	cAL10 (0.35)
ZNF445	chr3	44450969	.	SNV	c.599-7C>T	.	cAL10 (75)	cAL10 (33)	cAL10 (0.44)
ZNF502	chr3	44721013	4/4	SNV	c.196G>A	p.E66K	cAL9 (114)	cAL9 (38)	cAL9 (0.34)
PLXNB1	chr3	48412439	.	SNV	c.5033+3C>T	.	cAL10 (197)	cAL10 (71)	cAL10 (0.36)
PLXNB1	chr3	48420176	11/38	SNV	c.2110C>T	p.P704S	cAL5 (81)	cAL5 (19)	cAL5 (0.23)
PLXNB1	chr3	48420861	9/38	SNV	c.1906C>T	p.R636C	cAL3 (131)	cAL3 (54)	cAL3 (0.41)
COL7A1	chr3	48592668	7/118	SNV	c.878G>A	p.R293Q	cAL2 (287)	cAL2 (67)	cAL2 (0.23)
BSN	chr3	49655411	5/12	SNV	c.5855C>T	p.P1952L	cAL10 (141)	cAL10 (61)	cAL10 (0.43)
BSN	chr3	49662559	6/12	SNV	c.10714G>A	p.E3572K	cAL10 (180)	cAL10 (64)	cAL10 (0.36)
GMPPB	chr3	49723309	.	Subs	c.211-8_211-7delinsTT	.	cAL5 (354)	cAL5 (90)	cAL5 (0.25)
IQCF3	chr3	51830730	7/7	SNV	c.394G>A	p.G132S	cAL2 (182)	cAL2 (41)	cAL2 (0.23)
STAB1	chr3	52512846	29/69	SNV	c.3046C>T	p.P1016S	cAL10 (118)	cAL10 (37)	cAL10 (0.32)
ERC2	chr3	56434932	2/18	SNV	c.76C>T	p.R26C	cAL10 (73)	cAL10 (30)	cAL10 (0.41)
ADAMTS9	chr3	64561750	30/40	SNV	c.4526G>T	p.C1509F	cAL10 (140)	cAL10 (47)	cAL10 (0.34)
ADAMTS9	chr3	64594359	28/40	SNV	c.4255G>A	p.D1419N	cAL10 (130)	cAL10 (47)	cAL10 (0.36)
LRIG1	chr3	66410190	7/19	SNV	c.874A>C	p.N292H	cAL2 (164)	cAL2 (41)	cAL2 (0.25)
FRMD4B	chr3	69182725	.	SNV	c.1920-8C>A	.	cAL10 (109)	cAL10 (34)	cAL10 (0.32)
PDZRN3	chr3	73384632	10/10	SNV	c.1934G>A	p.R645H	cAL2 (328)	cAL2 (89)	cAL2 (0.27)
GBE1	chr3	81761371	.	SNV	c.143+4C>A	.	cAL5 (71)	cAL5 (25)	cAL5 (0.36)
PROS1	chr3	93896595	9/15	SNV	c.946C>T	p.R316C	cAL2 (77)	cAL2 (22)	cAL2 (0.29)
ST3GAL6	chr3	98770957	.	SNV	c.326+1G>A	.	cAL5 (83)	cAL5 (26)	cAL5 (0.32)
IMPG2	chr3	101244329	13/19	SNV	c.2002G>A	p.E668K	cAL10 (63)	cAL10 (30)	cAL10 (0.48)
LRRC58	chr3	120335036	3/4	SNV	c.733A>C	p.N245H	cAL10 (133)	cAL10 (94)	cAL10 (0.71)
GATA2	chr3	128486011	3/6	SNV	c.587C>A	p.S196Y	cAL10 (208)	cAL10 (78)	cAL10 (0.38)
ATP2C1	chr3	130994105	.	SNV	c.2159+7T>G	.	cAL10 (38)	cAL10 (14)	cAL10 (0.38)

SLC9A9	chr3	143796829	3/16	SNV	c.453G>T	p.K151N	cAL10 (49)	cAL10 (18)	cAL10 (0.37)
P2RY12	chr3	151338362	3/3	SNV	c.484C>A	p.L162M	cAL10 (154)	cAL10 (68)	cAL10 (0.44)
VEPH1	chr3	157364405	8/14	SNV	c.1235T>C	p.F412S	cAL3 (46)	cAL3 (13)	cAL3 (0.29)
FNDC3B	chr3	172378352	24/26	SNV	c.3091C>T	p.Q1031*	cAL9 (135)	cAL9 (35)	cAL9 (0.26)
LRRC15	chr3	194359704	3/3	SNV	c.1358C>T	p.T453M	cAL2 (190)	cAL2 (44)	cAL2 (0.23)
MUC4	chr3	195780280	2/25	SNV	c.11300C>T	p.S3767F	cAL5 (880)	cAL5 (337)	cAL5 (0.38)
MUC4	chr3	195784184	2/25	SNV	c.7396C>T	p.P2466S	cAL5 (1080)	cAL5 (248)	cAL5 (0.23)
ATP2B2	chr3	10340267	21/23	SNV	c.3212G>A	p.G1071E	cAL4 (71)	cAL5 (10)	cAL4 (0.12)
PLCH1	chr3	155514892	.	SNV	c.1435-8C>T	.	cAL4 (23)	cAL2 (9)	cAL4 (0.28)
RGS12	chr4	3415971	.	SNV	c.2284-7C>T	.	cAL10 (54)	cAL10 (24)	cAL10 (0.45)
SH3TC1	chr4	8233440	14/18	SNV	c.3209C>T	p.A1070V	cAL5 (97)	cAL5 (22)	cAL5 (0.23)
DRD5	chr4	9782919	1/1	SNV	c.890C>T	p.T297I	cAL10 (239)	cAL10 (108)	cAL10 (0.45)
PROM1	chr4	15979408	26/28	SNV	c.2569C>A	p.P857T	cAL11 (99)	cAL11 (16)	cAL11 (0.16)
NWD2	chr4	37325967	2/7	SNV	c.183A>T	p.E61D	cAL5 (100)	cAL5 (59)	cAL5 (0.59)
NWD2	chr4	37443310	7/7	SNV	c.1322C>T	p.T441I	cAL10 (144)	cAL10 (64)	cAL10 (0.45)
NWD2	chr4	37446534	7/7	SNV	c.4546C>T	p.R1516C	cAL10 (119)	cAL10 (46)	cAL10 (0.39)
FAM114A1	chr4	38905600	5/15	SNV	c.515G>A	p.G172E	cAL9 (92)	cAL9 (26)	cAL9 (0.29)
RBM47	chr4	40432710	6/7	SNV	c.1483G>A	p.A495T	cAL10 (39)	cAL10 (18)	cAL10 (0.46)
LNX1	chr4	53573903	2/11	SNV	c.100G>A	p.E34K	cAL10 (112)	cAL10 (44)	cAL10 (0.39)
ADGRL3	chr4	61948109	16/25	SNV	c.2434G>A	p.E812K	cAL9 (62)	cAL9 (16)	cAL9 (0.27)
YTHDC1	chr4	68320195	12/17	SNV	c.1612G>A	p.E538K	cAL10 (84)	cAL10 (31)	cAL10 (0.37)
HTN1	chr4	70055531	5/5	SNV	c.136T>A	p.Y46N	cAL9 (123)	cAL9 (36)	cAL9 (0.3)
ALB	chr4	73411996	7/15	SNV	c.714G>A	p.W238*	cAL2 (66)	cAL2 (16)	cAL2 (0.25)
EPGN	chr4	74313037	4/5	SNV	c.274G>C	p.G92R	cAL2 (39)	cAL2 (10)	cAL2 (0.27)
WDFY3	chr4	84691789	.	SNV	c.9050-4C>T	.	cAL10 (34)	cAL10 (16)	cAL10 (0.47)
NAP1L5	chr4	88697666	1/1	SNV	c.89G>A	p.G30D	cAL5 (167)	cAL5 (27)	cAL5 (0.16)
C4orf54	chr4	99650807	1/2	SNV	c.3842C>T	p.P1281L	cAL5 (210)	cAL5 (58)	cAL5 (0.28)
C4orf54	chr4	99652569	1/2	SNV	c.2080A>T	p.K694*	cAL9 (321)	cAL9 (100)	cAL9 (0.31)
CENPE	chr4	103140854	36/49	SNV	c.5714G>A	p.R1905K	cAL10 (77)	cAL10 (32)	cAL10 (0.42)
PDE5A	chr4	119562976	.	Ins	c.994-7dup	.	cAL10 (33)	cAL10 (14)	cAL10 (0.43)
PABPC4L	chr4	134200432	2/2	Ins	c.587dup	p.N196Kfs*5	cAL10 (133)	cAL10 (58)	cAL10 (0.43)
GAB1	chr4	143433493	3/11	SNV	c.370C>T	p.P124S	cAL9 (43)	cAL9 (19)	cAL9 (0.44)
ABCE1	chr4	145120087	11/18	SNV	c.1078T>C	p.F360L	cAL3 (31)	cAL3 (10)	cAL3 (0.33)
ZNF827	chr4	145892286	3/15	Subs	c.1222_1223delinsTT	p.P408L	cAL11 (64)	cAL11 (14)	cAL11 (0.21)

DCLK2	chr4	150220710	7/17	SNV	c.1115C>A	p.S372Y	cAL3 (71)	cAL3 (36)	cAL3 (0.51)
TMEM144	chr4	158215274	4/13	SNV	c.193T>G	p.W65G	cAL10 (241)	cAL10 (100)	cAL10 (0.42)
TKTL2	chr4	163472672	1/1	SNV	c.1063T>G	p.F355V	cAL5 (93)	cAL5 (29)	cAL5 (0.32)
ANXA10	chr4	168128159	2/12	SNV	c.94G>A	p.G32R	cAL9 (174)	cAL9 (52)	cAL9 (0.3)
WDR17	chr4	176177093	29/31	SNV	c.3602T>C	p.L1201S	cAL10 (81)	cAL10 (27)	cAL10 (0.34)
KIAA1109	chr4	122271388	47/86	Ins	c.7867_7869dup	p.R2623dup	cAL11 (69)	cAL3 (9)	cAL11 (0.13)
ICE1	chr5	5468991	.	SNV	c.6222+3G>A	.	cAL10 (79)	cAL10 (23)	cAL10 (0.3)
ADCY2	chr5	7717186	12/25	SNV	c.1652A>T	p.E551V	cAL10 (72)	cAL10 (31)	cAL10 (0.43)
DNAH5	chr5	13914640	10/79	SNV	c.1200G>A	p.V400%3D	cAL2 (62)	cAL2 (13)	cAL2 (0.2)
MYO10	chr5	16701361	25/41	SNV	c.3034G>C	p.E1012Q	cAL4 (211)	cAL4 (50)	cAL4 (0.24)
PRDM9	chr5	23526338	11/11	SNV	c.1250C>A	p.P417Q	cAL10 (189)	cAL10 (67)	cAL10 (0.36)
SLC1A3	chr5	36629443	.	SNV	c.182-7C>T	.	cAL5 (81)	cAL5 (16)	cAL5 (0.2)
CPLANE1	chr5	37125282	46/52	SNV	c.8758G>A	p.G2920R	cAL10 (133)	cAL10 (40)	cAL10 (0.3)
NNT	chr5	43615947	4/22	SNV	c.481C>T	p.P161S	cAL9 (151)	cAL9 (45)	cAL9 (0.3)
MAP3K1	chr5	56882493	14/20	SNV	c.3293G>A	p.S1098N	cAL3 (84)	cAL3 (29)	cAL3 (0.35)
MAST4	chr5	67164252	29/29	SNV	c.5073G>T	p.K1691N	cAL2 (170)	cAL2 (40)	cAL2 (0.24)
PIK3R1	chr5	68293835	.	SNV	c.1425+1G>A	.	cAL9 (77)	cAL9 (14)	cAL9 (0.18)
PIK3R1	chr5	68296342	.	SNV	c.1985+1G>T	.	cAL5 (122)	cAL5 (36)	cAL5 (0.3)
MARVELD2	chr5	69420086	2/7	SNV	c.701G>A	p.G234E	cAL10 (151)	cAL10 (62)	cAL10 (0.41)
ZNF366	chr5	72461113	2/5	SNV	c.384G>A	p.M128I	cAL9 (347)	cAL9 (117)	cAL9 (0.34)
ZBED3	chr5	77077212	3/3	SNV	c.667G>A	p.D223N	cAL10 (158)	cAL10 (64)	cAL10 (0.41)
MSH3	chr5	80875797	24/24	SNV	c.3349C>T	p.Q1117*	cAL2 (52)	cAL2 (13)	cAL2 (0.24)
VCAN	chr5	83521518	7/15	SNV	c.3212C>T	p.S1071L	cAL10 (108)	cAL10 (40)	cAL10 (0.37)
EDIL3	chr5	84060383	9/11	SNV	c.1054G>T	p.E352*	cAL11 (145)	cAL11 (23)	cAL11 (0.16)
CETN3	chr5	90399408	4/6	SNV	c.410A>G	p.E137G	cAL9 (95)	cAL9 (31)	cAL9 (0.33)
ADGRV1	chr5	90635273	10/90	SNV	c.1999G>T	p.D667Y	cAL11 (198)	cAL11 (29)	cAL11 (0.14)
TMEM232	chr5	110420719	14/14	SNV	c.1835C>A	p.A612E	cAL2 (85)	cAL2 (20)	cAL2 (0.24)
WDR36	chr5	111110257	13/23	SNV	c.1563T>G	p.Y521*	cAL10 (122)	cAL10 (55)	cAL10 (0.45)
MCC	chr5	113151391	4/19	SNV	c.659G>A	p.G220E	cAL10 (93)	cAL10 (34)	cAL10 (0.37)
PRR16	chr5	120686135	2/2	SNV	c.341T>C	p.L114P	cAL10 (80)	cAL10 (40)	cAL10 (0.5)
SRFBP1	chr5	122027037	8/8	SNV	c.1201C>A	p.H401N	cAL10 (117)	cAL10 (49)	cAL10 (0.42)
PPIC	chr5	123036522	1/5	SNV	c.104C>T	p.S35L	cAL2 (146)	cAL2 (28)	cAL2 (0.2)
PRDM6	chr5	123099764	3/8	SNV	c.703C>T	p.P235S	cAL9 (73)	cAL9 (24)	cAL9 (0.33)
MEGF10	chr5	127398695	7/25	SNV	c.679C>T	p.P227S	cAL3 (64)	cAL3 (31)	cAL3 (0.49)

MEGF10	chr5	127455577	24/25	SNV	c.3202A>G	p.T1068A	cAL10 (59)	cAL10 (22)	cAL10 (0.38)
FBN2	chr5	128446474	.	SNV	c.952+7C>T	.	cAL10 (68)	cAL10 (28)	cAL10 (0.41)
ADAMTS19	chr5	129620694	9/23	SNV	c.1555G>T	p.G519*	cAL2 (135)	cAL2 (35)	cAL2 (0.26)
TGFBI	chr5	136055764	11/17	Ins	c.1502dup	p.M502Nfs*15	cAL10 (121)	cAL10 (56)	cAL10 (0.46)
PCDHB4	chr5	141122368	1/1	SNV	c.370G>A	p.D124N	cAL5 (124)	cAL5 (42)	cAL5 (0.34)
PCDHB10	chr5	141193969	1/1	SNV	c.1417G>A	p.V473I	cAL3 (86)	cAL3 (31)	cAL3 (0.36)
FAT2	chr5	151549289	.	SNV	c.4789+6A>C	.	cAL5 (70)	cAL5 (26)	cAL5 (0.37)
GLRA1	chr5	151859870	4/9	SNV	c.391G>A	p.E131K	cAL3 (185)	cAL3 (75)	cAL3 (0.41)
NMUR2	chr5	152395451	.	SNV	c.937+8C>T	.	cAL10 (58)	cAL10 (20)	cAL10 (0.35)
MSX2	chr5	174724669	1/2	SNV	c.10C>T	p.P4S	cAL11 (110)	cAL11 (23)	cAL11 (0.21)
RGS14	chr5	177371382	13/15	Subs	c.1369_1370delinsTT	p.P457F	cAL5 (231)	cAL5 (62)	cAL5 (0.27)
DDX41	chr5	177514921	8/17	SNV	c.793C>T	p.P265S	cAL10 (170)	cAL10 (71)	cAL10 (0.42)
NIPBL	chr5	36985419	10/47	SNV	c.2239C>T	p.P747S	cAL2 (44)	cAL10 (9)	cAL2 (0.22)
ANKRD55	chr5	56116683	9/12	SNV	c.897C>A	p.S299R	cAL4 (84)	cAL9 (8)	cAL4 (0.1)
NUP153	chr6	17646064	.	SNV	c.1813+3A>T	.	cAL10 (80)	cAL10 (37)	cAL10 (0.46)
KIF13A	chr6	17787839	27/39	SNV	c.3298G>A	p.D1100N	cAL10 (152)	cAL10 (59)	cAL10 (0.39)
KIF13A	chr6	17855611	6/39	SNV	c.320G>A	p.G107E	cAL4 (90)	cAL4 (32)	cAL4 (0.36)
H2BC4	chr6	26123751	1/2	SNV	c.154G>A	p.D52N	cAL10 (346)	cAL10 (148)	cAL10 (0.43)
BTN3A2	chr6	26370561	5/11	SNV	c.673T>C	p.S225P	cAL4 (211)	cAL4 (62)	cAL4 (0.3)
OR11A1	chr6	29427326	5/5	SNV	c.316G>A	p.G106S	cAL10 (79)	cAL10 (27)	cAL10 (0.35)
HLA-B	chr6	31356443	.	SNV	c.344-1G>A	.	cAL10 (118)	cAL10 (65)	cAL10 (0.55)
HLA-B	chr6	31356786	2/8	Del	c.224_244del	p.W75_E82delins*	cAL10 (120)	cAL10 (56)	cAL10 (0.47)
TMEM217	chr6	37218745	2/4	SNV	c.286A>G	p.I96V	cAL5 (129)	cAL5 (36)	cAL5 (0.28)
DAAM2	chr6	39865014	5/25	SNV	c.368C>T	p.T123M	cAL11 (195)	cAL11 (25)	cAL11 (0.13)
BICRAL	chr6	42829166	6/13	Subs	c.833_834delinsGA	p.V278G	cAL9 (92)	cAL9 (20)	cAL9 (0.21)
RRP36	chr6	43029139	7/7	SNV	c.691C>T	p.R231C	cAL10 (79)	cAL10 (26)	cAL10 (0.33)
TNFRSF21	chr6	47234762	5/6	SNV	c.1646T>C	p.F549S	cAL5 (79)	cAL5 (15)	cAL5 (0.2)
CRISP1	chr6	49857338	2/8	SNV	c.63G>T	p.M21I	cAL10 (59)	cAL10 (24)	cAL10 (0.41)
PKHD1	chr6	51753194	.	SNV	c.8950+7G>A	.	cAL10 (111)	cAL10 (46)	cAL10 (0.42)
DST	chr6	56485477	.	SNV	c.14277-6C>T	.	cAL10 (43)	cAL10 (11)	cAL10 (0.27)
PHF3	chr6	63694761	6/16	Subs	c.2677_2678delinsTT	p.P893L	cAL5 (72)	cAL5 (29)	cAL5 (0.41)
ADGRB3	chr6	69048319	14/32	SNV	c.2242C>T	p.P748S	cAL10 (59)	cAL10 (24)	cAL10 (0.41)
COL12A1	chr6	75130167	37/66	SNV	c.6134G>A	p.W2045*	cAL3 (90)	cAL3 (33)	cAL3 (0.37)
GRIK2	chr6	101859495	.	SNV	c.1524+2T>A	.	cAL3 (49)	cAL3 (11)	cAL3 (0.22)

FRK	chr6	116060181	1/8	SNV	c.131G>C	p.G44A	cAL10 (114)	cAL10 (52)	cAL10 (0.46)
FAM162B	chr6	116752635	4/4	SNV	c.451G>A	p.E151K	cAL4 (54)	cAL4 (20)	cAL4 (0.38)
GPRC6A	chr6	116807146	3/6	SNV	c.559C>T	p.R187W	cAL2 (94)	cAL2 (22)	cAL2 (0.24)
SLC35F1	chr6	118267124	4/8	SNV	c.607G>A	p.D203N	cAL10 (127)	cAL10 (60)	cAL10 (0.47)
SMLR1	chr6	130827501	1/2	SNV	c.88C>T	p.P30S	cAL3 (202)	cAL3 (80)	cAL3 (0.4)
TCF21	chr6	133889484	1/2	SNV	c.87G>T	p.K29N	cAL11 (249)	cAL11 (27)	cAL11 (0.11)
HIVEP2	chr6	142772851	5/10	SNV	c.1888C>T	p.P630S	cAL5 (86)	cAL5 (26)	cAL5 (0.31)
SAMD5	chr6	147509250	1/2	SNV	c.322G>A	p.G108R	cAL11 (100)	cAL11 (23)	cAL11 (0.23)
ARID1B	chr6	157181057	12/20	SNV	c.3224G>A	p.R1075Q	cAL9 (87)	cAL9 (22)	cAL9 (0.26)
TTLL2	chr6	167340969	3/3	SNV	c.1069G>A	p.A357T	cAL10 (146)	cAL10 (50)	cAL10 (0.35)
FOXQ1	chr6	1313386	1/1	SNV	c.682C>T	p.R228W	cAL5 (48)	cAL10 (8)	cAL5 (0.2)
DST	chr6	56634950	22/95	SNV	c.2677G>A	p.E893K	cAL11 (61)	cAL9 (8)	cAL11 (0.16)
INTS1	chr7	1482686	27/48	SNV	c.3563C>T	p.A1188V	cAL10 (571)	cAL10 (268)	cAL10 (0.47)
EIF3B	chr7	2366566	8/19	Del	c.1332_1341del	p.D444Efs*16	cAL2 (91)	cAL2 (15)	cAL2 (0.16)
EIF3B	chr7	2366578	8/19	SNV	c.1343T>A	p.I448N	cAL2 (76)	cAL2 (15)	cAL2 (0.19)
CYTH3	chr7	6177944	.	Subs	c.250-4_250-3delinsGT	.	cAL3 (57)	cAL3 (19)	cAL3 (0.34)
IGF2BP3	chr7	23351393	6/15	SNV	c.595C>T	p.R199C	cAL2 (122)	cAL2 (46)	cAL2 (0.38)
GSDME	chr7	24719219	.	SNV	c.405-1G>A	.	cAL5 (64)	cAL5 (22)	cAL5 (0.35)
TAX1BP1	chr7	27800012	13/17	SNV	c.1686G>T	p.M562I	cAL10 (76)	cAL10 (42)	cAL10 (0.55)
BMPER	chr7	34079193	.	SNV	c.1408+7C>T	.	cAL10 (212)	cAL10 (46)	cAL10 (0.22)
VPS41	chr7	38795577	9/29	Del	c.604del	p.R202Efs*10	cAL3 (126)	cAL3 (41)	cAL3 (0.33)
HECW1	chr7	43444889	11/30	SNV	c.1717G>A	p.A573T	cAL9 (277)	cAL9 (76)	cAL9 (0.28)
RAMP3	chr7	45183150	.	SNV	c.192-7T>A	.	cAL10 (125)	cAL10 (26)	cAL10 (0.2)
VKORC1L1	chr7	65954132	2/2	SNV	c.253C>T	p.R85C	cAL5 (280)	cAL5 (72)	cAL5 (0.26)
SRRM3	chr7	76248228	3/15	SNV	c.274C>T	p.R92W	cAL10 (226)	cAL10 (52)	cAL10 (0.23)
GSAP	chr7	77381309	8/31	SNV	c.572G>T	p.R191I	cAL5 (112)	cAL5 (29)	cAL5 (0.26)
PCLO	chr7	82953083	5/25	SNV	c.7870C>T	p.P2624S	cAL4 (64)	cAL4 (15)	cAL4 (0.23)
SEMA3A	chr7	83981388	14/17	SNV	c.1585C>T	p.L529F	cAL10 (249)	cAL10 (44)	cAL10 (0.18)
SEMA3A	chr7	84060476	5/17	SNV	c.536C>T	p.S179F	cAL11 (199)	cAL11 (29)	cAL11 (0.14)
CDK14	chr7	90747747	4/15	SNV	c.436T>G	p.Y146D	cAL5 (118)	cAL5 (23)	cAL5 (0.19)
CDK14	chr7	91045936	11/15	SNV	c.1081C>T	p.H361Y	cAL3 (71)	cAL3 (29)	cAL3 (0.41)
PPP1R9A	chr7	95111320	3/20	SNV	c.1457C>T	p.A486V	cAL9 (103)	cAL9 (18)	cAL9 (0.18)
PON3	chr7	95367357	.	SNV	c.494+5G>A	.	cAL2 (37)	cAL2 (13)	cAL2 (0.36)
SEM1	chr7	96486387	2/3	SNV	c.43C>A	p.Q15K	cAL10 (284)	cAL10 (59)	cAL10 (0.21)

TRRAP	chr7	98967703	.	SNV	c.7491+5G>A	.	cAL10 (146)	cAL10 (59)	cAL10 (0.41)
TFR2	chr7	100621008	19/19	SNV	c.2255G>A	p.R752H	cAL10 (126)	cAL10 (22)	cAL10 (0.18)
MUC3A	chr7	100956014	2/12	SNV	c.4235C>T	p.T1412M	cAL10 (54)	cAL10 (11)	cAL10 (0.2)
MUC17	chr7	101034003	3/13	SNV	c.2587G>A	p.G863R	cAL10 (1267)	cAL10 (407)	cAL10 (0.32)
MUC17	chr7	101051826	9/13	SNV	c.12967G>A	p.E4323K	cAL10 (216)	cAL10 (88)	cAL10 (0.41)
PPP1R3A	chr7	113878078	4/4	SNV	c.3014A>G	p.E1005G	cAL9 (105)	cAL9 (18)	cAL9 (0.17)
CFTR	chr7	117540125	8/27	SNV	c.895G>A	p.A299T	cAL10 (193)	cAL10 (25)	cAL10 (0.13)
CFTR	chr7	117540219	8/27	SNV	c.989G>A	p.G330E	cAL9 (188)	cAL9 (45)	cAL9 (0.24)
KCND2	chr7	120275371	1/6	SNV	c.739C>T	p.R247C	cAL10 (324)	cAL10 (149)	cAL10 (0.46)
CADPS2	chr7	122388605	23/30	SNV	c.3142A>G	p.M1048V	cAL9 (139)	cAL9 (54)	cAL9 (0.39)
SND1	chr7	128081502	.	SNV	c.2110+1G>A	.	cAL10 (191)	cAL10 (40)	cAL10 (0.21)
FAM71F1	chr7	128729981	6/7	SNV	c.933G>A	p.W311*	cAL10 (293)	cAL10 (104)	cAL10 (0.36)
FLNC	chr7	128846909	.	SNV	c.4288+4T>C	.	cAL11 (154)	cAL11 (41)	cAL11 (0.27)
AKR1B15	chr7	134577015	10/12	SNV	c.878T>A	p.M293K	cAL9 (288)	cAL9 (85)	cAL9 (0.3)
SLC4A2	chr7	151062028	2/23	SNV	c.41C>T	p.S14F	cAL10 (311)	cAL10 (64)	cAL10 (0.21)
ABCF2	chr7	151222542	6/16	SNV	c.797G>A	p.W266*	cAL10 (299)	cAL10 (68)	cAL10 (0.23)
DPP6	chr7	154880947	.	SNV	c.2133+5G>A	.	cAL9 (117)	cAL9 (18)	cAL9 (0.15)
CSMD1	chr8	3157911	39/70	SNV	c.5900C>A	p.S1967Y	cAL2 (89)	cAL2 (20)	cAL2 (0.23)
CSMD1	chr8	3359249	21/70	SNV	c.3207T>A	p.F1069L	cAL9 (94)	cAL9 (22)	cAL9 (0.23)
TNKS	chr8	9615648	3/27	SNV	c.965C>G	p.A322G	cAL10 (51)	cAL10 (22)	cAL10 (0.43)
MICU3	chr8	17077832	4/15	SNV	c.617C>A	p.S206*	cAL5 (52)	cAL5 (21)	cAL5 (0.41)
SH2D4A	chr8	19333114	3/10	SNV	c.341G>T	p.R114I	cAL9 (100)	cAL9 (20)	cAL9 (0.2)
ADAM28	chr8	24341652	16/23	SNV	c.1725G>A	p.W575*	cAL11 (105)	cAL11 (14)	cAL11 (0.14)
TEX15	chr8	30845791	8/11	SNV	c.4376G>A	p.R1459K	cAL10 (87)	cAL10 (38)	cAL10 (0.44)
UNC5D	chr8	35750578	.	SNV	c.1936-4A>C	.	cAL3 (175)	cAL3 (68)	cAL3 (0.39)
CA8	chr8	60281126	1/9	SNV	c.22G>A	p.E8K	cAL10 (128)	cAL10 (57)	cAL10 (0.45)
MSC	chr8	71843833	1/2	SNV	c.346G>A	p.E116K	cAL9 (124)	cAL9 (42)	cAL9 (0.34)
KCNB2	chr8	72937516	3/3	SNV	c.2161G>A	p.E721K	cAL5 (196)	cAL5 (53)	cAL5 (0.27)
JPH1	chr8	74315600	2/6	Subs	c.399_400delinsAA	p.W133_A134delins*	cAL4 (84)	cAL4 (19)	cAL4 (0.23)
RIMS2	chr8	103936596	13/24	SNV	c.2421A>C	p.E807D	cAL2 (85)	cAL2 (16)	cAL2 (0.19)
CSMD3	chr8	112859211	11/71	SNV	c.1689C>A	p.N563K	cAL9 (222)	cAL9 (53)	cAL9 (0.24)
MRPL13	chr8	120396128	.	SNV	c.516-3C>T	.	cAL10 (213)	cAL10 (89)	cAL10 (0.42)
FER1L6	chr8	124066420	.	SNV	c.3556-8C>T	.	cAL2 (27)	cAL2 (12)	cAL2 (0.45)
FER1L6	chr8	124097859	37/41	SNV	c.4859A>C	p.K1620T	cAL10 (126)	cAL10 (52)	cAL10 (0.41)

SQLE	chr8	125020799	10/11	SNV	c.1460T>G	p.L487R	cAL5 (325)	cAL5 (83)	cAL5 (0.26)
LY6K	chr8	142703348	3/3	SNV	c.475G>T	p.A159S	cAL10 (24)	cAL10 (15)	cAL10 (0.62)
SCRIB	chr8	143803916	23/37	SNV	c.3145C>T	p.R1049C	cAL10 (162)	cAL10 (77)	cAL10 (0.48)
PPP1R16A	chr8	144500978	.	SNV	c.1037+7G>A	.	cAL10 (25)	cAL10 (10)	cAL10 (0.41)
ZNF34	chr8	144774279	6/6	SNV	c.670A>T	p.T224S	cAL2 (109)	cAL2 (33)	cAL2 (0.31)
KCNQ3	chr8	132480525	1/15	SNV	c.8T>C	p.L3P	cAL10 (35)	cAL11 (10)	cAL10 (0.19)
PTPRD	chr9	8486173	25/43	SNV	c.2644G>C	p.A882P	cAL9 (95)	cAL9 (22)	cAL9 (0.23)
MPDZ	chr9	13147591	26/47	SNV	c.3698A>T	p.N1233I	cAL9 (166)	cAL9 (40)	cAL9 (0.24)
PLIN2	chr9	19120901	5/8	SNV	c.574C>T	p.P192S	cAL11 (125)	cAL11 (24)	cAL11 (0.19)
DMRTA1	chr9	22451795	2/2	SNV	c.1399C>T	p.R467W	cAL10 (113)	cAL10 (48)	cAL10 (0.43)
ACO1	chr9	32430523	14/21	SNV	c.1675G>C	p.A559P	cAL10 (74)	cAL10 (33)	cAL10 (0.45)
DNAI1	chr9	34513178	16/20	SNV	c.1568G>A	p.G523E	cAL9 (120)	cAL9 (30)	cAL9 (0.25)
VCP	chr9	35068255	2/17	SNV	c.125C>T	p.S42F	cAL10 (35)	cAL10 (12)	cAL10 (0.35)
RUSC2	chr9	35547773	2/12	SNV	c.1252A>G	p.T418A	cAL3 (191)	cAL3 (75)	cAL3 (0.39)
TRPM3	chr9	70846548	4/25	SNV	c.506A>T	p.H169L	cAL11 (112)	cAL11 (19)	cAL11 (0.17)
RORB	chr9	74662570	6/10	SNV	c.856C>T	p.L286F	cAL10 (63)	cAL10 (19)	cAL10 (0.31)
PRUNE2	chr9	76854159	2/19	SNV	c.86C>T	p.S29L	cAL9 (102)	cAL9 (35)	cAL9 (0.35)
NTRK2	chr9	84724306	8/19	SNV	c.803C>T	p.A268V	cAL5 (104)	cAL5 (22)	cAL5 (0.21)
WNK2	chr9	93263711	14/30	SNV	c.3556C>T	p.R1186W	cAL10 (86)	cAL10 (40)	cAL10 (0.47)
ALDOB	chr9	101430836	2/9	SNV	c.52G>T	p.E18*	cAL4 (154)	cAL4 (42)	cAL4 (0.28)
GRIN3A	chr9	101737543	1/9	SNV	c.437T>G	p.L146R	cAL2 (176)	cAL2 (39)	cAL2 (0.22)
ABCA1	chr9	104806270	31/50	SNV	c.4435C>T	p.P1479S	cAL5 (31)	cAL5 (16)	cAL5 (0.51)
ACTL7B	chr9	108855048	1/1	SNV	c.883C>T	p.R295C	cAL2 (171)	cAL2 (51)	cAL2 (0.3)
ZNF483	chr9	111542301	6/6	SNV	c.1366A>G	p.K456E	cAL9 (98)	cAL9 (22)	cAL9 (0.23)
ZNF883	chr9	112997448	2/2	SNV	c.812G>A	p.G271E	cAL5 (104)	cAL5 (29)	cAL5 (0.28)
RGS3	chr9	113529271	.	SNV	c.1914+7C>T	.	cAL3 (147)	cAL3 (58)	cAL3 (0.4)
ORM1	chr9	114325116	5/6	SNV	c.504T>G	p.I168M	cAL10 (268)	cAL10 (97)	cAL10 (0.36)
TRUB2	chr9	128317220	3/8	SNV	c.248G>T	p.G83V	cAL5 (103)	cAL5 (32)	cAL5 (0.32)
COQ4	chr9	128323021	2/7	SNV	c.76C>G	p.P26A	cAL10 (86)	cAL10 (51)	cAL10 (0.59)
GTF3C4	chr9	132679298	2/5	SNV	c.1679C>G	p.A560G	cAL11 (108)	cAL11 (15)	cAL11 (0.14)
FCN2	chr9	134886444	7/8	SNV	c.574C>T	p.R192C	cAL3 (153)	cAL3 (67)	cAL3 (0.44)
ABCA2	chr9	137022975	4/49	SNV	c.241G>T	p.D81Y	cAL10 (111)	cAL10 (41)	cAL10 (0.37)
DIP2C	chr10	399140	10/37	SNV	c.1229C>T	p.P410L	cAL3 (307)	cAL3 (115)	cAL3 (0.37)
TUBAL3	chr10	5393858	4/4	SNV	c.1000G>A	p.E334K	cAL3 (188)	cAL3 (86)	cAL3 (0.46)

CDC123	chr10	12215770	5/13	SNV	c.268G>C	p.V90L	cAL11 (122)	cAL11 (14)	cAL11 (0.11)
FRMD4A	chr10	13674930	16/25	SNV	c.1232A>C	p.K411T	cAL5 (146)	cAL5 (33)	cAL5 (0.22)
MALRD1	chr10	19146323	11/40	SNV	c.1537C>T	p.H513Y	cAL10 (120)	cAL10 (48)	cAL10 (0.4)
MALRD1	chr10	19155105	12/40	SNV	c.1589C>T	p.S530F	cAL11 (98)	cAL11 (17)	cAL11 (0.18)
MLLT10	chr10	21617112	8/23	SNV	c.604A>C	p.K202Q	cAL10 (30)	cAL10 (12)	cAL10 (0.41)
ARMC3	chr10	22932038	2/19	Subs	c.42_43delinsAA	p.D15N	cAL5 (35)	cAL5 (13)	cAL5 (0.38)
PARD3	chr10	34284227	21/25	SNV	c.3093A>T	p.K1031N	cAL10 (84)	cAL10 (40)	cAL10 (0.48)
ANKRD30A	chr10	37141960	7/36	SNV	c.895G>A	p.E299K	cAL10 (165)	cAL10 (70)	cAL10 (0.42)
ZNF248	chr10	37831932	6/6	SNV	c.1423C>T	p.H475Y	cAL10 (147)	cAL10 (57)	cAL10 (0.39)
ZNF33A	chr10	38055078	6/6	Subs	c.1008_1009delinsTT	p.L337F	cAL9 (114)	cAL9 (38)	cAL9 (0.34)
RET	chr10	43123804	17/20	SNV	c.2935G>T	p.E979*	cAL2 (174)	cAL2 (41)	cAL2 (0.24)
MSMB	chr10	46040073	2/4	SNV	c.22G>A	p.V8I	cAL10 (69)	cAL10 (36)	cAL10 (0.52)
WDFY4	chr10	48832600	39/62	SNV	c.6554G>A	p.R2185H	cAL3 (232)	cAL3 (92)	cAL3 (0.4)
OGDHL	chr10	49750841	7/23	SNV	c.894C>A	p.H298Q	cAL10 (66)	cAL10 (22)	cAL10 (0.34)
ANK3	chr10	60073433	37/44	SNV	c.7448C>T	p.S2483L	cAL4 (84)	cAL4 (14)	cAL4 (0.16)
TMEM26	chr10	61410459	6/6	SNV	c.970G>A	p.G324R	cAL4 (299)	cAL4 (65)	cAL4 (0.22)
DDX21	chr10	68965441	5/15	Ins	c.857dup	p.L287Afs*17	cAL10 (122)	cAL10 (51)	cAL10 (0.42)
CDH23	chr10	71799586	52/70	SNV	c.7319G>A	p.S2440N	cAL11 (179)	cAL11 (24)	cAL11 (0.13)
LRIT2	chr10	84224819	2/4	SNV	c.406C>T	p.R136C	cAL10 (161)	cAL10 (63)	cAL10 (0.39)
LIPJ	chr10	88591480	4/11	SNV	c.112G>A	p.D38N	cAL10 (62)	cAL10 (22)	cAL10 (0.36)
HTR7	chr10	90857330	1/4	SNV	c.342G>C	p.Q114H	cAL2 (242)	cAL2 (44)	cAL2 (0.18)
CRTAC1	chr10	97908130	6/15	SNV	c.733G>A	p.V245M	cAL5 (238)	cAL5 (66)	cAL5 (0.28)
HPSE2	chr10	98459668	12/12	SNV	c.1685C>T	p.P562L	cAL5 (148)	cAL5 (40)	cAL5 (0.27)
CFAP58	chr10	104365862	5/18	SNV	c.646C>G	p.R216G	cAL10 (41)	cAL10 (13)	cAL10 (0.32)
PDZD8	chr10	117284819	5/5	Ins	c.1913dup	p.N638Kfs*12	cAL10 (78)	cAL10 (26)	cAL10 (0.34)
DOCK1	chr10	127106279	24/52	SNV	c.2494G>A	p.V832M	cAL10 (78)	cAL10 (32)	cAL10 (0.41)
MKI67	chr10	128115129	7/15	SNV	c.1279C>T	p.P427S	cAL10 (141)	cAL10 (54)	cAL10 (0.39)
TCERG1L	chr10	131146581	7/12	SNV	c.1114G>A	p.D372N	cAL4 (180)	cAL4 (42)	cAL4 (0.24)
MTG1	chr10	133398448	4/11	SNV	c.296A>G	p.H99R	cAL5 (148)	cAL5 (42)	cAL5 (0.29)
NLRP6	chr11	281283	4/8	SNV	c.1549G>C	p.G517R	cAL10 (315)	cAL10 (79)	cAL10 (0.25)
PHRF1	chr11	607279	14/18	SNV	c.1823C>T	p.P608L	cAL11 (196)	cAL11 (35)	cAL11 (0.18)
MUC5B	chr11	1244829	31/49	SNV	c.7949C>T	p.S2650F	cAL2 (65)	cAL2 (15)	cAL2 (0.24)
OSBPL5	chr11	3092503	19/22	Subs	c.2186_2188delinsATG	p.I729_L730delinsNV	cAL5 (116)	cAL5 (43)	cAL5 (0.37)
ART1	chr11	3659718	3/5	SNV	c.199A>G	p.T67A	cAL10 (235)	cAL10 (66)	cAL10 (0.28)

NUP98	chr11	3731551	14/33	SNV	c.1570C>T	p.Q524*	cAL2 (33)	cAL2 (10)	cAL2 (0.31)
UBQLNL	chr11	5515318	1/1	SNV	c.1124G>A	p.R375Q	cAL2 (126)	cAL2 (26)	cAL2 (0.2)
OR56A3	chr11	5947969	4/4	SNV	c.623G>T	p.W208L	cAL2 (324)	cAL2 (73)	cAL2 (0.23)
HPS5	chr11	18306286	7/23	SNV	c.673C>T	p.P225S	cAL10 (92)	cAL10 (55)	cAL10 (0.6)
LGR4	chr11	27384364	6/18	SNV	c.661T>A	p.F221I	cAL5 (109)	cAL5 (30)	cAL5 (0.28)
MPPED2	chr11	30411538	6/6	SNV	c.815C>T	p.T272M	cAL10 (235)	cAL10 (78)	cAL10 (0.33)
IFTAP	chr11	36648148	5/6	SNV	c.491C>T	p.T164M	cAL9 (63)	cAL9 (13)	cAL9 (0.2)
CREB3L1	chr11	46311177	5/12	Del	c.742_744del	p.T248del	cAL9 (101)	cAL9 (30)	cAL9 (0.3)
TRIM64C	chr11	49057145	.	SNV	c.738+3G>A	.	cAL10 (118)	cAL10 (71)	cAL10 (0.6)
LRRC55	chr11	57187289	2/2	SNV	c.835G>A	p.A279T	cAL9 (244)	cAL9 (67)	cAL9 (0.28)
SERPING1	chr11	57599917	3/8	SNV	c.90C>A	p.S30R	cAL10 (242)	cAL10 (115)	cAL10 (0.48)
CBLIF	chr11	59843880	2/9	SNV	c.255C>T	p.N85%3D	cAL9 (54)	cAL9 (14)	cAL9 (0.27)
MS4A10	chr11	60798460	7/8	SNV	c.668C>T	p.P223L	cAL5 (158)	cAL5 (31)	cAL5 (0.2)
AHNAK	chr11	62523272	5/5	SNV	c.11145C>A	p.D3715E	cAL10 (376)	cAL10 (208)	cAL10 (0.55)
SLC22A8	chr11	62993502	10/11	SNV	c.1451T>A	p.L484H	cAL9 (253)	cAL9 (83)	cAL9 (0.33)
SPINDOC	chr11	63817816	2/6	SNV	c.139G>A	p.E47K	cAL2 (85)	cAL2 (18)	cAL2 (0.21)
FRMD8	chr11	65396759	7/11	Del	c.582-36_607del	.	cAL3 (254)	cAL3 (38)	cAL3 (0.15)
FOLR2	chr11	72221712	5/5	Subs	c.718_719delinsAA	p.G240N	cAL5 (126)	cAL5 (29)	cAL5 (0.23)
TENM4	chr11	78903335	7/34	SNV	c.682G>A	p.G228S	cAL10 (52)	cAL10 (30)	cAL10 (0.57)
CCDC83	chr11	85898993	7/12	SNV	c.650A>G	p.E217G	cAL10 (81)	cAL10 (31)	cAL10 (0.39)
IZUMO1R	chr11	94307438	4/4	SNV	c.499C>T	p.P167S	cAL9 (235)	cAL9 (72)	cAL9 (0.31)
PGR	chr11	101050065	.	SNV	c.2358-6T>C	.	cAL5 (54)	cAL5 (13)	cAL5 (0.25)
MMP10	chr11	102779282	3/10	SNV	c.427G>A	p.V143M	cAL9 (53)	cAL9 (23)	cAL9 (0.44)
C11orf87	chr11	109424015	2/2	SNV	c.382G>A	p.E128K	cAL5 (216)	cAL5 (55)	cAL5 (0.26)
C11orf53	chr11	111285878	4/4	Subs	c.535_536delinsTT	p.P179L	cAL9 (317)	cAL9 (94)	cAL9 (0.3)
HSPB2	chr11	111913663	2/2	SNV	c.317G>A	p.R106H	cAL5 (320)	cAL5 (84)	cAL5 (0.26)
PDZD3	chr11	119188120	7/11	SNV	c.838G>A	p.E280K	cAL9 (127)	cAL9 (32)	cAL9 (0.25)
GRAMD1B	chr11	123577559	2/21	SNV	c.216C>G	p.S72R	cAL9 (53)	cAL9 (22)	cAL9 (0.42)
TMEM225	chr11	123883248	4/4	SNV	c.568G>A	p.D190N	cAL4 (67)	cAL4 (20)	cAL4 (0.3)
OR8B4	chr11	124424635	1/1	Ins	c.236_237insT	p.K80Qfs*5	cAL2 (90)	cAL2 (24)	cAL2 (0.27)
OR8B4	chr11	124424636	1/1	SNV	c.236C>T	p.P79L	cAL2 (90)	cAL2 (24)	cAL2 (0.27)
EI24	chr11	125581229	9/11	SNV	c.692G>A	p.R231Q	cAL2 (38)	cAL2 (11)	cAL2 (0.3)
GLB1L2	chr11	134374264	.	SNV	c.1707+8A>G	.	cAL10 (110)	cAL10 (38)	cAL10 (0.35)
KDM5A	chr12	328879	14/28	SNV	c.1924A>G	p.M642V	cAL10 (54)	cAL10 (21)	cAL10 (0.39)

C1S	chr12	7065844	10/15	SNV	c.745C>T	p.P249S	cAL4 (54)	cAL4 (13)	cAL4 (0.23)
CD163L1	chr12	7369447	15/20	SNV	c.3979G>A	p.G1327R	cAL9 (169)	cAL9 (54)	cAL9 (0.32)
AICDA	chr12	8605250	3/5	SNV	c.392G>A	p.R131H	cAL10 (104)	cAL10 (33)	cAL10 (0.32)
KLRC4	chr12	10409448	1/4	SNV	c.128T>A	p.L43*	cAL9 (130)	cAL9 (35)	cAL9 (0.27)
RERGL	chr12	18081435	6/6	SNV	c.374G>A	p.R125Q	cAL10 (161)	cAL10 (50)	cAL10 (0.31)
GYS2	chr12	21558303	11/16	SNV	c.1319T>C	p.L440S	cAL10 (128)	cAL10 (50)	cAL10 (0.39)
STK38L	chr12	27317976	11/14	Subs	c.1036_1037delinsTT	p.P346L	cAL9 (72)	cAL9 (17)	cAL9 (0.23)
AMN1	chr12	31697739	.	SNV	c.534+1G>T	.	cAL5 (112)	cAL5 (48)	cAL5 (0.43)
CNTN1	chr12	41016905	19/24	SNV	c.2408C>T	p.S803L	cAL10 (173)	cAL10 (81)	cAL10 (0.47)
GXYLT1	chr12	42097579	7/8	SNV	c.1024C>T	p.R342*	cAL10 (44)	cAL10 (16)	cAL10 (0.37)
ADAMTS20	chr12	43431400	22/39	SNV	c.3193A>T	p.K1065*	cAL3 (104)	cAL3 (31)	cAL3 (0.3)
FAM186A	chr12	50350659	4/8	SNV	c.6173A>C	p.Q2058P	cAL9 (217)	cAL9 (75)	cAL9 (0.35)
DIP2B	chr12	50723210	27/38	SNV	c.3175T>G	p.L1059V	cAL11 (163)	cAL11 (28)	cAL11 (0.17)
CSRNP2	chr12	51064248	5/5	SNV	c.1130C>T	p.A377V	cAL10 (103)	cAL10 (49)	cAL10 (0.48)
ANKRD33	chr12	51891061	5/5	SNV	c.1115C>T	p.P372L	cAL11 (168)	cAL11 (24)	cAL11 (0.15)
KRT1	chr12	52676450	7/9	SNV	c.1300G>A	p.E434K	cAL10 (198)	cAL10 (87)	cAL10 (0.44)
KRT76	chr12	52769051	9/9	Del	c.1578del	p.F526Lfs*68	cAL5 (147)	cAL5 (62)	cAL5 (0.42)
OR6C70	chr12	55469865	1/1	SNV	c.274T>G	p.C92G	cAL10 (135)	cAL10 (55)	cAL10 (0.41)
OS9	chr12	57694823	2/15	SNV	c.236C>A	p.A79D	cAL10 (149)	cAL10 (54)	cAL10 (0.36)
MON2	chr12	62537243	15/35	SNV	c.1993C>T	p.Q665*	cAL2 (146)	cAL2 (38)	cAL2 (0.26)
FRS2	chr12	69570407	4/7	SNV	c.143A>G	p.Y48C	cAL5 (225)	cAL5 (99)	cAL5 (0.44)
PPFIA2-AS1	chr12	81284209	.	SNV	n.284-7C>T	.	cAL10 (177)	cAL10 (77)	cAL10 (0.44)
TMTC2	chr12	82857320	2/12	SNV	c.394G>T	p.A132S	cAL11 (223)	cAL11 (29)	cAL11 (0.13)
SLC6A15	chr12	84861696	12/12	SNV	c.2129G>A	p.G710E	cAL4 (104)	cAL4 (22)	cAL4 (0.22)
LRRIQ1	chr12	85124362	17/27	SNV	c.3850G>A	p.E1284K	cAL5 (84)	cAL5 (29)	cAL5 (0.35)
LTA4H	chr12	96003021	18/19	SNV	c.1657C>T	p.P553S	cAL4 (200)	cAL4 (48)	cAL4 (0.24)
NEDD1	chr12	96934977	6/15	SNV	c.512C>T	p.S171F	cAL3 (48)	cAL3 (12)	cAL3 (0.26)
GAS2L3	chr12	100601670	5/10	SNV	c.220G>T	p.E74*	cAL10 (38)	cAL10 (12)	cAL10 (0.33)
ANO4	chr12	101111703	24/28	SNV	c.2443G>A	p.G815R	cAL10 (101)	cAL10 (30)	cAL10 (0.3)
KNTC1	chr12	122547451	11/64	SNV	c.853C>T	p.P285S	cAL10 (92)	cAL10 (36)	cAL10 (0.39)
HCAR2	chr12	122702724	1/1	SNV	c.560A>T	p.Q187L	cAL11 (161)	cAL11 (30)	cAL11 (0.19)
SBNO1	chr12	123340998	5/32	SNV	c.641C>T	p.S214F	cAL2 (67)	cAL2 (22)	cAL2 (0.33)
MMP17	chr12	131845170	7/10	SNV	c.1021C>T	p.Q341*	cAL5 (404)	cAL5 (77)	cAL5 (0.19)
MMP17	chr12	131851137	10/10	SNV	c.1675G>A	p.E559K	cAL5 (192)	cAL5 (38)	cAL5 (0.2)

GALNT9	chr12	132329065	1/11	SNV	c.139G>A	p.V47M	cAL4 (122)	cAL4 (20)	cAL4 (0.17)
MICU2	chr13	21521256	6/12	SNV	c.586G>A	p.E196K	cAL10 (40)	cAL10 (13)	cAL10 (0.33)
CENPJ	chr13	24885607	12/17	SNV	c.3365A>G	p.Q1122R	cAL10 (70)	cAL10 (17)	cAL10 (0.25)
FLT3	chr13	28037224	10/24	SNV	c.1270G>A	p.D424N	cAL10 (43)	cAL10 (12)	cAL10 (0.29)
NBEA	chr13	35606418	.	SNV	c.7297-8C>T	.	cAL10 (36)	cAL10 (11)	cAL10 (0.31)
FAM124A	chr13	51280639	5/5	SNV	c.1132G>A	p.E378K	cAL10 (260)	cAL10 (118)	cAL10 (0.46)
CCDC70	chr13	51865853	2/2	SNV	c.475G>A	p.E159K	cAL9 (186)	cAL9 (69)	cAL9 (0.37)
TBC1D4	chr13	75327804	9/21	SNV	c.1754G>A	p.R585Q	cAL9 (142)	cAL9 (46)	cAL9 (0.33)
FARP1	chr13	98395381	13/28	SNV	c.1319C>T	p.A440V	cAL9 (84)	cAL9 (26)	cAL9 (0.32)
STK24	chr13	98463731	7/11	SNV	c.925G>A	p.E309K	cAL10 (120)	cAL10 (45)	cAL10 (0.38)
NALCN	chr13	101083118	32/44	SNV	c.3664G>A	p.A1222T	cAL4 (110)	cAL4 (12)	cAL4 (0.11)
MCF2L	chr13	113096825	30/30	SNV	c.3344G>A	p.G1115D	cAL10 (30)	cAL10 (14)	cAL10 (0.47)
GRTP1	chr13	113350866	4/7	SNV	c.448G>A	p.G150R	cAL5 (75)	cAL5 (29)	cAL5 (0.39)
TFDP1	chr13	113633917	7/12	SNV	c.502C>T	p.R168C	cAL10 (219)	cAL10 (108)	cAL10 (0.49)
RASA3	chr13	113992594	.	SNV	c.2142-6G>A	.	cAL3 (104)	cAL3 (33)	cAL3 (0.32)
OR4Q3	chr14	19747483	1/1	SNV	c.56C>T	p.S19F	cAL2 (180)	cAL2 (20)	cAL2 (0.11)
OR11H6	chr14	20224569	1/1	SNV	c.860G>A	p.G287E	cAL5 (112)	cAL5 (38)	cAL5 (0.34)
RNASE3	chr14	20891868	2/2	SNV	c.182G>A	p.R61Q	cAL10 (220)	cAL10 (76)	cAL10 (0.35)
RNASE8	chr14	21058109	1/1	SNV	c.217G>A	p.E73K	cAL11 (215)	cAL11 (32)	cAL11 (0.15)
REM2	chr14	22884843	2/5	Ins	c.273_274insCCCAC	p.A92Pfs*30	cAL3 (196)	cAL3 (82)	cAL3 (0.42)
REM2	chr14	22884844	2/5	Ins	c.274_275insGCC	p.A92delinsGP	cAL3 (196)	cAL3 (82)	cAL3 (0.42)
NOVA1	chr14	26595561	.	SNV	c.137-8T>A	.	cAL5 (52)	cAL5 (16)	cAL5 (0.31)
FRMD6	chr14	51715345	10/14	SNV	c.870G>T	p.L290F	cAL10 (204)	cAL10 (80)	cAL10 (0.39)
PTGDR	chr14	52268028	1/2	SNV	c.214G>A	p.D72N	cAL10 (143)	cAL10 (62)	cAL10 (0.44)
SYNE2	chr14	64017690	34/116	SNV	c.4983G>A	p.W1661*	cAL10 (72)	cAL10 (21)	cAL10 (0.3)
SYNE2	chr14	64175136	95/116	SNV	c.17428G>T	p.E5810*	cAL10 (76)	cAL10 (34)	cAL10 (0.45)
LTBP2	chr14	74552916	5/36	SNV	c.1168G>A	p.D390N	cAL5 (44)	cAL5 (14)	cAL5 (0.33)
NRXN3	chr14	79861944	20/20	SNV	c.4696G>A	p.D1566N	cAL10 (56)	cAL10 (28)	cAL10 (0.5)
STON2	chr14	81396172	4/8	SNV	c.95C>T	p.T32M	cAL10 (41)	cAL10 (31)	cAL10 (0.77)
EVL	chr14	100135931	9/14	Subs	c.927_928delinsAA	p.G310R	cAL4 (124)	cAL4 (28)	cAL4 (0.22)
EXOC3L4	chr14	103102745	2/11	SNV	c.1022T>C	p.L341P	cAL10 (69)	cAL10 (20)	cAL10 (0.3)
GOLGA8M	chr15	28705618	12/19	Ins	c.995dup	p.S333Kfs*48	cAL10 (100)	cAL10 (43)	cAL10 (0.43)
RASGRP1	chr15	38512849	7/17	SNV	c.783G>C	p.M261I	cAL5 (102)	cAL5 (22)	cAL5 (0.21)
FBN1	chr15	48489920	25/66	SNV	c.3013G>A	p.E1005K	cAL2 (315)	cAL2 (103)	cAL2 (0.33)

FBN1	chr15	48596309	6/66	Subs	c.511_512delinsAA	p.G171K	cAL3 (192)	cAL3 (77)	cAL3 (0.4)
FAM227B	chr15	49577655	6/16	SNV	c.415G>A	p.E139K	cAL10 (88)	cAL10 (33)	cAL10 (0.38)
UNC13C	chr15	54500848	21/32	SNV	c.5171C>T	p.S1724F	cAL5 (134)	cAL5 (26)	cAL5 (0.19)
NEDD4	chr15	55915316	1/25	SNV	c.1516G>A	p.D506N	cAL10 (69)	cAL10 (28)	cAL10 (0.41)
VPS13C	chr15	61945710	.	SNV	c.5148+5G>C	.	cAL10 (42)	cAL10 (18)	cAL10 (0.43)
SCAPER	chr15	76434277	26/32	SNV	c.3112G>A	p.G1038R	cAL10 (68)	cAL10 (22)	cAL10 (0.33)
FSD2	chr15	82769891	.	SNV	c.1268-7T>C	.	cAL10 (51)	cAL10 (15)	cAL10 (0.3)
KIF7	chr15	89645028	10/19	SNV	c.2176G>A	p.E726K	cAL5 (216)	cAL5 (56)	cAL5 (0.26)
ZNF710	chr15	90067292	2/5	SNV	c.155C>T	p.S52L	cAL11 (120)	cAL11 (15)	cAL11 (0.12)
SELENOS	chr15	101275296	3/7	Del	c.274_276del	p.E92del	cAL10 (93)	cAL10 (42)	cAL10 (0.45)
PCSK6	chr15	101370468	12/22	SNV	c.1588G>A	p.E530K	cAL10 (59)	cAL10 (22)	cAL10 (0.38)
CHTF18	chr16	790548	7/22	SNV	c.776C>A	p.A259E	cAL9 (111)	cAL9 (26)	cAL9 (0.24)
PDPK1	chr16	2597274	13/14	SNV	c.1553C>T	p.T518M	cAL4 (70)	cAL4 (22)	cAL4 (0.32)
PDPK1	chr16	2597700	14/14	SNV	c.1604G>T	p.W535L	cAL10 (87)	cAL10 (51)	cAL10 (0.58)
CREBBP	chr16	3736113	28/31	Ins	c.4650dup	p.E1551Rfs*4	cAL10 (118)	cAL10 (83)	cAL10 (0.7)
MGRN1	chr16	4665094	.	SNV	c.629-8C>T	.	cAL10 (82)	cAL10 (43)	cAL10 (0.52)
ABAT	chr16	8764731	.	SNV	c.448-7C>A	.	cAL9 (127)	cAL9 (43)	cAL9 (0.34)
EMP2	chr16	10533014	5/5	SNV	c.395C>T	p.P132L	cAL2 (67)	cAL2 (20)	cAL2 (0.3)
ITPRIPL2	chr16	19114834	1/1	SNV	c.373C>T	p.R125W	cAL10 (117)	cAL10 (55)	cAL10 (0.47)
VPS35L	chr16	19633088	.	SNV	c.1822-4T>G	.	cAL10 (99)	cAL10 (33)	cAL10 (0.34)
DNAH3	chr16	21134365	7/62	Subs	c.975_976delinsTT	p.P326S	cAL3 (216)	cAL3 (69)	cAL3 (0.32)
IGSF6	chr16	21643566	4/6	SNV	c.567A>G	p.I189M	cAL10 (173)	cAL10 (76)	cAL10 (0.44)
SCNN1G	chr16	23186554	2/13	SNV	c.283C>T	p.P95S	cAL11 (128)	cAL11 (21)	cAL11 (0.17)
KIAA0556	chr16	27749686	16/28	Subs	c.2726_2727delinsTT	p.S909F	cAL2 (154)	cAL2 (32)	cAL2 (0.21)
SPN	chr16	29664722	2/2	SNV	c.994G>A	p.D332N	cAL5 (125)	cAL5 (41)	cAL5 (0.33)
ARMC5	chr16	31466650	8/8	SNV	c.2854C>T	p.R952C	cAL9 (109)	cAL9 (33)	cAL9 (0.31)
SALL1	chr16	51140729	2/3	SNV	c.1493G>A	p.R498H	cAL10 (151)	cAL10 (70)	cAL10 (0.46)
CNOT1	chr16	58538250	37/49	SNV	c.5152C>T	p.R1718*	cAL2 (31)	cAL2 (8)	cAL2 (0.24)
CNOT1	chr16	58546670	.	SNV	c.3828+2T>C	.	cAL9 (149)	cAL9 (51)	cAL9 (0.34)
DHX38	chr16	72096390	2/27	SNV	c.233C>T	p.S78F	cAL11 (98)	cAL11 (12)	cAL11 (0.12)
GLG1	chr16	74606895	1/27	SNV	c.200C>T	p.P67L	cAL10 (50)	cAL10 (19)	cAL10 (0.38)
ADAMTS18	chr16	77319913	16/23	SNV	c.2468G>A	p.R823H	cAL11 (166)	cAL11 (20)	cAL11 (0.12)
SLC38A8	chr16	84036810	2/10	SNV	c.280G>A	p.G94R	cAL10 (36)	cAL10 (12)	cAL10 (0.34)
CLUH	chr17	2701711	5/26	Subs	c.531_532delinsAA	p.E178K	cAL4 (56)	cAL4 (11)	cAL4 (0.21)

TRPV3	chr17	3516482	16/18	SNV	c.2173G>A	p.E725K	cAL10 (194)	cAL10 (90)	cAL10 (0.46)
ANKFY1	chr17	4197520	8/25	SNV	c.1082C>T	p.T361I	cAL5 (235)	cAL5 (63)	cAL5 (0.27)
ARHGEF15	chr17	8319086	13/16	SNV	c.2113C>T	p.P705S	cAL5 (287)	cAL5 (65)	cAL5 (0.23)
CFAP52	chr17	9628731	9/14	SNV	c.1085C>A	p.S362*	cAL5 (154)	cAL5 (35)	cAL5 (0.23)
USP43	chr17	9701428	12/15	SNV	c.1739C>T	p.T580M	cAL11 (195)	cAL11 (23)	cAL11 (0.12)
MYH13	chr17	10345277	14/40	SNV	c.1509C>A	p.Y503*	cAL11 (80)	cAL11 (11)	cAL11 (0.13)
CCDC144A	chr17	16707480	4/18	SNV	c.676T>A	p.S226T	cAL2 (51)	cAL2 (11)	cAL2 (0.21)
PIGS	chr17	28561430	6/12	SNV	c.668C>T	p.S223F	cAL2 (104)	cAL2 (26)	cAL2 (0.25)
SSH2	chr17	29632840	16/16	SNV	c.2354C>T	p.S785F	cAL5 (86)	cAL5 (28)	cAL5 (0.33)
EFCAB5	chr17	29969025	4/23	SNV	c.425A>G	p.E142G	cAL9 (72)	cAL9 (44)	cAL9 (0.61)
HEATR9	chr17	35864799	4/15	SNV	c.412T>G	p.L138V	cAL10 (111)	cAL10 (37)	cAL10 (0.34)
LYZL6	chr17	35934870	.	SNV	c.378-5C>T	.	cAL3 (189)	cAL3 (74)	cAL3 (0.39)
CCL15-CCL14	chr17	35997840	4/7	SNV	c.269G>A	p.R90Q	cAL4 (207)	cAL4 (42)	cAL4 (0.21)
ARHGAP23	chr17	38466972	7/24	Subs	c.1289_1290delinsTT	p.T430I	cAL4 (305)	cAL4 (58)	cAL4 (0.19)
KRTAP1-1	chr17	41041256	1/1	SNV	c.142A>G	p.S48G	cAL5 (202)	cAL5 (58)	cAL5 (0.29)
BECN1	chr17	42818341	7/12	SNV	c.563C>A	p.A188E	cAL4 (160)	cAL4 (21)	cAL4 (0.13)
MPP2	chr17	43909631	1/13	SNV	c.13C>T	p.P5S	cAL5 (84)	cAL5 (22)	cAL5 (0.27)
WNT9B	chr17	46875095	.	SNV	c.335-6A>G	.	cAL10 (458)	cAL10 (178)	cAL10 (0.39)
KIF2B	chr17	53824936	1/1	SNV	c.1903G>A	p.D635N	cAL11 (112)	cAL11 (17)	cAL11 (0.16)
ANKFN1	chr17	56440366	8/17	SNV	c.959G>A	p.G320E	cAL4 (135)	cAL4 (27)	cAL4 (0.2)
SRSF1	chr17	58007028	1/4	SNV	c.110A>C	p.Y37S	cAL10 (341)	cAL10 (152)	cAL10 (0.45)
ACE	chr17	63479911	4/25	SNV	c.654C>T	p.D218%3D	cAL5 (55)	cAL5 (16)	cAL5 (0.3)
LRRC37A3	chr17	64860950	11/14	SNV	c.3196C>T	p.P1066S	cAL9 (281)	cAL9 (152)	cAL9 (0.54)
ABCA8	chr17	68887484	25/40	SNV	c.3167G>A	p.R1056Q	cAL9 (141)	cAL9 (33)	cAL9 (0.24)
CD300E	chr17	74617355	2/4	SNV	c.151C>T	p.R51*	cAL10 (247)	cAL10 (108)	cAL10 (0.44)
HID1	chr17	74964550	2/19	SNV	c.149T>G	p.V50G	cAL10 (161)	cAL10 (58)	cAL10 (0.36)
UNK	chr17	75813198	5/16	SNV	c.743G>A	p.R248Q	cAL5 (110)	cAL5 (43)	cAL5 (0.39)
CBX8	chr17	79796237	.	Del	c.179+5_179+12del	.	cAL10 (85)	cAL10 (30)	cAL10 (0.36)
P4HB	chr17	81847354	.	SNV	c.625-7T>C	.	cAL10 (135)	cAL10 (48)	cAL10 (0.36)
CD7	chr17	82315349	4/4	SNV	c.695C>T	p.T232M	cAL10 (172)	cAL10 (71)	cAL10 (0.41)
SMCHD1	chr18	2718323	19/48	SNV	c.2347C>T	p.Q783*	cAL2 (90)	cAL2 (34)	cAL2 (0.38)
L3MBTL4	chr18	6138189	.	SNV	c.1199+5C>A	.	cAL10 (101)	cAL10 (39)	cAL10 (0.39)
TXNDC2	chr18	9887377	2/2	SNV	c.898C>T	p.P300S	cAL4 (299)	cAL4 (77)	cAL4 (0.26)

FHOD3	chr18	36709251	18/29	Subs	c.2393_2395delinsTTT	p.R798_A799delinsIS	cAL10 (150)	cAL10 (72)	cAL10 (0.48)
ST8SIA5	chr18	46680281	8/8	SNV	c.1000C>T	p.R334C	cAL10 (273)	cAL10 (114)	cAL10 (0.42)
CTIF	chr18	48761495	10/13	SNV	c.1183C>A	p.L395I	cAL10 (191)	cAL10 (62)	cAL10 (0.33)
CDH7	chr18	65862863	11/12	SNV	c.1810G>A	p.G604S	cAL2 (115)	cAL2 (35)	cAL2 (0.31)
DIPK1C	chr18	74436607	4/4	SNV	c.1154C>A	p.P385H	cAL10 (91)	cAL10 (32)	cAL10 (0.35)
SALL3	chr18	78993132	2/3	SNV	c.1141G>A	p.A381T	cAL10 (120)	cAL10 (62)	cAL10 (0.52)
CTDP1	chr18	79728965	11/13	Subs	c.2476_2477delinsAA	p.G826K	cAL9 (113)	cAL9 (40)	cAL9 (0.36)
FSTL3	chr19	676446	1/5	SNV	c.23C>T	p.P8L	cAL9 (33)	cAL9 (9)	cAL9 (0.28)
GPX4	chr19	1105364	.	Ins	c.180-1_189dup	.	cAL4 (169)	cAL4 (56)	cAL4 (0.33)
REXO1	chr19	1827154	2/16	SNV	c.1635C>G	p.S545R	cAL11 (121)	cAL11 (17)	cAL11 (0.14)
FSD1	chr19	4323072	11/13	SNV	c.1126C>T	p.R376C	cAL5 (93)	cAL5 (17)	cAL5 (0.19)
PTPRS	chr19	5221134	19/37	Del	c.3320del	p.G1107Afs*51	cAL10 (129)	cAL10 (63)	cAL10 (0.49)
COL5A3	chr19	9995584	16/67	SNV	c.1567C>T	p.P523S	cAL3 (193)	cAL3 (74)	cAL3 (0.38)
ACP5	chr19	11575222	7/7	SNV	c.766G>A	p.V256M	cAL2 (208)	cAL2 (28)	cAL2 (0.14)
ZNF564	chr19	12526682	4/4	SNV	c.1426C>T	p.P476S	cAL10 (211)	cAL10 (85)	cAL10 (0.4)
FBXW9	chr19	12696562	1/10	SNV	c.20G>A	p.R7Q	cAL10 (142)	cAL10 (58)	cAL10 (0.41)
ZNF43	chr19	21808070	4/4	SNV	c.1994G>C	p.G665A	cAL11 (327)	cAL11 (43)	cAL11 (0.13)
ZNF91	chr19	23374723	2/4	Del	c.71del	p.P24Rfs*18	cAL11 (272)	cAL11 (45)	cAL11 (0.17)
ZNF254	chr19	24126490	4/4	SNV	c.490T>C	p.Y164H	cAL10 (75)	cAL10 (31)	cAL10 (0.42)
ZNF599	chr19	34760463	4/4	SNV	c.338C>T	p.S113L	cAL3 (81)	cAL3 (27)	cAL3 (0.34)
HAMP	chr19	35284848	3/4	SNV	c.150G>A	p.M50I	cAL11 (160)	cAL11 (18)	cAL11 (0.11)
CAPN12	chr19	38742442	3/21	Subs	c.393_394delinsTT	p.Q132*	cAL4 (177)	cAL4 (44)	cAL4 (0.25)
IFNL1	chr19	39298091	3/5	SNV	c.377C>T	p.S126F	cAL10 (289)	cAL10 (105)	cAL10 (0.36)
FCGBP	chr19	39927946	2/28	SNV	c.416T>C	p.L139P	cAL10 (113)	cAL10 (38)	cAL10 (0.34)
SHKBP1	chr19	40591062	18/18	SNV	c.1979G>T	p.G660V	cAL11 (105)	cAL11 (20)	cAL11 (0.19)
PSG4	chr19	43195041	4/6	SNV	c.942C>A	p.D314E	cAL10 (244)	cAL10 (91)	cAL10 (0.37)
PSG9	chr19	43259027	4/6	SNV	c.818G>C	p.W273S	cAL9 (226)	cAL9 (70)	cAL9 (0.31)
SIGLECL1	chr19	51265878	4/6	SNV	c.406C>G	p.L136V	cAL11 (156)	cAL11 (27)	cAL11 (0.17)
ZNF415	chr19	53109809	4/4	SNV	c.236A>C	p.H79P	cAL9 (84)	cAL9 (18)	cAL9 (0.21)
NLRP8	chr19	55954656	3/10	Subs	c.598_599delinsAA	p.G200N	cAL4 (166)	cAL4 (39)	cAL4 (0.23)
ZSCAN5C	chr19	56208718	5/5	SNV	c.1009G>A	p.G337S	cAL2 (229)	cAL2 (33)	cAL2 (0.14)
ZNF805	chr19	57254179	4/4	Subs	c.1360_1361delinsTT	p.P454F	cAL5 (154)	cAL5 (55)	cAL5 (0.36)
ZNF776	chr19	57754113	3/3	SNV	c.983C>T	p.S328F	cAL9 (317)	cAL9 (86)	cAL9 (0.27)
ZSCAN18	chr19	58085152	7/7	SNV	c.1234C>A	p.Q412K	cAL10 (109)	cAL10 (71)	cAL10 (0.65)

SIRPB1	chr20	1571143	.	SNV	c.752-6T>C	.	cAL10 (159)	cAL10 (57)	cAL10 (0.36)
FERMT1	chr20	6096977	8/15	Subs	c.1013_1014delinsTT	p.S338F	cAL5 (127)	cAL5 (34)	cAL5 (0.27)
MACROD2	chr20	15933316	11/17	SNV	c.816G>T	p.M272I	cAL10 (58)	cAL10 (21)	cAL10 (0.37)
ASXL1	chr20	32436566	13/13	Del	c.3856_3866del	p.Q1286Gfs*4	cAL11 (110)	cAL11 (15)	cAL11 (0.13)
KIAA1755	chr20	38240731	3/14	SNV	c.1400C>G	p.P467R	cAL3 (137)	cAL3 (51)	cAL3 (0.37)
TOX2	chr20	44066724	.	SNV	c.1357-6C>A	.	cAL5 (162)	cAL5 (30)	cAL5 (0.19)
CSE1L	chr20	49068748	7/25	SNV	c.601G>T	p.D201Y	cAL10 (175)	cAL10 (83)	cAL10 (0.48)
STAU1	chr20	49154031	4/14	SNV	c.246G>T	p.M82I	cAL5 (104)	cAL5 (25)	cAL5 (0.25)
KCNB1	chr20	49373404	2/2	SNV	c.2156T>A	p.L719Q	cAL5 (132)	cAL5 (41)	cAL5 (0.31)
RNF114	chr20	49952077	6/6	SNV	c.623A>T	p.D208V	cAL10 (72)	cAL10 (30)	cAL10 (0.42)
KCNG1	chr20	51010336	2/3	SNV	c.3G>T	p.M1?	cAL2 (141)	cAL2 (24)	cAL2 (0.17)
SALL4	chr20	51790136	2/4	SNV	c.2347A>G	p.T783A	cAL5 (207)	cAL5 (61)	cAL5 (0.3)
ZNF217	chr20	53582127	2/6	SNV	c.700C>T	p.H234Y	cAL3 (173)	cAL3 (63)	cAL3 (0.37)
CSTF1	chr20	56397217	3/6	SNV	c.180C>G	p.N60K	cAL2 (106)	cAL2 (13)	cAL2 (0.12)
CDH26	chr20	60012728	18/18	Del	c.*8del	.	cAL10 (56)	cAL10 (28)	cAL10 (0.5)
CDH4	chr20	61928189	.	SNV	c.1772-1G>A	.	cAL5 (189)	cAL5 (54)	cAL5 (0.29)
CXADR	chr21	17547067	2/7	SNV	c.84G>T	p.M28I	cAL2 (78)	cAL2 (13)	cAL2 (0.16)
GRIK1	chr21	29537820	17/18	SNV	c.2672A>C	p.K891T	cAL11 (174)	cAL11 (27)	cAL11 (0.16)
ITSN1	chr21	33781544	15/40	SNV	c.1680G>T	p.L560F	cAL10 (36)	cAL10 (18)	cAL10 (0.5)
ITSN1	chr21	33875457	34/40	SNV	c.4277A>G	p.E1426G	cAL5 (99)	cAL5 (35)	cAL5 (0.36)
SIM2	chr21	36712618	3/11	SNV	c.344C>T	p.S115F	cAL10 (204)	cAL10 (86)	cAL10 (0.42)
TXNRD2	chr22	19878195	.	SNV	c.1348-8G>A	.	cAL5 (98)	cAL5 (28)	cAL5 (0.29)
SNAP29	chr22	20859203	1/5	Del	c.101_109del	p.G34_D36del	cAL10 (222)	cAL10 (101)	cAL10 (0.46)
MMP11	chr22	23781268	6/8	SNV	c.934A>G	p.K312E	cAL5 (253)	cAL5 (74)	cAL5 (0.29)
GSTT4	chr22	24000242	4/5	SNV	c.361C>T	p.P121S	cAL5 (107)	cAL5 (24)	cAL5 (0.23)
C1QTNF6	chr22	37182672	3/3	SNV	c.353G>A	p.G118E	cAL2 (280)	cAL2 (88)	cAL2 (0.32)
TNFRSF13C	chr22	41925513	3/3	SNV	c.409A>T	p.I137F	cAL11 (136)	cAL11 (17)	cAL11 (0.12)
EFCAB6	chr22	43615837	21/32	SNV	c.2551G>A	p.D851N	cAL10 (130)	cAL10 (52)	cAL10 (0.4)
PARVG	chr22	44187879	.	SNV	c.247+1G>C	.	cAL2 (214)	cAL2 (53)	cAL2 (0.25)
PKDREJ	chr22	46259942	1/1	SNV	c.3381G>A	p.W1127*	cAL5 (100)	cAL5 (23)	cAL5 (0.23)
MAGEB18	chrX	26139568	2/3	SNV	c.583C>T	p.P195S	cAL5 (42)	cAL5 (26)	cAL5 (0.61)
MAGEB6B	chrX	26160847	1/1	SNV	c.247G>A	p.D83N	cAL4 (262)	cAL4 (67)	cAL4 (0.26)
DMD	chrX	32389668	32/79	Ins	c.4350dup	p.L1451Ifs*18	cAL10 (33)	cAL10 (23)	cAL10 (0.69)
H2AP	chrX	37990909	1/1	SNV	c.70G>A	p.E24K	cAL2 (63)	cAL2 (39)	cAL2 (0.62)

BCOR	chrX	40064330	.	SNV	c.3502+6C>T	.	cAL9 (43)	cAL9 (19)	cAL9 (0.45)
CCNB3	chrX	50346729	10/13	Subs	c.3732_3733delinsAA	p.M1244_E1245delinsIK	cAL4 (135)	cAL4 (34)	cAL4 (0.26)
ALAS2	chrX	55021163	5/11	SNV	c.527C>T	p.P176L	cAL11 (47)	cAL11 (13)	cAL11 (0.29)
HNRNPH2	chrX	101413267	2/2	SNV	c.1279C>A	p.Q427K	cAL4 (158)	cAL4 (29)	cAL4 (0.18)
TCEAL6	chrX	102141295	3/3	SNV	c.37G>A	p.E13K	cAL2 (115)	cAL2 (54)	cAL2 (0.47)
RADX	chrX	106669266	13/14	SNV	c.2373C>A	p.Y791*	cAL10 (46)	cAL10 (39)	cAL10 (0.86)
TRPC5	chrX	111952300	2/11	SNV	c.121G>A	p.E41K	cAL4 (126)	cAL4 (33)	cAL4 (0.26)
INTS6L	chrX	135546750	5/18	SNV	c.478G>T	p.E160*	cAL10 (65)	cAL10 (45)	cAL10 (0.69)
ADGRG4	chrX	136349128	6/26	SNV	c.5422A>C	p.T1808P	cAL2 (99)	cAL2 (48)	cAL2 (0.49)
ADGRG4	chrX	136373056	15/26	SNV	c.7768G>T	p.D2590Y	cAL4 (143)	cAL4 (20)	cAL4 (0.14)
FLNA	chrX	154358448	27/48	SNV	c.4595G>A	p.R1532Q	cAL4 (268)	cAL4 (67)	cAL4 (0.25)
FLNA	chrX	154361523	21/48	SNV	c.2992G>A	p.A998T	cAL3 (326)	cAL3 (199)	cAL3 (0.61)

Supplementary Table S10. Genes recurrently affected by small-scale mutations in pcALCL.

Gene	Affected patient
ADAMTS4	cAL10, cAL11
APOB	cAL2, cAL10
C4orf54	cAL5, cAL9
CDK14	cAL3, cAL5
CFTR	cAL9, cAL10
CNOT1	cAL2, cAL9
CSMD1	cAL2, cAL9
DNAJC6	cAL2, cAL10
DST	cAL10, cAL11
FBN1	cAL2, cAL3
FLNA	cAL3, cAL4
HMCN1	cAL5, cAL10
ITSN1	cAL5, cAL10
KIF13A	cAL4, cAL10
LRP1B	cAL1, cAL3, cAL5, cAL7, cAL10
LRP2	cAL10, cAL11
MALRD1	cAL10, cAL11
MEGF10	cAL3, cAL10
MICU3	cAL5, cAL9
NRXN3	cAL10, cAL11
NWD2	cAL5, cAL10
PCLO	cAL4, cAL5
PDPK1	cAL4, cAL10
PIK3R1	cAL5, cAL9
PLXNB1	cAL3, cAL5, cAL10
PRDM6	cAL9, cAL11
RYR2	cAL3, cAL5
SEMA3A	cAL10, cAL11
SSPO	cAL5, cAL9
USH2A	cAL2, cAL5, cAL8, cAL9, cAL10

Supplementary Table S11. Genes affected by small-scale mutations in pcALCL implicated in cancer (NCG 6.0).

Gene type	Genes
Candidate cancer genes	ABCF2, ACE, ACO1, ACTL7B, ADAMTS18, ADAMTS20, ADAMTS9, ADGRB3, ADGRG4, ADGRL3, ADGRV1, AHNAK, ALB, ANK3, ANO4, APOB, BTN3A2, CD163L1, CD58, CDH23, CDK14, CENPJ, CNOT1, CNTN1, CNTN4, COL12A1, COL3A1, COL5A3, COL7A1, CREBBP, CSMD1, CTIF, DDX41, DIP2C, DMD, DNAH3, DNAH5, DPP6, DPYD, DRD5, DST, EI24, F5, FAT2, FBN2, FLG, FLNA, FOXQ1, GBE1, GSDME, GXYLT1, HECW1, HLA-B, HMCN1, HSPG2, IMPG2, KCNB2, KIF2B, LRIG1, LRP2, LRRC37A3, LRRC55, LRRC7, LRRIQ1, LTA4H, LTBP2, MALRD1, MKI67, MSH3, MUC17, MUC4, NALCN, NBEA, NEDD4, NIPBL, NRXN3, NTRK2, OBSCN, PARD3, PCLO, PCSK6, PDZRN3, PGR, PHF3, PKHD1, PLXNA2, PMS1, PPP1R3A, PPP1R9A, PRDM9, PROM1, PRUNE2, RGS12, RGS7, RIMS2, RYR2, SALL1, SALL3, SALL4, SCAPER, SCN11A, SCN5A, SERPING1, SHKBP1, SIRPB1, SLC1A3, SLC38A8, SLC44A3, SLC4A10, SLC6A15, SMG7, SPAG17, SPN, SRSF1, ST3GAL6, SYNE2, TEX15, TFDP1, TKTL2, TLR5, TMTC2, TRPM3, TTN, UNC13C, UNC5D, UNC80, USH2A, VCAN, WDFY3, XIRP2, ZNF217, ZNF483, ZNF638.
Oncogenes	ERBB4, FLT3, FSTL3, GATA2, KDM5A, MAP3K1, NUP98, PAX8, PRDM16, RET, SND1, TRRAP.
Tumor suppressors	ASXL1, ARID1B, BCOR, CAMTA1, CREB3L1, CSMD3, CREBBP, LRP1B, PIK3R1, PTPRD, TGFBR2, WNK2.

Supplementary Table S12. Gene set analysis of genes affected by small-scale mutations in pcALCL, Top 20 hits (Panther v.14.0).

Panther ID	Term	*P* value	Odds Ratio	Combined Score
P00026	Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway_Homo sapiens	0.001575513	2.882335216	18.60021105
P05912	Dopamine receptor mediated signaling pathway_Homo sapiens	0.019610047	3.199795213	12.58067717
P00048	PI3 kinase pathway_Homo sapiens	0.036724885	3.169320973	10.47238943
P04379	Beta3 adrenergic receptor signaling pathway_Homo sapiens	0.041429941	6.050521858	19.26335774
P00037	Ionotropic glutamate receptor pathway_Homo sapiens	0.04560785	2.958032908	9.13344552
P04378	Beta2 adrenergic receptor signaling pathway_Homo sapiens	0.050712979	3.565486095	10.6307585
P04377	Beta1 adrenergic receptor signaling pathway_Homo sapiens	0.050712979	3.565486095	10.6307585
P04373	5HT1 type receptor mediated signaling pathway_Homo sapiens	0.055346137	3.442538298	9.96321674
P00004	Alzheimer disease-presenilin pathway_Homo sapiens	0.077844522	2.016840619	5.14907829
P00039	Metabotropic glutamate receptor group III pathway_Homo sapiens	0.078733958	2.465027423	6.265312689
P04376	5HT4 type receptor mediated signaling pathway_Homo sapiens	0.081955874	4.159733777	10.4058831
P00007	Axon guidance mediated by semaphorins_Homo sapiens	0.091095485	3.915043555	9.379845498
P00027	Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway_Homo sapiens	0.100043461	1.883653031	4.336452905
P05916	Opioid prodynorphin pathway_Homo sapiens	0.100515236	3.697541135	8.494900952
P05915	Opioid proenkephalin pathway_Homo sapiens	0.100515236	3.697541135	8.494900952
P05917	Opioid proopiomelanocortin pathway_Homo sapiens	0.100515236	3.697541135	8.494900952
P00052	TGF-beta signaling pathway_Homo sapiens	0.125466864	1.89078808	3.924734511
P00030	Hypoxia response via HIF activation_Homo sapiens	0.16159984	2.773155851	5.054442933
P00059	p53 pathway_Homo sapiens	0.164866065	1.87480959	3.37957275
P00001	Adrenaline and noradrenaline biosynthesis_Homo sapiens	0.172346219	2.662229617	4.68086502

Supplementary Table S13. Genes screened for deleterious indels/SNVs in patients cAL1/6-8/12.

	Genes
A	AARS, ABCA1, ABCA2, ABCA8, ABCB4, ABCE1, ABCF2, AC002454.1, AC241952.1, ACE, ACE2, ACO1, ACOXL, ACP5, ADAM23, ADAM28, ADAMTS18, ADAMTS4, ADAMTS9, ADCY2, ADGRB3, ADGRG4, ADGRL3, ADGRV1, AGTRAP, AHNAK, AICDA, AKR1B15, AL035405.1, ALAS2, ALB, ALDOB, AMN1, ANK3, ANKFN1, ANKFY1, ANKRD11, ANKRD30A, ANKRD33, ANO4, ANTXR1, ANXA10, APOB, ARHGEF15, ARHGEF34P, ARHGEF35, ARHGEF5, ARID1B, ARMC3, ARMC5, ART1, ASPSCR1, ATAD1, ATF3, ATP2B2, ATP2C1, ATXN1, AXIN1.
B	BCOR, BECN1, BICRAL, BIRC6, BMPER, BOLL, BSN, BTN3A2.
C	C11orf53, C11orf74, C11orf87, C1QC, C1QTNF6, C1S, C3orf20, C4BPA, C4orf54, C9orf169, CA8, CADPS2, CALD1, CAMTA1, CAND2, CBX8, CCDC101, CCDC144A, CCDC57, CCDC66, CCDC70, CCDC83, CCNB3, CD163L1, CD300E, CD58, CD7, CDC42BPB, CDH26, CDH4, CDH7, CDK14, CENPE, CENPJ, CEP68, CETN3, CFAP52, CFAP58, CFTR, CGNL1, CHD3, CHTF18, CLK2, CLUH, CNOT1, CNTN1, CNTN2, CNTN4, CNTNAP2, COL12A1, COL26A1, COL3A1, COL4A3, COL5A3, COL7A1, COLEC11, COQ4, CPLANE1, CPNE7, CREB3L1, CREBBP, CRISP1, CRTAC1, CSE1L, CSMD1, CSMD3, CSRNP2, CSTF1, CTIF, CTTNBP2, CXADR, CYP4Z1, CYTH3.
D	DAAM2, DDX21, DDX41, DENND1B, DGKD, DGKI, DHX38, DIP2B, DIP2C, DIPK1C, DMD, DMRT1, DMRTA1, DMRTA2, DNAH17, DNAH3, DNAH5, DNAI1, DNAJC6, DOCK1, DPP6, DPY19L1P2, DRD5, DST, DUSP22.
E	EDIL3, EEF1AKNMT, EFCAB5, EFCAB6, EGR4, EI24, EIF3C, EMP2, EPB41L4A, EPGN, ERBB2IP, ERBB4, ERC2, ERICH3, ERO1B, ESCO1, ESPNP, ETS1, ETV7, EVL, EXO5, EXOC3L4, EXOC4, EZH2.
F	F2RL1, F5, FAM114A1, FAM124A, FAM135B, FAM161A, FAM162B, FAM163B, FAM174B, FAM186A, FAM213B, FAM227B, FAM234A, FAM3C, FAM71F1, FAM91A1, FANCL, FARP1, FAT2, FBLIM1, FBN1, FBN2, FBXW9, FCN2, FCRL5, FCRL6, FERMT1, FGD5, FGFR1, FLG, FLNA, FLNC, FLT3, FMN2, FNDC3B, FOLR2, FOXD4L5, FOXM1, FOXP2, FRK, FRMD4A, FRMD4B, FRMD6, FRMD8, FRS2, FSD1, FSD2, FSIP2, FSTL3.
G	GAB1, GADD45A, GALNT9, GAS2L3, GATA2, GBE1, GDF7, GIF, GLB1L2, GLG1, GLRA1, GNB2, GOLPH3, GP1BA, GPR31, GPR56, GPRC6A, GPS2, GPX4, GRAMD1B, GRIK1, GRIK2, GRM8, GRTP1, GSAP, GSDME, GTF3C1, GTF3C4, GTPBP2, GXYLT1, GYS2.
H	HAMP, HAO2, HCAR2, HCN4, HDAC4, HID1, HIPK2, HIST1H2BC, HIVEP2, HIVEP3, HMCN1, HNRNPH2, HORMAD1, HOXA4, HOXD10, HPS5, HPSE2, HSPB2, HSPG2, HTN1, HTR1D, HTR7, HYPM.
I	ICE1, IFNL1, IFT80, IGF2BP3, IGKV2D-24, IGSF6, IL12A, IMPG2, INSM2, INTS1, INTS6L, IQCF3, ITPRIPL2, ITSN1, IZUMO1R.
J	JMJD1C, JPH1.
K	KANK1, KCNB1, KCNB2, KCND2, KCNG1, KCNH7, KCTD20, KDM5A, KIAA0556, KIAA1109, KIAA1211, KIAA1217, KIAA1324L, KIAA1755, KIF13A, KIF1A, KIF26A, KIF2B, KIF7, KLHDC7A, KLHDC8A, KLHL29, KLRC4, KMT2C, KMT2E, KNTC1, KRT1, KRT6B, KRT76.

L	L3MBTL4, LAMC2, LCE5A, LEFTY2, LEPR, LGR4, LHPP, LIN28B, LINC00635, LINC-PINT, LIPJ, LNX1, LOC339862, LOR, LPCAT4, LRIG1, LRIT2, LRP1B, LRP2, LRRC15, LRRC37A3, LRRC55, LRRC58, LRRC7, LRRIQ1, LST1, LTA4H, LTBP2, LUC7L2, LY6K, LYST, LZTS2.
M	MACROD2, MAGEB18, MAGEB6B, MAGI3, MALRD1, MAP10, MAP3K1, MASP2, MAST4, MCC, MCF2L, MCF2L2, MCHR2, MECOM, MED27, MEGF10, MEGF6, MET, MGRN1, MICU2, MICU3, MIR100HG, MKI67, MKLN1, MLLT10, MMP10, MMP17, MON2, MPDZ, MPI, MPP2, MPPED2, MRNIP, MRPL13, MRPL19, MS4A10, MSC, MSH3, MSX2, MTG1, MT-ND5, MUC17, MUC3A, MUC5B, MYO10, MYPOP, MYRFL.
N	NAGPA, NAP1L5, NBEA, NCKAP5, NDUFA13, NEDD1, NEDD4, NES, NFKB2, NIPBL, NKX2-3, NLRP6, NLRP8, NMUR1, NMUR2, NNT, NOMO1, NOSIP, NOVA1, NPIPA1, NR_027155, NR_034111, NR_110155, NRBF2, NRXN3, NTRK2, NUMA1, NUP153, NUP98, NWD2.
O	OBSCN, OCA2, OGDHL, OR11H6, OR2G6, OR2M2, OR4Q3, OR56A3, OR6C70, OR8B4, ORAI3, ORM1, OS9, OTUB2, OXCT2.
P	P2RY12, P4HB, PABPC4L, PALM2, PAQR6, PARD3, PARVG, PAX8, PCDHB4, PCLO, PCSK6, PDE4D, PDE5A, PDGFD, PDPK1, PDXDC1, PDZD2, PDZD3, PDZD7, PDZD8, PDZRN3, PEG10, PGBD2, PGR, PHF19, PHF3, PHLPP1, PIEZO1, PIGS, PIK3C2B, PIK3R1, PKDREJ, PKHD1, PLA2G4A, PLCH1, PLEC, PLEKHM2, PLIN2, PLXNA2, PLXNB1, PMS1, POC1B, PODXL2, POF1B, POLR3A, PON3, PPFIA2-AS1, PPIC, PPM1L, PPP1R16A, PPP1R21, PPP1R3A, PPP1R9A, PPP6R3, PRDM1 , PRDM16, PRDM6, PRDM9, PRDX1, PRKAG2, PRMT7, PROKR1, PROM1, PROS1, PRPF40A, PRR16, PRR19, PRUNE2, PSG4, PSG9, PTCH2, PTGDR, PTK7, PTPRD, PTPRK, PTPRS.
R	RAB3GAP1, RABEPK, RADX, RAMP3, RASA1, RASA3, RASGRP1, RAVER2, RBFOX1, RBM47, RCOR1, REM2, RERGL, RET, REXO1, RGPD4, RGS11, RGS12, RGS14, RGS3, RGS7, RGSL1, RHBDD1, RIMS2, RNASE3, RNASE8, RNASEH2B, RNF114, RNF139, RNF32, RNLS, ROCK2, ROR1, RORB, RP11-219G17.4, RRP36, RUSC2, RYR2.
S	SALL1, SAMD11, SAMD5, SBNO1, SCAPER, SCN11A, SCN5A, SCNN1G, SCRT1, SEC14L5, SEC16B, SEM1, SEMA3A, SFSWAP, SGIP1, SH2D4A, SH3BP4, SH3TC1, SHKBP1, SIGLEC5, SIGLECL1, SIM2, SIPA1L2, SIRPB1, SIRT3, SKIDA1, SLC1A3, SLC22A16, SLC26A5, SLC35F1, SLC37A4, SLC38A8, SLC44A3, SLC4A10, SLC4A2, SLC6A15, SLC9A3, SLC9A9, SMARCAD1, SMCHD1, SMG1P1, SMG7, SMLR1, SMPD3, SNAP29, SND1, SPAG17, SPATA16, SPINDOC, SPN, SQRDL, SRFBP1, SRGAP2C, SRI, SRRM3, SRSF1, SSPO, ST3GAL6, ST7, ST8SIA5, STAB1, STAU1, STEAP3, STK24, STK39, STON2, SUPT3H, SUSD1, SYNE2.
T	TAX1BP1, TBC1D19, TBC1D4, TCEAL6, TCERG1L, TCF7L1, TENM4, TEX15, TFDP1, TFR2, TGFBI, TGFBR2, THEM6, TJAP1, TKTL2, TLR5, TMC1, TMEM144, TMEM178B, TMEM217, TMEM225, TMEM232, TMEM26, TMEM63A, TMEM72, TMTC2, TNFRSF14 , TNFRSF21, TNFRSF8, TNFRSF8 , TNIK, TNK1, TNKS, TOX2, TP53, TP63, TPGS1, TPM3, TRAPPC12, TRAV9-2, TRERF1, TRIM51GP, TRIM64C, TRPC5, TRPM3, TRPV3, TRRAP, TRUB2, TSEN2, TTLL2, TTN, TUBAL3, TULP3, TXNRD2.
U	UBAC1, UBQLNL, UNC13C, UNC5D, UNC80, UNC93B1, UNK, USH2A, USP34, USP43, USP7, UTRN.
V	VCAN, VCP, VEPH1, VKORC1L1, VN1R7P, VPS13C, VPS13D, VPS35L, VPS41, VPS9D1, VWA3B.
W	WDFY3, WDR17, WDR33, WDR36, WDR49, WDR63, WNK2, WRAP53.

X	XPO1
Z	ZAK, ZBED3, ZFYVE9, ZIC4, ZNF208, ZNF217, ZNF248, ZNF254, ZNF28, ZNF33A, ZNF34, ZNF366, ZNF415, ZNF445, ZNF483, ZNF502, ZNF564, ZNF599, ZNF638, ZNF710, ZNF776, ZNF783, ZNF805, ZNF827, ZNF883, ZNF890P, ZNF91, ZSCAN18, ZSCAN5C.

Supplementary Table S14. Small-scale mutations in patients cAL1/6-8/12 (WGS).

Gene	Chromosome	Position	Exon	Type	Nucleotide change	Peptide change	Samples
HSPG2	chr1	21847474	62/97	SNV	c.8044C>T	p.R2682W	cAL8
HSPG2	chr1	21850191	57/97	SNV	c.7296A>T	p.A2432%3D	cAL7
EXO5	chr1	40514996	3/3	SNV	c.452T>C	p.L151P	cAL8
DMRTA2	chr1	50418877	3/3	SNV	c.1417G>A	p.A473T	cAL6
SGIP1	chr1	66643594	8/27	SNV	c.346G>C	p.E116Q	cAL7
MAGI3	chr1	113590573	5/21	SNV	c.853T>C	p.Y285H	cAL12
MAGI3	chr1	113651069	14/21	SNV	c.2303G>A	p.R768H	cAL6
MAGI3	chr1	113683521	21/21	SNV	c.3953G>A	p.G1318D	cAL8
AC241952.1	chr1	120501112	35/42	SNV	n.5924A>G	-	cAL8
HORMAD1	chr1	150704198		deletion	c.851-5del	-	cAL1
FLG	chr1	152303983	3/3	SNV	c.10903G>A	p.D3635N	cAL7
FLG	chr1	152304285	3/3	SNV	c.10601A>G	p.N3534S	cAL12
FLG	chr1	152304286	3/3	SNV	c.10600A>T	p.N3534Y	cAL12
FLG	chr1	152305078	3/3	SNV	c.9808C>T	p.R3270C	cAL12
FLG	chr1	152309215	3/3	SNV	c.5671C>T	p.R1891W	cAL12
FLG	chr1	152309431	3/3	SNV	c.5455T>C	p.S1819P	cAL12
FLG	chr1	152310318	3/3	SNV	c.4568C>T	p.T1523I	cAL12
FLG	chr1	152312065	3/3	SNV	c.2821C>T	p.R941C	cAL12
FLG	chr1	152312100	3/3	SNV	c.2786G>T	p.G929V	cAL12
FLG	chr1	152312127	3/3	insertion	c.2758_2759insGG	p.A920Gfs*203	cAL12
FLG	chr1	152312652	3/3	SNV	c.2234G>C	p.S745T	cAL12
F5	chr1	169529762	16/25	SNV	c.5280A>G	p.I1760M	cAL6
SMG7	chr1	183512833		SNV	c.30-4C>T	-	cAL7
SMG7	chr1	183551071	21/22	SNV	c.3181C>T	p.L1061F	cAL7
USH2A	chr1	216073121	28/72	SNV	c.5752G>A	p.E1918K	cAL8
OBSCN	chr1	228282100	31/81	SNV	c.8365G>C	p.G2789R	cAL8
OBSCN	chr1	228294358	42/81	SNV	c.11338G>A	p.G3780R	cAL1
OBSCN	chr1	228338877	69/81	SNV	c.17109T>A	p.S5703R	cAL7
OBSCN	chr1	228370216	102/115	SNV	c.23015G>T	p.C7672F	cAL7
OBSCN	chr1	228371191	104/115	SNV	c.23284C>T	p.R7762W	cAL8
LYST	chr1	235775088		insertion	c.5461-3dup	-	cAL6

TUBAL3	chr10	5394110	4/4	SNV	c.748C>T	p.R250W	cAL1
FRMD4A	chr10	13657133	22/25	deletion	c.2447_2455del	p.A816_G818del	cAL8
SKIDA1	chr10	21516890	2/2	insertion	c.693_695dup	p.A239dup	cAL12
ANKRD30A	chr10	37189558		SNV	c.2344+1G>T	-	cAL1
ANK3	chr10	60196628		deletion	c.1690-4del	-	cAL8
CRTAC1	chr10	97865715		SNV	c.1820-1G>A	-	cAL6
HPSE2	chr10	98490168	10/13	SNV	c.1349G>A	p.R450H	cAL12
NKX2-3	chr10	99535442	2/2	deletion	c.837_845del	p.A284_A286del	cAL8
PDZD8	chr10	117284043	5/5	SNV	c.2690G>A	p.R897Q	cAL12
TCERG1L	chr10	131093202	12/12	SNV	c.1721G>A	p.R574Q	cAL7
MTG1	chr10	133402158	8/11	SNV	c.583C>T	p.R195W	cAL8
NLRP6	chr11	281784	4/8	deletion	c.2063_2065del	p.K688del	cAL6
MUC5B	chr11	1248948	31/49	SNV	c.12068C>T	p.T4023M	cAL1
NUP98	chr11	3720832		indel	c.2147-8_2147-7insTTT	-	cAL12
HPS5	chr11	18287933	17/23	SNV	c.2521G>T	p.V841F	cAL12
C11orf74	chr11	36659169	6/6	SNV	c.649G>A	p.E217K	cAL7
TRIM64C	chr11	49055411		insertion	c.762-7_762-5dup	-	cAL12
SPINDOC	chr11	63818795		SNV	c.734-7C>T	-	cAL8
FRMD8	chr11	65399767	8/11	SNV	c.835C>T	p.P279S	cAL6
FRMD8	chr11	65400815	9/11	SNV	c.1019G>T	p.G340V	cAL1
TENM4	chr11	78661540	33/34	SNV	c.7460C>A	p.P2487H	cAL7
PGR	chr11	101125999		SNV	c.1789+8C>T	-	cAL1
EI24	chr11	125575368	3/11	SNV	c.148G>A	p.A50T	cAL1
GLB1L2	chr11	134356350	6/20	SNV	c.608G>A	p.G203D	cAL8
GLB1L2	chr11	134356397		SNV	c.651+4A>G	-	cAL7
FOXM1	chr12	2858912	10/10	SNV	c.2132C>T	p.P711L	cAL6
TULP3	chr12	2938199	10/12	SNV	c.1109G>C	p.S370T	cAL8
CD163L1	chr12	7368967		insertion	c.4040-6_4040-3dup	-	cAL1
CD163L1	chr12	7451055	2/5	SNV	c.-309G>A	-	cAL1
FAM186A	chr12	50330661	7/8	SNV	c.6946C>G	p.Q2316E	cAL7
FAM186A	chr12	50350798	4/8	SNV	c.6034T>A	p.F2012I	cAL7
DIP2B	chr12	50686581	12/38	SNV	c.1450C>T	p.R484W	cAL1
KRT76	chr12	52771098	7/9	SNV	c.1385C>T	p.A462V	cAL1
SLC6A15	chr12	84873079		SNV	c.1109+8T>C	-	cAL12

LRRIQ1	chr12	85066893	10/27	SNV	c.2690G>A	p.R897Q	cAL12
KNTC1	chr12	122573245	26/64	SNV	c.2243A>G	p.H748R	cAL1
SBNO1	chr12	123313723		deletion	c.3118-5del	-	cAL7
SFSWAP	chr12	131753197	8/18	SNV	c.1156G>A	p.G386R	cAL1
FARP1	chr13	98440744	24/27	SNV	c.2704C>T	p.R902C	cAL6
MCF2L	chr13	112902269	2/30	SNV	c.67C>T	p.R23W	cAL6
MCF2L	chr13	113096439	7/9	SNV	c.656C>A	p.S219R	cAL7
MCF2L	chr13	113096573	8/9	SNV	c.724G>A	p.G242D	cAL7
CDC42BPB	chr14	102999711	5/37	SNV	c.450C>T	p.Y150%3D	cAL1
NEDD4	chr15	55916265	1/22	SNV	c.567T>G	p.S189R	cAL7
KIF7	chr15	89642378	11/19	SNV	c.2219A>G	p.Q740R	cAL6
PCSK6	chr15	101305277	19/19	SNV	c.2375C>T	p.T792M	cAL8
PCSK6	chr15	101370526		SNV	c.1533-3C>T	-	cAL6
PCSK6	chr15	101389569		SNV	c.1210-5C>T	-	cAL12
AXIN1	chr16	346689	2/11	SNV	c.337G>A	p.D113N	cAL7
MGRN1	chr16	4652815	4/17	SNV	c.434G>T	p.G145V	cAL6
ITPRIPL2	chr16	19114478	1/1	SNV	c.17C>T	p.T6I	cAL7
DNAH3	chr16	21051712	29/62	SNV	c.4196C>A	p.S1399Y	cAL7
CNOT1	chr16	58555913		SNV	c.2480-5A>G	-	cAL6
PIEZO1	chr16	88723091		SNV	c.4495+4C>T	-	cAL7
VPS9D1	chr16	89710715	10/15	SNV	c.1129G>A	p.D377N	cAL12
CLUH	chr17	2701524		SNV	c.631-4G>A	-	cAL7
CFAP52	chr17	9594243	4/14	SNV	c.458C>T	p.A153V	cAL12
KIF2B	chr17	53824465	1/1	SNV	c.1432C>A	p.L478I	cAL7
CD300E	chr17	74617195	2/4	SNV	c.311G>A	p.C104Y	cAL6
DNAH17	chr17	78453332		deletion	c.10529+8_10529+10del	-	cAL6
DNAH17	chr17	78454485	64/81	SNV	c.10391G>A	p.R3464H	cAL6
DNAH17	chr17	78505418	31/81	SNV	c.4831G>C	p.D1611H	cAL8
DNAH17	chr17	78529510	22/81	SNV	c.3469G>A	p.G1157R	cAL7
CD7	chr17	82315358	4/4	SNV	c.686G>A	p.R229H	cAL12
PHLPP1	chr18	62715770	1/17	insertion	c.99_104dup	p.A39_A40dup	cAL12
ZNF91	chr19	23360746	4/4	SNV	c.2233G>A	p.E745K	cAL8
ZNF599	chr19	34769537	2/4	SNV	c.37G>A	p.D13N	cAL6
PSG4	chr19	43205529	1/5	SNV	c.8C>T	p.P3L	cAL6

ZNF415	chr19	53108549	4/4	SNV	c.1496A>C	p.N499T	cAL8
VWA3B	chr2	98162976	8/23	SNV	n.1320G>T	-	cAL8
VWA3B	chr2	98211926		SNV	n.1944-4G>A	-	cAL8
RGPD4	chr2	107866325	18/23	SNV	c.2605G>T	p.V869F	cAL7
RGPD4	chr2	107871440	20/23	SNV	c.3436C>T	p.R1146W	cAL8
LRP1B	chr2	140536716		deletion	c.7514-8del	-	cAL1
LRP1B	chr2	140716048	37/91	SNV	c.5948A>G	p.N1983S	cAL7
LRP1B	chr2	140770874		SNV	c.5626+7G>A	-	cAL7
LRP2	chr2	169294717		deletion	c.428-10_428-8del	-	cAL12
TTN	chr2	178528797	188/191	SNV	c.80335C>T	p.R26779*	cAL7
TTN	chr2	178588702	132/191	SNV	c.36404C>T	p.T12135I	cAL12
KIF1A	chr2	240761261	23/48	SNV	c.2206G>T	p.A736S	cAL7
KIF1A	chr2	240788044		SNV	c.363+7A>G	-	cAL6
KIF1A	chr2	240788047		SNV	c.363+4C>G	-	cAL6
SIM2	chr21	36744720		SNV	c.1168-8C>T	-	cAL12
EFCAB6	chr22	43672313		SNV	c.1420-8C>T	-	cAL6
EFCAB6	chr22	43735906	7/32	SNV	c.595A>G	p.R199G	cAL8
TSEN2	chr3	12539173	3/3	SNV	c.106G>A	p.V36I	cAL7
CAND2	chr3	12810332		SNV	c.478+8G>A	-	cAL6
CAND2	chr3	12816797	8/13	SNV	c.1586G>A	p.R529Q	cAL12
COL7A1	chr3	48571132	93/118	SNV	c.7133C>T	p.S2378F	cAL1
COL7A1	chr3	48573318	83/118	SNV	c.6649C>T	p.R2217W	cAL1
COL7A1	chr3	48585562	31/118	SNV	c.3889G>A	p.E1297K	cAL7
BSN	chr3	49660682	6/12	SNV	c.8837G>A	p.R2946Q	cAL7
STAB1	chr3	52505030	13/69	SNV	c.1405C>A	p.P469T	cAL7
ERC2	chr3	56080833	7/18	SNV	c.1625A>G	p.N542S	cAL7
CCDC66	chr3	56619396	16/18	SNV	c.2402A>T	p.E801V	cAL1
FRMD4B	chr3	69181256	21/23	SNV	c.2494C>G	p.Q832E	cAL12
MCF2L2	chr3	183289227		SNV	c.1676-7C>T	-	cAL1
SH3TC1	chr4	8205279	2/18	SNV	c.85C>T	p.R29W	cAL8
NWD2	chr4	37245192	1/7	SNV	c.125G>T	p.R42L	cAL7
RBM47	chr4	40432685	6/7	deletion	c.1499_1507del	p.A500_A502del	cAL1
KIAA1211	chr4	56298339	4/11	SNV	c.110A>G	p.K37R	cAL6
C4orf54	chr4	99650409	1/2	SNV	c.4240A>G	p.K1414E	cAL1

C4orf54	chr4	99652754	1/2	SNV	c.1895G>A	p.R632Q	cAL12
C4orf54	chr4	99654332	1/2	SNV	c.317G>A	p.R106H	cAL1
KIAA1109	chr4	122258745	42/86	SNV	c.6664C>T	p.R2222W	cAL1
KIAA1109	chr4	122272382	48/86	SNV	c.8423T>G	p.F2808C	cAL12
PABPC4L	chr4	134200566	2/2	SNV	c.454A>G	p.R152G	cAL6
WDR17	chr4	176174622	28/31	SNV	c.3470G>A	p.R1157Q	cAL1
MYO10	chr5	16689924		SNV	c.3834-5T>G	-	cAL6
PRDM9	chr5	23524407	10/11	SNV	c.1024A>G	p.R342G	cAL6
MSH3	chr5	80654905	1/24	insertion	c.186_187insGCCGCAGCGCCCGCAGCG	p.A62_P63insAAAPAA	cAL1
MCC	chr5	113028992	16/17	SNV	c.2251A>T	p.S751C	cAL6
MCC	chr5	113488351	1/19	SNV	c.64A>G	p.S22G	cAL1
TGFBI	chr5	136063181		SNV	c.2012-5T>C	-	cAL7
TRERF1	chr6	42228389	16/16	SNV	c.3346G>A	p.D1116N	cAL12
PHF3	chr6	63685295	4/16	SNV	c.1573G>A	p.V525I	cAL12
HIVEP2	chr6	142771617	4/9	SNV	c.3122C>T	p.A1041V	cAL6
UTRN	chr6	144421879	3/74	SNV	c.143G>A	p.S48N	cAL6
INTS1	chr7	1473187		SNV	c.5958-3C>T	-	cAL6
INTS1	chr7	1484062	25/48	SNV	c.3370T>A	p.F1124I	cAL12
VPS41	chr7	38765615	16/29	SNV	c.1294G>A	p.E432K	cAL12
PCLO	chr7	83155517	2/25	insertion	c.1094_1123dup	p.P365_Q374dup	cAL6
SEMA3A	chr7	84005396	11/17	SNV	c.1303G>A	p.V435I	cAL8
TFR2	chr7	100626861	17/18	SNV	c.2038G>T	p.D680Y	cAL1
MUC3A	chr7	100959093	2/12	SNV	c.7314G>C	p.E2438D	cAL7
MUC3A	chr7	100959106	2/12	SNV	c.7327C>T	p.L2443F	cAL7
MUC17	chr7	101033929	3/13	SNV	c.2513C>T	p.T838I	cAL1
MUC17	chr7	101038470	3/13	SNV	c.7054A>G	p.S2352G	cAL8
MUC17	chr7	101041369	3/13	SNV	c.9953C>G	p.A3318G	cAL8
MUC17	chr7	101053335		SNV	c.13266-4C>A	-	cAL7
COL26A1	chr7	101545391	7/13	SNV	c.757G>A	p.G253S	cAL8
CFTR	chr7	117509093	3/27	SNV	c.224G>A	p.R75Q	cAL12
ZNF783	chr7	149294533		SNV	c.*973-7C>T	-	cAL6
SSPO	chr7	149809059	62/107	SNV	c.9142G>A	p.G3048S	cAL8
TEX15	chr8	30836916	3/4	SNV	c.8219C>T	p.S2740F	cAL8
MPDZ	chr9	13223593	5/47	SNV	c.511C>G	p.Q171E	cAL12

PLIN2	chr9	19126187	3/8	SNV	c.153G>C	p.E51D	cAL7
ABCA1	chr9	104794512		insertion	c.5383-6_5383-3dup	-	cAL12
ZNF883	chr9	112968948		indel	n.882-8_882-7insTTT	-	cAL12
ADGRG4	chrX	136323161	3/24	SNV	c.454C>A	p.L152M	cAL1

Supplementary Table S15. Differentially expressed genes (FDR < 0.01) in pcALCL when compared to CD4+ T cells.

Gene symbol	Ensembl code	Log2FC	P.Value	adj.P.Val
AL138963.3	ENSG00000273149	-10.62838094	1.39E-46	1.89E-42
AC245140.2	ENSG00000280195	-9.337416652	2.81E-41	1.90E-37
ATP1A1-AS1	ENSG00000203865	-5.846196197	7.60E-38	3.43E-34
ATG10	ENSG00000152348	-5.613521178	2.95E-37	9.99E-34
AC068888.1	ENSG00000257337	-6.698110463	4.80E-37	1.30E-33
AC021739.4	ENSG00000259544	-9.377413567	1.50E-36	2.84E-33
AC010761.1	ENSG00000264577	-10.23830384	1.72E-36	2.84E-33
AC008105.1	ENSG00000233175	-7.369385175	1.80E-36	2.84E-33
AL355388.3	ENSG00000285677	-9.710340251	1.89E-36	2.84E-33
LIX1L-AS1	ENSG00000234222	-8.215857457	2.13E-36	2.88E-33
AC025682.1	ENSG00000263766	-5.385200947	2.86E-36	3.51E-33
AP003352.1	ENSG00000245970	-11.32243691	1.90E-35	2.14E-32
AL645941.3	ENSG00000263756	-9.418517789	4.01E-35	4.05E-32
BGN	ENSG00000182492	11.37476049	4.39E-35	4.05E-32
SPARC	ENSG00000113140	11.3914239	4.49E-35	4.05E-32
AC006449.7	ENSG00000279119	-10.155796	5.35E-35	4.53E-32
TNFRSF8	ENSG00000120949	10.81463822	6.14E-35	4.86E-32
AL354733.3	ENSG00000235298	-8.911533424	6.46E-35	4.86E-32
CARS-AS1	ENSG00000247473	-8.065078394	7.40E-35	5.28E-32
AC018362.1	ENSG00000261684	-8.506695671	9.08E-35	5.99E-32
AC005726.2	ENSG00000264044	-9.224311293	9.30E-35	5.99E-32
AC067930.6	ENSG00000279605	-9.076477739	1.31E-34	8.03E-32
SH3D19	ENSG00000109686	-5.873069994	1.56E-34	9.19E-32
AC083798.2	ENSG00000272758	-5.36953506	2.37E-34	1.34E-31
AL671277.1	ENSG00000227766	-9.023330909	3.61E-34	1.85E-31
BATF3	ENSG00000123685	9.068945615	3.69E-34	1.85E-31
AL365277.1	ENSG00000228060	-9.171763311	3.81E-34	1.85E-31
AC005944.1	ENSG00000267469	-9.312116612	3.83E-34	1.85E-31
PKD2L2	ENSG00000078795	-7.415850245	5.13E-34	2.40E-31
AP002490.1	ENSG00000251143	-7.746251914	5.71E-34	2.50E-31
AL671883.2	ENSG00000271581	-9.461473216	5.72E-34	2.50E-31
AC006449.3	ENSG00000275665	-10.00097845	6.43E-34	2.68E-31
NCBP2-AS1	ENSG00000225578	-7.304633111	6.56E-34	2.68E-31
AC107081.2	ENSG00000236498	-8.185504616	6.73E-34	2.68E-31
AC005253.1	ENSG00000268030	-8.63530346	7.13E-34	2.76E-31
AC141586.3	ENSG00000261093	-7.782629424	8.14E-34	3.03E-31
RNF219-AS1	ENSG00000234377	-7.751754535	8.29E-34	3.03E-31
AC090617.3	ENSG00000262533	-8.509406679	8.60E-34	3.07E-31
MYCBP2-AS1	ENSG00000236051	-8.534534904	8.88E-34	3.08E-31
AC022400.8	ENSG00000279689	-6.417298334	1.15E-33	3.88E-31
AC124068.1	ENSG00000259948	-7.943461522	1.32E-33	4.29E-31
AC003681.1	ENSG00000279159	-10.04952542	1.33E-33	4.29E-31
SPAG5-AS1	ENSG00000227543	-6.023299329	1.89E-33	5.96E-31
AP001267.1	ENSG00000254873	-9.530146731	2.11E-33	6.34E-31
AC133550.1	ENSG00000260570	-8.639733939	2.11E-33	6.34E-31
COL3A1	ENSG00000168542	14.18328869	2.54E-33	7.47E-31
LRRC75A	ENSG00000181350	-6.053016089	2.86E-33	8.24E-31
COL1A2	ENSG00000164692	13.08160451	2.96E-33	8.35E-31
AC125494.1	ENSG00000219410	-9.177221894	3.16E-33	8.72E-31

MRNIP	ENSG00000161010	-3.939802773	3.55E-33	9.47E-31
AC087164.2	ENSG00000279428	-7.280951746	3.57E-33	9.47E-31
AC004542.2	ENSG00000269987	-9.589866912	4.36E-33	1.14E-30
AP003096.1	ENSG00000260808	-7.986692217	5.88E-33	1.50E-30
AC013356.2	ENSG00000259211	-8.04260824	9.23E-33	2.30E-30
AC120057.3	ENSG00000279641	-8.128484155	9.33E-33	2.30E-30
AC004542.1	ENSG00000269972	-9.4174159	9.85E-33	2.38E-30
AC069287.2	ENSG00000254559	-8.752228484	1.02E-32	2.43E-30
AC005921.2	ENSG00000262967	-7.814590093	1.44E-32	3.36E-30
AC020913.1	ENSG00000268056	-8.695885699	1.54E-32	3.53E-30
C5orf58	ENSG00000234511	-9.145606396	1.84E-32	4.15E-30
AC009133.1	ENSG00000238045	-5.682648744	1.90E-32	4.22E-30
AC093495.1	ENSG00000228242	-8.045469854	2.05E-32	4.48E-30
AC087276.2	ENSG00000254907	-8.462797133	2.63E-32	5.66E-30
AC114271.1	ENSG00000274425	-4.634439872	2.76E-32	5.80E-30
AC025257.1	ENSG00000257386	-8.717877141	2.79E-32	5.80E-30
AC034102.4	ENSG00000257553	-6.697535179	2.89E-32	5.93E-30
RBFOX2	ENSG00000100320	5.374833939	3.57E-32	7.22E-30
AC006128.1	ENSG00000279716	-8.5886737	4.23E-32	8.43E-30
MLLT11	ENSG00000213190	-4.574882235	4.40E-32	8.64E-30
AC138811.1	ENSG00000260017	-8.710381621	5.09E-32	9.84E-30
AC138956.1	ENSG00000250909	-7.521540329	5.20E-32	9.91E-30
AC114546.3	ENSG00000279364	-8.961477166	5.40E-32	1.02E-29
AL592166.1	ENSG00000225721	-8.951939808	5.75E-32	1.07E-29
AC027601.1	ENSG00000260005	-8.203968935	5.89E-32	1.08E-29
MFSD11	ENSG00000092931	-3.095006515	6.34E-32	1.14E-29
CD44-AS1	ENSG00000255443	-10.30607775	7.71E-32	1.37E-29
AC025262.3	ENSG00000280320	-9.196192064	8.24E-32	1.45E-29
CDC20	ENSG00000117399	7.773801172	9.84E-32	1.71E-29
TOP2A	ENSG00000131747	7.811079355	1.10E-31	1.89E-29
AL512770.1	ENSG00000228302	-8.268079053	1.15E-31	1.95E-29
SREBF2-AS1	ENSG00000184068	-5.183168626	1.19E-31	1.97E-29
EDRF1-AS1	ENSG00000236991	-7.910617671	1.19E-31	1.97E-29
CFLAR-AS1	ENSG00000226312	-8.394706396	1.38E-31	2.26E-29
AC114947.2	ENSG00000261604	-7.822161449	1.43E-31	2.31E-29
ZRANB2-AS1	ENSG00000235079	-7.906952066	1.48E-31	2.36E-29
AC245452.1	ENSG00000224086	-5.359233562	1.54E-31	2.40E-29
AC073254.1	ENSG00000237126	-8.004629202	1.54E-31	2.40E-29
AL139022.1	ENSG00000259118	-8.850861094	1.61E-31	2.48E-29
PXN-AS1	ENSG00000255857	-5.53949512	1.67E-31	2.54E-29
AC012645.3	ENSG00000261416	-5.508054523	1.69E-31	2.55E-29
ZACN	ENSG00000186919	-7.896026711	1.83E-31	2.73E-29
AC068831.4	ENSG00000259661	-9.337478208	1.86E-31	2.74E-29
AC008781.1	ENSG00000228737	-6.877456536	2.13E-31	3.09E-29
DDX39B	ENSG00000198563	-3.395840846	2.14E-31	3.09E-29
AC005253.2	ENSG00000268983	-7.779901846	2.31E-31	3.29E-29
C1orf56	ENSG00000143443	-5.134721747	2.35E-31	3.32E-29
COL6A3	ENSG00000163359	8.262745315	2.67E-31	3.73E-29
FSTL1	ENSG00000163430	9.75918891	2.96E-31	4.09E-29
PCBP1-AS1	ENSG00000179818	-3.222055525	3.04E-31	4.15E-29
SH3BP5-AS1	ENSG00000224660	-4.091191766	3.52E-31	4.76E-29

C6orf201	ENSG00000185689	-8.565519441	3.64E-31	4.88E-29
AC090984.1	ENSG00000279033	-8.361453177	3.77E-31	5.01E-29
EMP2	ENSG00000213853	8.166724591	4.08E-31	5.36E-29
CCDC151	ENSG00000198003	-5.837494764	4.13E-31	5.38E-29
PRMT5-AS1	ENSG00000237054	-8.02740084	4.22E-31	5.40E-29
EFCAB14-AS1	ENSG00000228237	-7.806244517	4.23E-31	5.40E-29
AC025165.2	ENSG00000257342	-8.162511914	4.28E-31	5.41E-29
AP4B1-AS1	ENSG00000226167	-8.941850222	4.32E-31	5.42E-29
AC112907.3	ENSG00000263826	-8.509753245	4.39E-31	5.46E-29
AC008635.1	ENSG00000269487	-7.62090024	4.57E-31	5.62E-29
AL583722.2	ENSG00000258430	-7.033391753	4.63E-31	5.65E-29
AC008735.2	ENSG00000267523	-8.498624408	4.99E-31	6.04E-29
AC132812.1	ENSG00000265298	-8.56084942	5.47E-31	6.55E-29
IGFBP7	ENSG00000163453	4.76359135	6.00E-31	7.13E-29
AP002433.1	ENSG00000255467	-7.275361208	6.85E-31	8.06E-29
MBNL1-AS1	ENSG00000229619	-4.469561705	7.48E-31	8.73E-29
AC087286.3	ENSG00000259375	-8.22705553	8.30E-31	9.60E-29
TSNAXIP1	ENSG00000102904	-5.529131809	8.81E-31	1.01E-28
COL4A2	ENSG00000134871	10.20222417	8.88E-31	1.01E-28
GAS2L3	ENSG00000139354	6.198003009	9.52E-31	1.07E-28
AC008264.2	ENSG00000273489	-9.079847393	9.77E-31	1.09E-28
TUBA1B	ENSG00000123416	4.036773736	1.01E-30	1.13E-28
CORO1C	ENSG00000110880	5.096279096	1.14E-30	1.25E-28
AC005696.2	ENSG00000272770	-8.964660944	1.19E-30	1.29E-28
RNASE1	ENSG00000129538	8.683110938	1.34E-30	1.45E-28
AC135457.1	ENSG00000272742	-9.625308369	1.35E-30	1.45E-28
GPS2	ENSG00000132522	-6.407531223	1.38E-30	1.47E-28
AC009303.2	ENSG00000235066	-7.605889362	1.39E-30	1.47E-28
TIMP3	ENSG00000100234	9.118268854	1.50E-30	1.58E-28
ZNF337-AS1	ENSG00000213742	-4.8634315	1.52E-30	1.59E-28
AC018521.4	ENSG00000264701	-8.941316745	1.55E-30	1.60E-28
AL031595.1	ENSG00000279933	-10.06539934	1.57E-30	1.61E-28
PLXNB2	ENSG00000196576	6.147876176	1.68E-30	1.71E-28
GTSE1	ENSG00000075218	7.014757882	1.69E-30	1.71E-28
AL118558.1	ENSG00000258959	-8.92574456	1.72E-30	1.72E-28
AC137590.1	ENSG00000257000	-7.645112122	1.97E-30	1.96E-28
U91328.2	ENSG00000272558	-8.230089863	2.07E-30	2.05E-28
CATSPER2P1	ENSG00000205771	-4.516966147	2.41E-30	2.37E-28
AC008105.2	ENSG00000233483	-6.473836263	2.45E-30	2.39E-28
AC106886.4	ENSG00000280211	-7.232831662	2.50E-30	2.42E-28
RUSC1-AS1	ENSG00000225855	-5.350864713	2.67E-30	2.56E-28
AL161668.3	ENSG00000258471	-7.786843842	2.99E-30	2.84E-28
CLEC14A	ENSG00000176435	6.99330703	3.00E-30	2.84E-28
AC009088.2	ENSG00000260304	-10.19146636	3.04E-30	2.86E-28
AC012157.1	ENSG00000258034	-7.862378191	3.52E-30	3.29E-28
CCNB1	ENSG00000134057	5.872243547	3.71E-30	3.44E-28
MCM3AP-AS1	ENSG00000215424	-5.091643187	3.97E-30	3.62E-28
AC084876.1	ENSG00000277299	-7.621776121	3.98E-30	3.62E-28
LAMA4	ENSG00000112769	8.186520186	3.98E-30	3.62E-28
MCM4	ENSG00000104738	4.02051676	4.09E-30	3.67E-28
SLC5A2	ENSG00000140675	-6.810834026	4.11E-30	3.67E-28

AC004824.1	ENSG00000227751	-6.923493397	4.12E-30	3.67E-28
BEST1	ENSG00000167995	-8.775895402	4.46E-30	3.95E-28
GTF3C2-AS1	ENSG00000234945	-8.57500802	4.51E-30	3.97E-28
SPATA21	ENSG00000187144	-8.616344013	5.11E-30	4.47E-28
AC124319.3	ENSG00000276863	-8.262053463	5.88E-30	5.10E-28
AC010894.4	ENSG00000237798	-10.32602773	6.32E-30	5.45E-28
SPARCL1	ENSG00000152583	9.040397473	6.59E-30	5.64E-28
AC007728.1	ENSG00000260616	-8.850289749	6.66E-30	5.67E-28
SNAI2	ENSG00000019549	7.647902957	6.70E-30	5.67E-28
KIF4A	ENSG00000090889	7.166004147	7.56E-30	6.36E-28
AC012615.3	ENSG00000267125	-7.603659478	8.17E-30	6.83E-28
AC245052.4	ENSG00000237017	-6.864054441	8.29E-30	6.86E-28
AL512656.1	ENSG00000233144	-9.282008832	8.30E-30	6.86E-28
LAMC1	ENSG00000135862	9.504095905	8.93E-30	7.33E-28
AC020913.2	ENSG00000269480	-8.223467318	9.11E-30	7.43E-28
COL4A1	ENSG00000187498	10.95252684	9.27E-30	7.52E-28
AC007314.1	ENSG00000234818	-7.137302552	9.36E-30	7.54E-28
AC005288.1	ENSG00000266469	-4.811799993	9.44E-30	7.57E-28
ARAP1-AS2	ENSG00000245148	-7.283613233	9.60E-30	7.64E-28
ZNF451-AS1	ENSG00000226803	-7.732979638	9.92E-30	7.86E-28
AC024267.6	ENSG00000266642	-7.668594088	1.16E-29	9.07E-28
PLK1	ENSG00000166851	4.598944728	1.19E-29	9.28E-28
AL158834.2	ENSG00000227253	-9.88611348	1.23E-29	9.48E-28
SEMA3F-AS1	ENSG00000235016	-8.98011526	1.31E-29	1.01E-27
AC092069.1	ENSG00000267458	-7.746689757	1.33E-29	1.02E-27
CYYR1	ENSG00000166265	6.221921208	1.36E-29	1.03E-27
AC109587.1	ENSG00000244513	-5.50814289	1.41E-29	1.07E-27
KDR	ENSG00000128052	7.171889124	1.51E-29	1.13E-27
AC010320.2	ENSG00000268015	-7.03251704	1.57E-29	1.16E-27
SENP7	ENSG00000138468	-3.554181552	1.75E-29	1.29E-27
RBM5-AS1	ENSG00000281691	-9.008530204	1.76E-29	1.29E-27
AL031714.1	ENSG00000261505	-9.674857326	1.82E-29	1.33E-27
COL6A1	ENSG00000142156	7.389674611	1.98E-29	1.43E-27
AL671710.1	ENSG00000273192	-4.876835935	1.98E-29	1.43E-27
MARCKS	ENSG00000277443	8.754428231	2.06E-29	1.48E-27
TSSK4	ENSG00000139908	-7.995431561	2.08E-29	1.48E-27
ARAP1-AS1	ENSG00000256007	-7.621017853	2.19E-29	1.55E-27
AURKB	ENSG00000178999	5.710722281	2.21E-29	1.56E-27
AC004477.2	ENSG00000266341	-7.255108559	2.44E-29	1.71E-27
AL133453.1	ENSG00000258757	-8.825099611	2.44E-29	1.71E-27
AC005523.2	ENSG00000269604	-8.23444167	2.46E-29	1.71E-27
AL161452.1	ENSG00000226706	-7.304587441	2.54E-29	1.75E-27
AC006059.1	ENSG00000230084	-7.398155517	2.68E-29	1.84E-27
AL356481.3	ENSG00000280758	-6.7768099	2.73E-29	1.87E-27
AC009133.2	ENSG00000259952	-6.33567879	2.83E-29	1.92E-27
IGBP1-AS2	ENSG00000220925	-7.936689991	2.86E-29	1.94E-27
AC068789.1	ENSG00000257824	-9.228289232	2.94E-29	1.98E-27
AL445686.2	ENSG00000264443	-10.525039	3.34E-29	2.24E-27
SNX22	ENSG00000157734	-5.060678564	3.57E-29	2.37E-27
AC010976.1	ENSG00000231731	-8.464606305	3.58E-29	2.37E-27
AC073896.2	ENSG00000257303	-4.675154298	3.60E-29	2.38E-27

FN1	ENSG00000115414	7.804659782	3.76E-29	2.47E-27
CTTN	ENSG00000085733	6.656211829	3.78E-29	2.47E-27
AC008676.3	ENSG00000285868	-7.816092692	3.82E-29	2.49E-27
AC055713.1	ENSG00000247373	-4.501864682	3.90E-29	2.52E-27
MMP24	ENSG00000125966	-5.977323018	4.51E-29	2.87E-27
CHCHD10	ENSG00000250479	3.910897496	4.79E-29	3.03E-27
HTR5BP	ENSG00000125631	-7.722104364	5.26E-29	3.31E-27
ERICH6B	ENSG00000165837	-7.925876819	5.40E-29	3.39E-27
AC005480.1	ENSG00000258891	-6.172751648	5.48E-29	3.42E-27
AC009690.2	ENSG00000261460	-7.902180191	6.05E-29	3.76E-27
AC020659.2	ENSG00000250379	-7.174351527	6.22E-29	3.84E-27
AP001107.4	ENSG00000254461	-7.26093664	6.24E-29	3.84E-27
AC087362.1	ENSG00000254898	-8.739678664	6.41E-29	3.93E-27
KIFC1	ENSG00000237649	6.252858105	6.65E-29	4.04E-27
AL928654.2	ENSG00000257270	-7.114639347	7.17E-29	4.33E-27
MT-TP	ENSG00000210196	-6.68064178	7.35E-29	4.42E-27
AC005954.2	ENSG00000267205	-7.16737011	7.71E-29	4.62E-27
AC003070.1	ENSG00000267344	-7.344717527	7.78E-29	4.63E-27
UBE2Q1-AS1	ENSG00000229780	-7.749707295	7.80E-29	4.63E-27
BIRC5	ENSG00000089685	7.447517142	8.07E-29	4.77E-27
COL15A1	ENSG00000204291	10.06069164	8.18E-29	4.82E-27
AC005104.1	ENSG00000223374	-9.287435573	8.48E-29	4.97E-27
AC037459.3	ENSG00000253200	-4.699324738	8.55E-29	4.97E-27
AC006435.2	ENSG00000263345	-9.368499417	8.55E-29	4.97E-27
AC023906.3	ENSG00000259327	-6.711260087	8.97E-29	5.19E-27
ASB14	ENSG00000239388	-7.544176246	9.40E-29	5.42E-27
DPP9-AS1	ENSG00000205790	-7.732513673	9.58E-29	5.49E-27
AP003108.2	ENSG00000256591	-5.62374011	9.88E-29	5.64E-27
VCAM1	ENSG00000162692	8.755075492	1.04E-28	5.89E-27
AC096649.1	ENSG00000229750	-7.406972871	1.18E-28	6.67E-27
SMARCA5-AS1	ENSG00000245112	-7.229439421	1.23E-28	6.91E-27
A2M	ENSG00000175899	7.394081258	1.28E-28	7.16E-27
AL590714.1	ENSG00000224985	-7.134417913	1.35E-28	7.50E-27
B3GNT4	ENSG00000176383	-6.610184749	1.37E-28	7.58E-27
AC093484.3	ENSG00000265401	-8.141965781	1.39E-28	7.70E-27
AC137630.2	ENSG00000235236	-6.220942144	1.42E-28	7.83E-27
AP000873.2	ENSG00000247137	-4.009569836	1.44E-28	7.87E-27
ADGRL4	ENSG00000162618	7.375296234	1.44E-28	7.87E-27
AC016888.1	ENSG00000266036	-7.365673688	1.46E-28	7.91E-27
AC087292.1	ENSG00000263165	-7.658483505	1.47E-28	7.95E-27
AC090971.1	ENSG00000259185	-8.120557017	1.53E-28	8.25E-27
AC005037.1	ENSG00000183308	-5.148934761	1.58E-28	8.48E-27
PLCG1-AS1	ENSG00000226648	-6.660915134	1.67E-28	8.92E-27
CNTD1	ENSG00000176563	-8.694825797	1.70E-28	9.09E-27
AC012184.4	ENSG00000285710	-6.672887809	1.74E-28	9.23E-27
AC145207.2	ENSG00000262413	-6.648496397	1.75E-28	9.27E-27
CTSZ	ENSG00000101160	4.834369481	1.76E-28	9.29E-27
ANKRD23	ENSG00000163126	-4.328342165	1.77E-28	9.30E-27
AC009228.1	ENSG00000242628	-7.211602405	1.79E-28	9.33E-27
AC091133.1	ENSG00000230532	-3.514592091	1.80E-28	9.39E-27
AP000879.1	ENSG00000254721	-7.530420544	1.82E-28	9.39E-27

AL035658.1	ENSG00000232754	-7.905221968	1.83E-28	9.39E-27
PRR11	ENSG00000068489	6.676147084	1.83E-28	9.39E-27
CAV2	ENSG00000105971	6.995927254	1.83E-28	9.39E-27
DDAH1	ENSG00000153904	5.747466339	1.84E-28	9.39E-27
AC137630.1	ENSG00000223343	-5.547895286	1.86E-28	9.47E-27
DCN	ENSG00000011465	11.58546116	1.92E-28	9.75E-27
AC006435.1	ENSG00000262456	-8.033638818	2.03E-28	1.03E-26
AP006621.1	ENSG00000255108	-7.796039025	2.13E-28	1.07E-26
AC129510.1	ENSG00000265678	-8.032388023	2.13E-28	1.07E-26
LUM	ENSG00000139329	10.83700173	2.22E-28	1.11E-26
AL670729.2	ENSG00000270094	-7.443026264	2.23E-28	1.11E-26
ANKRD36BP1	ENSG00000214262	-8.804605952	2.24E-28	1.11E-26
AP001458.1	ENSG00000254964	-8.327282798	2.30E-28	1.14E-26
AC020900.1	ENSG00000249180	-8.307113735	2.31E-28	1.14E-26
AC007292.1	ENSG00000267980	-4.416946923	2.32E-28	1.14E-26
PITRM1-AS1	ENSG00000237399	-5.767807447	2.51E-28	1.22E-26
AL645933.1	ENSG00000233902	-6.950537643	2.55E-28	1.24E-26
AP001001.1	ENSG00000254433	-7.607818365	2.70E-28	1.30E-26
SERINC4	ENSG00000184716	-7.062337745	2.70E-28	1.30E-26
AC001226.2	ENSG00000283208	-7.779250302	2.70E-28	1.30E-26
AL031670.1	ENSG00000275582	-7.098143833	2.88E-28	1.38E-26
AL590133.2	ENSG00000259357	-6.687460246	2.89E-28	1.38E-26
AC036103.1	ENSG00000261002	-8.561742506	2.98E-28	1.42E-26
PRRX1	ENSG00000116132	9.512261556	3.03E-28	1.44E-26
AC010273.1	ENSG00000248664	-5.725061983	3.11E-28	1.47E-26
AL109811.1	ENSG00000226849	-5.536111323	3.19E-28	1.50E-26
KIF2C	ENSG00000142945	4.932773043	3.37E-28	1.58E-26
AC009060.1	ENSG00000247228	-10.15464469	3.46E-28	1.61E-26
EHMT2-AS1	ENSG00000237080	-7.730777219	3.53E-28	1.64E-26
CAVIN1	ENSG00000177469	8.293123762	3.60E-28	1.67E-26
U47924.2	ENSG00000272173	-5.995084616	3.83E-28	1.77E-26
SPC25	ENSG00000152253	7.037423533	3.96E-28	1.82E-26
SRRM5	ENSG00000226763	-4.84463022	3.97E-28	1.82E-26
AC008649.1	ENSG00000267291	-7.022096823	4.01E-28	1.83E-26
AL138478.1	ENSG00000277801	-8.694529208	4.11E-28	1.87E-26
AL358472.5	ENSG00000284738	-5.290495734	4.20E-28	1.91E-26
CEP164P1	ENSG00000226937	-8.013698524	4.24E-28	1.92E-26
AL157871.6	ENSG00000259052	-7.747949869	4.40E-28	1.99E-26
SLC29A1	ENSG00000112759	6.09335901	4.51E-28	2.03E-26
THY1	ENSG00000154096	9.063613575	4.59E-28	2.06E-26
MT-TY	ENSG00000210144	-7.659182139	4.66E-28	2.07E-26
AL157838.1	ENSG00000197670	-8.042789628	4.66E-28	2.07E-26
AC002094.2	ENSG00000265618	-7.42149966	4.67E-28	2.07E-26
CNNM2	ENSG00000148842	-3.062052687	4.69E-28	2.08E-26
C1QC	ENSG00000159189	10.24756181	4.77E-28	2.10E-26
SZT2-AS1	ENSG00000229372	-7.933104491	4.85E-28	2.13E-26
TNC	ENSG00000041982	10.42769951	4.88E-28	2.14E-26
TAB3-AS2	ENSG00000235512	-8.013869727	5.06E-28	2.21E-26
AP001453.1	ENSG00000256116	-4.858185102	5.09E-28	2.22E-26
AC009630.3	ENSG00000264578	-7.818896449	5.18E-28	2.25E-26
PGM5P2	ENSG00000277778	-6.959301967	5.20E-28	2.25E-26

CAVIN3	ENSG00000170955	9.664677203	5.30E-28	2.29E-26
AC015674.1	ENSG00000264558	-7.847116247	5.34E-28	2.29E-26
MXRA5	ENSG00000101825	9.269360638	5.38E-28	2.29E-26
AC139530.1	ENSG00000262049	-3.235995376	5.39E-28	2.29E-26
MCMDC2	ENSG00000178460	-6.587673527	5.39E-28	2.29E-26
CD276	ENSG00000103855	8.115984805	5.64E-28	2.39E-26
AC011603.2	ENSG00000258017	-5.920437376	5.82E-28	2.46E-26
AC010642.2	ENSG00000283103	-4.508818325	6.05E-28	2.54E-26
TATDN2P2	ENSG00000218226	-8.711207507	6.27E-28	2.63E-26
CAV1	ENSG00000105974	8.816972519	6.40E-28	2.68E-26
CCND1	ENSG00000110092	4.842503194	6.52E-28	2.72E-26
AC073167.1	ENSG00000259589	-9.166247798	6.65E-28	2.76E-26
AL589990.1	ENSG00000228086	-8.274830628	6.79E-28	2.81E-26
APOM	ENSG00000204444	-3.103960901	7.15E-28	2.95E-26
AL358781.1	ENSG00000176868	-8.091824555	7.28E-28	2.99E-26
AC025918.1	ENSG00000225798	-7.115455564	7.33E-28	3.00E-26
AL592148.3	ENSG00000272750	-4.844709927	7.34E-28	3.00E-26
SARAF	ENSG00000133872	-3.056813147	7.53E-28	3.07E-26
CTBP1-AS	ENSG00000280927	-7.459504678	7.95E-28	3.23E-26
TROAP	ENSG00000135451	5.74510006	8.10E-28	3.28E-26
TIMP2	ENSG00000035862	5.120162416	8.15E-28	3.29E-26
FBN1	ENSG00000166147	7.936038443	8.24E-28	3.32E-26
AC093162.2	ENSG00000246575	-8.255608455	8.41E-28	3.38E-26
MRC2	ENSG00000011028	4.417257476	1.07E-27	4.28E-26
ACVRL1	ENSG00000139567	7.253609829	1.12E-27	4.48E-26
ANTXR1	ENSG00000169604	8.64039905	1.15E-27	4.57E-26
EMILIN1	ENSG00000138080	6.157186166	1.19E-27	4.71E-26
TBL1XR1-AS1	ENSG00000231310	-7.411693227	1.21E-27	4.78E-26
PDGFRB	ENSG00000113721	8.97099194	1.24E-27	4.88E-26
AC021739.2	ENSG00000259407	-7.901725684	1.26E-27	4.94E-26
CENPE	ENSG00000138778	5.118902389	1.26E-27	4.95E-26
SH3GL1P3	ENSG00000267352	-7.997519008	1.28E-27	5.01E-26
C22orf23	ENSG00000128346	-6.098318665	1.33E-27	5.19E-26
AC109460.2	ENSG00000260853	-8.560235841	1.35E-27	5.27E-26
AL513550.1	ENSG00000228506	-4.707226228	1.38E-27	5.34E-26
LHFPL6	ENSG00000183722	6.912859343	1.39E-27	5.35E-26
ABCB9	ENSG00000150967	-4.185405722	1.39E-27	5.36E-26
AC015813.5	ENSG00000279069	-6.79286682	1.40E-27	5.37E-26
AP001107.1	ENSG00000245156	-7.993912989	1.40E-27	5.37E-26
AC008443.1	ENSG00000247049	-7.136385116	1.48E-27	5.65E-26
PMP22	ENSG00000109099	8.034103381	1.49E-27	5.67E-26
AC090510.3	ENSG00000278769	-6.540511517	1.50E-27	5.68E-26
B3GAT2	ENSG00000112309	-8.264470566	1.50E-27	5.68E-26
LRRC37A16P	ENSG00000267023	-9.670984459	1.51E-27	5.68E-26
AL450998.2	ENSG00000237938	-8.083183729	1.52E-27	5.70E-26
AC007679.1	ENSG00000225610	-8.661658318	1.54E-27	5.77E-26
AL157938.2	ENSG00000236986	-7.989326496	1.59E-27	5.94E-26
NR2F2	ENSG00000185551	8.085753495	1.60E-27	5.97E-26
AC004906.1	ENSG00000237286	-8.920424199	1.61E-27	5.97E-26
AP003392.1	ENSG00000254428	-9.002426764	1.65E-27	6.12E-26
AC002350.1	ENSG00000278993	-5.671995232	1.66E-27	6.13E-26

AC080112.3	ENSG00000278918	-8.807048485	1.68E-27	6.20E-26
AC026401.1	ENSG00000257769	-7.149140707	1.70E-27	6.26E-26
AL731566.1	ENSG00000273891	-7.384755623	1.72E-27	6.31E-26
AC139887.1	ENSG00000233799	-7.127868173	2.00E-27	7.32E-26
SOD2	ENSG00000285441	-8.824272374	2.03E-27	7.40E-26
AC011450.1	ENSG00000197813	-6.257948944	2.11E-27	7.70E-26
SERPINF1	ENSG00000132386	5.369539443	2.16E-27	7.83E-26
CACTIN-AS1	ENSG00000226800	-7.243656607	2.21E-27	7.99E-26
AL024507.2	ENSG00000272476	-3.944264325	2.25E-27	8.11E-26
AC104083.1	ENSG00000260244	6.215160136	2.28E-27	8.22E-26
CDCA8	ENSG00000134690	5.706732423	2.33E-27	8.35E-26
CDCA5	ENSG00000146670	6.459845958	2.40E-27	8.58E-26
SAPCD2	ENSG00000186193	7.378093854	2.40E-27	8.58E-26
C5orf66	ENSG00000224186	-8.250917938	2.45E-27	8.73E-26
AC044849.1	ENSG00000272256	-10.36689467	2.46E-27	8.73E-26
AC107871.1	ENSG00000260007	-4.718991742	2.47E-27	8.77E-26
AC211433.1	ENSG00000232729	-7.834516838	2.54E-27	8.93E-26
TSPYL2	ENSG00000184205	-4.400321303	2.65E-27	9.31E-26
SGO2	ENSG00000163535	4.209814292	2.67E-27	9.35E-26
SH3RF2	ENSG00000156463	7.097751299	2.72E-27	9.51E-26
TTC3-AS1	ENSG00000228677	-8.419081933	2.80E-27	9.73E-26
AF230666.1	ENSG00000223697	-9.110164023	2.94E-27	1.02E-25
ITIH4-AS1	ENSG00000239799	-7.711062144	3.02E-27	1.04E-25
SLC1A3	ENSG00000079215	7.085998131	3.26E-27	1.12E-25
AC022400.1	ENSG00000224195	-7.336873789	3.31E-27	1.14E-25
AL021707.5	ENSG00000244491	-9.156988885	3.42E-27	1.17E-25
AL135999.1	ENSG00000258727	-4.245620365	3.56E-27	1.22E-25
CDK2AP1	ENSG00000111328	3.721568059	3.62E-27	1.23E-25
MAP3K14-AS1	ENSG00000267278	-3.86486658	3.63E-27	1.23E-25
AL354740.1	ENSG00000225339	-6.26358139	3.64E-27	1.23E-25
AL162377.3	ENSG00000285444	-7.908429045	3.70E-27	1.25E-25
VIM-AS1	ENSG00000229124	-4.140412804	3.78E-27	1.27E-25
AC037459.2	ENSG00000251034	-7.691140908	4.11E-27	1.38E-25
TMEM262	ENSG00000187066	-6.771959397	4.20E-27	1.41E-25
CCNB2	ENSG00000157456	7.145989488	4.28E-27	1.43E-25
AC004771.4	ENSG00000262429	-6.609953582	4.45E-27	1.48E-25
AP000648.3	ENSG00000280385	-8.647475896	4.65E-27	1.55E-25
AC009090.6	ENSG00000285979	-9.747736844	4.71E-27	1.56E-25
AL139021.1	ENSG00000258378	-7.57838459	4.74E-27	1.57E-25
SLC25A5-AS1	ENSG00000224281	-4.595728538	4.81E-27	1.59E-25
TK1	ENSG00000167900	5.351329861	4.95E-27	1.63E-25
AC021092.1	ENSG00000186019	-6.792487084	4.98E-27	1.64E-25
AL442663.3	ENSG00000258813	-6.181482196	5.21E-27	1.71E-25
GOLIM4	ENSG00000173905	6.883982846	5.23E-27	1.71E-25
AL031600.1	ENSG00000260051	-8.01318613	5.60E-27	1.82E-25
PHC3	ENSG00000173889	-3.127875714	5.68E-27	1.84E-25
AC005070.3	ENSG00000272918	-5.805504249	5.79E-27	1.87E-25
AC103858.1	ENSG00000271725	-8.722544988	5.82E-27	1.88E-25
AL031600.3	ENSG00000261641	-8.249559132	5.97E-27	1.92E-25
TPX2	ENSG00000088325	5.711546727	6.72E-27	2.15E-25
AC087362.2	ENSG00000255487	-6.449297736	6.75E-27	2.16E-25

MED4-AS1	ENSG00000229111	-8.900410765	6.86E-27	2.19E-25
NCAPG	ENSG00000109805	5.235199564	6.96E-27	2.21E-25
AC087393.2	ENSG00000263986	-8.597899767	7.24E-27	2.30E-25
AP001267.3	ENSG00000255435	-5.140389334	7.43E-27	2.35E-25
PHKA2-AS1	ENSG00000237836	-5.518669917	7.58E-27	2.39E-25
AC069234.3	ENSG00000256569	-7.715739143	7.99E-27	2.52E-25
NABP2	ENSG00000139579	3.051986219	8.11E-27	2.55E-25
TRIO	ENSG00000038382	4.258306467	8.29E-27	2.59E-25
FANCD2OS	ENSG00000163705	-7.479770367	8.40E-27	2.62E-25
TCF4	ENSG00000196628	7.277831479	8.53E-27	2.66E-25
AC020909.3	ENSG00000268854	-7.550922806	9.48E-27	2.94E-25
NES	ENSG00000132688	6.628204299	9.66E-27	2.99E-25
CD34	ENSG00000174059	7.369138434	9.92E-27	3.06E-25
AC073611.1	ENSG00000257605	-4.486298207	1.00E-26	3.09E-25
CDC45	ENSG00000093009	5.408743447	1.01E-26	3.10E-25
PLVAP	ENSG00000130300	7.13075595	1.04E-26	3.19E-25
ARNTL2	ENSG00000029153	7.210265446	1.07E-26	3.28E-25
BBIP1	ENSG00000214413	-3.748119468	1.08E-26	3.29E-25
AC024075.3	ENSG00000269427	-6.695730242	1.09E-26	3.31E-25
AL121985.1	ENSG00000228863	-7.677449038	1.10E-26	3.33E-25
AC104134.1	ENSG00000225420	-8.723088483	1.14E-26	3.46E-25
HJURP	ENSG00000123485	7.815383086	1.16E-26	3.51E-25
RAB31	ENSG00000168461	7.610817976	1.17E-26	3.54E-25
DAB2	ENSG00000153071	7.973700026	1.26E-26	3.78E-25
AL391069.1	ENSG00000224645	-6.995493791	1.32E-26	3.97E-25
PRDX4	ENSG00000123131	3.271764515	1.36E-26	4.07E-25
AC025283.2	ENSG00000262621	-7.24058303	1.41E-26	4.22E-25
AC026202.3	ENSG00000268509	-7.18851902	1.45E-26	4.31E-25
AC008040.5	ENSG00000268220	-8.545821375	1.54E-26	4.59E-25
AP001350.1	ENSG00000269570	-7.876346636	1.62E-26	4.81E-25
AC124319.2	ENSG00000263069	-7.717506487	1.66E-26	4.91E-25
AL031846.2	ENSG00000279833	-10.52890034	1.71E-26	5.05E-25
NDN	ENSG00000182636	6.619708984	1.77E-26	5.23E-25
ASF1B	ENSG00000105011	5.560989048	1.79E-26	5.28E-25
CFAP73	ENSG00000186710	-5.013246625	1.83E-26	5.36E-25
CALML4	ENSG00000129007	-5.395842992	1.84E-26	5.39E-25
TM4SF1	ENSG00000169908	6.982563695	1.88E-26	5.49E-25
AC008149.1	ENSG00000258177	-7.145608278	1.92E-26	5.60E-25
AC007163.1	ENSG00000230408	-7.42191763	1.95E-26	5.67E-25
AC137932.3	ENSG00000268218	-9.354095039	2.09E-26	6.07E-25
CDK1	ENSG00000170312	5.70139564	2.09E-26	6.07E-25
KIF18B	ENSG00000186185	6.425042545	2.10E-26	6.07E-25
MKNK1-AS1	ENSG00000269956	-7.224231927	2.15E-26	6.21E-25
AP002907.1	ENSG00000272037	-7.900541969	2.32E-26	6.68E-25
AC127024.6	ENSG00000276250	-6.838770393	2.36E-26	6.79E-25
RAB32	ENSG00000118508	5.834736496	2.42E-26	6.93E-25
AC097460.1	ENSG00000245322	-6.863335263	2.47E-26	7.06E-25
AC009065.6	ENSG00000261240	-6.772414972	2.50E-26	7.12E-25
SYNPO	ENSG00000171992	6.681352754	2.60E-26	7.37E-25
CDT1	ENSG00000167513	5.326236828	2.61E-26	7.38E-25
DGKA	ENSG00000065357	-3.356801343	2.69E-26	7.59E-25

AL442003.1	ENSG00000285803	-7.79366419	2.69E-26	7.59E-25
AC008937.2	ENSG00000237705	-8.406531577	2.71E-26	7.63E-25
AC010978.1	ENSG00000235522	-8.549520736	2.72E-26	7.65E-25
AC020651.1	ENSG00000249474	-7.760510286	2.75E-26	7.71E-25
AC084024.3	ENSG00000253356	-6.833241777	2.85E-26	7.97E-25
H2AFX	ENSG00000188486	4.662629799	2.98E-26	8.32E-25
AC004528.2	ENSG00000274177	-8.85394036	3.02E-26	8.41E-25
AC005785.1	ENSG00000268189	-7.148933556	3.05E-26	8.46E-25
AC022558.3	ENSG00000273747	-6.195514982	3.05E-26	8.46E-25
AL133230.1	ENSG00000232043	-8.9035829	3.08E-26	8.52E-25
AC022400.6	ENSG00000272916	-6.381196677	3.09E-26	8.53E-25
KLF12	ENSG00000118922	-3.494507999	3.09E-26	8.53E-25
AL512791.1	ENSG00000258424	-9.110257434	3.10E-26	8.54E-25
JCAD	ENSG00000165757	6.703306486	3.13E-26	8.59E-25
CSDC2	ENSG00000172346	-5.820270556	3.16E-26	8.66E-25
AC004771.2	ENSG00000234203	-7.331739231	3.49E-26	9.54E-25
KIF20A	ENSG00000112984	5.446039572	3.50E-26	9.55E-25
AC010245.1	ENSG00000248881	-7.151461839	3.53E-26	9.61E-25
TNFRSF10A-AS1	ENSG00000253930	-7.925708052	3.79E-26	1.03E-24
SNX32	ENSG00000172803	-7.30982471	3.99E-26	1.08E-24
WDR34	ENSG00000119333	4.314284602	4.34E-26	1.17E-24
SOX18	ENSG00000203883	6.804931334	4.48E-26	1.21E-24
DDR2	ENSG00000162733	5.210796574	4.74E-26	1.27E-24
DAB2IP	ENSG00000136848	8.331191319	4.84E-26	1.29E-24
AC019163.1	ENSG00000248980	-4.648847081	4.90E-26	1.31E-24
AC125257.2	ENSG00000274630	-7.122260511	4.96E-26	1.32E-24
VWF	ENSG00000110799	6.924245796	4.98E-26	1.32E-24
CENPF	ENSG00000117724	5.705643572	5.15E-26	1.36E-24
AL136038.2	ENSG00000258800	-7.506271408	5.18E-26	1.37E-24
SNRK-AS1	ENSG00000234617	-7.768512971	5.44E-26	1.43E-24
UNC5B	ENSG00000107731	7.731756278	5.49E-26	1.44E-24
AL133415.1	ENSG00000234961	-7.460403882	5.61E-26	1.47E-24
SERPING1	ENSG00000149131	8.965323539	5.66E-26	1.48E-24
HTRA1	ENSG00000166033	8.996724461	5.86E-26	1.53E-24
AP000781.1	ENSG00000254662	-6.495025826	5.91E-26	1.54E-24
CLSPN	ENSG00000092853	7.76324598	6.17E-26	1.61E-24
AC078795.1	ENSG00000269984	-7.001883169	6.22E-26	1.62E-24
CST3	ENSG00000101439	9.404111376	6.33E-26	1.64E-24
OLFML2B	ENSG00000162745	8.329407374	6.34E-26	1.64E-24
ANGPTL2	ENSG00000136859	8.830886031	6.43E-26	1.66E-24
AC003101.3	ENSG00000278977	-8.199844012	6.48E-26	1.67E-24
IFITM3	ENSG00000142089	5.41289496	6.58E-26	1.69E-24
AC092115.3	ENSG00000262136	-6.426959298	6.60E-26	1.70E-24
DNAJC9-AS1	ENSG00000236756	-5.070996941	6.73E-26	1.73E-24
UBOX5-AS1	ENSG00000235958	-7.321750218	6.79E-26	1.74E-24
GNG12	ENSG00000172380	8.156392353	7.10E-26	1.81E-24
DNAH1	ENSG00000114841	-3.112053547	7.11E-26	1.81E-24
AC004974.1	ENSG00000285612	-8.987978825	7.49E-26	1.91E-24
IL13RA1	ENSG00000131724	7.149693847	7.69E-26	1.95E-24
TYMS	ENSG00000176890	4.311797077	7.91E-26	2.00E-24
LGALS8-AS1	ENSG00000223776	-6.859891833	8.31E-26	2.10E-24

RRM2	ENSG00000171848	9.183184716	8.44E-26	2.13E-24
WDR38	ENSG00000136918	-7.374168161	8.47E-26	2.13E-24
MKI67	ENSG00000148773	7.742973257	8.50E-26	2.14E-24
CDCA2	ENSG00000184661	6.495024187	8.71E-26	2.18E-24
AP003392.2	ENSG00000254909	-7.698132102	8.78E-26	2.20E-24
AC004148.2	ENSG00000263272	-8.642764633	8.80E-26	2.20E-24
MYL9	ENSG00000101335	8.041021317	9.26E-26	2.31E-24
AL031772.1	ENSG00000231329	-10.35891077	9.70E-26	2.41E-24
EML1	ENSG00000066629	6.842092892	9.74E-26	2.42E-24
AC091045.1	ENSG00000259536	-6.809059464	9.77E-26	2.42E-24
TMEM47	ENSG00000147027	5.874516728	1.01E-25	2.49E-24
DDTL	ENSG00000099974	-4.708700539	1.01E-25	2.49E-24
TFPI	ENSG00000003436	6.867612818	1.01E-25	2.49E-24
ACBD3-AS1	ENSG00000234478	-6.36585025	1.02E-25	2.52E-24
AP003068.1	ENSG00000254501	-7.450242872	1.03E-25	2.53E-24
NRP1	ENSG00000099250	6.622987507	1.03E-25	2.54E-24
AC005899.8	ENSG00000279762	-6.637458433	1.05E-25	2.58E-24
KCNJ8	ENSG00000121361	5.673691163	1.06E-25	2.58E-24
RASSF8	ENSG00000123094	6.536390107	1.07E-25	2.62E-24
AC132872.3	ENSG00000275888	-8.88480907	1.08E-25	2.62E-24
ISLR	ENSG00000129009	7.4562552	1.16E-25	2.81E-24
AP001273.1	ENSG00000279696	-4.038622976	1.21E-25	2.93E-24
C14orf178	ENSG00000197734	-6.376442437	1.24E-25	2.99E-24
AC015795.1	ENSG00000250751	-7.491632009	1.24E-25	2.99E-24
EME2	ENSG00000197774	-3.276626212	1.25E-25	3.02E-24
LGMN	ENSG00000100600	4.910069054	1.29E-25	3.10E-24
PRRX2	ENSG00000167157	6.604610364	1.30E-25	3.11E-24
AC025917.1	ENSG00000260618	-9.489899421	1.30E-25	3.11E-24
FAM198B	ENSG00000164125	8.143689321	1.30E-25	3.11E-24
AC011558.1	ENSG00000279753	-7.386941938	1.31E-25	3.13E-24
AC011511.2	ENSG00000266978	-6.381183665	1.33E-25	3.15E-24
AC006547.2	ENSG00000243762	-6.178243816	1.33E-25	3.16E-24
CTSD	ENSG00000117984	3.964960524	1.40E-25	3.31E-24
AC087289.2	ENSG00000267342	-6.846227578	1.41E-25	3.34E-24
DLGAP5	ENSG00000126787	7.784054616	1.45E-25	3.43E-24
AC106864.1	ENSG00000249532	-7.761825892	1.51E-25	3.55E-24
FKBP9	ENSG00000122642	4.882339621	1.58E-25	3.71E-24
MYOF	ENSG00000138119	8.070813609	1.62E-25	3.79E-24
THBD	ENSG00000178726	7.154282166	1.63E-25	3.81E-24
AP001107.2	ENSG00000254452	-6.110519249	1.64E-25	3.81E-24
AP005329.1	ENSG00000264235	-7.744241804	1.67E-25	3.89E-24
AC009554.1	ENSG00000259564	-7.643206894	1.67E-25	3.89E-24
AC020931.1	ENSG00000267387	-8.910294178	1.70E-25	3.95E-24
AL355075.2	ENSG00000258515	-8.044218856	1.75E-25	4.06E-24
AP000892.3	ENSG00000280143	-4.893439323	1.82E-25	4.19E-24
FAM184B	ENSG00000047662	-7.996947375	1.82E-25	4.20E-24
AL031281.3	ENSG00000285752	-5.857071137	2.00E-25	4.57E-24
NLRP1	ENSG00000091592	-3.208723562	2.02E-25	4.61E-24
CCDC73	ENSG00000186714	-5.30586854	2.03E-25	4.62E-24
AL451070.1	ENSG00000229044	-7.184285838	2.05E-25	4.66E-24
AC023906.4	ENSG00000259709	-7.886025859	2.08E-25	4.71E-24

CREG1	ENSG00000143162	3.538627444	2.08E-25	4.71E-24
AC010336.4	ENSG00000268149	-6.772909575	2.13E-25	4.82E-24
RASA3	ENSG00000185989	-4.453926098	2.18E-25	4.94E-24
MRPS18AP1	ENSG00000229759	-7.125107319	2.19E-25	4.95E-24
GINS1	ENSG00000101003	5.118596942	2.20E-25	4.96E-24
HMOX1	ENSG00000100292	5.959328055	2.23E-25	5.02E-24
HCG25	ENSG00000232940	-4.421483547	2.30E-25	5.17E-24
NFIB	ENSG00000147862	7.585904534	2.35E-25	5.26E-24
AC009133.4	ENSG00000275857	-6.838902172	2.40E-25	5.38E-24
HYAL2	ENSG00000068001	4.713581212	2.44E-25	5.46E-24
C1S	ENSG00000182326	5.703932393	2.52E-25	5.62E-24
AC010335.1	ENSG00000268199	-7.565087923	2.56E-25	5.70E-24
AC002558.2	ENSG00000261872	-7.391837029	2.60E-25	5.78E-24
C20orf27	ENSG00000101220	3.354695901	2.63E-25	5.85E-24
AC012184.3	ENSG00000261777	-3.676878689	2.64E-25	5.86E-24
AC069282.1	ENSG00000225507	-7.585090493	2.80E-25	6.19E-24
GPCPD1	ENSG00000125772	-3.138219021	2.80E-25	6.19E-24
AC007298.1	ENSG00000257715	-7.409011079	2.84E-25	6.26E-24
AC008906.1	ENSG00000248734	-6.075843945	3.00E-25	6.61E-24
AL161665.1	ENSG00000285608	-9.478125423	3.01E-25	6.61E-24
AC017083.2	ENSG00000273275	-6.496694557	3.01E-25	6.61E-24
USP3-AS1	ENSG00000259248	-8.016217619	3.04E-25	6.67E-24
ZNF503	ENSG00000165655	7.116892823	3.13E-25	6.85E-24
SLC7A6OS	ENSG00000103061	-3.096515979	3.14E-25	6.85E-24
AC007728.2	ENSG00000261644	-4.70361829	3.16E-25	6.89E-24
TMEM98	ENSG00000006042	5.774466269	3.18E-25	6.92E-24
DTL	ENSG00000143476	6.615824411	3.20E-25	6.96E-24
AL022328.2	ENSG00000273137	-4.823041725	3.29E-25	7.12E-24
PRKCQ	ENSG00000065675	-4.404151234	3.33E-25	7.19E-24
SRM	ENSG00000116649	3.744461087	3.59E-25	7.75E-24
GGNBP1	ENSG00000204188	-6.208631174	3.61E-25	7.79E-24
FSCN1	ENSG00000075618	5.908979434	3.63E-25	7.81E-24
AC007622.2	ENSG00000258136	-6.82972262	3.64E-25	7.83E-24
AC087164.1	ENSG00000266677	-5.171263135	3.75E-25	8.05E-24
AC093512.1	ENSG00000274904	-7.336906671	3.89E-25	8.32E-24
MDC1-AS1	ENSG00000224328	-7.134029981	3.99E-25	8.52E-24
NUF2	ENSG00000143228	4.39635044	4.00E-25	8.53E-24
GUCY1A1	ENSG00000164116	6.767254305	4.07E-25	8.67E-24
TNS3	ENSG00000136205	7.243247357	4.28E-25	9.09E-24
C6orf47-AS1	ENSG00000227198	-6.508198616	4.42E-25	9.36E-24
HERC1	ENSG00000103657	-3.141027569	4.43E-25	9.37E-24
AL157786.1	ENSG00000232934	-4.966411604	4.50E-25	9.51E-24
CDC14A	ENSG00000079335	-3.480276743	4.53E-25	9.55E-24
AC022395.1	ENSG00000231104	-7.519151932	4.59E-25	9.65E-24
GUCY1B1	ENSG00000061918	7.063761039	4.60E-25	9.65E-24
AC092953.2	ENSG00000273261	-6.749474302	4.65E-25	9.74E-24
ACTB	ENSG00000075624	3.062681405	4.76E-25	9.96E-24
PTMS	ENSG00000159335	8.395798166	4.77E-25	9.96E-24
HSPG2	ENSG00000142798	6.192421245	4.89E-25	1.02E-23
APBB2	ENSG00000163697	5.350105492	4.95E-25	1.03E-23
FAM114A1	ENSG00000197712	7.129141978	5.13E-25	1.07E-23

AC097641.2	ENSG00000277728	-5.008309854	5.16E-25	1.07E-23
AL589765.7	ENSG00000269621	-7.686562813	5.22E-25	1.08E-23
FAT1	ENSG00000083857	7.10282029	5.25E-25	1.09E-23
MIF-AS1	ENSG00000218537	-4.557627941	5.29E-25	1.09E-23
IL33	ENSG00000137033	6.866997134	5.34E-25	1.10E-23
CYP26B1	ENSG00000003137	6.810503912	5.55E-25	1.14E-23
VCAN	ENSG00000038427	7.983965056	5.69E-25	1.17E-23
AC090510.1	ENSG00000246283	-5.706195416	5.81E-25	1.19E-23
AL365330.1	ENSG00000272153	-5.809801937	5.94E-25	1.22E-23
CTSB	ENSG00000164733	3.19406458	5.98E-25	1.22E-23
AC005697.2	ENSG00000266527	-6.949774222	6.09E-25	1.24E-23
AC009120.2	ENSG00000259972	-3.450835608	6.26E-25	1.28E-23
AL355312.2	ENSG00000231760	-5.971957592	6.40E-25	1.30E-23
WDFY3	ENSG00000163625	6.486103632	6.51E-25	1.32E-23
AC145285.6	ENSG00000275807	-4.222626324	6.57E-25	1.33E-23
RASL12	ENSG00000103710	5.601090779	6.76E-25	1.37E-23
AC016727.1	ENSG00000270820	-4.004232729	6.78E-25	1.37E-23
EHD2	ENSG00000024422	7.288974461	7.20E-25	1.46E-23
AC090772.4	ENSG00000279332	-7.547325195	7.33E-25	1.48E-23
RAI14	ENSG00000039560	6.503662918	7.59E-25	1.53E-23
AC092881.1	ENSG00000279530	-7.338715811	7.60E-25	1.53E-23
RHOBTB1	ENSG00000072422	6.105869528	7.64E-25	1.53E-23
PLCD4	ENSG00000115556	-4.822843423	7.86E-25	1.57E-23
AC025423.4	ENSG00000257181	-6.231294542	7.94E-25	1.59E-23
AC120114.2	ENSG00000278713	-6.80878931	8.03E-25	1.60E-23
AL023584.1	ENSG00000233138	-8.646871644	8.03E-25	1.60E-23
COL5A2	ENSG00000204262	8.079474278	8.49E-25	1.69E-23
VIL1	ENSG00000127831	-8.047494544	8.62E-25	1.71E-23
GNG11	ENSG00000127920	6.759836862	8.84E-25	1.76E-23
AL109918.1	ENSG00000216775	5.999935096	9.09E-25	1.80E-23
RPL23AP64	ENSG00000240970	-8.312183802	9.14E-25	1.81E-23
UHRF1	ENSG00000276043	4.513348355	9.19E-25	1.82E-23
MYBL2	ENSG00000101057	7.484373032	9.33E-25	1.84E-23
SKA3	ENSG00000165480	6.78894183	9.89E-25	1.95E-23
AC005606.1	ENSG00000260107	-7.766963154	1.00E-24	1.97E-23
PLOD1	ENSG00000083444	5.402472449	1.01E-24	1.99E-23
GSN	ENSG00000148180	5.758004671	1.03E-24	2.01E-23
VWA1	ENSG00000179403	8.007685494	1.03E-24	2.01E-23
AC016027.1	ENSG00000225335	-4.100744148	1.05E-24	2.05E-23
AL359921.1	ENSG00000230325	-4.923770563	1.06E-24	2.07E-23
CHMP1B-AS1	ENSG00000267165	-9.979762453	1.08E-24	2.10E-23
ZNF814	ENSG00000204514	-3.771742714	1.08E-24	2.10E-23
GRN	ENSG00000030582	4.918412638	1.08E-24	2.11E-23
AC093503.2	ENSG00000269292	-7.829345668	1.10E-24	2.14E-23
AL021707.1	ENSG00000225450	-6.469052065	1.14E-24	2.20E-23
P2RX5-TAX1BP3	ENSG00000257950	-6.298904114	1.14E-24	2.20E-23
ADD3-AS1	ENSG00000203876	-5.53100368	1.14E-24	2.20E-23
PLAU	ENSG00000122861	7.467192153	1.15E-24	2.23E-23
CDC6	ENSG00000094804	5.00965202	1.18E-24	2.27E-23
AC008894.2	ENSG00000269243	-7.47731397	1.27E-24	2.43E-23
TSSK3	ENSG00000162526	-7.077934041	1.29E-24	2.47E-23

GJA1	ENSG00000152661	8.738094524	1.34E-24	2.56E-23
GGH	ENSG00000137563	6.405355255	1.35E-24	2.58E-23
ZWINT	ENSG00000122952	4.773647612	1.36E-24	2.58E-23
PLLP	ENSG00000102934	-5.335308718	1.40E-24	2.67E-23
AP000442.2	ENSG00000255139	-5.006441459	1.41E-24	2.67E-23
AF131216.1	ENSG00000246477	-7.672235353	1.46E-24	2.76E-23
GJA4	ENSG00000187513	5.572898989	1.48E-24	2.80E-23
AC007342.6	ENSG00000279344	-7.654401024	1.50E-24	2.83E-23
AC008764.3	ENSG00000268309	-7.950880544	1.53E-24	2.89E-23
UPK2	ENSG00000110375	-7.600829755	1.54E-24	2.90E-23
AL139095.4	ENSG00000238221	-7.857242771	1.56E-24	2.93E-23
AC018557.1	ENSG00000260465	-10.24016807	1.61E-24	3.01E-23
PRELID1	ENSG00000169230	3.265271354	1.61E-24	3.02E-23
MT-TS1	ENSG00000210151	-8.024084181	1.64E-24	3.06E-23
AC055811.1	ENSG00000263624	-6.849406193	1.65E-24	3.06E-23
PLPP3	ENSG00000162407	7.717627034	1.65E-24	3.07E-23
SCAND2P	ENSG00000176700	-3.000991913	1.66E-24	3.09E-23
AC134772.1	ENSG00000244380	-7.384779696	1.70E-24	3.15E-23
FMOD	ENSG00000122176	7.804505874	1.73E-24	3.21E-23
MITF	ENSG00000187098	5.835677206	1.78E-24	3.29E-23
GM2A	ENSG00000196743	3.912865606	1.83E-24	3.39E-23
TUBB	ENSG00000196230	3.657579025	1.91E-24	3.52E-23
NID1	ENSG00000116962	6.813910028	1.92E-24	3.53E-23
C1QA	ENSG00000173372	9.4441313	1.93E-24	3.55E-23
BACH2	ENSG00000112182	-5.61177439	1.94E-24	3.56E-23
AC006027.1	ENSG00000272638	-5.594252978	1.94E-24	3.56E-23
TNFRSF21	ENSG00000146072	7.339571903	1.97E-24	3.60E-23
PLSCR4	ENSG00000114698	6.094829533	2.05E-24	3.74E-23
UBE2C	ENSG00000175063	7.493589766	2.05E-24	3.75E-23
H3F3AP4	ENSG00000235655	3.288432682	2.14E-24	3.89E-23
AC105020.6	ENSG00000275454	-5.002888904	2.19E-24	3.99E-23
MT-ND6	ENSG00000198695	-4.877797324	2.22E-24	4.03E-23
C13orf46	ENSG00000283199	-7.924377918	2.29E-24	4.15E-23
APOE	ENSG00000130203	7.298920097	2.36E-24	4.27E-23
UACA	ENSG00000137831	6.83023347	2.39E-24	4.32E-23
AC104532.2	ENSG00000267571	-7.087464802	2.44E-24	4.41E-23
GRPEL2-AS1	ENSG00000253618	-6.848437102	2.45E-24	4.42E-23
SMPDL3A	ENSG00000172594	5.799475393	2.50E-24	4.51E-23
CD74	ENSG00000019582	5.96759329	2.52E-24	4.53E-23
AL133375.1	ENSG00000245261	-5.840942737	2.68E-24	4.82E-23
AC010186.2	ENSG00000256594	-3.915805871	2.69E-24	4.82E-23
AQP1	ENSG00000240583	6.897430455	2.74E-24	4.90E-23
AC136469.2	ENSG00000279827	-6.910413431	2.81E-24	5.02E-23
SPI1	ENSG00000066336	6.579832822	2.86E-24	5.11E-23
AC006441.3	ENSG00000265784	-8.722354221	2.88E-24	5.14E-23
AC104116.1	ENSG00000249971	-7.60664403	2.90E-24	5.17E-23
AD000864.1	ENSG00000280194	-5.90554667	2.94E-24	5.23E-23
AL021707.3	ENSG00000230149	-7.407361885	2.97E-24	5.28E-23
AC234582.1	ENSG00000231064	-5.820572772	2.98E-24	5.29E-23
SDC2	ENSG00000169439	6.097597759	3.04E-24	5.39E-23
AC004494.1	ENSG00000262312	-8.394777725	3.13E-24	5.52E-23

SPRED1	ENSG00000166068	6.393287528	3.18E-24	5.58E-23
AL049840.2	ENSG00000269910	-6.361248199	3.35E-24	5.88E-23
C1QB	ENSG00000173369	9.612507579	3.38E-24	5.92E-23
CPXM2	ENSG00000121898	6.081904433	3.42E-24	5.99E-23
RGL4	ENSG00000159496	-5.279745409	3.64E-24	6.36E-23
SMTN	ENSG00000183963	4.497624853	3.65E-24	6.36E-23
CIT	ENSG00000122966	3.714090172	3.65E-24	6.36E-23
PHKG1	ENSG00000164776	-4.381277613	3.88E-24	6.74E-23
MIR3661	ENSG00000266751	-7.514851837	3.92E-24	6.80E-23
TTYH3	ENSG00000136295	3.613985857	4.04E-24	7.00E-23
AL031282.1	ENSG00000227775	-7.437330636	4.07E-24	7.03E-23
COL1A1	ENSG00000108821	9.04634797	4.10E-24	7.07E-23
AC078777.1	ENSG00000235872	-9.243005535	4.12E-24	7.09E-23
CEP55	ENSG00000138180	7.562114664	4.17E-24	7.18E-23
AC004596.1	ENSG00000267394	-6.830883782	4.31E-24	7.41E-23
SORL1	ENSG00000137642	-5.000635818	4.43E-24	7.60E-23
AC022167.1	ENSG00000259939	-5.400707542	4.53E-24	7.76E-23
AC023355.1	ENSG00000259488	-4.30834099	4.74E-24	8.10E-23
AL139011.1	ENSG00000228606	-6.680534406	4.76E-24	8.11E-23
ITGA9	ENSG00000144668	4.844994957	4.77E-24	8.13E-23
PCTP	ENSG00000141179	3.138711322	4.78E-24	8.13E-23
AURKA	ENSG00000087586	5.579449343	4.94E-24	8.38E-23
PCAT1	ENSG00000253438	-5.866804264	4.99E-24	8.46E-23
PTPRB	ENSG00000127329	5.518345148	5.20E-24	8.81E-23
AL603832.1	ENSG00000225075	-7.531316023	5.33E-24	8.99E-23
AC008569.1	ENSG00000267379	-8.41734859	5.40E-24	9.10E-23
SPDYE3	ENSG00000214300	-7.235637615	5.48E-24	9.23E-23
HSPB8	ENSG00000152137	6.187396926	5.53E-24	9.30E-23
RAB11FIP1P1	ENSG00000228492	-8.149096477	5.67E-24	9.52E-23
AVPR1A	ENSG00000166148	6.221185478	5.68E-24	9.53E-23
CKS1B	ENSG00000173207	4.269909114	5.75E-24	9.64E-23
CDH5	ENSG00000179776	6.289903573	5.84E-24	9.77E-23
AC022382.1	ENSG00000269886	-6.094981964	5.88E-24	9.82E-23
AC006064.2	ENSG00000247853	-5.887565372	5.90E-24	9.84E-23
RAMP2	ENSG00000131477	6.246039157	6.00E-24	9.99E-23
UXT-AS1	ENSG00000267064	-7.144777434	6.02E-24	1.00E-22
AC109460.1	ENSG00000260367	-7.019728623	6.28E-24	1.04E-22
MASP2	ENSG00000009724	-8.877711728	6.28E-24	1.04E-22
BASP1	ENSG00000176788	7.233928861	6.43E-24	1.07E-22
AC079880.1	ENSG00000270228	-7.029690706	6.48E-24	1.07E-22
SULF1	ENSG00000137573	9.063158737	6.70E-24	1.11E-22
GPX8	ENSG00000164294	6.779368176	6.84E-24	1.13E-22
C1orf147	ENSG00000162888	-6.811018951	6.85E-24	1.13E-22
POC1A	ENSG00000164087	4.509986621	7.00E-24	1.15E-22
CCDC80	ENSG00000091986	6.820787528	7.25E-24	1.19E-22
AC023509.2	ENSG00000257550	-7.897530447	7.29E-24	1.19E-22
FZD1	ENSG00000157240	7.086046504	7.64E-24	1.25E-22
KIF15	ENSG00000163808	6.133224795	7.81E-24	1.28E-22
PPIC	ENSG00000168938	5.7796035	8.36E-24	1.36E-22
PALMD	ENSG00000099260	6.334611613	8.87E-24	1.44E-22
TICRR	ENSG00000140534	4.944477041	8.98E-24	1.46E-22

CENPA	ENSG00000115163	5.124880558	8.98E-24	1.46E-22
KCNE4	ENSG00000152049	5.70098532	9.00E-24	1.46E-22
HNMT	ENSG00000150540	6.352657319	9.11E-24	1.47E-22
RSPH9	ENSG00000172426	-5.603978505	9.41E-24	1.52E-22
AC234917.2	ENSG00000285599	-6.926999566	9.48E-24	1.53E-22
SSPN	ENSG00000123096	6.239655467	9.54E-24	1.54E-22
ERG	ENSG00000157554	5.431904733	9.68E-24	1.56E-22
FGD5	ENSG00000154783	5.089067112	1.01E-23	1.62E-22
PIF1	ENSG00000140451	5.596406182	1.03E-23	1.65E-22
KIF23	ENSG00000137807	6.536618794	1.04E-23	1.66E-22
AC098484.4	ENSG00000285728	-6.255964276	1.04E-23	1.66E-22
AC009542.1	ENSG00000231794	-7.402932295	1.06E-23	1.70E-22
AL161725.1	ENSG00000227155	-8.602966572	1.06E-23	1.70E-22
AL354836.1	ENSG00000226332	-5.454318799	1.07E-23	1.71E-22
CKAP2L	ENSG00000169607	6.922356787	1.08E-23	1.72E-22
LTBP1	ENSG00000049323	6.306345403	1.09E-23	1.73E-22
MCM10	ENSG00000065328	5.337532908	1.11E-23	1.77E-22
AC024896.1	ENSG00000247903	-6.987805822	1.13E-23	1.79E-22
AL109761.1	ENSG00000244676	-6.666285372	1.16E-23	1.83E-22
AL035681.1	ENSG00000235513	-3.774729143	1.16E-23	1.84E-22
TNFAIP2	ENSG00000185215	6.33597332	1.17E-23	1.84E-22
UBXN11	ENSG00000158062	-3.305585242	1.17E-23	1.85E-22
COL6A2	ENSG00000142173	5.788238974	1.18E-23	1.86E-22
KIF14	ENSG00000118193	6.300851086	1.20E-23	1.88E-22
PCOLCE	ENSG00000106333	4.938905243	1.22E-23	1.92E-22
OCIAD1-AS1	ENSG00000248256	-7.695301175	1.23E-23	1.92E-22
FOXM1	ENSG00000111206	3.024340341	1.25E-23	1.95E-22
GNB4	ENSG00000114450	4.300743999	1.25E-23	1.96E-22
AL049840.1	ENSG00000246451	-7.426257809	1.25E-23	1.96E-22
ACOT7	ENSG00000097021	4.53580302	1.27E-23	1.98E-22
AC007364.1	ENSG00000231969	-6.205635376	1.28E-23	1.99E-22
ESCO2	ENSG00000171320	5.934486788	1.28E-23	2.00E-22
MMP14	ENSG00000157227	5.069725413	1.29E-23	2.01E-22
EMCN	ENSG00000164035	5.990420652	1.32E-23	2.04E-22
MSRB3	ENSG00000174099	6.081743847	1.34E-23	2.08E-22
NOTCH3	ENSG00000074181	7.806005755	1.35E-23	2.08E-22
FEN1	ENSG00000168496	3.320788023	1.35E-23	2.08E-22
CD14	ENSG00000170458	6.418235017	1.36E-23	2.09E-22
KIRREL1	ENSG00000183853	6.543129964	1.36E-23	2.10E-22
ADAMTS1	ENSG00000154734	7.278949314	1.37E-23	2.11E-22
AC114730.2	ENSG00000234793	-7.283168087	1.41E-23	2.16E-22
AC012170.2	ENSG00000259298	-7.161360591	1.43E-23	2.19E-22
SHCBP1	ENSG00000171241	4.806503003	1.46E-23	2.23E-22
AC087289.1	ENSG00000266980	-6.369092141	1.50E-23	2.29E-22
AC115618.1	ENSG00000204620	-7.710644436	1.52E-23	2.32E-22
TEDC2	ENSG00000162062	6.003387922	1.56E-23	2.38E-22
CDCA3	ENSG00000111665	4.797936087	1.57E-23	2.38E-22
LHFPL2	ENSG00000145685	5.377278215	1.62E-23	2.45E-22
AC069234.2	ENSG00000256364	-8.255700134	1.62E-23	2.46E-22
AL160408.2	ENSG00000228830	-9.539813137	1.66E-23	2.51E-22
SPECC1	ENSG00000128487	4.286375844	1.67E-23	2.52E-22

SMCHD1	ENSG00000101596	-3.893273145	1.69E-23	2.54E-22
AL391839.2	ENSG00000233825	-8.494681235	1.71E-23	2.57E-22
CYR61	ENSG00000142871	7.510195466	1.72E-23	2.59E-22
AC132872.4	ENSG00000280407	-8.737798186	1.75E-23	2.63E-22
AC037459.4	ENSG00000254230	-7.716439214	1.75E-23	2.63E-22
AC006064.4	ENSG00000269968	-5.58531522	1.78E-23	2.67E-22
ARHGAP29	ENSG00000137962	6.216965723	1.82E-23	2.73E-22
ATM	ENSG00000149311	-3.384379198	1.84E-23	2.75E-22
ARHGEF38	ENSG00000236699	-6.605805452	1.86E-23	2.78E-22
AC025442.1	ENSG00000253744	-8.13893405	1.88E-23	2.80E-22
PPP1R14B	ENSG00000173457	4.295538286	1.91E-23	2.84E-22
TNS1	ENSG00000079308	6.651334128	1.92E-23	2.85E-22
DIAPH3	ENSG00000139734	6.576538781	1.93E-23	2.86E-22
AC005091.1	ENSG00000229893	-8.165795648	1.96E-23	2.91E-22
AC020765.2	ENSG00000275441	-5.129567294	1.96E-23	2.91E-22
AC010761.3	ENSG00000265205	-7.294806093	1.98E-23	2.92E-22
GTF2IRD1P1	ENSG00000230583	-4.94556072	1.98E-23	2.93E-22
APLNR	ENSG00000134817	7.305192206	2.07E-23	3.06E-22
CDH11	ENSG00000140937	8.141375547	2.09E-23	3.08E-22
APCDD1	ENSG00000154856	8.159648282	2.11E-23	3.11E-22
AC137932.1	ENSG00000260279	-8.175457825	2.13E-23	3.13E-22
IRX2	ENSG00000170561	5.731871805	2.15E-23	3.16E-22
AC006547.3	ENSG00000268292	-6.79386291	2.19E-23	3.22E-22
MS4A4A	ENSG00000110079	7.009194789	2.20E-23	3.22E-22
SERHL	ENSG00000172250	-7.481430311	2.24E-23	3.28E-22
E2F8	ENSG00000129173	6.800677152	2.28E-23	3.33E-22
AC084824.4	ENSG00000275854	-3.961618867	2.34E-23	3.41E-22
MAFB	ENSG00000204103	7.888598588	2.35E-23	3.42E-22
DND1	ENSG00000256453	-4.316627543	2.36E-23	3.43E-22
ITK	ENSG00000113263	-4.041515025	2.36E-23	3.43E-22
AL645939.1	ENSG00000225864	-7.180006314	2.38E-23	3.46E-22
SKA1	ENSG00000154839	6.850043625	2.42E-23	3.51E-22
AC145207.3	ENSG00000262831	-7.241544279	2.45E-23	3.54E-22
PCBD1	ENSG00000166228	3.324612666	2.47E-23	3.57E-22
CDKN3	ENSG00000100526	4.733921894	2.55E-23	3.67E-22
ANGPTL6	ENSG00000130812	-5.051872132	2.55E-23	3.67E-22
MYO1B	ENSG00000128641	6.648936819	2.58E-23	3.71E-22
AL139099.1	ENSG00000258377	-7.267068431	2.59E-23	3.72E-22
AC012173.1	ENSG00000260350	-5.082776236	2.61E-23	3.74E-22
PALLD	ENSG00000129116	5.740636289	2.62E-23	3.75E-22
NUDT8	ENSG00000167799	5.303891277	2.64E-23	3.77E-22
PARVA	ENSG00000197702	5.59375223	2.70E-23	3.86E-22
EFEMP1	ENSG00000115380	8.142673843	2.75E-23	3.92E-22
CCNL1	ENSG00000163660	-3.580950412	2.77E-23	3.94E-22
CLU	ENSG00000120885	6.65164579	2.77E-23	3.94E-22
DOCK1	ENSG00000150760	6.055668689	2.77E-23	3.94E-22
TRIM47	ENSG00000132481	3.728129486	2.80E-23	3.98E-22
MIR1282	ENSG00000221792	-5.449166696	2.82E-23	4.00E-22
AC005329.3	ENSG00000280486	-5.746239597	2.82E-23	4.00E-22
SLC5A10	ENSG00000154025	-7.870101022	2.82E-23	4.00E-22
BICC1	ENSG00000122870	7.520615512	2.91E-23	4.12E-22

AC000068.2	ENSG00000273212	-6.121712815	3.01E-23	4.24E-22
COPRS	ENSG00000172301	3.629146195	3.09E-23	4.36E-22
ACTA2	ENSG00000107796	3.585939821	3.10E-23	4.36E-22
AC092849.2	ENSG00000241357	-6.427201842	3.10E-23	4.36E-22
AP000487.1	ENSG00000246889	-5.233841261	3.10E-23	4.36E-22
IFI27	ENSG00000165949	6.134879723	3.20E-23	4.50E-22
MMP2	ENSG00000087245	11.03755873	3.27E-23	4.59E-22
AL080317.3	ENSG00000272356	-3.37790818	3.31E-23	4.64E-22
AC005606.2	ENSG00000261790	-6.80878813	3.33E-23	4.66E-22
MYLK	ENSG00000065534	4.628844501	3.34E-23	4.67E-22
PCDH18	ENSG00000189184	6.742465691	3.41E-23	4.75E-22
GPX1	ENSG00000233276	3.231072777	3.47E-23	4.84E-22
ANKRD18EP	ENSG00000217165	-7.887088216	3.50E-23	4.87E-22
ADGRL2	ENSG00000117114	6.281933367	3.52E-23	4.89E-22
RCAN3	ENSG00000117602	-3.132383501	3.63E-23	5.03E-22
AC015849.3	ENSG00000270871	-7.691716292	3.64E-23	5.04E-22
C5orf56	ENSG00000197536	-3.82236719	3.68E-23	5.09E-22
HEATR4	ENSG00000187105	-5.788977065	3.71E-23	5.12E-22
AC022201.2	ENSG00000233849	-5.289602324	3.75E-23	5.17E-22
DAPK1	ENSG00000196730	5.89404519	3.79E-23	5.22E-22
DEPDC1B	ENSG00000035499	6.148447245	3.82E-23	5.26E-22
SHANK3	ENSG00000251322	5.820680975	3.85E-23	5.29E-22
AP003465.1	ENSG00000254224	-10.2311282	4.01E-23	5.51E-22
DEPDC1	ENSG00000024526	7.494547969	4.04E-23	5.55E-22
TNFRSF25	ENSG00000215788	-4.373245876	4.13E-23	5.66E-22
YEATS2-AS1	ENSG00000233885	-6.599794734	4.17E-23	5.72E-22
TMEM176A	ENSG00000002933	6.643635652	4.26E-23	5.84E-22
AL049776.1	ENSG00000279434	-5.90158911	4.35E-23	5.95E-22
AP000919.2	ENSG00000265907	-8.019433635	4.45E-23	6.08E-22
RICTOR	ENSG00000164327	-3.661409875	4.56E-23	6.22E-22
SMC2	ENSG00000136824	3.90475218	4.69E-23	6.39E-22
DRAM1	ENSG00000136048	3.896002454	4.75E-23	6.45E-22
MBOAT4	ENSG00000177669	-7.615350499	4.93E-23	6.68E-22
AC025043.1	ENSG00000259595	-8.675968154	4.95E-23	6.70E-22
PBK	ENSG00000168078	6.562394984	5.02E-23	6.80E-22
KDM4A-AS1	ENSG00000236200	-4.580231846	5.08E-23	6.87E-22
COL12A1	ENSG00000111799	8.054761771	5.11E-23	6.90E-22
ERVK3-1	ENSG00000142396	-4.288381964	5.39E-23	7.27E-22
AC004466.1	ENSG00000268069	-6.490353811	5.42E-23	7.30E-22
LMBR1L	ENSG00000139636	-3.113941219	5.52E-23	7.43E-22
AL121787.1	ENSG00000226455	-8.279490667	5.53E-23	7.44E-22
MECOM	ENSG00000085276	5.67348771	5.71E-23	7.67E-22
AL691432.1	ENSG00000269737	-7.260886106	5.73E-23	7.69E-22
NNMT	ENSG00000166741	8.017248599	5.88E-23	7.87E-22
TMEM51	ENSG00000171729	5.82327543	5.94E-23	7.94E-22
BLVRB	ENSG00000090013	4.442511014	5.95E-23	7.95E-22
OAZ3	ENSG00000143450	-4.551040726	5.98E-23	7.97E-22
AL034550.1	ENSG00000236772	-6.84322867	6.06E-23	8.08E-22
ZNF32-AS2	ENSG00000230565	-5.757513681	6.16E-23	8.20E-22
MELK	ENSG00000165304	6.424562033	6.19E-23	8.23E-22
N4BP2L2-IT2	ENSG00000281026	-4.035070976	6.28E-23	8.33E-22

AC009065.2	ENSG00000259933	-5.190642224	6.33E-23	8.40E-22
AL138921.1	ENSG00000227492	-8.233374026	6.39E-23	8.46E-22
RHD	ENSG00000187010	-7.512477966	6.77E-23	8.95E-22
EAF1-AS1	ENSG00000249786	-6.709885867	6.84E-23	9.04E-22
AC092718.4	ENSG00000261061	5.235188498	6.96E-23	9.19E-22
BCL6B	ENSG00000161940	5.13962247	7.11E-23	9.37E-22
RND3	ENSG00000115963	6.907794247	7.13E-23	9.39E-22
RHOXF1P3	ENSG00000282933	-6.28149112	7.24E-23	9.53E-22
DPYSL3	ENSG00000113657	8.292550228	7.34E-23	9.64E-22
FCER1G	ENSG00000158869	5.559196821	7.41E-23	9.72E-22
AC009118.3	ENSG00000276259	-4.394284643	7.41E-23	9.72E-22
CNN3	ENSG00000117519	5.502265083	7.79E-23	1.02E-21
GALK1	ENSG00000108479	3.220610168	7.91E-23	1.04E-21
AL133227.1	ENSG00000273828	-7.759855791	7.92E-23	1.04E-21
AC087190.1	ENSG00000260349	-9.756240162	8.28E-23	1.08E-21
AL020996.1	ENSG00000228172	-4.640208819	8.33E-23	1.09E-21
KREMEN1	ENSG00000183762	6.611452603	8.44E-23	1.10E-21
HLA-DMA	ENSG00000204257	3.712913928	8.60E-23	1.12E-21
S1PR3	ENSG00000213694	6.724671537	8.62E-23	1.12E-21
B4GALT2	ENSG00000117411	5.253104946	8.99E-23	1.17E-21
UBE2T	ENSG00000077152	4.490084426	9.06E-23	1.17E-21
ARHGAP23	ENSG00000275832	5.977062931	9.34E-23	1.21E-21
FBLN2	ENSG00000163520	8.392518532	9.36E-23	1.21E-21
AC003991.2	ENSG00000254003	-5.942150536	9.60E-23	1.24E-21
LAMB2	ENSG00000172037	6.075990665	9.74E-23	1.26E-21
AC015911.7	ENSG00000267369	-8.234422242	9.93E-23	1.28E-21
RAD51AP1	ENSG00000111247	5.111836229	9.95E-23	1.28E-21
SLCO2A1	ENSG00000174640	5.970782367	1.00E-22	1.29E-21
AL358852.1	ENSG00000278899	-6.319859586	1.01E-22	1.30E-21
CHST3	ENSG00000122863	5.53088957	1.01E-22	1.30E-21
AC127024.5	ENSG00000266490	-3.958198257	1.02E-22	1.31E-21
PCNA	ENSG00000132646	3.101937953	1.02E-22	1.31E-21
AL662797.1	ENSG00000272540	-5.276662258	1.06E-22	1.35E-21
KIF11	ENSG00000138160	4.948424668	1.07E-22	1.37E-21
GAS5-AS1	ENSG00000270084	-4.531162144	1.11E-22	1.41E-21
POLQ	ENSG00000051341	4.206679202	1.14E-22	1.46E-21
LDLRAD3	ENSG00000179241	5.893881079	1.17E-22	1.49E-21
MPZL1	ENSG00000197965	4.443468152	1.19E-22	1.51E-21
AC008522.1	ENSG00000279232	-7.22732481	1.22E-22	1.56E-21
CDH13	ENSG00000140945	5.68851447	1.25E-22	1.59E-21
FAM110B	ENSG00000169122	5.596273592	1.28E-22	1.62E-21
MS4A6A	ENSG00000110077	7.824361699	1.28E-22	1.63E-21
AL117332.1	ENSG00000275457	-3.359795678	1.30E-22	1.64E-21
AC020904.3	ENSG00000279172	-9.199417559	1.31E-22	1.65E-21
AC007390.2	ENSG00000272054	-4.239309989	1.34E-22	1.70E-21
ROBO1	ENSG00000169855	7.088215896	1.36E-22	1.71E-21
FKBP10	ENSG00000141756	6.988931766	1.38E-22	1.74E-21
KF459542.1	ENSG00000231880	-5.851859887	1.40E-22	1.76E-21
SPRY2	ENSG00000136158	5.903289263	1.41E-22	1.77E-21
ADAMTS2	ENSG00000087116	8.156940081	1.42E-22	1.77E-21
AL022322.2	ENSG00000279080	-7.114804599	1.44E-22	1.79E-21

LINC00334	ENSG00000182586	-7.407322258	1.44E-22	1.80E-21
ZYG11A	ENSG00000203995	4.866853743	1.47E-22	1.83E-21
NDST1	ENSG00000070614	5.276274878	1.48E-22	1.84E-21
TMEM176B	ENSG00000106565	6.37509882	1.51E-22	1.87E-21
ANLN	ENSG00000011426	6.153393342	1.54E-22	1.91E-21
LINC00641	ENSG00000258441	-3.941689897	1.54E-22	1.91E-21
AC116348.3	ENSG00000261346	-8.925675564	1.55E-22	1.92E-21
FOXRED2	ENSG00000100350	3.972922767	1.57E-22	1.94E-21
AC138932.5	ENSG00000275910	-5.217537528	1.58E-22	1.95E-21
CCDC39	ENSG00000284862	-8.547775996	1.62E-22	1.99E-21
AC103739.2	ENSG00000259314	-7.698420526	1.63E-22	2.01E-21
CCNF	ENSG00000162063	3.646213875	1.64E-22	2.01E-21
NREP	ENSG00000134986	5.244314603	1.65E-22	2.02E-21
TGFBI	ENSG00000120708	6.575049037	1.65E-22	2.03E-21
SNX7	ENSG00000162627	7.112670841	1.71E-22	2.09E-21
NECTIN2	ENSG00000130202	4.758431151	1.74E-22	2.14E-21
AC073052.2	ENSG00000274629	-8.411994314	1.82E-22	2.23E-21
AC015912.1	ENSG00000262112	-8.075231585	1.85E-22	2.26E-21
DHFR	ENSG00000228716	4.539418454	1.87E-22	2.28E-21
AC025164.1	ENSG00000245904	-5.889964772	1.97E-22	2.40E-21
PP2D1	ENSG00000183977	-8.650393089	2.00E-22	2.43E-21
AC073573.1	ENSG00000257808	-7.613448175	2.01E-22	2.44E-21
AC136604.2	ENSG00000244945	-4.982921764	2.07E-22	2.51E-21
AC027682.3	ENSG00000260894	-6.723071244	2.08E-22	2.52E-21
ASPM	ENSG00000066279	5.665362996	2.16E-22	2.62E-21
FZD4	ENSG00000174804	5.569245286	2.16E-22	2.62E-21
AC100778.3	ENSG00000265496	-8.975989746	2.19E-22	2.65E-21
AC006547.1	ENSG00000236540	-7.361066974	2.37E-22	2.85E-21
CDON	ENSG00000064309	3.566347313	2.44E-22	2.93E-21
SPDYA	ENSG00000163806	-4.410725751	2.45E-22	2.94E-21
WLS	ENSG00000116729	5.93963771	2.55E-22	3.07E-21
AC018638.1	ENSG00000229413	-8.335518316	2.65E-22	3.18E-21
CDC42EP5	ENSG00000167617	6.009330968	2.70E-22	3.24E-21
C1R	ENSG00000159403	5.681374358	2.70E-22	3.24E-21
TGM2	ENSG00000198959	6.489568561	2.75E-22	3.29E-21
PDLIM3	ENSG00000154553	5.085201253	2.83E-22	3.38E-21
E2F1	ENSG00000101412	3.467839056	2.92E-22	3.49E-21
TPSB2	ENSG00000197253	6.965175788	2.94E-22	3.51E-21
SYNGAP1-AS1	ENSG00000274259	-4.886648592	2.98E-22	3.54E-21
OLFML1	ENSG00000183801	6.190430378	3.05E-22	3.62E-21
PEG13	ENSG00000282164	-4.079374932	3.10E-22	3.68E-21
PKM	ENSG00000067225	3.343561593	3.16E-22	3.74E-21
SLC3A1	ENSG00000138079	-6.898048397	3.19E-22	3.77E-21
TWIST1	ENSG00000122691	7.018134037	3.21E-22	3.79E-21
AL603756.1	ENSG00000271933	-6.085100041	3.27E-22	3.85E-21
HAVCR2	ENSG00000135077	3.321118356	3.27E-22	3.85E-21
VSTM4	ENSG00000165633	5.618294795	3.38E-22	3.97E-21
FAM111B	ENSG00000189057	6.072205211	3.56E-22	4.17E-21
LY6G5B	ENSG00000240053	-3.79406213	3.68E-22	4.32E-21
ETV5	ENSG00000244405	5.334322892	3.74E-22	4.38E-21
TCN2	ENSG00000185339	6.822413184	3.74E-22	4.38E-21

MARVELD1	ENSG00000155254	5.849851674	3.77E-22	4.41E-21
FXYD6	ENSG00000137726	5.41583424	3.78E-22	4.41E-21
AC079203.2	ENSG00000259468	-7.333553478	3.79E-22	4.42E-21
LAMB1	ENSG00000091136	4.412995579	3.81E-22	4.44E-21
PIK3IP1	ENSG00000100100	-4.715585284	4.02E-22	4.68E-21
TMEM202-AS1	ENSG00000261423	-4.931320118	4.05E-22	4.72E-21
STMN1	ENSG00000117632	4.371745361	4.06E-22	4.72E-21
NUPR1	ENSG00000176046	6.552316056	4.07E-22	4.73E-21
AC011498.6	ENSG00000267769	-5.404075616	4.09E-22	4.74E-21
PGD	ENSG00000142657	3.132690318	4.19E-22	4.86E-21
JDP2	ENSG00000140044	5.183754011	4.26E-22	4.94E-21
SPATA1	ENSG00000122432	-4.933499366	4.32E-22	5.00E-21
MCM2	ENSG00000073111	3.052735871	4.33E-22	5.00E-21
CALD1	ENSG00000122786	7.724087568	4.40E-22	5.08E-21
AC007566.1	ENSG00000244055	-3.904702149	4.44E-22	5.11E-21
GPNMB	ENSG00000136235	8.838444693	4.64E-22	5.34E-21
NUCB1-AS1	ENSG00000235191	-7.132266782	4.65E-22	5.35E-21
CNOT6L	ENSG00000138767	-3.908368109	4.76E-22	5.46E-21
FERP1	ENSG00000232149	-6.658638837	4.76E-22	5.46E-21
ARHGAP42	ENSG00000165895	5.91898229	4.88E-22	5.59E-21
CALCRL	ENSG00000064989	5.978707748	4.92E-22	5.63E-21
CDC42EP1	ENSG00000128283	7.735618617	4.99E-22	5.72E-21
KANK2	ENSG00000197256	5.816372631	5.10E-22	5.83E-21
Z97986.1	ENSG00000261691	-6.575648872	5.20E-22	5.94E-21
AC116348.2	ENSG00000261332	-8.394035283	5.25E-22	5.99E-21
CACNA2D1	ENSG00000153956	5.731048408	5.27E-22	6.00E-21
SLC9A3R2	ENSG00000065054	5.042379569	5.28E-22	6.01E-21
AL109628.2	ENSG00000285830	-7.914185604	5.30E-22	6.03E-21
DPYSL2	ENSG00000092964	3.949004578	5.41E-22	6.14E-21
AC008676.1	ENSG00000248544	-6.627813362	5.61E-22	6.36E-21
SDC3	ENSG00000162512	7.094494416	5.75E-22	6.51E-21
ZCCHC24	ENSG00000165424	3.580982502	5.86E-22	6.64E-21
CRNDE	ENSG00000245694	4.79896048	5.88E-22	6.65E-21
AC072022.1	ENSG00000228804	-7.135241521	5.89E-22	6.66E-21
AC012615.6	ENSG00000267244	-8.196331846	6.13E-22	6.92E-21
OLFML2A	ENSG00000185585	5.687802905	6.24E-22	7.04E-21
SERPINH1	ENSG00000149257	3.813105768	6.33E-22	7.13E-21
CDC25A	ENSG00000164045	5.287390373	6.51E-22	7.33E-21
IL10RB-DT	ENSG00000223799	-7.151812243	6.60E-22	7.42E-21
ABCC9	ENSG00000069431	6.436934488	6.61E-22	7.43E-21
ARHGEF18	ENSG00000104880	-3.389922039	6.69E-22	7.51E-21
PDLIM4	ENSG00000131435	6.187978192	6.81E-22	7.63E-21
AC017083.3	ENSG00000273398	-6.583515666	6.90E-22	7.74E-21
ARPIN	ENSG00000242498	5.691780524	7.05E-22	7.88E-21
LRIG3	ENSG00000139263	6.601028984	7.05E-22	7.88E-21
HOXD8	ENSG00000175879	5.351191131	7.38E-22	8.22E-21
ARIH2OS	ENSG00000221883	-4.000817891	7.41E-22	8.25E-21
RASSF4	ENSG00000107551	6.200672488	7.63E-22	8.48E-21
PRRG4	ENSG00000135378	6.314600585	7.65E-22	8.50E-21
ENPP2	ENSG00000136960	5.833454555	7.68E-22	8.53E-21
AC034102.6	ENSG00000258317	-5.884190415	7.74E-22	8.58E-21

HLA-DRA	ENSG00000204287	7.592059601	7.76E-22	8.59E-21
AC018635.1	ENSG00000242261	-6.899620994	7.99E-22	8.84E-21
AP002954.1	ENSG00000255422	-6.727473914	8.09E-22	8.94E-21
AL606760.2	ENSG00000236723	-4.024121456	8.18E-22	9.03E-21
GPR174	ENSG00000147138	-3.733564298	8.40E-22	9.26E-21
AC023510.2	ENSG00000276842	-7.58121019	8.87E-22	9.75E-21
AC112491.1	ENSG00000269888	-7.765909298	9.04E-22	9.93E-21
RCN1	ENSG00000049449	4.290257941	9.09E-22	9.96E-21
AC008555.2	ENSG00000269086	-7.006504879	9.09E-22	9.96E-21
FAM20C	ENSG00000177706	6.976906577	9.44E-22	1.03E-20
PXDC1	ENSG00000168994	6.17693715	9.86E-22	1.08E-20
AC092755.2	ENSG00000259238	-6.220150007	1.03E-21	1.13E-20
ZNF703	ENSG00000183779	4.490727538	1.05E-21	1.15E-20
ADAMTS5	ENSG00000154736	7.13546838	1.09E-21	1.19E-20
THBS2	ENSG00000186340	8.040880014	1.11E-21	1.21E-20
CENPU	ENSG00000151725	4.063001655	1.13E-21	1.23E-20
RHOJ	ENSG00000126785	5.624969876	1.13E-21	1.23E-20
BUB1	ENSG00000169679	4.402713294	1.15E-21	1.25E-20
PRR29	ENSG00000224383	-7.714161111	1.17E-21	1.27E-20
Sep-10	ENSG00000186522	6.5157769	1.17E-21	1.27E-20
TYROBP	ENSG00000011600	5.525874348	1.17E-21	1.27E-20
AC079921.1	ENSG00000249207	-7.844111891	1.20E-21	1.30E-20
TCP11L2	ENSG00000166046	-3.985047168	1.21E-21	1.30E-20
NMU	ENSG00000109255	6.774213622	1.22E-21	1.31E-20
AC022211.4	ENSG00000279035	-5.216472132	1.23E-21	1.33E-20
COPZ2	ENSG00000005243	5.333125977	1.25E-21	1.34E-20
FAM173A	ENSG00000103254	3.829394846	1.26E-21	1.35E-20
HLA-DMB	ENSG00000242574	4.541814342	1.29E-21	1.39E-20
AL078581.3	ENSG00000281021	-7.575062143	1.30E-21	1.39E-20
LTBR	ENSG00000111321	5.692069839	1.30E-21	1.39E-20
FAM71E1	ENSG00000142530	-4.867849621	1.34E-21	1.43E-20
C1orf167	ENSG00000215910	-5.799669923	1.35E-21	1.44E-20
WWTR1	ENSG00000018408	4.632780383	1.38E-21	1.47E-20
PCLAF	ENSG00000166803	6.275936879	1.40E-21	1.48E-20
PAXBP1-AS1	ENSG00000238197	-3.564038087	1.40E-21	1.49E-20
ADGRF5	ENSG00000069122	7.338066931	1.40E-21	1.49E-20
TLR4	ENSG00000136869	6.347410565	1.43E-21	1.52E-20
ISOC2	ENSG00000063241	4.120838427	1.45E-21	1.54E-20
NEGR1	ENSG00000172260	5.698699217	1.46E-21	1.55E-20
LINC00565	ENSG00000260910	-6.606482883	1.48E-21	1.56E-20
TRBV2	ENSG00000226660	-5.182702116	1.51E-21	1.59E-20
AC138028.3	ENSG00000259813	-9.47210192	1.55E-21	1.63E-20
IMPDH1P10	ENSG00000232133	-8.552431409	1.55E-21	1.63E-20
RAB11FIP4	ENSG00000131242	-3.541129871	1.59E-21	1.67E-20
BHLHE41	ENSG00000123095	6.608028312	1.64E-21	1.72E-20
STK3	ENSG00000104375	3.472181031	1.68E-21	1.76E-20
PLTP	ENSG00000100979	4.809293558	1.68E-21	1.76E-20
HMMR	ENSG00000072571	5.771858172	1.70E-21	1.78E-20
HLA-F-AS1	ENSG00000214922	-3.192113576	1.77E-21	1.84E-20
UGGT2	ENSG00000102595	5.706632628	1.81E-21	1.88E-20
SLC41A2	ENSG00000136052	4.708455688	1.81E-21	1.88E-20

AC008750.4	ENSG00000267984	-6.601152811	1.82E-21	1.89E-20
VGLL3	ENSG00000206538	7.608819285	1.82E-21	1.89E-20
LMO2	ENSG00000135363	5.538628889	1.85E-21	1.92E-20
SPTY2D1OS	ENSG00000247595	-4.293847222	1.88E-21	1.94E-20
BRCA1	ENSG00000012048	4.541056528	1.88E-21	1.94E-20
MIR497HG	ENSG00000267532	-5.300057116	1.89E-21	1.95E-20
EFCAB10	ENSG00000185055	-6.535940374	1.90E-21	1.96E-20
CTGF	ENSG00000118523	8.857061565	1.95E-21	2.01E-20
AC074050.3	ENSG00000261731	-7.490594576	1.97E-21	2.02E-20
RTL8C	ENSG00000134590	3.198364244	1.99E-21	2.04E-20
PHETA2	ENSG00000177096	3.771911317	2.00E-21	2.05E-20
SRD5A3	ENSG00000128039	3.928987842	2.13E-21	2.18E-20
OPRM1	ENSG00000112038	-6.923874585	2.16E-21	2.20E-20
TMTC1	ENSG00000133687	5.336935406	2.26E-21	2.31E-20
AC129492.7	ENSG00000279152	-4.50244033	2.29E-21	2.33E-20
ROBO4	ENSG00000154133	5.990603268	2.33E-21	2.36E-20
AEBP1	ENSG00000106624	5.459984866	2.33E-21	2.37E-20
PCDH7	ENSG00000169851	6.123305378	2.35E-21	2.39E-20
SIRPA	ENSG00000198053	6.845133539	2.45E-21	2.48E-20
PLEKHH3	ENSG00000068137	5.479777136	2.45E-21	2.48E-20
AC002553.1	ENSG00000227782	-5.467849061	2.46E-21	2.49E-20
POSTN	ENSG00000133110	10.80672093	2.46E-21	2.49E-20
AC136632.1	ENSG00000218227	-4.452078931	2.47E-21	2.49E-20
AC138150.1	ENSG00000224505	-3.711416219	2.50E-21	2.52E-20
PHKA1	ENSG00000067177	5.789154141	2.61E-21	2.63E-20
CD63	ENSG00000135404	4.432692669	2.70E-21	2.71E-20
NRM	ENSG00000137404	3.381511721	2.71E-21	2.72E-20
LPAR1	ENSG00000198121	6.662357378	2.74E-21	2.75E-20
DHPS	ENSG00000095059	-3.487345012	2.78E-21	2.79E-20
AC020978.5	ENSG00000262160	-5.713109668	2.85E-21	2.85E-20
AC093110.1	ENSG00000238018	-7.772652695	2.87E-21	2.86E-20
FBLIM1	ENSG00000162458	5.928538591	2.90E-21	2.89E-20
AC022167.2	ENSG00000260276	-3.659319433	2.92E-21	2.91E-20
A4GALT	ENSG00000128274	5.624649417	2.97E-21	2.96E-20
FAP	ENSG00000078098	7.308706	3.03E-21	3.01E-20
TSKU	ENSG00000182704	6.198818666	3.10E-21	3.08E-20
AC135050.7	ENSG00000280160	-6.745454045	3.12E-21	3.09E-20
TMEM110-MUSTN1	ENSG00000248592	-4.52692384	3.16E-21	3.13E-20
EFNB2	ENSG00000125266	4.707123425	3.19E-21	3.15E-20
AL359076.1	ENSG00000236199	-8.217173282	3.22E-21	3.18E-20
KRR1P1	ENSG00000237672	-7.254476742	3.24E-21	3.19E-20
EGFL7	ENSG00000172889	6.296170527	3.29E-21	3.24E-20
YBX3	ENSG00000060138	4.260332656	3.29E-21	3.24E-20
PALD1	ENSG00000107719	4.711747194	3.33E-21	3.28E-20
STARD13	ENSG00000133121	7.019415419	3.44E-21	3.38E-20
TUSC3	ENSG00000104723	4.998988882	3.44E-21	3.39E-20
GDF9	ENSG00000164404	-3.90688605	3.49E-21	3.43E-20
GCC2-AS1	ENSG00000214184	-3.575910572	3.68E-21	3.61E-20
ADAP2	ENSG00000184060	5.514406435	3.73E-21	3.66E-20
SMIM30	ENSG00000214194	3.078640303	3.77E-21	3.69E-20
AL157955.1	ENSG00000258407	-7.332677959	3.80E-21	3.71E-20

AL109811.2	ENSG00000230337	-3.730392174	4.02E-21	3.91E-20
AC002401.1	ENSG00000236472	-7.947003133	4.12E-21	4.00E-20
HSPB1	ENSG00000106211	3.858152558	4.12E-21	4.01E-20
PYCR1	ENSG00000183010	5.76464257	4.15E-21	4.02E-20
EGFLAM	ENSG00000164318	5.394367261	4.15E-21	4.02E-20
PDLIM1	ENSG00000107438	5.731189588	4.22E-21	4.09E-20
HMGB3	ENSG00000029993	4.067581292	4.24E-21	4.11E-20
SLC25A25-AS1	ENSG00000234771	-3.065952742	4.65E-21	4.49E-20
CENPW	ENSG00000203760	5.684378873	4.66E-21	4.50E-20
SLC7A2	ENSG00000003989	6.009611328	4.86E-21	4.69E-20
NT5DC2	ENSG00000168268	5.126051975	5.00E-21	4.82E-20
CXXC5	ENSG00000171604	3.91926834	5.07E-21	4.89E-20
TCF19	ENSG00000137310	3.062672106	5.30E-21	5.09E-20
AC020907.4	ENSG00000271032	-7.549076604	5.31E-21	5.10E-20
PRSS23	ENSG00000150687	7.304716837	5.41E-21	5.19E-20
SPRED2	ENSG00000198369	4.031738375	5.52E-21	5.29E-20
AC011466.3	ENSG00000269534	-6.745259495	5.56E-21	5.33E-20
CD86	ENSG00000114013	7.436450133	5.60E-21	5.36E-20
RPS6KB2-AS1	ENSG00000255949	-5.77253101	5.66E-21	5.41E-20
ALDH1B1	ENSG00000137124	3.372718302	5.78E-21	5.52E-20
RAPGEF5	ENSG00000136237	6.19911415	5.84E-21	5.57E-20
NDUFA4L2	ENSG00000185633	5.158061399	5.93E-21	5.65E-20
CEMP1	ENSG00000205923	-7.029312268	5.94E-21	5.65E-20
AL162458.1	ENSG00000285796	-3.42697898	6.01E-21	5.71E-20
CADM1	ENSG00000182985	6.546274248	6.04E-21	5.74E-20
XRCC2	ENSG00000196584	3.545600686	6.32E-21	6.00E-20
PRKCQ-AS1	ENSG00000237943	-4.726988346	6.38E-21	6.04E-20
MMRN2	ENSG00000173269	5.043353632	6.39E-21	6.05E-20
AL451165.2	ENSG00000272288	-3.444348044	6.48E-21	6.13E-20
PGAM2	ENSG00000164708	-7.611553459	6.50E-21	6.14E-20
FOXC1	ENSG00000054598	5.68634935	6.56E-21	6.19E-20
TIMP1	ENSG00000102265	4.018418753	6.75E-21	6.36E-20
CXorf36	ENSG00000147113	5.311911925	6.82E-21	6.42E-20
CTTNBP2NL	ENSG00000143079	4.920156074	6.97E-21	6.56E-20
SYK	ENSG00000165025	6.367804222	7.34E-21	6.89E-20
AC109460.4	ENSG00000261552	-8.867093905	7.47E-21	7.00E-20
P2RY11	ENSG00000244165	-3.14380719	7.69E-21	7.20E-20
JAM2	ENSG00000154721	5.460151345	7.83E-21	7.32E-20
AC067930.5	ENSG00000255050	-6.758304459	7.85E-21	7.33E-20
AC015802.6	ENSG00000284526	-7.223580338	7.85E-21	7.33E-20
F3	ENSG00000117525	5.93175821	7.89E-21	7.36E-20
CDC42BPA	ENSG00000143776	5.676620563	7.90E-21	7.36E-20
HOXC4	ENSG00000198353	5.31933427	7.97E-21	7.42E-20
AL137856.1	ENSG00000231128	-7.06671406	8.12E-21	7.56E-20
UBE2S	ENSG00000108106	3.892243689	8.50E-21	7.91E-20
AC010503.4	ENSG00000275234	-3.791128972	8.54E-21	7.93E-20
ECM1	ENSG00000143369	4.654726575	8.56E-21	7.95E-20
YAP1	ENSG00000137693	7.905144604	8.75E-21	8.11E-20
LAMTOR5-AS1	ENSG00000224699	-3.809691592	8.75E-21	8.11E-20
AC023055.1	ENSG00000257390	-4.892976313	8.86E-21	8.21E-20
AC008686.1	ENSG00000267633	-7.725301269	8.99E-21	8.31E-20

ACAD11	ENSG00000240303	-4.2160594	9.25E-21	8.54E-20
RBBP8	ENSG00000101773	4.023285424	9.61E-21	8.86E-20
AC124014.1	ENSG00000285165	-8.033323038	9.64E-21	8.88E-20
DNAH17	ENSG00000187775	-4.028813383	9.86E-21	9.06E-20
DMC1	ENSG00000100206	5.752787127	9.88E-21	9.07E-20
AC130456.5	ENSG00000260934	-7.028933308	1.02E-20	9.31E-20
LAMC2	ENSG00000058085	5.456152821	1.02E-20	9.34E-20
RAB42	ENSG00000188060	4.946345257	1.04E-20	9.51E-20
AC018754.1	ENSG00000285190	-7.754931191	1.07E-20	9.76E-20
PTPRG	ENSG00000144724	6.373759421	1.07E-20	9.77E-20
AL137186.2	ENSG00000232807	-4.494122546	1.08E-20	9.90E-20
COL5A1	ENSG00000130635	7.030329566	1.10E-20	1.00E-19
ANKHD1	ENSG00000131503	-3.240744373	1.10E-20	1.00E-19
GINS2	ENSG00000131153	4.714892498	1.11E-20	1.01E-19
TBC1D9	ENSG00000109436	5.194108764	1.12E-20	1.02E-19
AC087481.3	ENSG00000270015	-3.174628809	1.16E-20	1.05E-19
ITGB5	ENSG00000082781	5.409264206	1.16E-20	1.06E-19
CCNA2	ENSG00000145386	3.114110402	1.18E-20	1.07E-19
AL139317.3	ENSG00000259049	-4.723237244	1.25E-20	1.13E-19
ANKRD50	ENSG00000151458	4.586126309	1.26E-20	1.14E-19
ENTPD1	ENSG00000138185	3.779442556	1.27E-20	1.15E-19
JPT1	ENSG00000189159	3.285908388	1.29E-20	1.16E-19
GGTA1P	ENSG00000204136	6.083675497	1.29E-20	1.17E-19
CASK-AS1	ENSG00000233033	-6.959807352	1.31E-20	1.18E-19
CRTC3-AS1	ENSG00000259736	-5.162401772	1.31E-20	1.18E-19
KCP	ENSG00000135253	-3.246114643	1.32E-20	1.18E-19
PROS1	ENSG00000184500	6.100878318	1.32E-20	1.19E-19
AC011342.1	ENSG00000285420	-7.07717475	1.36E-20	1.22E-19
CENPI	ENSG00000102384	4.154688983	1.40E-20	1.25E-19
TMEM54	ENSG00000121900	5.426971656	1.40E-20	1.25E-19
PDE3B	ENSG00000152270	-4.604995475	1.40E-20	1.26E-19
AL022328.4	ENSG00000273253	-5.089425133	1.43E-20	1.28E-19
FAM13A-AS1	ENSG00000248019	-3.704612844	1.43E-20	1.28E-19
PAFAH1B3	ENSG00000079462	3.051664119	1.45E-20	1.29E-19
DLC1	ENSG00000164741	5.203837435	1.47E-20	1.31E-19
TENM3	ENSG00000218336	6.45342026	1.51E-20	1.34E-19
ADAMTS7	ENSG00000136378	4.982209753	1.54E-20	1.37E-19
TMEM120B	ENSG00000188735	-3.053045476	1.56E-20	1.39E-19
AP1S1	ENSG00000106367	4.630884187	1.57E-20	1.40E-19
RAMP3	ENSG00000122679	6.259104123	1.60E-20	1.42E-19
BCAT1	ENSG00000060982	7.858588214	1.60E-20	1.42E-19
AFMID	ENSG00000183077	3.26291198	1.60E-20	1.42E-19
SLAMF8	ENSG00000158714	4.75124545	1.62E-20	1.44E-19
EBLN2	ENSG00000255423	-3.086404189	1.65E-20	1.45E-19
SLC51A	ENSG00000163959	-5.447683194	1.68E-20	1.48E-19
KIAA1211L	ENSG00000196872	6.0732536	1.69E-20	1.49E-19
ALKBH6	ENSG00000239382	-3.167658186	1.69E-20	1.49E-19
AC114730.1	ENSG00000215692	-5.252367174	1.69E-20	1.49E-19
OLFM1	ENSG00000130558	5.42503987	1.71E-20	1.50E-19
AC021242.3	ENSG00000272267	-5.3340808	1.76E-20	1.55E-19
TPBG	ENSG00000146242	5.818036194	1.76E-20	1.55E-19

CXCL12	ENSG00000107562	9.172481373	1.80E-20	1.59E-19
HYPK	ENSG00000242028	-3.118828634	1.82E-20	1.59E-19
AC090607.4	ENSG00000272418	-7.440923879	1.83E-20	1.61E-19
IRF4	ENSG00000137265	4.332478522	1.85E-20	1.62E-19
CIITA	ENSG00000179583	3.700627234	1.89E-20	1.65E-19
AC116903.1	ENSG00000258761	-7.655798573	1.91E-20	1.67E-19
CXCR5	ENSG00000160683	-6.614080838	1.91E-20	1.67E-19
AC114730.3	ENSG00000235351	-6.979992301	1.95E-20	1.70E-19
TTK	ENSG00000112742	5.875212979	2.01E-20	1.75E-19
ELF3-AS1	ENSG00000234678	-7.635283308	2.01E-20	1.75E-19
CD248	ENSG00000174807	6.870165739	2.03E-20	1.76E-19
C9orf64	ENSG00000165118	3.250282737	2.04E-20	1.77E-19
PLS3	ENSG00000102024	6.738783236	2.06E-20	1.79E-19
SHROOM1	ENSG00000164403	5.906897451	2.13E-20	1.85E-19
AF129075.2	ENSG00000273254	-7.449603884	2.14E-20	1.85E-19
AL121928.1	ENSG00000273262	-5.283860454	2.14E-20	1.85E-19
SAC3D1	ENSG00000168061	4.328905594	2.16E-20	1.86E-19
AC027290.1	ENSG00000256152	-7.408062156	2.16E-20	1.87E-19
AP001793.1	ENSG00000266708	-8.34797304	2.16E-20	1.87E-19
SGMS2	ENSG00000164023	5.572168443	2.20E-20	1.89E-19
MNDA	ENSG00000163563	6.814134104	2.21E-20	1.90E-19
AC005540.1	ENSG00000235852	-4.219658108	2.23E-20	1.92E-19
RGS5	ENSG00000143248	5.214981275	2.25E-20	1.93E-19
NEIL1	ENSG00000140398	-5.001410306	2.27E-20	1.95E-19
CPE	ENSG00000109472	6.909839925	2.29E-20	1.97E-19
ARHGEF10L	ENSG00000074964	5.756013916	2.31E-20	1.98E-19
P2RY6	ENSG00000171631	4.520486803	2.40E-20	2.05E-19
CENPM	ENSG00000100162	4.306081703	2.52E-20	2.15E-19
WDR86	ENSG00000187260	-4.393474561	2.52E-20	2.15E-19
AC130343.2	ENSG00000277597	-6.208270808	2.52E-20	2.15E-19
TINAGL1	ENSG00000142910	5.491435583	2.55E-20	2.18E-19
SH3PXD2B	ENSG00000174705	5.629054223	2.60E-20	2.21E-19
LILRB4	ENSG00000186818	6.924073739	2.61E-20	2.22E-19
NFATC4	ENSG00000100968	5.909817149	2.73E-20	2.32E-19
FABP5	ENSG00000164687	5.117417363	2.74E-20	2.33E-19
DLEC1	ENSG00000008226	-5.100655917	2.77E-20	2.35E-19
GNAI1	ENSG00000127955	4.927454472	2.77E-20	2.35E-19
SYDE1	ENSG00000105137	4.719376252	2.79E-20	2.36E-19
PODXL	ENSG00000128567	3.975338414	2.80E-20	2.37E-19
PTGFRN	ENSG00000134247	5.104177125	2.82E-20	2.39E-19
AP001010.1	ENSG00000266954	-7.020455089	2.94E-20	2.49E-19
IGF1	ENSG00000017427	7.043461688	2.95E-20	2.49E-19
MANEAL	ENSG00000185090	4.053793414	2.98E-20	2.52E-19
SOD3	ENSG00000109610	7.968408284	2.99E-20	2.52E-19
AC114760.2	ENSG00000272211	-7.857234476	3.02E-20	2.55E-19
TRBV23-1	ENSG00000211749	-5.729563783	3.06E-20	2.58E-19
UCKL1-AS1	ENSG00000280213	-5.559883734	3.10E-20	2.61E-19
EXO1	ENSG00000174371	6.421313485	3.13E-20	2.63E-19
GPRASP1	ENSG00000198932	-5.882991551	3.20E-20	2.69E-19
CEBPB	ENSG00000172216	3.154653562	3.22E-20	2.70E-19
SCARB1	ENSG00000073060	4.638127485	3.34E-20	2.79E-19

NRARP	ENSG00000198435	4.400737226	3.34E-20	2.79E-19
AL136368.1	ENSG00000232470	-6.457409555	3.36E-20	2.81E-19
RRM1-AS1	ENSG00000255276	-7.048194153	3.37E-20	2.81E-19
TPSAB1	ENSG00000172236	7.474677483	3.38E-20	2.82E-19
RIN2	ENSG00000132669	6.024664546	3.55E-20	2.96E-19
AC097382.2	ENSG00000245748	-6.900644074	3.55E-20	2.96E-19
CNRIP1	ENSG00000119865	4.948737434	3.59E-20	2.99E-19
Z92544.2	ENSG00000261659	-3.404686407	3.59E-20	2.99E-19
AL031733.2	ENSG00000241666	-4.015902055	3.60E-20	3.00E-19
C17orf58	ENSG00000186665	4.516221196	3.63E-20	3.02E-19
AC004623.1	ENSG00000279488	-6.437706593	3.83E-20	3.18E-19
CEACAM21	ENSG00000007129	-3.63832502	4.02E-20	3.33E-19
BACE2	ENSG00000182240	5.896324033	4.15E-20	3.43E-19
AC099063.4	ENSG00000284734	-4.217038494	4.15E-20	3.43E-19
ANK2	ENSG00000145362	6.166434666	4.22E-20	3.49E-19
RPP25	ENSG00000178718	4.934891993	4.25E-20	3.50E-19
UBAP1L	ENSG00000246922	-3.124588448	4.41E-20	3.63E-19
GLI3	ENSG00000106571	5.853780244	4.41E-20	3.63E-19
AP001318.2	ENSG00000255062	-5.094633188	4.49E-20	3.69E-19
AC091180.3	ENSG00000250186	-6.517479646	4.52E-20	3.71E-19
LRP1	ENSG00000123384	4.277517044	4.55E-20	3.73E-19
PHLDA3	ENSG00000174307	5.333926654	4.62E-20	3.79E-19
STC2	ENSG00000113739	5.288212441	4.64E-20	3.80E-19
CCDC85C	ENSG00000205476	-3.007529753	4.64E-20	3.80E-19
PSTK	ENSG00000179988	-3.49513276	4.65E-20	3.80E-19
AL662907.2	ENSG00000279179	-6.236910141	4.76E-20	3.89E-19
AL360270.1	ENSG00000232811	-4.331481511	4.78E-20	3.91E-19
AC233300.1	ENSG00000279155	-7.661205095	4.79E-20	3.91E-19
RAB7B	ENSG00000276600	5.532427314	4.79E-20	3.91E-19
MSMP	ENSG00000215183	-6.111670872	5.04E-20	4.10E-19
EFS	ENSG00000100842	5.4213265	5.06E-20	4.12E-19
PDPN	ENSG00000162493	7.244487484	5.24E-20	4.26E-19
AC115618.2	ENSG00000228343	-6.185088176	5.37E-20	4.36E-19
ZNRD1ASP	ENSG00000204623	-4.28731189	5.38E-20	4.36E-19
MAP3K20	ENSG00000091436	5.375831986	5.43E-20	4.40E-19
AL355802.2	ENSG00000271754	-4.077960907	5.45E-20	4.41E-19
DYSF	ENSG00000135636	5.214280511	5.61E-20	4.54E-19
AC069281.2	ENSG00000274272	-4.969362568	5.74E-20	4.64E-19
STAT4	ENSG00000138378	-3.942240313	5.79E-20	4.67E-19
PLBD1	ENSG00000121316	4.928273715	5.87E-20	4.74E-19
ANO1	ENSG00000131620	5.172707611	5.91E-20	4.76E-19
CD93	ENSG00000125810	5.947768074	6.14E-20	4.94E-19
AC007192.2	ENSG00000269145	-6.197620147	6.17E-20	4.96E-19
PMFBP1	ENSG00000118557	-3.43516441	6.28E-20	5.04E-19
GRIN2C	ENSG00000161509	-5.659070092	6.30E-20	5.06E-19
SOX4	ENSG00000124766	5.616910012	6.34E-20	5.09E-19
AC009065.7	ENSG00000261532	-6.186126126	6.40E-20	5.13E-19
PYCR3	ENSG00000104524	3.768035719	6.50E-20	5.20E-19
AL354920.1	ENSG00000254473	-3.632175385	6.51E-20	5.20E-19
C11orf65	ENSG00000166323	-5.441145594	6.82E-20	5.44E-19
PIK3R3	ENSG00000117461	5.119948134	7.07E-20	5.63E-19

SLCO2B1	ENSG00000137491	7.526549797	7.10E-20	5.66E-19
AC008537.4	ENSG00000282951	-6.148974396	7.16E-20	5.70E-19
PTOV1-AS1	ENSG00000268006	-4.746874587	7.29E-20	5.79E-19
TWIST2	ENSG00000233608	6.702964472	7.30E-20	5.80E-19
AC083949.1	ENSG00000224875	-6.738891958	7.41E-20	5.87E-19
IGFBP4	ENSG00000141753	5.583406534	7.57E-20	5.99E-19
CASKIN2	ENSG00000177303	3.568138077	7.78E-20	6.15E-19
C9orf3	ENSG00000148120	3.157570036	7.88E-20	6.23E-19
ABHD14A	ENSG00000248487	-3.018075353	7.94E-20	6.28E-19
SCCPDH	ENSG00000143653	4.539619892	8.10E-20	6.40E-19
AC007613.1	ENSG00000262420	-5.237294453	8.18E-20	6.46E-19
AL157935.1	ENSG00000227218	-9.612454581	8.20E-20	6.47E-19
GSTA4	ENSG00000170899	5.606433696	8.24E-20	6.50E-19
TRBV29-1	ENSG00000232869	-5.808063176	8.24E-20	6.50E-19
PTGES	ENSG00000148344	5.246755565	8.30E-20	6.53E-19
GLIS2	ENSG00000126603	3.33349014	8.42E-20	6.62E-19
IKBIP	ENSG00000166130	3.326776836	8.61E-20	6.77E-19
TMEM238	ENSG00000233493	3.222821537	8.65E-20	6.79E-19
SH3BP4	ENSG00000130147	4.604014348	8.70E-20	6.82E-19
GOLGA2P5	ENSG00000238105	-3.100132629	8.88E-20	6.96E-19
BAHCC1	ENSG00000266074	5.014748063	8.90E-20	6.96E-19
ASB16	ENSG00000161664	-6.071202409	8.93E-20	6.99E-19
TBX3	ENSG00000135111	5.643511275	8.94E-20	6.99E-19
MTND2P28	ENSG00000225630	-5.421793883	9.11E-20	7.11E-19
AC012615.2	ENSG00000267007	-5.896549307	9.15E-20	7.14E-19
GPR153	ENSG00000158292	5.118059488	9.45E-20	7.36E-19
TRAV8-3	ENSG00000211787	-4.478031173	9.47E-20	7.37E-19
SMTNL1	ENSG00000214872	-7.717864784	9.48E-20	7.38E-19
RAB3IL1	ENSG00000167994	5.528052472	9.58E-20	7.45E-19
TMEM45A	ENSG00000181458	7.047214853	9.73E-20	7.56E-19
EDNRA	ENSG00000151617	6.667230194	9.90E-20	7.68E-19
AC130304.1	ENSG00000280064	-8.704353498	1.00E-19	7.76E-19
AC009950.1	ENSG00000225963	-7.02125856	1.02E-19	7.87E-19
CTSH	ENSG00000103811	3.97768633	1.02E-19	7.89E-19
CD163L1	ENSG00000177675	6.285506829	1.03E-19	7.95E-19
EPAS1	ENSG00000116016	6.858319959	1.04E-19	8.06E-19
ZNF483	ENSG00000173258	-4.442028429	1.04E-19	8.06E-19
CHRNE	ENSG00000108556	-3.297290438	1.05E-19	8.11E-19
PDLIM7	ENSG00000196923	4.605115926	1.06E-19	8.15E-19
HCK	ENSG00000101336	6.841777746	1.07E-19	8.25E-19
PAQR4	ENSG00000162073	4.602350439	1.09E-19	8.36E-19
E2F7	ENSG00000165891	5.15733612	1.13E-19	8.64E-19
NRP2	ENSG00000118257	6.055401542	1.16E-19	8.90E-19
AL355310.2	ENSG00000228703	-8.328392826	1.16E-19	8.90E-19
RECQL4	ENSG00000160957	3.171255547	1.18E-19	9.01E-19
RTKN	ENSG00000114993	4.096297455	1.23E-19	9.39E-19
S100A16	ENSG00000188643	6.679041276	1.23E-19	9.39E-19
FBLN1	ENSG00000077942	7.253872752	1.26E-19	9.64E-19
C4orf48	ENSG00000243449	4.136138849	1.34E-19	1.02E-18
FAM72B	ENSG00000188610	5.416459156	1.36E-19	1.03E-18
SORT1	ENSG00000134243	5.138161475	1.39E-19	1.06E-18

HIVEP2	ENSG00000010818	-3.102811813	1.39E-19	1.06E-18
AC243960.1	ENSG00000268027	-3.966227168	1.40E-19	1.06E-18
TXN	ENSG00000136810	3.333279212	1.42E-19	1.08E-18
HIF1A-AS1	ENSG00000258777	-7.26328059	1.42E-19	1.08E-18
DRC3	ENSG00000171962	-3.923861401	1.43E-19	1.09E-18
TST	ENSG00000128311	5.46706542	1.45E-19	1.10E-18
SNRPN	ENSG00000128739	-4.209317073	1.47E-19	1.11E-18
FCGR2A	ENSG00000143226	6.701577898	1.47E-19	1.12E-18
AC010260.1	ENSG00000251675	-8.48675522	1.49E-19	1.13E-18
CRLF1	ENSG00000006016	-5.438007942	1.50E-19	1.13E-18
BCL9L	ENSG00000186174	-3.153633345	1.50E-19	1.14E-18
Sep-11	ENSG00000138758	3.680538489	1.51E-19	1.14E-18
PKMYT1	ENSG00000127564	5.244123302	1.51E-19	1.14E-18
ALDH1L2	ENSG00000136010	4.664018363	1.53E-19	1.16E-18
AC021224.1	ENSG00000262477	-7.337471762	1.62E-19	1.21E-18
MND1	ENSG00000121211	6.19153388	1.63E-19	1.22E-18
AL031595.2	ENSG00000280011	-7.157296564	1.65E-19	1.24E-18
AL158163.1	ENSG00000270589	-5.48833522	1.65E-19	1.24E-18
IL7R	ENSG00000168685	-4.385996361	1.69E-19	1.26E-18
LIMD1-AS1	ENSG00000230530	-3.988375221	1.70E-19	1.27E-18
CALM2P2	ENSG00000229097	-6.211677157	1.75E-19	1.31E-18
AP002770.1	ENSG00000256034	-3.87110795	1.76E-19	1.31E-18
MORC2-AS1	ENSG00000235989	-4.758730547	1.77E-19	1.32E-18
DNHD1	ENSG00000179532	-3.040807057	1.78E-19	1.33E-18
AL358333.3	ENSG00000259007	-9.000065517	1.78E-19	1.33E-18
IL21R-AS1	ENSG00000259954	-7.374252612	1.79E-19	1.34E-18
PSRC1	ENSG00000134222	4.499977932	1.84E-19	1.37E-18
RSPO3	ENSG00000146374	5.077774064	1.87E-19	1.39E-18
GDPGP1	ENSG00000183208	-5.673029222	1.88E-19	1.39E-18
Z83844.2	ENSG00000233360	-7.034942705	1.91E-19	1.41E-18
FBXL7	ENSG00000183580	5.526837408	1.92E-19	1.42E-18
RASGRP2	ENSG00000068831	-4.978219689	1.96E-19	1.45E-18
AL356599.1	ENSG00000235652	-3.24818339	2.00E-19	1.48E-18
IL23A	ENSG00000110944	-4.435032102	2.11E-19	1.56E-18
AC009831.1	ENSG00000263823	-3.604390222	2.14E-19	1.58E-18
PARD3	ENSG00000148498	5.430098109	2.16E-19	1.59E-18
AL157938.3	ENSG00000246851	-7.669772218	2.17E-19	1.59E-18
CCDC88A	ENSG00000115355	3.322663146	2.21E-19	1.62E-18
SLC15A3	ENSG00000110446	5.052612938	2.27E-19	1.67E-18
ABALON	ENSG00000281376	-5.982160159	2.33E-19	1.70E-18
AC026191.1	ENSG00000254485	-5.715908051	2.37E-19	1.74E-18
FPR3	ENSG00000187474	6.563121257	2.38E-19	1.74E-18
LRRC39	ENSG00000122477	-3.619647925	2.38E-19	1.74E-18
STAG3	ENSG00000066923	-3.132380508	2.40E-19	1.76E-18
AC108863.1	ENSG00000253645	-10.42581028	2.42E-19	1.76E-18
FUCA1	ENSG00000179163	3.088212929	2.42E-19	1.77E-18
COBLL1	ENSG00000082438	5.272187756	2.49E-19	1.81E-18
ALDH1A1	ENSG00000165092	6.396613416	2.58E-19	1.87E-18
FOXH1	ENSG00000160973	-6.133670259	2.62E-19	1.90E-18
NEIL3	ENSG00000109674	7.311852021	2.65E-19	1.93E-18
AC091059.1	ENSG00000266002	-7.66549744	2.72E-19	1.98E-18

Z99129.1	ENSG00000275339	-7.187228322	2.76E-19	2.00E-18
EIF4EBP1	ENSG00000187840	3.889975585	2.77E-19	2.01E-18
LTBP2	ENSG00000119681	3.835125883	2.77E-19	2.01E-18
GRHL1	ENSG00000134317	4.877484914	2.81E-19	2.03E-18
ICAM1	ENSG00000090339	3.759326814	2.83E-19	2.05E-18
LRFN4	ENSG00000173621	4.145314563	2.93E-19	2.11E-18
STAB1	ENSG00000010327	6.232725438	2.95E-19	2.13E-18
ZNF521	ENSG00000198795	6.025595658	2.95E-19	2.13E-18
AMOTL2	ENSG00000114019	5.914391831	2.96E-19	2.13E-18
AC012640.4	ENSG00000271980	-7.120078152	2.96E-19	2.13E-18
TFEC	ENSG00000105967	5.598159993	3.01E-19	2.16E-18
ARHGEF25	ENSG00000240771	5.048330543	3.02E-19	2.17E-18
APOL4	ENSG00000100336	5.595096168	3.03E-19	2.18E-18
LGALS1	ENSG00000100097	5.232269183	3.06E-19	2.20E-18
TRBV5-1	ENSG00000211734	-5.189586709	3.13E-19	2.25E-18
AXL	ENSG00000167601	3.590810565	3.15E-19	2.25E-18
MRPS31P5	ENSG00000243406	-5.305194387	3.16E-19	2.27E-18
SOWAHC	ENSG00000198142	5.652718227	3.29E-19	2.35E-18
TJP1	ENSG00000104067	6.361640633	3.33E-19	2.38E-18
CSPG4	ENSG00000173546	4.715291322	3.41E-19	2.43E-18
LRRCC1	ENSG00000133739	3.732603067	3.53E-19	2.52E-18
KLF3-AS1	ENSG00000231160	-5.969752897	3.54E-19	2.52E-18
MRPL23	ENSG00000214026	3.60905988	3.68E-19	2.61E-18
MYH7B	ENSG00000078814	-3.508034524	3.72E-19	2.64E-18
LRRK1	ENSG00000154237	4.774151691	3.72E-19	2.64E-18
DSCC1	ENSG00000136982	4.926965007	3.73E-19	2.65E-18
SCD	ENSG00000099194	4.825618372	3.88E-19	2.75E-18
AP000919.4	ENSG00000272625	-5.721348153	3.97E-19	2.81E-18
CSF1R	ENSG00000182578	5.034949893	4.11E-19	2.91E-18
NPL	ENSG00000135838	4.043531557	4.15E-19	2.94E-18
AP001972.1	ENSG00000254429	-6.018050167	4.18E-19	2.95E-18
ARHGAP18	ENSG00000146376	4.254518096	4.20E-19	2.97E-18
H1FX-AS1	ENSG00000206417	-3.525867953	4.26E-19	3.01E-18
GAPDHS	ENSG00000105679	-5.411822528	4.27E-19	3.01E-18
COPG2	ENSG00000158623	3.206192934	4.46E-19	3.14E-18
PPFIBP1	ENSG00000110841	3.872044712	4.50E-19	3.16E-18
ATXN7	ENSG00000163635	-3.381036419	4.50E-19	3.16E-18
CD9	ENSG00000010278	6.290078888	4.57E-19	3.21E-18
TENM4	ENSG00000149256	6.144406479	4.67E-19	3.28E-18
ACKR1	ENSG00000213088	6.188434536	4.80E-19	3.36E-18
TUSC1	ENSG00000198680	4.760209139	4.80E-19	3.36E-18
PSMD6-AS2	ENSG00000239653	-4.348733311	4.96E-19	3.47E-18
AP001011.1	ENSG00000266049	-8.653941105	5.05E-19	3.53E-18
SLC8A1	ENSG00000183023	5.273073054	5.11E-19	3.57E-18
EZR-AS1	ENSG00000233893	-8.395606728	5.19E-19	3.63E-18
TCF7	ENSG00000081059	-5.078719239	5.23E-19	3.65E-18
SOGA1	ENSG00000149639	3.164727732	5.25E-19	3.66E-18
IL23R	ENSG00000162594	6.240644326	5.40E-19	3.76E-18
CYBRD1	ENSG00000071967	5.855936252	5.40E-19	3.76E-18
WISP1	ENSG00000104415	6.136237699	5.43E-19	3.78E-18
PHLDB1	ENSG00000019144	3.090007302	5.44E-19	3.78E-18

NRN1	ENSG00000124785	5.582496428	5.46E-19	3.80E-18
GSTP1	ENSG00000084207	4.09958134	5.51E-19	3.83E-18
GPC1	ENSG00000063660	4.459225886	5.55E-19	3.85E-18
SOBP	ENSG00000112320	4.464591878	5.57E-19	3.86E-18
TIMELESS	ENSG00000111602	3.375558738	5.58E-19	3.87E-18
OAF	ENSG00000184232	5.008756212	5.63E-19	3.90E-18
AP000763.4	ENSG00000256928	-7.558359393	5.69E-19	3.94E-18
EP300-AS1	ENSG00000231993	-5.968904443	5.76E-19	3.98E-18
MRAS	ENSG00000158186	4.818627995	5.81E-19	4.01E-18
CCDC34	ENSG00000109881	6.094781188	5.82E-19	4.01E-18
AC068631.1	ENSG00000197099	-3.373299106	5.96E-19	4.11E-18
LPCAT2	ENSG00000087253	5.189061291	6.02E-19	4.15E-18
MRPL38	ENSG00000204316	-3.383913586	6.21E-19	4.27E-18
CLN3	ENSG00000188603	-4.19634204	6.28E-19	4.32E-18
AGPAT2	ENSG00000169692	3.815137735	6.51E-19	4.47E-18
GPRIN1	ENSG00000169258	4.517391891	6.77E-19	4.65E-18
AC010422.8	ENSG00000285589	-3.696139753	7.08E-19	4.85E-18
LRRC15	ENSG00000172061	8.046301752	7.12E-19	4.87E-18
MT-TE	ENSG00000210194	-6.360814126	7.19E-19	4.91E-18
CPPED1	ENSG00000103381	3.473238667	7.27E-19	4.96E-18
HOXB7	ENSG00000260027	5.303504801	7.42E-19	5.07E-18
CPVL	ENSG00000106066	6.894367072	7.57E-19	5.16E-18
AC008894.3	ENSG00000279198	-4.394290277	7.61E-19	5.19E-18
AP003392.3	ENSG00000255114	-7.089197106	7.68E-19	5.23E-18
SGO1	ENSG00000129810	3.627307757	7.75E-19	5.27E-18
ORC6	ENSG00000091651	3.175691187	7.75E-19	5.27E-18
NLN	ENSG00000123213	3.695191704	7.78E-19	5.29E-18
RCN3	ENSG00000142552	4.217058241	7.89E-19	5.35E-18
AC015971.1	ENSG00000228363	-9.270994141	7.91E-19	5.36E-18
IGFBP5	ENSG00000115461	8.930576885	8.03E-19	5.44E-18
AL162742.2	ENSG00000270075	-7.419629149	8.14E-19	5.51E-18
HAS2	ENSG00000170961	6.130349984	8.20E-19	5.54E-18
GLS2	ENSG00000135423	-4.251330679	8.37E-19	5.64E-18
ALDH1A3	ENSG00000184254	5.039315863	8.84E-19	5.95E-18
RARRES1	ENSG00000118849	5.015371954	8.93E-19	6.01E-18
PSPH	ENSG00000146733	3.15442244	8.96E-19	6.03E-18
SCARF1	ENSG00000074660	3.531939319	9.05E-19	6.08E-18
SLC26A1	ENSG00000145217	-6.006104112	9.15E-19	6.14E-18
STX16-NPEPL1	ENSG00000254995	-4.69627562	9.34E-19	6.26E-18
MEIOC	ENSG00000180336	-6.889531333	9.75E-19	6.53E-18
DDX47	ENSG00000213782	-4.583682353	9.92E-19	6.62E-18
CD28	ENSG00000178562	-4.920894627	9.93E-19	6.63E-18
PTAFR	ENSG00000169403	4.489021761	1.02E-18	6.79E-18
HEPH	ENSG00000089472	4.860830687	1.03E-18	6.87E-18
CCL2	ENSG00000108691	6.943246043	1.09E-18	7.24E-18
LRRC25	ENSG00000175489	5.118995868	1.11E-18	7.35E-18
AC067945.3	ENSG00000231858	-8.888808361	1.13E-18	7.44E-18
AC073957.3	ENSG00000273151	-5.301578804	1.14E-18	7.51E-18
LY86	ENSG00000112799	4.45954843	1.15E-18	7.62E-18
ESPL1	ENSG00000135476	3.817945602	1.16E-18	7.63E-18
AL355075.3	ENSG00000258908	-8.331587077	1.17E-18	7.73E-18

COL16A1	ENSG00000084636	6.66867953	1.17E-18	7.74E-18
COL4A5	ENSG00000188153	6.501936103	1.18E-18	7.78E-18
AC022087.1	ENSG00000259715	-7.003413777	1.18E-18	7.79E-18
ECT2	ENSG00000114346	4.342387333	1.22E-18	8.01E-18
AC010761.4	ENSG00000265474	-7.088191116	1.22E-18	8.04E-18
OBSL1	ENSG00000124006	4.773563835	1.23E-18	8.05E-18
H1F0	ENSG00000189060	3.877566031	1.23E-18	8.09E-18
AC092794.2	ENSG00000275197	-6.730873218	1.26E-18	8.25E-18
MEF2C	ENSG00000081189	7.203118116	1.28E-18	8.40E-18
EPHA2	ENSG00000142627	5.02233111	1.29E-18	8.42E-18
AC005726.4	ENSG00000265168	-6.491110348	1.30E-18	8.53E-18
SERHL2	ENSG00000183569	-3.84164175	1.30E-18	8.53E-18
EIF4A1	ENSG00000161960	-4.178662041	1.32E-18	8.63E-18
PLXDC2	ENSG00000120594	6.481317254	1.35E-18	8.82E-18
BCAR1	ENSG00000050820	5.392250152	1.35E-18	8.82E-18
PXDN	ENSG00000130508	6.789580554	1.38E-18	9.02E-18
AC011825.4	ENSG00000265008	-4.601913576	1.42E-18	9.23E-18
WHAMM	ENSG00000156232	-3.420658214	1.43E-18	9.28E-18
TMEM63A	ENSG00000196187	-3.281111059	1.44E-18	9.34E-18
TBX2	ENSG00000121068	5.793726085	1.48E-18	9.60E-18
AL590627.1	ENSG00000255585	-6.944279821	1.48E-18	9.60E-18
AC020978.9	ENSG00000279649	-6.254289934	1.49E-18	9.65E-18
AC079313.1	ENSG00000258086	-7.080342669	1.49E-18	9.66E-18
RF00019	ENSG00000201778	-9.783944871	1.52E-18	9.80E-18
CCDC144NL-AS1	ENSG00000233098	-4.649654949	1.52E-18	9.83E-18
MORN3	ENSG00000139714	-4.179961725	1.53E-18	9.85E-18
AC048382.5	ENSG00000275120	-3.187001235	1.53E-18	9.86E-18
MAP3K6	ENSG00000142733	3.067820629	1.57E-18	1.01E-17
BRI3BP	ENSG00000184992	3.163922996	1.65E-18	1.06E-17
PIMREG	ENSG00000129195	5.535138144	1.70E-18	1.09E-17
ARHGEF17	ENSG00000110237	5.436253935	1.72E-18	1.11E-17
PLA2R1	ENSG00000153246	5.162481651	1.72E-18	1.11E-17
MREG	ENSG00000118242	3.618616708	1.74E-18	1.12E-17
CELF2-AS1	ENSG00000181800	-8.661574935	1.75E-18	1.12E-17
LOXL2	ENSG00000134013	3.011492906	1.80E-18	1.15E-17
CRISPLD2	ENSG00000103196	5.377511384	1.81E-18	1.16E-17
MPEG1	ENSG00000197629	6.857633341	1.82E-18	1.16E-17
DENND6A-AS1	ENSG00000239801	-7.676992037	1.83E-18	1.17E-17
CENPQ	ENSG00000031691	3.049109524	1.84E-18	1.17E-17
AC018665.1	ENSG00000279382	-7.372090848	1.84E-18	1.18E-17
PDGFC	ENSG00000145431	5.557808911	1.85E-18	1.18E-17
DDIAS	ENSG00000165490	3.706470232	1.88E-18	1.20E-17
CERCAM	ENSG00000167123	5.504032759	1.89E-18	1.20E-17
MAGI2-AS3	ENSG00000234456	4.785523133	1.92E-18	1.22E-17
PRKCA	ENSG00000154229	-3.803216142	1.95E-18	1.24E-17
COL8A1	ENSG00000144810	5.544799294	2.00E-18	1.27E-17
ERCC5	ENSG00000134899	-4.036369268	2.06E-18	1.30E-17
KITLG	ENSG00000049130	7.117622044	2.06E-18	1.30E-17
AP001160.1	ENSG00000256690	-5.581332364	2.08E-18	1.32E-17
PRDX1	ENSG00000117450	3.311209318	2.08E-18	1.32E-17
MMP16	ENSG00000156103	5.407622395	2.10E-18	1.33E-17

CD40	ENSG00000101017	4.544660555	2.22E-18	1.40E-17
AC012676.5	ENSG00000280063	-3.224294371	2.29E-18	1.44E-17
CTHRC1	ENSG00000164932	7.029231678	2.29E-18	1.45E-17
AP000779.1	ENSG00000285921	-6.65781161	2.44E-18	1.54E-17
STEAP2	ENSG00000157214	5.846334298	2.50E-18	1.57E-17
CD163	ENSG00000177575	8.06677737	2.50E-18	1.57E-17
ENAH	ENSG00000154380	6.28106099	2.54E-18	1.59E-17
GPT2	ENSG00000166123	3.822487658	2.54E-18	1.60E-17
EPOP	ENSG00000273604	4.286045233	2.59E-18	1.62E-17
RORA	ENSG00000069667	-3.087462257	2.86E-18	1.79E-17
COLEC12	ENSG00000158270	6.462541512	2.88E-18	1.80E-17
MYH3	ENSG00000109063	-3.518173868	2.92E-18	1.82E-17
APOBEC3B	ENSG00000179750	6.668965602	2.95E-18	1.84E-17
CADPS2	ENSG00000081803	5.134251857	2.97E-18	1.85E-17
ITIH5	ENSG00000123243	5.352357775	2.98E-18	1.86E-17
MATN1	ENSG00000162510	-5.347559539	3.02E-18	1.88E-17
FMO3	ENSG00000007933	5.797898526	3.08E-18	1.91E-17
NQO1	ENSG00000181019	3.767971697	3.09E-18	1.92E-17
AC073861.1	ENSG00000242299	-4.295776288	3.09E-18	1.92E-17
CXCL13	ENSG00000156234	8.285485475	3.18E-18	1.97E-17
RNASE6	ENSG00000169413	5.645303467	3.22E-18	2.00E-17
NR2F6	ENSG00000160113	3.72347727	3.27E-18	2.02E-17
AC135050.1	ENSG00000232748	-5.803092121	3.31E-18	2.05E-17
TRBJ1-4	ENSG00000281958	-5.374493327	3.32E-18	2.05E-17
DGUOK-AS1	ENSG00000237883	-4.317166741	3.34E-18	2.06E-17
CLEC7A	ENSG00000172243	4.706700454	3.35E-18	2.07E-17
EMP1	ENSG00000134531	5.709118333	3.37E-18	2.08E-17
AL158163.2	ENSG00000278601	-4.712796911	3.38E-18	2.08E-17
TJP3	ENSG00000105289	-4.043234707	3.41E-18	2.10E-17
SIAH2-AS1	ENSG00000244265	-6.473151449	3.43E-18	2.11E-17
AMOTL1	ENSG00000166025	5.142580751	3.48E-18	2.14E-17
PMS2P7	ENSG00000229018	-5.098945591	3.48E-18	2.14E-17
PRICKLE2	ENSG00000163637	4.832940169	3.49E-18	2.14E-17
IGF2BP2	ENSG00000073792	5.249509369	3.59E-18	2.21E-17
FCMR	ENSG00000162894	-4.665100837	3.66E-18	2.25E-17
SHTN1	ENSG00000187164	4.306421518	3.68E-18	2.25E-17
SPC24	ENSG00000161888	3.399756474	3.69E-18	2.26E-17
AC241377.3	ENSG00000281741	-5.819267313	3.71E-18	2.27E-17
STAG3L5P	ENSG00000242294	-3.360936203	3.77E-18	2.31E-17
HLA-DPA1	ENSG00000231389	5.24309565	3.81E-18	2.33E-17
RBM47	ENSG00000163694	4.22387681	3.90E-18	2.38E-17
ANPEP	ENSG00000166825	5.735370126	3.92E-18	2.39E-17
FILIP1L	ENSG00000168386	5.657498377	3.96E-18	2.41E-17
RUNX1T1	ENSG00000079102	4.989481352	4.02E-18	2.45E-17
FAM102A	ENSG00000167106	-3.420304127	4.10E-18	2.49E-17
NCEH1	ENSG00000144959	4.061660044	4.13E-18	2.51E-17
GNRHR2	ENSG00000211451	-3.079608889	4.28E-18	2.60E-17
GCNT4	ENSG00000176928	-4.32419956	4.30E-18	2.61E-17
AC023818.1	ENSG00000280067	-6.008435368	4.36E-18	2.65E-17
UBTD1	ENSG00000165886	3.51960004	4.37E-18	2.65E-17
ARHGEF40	ENSG00000165801	3.73096272	4.47E-18	2.70E-17

IRF5	ENSG00000128604	3.564710995	4.49E-18	2.72E-17
SEMA4A	ENSG00000196189	4.332133439	4.52E-18	2.73E-17
TRBJ2-7	ENSG00000211771	-4.561172254	4.60E-18	2.78E-17
PLOD2	ENSG00000152952	7.277138021	4.67E-18	2.81E-17
IQGAP3	ENSG00000183856	4.810659407	4.67E-18	2.81E-17
CDR2L	ENSG00000109089	4.597977859	4.73E-18	2.85E-17
LRRC24	ENSG00000254402	-3.250009832	4.75E-18	2.86E-17
IGFLR1	ENSG00000126246	-3.084402764	4.80E-18	2.89E-17
NDUFV2-AS1	ENSG00000266053	-3.304020287	4.82E-18	2.89E-17
FMO1	ENSG00000010932	6.360318065	4.98E-18	2.99E-17
RHBDF1	ENSG00000007384	3.892924456	5.06E-18	3.03E-17
SDC1	ENSG00000115884	7.758141112	5.50E-18	3.28E-17
FO704657.1	ENSG00000272004	-5.140720974	5.51E-18	3.29E-17
TMEM132A	ENSG00000006118	4.670142271	5.54E-18	3.31E-17
POU6F1	ENSG00000184271	-3.160650204	5.58E-18	3.32E-17
PHBP9	ENSG00000230224	-7.938891365	5.59E-18	3.33E-17
CD151	ENSG00000177697	3.478929841	5.63E-18	3.35E-17
AL031282.2	ENSG00000268575	-3.546736607	5.64E-18	3.36E-17
AC253536.3	ENSG00000232545	-4.2927306	5.65E-18	3.36E-17
AC004877.1	ENSG00000273419	-6.548451021	5.69E-18	3.38E-17
RHOBTB3	ENSG00000164292	4.229538034	5.88E-18	3.49E-17
RPS11P5	ENSG00000232888	-4.874589121	5.92E-18	3.51E-17
C1orf198	ENSG00000119280	3.01223602	5.94E-18	3.52E-17
CRYAB	ENSG00000109846	4.729935817	5.98E-18	3.54E-17
CYBB	ENSG00000165168	6.84064798	5.99E-18	3.54E-17
LOXL1	ENSG00000129038	3.238596372	6.00E-18	3.55E-17
SERINC5	ENSG00000164300	-3.362173726	6.08E-18	3.59E-17
PTPN21	ENSG00000070778	4.378367932	6.19E-18	3.66E-17
PTPRN2	ENSG00000155093	5.263293168	6.28E-18	3.71E-17
RPL24P4	ENSG00000181524	-4.541569908	6.34E-18	3.74E-17
ST14	ENSG00000149418	5.41770569	6.34E-18	3.74E-17
PER1	ENSG00000179094	-4.119636532	6.38E-18	3.76E-17
TCEAL9	ENSG00000185222	5.460779815	6.44E-18	3.79E-17
AC010973.2	ENSG00000244151	-4.418417518	6.49E-18	3.82E-17
SLC37A2	ENSG00000134955	4.015878319	6.58E-18	3.88E-17
C1QTNF1	ENSG00000173918	5.622244422	6.61E-18	3.89E-17
FCGRT	ENSG00000104870	3.070712883	6.63E-18	3.90E-17
RMI2	ENSG00000175643	4.374291943	6.63E-18	3.90E-17
COL8A2	ENSG00000171812	4.966317976	6.73E-18	3.95E-17
HIP1	ENSG00000127946	4.516876658	6.87E-18	4.03E-17
LDB2	ENSG00000169744	5.348972721	7.05E-18	4.13E-17
KCTD21-AS1	ENSG00000246174	-3.604060961	7.09E-18	4.15E-17
RCAN1	ENSG00000159200	3.296032957	7.14E-18	4.18E-17
NEK2	ENSG00000117650	5.710704886	7.20E-18	4.21E-17
JMJD7-PLA2G4B	ENSG00000168970	-4.479463482	7.28E-18	4.25E-17
AC119396.1	ENSG00000263264	-5.647006825	7.50E-18	4.37E-17
LIMCH1	ENSG00000064042	5.311840494	7.54E-18	4.40E-17
TH2LCRR	ENSG00000223442	-5.055050629	7.58E-18	4.41E-17
ADAMTS12	ENSG00000151388	5.722231112	7.67E-18	4.46E-17
TRBV3-1	ENSG00000237702	-4.993953436	7.80E-18	4.54E-17
TNK2-AS1	ENSG00000224614	-4.468373188	7.87E-18	4.57E-17

MIR3648-1	ENSG00000275708	5.831684892	7.90E-18	4.59E-17
PTK7	ENSG00000112655	4.507963775	8.08E-18	4.69E-17
ZDHHC1	ENSG00000159714	4.600535603	8.22E-18	4.76E-17
BHLHE22	ENSG00000180828	6.238683603	8.40E-18	4.86E-17
AC004453.1	ENSG00000146677	-4.211999797	8.43E-18	4.88E-17
AC040162.1	ENSG00000261884	-3.910691099	8.62E-18	4.98E-17
AC116366.1	ENSG00000234290	-7.049031956	8.85E-18	5.11E-17
NRIP2	ENSG00000053702	-4.906629016	9.13E-18	5.26E-17
PDCD1LG2	ENSG00000197646	4.555817359	9.28E-18	5.34E-17
STEAP3	ENSG00000115107	6.453724614	9.49E-18	5.46E-17
KNL1	ENSG00000137812	4.043042767	9.70E-18	5.57E-17
MOXD1	ENSG00000079931	6.405089538	9.85E-18	5.65E-17
CLIC6	ENSG00000159212	4.439301559	9.90E-18	5.67E-17
AC005329.1	ENSG00000248015	-3.555491109	9.97E-18	5.71E-17
C9orf43	ENSG00000157653	-5.337053388	1.05E-17	5.99E-17
AC135507.1	ENSG00000272182	-3.353910455	1.05E-17	6.00E-17
BTK	ENSG00000010671	4.719050352	1.06E-17	6.04E-17
HOXC6	ENSG00000197757	5.29221548	1.08E-17	6.13E-17
NRSN2	ENSG00000125841	3.809966665	1.08E-17	6.13E-17
MIR100HG	ENSG00000255248	4.753412905	1.08E-17	6.14E-17
FAM72A	ENSG00000196550	4.491895155	1.09E-17	6.20E-17
SUPT4H1	ENSG00000213246	-5.507912043	1.09E-17	6.22E-17
ASPN	ENSG00000106819	5.417521508	1.10E-17	6.23E-17
CADM3	ENSG00000162706	5.515986631	1.13E-17	6.43E-17
AC007608.3	ENSG00000260249	-6.499756363	1.14E-17	6.48E-17
SCARA3	ENSG00000168077	6.065933418	1.15E-17	6.53E-17
TGFB1I1	ENSG00000140682	4.649344754	1.18E-17	6.66E-17
EML5	ENSG00000165521	-4.045148523	1.18E-17	6.68E-17
LMCD1	ENSG00000071282	5.524272012	1.18E-17	6.68E-17
SMOC2	ENSG00000112562	6.120161373	1.19E-17	6.71E-17
AC084337.1	ENSG00000254595	-4.244633923	1.22E-17	6.88E-17
KLHDC8B	ENSG00000185909	3.309507933	1.22E-17	6.89E-17
HLX	ENSG00000136630	5.628166898	1.24E-17	6.97E-17
SAMD1	ENSG00000141858	3.111174287	1.25E-17	7.06E-17
ADRA2A	ENSG00000150594	6.826780598	1.27E-17	7.16E-17
RORA-AS1	ENSG00000245534	-6.438332027	1.32E-17	7.44E-17
LRP3	ENSG00000130881	5.502857493	1.32E-17	7.44E-17
CLDN5	ENSG00000184113	5.373399036	1.37E-17	7.65E-17
LYN	ENSG00000254087	5.018737022	1.39E-17	7.77E-17
AC068580.3	ENSG00000235027	-6.72591	1.40E-17	7.81E-17
SLIT2	ENSG00000145147	4.901337304	1.42E-17	7.91E-17
CLEC11A	ENSG00000105472	5.020312471	1.44E-17	8.02E-17
AC011446.2	ENSG00000267598	-9.34720788	1.46E-17	8.15E-17
COL14A1	ENSG00000187955	6.776565965	1.47E-17	8.18E-17
CCDC112	ENSG00000164221	3.574688218	1.50E-17	8.36E-17
GCAT	ENSG00000100116	3.728788113	1.54E-17	8.57E-17
TRAV8-2	ENSG00000211786	-4.160881354	1.55E-17	8.62E-17
DST	ENSG00000151914	3.879442005	1.59E-17	8.80E-17
RARRES2	ENSG00000106538	5.758703573	1.59E-17	8.81E-17
AC108010.1	ENSG00000242588	-3.571746358	1.59E-17	8.81E-17
AC137834.2	ENSG00000276727	-6.317813254	1.60E-17	8.83E-17

RPS28P7	ENSG00000227097	-3.590642776	1.60E-17	8.83E-17
AL355581.1	ENSG00000227678	-5.040826905	1.60E-17	8.85E-17
C3	ENSG00000125730	7.087217832	1.62E-17	8.95E-17
CUEDC1	ENSG00000180891	4.666916182	1.62E-17	8.95E-17
SPOCK1	ENSG00000152377	5.276074	1.64E-17	9.04E-17
CCR1	ENSG00000163823	6.321335243	1.70E-17	9.39E-17
HES1	ENSG00000114315	5.201598173	1.72E-17	9.44E-17
AC005786.3	ENSG00000267436	-4.980120438	1.76E-17	9.69E-17
HSD17B1	ENSG00000108786	-3.725062634	1.77E-17	9.74E-17
GJC1	ENSG00000182963	4.262873464	1.78E-17	9.79E-17
AC004918.3	ENSG00000270157	-3.475611421	1.80E-17	9.85E-17
SELE	ENSG00000007908	5.188141134	1.81E-17	9.92E-17
PIK3R1	ENSG00000145675	-3.410941195	1.84E-17	1.01E-16
AP000759.1	ENSG00000255320	-6.773134975	1.85E-17	1.01E-16
SPRY4	ENSG00000187678	4.692573641	1.86E-17	1.02E-16
DIO2	ENSG00000211448	8.245794953	1.87E-17	1.02E-16
SLC12A6	ENSG00000140199	-3.058583378	1.90E-17	1.04E-16
APOD	ENSG00000189058	6.782910836	1.90E-17	1.04E-16
HK3	ENSG00000160883	4.746544062	1.91E-17	1.04E-16
FOLR2	ENSG00000165457	6.891767428	1.92E-17	1.05E-16
FLNB-AS1	ENSG00000244161	-7.432709792	1.94E-17	1.05E-16
HHEX	ENSG00000152804	4.235018919	1.94E-17	1.05E-16
TRBJ1-6	ENSG00000282780	-5.109476205	1.94E-17	1.06E-16
AC068338.2	ENSG00000260274	-3.865426212	1.99E-17	1.08E-16
PWAR5	ENSG00000279192	-6.185413254	2.04E-17	1.11E-16
ZNF331	ENSG00000130844	-3.440525287	2.05E-17	1.11E-16
PDGFRA	ENSG00000134853	7.528384349	2.05E-17	1.11E-16
ITGB4	ENSG00000132470	4.331997572	2.06E-17	1.12E-16
ALDH3B1	ENSG00000006534	4.735776085	2.07E-17	1.13E-16
ZNF608	ENSG00000168916	4.871468796	2.08E-17	1.13E-16
NFAM1	ENSG00000235568	4.609027216	2.14E-17	1.15E-16
PYGM	ENSG00000068976	-4.946967351	2.14E-17	1.15E-16
FAM171B	ENSG00000144369	4.222776536	2.14E-17	1.16E-16
AC018529.2	ENSG00000278330	-5.139948317	2.15E-17	1.16E-16
MGST2	ENSG00000085871	3.493208158	2.15E-17	1.16E-16
UCK2	ENSG00000143179	3.976787605	2.18E-17	1.17E-16
AC007899.1	ENSG00000224891	-7.170655479	2.18E-17	1.18E-16
SLC1A5	ENSG00000105281	3.59354824	2.19E-17	1.18E-16
KIF18A	ENSG00000121621	3.831216167	2.22E-17	1.19E-16
ZFHX3	ENSG00000140836	3.474618775	2.25E-17	1.21E-16
AC015813.1	ENSG00000264112	-3.901763283	2.31E-17	1.23E-16
CIRBP-AS1	ENSG00000267493	-3.878947819	2.32E-17	1.24E-16
SDK1	ENSG00000146555	4.400359594	2.42E-17	1.29E-16
THSD7A	ENSG00000005108	4.939434155	2.44E-17	1.30E-16
PSEN2	ENSG00000143801	4.184300318	2.47E-17	1.32E-16
AC115676.1	ENSG00000255958	-7.458359013	2.48E-17	1.32E-16
STEAP1	ENSG00000164647	5.671427482	2.50E-17	1.33E-16
ITGA8	ENSG00000077943	4.610330695	2.52E-17	1.34E-16
TPPP3	ENSG00000159713	5.441876003	2.56E-17	1.36E-16
CYGB	ENSG00000161544	5.341569964	2.58E-17	1.37E-16
SMAD1	ENSG00000170365	4.03939557	2.60E-17	1.38E-16

TC2N	ENSG00000165929	-3.978775182	2.63E-17	1.39E-16
IRX3	ENSG00000177508	5.959081685	2.72E-17	1.44E-16
MEX3D	ENSG00000181588	3.894985085	2.82E-17	1.49E-16
MSX1	ENSG00000163132	5.466719869	2.82E-17	1.49E-16
NFKBIZ	ENSG00000144802	-3.360037526	2.91E-17	1.54E-16
AC026771.1	ENSG00000260545	-7.155209128	2.93E-17	1.54E-16
DLL4	ENSG00000128917	3.518857343	2.96E-17	1.56E-16
HES4	ENSG00000188290	4.724862616	2.98E-17	1.57E-16
IMPA2	ENSG00000141401	3.766374659	3.12E-17	1.64E-16
RASAL2	ENSG00000075391	5.552546025	3.23E-17	1.70E-16
AL121987.2	ENSG00000227741	-4.273291931	3.28E-17	1.72E-16
OPN3	ENSG00000054277	4.113628827	3.40E-17	1.78E-16
WNT5B	ENSG00000111186	6.884889655	3.44E-17	1.80E-16
ACTA2-AS1	ENSG00000180139	-3.260482322	3.44E-17	1.80E-16
DNAAF1	ENSG00000154099	-6.405859918	3.45E-17	1.80E-16
PTGFR	ENSG00000122420	6.175733318	3.49E-17	1.82E-16
MYO1E	ENSG00000157483	5.843915181	3.52E-17	1.84E-16
GRIN3B	ENSG00000116032	-5.216062984	3.53E-17	1.84E-16
SMARCA1	ENSG00000102038	4.125538572	3.62E-17	1.89E-16
ESAM	ENSG00000149564	3.933900616	3.68E-17	1.92E-16
PDXDC2P-NPIPB14P	ENSG00000196696	-3.144257203	3.69E-17	1.92E-16
TRBV6-2	ENSG00000283063	-4.789109498	3.71E-17	1.93E-16
OLFML3	ENSG00000116774	5.617099436	3.71E-17	1.93E-16
MME	ENSG00000196549	5.868071388	3.94E-17	2.04E-16
SRPX	ENSG00000101955	5.916838989	3.95E-17	2.04E-16
ZNF815P	ENSG00000235944	-3.604740089	4.11E-17	2.12E-16
REL	ENSG00000162924	-3.448769532	4.13E-17	2.14E-16
TLR7	ENSG00000196664	5.048558221	4.16E-17	2.15E-16
AC008914.1	ENSG00000262211	-10.22134923	4.28E-17	2.21E-16
MGLL	ENSG00000074416	4.855855432	4.31E-17	2.22E-16
CLIC4	ENSG00000169504	5.152318119	4.31E-17	2.22E-16
CMKLR1	ENSG00000174600	5.810435403	4.36E-17	2.25E-16
MSR1	ENSG00000038945	6.013189449	4.39E-17	2.26E-16
CDS1	ENSG00000163624	3.568915627	4.44E-17	2.29E-16
PTN	ENSG00000105894	6.798333755	4.45E-17	2.29E-16
JAG1	ENSG00000101384	5.263318143	4.54E-17	2.34E-16
GGT5	ENSG00000099998	4.976292162	4.56E-17	2.35E-16
TRBV6-5	ENSG00000211721	-4.34617361	4.60E-17	2.36E-16
TCAP	ENSG00000173991	-3.886968486	4.76E-17	2.44E-16
BCAM	ENSG00000187244	4.996747589	4.82E-17	2.47E-16
MS4A7	ENSG00000166927	6.9830668	4.88E-17	2.50E-16
RYR3	ENSG00000198838	-4.498507501	4.88E-17	2.50E-16
MYB	ENSG00000118513	3.832674945	4.96E-17	2.54E-16
KYNU	ENSG00000115919	4.26576388	5.06E-17	2.59E-16
BUB1B	ENSG00000156970	4.148925849	5.10E-17	2.60E-16
IL11RA	ENSG00000137070	-3.217023018	5.19E-17	2.65E-16
MEIS2	ENSG00000134138	5.714270085	5.24E-17	2.67E-16
MAP1B	ENSG00000131711	6.28299972	5.40E-17	2.74E-16
AC068724.1	ENSG00000261687	-5.943194765	5.54E-17	2.81E-16
AC090589.3	ENSG00000270060	-4.305480532	5.57E-17	2.83E-16
ID4	ENSG00000172201	5.997413664	5.64E-17	2.85E-16

DOC2B	ENSG00000272636	5.101734631	5.65E-17	2.86E-16
ESR2	ENSG00000140009	-5.250124308	5.66E-17	2.86E-16
RHOH	ENSG00000168421	-3.141725429	5.66E-17	2.86E-16
PANX2	ENSG00000073150	5.194205558	5.72E-17	2.89E-16
MET	ENSG00000105976	6.202770861	5.90E-17	2.98E-16
KCTD3	ENSG00000136636	4.618825343	5.97E-17	3.01E-16
JUP	ENSG00000173801	6.601908552	5.98E-17	3.01E-16
CCDC65	ENSG00000139537	-4.514059439	6.00E-17	3.02E-16
MEDAG	ENSG00000102802	5.678232901	6.11E-17	3.07E-16
FCGR1A	ENSG00000150337	5.928600145	6.13E-17	3.08E-16
HPCAL4	ENSG00000116983	-6.105146472	6.28E-17	3.16E-16
KLF3	ENSG00000109787	-3.294986059	6.29E-17	3.16E-16
CSTA	ENSG00000121552	6.729184845	6.44E-17	3.24E-16
MIR3918	ENSG00000265558	-7.413345486	6.91E-17	3.46E-16
AC137630.3	ENSG00000272434	-3.465262255	6.98E-17	3.49E-16
KIFC3	ENSG00000140859	4.384012579	7.07E-17	3.53E-16
PERP	ENSG00000112378	4.90238451	7.23E-17	3.61E-16
AC003957.1	ENSG00000279825	-6.999630093	7.24E-17	3.62E-16
SOWAHD	ENSG00000187808	3.790459963	7.39E-17	3.69E-16
ST3GAL4	ENSG00000110080	3.017714222	7.40E-17	3.69E-16
CCL18	ENSG00000275385	9.691922396	7.83E-17	3.90E-16
LGALSL	ENSG00000119862	5.320910118	7.88E-17	3.92E-16
PARVB	ENSG00000188677	3.161973724	8.03E-17	3.99E-16
PYGL	ENSG00000100504	6.496540985	8.06E-17	4.00E-16
PTTG1	ENSG00000164611	3.693448278	8.08E-17	4.01E-16
ABI3BP	ENSG00000154175	6.406004176	8.20E-17	4.07E-16
CTDSPL	ENSG00000144677	5.831044201	8.22E-17	4.07E-16
CPXM1	ENSG00000088882	6.882265221	8.78E-17	4.34E-16
AC006030.1	ENSG00000264324	-4.913661882	8.92E-17	4.41E-16
TCTEX1D4	ENSG00000188396	-5.992792141	8.94E-17	4.41E-16
TSPAN11	ENSG00000110900	6.363497604	8.99E-17	4.44E-16
MOB3B	ENSG00000120162	3.279527455	9.00E-17	4.44E-16
LILRB2	ENSG00000131042	5.818243346	9.11E-17	4.49E-16
PTPN3	ENSG00000070159	6.481977741	9.75E-17	4.80E-16
NAPSB	ENSG00000131401	6.527368432	9.86E-17	4.85E-16
POLR2J4	ENSG00000214783	-3.497035457	1.03E-16	5.07E-16
SESN3	ENSG00000149212	-3.932898008	1.05E-16	5.16E-16
S100A9	ENSG00000163220	7.53668388	1.05E-16	5.17E-16
PSAT1	ENSG00000135069	4.338238846	1.07E-16	5.22E-16
MAP2	ENSG00000078018	4.775606469	1.11E-16	5.42E-16
HLA-DPB1	ENSG00000223865	4.21784233	1.11E-16	5.43E-16
CDCP1	ENSG00000163814	4.685055667	1.18E-16	5.76E-16
CYP27A1	ENSG00000135929	4.772439561	1.21E-16	5.88E-16
AC073130.3	ENSG00000279086	-4.635816262	1.24E-16	6.03E-16
AP002387.1	ENSG00000254682	-3.309824761	1.25E-16	6.08E-16
TRBJ1-5	ENSG00000282173	-5.074730676	1.27E-16	6.17E-16
GAS7	ENSG00000007237	5.333427029	1.28E-16	6.20E-16
PFN1P6	ENSG00000227212	-7.021584491	1.30E-16	6.29E-16
LOX	ENSG00000113083	5.154043952	1.32E-16	6.42E-16
SATB1	ENSG00000182568	-4.005116864	1.36E-16	6.57E-16
AL360181.2	ENSG00000235245	-4.141836774	1.41E-16	6.80E-16

RACGAP1	ENSG00000161800	3.420941702	1.42E-16	6.86E-16
NBL1	ENSG00000158747	3.260718512	1.45E-16	7.01E-16
MSC	ENSG00000178860	6.761547219	1.46E-16	7.04E-16
KCNJ5	ENSG00000120457	4.67746093	1.46E-16	7.04E-16
OSBPL6	ENSG00000079156	4.420548484	1.50E-16	7.19E-16
KCNMB3	ENSG00000171121	-3.752210873	1.50E-16	7.22E-16
AC108449.2	ENSG00000259366	-3.354588635	1.52E-16	7.30E-16
PRR33	ENSG00000283787	-6.001777781	1.52E-16	7.31E-16
CNTLN	ENSG00000044459	4.764607171	1.60E-16	7.67E-16
C18orf54	ENSG00000166845	4.250471194	1.60E-16	7.67E-16
ABHD17C	ENSG00000136379	5.367067731	1.61E-16	7.73E-16
SMCO4	ENSG00000166002	4.761868235	1.64E-16	7.85E-16
AL589935.1	ENSG00000232295	-5.653024476	1.65E-16	7.89E-16
DNAJB13	ENSG00000187726	-6.863560776	1.66E-16	7.94E-16
SATB2	ENSG00000119042	5.324608503	1.67E-16	7.95E-16
SPNS1	ENSG00000169682	-3.720249533	1.67E-16	7.98E-16
RPL14P1	ENSG00000139239	-3.102423293	1.70E-16	8.13E-16
CAPG	ENSG00000042493	4.730927432	1.75E-16	8.31E-16
SIGLEC10	ENSG00000142512	3.857310621	1.78E-16	8.49E-16
SPRN	ENSG00000203772	-4.336063395	1.80E-16	8.55E-16
CDC42EP4	ENSG00000179604	3.797863252	1.80E-16	8.57E-16
AC073548.1	ENSG00000279861	-3.840402063	1.83E-16	8.70E-16
AC010616.1	ENSG00000268041	-6.59055211	1.84E-16	8.72E-16
TRBV10-3	ENSG00000275791	-4.828118729	1.85E-16	8.75E-16
SASH1	ENSG00000111961	4.430157508	1.89E-16	8.93E-16
TBC1D12	ENSG00000108239	3.891048524	1.89E-16	8.95E-16
AC138028.2	ENSG00000224888	-6.176659349	1.90E-16	8.99E-16
GAS1	ENSG00000180447	7.449899518	1.91E-16	9.01E-16
LINC01772	ENSG00000226029	-3.404664279	1.91E-16	9.04E-16
IGFBP3	ENSG00000146674	4.893147693	1.92E-16	9.05E-16
TRBV30	ENSG00000237254	-5.35040181	1.93E-16	9.13E-16
AC084018.1	ENSG00000272849	-7.84971069	1.94E-16	9.13E-16
DSTNP1	ENSG00000230982	-6.801338199	1.96E-16	9.22E-16
MAOB	ENSG00000069535	5.670786101	1.96E-16	9.25E-16
AC018761.2	ENSG00000267062	-5.944954229	1.97E-16	9.27E-16
STON2	ENSG00000140022	5.847630886	2.13E-16	1.00E-15
DNAJB1	ENSG00000132002	-3.951803049	2.16E-16	1.01E-15
FLRT2	ENSG00000185070	5.223259915	2.17E-16	1.02E-15
JAG2	ENSG00000184916	3.683014396	2.22E-16	1.04E-15
HLA-DOA	ENSG00000204252	5.021864764	2.23E-16	1.04E-15
AC106739.1	ENSG00000274092	-7.39970748	2.26E-16	1.06E-15
ICOS	ENSG00000163600	-4.743224716	2.36E-16	1.10E-15
P2RY13	ENSG00000181631	5.861306341	2.40E-16	1.12E-15
CDK11A	ENSG00000008128	-4.03717444	2.45E-16	1.14E-15
ATP9A	ENSG00000054793	4.222485056	2.48E-16	1.15E-15
AL390208.1	ENSG00000271730	-6.215746665	2.57E-16	1.20E-15
ALDH2	ENSG00000111275	4.686405393	2.60E-16	1.21E-15
GFI1	ENSG00000162676	-3.730610074	2.62E-16	1.22E-15
KRT8P33	ENSG00000250539	-3.574153701	2.62E-16	1.22E-15
TPI1	ENSG00000111669	3.154631062	2.62E-16	1.22E-15
DLGAP4-AS1	ENSG00000232907	-3.519613782	2.69E-16	1.25E-15

AC069542.1	ENSG00000229190	-7.337335827	2.74E-16	1.27E-15
EVI5	ENSG00000067208	3.367271319	2.74E-16	1.27E-15
TYMP	ENSG00000025708	4.243959405	2.75E-16	1.28E-15
AC084018.2	ENSG00000274292	-5.35509921	2.81E-16	1.30E-15
TSHZ3	ENSG00000121297	4.943480499	2.86E-16	1.32E-15
SLC25A43	ENSG00000077713	3.720733233	2.91E-16	1.34E-15
PBX1	ENSG00000185630	3.904641794	2.93E-16	1.35E-15
ADCY6	ENSG00000174233	3.985312495	2.93E-16	1.35E-15
TSPAN9	ENSG00000011105	4.279722551	2.94E-16	1.36E-15
TEAD1	ENSG00000187079	5.093016073	2.98E-16	1.37E-15
PROCR	ENSG00000101000	3.201614039	2.99E-16	1.38E-15
ARMCX1	ENSG00000126947	3.858907033	2.99E-16	1.38E-15
ABLIM1	ENSG00000099204	-3.272749861	3.02E-16	1.39E-15
TTLL7	ENSG00000137941	6.291293456	3.02E-16	1.39E-15
AL359220.1	ENSG00000247287	-3.091272914	3.07E-16	1.41E-15
CA12	ENSG00000074410	7.44427076	3.13E-16	1.44E-15
CCDC3	ENSG00000151468	6.718437913	3.24E-16	1.49E-15
MEIS1	ENSG00000143995	4.706195028	3.26E-16	1.50E-15
DAAM2	ENSG00000146122	4.137427851	3.28E-16	1.50E-15
P4HA2	ENSG00000072682	4.799797106	3.29E-16	1.51E-15
AC104971.1	ENSG00000267226	-3.634747628	3.30E-16	1.51E-15
SEMA3F	ENSG00000001617	4.556984995	3.42E-16	1.57E-15
AC004890.2	ENSG00000244560	-3.80770223	3.50E-16	1.60E-15
CLMP	ENSG00000166250	4.133948571	3.53E-16	1.61E-15
CD6	ENSG00000013725	-4.839816564	3.53E-16	1.61E-15
MRVI1	ENSG00000072952	4.866173783	3.62E-16	1.65E-15
TANC1	ENSG00000115183	3.862709869	3.63E-16	1.66E-15
KAZN	ENSG00000189337	4.09887636	3.63E-16	1.66E-15
S100A11	ENSG00000163191	3.681531114	3.71E-16	1.69E-15
AC124283.1	ENSG00000261845	-5.722240236	3.78E-16	1.72E-15
HSPA2	ENSG00000126803	3.511390851	3.78E-16	1.72E-15
FRMD6	ENSG00000139926	4.96519212	3.89E-16	1.77E-15
NEURL1B	ENSG00000214357	5.352361759	3.90E-16	1.78E-15
SERPINE1	ENSG00000106366	4.397436467	3.96E-16	1.80E-15
PTPRK	ENSG00000152894	4.060045338	4.05E-16	1.84E-15
DEPP1	ENSG00000165507	6.296972317	4.08E-16	1.85E-15
AC008115.3	ENSG00000275560	-4.339575092	4.12E-16	1.87E-15
FAM84A	ENSG00000162981	5.638190522	4.12E-16	1.87E-15
RIC3	ENSG00000166405	-4.405870182	4.19E-16	1.90E-15
TRAV12-3	ENSG00000211794	-4.431284248	4.30E-16	1.94E-15
CHST1	ENSG00000175264	5.312240615	4.34E-16	1.96E-15
FLT3LG	ENSG00000090554	-4.975955367	4.56E-16	2.06E-15
IGSF3	ENSG00000143061	5.438083473	4.57E-16	2.06E-15
AC012615.5	ENSG00000267232	-7.85711516	4.59E-16	2.07E-15
INTS7	ENSG00000143493	3.097318116	4.79E-16	2.16E-15
MATR3	ENSG00000015479	-3.742497742	4.86E-16	2.18E-15
CCDC102B	ENSG00000150636	3.319668191	4.87E-16	2.19E-15
LIMA1	ENSG00000050405	3.179641131	4.95E-16	2.22E-15
MFAP2	ENSG00000117122	5.434607548	4.97E-16	2.23E-15
ADAMDEC1	ENSG00000134028	7.331132683	5.02E-16	2.25E-15
GREM1	ENSG00000166923	7.007235945	5.09E-16	2.28E-15

KIAA1024L	ENSG00000186367	6.984968579	5.13E-16	2.30E-15
ASS1	ENSG00000130707	5.268633879	5.22E-16	2.33E-15
AC241585.2	ENSG00000281571	-3.162068501	5.36E-16	2.40E-15
AC011466.1	ENSG00000268583	-6.506446901	5.54E-16	2.47E-15
OIP5	ENSG00000104147	3.300435313	5.79E-16	2.58E-15
LINC02381	ENSG00000250742	4.46434508	6.04E-16	2.69E-15
LAMA2	ENSG00000196569	4.584705574	6.22E-16	2.77E-15
AC008982.2	ENSG00000269688	-3.862607608	6.43E-16	2.86E-15
LAMB3	ENSG00000196878	6.292895326	6.68E-16	2.97E-15
TPST1	ENSG00000169902	3.060314266	6.68E-16	2.97E-15
CLIC2	ENSG00000155962	6.320925499	6.85E-16	3.04E-15
SPHK1	ENSG00000176170	4.322161255	6.85E-16	3.04E-15
EPS8	ENSG00000151491	3.211843859	6.88E-16	3.05E-15
AC127502.2	ENSG00000270055	-3.837548729	6.95E-16	3.08E-15
FGF7	ENSG00000140285	5.206163226	7.02E-16	3.11E-15
DPT	ENSG00000143196	5.058320737	7.29E-16	3.22E-15
TMEM150C	ENSG00000249242	4.006342399	7.40E-16	3.26E-15
CHST15	ENSG00000182022	4.241052466	7.44E-16	3.28E-15
PARM1	ENSG00000169116	5.412167215	7.56E-16	3.33E-15
TESPA1	ENSG00000135426	-3.461166779	7.68E-16	3.38E-15
YPEL2	ENSG00000175155	-3.017846209	7.82E-16	3.44E-15
FAM129B	ENSG00000136830	4.164057866	7.84E-16	3.44E-15
ARAP2	ENSG00000047365	-3.208709432	7.99E-16	3.50E-15
BMP2	ENSG00000125845	5.852532155	8.06E-16	3.53E-15
TSPAN33	ENSG00000158457	4.004952592	8.07E-16	3.54E-15
LRRC7	ENSG00000033122	-5.714927522	8.11E-16	3.55E-15
GPR161	ENSG00000143147	4.789276304	8.57E-16	3.75E-15
APLN	ENSG00000171388	5.489895786	8.70E-16	3.80E-15
MMEL1	ENSG00000142606	-3.799834111	8.89E-16	3.88E-15
IRF8	ENSG00000140968	4.448752026	8.97E-16	3.91E-15
RGL1	ENSG00000143344	4.072386081	9.18E-16	4.00E-15
AC139769.2	ENSG00000267924	-6.712321	9.19E-16	4.00E-15
DCLK1	ENSG00000133083	5.806217104	9.36E-16	4.07E-15
CKS2	ENSG00000123975	3.486897738	9.41E-16	4.09E-15
NPM1P26	ENSG00000235677	-6.773201373	9.51E-16	4.13E-15
RUSC2	ENSG00000198853	3.556150095	9.61E-16	4.17E-15
DOCK4	ENSG00000128512	3.820864896	9.66E-16	4.19E-15
GJA5	ENSG00000265107	4.878435047	9.69E-16	4.20E-15
Z98885.3	ENSG00000279345	-6.576592576	9.75E-16	4.22E-15
KIF13A	ENSG00000137177	3.313591826	9.90E-16	4.28E-15
MTFR2	ENSG00000146410	3.054059048	1.01E-15	4.36E-15
AL391863.1	ENSG00000229502	-8.180213722	1.02E-15	4.40E-15
ZNF618	ENSG00000157657	3.727906892	1.02E-15	4.41E-15
ANXA5	ENSG00000164111	3.766222176	1.03E-15	4.45E-15
PYCARD	ENSG00000103490	3.349417038	1.04E-15	4.50E-15
PRKAR2B	ENSG00000005249	3.713291898	1.05E-15	4.53E-15
SLC9A3	ENSG00000066230	-6.38272778	1.07E-15	4.63E-15
AC091564.6	ENSG00000255680	-6.642067893	1.09E-15	4.67E-15
TNFSF8	ENSG00000106952	-4.315046338	1.10E-15	4.74E-15
S100B	ENSG00000160307	4.745029026	1.11E-15	4.76E-15
MOCS1	ENSG00000124615	3.717804235	1.12E-15	4.81E-15

AC005912.1	ENSG00000227081	-3.040304357	1.16E-15	4.95E-15
TIFAB	ENSG00000255833	4.743946435	1.16E-15	4.99E-15
AC004492.1	ENSG00000272072	-3.630324735	1.17E-15	5.00E-15
FERMT1	ENSG00000101311	6.558271169	1.19E-15	5.10E-15
TRAT1	ENSG00000163519	-4.299852455	1.25E-15	5.33E-15
ECM2	ENSG00000106823	5.38565273	1.25E-15	5.33E-15
ASRGL1	ENSG00000162174	3.77870216	1.28E-15	5.45E-15
PDZRN3	ENSG00000121440	5.895157281	1.31E-15	5.57E-15
CA2	ENSG00000104267	6.256386015	1.40E-15	5.94E-15
TLDC2	ENSG00000101342	-6.22088722	1.42E-15	6.03E-15
ITGAX	ENSG00000140678	4.685339044	1.44E-15	6.09E-15
DGAT2	ENSG00000062282	5.398283567	1.46E-15	6.19E-15
MYO10	ENSG00000145555	5.785443793	1.53E-15	6.46E-15
ARMC9	ENSG00000135931	3.468837618	1.54E-15	6.52E-15
AC007878.1	ENSG00000281195	-4.707122006	1.55E-15	6.52E-15
BLNK	ENSG00000095585	4.69796305	1.56E-15	6.56E-15
AC099811.1	ENSG00000236194	-5.559822102	1.57E-15	6.62E-15
EPDR1	ENSG00000086289	5.543032493	1.58E-15	6.67E-15
IPCEF1	ENSG00000074706	-3.96392667	1.63E-15	6.85E-15
BICDL1	ENSG00000135127	-3.179910246	1.67E-15	7.01E-15
NOTCH4	ENSG00000204301	3.339455635	1.69E-15	7.10E-15
AC012254.3	ENSG00000267724	-5.694251484	1.74E-15	7.33E-15
LGI2	ENSG00000153012	5.47164499	1.81E-15	7.60E-15
DDIT4-AS1	ENSG00000269926	-9.93187118	1.81E-15	7.60E-15
SLC2A5	ENSG00000142583	4.571485912	1.87E-15	7.82E-15
RPS7P1	ENSG00000263266	-3.735402435	1.89E-15	7.91E-15
ANKRD22	ENSG00000152766	5.351507263	1.90E-15	7.93E-15
ITPRIPL2	ENSG00000205730	4.738468848	1.92E-15	8.02E-15
AC104581.4	ENSG00000280046	-5.054760726	1.94E-15	8.10E-15
DEGS2	ENSG00000168350	-3.966660231	2.01E-15	8.39E-15
AC000068.3	ENSG00000273300	-5.039478401	2.02E-15	8.41E-15
HLA-DQA1	ENSG00000196735	7.705009301	2.04E-15	8.51E-15
EPB41L1	ENSG00000088367	4.110770623	2.13E-15	8.86E-15
CYP7B1	ENSG00000172817	4.577796611	2.17E-15	9.00E-15
COL7A1	ENSG00000114270	4.20124649	2.19E-15	9.10E-15
VIPR1-AS1	ENSG00000232354	-7.610258363	2.20E-15	9.14E-15
CSF2RA	ENSG00000198223	4.218748798	2.22E-15	9.19E-15
ABCC2	ENSG00000023839	-3.526452014	2.23E-15	9.23E-15
GATM	ENSG00000171766	5.130803789	2.23E-15	9.25E-15
VAV2	ENSG00000160293	3.802114989	2.25E-15	9.30E-15
EBF1	ENSG00000164330	5.039341315	2.28E-15	9.41E-15
SPOCK2	ENSG00000107742	-3.33560715	2.34E-15	9.68E-15
ACPP	ENSG00000014257	5.076062134	2.36E-15	9.74E-15
PSD	ENSG00000059915	-3.085942063	2.41E-15	9.95E-15
AC091814.1	ENSG00000255882	-5.175204456	2.43E-15	1.00E-14
AC026470.2	ENSG00000261267	-6.72640548	2.45E-15	1.01E-14
ANKRD29	ENSG00000154065	5.095116823	2.50E-15	1.03E-14
BCL11B	ENSG00000127152	-3.026853315	2.51E-15	1.03E-14
AC116158.1	ENSG00000259326	-6.444047989	2.51E-15	1.03E-14
CTNNA1	ENSG00000044115	3.801469147	2.61E-15	1.07E-14
CAVIN2	ENSG00000168497	4.649424933	2.73E-15	1.12E-14

HR	ENSG00000168453	5.31367808	2.77E-15	1.13E-14
MAGI1	ENSG00000151276	5.287006504	2.78E-15	1.14E-14
HOXA10	ENSG00000253293	6.24009498	2.81E-15	1.15E-14
IGHD	ENSG00000211898	4.578053855	2.85E-15	1.16E-14
KCNMA1	ENSG00000156113	6.911971879	2.86E-15	1.17E-14
HLA-DRB1	ENSG00000196126	6.553438301	2.90E-15	1.18E-14
SGIP1	ENSG00000118473	4.484097443	2.91E-15	1.19E-14
RHOC	ENSG00000155366	3.495858846	2.93E-15	1.19E-14
CICP14	ENSG00000281490	-8.627386423	2.97E-15	1.21E-14
AC055748.1	ENSG00000244720	-3.576667772	3.16E-15	1.28E-14
ALOX12	ENSG00000108839	-4.912154122	3.22E-15	1.31E-14
FOXD1	ENSG00000251493	5.411249642	3.23E-15	1.31E-14
CERKL	ENSG00000188452	-7.955840951	3.24E-15	1.31E-14
FJX1	ENSG00000179431	4.846992635	3.24E-15	1.32E-14
FGF2	ENSG00000138685	4.728177516	3.29E-15	1.34E-14
MMP15	ENSG00000102996	3.180360181	3.41E-15	1.38E-14
SLC39A14	ENSG00000104635	3.156152015	3.48E-15	1.41E-14
TRBV7-2	ENSG00000282939	-4.751294737	3.55E-15	1.43E-14
JADE3	ENSG00000102221	5.654236929	3.56E-15	1.44E-14
TNNT3	ENSG00000130595	-4.956888139	3.58E-15	1.45E-14
LINC01422	ENSG00000223704	-4.058597623	3.67E-15	1.48E-14
RPL39L	ENSG00000163923	3.450437159	3.74E-15	1.51E-14
TRBV6-6	ENSG00000211724	-4.16064724	3.80E-15	1.53E-14
ASAP3	ENSG00000088280	3.258015339	3.85E-15	1.55E-14
AP000977.1	ENSG00000246790	-5.422221048	3.87E-15	1.55E-14
NME1	ENSG00000239672	3.310336384	3.89E-15	1.56E-14
C11orf96	ENSG00000187479	5.046933352	4.02E-15	1.62E-14
GAB1	ENSG00000109458	4.681912356	4.12E-15	1.65E-14
MSRB2	ENSG00000148450	3.812083142	4.16E-15	1.67E-14
SOX9	ENSG00000125398	5.956457019	4.26E-15	1.70E-14
EZH2	ENSG00000106462	3.285751087	4.37E-15	1.75E-14
BMP1	ENSG00000168487	3.291753523	4.46E-15	1.78E-14
AP001486.2	ENSG00000260966	-3.122903123	4.54E-15	1.81E-14
SDC4	ENSG00000124145	3.738801627	4.55E-15	1.81E-14
PDE4D	ENSG00000113448	-3.524837067	4.66E-15	1.85E-14
ARHGEF15	ENSG00000198844	4.036036758	4.73E-15	1.88E-14
DBN1	ENSG00000113758	4.515400302	4.84E-15	1.92E-14
ALDH7A1	ENSG00000164904	3.275831202	5.06E-15	2.01E-14
ATP10D	ENSG00000145246	3.444313023	5.16E-15	2.05E-14
AC010343.1	ENSG00000240376	-3.068960171	5.26E-15	2.08E-14
CD109	ENSG00000156535	3.520264261	5.34E-15	2.11E-14
WNT5A	ENSG00000114251	5.933029909	5.35E-15	2.12E-14
AOX1	ENSG00000138356	5.518761096	5.37E-15	2.12E-14
HECW2	ENSG00000138411	3.720453782	5.55E-15	2.19E-14
TRAV8-6	ENSG00000211795	-4.174428564	5.58E-15	2.20E-14
DZIP1	ENSG00000134874	5.578370329	5.60E-15	2.21E-14
AP006284.1	ENSG00000254815	-3.632412127	5.64E-15	2.22E-14
TRIP10	ENSG00000125733	3.246109598	5.87E-15	2.31E-14
FAM84B	ENSG00000168672	-3.423834993	5.96E-15	2.34E-14
CREB3L1	ENSG00000157613	5.161966762	6.02E-15	2.37E-14
EVA1B	ENSG00000142694	3.577392867	6.20E-15	2.44E-14

AC027290.2	ENSG00000280138	-4.815517883	6.25E-15	2.46E-14
AIF1	ENSG00000204472	3.643397145	6.27E-15	2.46E-14
SPATS2L	ENSG00000196141	4.140599023	6.31E-15	2.48E-14
PTPN14	ENSG00000152104	5.20075468	6.47E-15	2.54E-14
CD36	ENSG00000135218	5.452984826	6.55E-15	2.57E-14
SCD5	ENSG00000145284	4.254640297	6.75E-15	2.64E-14
CACNB2	ENSG00000165995	-3.212982381	6.90E-15	2.69E-14
PLD1	ENSG00000075651	5.296616599	7.06E-15	2.75E-14
AL161787.1	ENSG00000219928	-6.392576909	7.63E-15	2.97E-14
AC093525.8	ENSG00000279520	-4.129015365	7.72E-15	3.00E-14
RN7SL834P	ENSG00000243650	-3.641329384	7.93E-15	3.08E-14
APC2	ENSG00000115266	-4.366132742	8.04E-15	3.12E-14
TMEM44	ENSG00000145014	3.322938908	8.13E-15	3.15E-14
VASN	ENSG00000168140	3.727221899	8.18E-15	3.17E-14
ASAP2	ENSG00000151693	4.607438361	8.22E-15	3.19E-14
PGF	ENSG00000119630	3.055063859	8.27E-15	3.20E-14
PDIA5	ENSG00000065485	3.289694965	8.29E-15	3.21E-14
AC010768.1	ENSG00000254693	-6.707857817	8.45E-15	3.27E-14
AL035530.2	ENSG00000271913	-6.530341146	8.57E-15	3.31E-14
C5orf30	ENSG00000181751	3.478034819	8.89E-15	3.43E-14
AC080112.1	ENSG00000266208	3.038714999	8.91E-15	3.44E-14
F2RL2	ENSG00000164220	4.772940936	9.00E-15	3.47E-14
REXO5	ENSG00000005189	3.620194113	9.17E-15	3.53E-14
CTSL	ENSG00000135047	3.756879547	9.19E-15	3.54E-14
AC091887.1	ENSG00000251556	-5.122780689	9.22E-15	3.55E-14
STEAP4	ENSG00000127954	6.617252112	9.73E-15	3.73E-14
TRBV18	ENSG00000276557	-4.856715435	9.75E-15	3.74E-14
BOC	ENSG00000144857	3.514193232	1.04E-14	3.96E-14
ADAMTS9	ENSG00000163638	4.615645672	1.04E-14	3.98E-14
RNF43	ENSG00000108375	-3.381273603	1.05E-14	4.00E-14
RF00019	ENSG00000252759	-5.626380043	1.05E-14	4.03E-14
CEBPD	ENSG00000221869	5.225852628	1.07E-14	4.08E-14
TFAP2C	ENSG00000087510	4.65107127	1.08E-14	4.13E-14
AD000671.3	ENSG00000267439	-5.619534414	1.10E-14	4.19E-14
SERPINA1	ENSG00000197249	6.847539901	1.10E-14	4.21E-14
RALB	ENSG00000144118	3.243197895	1.13E-14	4.29E-14
FERMT2	ENSG00000073712	3.393253078	1.13E-14	4.30E-14
SELENOP	ENSG00000250722	4.853910984	1.13E-14	4.31E-14
PCDH1	ENSG00000156453	4.513982209	1.13E-14	4.31E-14
TIE1	ENSG00000066056	3.403969944	1.14E-14	4.32E-14
AC099489.1	ENSG00000188897	-4.40513641	1.20E-14	4.55E-14
MYCN	ENSG00000134323	5.115740826	1.23E-14	4.67E-14
PLCG2	ENSG00000197943	3.667874035	1.24E-14	4.70E-14
LONRF3	ENSG00000175556	-3.999443841	1.25E-14	4.73E-14
HGD	ENSG00000113924	-4.592415916	1.25E-14	4.73E-14
SIX5	ENSG00000177045	3.058503045	1.25E-14	4.73E-14
CIB2	ENSG00000136425	3.204939668	1.27E-14	4.79E-14
FLT1	ENSG00000102755	3.658964021	1.30E-14	4.91E-14
ABLIM3	ENSG00000173210	5.1245419	1.30E-14	4.92E-14
VANGL1	ENSG00000173218	3.361391277	1.34E-14	5.06E-14
TFAP2A	ENSG00000137203	5.639013135	1.36E-14	5.09E-14

RPL39P3	ENSG00000235174	-3.483778584	1.39E-14	5.22E-14
AL109955.1	ENSG00000218018	-5.953399866	1.42E-14	5.35E-14
GPX3	ENSG00000211445	3.717875267	1.44E-14	5.41E-14
TRBV5-4	ENSG00000230099	-4.11571236	1.48E-14	5.56E-14
AL139423.1	ENSG00000272078	-6.850723761	1.52E-14	5.69E-14
LAT	ENSG00000213658	-4.008313908	1.53E-14	5.72E-14
COL27A1	ENSG00000196739	3.170465483	1.58E-14	5.89E-14
MPZL2	ENSG00000149573	4.122023911	1.58E-14	5.91E-14
CREB5	ENSG00000146592	4.199630653	1.58E-14	5.91E-14
NCALD	ENSG00000104490	4.041251761	1.61E-14	6.01E-14
FAM107A	ENSG00000168309	4.396283636	1.65E-14	6.16E-14
LINC00888	ENSG00000240024	3.239182782	1.71E-14	6.35E-14
TEX52	ENSG00000283297	-6.677089134	1.73E-14	6.42E-14
SBK1	ENSG00000188322	-3.031645038	1.78E-14	6.62E-14
AP003717.1	ENSG00000255847	-4.709051703	1.79E-14	6.64E-14
IL1RN	ENSG00000136689	4.795084801	1.83E-14	6.78E-14
TRBV19	ENSG00000211746	-4.909714368	1.88E-14	6.96E-14
SLC7A7	ENSG00000155465	3.318238748	1.88E-14	6.98E-14
RPS3AP6	ENSG00000234797	-3.065097126	1.88E-14	6.98E-14
CXCL10	ENSG00000169245	7.348582255	1.88E-14	6.98E-14
AL513190.1	ENSG00000278831	-4.828438434	1.90E-14	7.02E-14
TSPAN13	ENSG00000106537	4.449224326	1.90E-14	7.04E-14
C19orf71	ENSG00000183397	-4.136545121	1.90E-14	7.04E-14
IGSF6	ENSG00000140749	3.153411482	1.94E-14	7.16E-14
AC099560.2	ENSG00000234287	-3.449301347	1.95E-14	7.20E-14
HOXC9	ENSG00000180806	5.108578552	2.01E-14	7.43E-14
AL390195.2	ENSG00000260948	-3.373276416	2.03E-14	7.47E-14
CHST2	ENSG00000175040	3.672878694	2.08E-14	7.66E-14
SGCE	ENSG00000127990	3.450099602	2.11E-14	7.78E-14
AC009318.1	ENSG00000257176	-3.027791659	2.15E-14	7.92E-14
CCND2-AS1	ENSG00000255920	-4.8680949	2.23E-14	8.20E-14
LINC00304	ENSG00000180422	-5.711923189	2.26E-14	8.29E-14
DLGAP1-AS2	ENSG00000262001	-3.003338626	2.29E-14	8.39E-14
IDI2-AS1	ENSG00000232656	-8.297470402	2.32E-14	8.49E-14
IGKC	ENSG00000211592	8.702604886	2.43E-14	8.87E-14
ADPRH	ENSG00000144843	4.104859262	2.44E-14	8.93E-14
AC092143.2	ENSG00000259006	-5.064119309	2.51E-14	9.18E-14
NECTIN1	ENSG00000110400	4.320671894	2.58E-14	9.41E-14
AC008555.5	ENSG00000271109	-4.137402475	2.62E-14	9.54E-14
CCDC170	ENSG00000120262	4.045068673	2.72E-14	9.90E-14
ADAM28	ENSG00000042980	4.4330835	2.72E-14	9.91E-14
GLT8D2	ENSG00000120820	3.463323109	2.81E-14	1.02E-13
RNF157-AS1	ENSG00000267128	-5.908236351	2.83E-14	1.03E-13
SERINC2	ENSG00000168528	3.965690437	2.86E-14	1.04E-13
OSCAR	ENSG00000170909	3.26873148	3.00E-14	1.09E-13
DTX4	ENSG00000110042	3.032482108	3.01E-14	1.09E-13
MERTK	ENSG00000153208	4.403573665	3.02E-14	1.09E-13
SPIRE1	ENSG00000134278	3.034047009	3.12E-14	1.13E-13
DUSP16	ENSG00000111266	-3.053758508	3.19E-14	1.15E-13
SMIM10	ENSG00000184785	5.501469778	3.19E-14	1.15E-13
RIMS3	ENSG00000117016	3.126780189	3.20E-14	1.15E-13

DBH	ENSG00000123454	-7.747867214	3.27E-14	1.18E-13
RAB13	ENSG00000143545	5.570780206	3.29E-14	1.18E-13
TLR8	ENSG00000101916	4.625076963	3.35E-14	1.20E-13
AC099336.2	ENSG00000236439	-5.61077577	3.44E-14	1.24E-13
WWC1	ENSG00000113645	3.222386097	3.44E-14	1.24E-13
AP000254.1	ENSG00000273271	-3.171064676	3.54E-14	1.27E-13
DIABLO	ENSG00000184047	-3.019365122	3.57E-14	1.28E-13
CFAP126	ENSG00000188931	-5.625099906	3.59E-14	1.29E-13
AC007969.1	ENSG00000233762	-3.964062249	3.61E-14	1.29E-13
CFAP70	ENSG00000156042	-3.156184484	3.63E-14	1.30E-13
AC022113.1	ENSG00000246214	-6.66455242	3.63E-14	1.30E-13
AC090616.6	ENSG00000278867	-3.886573033	3.68E-14	1.32E-13
FAM166A	ENSG00000188163	-4.792581392	3.78E-14	1.35E-13
CX3CL1	ENSG00000006210	4.469534717	3.85E-14	1.38E-13
AC138028.4	ENSG00000260121	-6.695451151	3.86E-14	1.38E-13
BCL11A	ENSG00000119866	3.684184855	3.89E-14	1.39E-13
ADM	ENSG00000148926	4.562461329	4.00E-14	1.43E-13
INHBB	ENSG00000163083	4.41996689	4.07E-14	1.45E-13
CCL8	ENSG00000108700	5.162131845	4.38E-14	1.55E-13
NUAK1	ENSG00000074590	4.995397951	4.39E-14	1.56E-13
FGD2	ENSG00000146192	4.36269143	4.46E-14	1.58E-13
RTN1	ENSG00000139970	5.474093533	4.53E-14	1.60E-13
LIPG	ENSG00000101670	3.690159749	4.60E-14	1.63E-13
PLA2G7	ENSG00000146070	5.570586843	4.63E-14	1.64E-13
EGFR	ENSG00000146648	5.973386273	4.67E-14	1.65E-13
TMEM269	ENSG00000274386	-3.392333849	4.71E-14	1.67E-13
ETV1	ENSG00000006468	6.687067751	4.91E-14	1.73E-13
FOXP2	ENSG00000128573	6.266697272	4.92E-14	1.74E-13
AK4	ENSG00000162433	5.488655009	4.94E-14	1.74E-13
LINC01215	ENSG00000271856	-3.690495342	4.95E-14	1.75E-13
NXN	ENSG00000167693	4.145257596	5.07E-14	1.79E-13
HMGN2P3	ENSG00000230330	3.025102215	5.39E-14	1.89E-13
CXCL9	ENSG00000138755	9.905061527	5.40E-14	1.90E-13
CCBE1	ENSG00000183287	4.017600474	5.44E-14	1.91E-13
PECAM1	ENSG00000261371	3.992828981	5.45E-14	1.92E-13
SERPINE2	ENSG00000135919	4.635047261	5.51E-14	1.93E-13
RNF208	ENSG00000212864	3.726825637	5.54E-14	1.94E-13
OVGP1	ENSG00000085465	-3.346402626	5.62E-14	1.97E-13
CDK14	ENSG00000058091	4.677805389	5.73E-14	2.01E-13
AC010653.2	ENSG00000279592	-6.428952923	5.74E-14	2.01E-13
ROR2	ENSG00000169071	4.81917579	6.15E-14	2.15E-13
MSC-AS1	ENSG00000235531	4.220288613	6.24E-14	2.18E-13
UBE2E2	ENSG00000182247	3.114898301	6.46E-14	2.25E-13
AC135983.2	ENSG00000223509	-3.678377627	6.80E-14	2.36E-13
RNF125	ENSG00000101695	-3.435289874	7.01E-14	2.43E-13
BX679664.3	ENSG00000244716	-3.131843891	7.58E-14	2.62E-13
PTGS1	ENSG00000095303	4.798006405	7.59E-14	2.63E-13
IL24	ENSG00000162892	-7.26245105	7.67E-14	2.65E-13
ZC3H12C	ENSG00000149289	4.792875082	7.80E-14	2.70E-13
AC007540.1	ENSG00000257579	-6.845113052	7.96E-14	2.75E-13
ZNF256	ENSG00000152454	-3.135068078	8.25E-14	2.84E-13

CMBL	ENSG00000164237	4.48996105	8.33E-14	2.87E-13
MOCOS	ENSG00000075643	4.574585406	8.35E-14	2.88E-13
NFIX	ENSG00000008441	4.421216792	8.38E-14	2.88E-13
CYB5D1	ENSG00000182224	-3.002066807	8.60E-14	2.95E-13
TMEM158	ENSG00000249992	5.95780087	8.85E-14	3.04E-13
AC092645.1	ENSG00000278962	-4.29635152	8.87E-14	3.04E-13
MPST	ENSG00000128309	3.743702567	8.91E-14	3.06E-13
AL022328.3	ENSG00000273188	-6.70644756	8.97E-14	3.07E-13
DSG3	ENSG00000134757	7.807923981	9.01E-14	3.08E-13
CPA3	ENSG00000163751	6.098895826	9.16E-14	3.13E-13
IQCN	ENSG00000130518	-3.353653669	9.38E-14	3.21E-13
SEMA3C	ENSG00000075223	5.814629501	9.44E-14	3.22E-13
HLA-J	ENSG00000204622	-4.513684854	9.66E-14	3.30E-13
NLGN4X	ENSG00000146938	4.148630585	9.71E-14	3.31E-13
TSPAN7	ENSG00000156298	4.66047595	9.78E-14	3.33E-13
SFRP2	ENSG00000145423	8.326642584	9.97E-14	3.39E-13
Sep-04	ENSG00000108387	3.5201579	1.02E-13	3.48E-13
GRAP2	ENSG00000100351	-3.441914732	1.04E-13	3.53E-13
AC090948.2	ENSG00000272498	-4.759745568	1.05E-13	3.56E-13
CYP2D6	ENSG00000100197	-4.016766047	1.05E-13	3.56E-13
VSIG4	ENSG00000155659	6.269389417	1.05E-13	3.57E-13
KCNAB1	ENSG00000169282	-3.28832884	1.10E-13	3.73E-13
IL18	ENSG00000150782	5.60014594	1.11E-13	3.78E-13
NKD2	ENSG00000145506	4.218650747	1.13E-13	3.82E-13
CHI3L1	ENSG00000133048	6.811182773	1.17E-13	3.94E-13
RCAN2	ENSG00000172348	6.872281569	1.19E-13	4.01E-13
P2RY10	ENSG00000078589	-3.008157385	1.21E-13	4.07E-13
CYP1B1	ENSG00000138061	6.481665023	1.23E-13	4.15E-13
COL9A2	ENSG00000049089	3.654765016	1.24E-13	4.18E-13
PASK	ENSG00000115687	-3.037743579	1.26E-13	4.25E-13
KCND3	ENSG00000171385	3.876438785	1.28E-13	4.32E-13
ARMH4	ENSG00000139971	4.694266885	1.31E-13	4.42E-13
PYGO1	ENSG00000171016	5.751006603	1.32E-13	4.43E-13
MIAT	ENSG00000225783	-5.140741527	1.33E-13	4.48E-13
LARGE1	ENSG00000133424	4.815669122	1.35E-13	4.52E-13
PODN	ENSG00000174348	5.877673229	1.37E-13	4.58E-13
TEAD3	ENSG00000007866	3.650906147	1.37E-13	4.60E-13
SAMD11	ENSG00000187634	-3.070931324	1.38E-13	4.64E-13
IL4I1	ENSG00000104951	4.986830885	1.39E-13	4.66E-13
MMP11	ENSG00000099953	4.594908406	1.40E-13	4.71E-13
FAM167A	ENSG00000154319	3.854007772	1.43E-13	4.77E-13
WDFY4	ENSG00000128815	5.054312287	1.43E-13	4.78E-13
OR10AH1P	ENSG00000272595	-6.149823519	1.43E-13	4.79E-13
KL	ENSG00000133116	4.331283978	1.43E-13	4.79E-13
SYNPO2	ENSG00000172403	3.504958894	1.43E-13	4.79E-13
FPR1	ENSG00000171051	4.673137368	1.45E-13	4.85E-13
AL109930.1	ENSG00000271774	-6.611529764	1.47E-13	4.90E-13
PCDH17	ENSG00000118946	5.679433221	1.52E-13	5.08E-13
SLC2A6	ENSG00000160326	3.002300329	1.54E-13	5.14E-13
AC127502.1	ENSG00000215302	-3.782256776	1.55E-13	5.16E-13
ARHGAP10	ENSG00000071205	3.074918974	1.58E-13	5.25E-13

BVES	ENSG00000112276	6.522535809	1.65E-13	5.49E-13
FAM49A	ENSG00000197872	3.917731777	1.71E-13	5.68E-13
IER5L	ENSG00000188483	3.387679392	1.71E-13	5.69E-13
TRBV28	ENSG00000211753	-4.290709213	1.75E-13	5.80E-13
CD180	ENSG00000134061	4.996903348	1.75E-13	5.81E-13
ZC3H12B	ENSG00000102053	-3.667471685	1.77E-13	5.86E-13
HOXA7	ENSG00000122592	6.549227139	1.83E-13	6.06E-13
PACSIN3	ENSG00000165912	3.419958314	1.84E-13	6.08E-13
KIAA1217	ENSG00000120549	6.200508329	1.87E-13	6.17E-13
MXRA8	ENSG00000162576	3.719524598	1.88E-13	6.22E-13
CD69	ENSG00000110848	-4.534107867	1.91E-13	6.29E-13
F13A1	ENSG00000124491	7.930744005	1.96E-13	6.47E-13
PLAUR	ENSG00000011422	3.510823049	1.97E-13	6.51E-13
LHX4	ENSG00000121454	-5.624157265	2.06E-13	6.79E-13
TEAD4	ENSG00000197905	4.239262264	2.07E-13	6.80E-13
DNM1	ENSG00000106976	3.040028998	2.18E-13	7.16E-13
HSD3B7	ENSG00000099377	3.978434447	2.22E-13	7.28E-13
IL1R1	ENSG00000115594	5.198649378	2.24E-13	7.34E-13
FXYD7	ENSG00000221946	-4.203385711	2.27E-13	7.45E-13
XG	ENSG00000124343	3.749951949	2.28E-13	7.48E-13
TENM1	ENSG00000009694	-5.461928897	2.30E-13	7.54E-13
ITGA6-AS1	ENSG00000232788	-4.08485428	2.33E-13	7.63E-13
GAS2L1	ENSG00000185340	3.725765938	2.42E-13	7.93E-13
CFD	ENSG00000197766	4.743054667	2.52E-13	8.21E-13
FZD7	ENSG00000155760	3.879072075	2.55E-13	8.30E-13
KLHL23	ENSG00000213160	4.282561066	2.60E-13	8.46E-13
SORD	ENSG00000140263	3.112535549	2.67E-13	8.70E-13
ME1	ENSG00000065833	4.553989171	2.74E-13	8.92E-13
AC136475.3	ENSG00000255026	-5.954434961	2.79E-13	9.08E-13
CPED1	ENSG00000106034	5.119765537	2.80E-13	9.11E-13
PTPRF	ENSG00000142949	6.356682515	2.95E-13	9.56E-13
CASKIN1	ENSG00000167971	-3.984114337	2.95E-13	9.57E-13
PPM1H	ENSG00000111110	6.617299229	2.99E-13	9.68E-13
SH3GL1P1	ENSG00000266777	-3.037129191	3.08E-13	9.96E-13
AC119044.1	ENSG00000258352	-3.41162668	3.11E-13	1.01E-12
AC011379.2	ENSG00000254363	-3.426414528	3.29E-13	1.06E-12
FAM20A	ENSG00000108950	3.523725686	3.34E-13	1.08E-12
TRAV13-1	ENSG00000211788	-3.809323623	3.36E-13	1.08E-12
AP000787.1	ENSG00000245552	-3.30932486	3.39E-13	1.09E-12
PDGFA	ENSG00000197461	5.040839629	3.51E-13	1.13E-12
LINC01605	ENSG00000253161	4.688656025	3.69E-13	1.18E-12
TDO2	ENSG00000151790	6.969728168	3.75E-13	1.20E-12
ERN1	ENSG00000178607	-3.316103389	3.85E-13	1.23E-12
AC096921.2	ENSG00000261468	-4.693541258	3.87E-13	1.24E-12
SERPINB5	ENSG00000206075	6.658745434	3.90E-13	1.25E-12
LINGO3	ENSG00000220008	-5.465206131	3.99E-13	1.27E-12
ERMN	ENSG00000136541	-4.884293841	4.06E-13	1.29E-12
OPLAH	ENSG00000178814	3.685148098	4.21E-13	1.34E-12
AC125611.3	ENSG00000258232	-6.351081909	4.24E-13	1.35E-12
AL590867.2	ENSG00000218426	-3.623457714	4.25E-13	1.35E-12
CCDC74A	ENSG00000163040	4.517422072	4.27E-13	1.36E-12

AL137145.1	ENSG00000212743	-4.152993176	4.30E-13	1.36E-12
C3orf35	ENSG00000198590	-3.328581955	4.43E-13	1.40E-12
SKAP2	ENSG00000005020	3.666270311	4.48E-13	1.42E-12
KHDRBS3	ENSG00000131773	6.952517802	4.51E-13	1.43E-12
SLC7A8	ENSG00000092068	3.574557217	4.54E-13	1.44E-12
PGGHG	ENSG00000142102	-3.097451162	4.62E-13	1.46E-12
LAMA3	ENSG00000053747	5.201019683	4.67E-13	1.48E-12
AC246817.2	ENSG00000254319	4.715969825	4.71E-13	1.49E-12
PARD3B	ENSG00000116117	3.435547084	4.76E-13	1.50E-12
NR3C2	ENSG00000151623	-3.624439131	4.79E-13	1.51E-12
CHRD	ENSG00000090539	4.570249389	5.14E-13	1.62E-12
TNFRSF19	ENSG00000127863	5.588894668	5.33E-13	1.68E-12
ST5	ENSG00000166444	3.322532319	5.40E-13	1.70E-12
AC003102.1	ENSG00000260793	-3.296247389	5.66E-13	1.78E-12
NKD1	ENSG00000140807	-3.309451494	5.67E-13	1.78E-12
PPT2-EGFL8	ENSG00000258388	-6.089374209	5.80E-13	1.82E-12
GIMAP5	ENSG00000196329	-4.823315843	6.04E-13	1.89E-12
CALHM6	ENSG00000188820	4.223375559	6.12E-13	1.91E-12
EGFL6	ENSG00000198759	5.267959559	6.21E-13	1.94E-12
SPON1-AS1	ENSG00000254418	-5.868470271	6.49E-13	2.02E-12
METTL7A	ENSG00000185432	3.743375227	6.75E-13	2.10E-12
WHAMMP3	ENSG00000276141	-3.297859762	6.77E-13	2.11E-12
TERT	ENSG00000164362	4.192125703	7.25E-13	2.25E-12
DSC2	ENSG00000134755	6.148065174	7.53E-13	2.34E-12
THSD4	ENSG00000187720	3.932353952	7.81E-13	2.42E-12
TMEM56	ENSG00000152078	5.346019363	7.98E-13	2.47E-12
AGRN	ENSG00000188157	3.00293008	8.13E-13	2.51E-12
AC006460.1	ENSG00000228509	-4.669856918	8.19E-13	2.53E-12
MMP12	ENSG00000262406	6.190263615	8.21E-13	2.54E-12
TACC2	ENSG00000138162	3.836896589	8.22E-13	2.54E-12
MYO6	ENSG00000196586	3.676975486	8.31E-13	2.56E-12
AL096816.1	ENSG00000280135	-5.211899514	8.42E-13	2.60E-12
ZNF831	ENSG00000124203	-3.426452143	8.53E-13	2.63E-12
TACSTD2	ENSG00000184292	6.028370353	8.74E-13	2.69E-12
MFAP5	ENSG00000197614	5.801934097	8.77E-13	2.70E-12
GEM	ENSG00000164949	3.110781819	8.91E-13	2.74E-12
AC012507.1	ENSG00000230385	-5.843630897	9.19E-13	2.82E-12
FCGR3A	ENSG00000203747	5.46078916	9.25E-13	2.84E-12
ACKR3	ENSG00000144476	3.508751586	9.27E-13	2.85E-12
COL4A4	ENSG00000081052	4.062853588	9.31E-13	2.86E-12
PLCL1	ENSG00000115896	-3.322980988	9.35E-13	2.87E-12
OVCH1-AS1	ENSG00000257599	-4.115368575	1.01E-12	3.08E-12
AC090948.1	ENSG00000271964	-5.045948235	1.01E-12	3.08E-12
AL162151.2	ENSG00000234648	-5.93957923	1.02E-12	3.11E-12
CLCA2	ENSG00000137975	6.740076539	1.06E-12	3.23E-12
NAV2	ENSG00000166833	3.037555836	1.07E-12	3.25E-12
CGN	ENSG00000143375	3.065448787	1.08E-12	3.30E-12
LCK	ENSG00000182866	-3.271891242	1.13E-12	3.42E-12
TPT1P9	ENSG00000234782	-4.115314129	1.17E-12	3.54E-12
IRAK3	ENSG00000090376	4.362715036	1.18E-12	3.60E-12
B4GALNT1	ENSG00000135454	5.348192953	1.19E-12	3.62E-12

XCR1	ENSG00000173578	3.814479425	1.26E-12	3.80E-12
PHLDA2	ENSG00000181649	4.117151471	1.26E-12	3.80E-12
AP005899.1	ENSG00000263847	-8.85105412	1.27E-12	3.83E-12
KCNK1	ENSG00000135750	4.371528328	1.31E-12	3.95E-12
CD52	ENSG00000169442	-3.093033862	1.32E-12	3.97E-12
FBXO17	ENSG00000269190	6.198596757	1.36E-12	4.08E-12
MAP7	ENSG00000135525	3.11456923	1.37E-12	4.13E-12
SEMA6B	ENSG00000167680	3.473762413	1.40E-12	4.20E-12
STARD8	ENSG00000130052	3.394271971	1.40E-12	4.20E-12
PRR7-AS1	ENSG00000246334	-6.188516231	1.43E-12	4.30E-12
ANKRD18B	ENSG00000230453	6.642192706	1.43E-12	4.30E-12
DDN-AS1	ENSG00000257913	-3.457378811	1.44E-12	4.31E-12
ITGBL1	ENSG00000198542	5.2837292	1.44E-12	4.32E-12
HSPA4L	ENSG00000164070	3.561078868	1.46E-12	4.36E-12
MATN2	ENSG00000132561	3.156192814	1.50E-12	4.50E-12
S100A14	ENSG00000189334	6.420687903	1.52E-12	4.55E-12
ID1	ENSG00000125968	3.521593561	1.53E-12	4.57E-12
AC026748.1	ENSG00000279908	-4.231835001	1.58E-12	4.72E-12
TRBV9	ENSG00000211716	-3.451492351	1.59E-12	4.73E-12
RASSF1-AS1	ENSG00000281358	-3.161663553	1.59E-12	4.75E-12
HDGFL3	ENSG00000166503	4.266973282	1.61E-12	4.81E-12
CD5	ENSG00000110448	-4.30995096	1.63E-12	4.87E-12
PRKXP1	ENSG00000259205	-4.067825115	1.64E-12	4.87E-12
CD24	ENSG00000272398	5.665061255	1.65E-12	4.90E-12
ZNF135	ENSG00000176293	-4.086569651	1.68E-12	4.99E-12
TSPAN15	ENSG00000099282	3.87674103	1.74E-12	5.16E-12
VSIG1	ENSG00000101842	-4.648282396	1.87E-12	5.53E-12
RPL3P4	ENSG00000232573	-3.181872737	1.89E-12	5.59E-12
CACNA1I	ENSG00000100346	-6.860233732	1.97E-12	5.82E-12
INHBA	ENSG00000122641	6.909387471	2.04E-12	6.01E-12
DOCK5	ENSG00000147459	3.145429074	2.09E-12	6.16E-12
BEX2	ENSG00000133134	-4.018449315	2.11E-12	6.22E-12
DOK3	ENSG00000146094	4.25625197	2.12E-12	6.25E-12
AC116533.1	ENSG00000244398	-3.064994484	2.12E-12	6.25E-12
TRBV7-9	ENSG00000278030	-3.947474025	2.16E-12	6.35E-12
ITGA4	ENSG00000115232	-3.032055752	2.19E-12	6.43E-12
TNFAIP6	ENSG00000123610	5.11230965	2.25E-12	6.60E-12
DSG2	ENSG00000046604	5.811070625	2.27E-12	6.66E-12
TRBV20-1	ENSG00000211747	-4.145720981	2.35E-12	6.88E-12
RPS27AP16	ENSG00000224631	-3.230628024	2.48E-12	7.27E-12
DNASE1L3	ENSG00000163687	4.221217798	2.50E-12	7.32E-12
MDK	ENSG00000110492	3.450860246	2.51E-12	7.33E-12
TNFAIP3	ENSG00000118503	-3.391782674	2.54E-12	7.42E-12
PLCXD2	ENSG00000240891	-3.524021845	2.57E-12	7.50E-12
EPB41L3	ENSG00000082397	3.53124418	2.64E-12	7.71E-12
SCN9A	ENSG00000169432	4.747532563	2.68E-12	7.81E-12
SLC7A11	ENSG00000151012	4.705463266	2.88E-12	8.37E-12
WNT4	ENSG00000162552	3.772952288	2.89E-12	8.41E-12
DMD	ENSG00000198947	3.102221172	2.99E-12	8.67E-12
RPS3AP26	ENSG00000214389	-3.20923248	3.05E-12	8.84E-12
LINC01619	ENSG00000257242	-5.936014574	3.19E-12	9.21E-12

AL136295.5	ENSG00000259529	-3.043669822	3.28E-12	9.45E-12
KRTAP5-AS1	ENSG00000233930	-4.970964982	3.33E-12	9.60E-12
KRT14	ENSG00000186847	10.66299038	3.44E-12	9.90E-12
SEMA4G	ENSG00000095539	-3.239463714	3.57E-12	1.03E-11
S100A8	ENSG00000143546	6.73774265	3.62E-12	1.04E-11
FGD4	ENSG00000139132	3.732659556	3.63E-12	1.04E-11
AL008726.1	ENSG00000271984	-4.389814438	3.67E-12	1.05E-11
CLIC1	ENSG00000213719	3.156702326	3.67E-12	1.06E-11
UGDH	ENSG00000109814	3.088064618	3.68E-12	1.06E-11
SGCD	ENSG00000170624	3.934014344	3.85E-12	1.10E-11
CACNA2D2	ENSG00000007402	-3.772809813	3.94E-12	1.13E-11
SHOX2	ENSG00000168779	5.692869473	3.95E-12	1.13E-11
EVC	ENSG00000072840	3.695654179	4.10E-12	1.17E-11
S100A2	ENSG00000196754	4.652042493	4.12E-12	1.18E-11
PI15	ENSG00000137558	6.362744645	4.28E-12	1.22E-11
GRM2	ENSG00000164082	-3.844942255	4.41E-12	1.26E-11
SLC43A3	ENSG00000134802	3.239628629	4.42E-12	1.26E-11
GRHL3	ENSG00000158055	4.420803398	4.49E-12	1.28E-11
RAB43	ENSG00000172780	-3.348713558	4.87E-12	1.38E-11
CDC42	ENSG00000070831	-3.819229746	5.02E-12	1.42E-11
ANXA2	ENSG00000182718	4.02013752	5.21E-12	1.47E-11
IGFBP2	ENSG00000115457	5.486147799	5.24E-12	1.48E-11
LAD1	ENSG00000159166	5.838447932	5.30E-12	1.49E-11
GJB2	ENSG00000165474	7.39843002	5.51E-12	1.55E-11
LYZ	ENSG00000090382	6.360965586	5.52E-12	1.56E-11
FP671120.4	ENSG00000281383	-7.010693283	5.53E-12	1.56E-11
LGR4	ENSG00000205213	3.147842245	5.65E-12	1.59E-11
SAMD5	ENSG00000203727	4.578291285	5.70E-12	1.60E-11
RASGRP1	ENSG00000172575	-3.103137042	5.72E-12	1.61E-11
LILRB5	ENSG00000105609	4.683062197	5.78E-12	1.62E-11
AHNAK2	ENSG00000185567	5.604707802	6.03E-12	1.69E-11
PKP3	ENSG00000184363	6.140452485	6.11E-12	1.71E-11
DOCK6	ENSG00000130158	3.088641074	6.15E-12	1.72E-11
ANXA8L1	ENSG00000264230	5.67525396	6.44E-12	1.80E-11
SERPINB4	ENSG00000206073	5.866955894	6.56E-12	1.83E-11
SCML4	ENSG00000146285	-4.34138021	6.74E-12	1.88E-11
E2F2	ENSG00000007968	5.090689088	6.83E-12	1.90E-11
RGCC	ENSG00000102760	-3.018123016	6.96E-12	1.94E-11
GP1BA	ENSG00000185245	-3.651835516	7.02E-12	1.95E-11
CXADR	ENSG00000154639	3.772973082	7.20E-12	2.00E-11
EHHADH	ENSG00000113790	3.297221134	7.26E-12	2.02E-11
SFN	ENSG00000175793	5.502517829	7.32E-12	2.03E-11
SETBP1	ENSG00000152217	3.525297017	7.35E-12	2.04E-11
COL17A1	ENSG00000065618	6.742340218	7.36E-12	2.04E-11
FADS1	ENSG00000149485	3.401761533	7.94E-12	2.20E-11
CEBPA	ENSG00000245848	4.438900341	8.27E-12	2.29E-11
SYDE2	ENSG00000097096	-3.664473609	8.33E-12	2.30E-11
SHISAL2A	ENSG00000182183	-3.564164167	8.63E-12	2.38E-11
DDIT4L	ENSG00000145358	4.973889219	8.71E-12	2.40E-11
MYO15A	ENSG00000091536	-3.31233587	8.93E-12	2.46E-11
CXCL11	ENSG00000169248	5.366333349	9.08E-12	2.50E-11

IDO1	ENSG00000131203	5.953468223	9.46E-12	2.60E-11
COL18A1	ENSG00000182871	3.310185491	9.52E-12	2.61E-11
ADPGK-AS1	ENSG00000260898	-3.336309554	9.61E-12	2.64E-11
PLD4	ENSG00000166428	4.197214167	9.66E-12	2.65E-11
CNTNAP1	ENSG00000108797	3.059521948	9.83E-12	2.70E-11
MCAM	ENSG00000076706	4.229399029	9.84E-12	2.70E-11
RFLNA	ENSG00000178882	4.307832571	9.97E-12	2.73E-11
LINC02363	ENSG00000180712	4.754730402	9.97E-12	2.73E-11
CEND1	ENSG00000184524	3.992898788	1.01E-11	2.77E-11
MAPK12	ENSG00000188130	3.989418546	1.02E-11	2.80E-11
PLEK	ENSG00000115956	3.318435961	1.05E-11	2.87E-11
TYRP1	ENSG00000107165	6.209682437	1.05E-11	2.89E-11
MIR29B2CHG	ENSG00000203709	-3.096629971	1.07E-11	2.94E-11
LRRK2	ENSG00000188906	3.423922443	1.07E-11	2.94E-11
C6orf132	ENSG00000188112	3.861488559	1.07E-11	2.94E-11
CERS6-AS1	ENSG00000227617	-7.145214602	1.13E-11	3.07E-11
KRT5	ENSG00000186081	9.926099599	1.13E-11	3.07E-11
PLAC8	ENSG00000145287	-4.196684636	1.13E-11	3.09E-11
TENM2	ENSG00000145934	5.22551804	1.14E-11	3.09E-11
PTGIS	ENSG00000124212	4.903746769	1.15E-11	3.12E-11
AC138819.1	ENSG00000249849	-6.104037038	1.15E-11	3.14E-11
TNFRSF12A	ENSG00000006327	3.221689677	1.18E-11	3.21E-11
AR	ENSG00000169083	4.813021747	1.21E-11	3.28E-11
HS3ST2	ENSG00000122254	4.289539752	1.22E-11	3.31E-11
CCR9	ENSG00000173585	-6.23457128	1.29E-11	3.49E-11
CBFA2T3	ENSG00000129993	4.416871965	1.30E-11	3.52E-11
ADAMTS4	ENSG00000158859	3.252135643	1.30E-11	3.52E-11
AIM2	ENSG00000163568	3.680363143	1.34E-11	3.62E-11
FLJ22447	ENSG00000232774	-3.337313174	1.35E-11	3.65E-11
AC009133.3	ENSG00000260719	-3.468166982	1.37E-11	3.70E-11
SLC27A2	ENSG00000140284	3.788494189	1.37E-11	3.71E-11
FNDC7	ENSG00000143107	-5.647765776	1.39E-11	3.76E-11
HTRA3	ENSG00000170801	7.581108723	1.41E-11	3.81E-11
FBXO27	ENSG00000161243	5.302839188	1.45E-11	3.91E-11
MFSD14A	ENSG00000156875	-3.683168511	1.46E-11	3.93E-11
CDKN2B	ENSG00000147883	4.229059485	1.49E-11	4.03E-11
QPCT	ENSG00000115828	3.057077009	1.53E-11	4.11E-11
AL390755.1	ENSG00000279965	6.001454381	1.54E-11	4.15E-11
LEF1-AS1	ENSG00000232021	-5.405805511	1.55E-11	4.16E-11
ZNF358	ENSG00000198816	3.061226266	1.55E-11	4.18E-11
AP001610.1	ENSG00000228318	-8.619273436	1.62E-11	4.35E-11
LRP5	ENSG00000162337	3.716809275	1.71E-11	4.58E-11
GPA33	ENSG00000143167	-5.830735421	1.71E-11	4.58E-11
ITGA7	ENSG00000135424	3.455977563	1.72E-11	4.61E-11
COL4A6	ENSG00000197565	5.486000429	1.77E-11	4.72E-11
GDPD5	ENSG00000158555	-3.738493958	1.83E-11	4.88E-11
SLC28A3	ENSG00000197506	5.543523305	1.91E-11	5.10E-11
AC092053.2	ENSG00000283849	-7.376404734	1.96E-11	5.21E-11
CUBN	ENSG00000107611	-3.435345437	1.96E-11	5.21E-11
SPRR2E	ENSG00000203785	6.197427658	2.16E-11	5.73E-11
STARD5	ENSG00000172345	-3.071840553	2.19E-11	5.79E-11

MMP1	ENSG00000196611	10.80265361		2.20E-11	5.81E-11
NDUFV2	ENSG00000178127	-6.874289853		2.27E-11	5.99E-11
PRELP	ENSG00000188783	6.628307586		2.33E-11	6.16E-11
MBOAT2	ENSG00000143797	3.788594022		2.37E-11	6.25E-11
AL137145.2	ENSG00000215244	-4.722092083		2.38E-11	6.27E-11
CRACR2B	ENSG00000177685	4.697048594		2.44E-11	6.45E-11
VASH2	ENSG00000143494	4.009854933		2.47E-11	6.52E-11
PRUNE2	ENSG00000106772	3.704142772		2.49E-11	6.55E-11
PTGER3	ENSG00000050628	4.957074661		2.65E-11	6.96E-11
LINC00402	ENSG00000235532	-5.691720246		2.67E-11	7.01E-11
HOOK2	ENSG00000095066	-3.022694806		2.73E-11	7.16E-11
LILRA6	ENSG00000244482	3.310459886		2.74E-11	7.18E-11
AC027601.4	ENSG00000276101	-3.747848866		2.77E-11	7.26E-11
AKAP12	ENSG00000131016	3.844020678		2.94E-11	7.68E-11
CXCL14	ENSG00000145824	8.759021252		2.97E-11	7.75E-11
RP9P	ENSG00000205763	3.600153902		3.09E-11	8.06E-11
CTD-2201I18.1	ENSG00000249825	-3.222363866		3.11E-11	8.12E-11
DSC3	ENSG00000134762	7.896221404		3.16E-11	8.21E-11
NT5E	ENSG00000135318	3.375408874		3.18E-11	8.27E-11
MAL2	ENSG00000147676	5.487532498		3.21E-11	8.35E-11
MZB1	ENSG00000170476	5.265767139		3.23E-11	8.40E-11
HIST1H2BK	ENSG00000197903	3.261907782		3.25E-11	8.45E-11
EBI3	ENSG00000105246	4.089234713		3.32E-11	8.61E-11
CYB5R2	ENSG00000166394	4.123090508		3.33E-11	8.63E-11
SPP1	ENSG00000118785	5.792518678		3.33E-11	8.64E-11
HMGN5	ENSG00000198157	5.901831793		3.40E-11	8.81E-11
ZNF80	ENSG00000174255	-5.015545479		3.60E-11	9.30E-11
RPL10AP6	ENSG00000226360	-3.108851977		3.72E-11	9.60E-11
CLDN1	ENSG00000163347	5.553329689		3.77E-11	9.72E-11
MST1R	ENSG00000164078	3.662415188		3.86E-11	9.93E-11
REM2	ENSG00000139890	-3.851997503		3.99E-11	1.03E-10
TRBV4-2	ENSG00000211745	-3.87867715		4.01E-11	1.03E-10
CAMK4	ENSG00000152495	-3.258246009		4.05E-11	1.04E-10
MAATS1	ENSG00000183833	4.822206015		4.06E-11	1.04E-10
SFRP1	ENSG00000104332	4.909600611		4.09E-11	1.05E-10
ROBO2	ENSG00000185008	5.045045731		4.12E-11	1.06E-10
AL683807.1	ENSG00000223511	-3.254083096		4.23E-11	1.08E-10
SELENBP1	ENSG00000143416	3.099233756		4.38E-11	1.12E-10
LGALS7B	ENSG00000178934	6.982559803		4.48E-11	1.15E-10
AL353593.1	ENSG00000269890	-3.498118857		4.55E-11	1.16E-10
SLC17A9	ENSG00000101194	3.108551471		4.72E-11	1.21E-10
AC126696.2	ENSG00000260466	-6.991017587		4.91E-11	1.25E-10
ITGB8	ENSG00000105855	4.125125133		4.98E-11	1.27E-10
VEGFA	ENSG00000112715	3.99653561		5.11E-11	1.30E-10
TNS4	ENSG00000131746	3.212022695		5.14E-11	1.31E-10
TMEM200A	ENSG00000164484	3.246424979		5.24E-11	1.33E-10
NCS1	ENSG00000107130	4.975463914		5.38E-11	1.36E-10
FSD1L	ENSG00000106701	3.019119067		5.47E-11	1.39E-10
SIGLEC1	ENSG00000088827	4.389990681		5.49E-11	1.39E-10
KLF2	ENSG00000127528	-3.132994978		5.51E-11	1.40E-10
HLA-DQB1	ENSG00000179344	5.533065413		5.57E-11	1.41E-10

ITPKA	ENSG00000137825	4.878093939	5.68E-11	1.44E-10
C1orf21	ENSG00000116667	4.312007238	5.83E-11	1.47E-10
Z99774.1	ENSG00000206028	-9.223819952	5.89E-11	1.49E-10
LILRB1	ENSG00000104972	4.040429106	6.16E-11	1.55E-10
TOX2	ENSG00000124191	3.889763582	6.41E-11	1.61E-10
POU3F1	ENSG00000185668	4.172804811	6.46E-11	1.62E-10
AC027020.2	ENSG00000270127	-3.30176805	6.71E-11	1.69E-10
HBB	ENSG00000244734	4.833131567	6.88E-11	1.73E-10
LTF	ENSG00000012223	4.394151201	7.20E-11	1.80E-10
POPDC3	ENSG00000132429	4.830673833	7.52E-11	1.88E-10
KRT80	ENSG00000167767	5.705762015	7.64E-11	1.91E-10
AC245060.5	ENSG00000274422	4.497735768	7.67E-11	1.91E-10
HIP1R	ENSG00000130787	-3.200615126	7.72E-11	1.93E-10
PVR	ENSG00000073008	3.04732302	7.79E-11	1.94E-10
PAWR	ENSG00000177425	3.615929137	8.08E-11	2.01E-10
ZNF890P	ENSG00000159904	-4.327191074	8.18E-11	2.04E-10
TP63	ENSG00000073282	6.472940374	8.20E-11	2.04E-10
AL512306.2	ENSG00000240219	-4.698962732	8.28E-11	2.06E-10
Sep-03	ENSG00000100167	4.004609304	8.32E-11	2.07E-10
CSPG4P10	ENSG00000276710	-5.261146452	8.50E-11	2.11E-10
LY6D	ENSG00000167656	6.912644834	8.66E-11	2.15E-10
COL11A1	ENSG00000060718	5.813127845	8.70E-11	2.16E-10
AC093010.2	ENSG00000241490	-4.488161203	8.89E-11	2.20E-10
KIF26B	ENSG00000162849	3.703970624	8.95E-11	2.22E-10
DPEP2	ENSG00000167261	-4.059791302	9.07E-11	2.25E-10
EFNA5	ENSG00000184349	4.348952554	9.21E-11	2.28E-10
MEG3	ENSG00000214548	4.695616754	9.69E-11	2.39E-10
HIST1H1C	ENSG00000187837	4.097069197	9.75E-11	2.41E-10
MEOX1	ENSG00000005102	3.982890357	9.92E-11	2.45E-10
MT1E	ENSG00000169715	4.083660609	1.00E-10	2.47E-10
AC118344.2	ENSG00000279759	-3.113433855	1.02E-10	2.51E-10
GABARAPL1	ENSG00000139112	-3.192791601	1.03E-10	2.52E-10
FNDC1	ENSG00000164694	6.927378429	1.03E-10	2.53E-10
SLIT3	ENSG00000184347	5.450716065	1.05E-10	2.59E-10
ITGA11	ENSG00000137809	3.228825151	1.10E-10	2.71E-10
ATP8B4	ENSG00000104043	3.384877029	1.13E-10	2.77E-10
TRAV9-2	ENSG00000211793	-3.832234782	1.13E-10	2.77E-10
HOOK1	ENSG00000134709	-3.089307651	1.13E-10	2.78E-10
NLGN1	ENSG00000169760	5.793166374	1.14E-10	2.79E-10
LGALS3	ENSG00000131981	4.577025042	1.15E-10	2.81E-10
BCHE	ENSG00000114200	5.283002308	1.15E-10	2.81E-10
IVL	ENSG00000163207	6.168874442	1.16E-10	2.83E-10
SPRR2G	ENSG00000159516	5.334048768	1.18E-10	2.89E-10
AC017002.3	ENSG00000240350	3.745148351	1.19E-10	2.90E-10
FBXO40	ENSG00000163833	-5.084729962	1.19E-10	2.91E-10
MT2A	ENSG00000125148	3.265365441	1.24E-10	3.03E-10
AC006369.1	ENSG00000236213	-5.014723206	1.30E-10	3.17E-10
EVA1A	ENSG00000115363	4.593471821	1.31E-10	3.19E-10
LZTS3	ENSG00000088899	-3.072567132	1.34E-10	3.26E-10
AC109326.1	ENSG00000279602	-3.855240986	1.37E-10	3.34E-10
AL353597.3	ENSG00000279942	-3.854972256	1.44E-10	3.50E-10

MYO3B	ENSG00000071909	6.560921928	1.44E-10	3.51E-10
AC007384.1	ENSG00000237513	-3.447038816	1.45E-10	3.52E-10
MIR616	ENSG00000208028	-4.169842051	1.47E-10	3.57E-10
IGHA2	ENSG00000211890	6.737314961	1.51E-10	3.66E-10
MIR205HG	ENSG00000230937	4.481147875	1.52E-10	3.67E-10
GAD1	ENSG00000128683	4.171572086	1.55E-10	3.75E-10
CD209	ENSG00000090659	5.93763455	1.64E-10	3.96E-10
RAI2	ENSG00000131831	3.40431161	1.67E-10	4.04E-10
PNMA3	ENSG00000183837	-4.448220139	1.70E-10	4.08E-10
AL592430.1	ENSG00000232682	-6.774674875	1.75E-10	4.21E-10
IGHA1	ENSG00000211895	8.51960417	1.76E-10	4.23E-10
RUBCNL	ENSG00000102445	4.635201792	1.79E-10	4.30E-10
PRG4	ENSG00000116690	-4.065176714	1.82E-10	4.36E-10
LINC00996	ENSG00000242258	3.441366423	1.88E-10	4.51E-10
AL645929.1	ENSG00000230521	-3.91567968	1.91E-10	4.59E-10
DSP	ENSG00000096696	8.184519805	1.97E-10	4.72E-10
FADS2	ENSG00000134824	4.097528289	1.98E-10	4.73E-10
SPIB	ENSG00000269404	3.73848931	1.99E-10	4.75E-10
SCARA5	ENSG00000168079	5.118347552	2.00E-10	4.79E-10
LIFR	ENSG00000113594	4.658513109	2.20E-10	5.25E-10
LINC00861	ENSG00000245164	-4.613564783	2.27E-10	5.41E-10
AL121839.2	ENSG00000260711	-3.202532115	2.39E-10	5.68E-10
PRAL	ENSG00000279296	-9.854834238	2.42E-10	5.76E-10
SCML1	ENSG00000047634	-3.534272599	2.43E-10	5.77E-10
ADGRG1	ENSG00000205336	3.891364386	2.48E-10	5.88E-10
IGKV4-1	ENSG00000211598	4.292522969	2.50E-10	5.94E-10
HLA-DQB2	ENSG00000232629	6.073408047	2.65E-10	6.26E-10
FBLN5	ENSG00000140092	4.599402441	2.67E-10	6.32E-10
CCL21	ENSG00000137077	6.365610997	2.80E-10	6.61E-10
DBH-AS1	ENSG00000225756	-3.846086534	2.87E-10	6.77E-10
ZNF204P	ENSG00000204789	-3.501221849	2.87E-10	6.77E-10
WNT6	ENSG00000115596	4.619918697	2.95E-10	6.94E-10
PDGFD	ENSG00000170962	4.792975167	2.95E-10	6.95E-10
TSC22D3	ENSG00000157514	-3.100688624	3.10E-10	7.30E-10
SARDH	ENSG00000123453	-3.201538153	3.11E-10	7.31E-10
MYCL	ENSG00000116990	3.782459145	3.34E-10	7.83E-10
REPS2	ENSG00000169891	3.244059515	3.62E-10	8.45E-10
AC099063.1	ENSG00000237568	-9.308570952	3.69E-10	8.62E-10
AL034550.2	ENSG00000277301	-3.693518836	3.79E-10	8.83E-10
IRF6	ENSG00000117595	3.639915236	3.86E-10	9.00E-10
FMNL2	ENSG00000157827	3.037736634	3.92E-10	9.12E-10
DKK3	ENSG00000050165	3.274508628	4.10E-10	9.53E-10
RPL10P16	ENSG00000178464	-3.307378227	4.11E-10	9.55E-10
AC020763.4	ENSG00000279569	-5.128346623	4.19E-10	9.72E-10
AC092053.3	ENSG00000284669	-6.742819545	4.25E-10	9.87E-10
EFCAB12	ENSG00000172771	-4.013101275	4.33E-10	1.00E-09
CNKSR2	ENSG00000149970	-4.260971206	4.38E-10	1.01E-09
CDH2	ENSG00000170558	6.101717851	4.39E-10	1.02E-09
KRT17	ENSG00000128422	8.693610316	4.55E-10	1.05E-09
LRRN2	ENSG00000170382	-5.782981909	4.58E-10	1.06E-09
MMP9	ENSG00000100985	5.900792795	4.75E-10	1.10E-09

TRAV12-1	ENSG00000211785	-3.434075382	4.81E-10	1.11E-09
RORB	ENSG00000198963	6.44276326	5.18E-10	1.19E-09
IGF2BP3	ENSG00000136231	4.091756289	5.23E-10	1.20E-09
WNT10B	ENSG00000169884	-3.275919108	5.38E-10	1.24E-09
ADAM33	ENSG00000149451	4.319045206	5.43E-10	1.25E-09
CSF2RB	ENSG00000100368	4.274234265	5.50E-10	1.26E-09
RBM11	ENSG00000185272	-4.202532705	5.54E-10	1.27E-09
SP5	ENSG00000204335	5.089573576	6.32E-10	1.44E-09
AC008440.2	ENSG00000232220	-8.978466557	6.34E-10	1.45E-09
AP001324.1	ENSG00000227615	-3.197580828	6.35E-10	1.45E-09
SOX5	ENSG00000134532	4.658557425	6.58E-10	1.50E-09
CNFN	ENSG00000105427	5.171570273	6.62E-10	1.51E-09
AC015921.1	ENSG00000262884	-6.206190751	6.88E-10	1.56E-09
GFRA1	ENSG00000151892	4.990203059	6.92E-10	1.57E-09
AMIGO1	ENSG00000181754	-3.365212217	6.93E-10	1.57E-09
SBSN	ENSG00000189001	7.140828762	6.93E-10	1.58E-09
RSPH4A	ENSG00000111834	-3.336278614	6.97E-10	1.58E-09
LINC02325	ENSG00000246084	-3.78538249	7.03E-10	1.60E-09
AL450306.1	ENSG00000228748	-6.168028787	7.03E-10	1.60E-09
CYS1	ENSG00000205795	4.430587901	7.15E-10	1.62E-09
VIPR1	ENSG00000114812	-4.356849922	7.18E-10	1.63E-09
NTN1	ENSG00000065320	3.471951121	7.55E-10	1.71E-09
SLITRK6	ENSG00000184564	4.830583879	7.64E-10	1.73E-09
AC004585.1	ENSG00000266088	3.768897685	8.29E-10	1.87E-09
KRT6B	ENSG00000185479	7.844021238	8.72E-10	1.96E-09
FCGR2C	ENSG00000244682	4.015288585	9.42E-10	2.11E-09
KRT15	ENSG00000171346	5.524335392	9.74E-10	2.18E-09
NCCRP1	ENSG00000188505	4.655220838	9.74E-10	2.18E-09
SERPINB3	ENSG00000057149	5.501175725	9.85E-10	2.21E-09
FGFR3	ENSG00000068078	5.820735844	9.92E-10	2.22E-09
AARD	ENSG00000205002	6.94746193	9.96E-10	2.23E-09
HMCN1	ENSG00000143341	4.265127465	1.01E-09	2.26E-09
TRPM6	ENSG00000119121	4.078376801	1.03E-09	2.31E-09
LARP6	ENSG00000166173	4.340671215	1.05E-09	2.35E-09
VSTM2L	ENSG00000132821	7.29030005	1.09E-09	2.42E-09
CALML5	ENSG00000178372	7.295970448	1.12E-09	2.49E-09
NGFR	ENSG00000064300	3.79510357	1.17E-09	2.60E-09
AC009090.4	ENSG00000279019	-4.148171463	1.17E-09	2.61E-09
SPINK5	ENSG00000133710	8.199711961	1.17E-09	2.61E-09
SPRR2D	ENSG00000163216	4.534604015	1.17E-09	2.61E-09
FAM153A	ENSG00000170074	-5.943481879	1.20E-09	2.67E-09
ST6GALNAC1	ENSG00000070526	-4.090093475	1.26E-09	2.78E-09
LINC00954	ENSG00000228784	-3.503025579	1.31E-09	2.91E-09
DUSP8	ENSG00000184545	-3.726916213	1.35E-09	2.98E-09
CD1E	ENSG00000158488	4.30830226	1.38E-09	3.06E-09
CHRDL1	ENSG00000101938	5.113639916	1.44E-09	3.17E-09
SEMA5A	ENSG00000112902	3.750463751	1.44E-09	3.18E-09
TNFRSF17	ENSG00000048462	4.950749651	1.46E-09	3.21E-09
WHAMMP2	ENSG00000248334	-4.104906436	1.54E-09	3.38E-09
CD40LG	ENSG00000102245	-4.258997725	1.58E-09	3.48E-09
PLA2G4E	ENSG00000188089	4.668656377	1.64E-09	3.59E-09

AL139327.1	ENSG00000121388	4.898105544	1.76E-09	3.85E-09
GPR63	ENSG00000112218	3.669410128	1.78E-09	3.88E-09
FCGR2B	ENSG00000072694	4.185494358	1.82E-09	3.97E-09
ARHGAP44	ENSG00000006740	3.430707367	1.91E-09	4.15E-09
STC1	ENSG00000159167	4.058783019	1.93E-09	4.20E-09
SLC9A7P1	ENSG00000227825	4.994197557	1.94E-09	4.23E-09
TRAV12-2	ENSG00000211789	-3.270956362	1.99E-09	4.33E-09
FUT7	ENSG00000180549	4.349012518	2.01E-09	4.37E-09
BTBD11	ENSG00000151136	-4.268477118	2.03E-09	4.42E-09
CCL13	ENSG00000181374	5.831764454	2.09E-09	4.54E-09
STRIP2	ENSG00000128578	3.364906046	2.12E-09	4.61E-09
CPNE7	ENSG00000178773	3.252807894	2.21E-09	4.79E-09
AP000769.1	ENSG00000173727	3.026125793	2.35E-09	5.08E-09
MFAP4	ENSG00000166482	5.05171773	2.35E-09	5.08E-09
PTPRU	ENSG00000060656	3.028475822	2.38E-09	5.14E-09
BATF2	ENSG00000168062	3.538502828	2.50E-09	5.40E-09
AC020659.1	ENSG00000174171	-3.389759023	2.53E-09	5.45E-09
AC245100.4	ENSG00000231551	-3.184430535	2.57E-09	5.53E-09
AC026979.2	ENSG00000271869	-3.491149237	2.59E-09	5.59E-09
DMKN	ENSG00000161249	6.611467823	2.61E-09	5.61E-09
ARMH1	ENSG00000198520	-3.05912557	2.63E-09	5.65E-09
TRIM29	ENSG00000137699	7.154130454	2.69E-09	5.78E-09
AC139491.7	ENSG00000285476	-5.011350929	2.71E-09	5.82E-09
ASTL	ENSG00000188886	-4.769171973	2.77E-09	5.95E-09
POF1B	ENSG00000124429	4.622733893	2.98E-09	6.38E-09
PPP1R1A	ENSG00000135447	-3.406335081	3.15E-09	6.73E-09
KRTDAP	ENSG00000188508	5.616251336	3.17E-09	6.76E-09
SLC16A14	ENSG00000163053	3.431916047	3.18E-09	6.79E-09
ACVR1C	ENSG00000123612	-3.585203985	3.26E-09	6.95E-09
AC245297.1	ENSG00000215861	3.473138683	3.34E-09	7.12E-09
LTB	ENSG00000227507	-3.153231415	3.39E-09	7.22E-09
LUCAT1	ENSG00000248323	3.072216441	3.49E-09	7.43E-09
TNFRSF9	ENSG00000049249	3.788064185	3.63E-09	7.71E-09
MRC1	ENSG00000260314	4.369810551	3.70E-09	7.85E-09
C9orf139	ENSG00000180539	3.109539933	3.75E-09	7.94E-09
ADAMTS14	ENSG00000138316	4.408716876	3.75E-09	7.94E-09
HLA-DRB5	ENSG00000198502	5.894057597	3.79E-09	8.03E-09
SEC14L2	ENSG00000100003	-3.595505817	3.84E-09	8.12E-09
CA14	ENSG00000118298	-6.735802978	3.91E-09	8.28E-09
PKP1	ENSG00000081277	7.211933007	3.97E-09	8.40E-09
RPS23P8	ENSG00000230629	-3.420389396	4.11E-09	8.69E-09
FGL2	ENSG00000127951	3.110328046	4.25E-09	8.96E-09
EIF4BP7	ENSG00000225031	-3.408603482	4.27E-09	9.01E-09
ADAM12	ENSG00000148848	4.594976564	4.35E-09	9.18E-09
CXXC4	ENSG00000168772	6.382377792	4.37E-09	9.22E-09
PAPPA	ENSG00000182752	3.034785863	4.50E-09	9.48E-09
SATB1-AS1	ENSG00000228956	-3.915348411	4.50E-09	9.48E-09
CLEC10A	ENSG00000132514	4.689483715	4.59E-09	9.67E-09
IGHG2	ENSG00000211893	6.094431003	4.77E-09	1.00E-08
COL6A5	ENSG00000172752	5.490848071	4.98E-09	1.04E-08
APBA2	ENSG00000034053	-3.603581748	4.99E-09	1.05E-08

IGHM	ENSG00000211899	7.112266759	5.03E-09	1.05E-08
TXK	ENSG00000074966	-3.709575635	5.13E-09	1.07E-08
GFPT2	ENSG00000131459	3.208456316	5.24E-09	1.10E-08
RHOU	ENSG00000116574	3.68084598	5.25E-09	1.10E-08
PLIN4	ENSG00000167676	-3.379362291	5.29E-09	1.11E-08
SMIM35	ENSG00000255274	-5.048577165	6.28E-09	1.31E-08
BTG3-AS1	ENSG00000280594	-3.464907533	6.36E-09	1.32E-08
COL5A3	ENSG00000080573	3.779115403	6.46E-09	1.34E-08
LINC00184	ENSG00000224939	5.173087547	6.51E-09	1.35E-08
CFH	ENSG00000000971	4.518516864	7.16E-09	1.49E-08
GSDME	ENSG00000105928	5.600224794	7.33E-09	1.52E-08
DSG1	ENSG00000134760	7.397678541	7.39E-09	1.53E-08
ANXA8	ENSG00000265190	5.192346635	7.66E-09	1.59E-08
CNTD2	ENSG00000105219	-4.069843171	8.21E-09	1.70E-08
SLC2A8	ENSG00000136856	3.17602572	8.37E-09	1.73E-08
PIK3AP1	ENSG00000155629	3.322430533	8.50E-09	1.75E-08
RASGRP4	ENSG00000171777	3.055947798	9.57E-09	1.96E-08
ADCY1	ENSG00000164742	5.648636749	9.66E-09	1.98E-08
HMSD	ENSG00000221887	4.844495514	9.94E-09	2.04E-08
KRT10	ENSG00000186395	3.20560115	1.02E-08	2.08E-08
LOR	ENSG00000203782	5.301149908	1.03E-08	2.11E-08
NELL2	ENSG00000184613	-5.018630804	1.04E-08	2.12E-08
DRD2	ENSG00000149295	5.256830986	1.11E-08	2.26E-08
AC006042.3	ENSG00000233264	-3.271793265	1.13E-08	2.31E-08
MYO7A	ENSG00000137474	3.379394519	1.13E-08	2.31E-08
PLD5	ENSG00000180287	5.766839395	1.15E-08	2.34E-08
LINC02384	ENSG00000251301	3.845692352	1.16E-08	2.35E-08
LAYN	ENSG00000204381	3.421047942	1.18E-08	2.41E-08
AQP9	ENSG00000103569	3.372761948	1.20E-08	2.43E-08
KRT6A	ENSG00000205420	9.60962687	1.27E-08	2.57E-08
TMEM155	ENSG00000164112	5.162985812	1.27E-08	2.58E-08
TRIB1	ENSG00000173334	3.13370779	1.28E-08	2.59E-08
IL34	ENSG00000157368	3.688273643	1.28E-08	2.60E-08
CDKN2A	ENSG00000147889	3.467664618	1.31E-08	2.65E-08
U2AF1L5	ENSG00000275895	-3.22640292	1.35E-08	2.74E-08
FAT2	ENSG00000086570	3.325765617	1.41E-08	2.85E-08
KLK10	ENSG00000129451	3.680776552	1.45E-08	2.93E-08
MUC15	ENSG00000169550	4.646076673	1.53E-08	3.09E-08
S100A7	ENSG00000143556	6.825524494	1.60E-08	3.23E-08
IL1R2	ENSG00000115590	4.433895786	1.71E-08	3.43E-08
PLA2G2D	ENSG00000117215	6.774112265	1.73E-08	3.48E-08
NLRP6	ENSG00000174885	-4.450173416	1.74E-08	3.49E-08
IGLC2	ENSG00000211677	5.352428179	1.74E-08	3.50E-08
AC020951.1	ENSG00000278897	-3.918558071	1.80E-08	3.61E-08
NIPAL2	ENSG00000104361	3.266143623	1.82E-08	3.64E-08
PLA2G2A	ENSG00000188257	3.922451963	1.86E-08	3.73E-08
CCR10	ENSG00000184451	5.003884738	1.94E-08	3.87E-08
SPRR1B	ENSG00000169469	6.801010226	2.06E-08	4.12E-08
JCHAIN	ENSG00000132465	5.726019332	2.15E-08	4.29E-08
TULP2	ENSG00000104804	-4.231901936	2.28E-08	4.52E-08
CALML3	ENSG00000178363	6.102604791	2.37E-08	4.70E-08

HRH1	ENSG00000196639	3.516915045	2.38E-08	4.71E-08
XIRP1	ENSG00000168334	3.888764304	2.45E-08	4.86E-08
DUSP2	ENSG00000158050	-3.147229549	2.50E-08	4.95E-08
STOX2	ENSG00000173320	4.445465319	2.52E-08	4.98E-08
BAALC	ENSG00000164929	3.908179803	2.56E-08	5.05E-08
PPL	ENSG00000118898	4.039717539	2.56E-08	5.06E-08
ZEB2	ENSG00000169554	3.143887093	2.58E-08	5.09E-08
NKX6-1	ENSG00000163623	4.370428381	2.70E-08	5.32E-08
FRZB	ENSG00000162998	5.192719433	2.72E-08	5.36E-08
LRRC49	ENSG00000137821	3.255628615	2.83E-08	5.57E-08
CCL19	ENSG00000172724	7.436182144	2.87E-08	5.64E-08
KRT16	ENSG00000186832	8.284035909	3.10E-08	6.08E-08
FOXB1	ENSG00000171956	3.827981603	3.42E-08	6.70E-08
IGHG1	ENSG00000211896	7.675692033	3.45E-08	6.76E-08
ALPL	ENSG00000162551	5.814814366	3.45E-08	6.76E-08
SIPA1L2	ENSG00000116991	3.395451227	3.48E-08	6.81E-08
COL6A6	ENSG00000206384	5.203561755	3.55E-08	6.95E-08
HIST1H2BJ	ENSG00000124635	3.209038402	3.58E-08	6.99E-08
CDH3	ENSG00000062038	3.29985483	3.65E-08	7.12E-08
TRAV8-4	ENSG00000211790	-3.058132999	3.69E-08	7.20E-08
ALDH3B2	ENSG00000132746	4.869103971	3.77E-08	7.34E-08
KIAA1549	ENSG00000122778	3.111219839	3.77E-08	7.35E-08
WISP2	ENSG00000064205	6.512305835	3.91E-08	7.61E-08
DEPTOR	ENSG00000155792	3.216494748	3.95E-08	7.69E-08
RDM1P5	ENSG00000263818	-3.01324652	4.05E-08	7.88E-08
SORD2P	ENSG00000259479	4.846853122	4.28E-08	8.30E-08
NRCAM	ENSG00000091129	3.507665267	4.50E-08	8.71E-08
KLK7	ENSG00000169035	5.54951526	4.58E-08	8.87E-08
CDSN	ENSG00000204539	6.026442232	4.61E-08	8.91E-08
PTGS2	ENSG00000073756	3.165866705	4.64E-08	8.98E-08
NCAPH	ENSG00000121152	3.393397637	4.83E-08	9.33E-08
CHRM3-AS2	ENSG00000233355	-3.668599775	5.05E-08	9.75E-08
LINC00243	ENSG00000214894	-3.508892187	5.44E-08	1.05E-07
CARD9	ENSG00000187796	3.230458536	5.49E-08	1.06E-07
WNT7A	ENSG00000154764	-4.858447166	5.50E-08	1.06E-07
RAMP1	ENSG00000132329	4.110397647	5.53E-08	1.06E-07
FAM153C	ENSG00000204677	-3.651135384	5.56E-08	1.07E-07
AZGP1	ENSG00000160862	4.669803772	5.85E-08	1.12E-07
MGAT5B	ENSG00000167889	-3.583449133	6.49E-08	1.24E-07
AC036108.2	ENSG00000261054	-6.208071259	6.66E-08	1.27E-07
RET	ENSG00000165731	4.12463766	7.60E-08	1.45E-07
TLR3	ENSG00000164342	3.132946537	7.85E-08	1.49E-07
TMEM163	ENSG00000152128	4.104942272	8.81E-08	1.67E-07
PABPC3	ENSG00000151846	-3.056403794	9.04E-08	1.71E-07
FLG2	ENSG00000143520	6.390139768	9.29E-08	1.75E-07
FLNC	ENSG00000128591	3.040738701	9.33E-08	1.76E-07
TUBB2B	ENSG00000137285	3.165983992	9.65E-08	1.82E-07
AC004551.1	ENSG00000257452	-5.447594342	9.87E-08	1.86E-07
PHGDH	ENSG00000092621	3.963364318	9.99E-08	1.88E-07
IL31RA	ENSG00000164509	4.038279017	1.01E-07	1.90E-07
GREB1	ENSG00000196208	5.301196785	1.02E-07	1.91E-07

ZNRF1	ENSG00000186187	3.216341042	1.02E-07	1.93E-07
AC011611.3	ENSG00000257453	-6.438653981	1.03E-07	1.93E-07
SSTR3	ENSG00000278195	-3.349734697	1.06E-07	1.99E-07
TCTE1	ENSG00000146221	-4.111333661	1.07E-07	2.01E-07
TEX45	ENSG00000198723	-5.303945448	1.09E-07	2.05E-07
G0S2	ENSG00000123689	4.575343167	1.19E-07	2.22E-07
APBA1	ENSG00000107282	3.959040824	1.20E-07	2.24E-07
F2R	ENSG00000181104	3.422113876	1.21E-07	2.26E-07
AC093642.1	ENSG00000226423	-4.344663411	1.25E-07	2.33E-07
CABLES1	ENSG00000134508	3.285539322	1.27E-07	2.37E-07
CD300E	ENSG00000186407	3.470120117	1.29E-07	2.41E-07
AL137186.1	ENSG00000229664	-5.102131521	1.31E-07	2.45E-07
WNT10A	ENSG00000135925	4.05805654	1.32E-07	2.47E-07
RHBDL1	ENSG00000103269	-3.385641579	1.41E-07	2.62E-07
EMID1	ENSG00000186998	4.347320639	1.53E-07	2.84E-07
ONECUT2	ENSG00000119547	7.127666624	1.70E-07	3.14E-07
HOXB9	ENSG00000170689	5.276619675	1.76E-07	3.25E-07
KRT6C	ENSG00000170465	7.437215309	1.86E-07	3.43E-07
AP001189.1	ENSG00000236304	-4.783177884	1.86E-07	3.44E-07
NTRK2	ENSG00000148053	5.355388887	2.20E-07	4.04E-07
TP73	ENSG00000078900	4.35512207	2.33E-07	4.27E-07
IGKV3-20	ENSG00000239951	4.461297004	2.41E-07	4.40E-07
CASP14	ENSG00000105141	5.900481593	2.43E-07	4.45E-07
DHCR24	ENSG00000116133	3.182131132	2.44E-07	4.45E-07
MACC1	ENSG00000183742	4.829845992	2.52E-07	4.61E-07
SLC27A6	ENSG00000113396	5.75138049	2.56E-07	4.67E-07
AC095055.1	ENSG00000270681	-4.218092185	2.68E-07	4.88E-07
FAM106A	ENSG00000273018	-3.646896213	2.84E-07	5.17E-07
AC133644.2	ENSG00000273445	-4.048422449	2.99E-07	5.43E-07
METRNL	ENSG00000176845	3.093502709	3.02E-07	5.47E-07
SCN3A	ENSG00000153253	3.967941974	3.04E-07	5.52E-07
IGKV1-5	ENSG00000243466	3.943610831	3.09E-07	5.61E-07
DES	ENSG00000175084	4.170545173	3.50E-07	6.32E-07
ADGRG2	ENSG00000173698	6.550521954	3.51E-07	6.34E-07
ACSL6	ENSG00000164398	-3.280852836	3.54E-07	6.38E-07
NR4A2	ENSG00000153234	-4.1713136	3.61E-07	6.50E-07
SLAMF7	ENSG00000026751	3.050368304	3.62E-07	6.52E-07
KLHL4	ENSG00000102271	4.308098305	3.79E-07	6.82E-07
AL049836.1	ENSG00000258919	-4.437626117	3.87E-07	6.97E-07
SLC16A9	ENSG00000165449	5.17533395	3.89E-07	6.99E-07
BCAS1	ENSG00000064787	4.21020142	3.98E-07	7.16E-07
ELN	ENSG00000049540	3.284962723	4.05E-07	7.27E-07
GPR55	ENSG00000135898	-3.682790005	4.49E-07	8.03E-07
FAM149A	ENSG00000109794	3.388397989	5.33E-07	9.49E-07
HLA-DQA2	ENSG00000237541	5.621815327	5.38E-07	9.57E-07
CHRNA6	ENSG00000147434	3.858999493	5.58E-07	9.91E-07
FCN1	ENSG00000085265	3.704563363	5.60E-07	9.95E-07
LRG1	ENSG00000171236	3.429045539	5.76E-07	1.02E-06
LINC01102	ENSG00000235597	3.467747491	5.89E-07	1.04E-06
KRT73-AS1	ENSG00000257495	-6.834032904	6.15E-07	1.09E-06
GALNT14	ENSG00000158089	4.993808498	6.35E-07	1.12E-06

ETV7	ENSG00000010030	3.305958724	6.50E-07	1.15E-06
HNRNPA1P21	ENSG00000228168	5.357584404	7.36E-07	1.29E-06
ANKRD26P3	ENSG00000237636	4.172511022	7.36E-07	1.29E-06
RGS1	ENSG00000090104	-3.148896119	7.85E-07	1.38E-06
DUSP1	ENSG00000120129	-3.696002252	7.95E-07	1.39E-06
MIR6723	ENSG00000278791	-6.032167566	8.60E-07	1.50E-06
KRT7	ENSG00000135480	5.148870973	9.49E-07	1.65E-06
SPRR2A	ENSG00000241794	4.047841457	9.86E-07	1.72E-06
TUBA3C	ENSG00000198033	4.489948312	1.01E-06	1.76E-06
IL6	ENSG00000136244	3.314756034	1.02E-06	1.77E-06
DNAH7	ENSG00000118997	3.359526038	1.05E-06	1.83E-06
DUXAP10	ENSG00000244306	3.179564571	1.16E-06	2.02E-06
MIR155HG	ENSG00000234883	3.910401468	1.26E-06	2.17E-06
GOLGA8M	ENSG00000188626	-3.730594964	1.26E-06	2.17E-06
NLGN4Y	ENSG00000165246	3.658714178	1.30E-06	2.24E-06
GZMB	ENSG00000100453	4.440634826	1.31E-06	2.25E-06
TRGV10	ENSG00000211694	-3.29392187	1.34E-06	2.31E-06
UNC13C	ENSG00000137766	4.814510614	1.38E-06	2.37E-06
GRIK4	ENSG00000149403	3.313877649	1.43E-06	2.46E-06
FGFR2	ENSG00000066468	3.485154107	1.54E-06	2.64E-06
ALPK2	ENSG00000198796	3.740502657	1.60E-06	2.73E-06
OPCML	ENSG00000183715	4.170702601	1.69E-06	2.88E-06
AC020656.2	ENSG00000274979	-3.347765539	1.69E-06	2.89E-06
IGLC3	ENSG00000211679	4.839251932	1.77E-06	3.01E-06
AC009041.2	ENSG00000260807	-3.238568766	1.79E-06	3.04E-06
CCR12P	ENSG00000238241	-4.620273927	1.87E-06	3.18E-06
MMP3	ENSG00000149968	7.790202867	1.88E-06	3.20E-06
LGALS7	ENSG00000205076	3.719673044	1.92E-06	3.26E-06
ANK3	ENSG00000151150	-3.079658722	2.37E-06	4.00E-06
CDHR1	ENSG00000148600	3.557407404	2.44E-06	4.12E-06
FOS	ENSG00000170345	-4.883584245	2.55E-06	4.29E-06
FHIT	ENSG00000189283	-3.044824063	2.58E-06	4.34E-06
PAX9	ENSG00000198807	4.473356528	2.64E-06	4.44E-06
IGKV3-15	ENSG00000244437	3.19582949	2.71E-06	4.55E-06
COMP	ENSG00000105664	3.704976644	3.00E-06	5.02E-06
LIAS	ENSG00000121897	-3.351373707	3.22E-06	5.37E-06
AC092821.3	ENSG00000284634	-6.224243983	3.36E-06	5.60E-06
FLG	ENSG00000143631	7.091039754	3.83E-06	6.35E-06
EDAR	ENSG00000135960	-3.838461702	3.88E-06	6.43E-06
DUXAP8	ENSG00000206195	3.324280357	4.01E-06	6.64E-06
CD70	ENSG00000125726	4.465600334	4.37E-06	7.21E-06
AC007278.1	ENSG00000234389	-4.57975139	4.48E-06	7.39E-06
IGSF9B	ENSG00000080854	-4.856182553	5.26E-06	8.64E-06
KLRB1	ENSG00000111796	-5.402721915	5.67E-06	9.29E-06
HLA-V	ENSG00000181126	-3.520515933	5.77E-06	9.45E-06
IGLV1-40	ENSG00000211653	3.681550098	6.06E-06	9.91E-06
FAAHP1	ENSG00000232022	-4.466652669	7.15E-06	1.16E-05
RTKN2	ENSG00000182010	-3.195464575	7.21E-06	1.17E-05
GPR15	ENSG00000154165	-4.984857833	7.48E-06	1.21E-05
CCR8	ENSG00000179934	4.558578735	7.91E-06	1.28E-05
CFTR	ENSG00000001626	3.474878918	8.27E-06	1.34E-05

CXCL1	ENSG00000163739	3.568497218	8.48E-06	1.37E-05
EVPL	ENSG00000167880	3.264503023	8.59E-06	1.39E-05
ADD2	ENSG00000075340	3.67303738	9.03E-06	1.45E-05
SIAH3	ENSG00000215475	-4.389703951	1.28E-05	2.04E-05
SSTR2	ENSG00000180616	3.637234151	1.30E-05	2.07E-05
SYT1	ENSG00000067715	4.358995874	1.34E-05	2.13E-05
SULT1B1	ENSG00000173597	-3.245951518	1.55E-05	2.46E-05
DMRT2	ENSG00000173253	3.392513989	1.56E-05	2.47E-05
CALN1	ENSG00000183166	3.863996783	1.66E-05	2.62E-05
UTS2B	ENSG00000188958	3.280826761	1.67E-05	2.63E-05
AC025259.3	ENSG00000259884	-8.149228194	1.72E-05	2.71E-05
CDH1	ENSG00000039068	3.140177071	1.84E-05	2.89E-05
AC034238.1	ENSG00000240535	-5.670993996	2.05E-05	3.22E-05
SOX9-AS1	ENSG00000234899	3.489359504	2.15E-05	3.36E-05
ZDHHC11B	ENSG00000206077	-3.172035115	2.23E-05	3.49E-05
S100A7A	ENSG00000184330	3.646261332	2.24E-05	3.50E-05
KRT2	ENSG00000172867	4.647813953	2.31E-05	3.61E-05
HAND1	ENSG00000113196	5.749975914	2.34E-05	3.66E-05
AC008011.2	ENSG00000257042	3.742283936	2.52E-05	3.93E-05
IGKV3-11	ENSG00000241351	3.344786862	2.76E-05	4.28E-05
KRT72	ENSG00000170486	-5.701742648	2.85E-05	4.41E-05
MIR4697HG	ENSG00000280237	-4.657923676	3.00E-05	4.64E-05
SLC35F3	ENSG00000183780	3.282224355	3.05E-05	4.72E-05
KRT73	ENSG00000186049	-6.07153253	3.09E-05	4.78E-05
PI3	ENSG00000124102	4.30249586	3.14E-05	4.85E-05
PAX5	ENSG00000196092	3.18467972	3.30E-05	5.08E-05
BCORP1	ENSG00000215580	-4.466322956	3.61E-05	5.55E-05
FUT3	ENSG00000171124	-3.087638701	3.67E-05	5.63E-05
DCT	ENSG00000080166	3.142273369	3.71E-05	5.70E-05
PROK2	ENSG00000163421	3.128624641	3.88E-05	5.94E-05
ETV3L	ENSG00000253831	3.481159951	4.30E-05	6.56E-05
IGHG3	ENSG00000211897	5.446885618	4.59E-05	7.00E-05
HLA-DQB1-AS1	ENSG00000223534	-3.834494378	5.10E-05	7.75E-05
FAM30A	ENSG00000226777	3.824851005	5.40E-05	8.19E-05
TNFSF9	ENSG00000125657	3.01841419	5.91E-05	8.93E-05
PEG10	ENSG00000242265	3.356396401	6.16E-05	9.31E-05
FOSB	ENSG00000125740	-6.706026157	8.31E-05	0.000125
SCN5A	ENSG00000183873	-3.020839505	8.46E-05	0.000127
SIK1	ENSG00000142178	-3.227928034	8.59E-05	0.000129
NOG	ENSG00000183691	-3.817103758	8.87E-05	0.000132
KRT1	ENSG00000167768	4.331564098	9.92E-05	0.000147
POU2AF1	ENSG00000110777	3.272959866	0.000102	0.000152
IGLV1-44	ENSG00000211651	3.50040403	0.000117	0.000173
DSC1	ENSG00000134765	3.597768536	0.000123	0.000181
AC020656.1	ENSG00000257764	-3.075379762	0.000159	0.000233
AC103702.2	ENSG00000272763	3.185574655	0.000192	0.000278
NEFL	ENSG00000277586	-3.396221882	0.000373	0.000528
AC010889.1	ENSG00000260197	-3.111783822	0.000549	0.000769
IGHV1-2	ENSG00000211934	3.30020287	0.00056	0.000784
CCR6	ENSG00000112486	-4.056285618	0.000736	0.00102
IGLV3-12	ENSG00000211667	-3.26721665	0.001693	0.002284

AC099552.1	ENSG00000217825	3.517659149		0.003078	0.004059
USP9Y	ENSG00000114374	-3.132477675		0.004983	0.006444

Supplementary Table S16. Fusion transcripts in pcALCL detected by RNA-seq.

Sample	Fusion transcript	Left Chr	Left Breakpoint	Strand	Right Chr	Right Breakpoint	Strand	Predicted effect
cAL1	NLRP1–DERL2	17	5558339	-	17	5474789	-	in-frame
cAL1	ANKRD11–VPS9D1-AS1	16	89316936	-	16	89717344	+	CDS(truncated)/exonic(no-known-CDS)
cAL1	INPP5B–GNL2	1	37931673	-	1	37583933	-	out-of-frame
cAL2	IGSF3–CD58	1	116579392	-	1	116521983	-	in-frame
cAL3	TNK1–GPS2	17	7387074	+	17	7315061	-	CDS(truncated)/CDS(no-known-start-or-end)
cAL3	TP53–TNK1	17	7687377	-	17	7382836	+	UTR/UTR
cAL4	GPS2–CHD3	17	7314488	-	17	7887029	+	CDS(truncated)/intronic
cAL5	LINC-PINT–RNASEH2B-AS1	7	130945720	-	13	50889735	-	exonic(no-known-CDS)/exonic(no-known-CDS)
cAL5	SMARCAD1–TP63	4	94241006	+	3	189808272	+	in-frame
cAL5	TP63–SMARCAD1	3	189738774	+	4	94249654	+	in-frame
cAL5	ETS1–SLC37A4	11	128521913	-	11	119025076	-	in-frame
cAL7	NFKB2–SIRT3	10	102400824	+	11	216718	-	N/A
cAL7	GTPBP2–TRERF1	6	43623737	-	6	42228669	-	N/A
cAL7	SIRT3–NFKB2	11	218832	-	10	102401180	+	N/A
cAL8	USP7–SAMD11	16	8963207	-	1	942410	+	in-frame
cAL8	MMS19–RRP12	10	97462017	-	10	97409859	-	CDS(truncated)/UTR
cAL9	NFAT5–WWP2	16	69566374	+	16	69840126	+	in-frame
cAL10	RABEPK–UBAC1	9	125220700	+	9	135955415	-	out-of-frame
cAL10	HIVEP3–MRPL43	1	41918413	-	10	100987468	-	UTR/UTR
cAL10	DUSP22–UNC93B1	6	311962	+	11	67991857	-	N/A
cAL11	AGTRAP–LST1	1	11736235	+	6	31588518	+	in-frame
cAL11	CLK2–NUMA1	1	155268010	-	11	72035975	-	N/A
cAL11	KANSL1–ARL17B	17	46094560	-	17	46352930	-	N/A
cAL12	ERBB2IP–SQRDL	5	65926806	+	15	45658907	+	UTR/UTR
cAL12	RBPJ–TRAPPC12	4	26163614	+	2	3443779	+	UTR/CDS(truncated)

CDS, coding sequence; UTR, untranslated region of mRNA; N/A, not available.

Supplementary Table S17. Upregulated and downregulated processes/pathways in pcALCL (GeneAnalytics).

Upregulated processes/pathways in pcALCL

Name	Enrichment Score	Source	Number Matched	Total Genes
SuperPath: ERK Signaling	166.1	Qiagen	224	1180
SuperPath: Integrin pathway	94.03	Qiagen	135	568
SuperPath: Phospholipase-C Pathway	86.47	Qiagen	121	500
SuperPath: Collagen Chain Trimerization	67.65	Reactome, Qiagen, KEGG	63	184
SuperPath: PAK pathway	59.21	Qiagen	127	683
SuperPath: Focal Adhesion	57.48	KEGG, Qiagen, BioSystems	73	283
SuperPath: AKT Signaling	49.09	Qiagen	119	682
SuperPath: GPCR Pathway	48.91	Qiagen	122	709
SuperPath: Actin Nucleation by ARP-WASP Complex	39.41	Qiagen	70	342
SuperPath: Allograft Rejection	26.53	KEGG, Qiagen, BioSystems	49	249

Downregulated processes/pathways in pcALCL

Name	Enrichment Score	Source	Number Matched	Total Genes
SuperPath: Icos-ICosL Pathway in T-Helper Cell	13.3	Qiagen	14	131
SuperPath: TCR Signaling	11.75	Qiagen	19	239
SuperPath: Fc-GammaR Pathway	5.75	Qiagen	7	84

Supplementary Table S18. Human kinases for which known co-expressed genes were overrepresented in RNA-seq data of pcALCL, Top 20 hits (ARCHS4 database).

Term	Overlap	Odds Ratio	*P*-value	Combined Score
DDR2 human kinase ARCHS4 coexpression	178/299	6.938435	2.70E-112	1782.45
PDGFRB human kinase ARCHS4 coexpression	176/299	6.860475	7.92E-110	1723.45
PDGFRA human kinase ARCHS4 coexpression	161/299	6.275776	4.06E-92	1320.66
MYLK human kinase ARCHS4 coexpression	159/299	6.197816	7.32E-90	1272.05
RPS6KA2 human kinase ARCHS4 coexpression	152/299	5.924956	3.71E-82	1110.93
TEK human kinase ARCHS4 coexpression	144/299	5.613116	1.02E-73	943.37
ACVRL1 human kinase ARCHS4 coexpression	134/299	5.223316	1.03E-63	757.56
NEK7 human kinase ARCHS4 coexpression	133/299	5.184336	9.52E-63	740.37
KDR human kinase ARCHS4 coexpression	121/299	4.716577	1.24E-51	552.85
MELK human kinase ARCHS4 coexpression	119/299	4.638617	7.24E-50	524.86
MERTK human kinase ARCHS4 coexpression	119/299	4.638617	7.24E-50	524.86
PBK human kinase ARCHS4 coexpression	115/299	4.482697	2.06E-46	471.56
TIE1 human kinase ARCHS4 coexpression	115/299	4.482697	2.06E-46	471.56
CSF1R human kinase ARCHS4 coexpression	113/299	4.404737	1.01E-44	446.23
EGFR human kinase ARCHS4 coexpression	113/299	4.404737	1.01E-44	446.23
CDK1 human kinase ARCHS4 coexpression	112/299	4.365757	6.89E-44	433.89
ACVR1 human kinase ARCHS4 coexpression	112/299	4.365757	6.89E-44	433.89
AURKB human kinase ARCHS4 coexpression	111/299	4.326777	4.64E-43	421.76
NEK2 human kinase ARCHS4 coexpression	108/299	4.209837	1.30E-40	386.65
PLK4 human kinase ARCHS4 coexpression	105/299	4.092897	3.16E-38	353.41

Supplementary Table S19. Copy numbers of cancer genes recurrently affected by CNAs in pcALCL as estimated by WGS and ddPCR.

TNFRSF8

	WGS[1]		ddPCR[2]	
Patient	Copy number	Type of CNA	Copy number	Type of CNA
cAL1	6	Gain	5.81	Gain
cAL9	3	Gain	3.36	Gain

RBFOX1

	WGS[1]		ddPCR[2]	
Patient	Copy number	Type of CNA	Copy number	Type of CNA
cAL8	1	Loss	1.11	Loss
cAL10	1	Loss	1.29	Loss

STK24

	WGS[1]		ddPCR[2]	
Patient	Copy number	Type of CNA	Copy number	Type of CNA
cAL5	1	Loss	1.37	Loss
cAL8	1	Loss	1.21	Loss
cAL10	1	Loss	1.42	Loss

EZH2

	WGS[1]		ddPCR[2]	
Patient	Copy number	Type of CNA	Copy number	Type of CNA
cAL1	3	Gain	3.48	Gain
cAL5	3	Gain	2.85	Gain
cAL6	3	Gain	3.50	Gain
cAL7	3	Gain	2.43	Gain
cAL10	4	Gain	4.37	Gain
cAL11	3	Gain	2.22	Gain

PRDM1

	WGS[1]		ddPCR[2]	
Patient	Copy number	Type of CNA	Copy number	Type of CNA
cAL1	1	Loss	1.31	Loss
cAL5	1	Loss	1.45	Loss
cAL6	1	Loss	1.18	Loss
cAL8	1	Loss	1.28	Loss
cAL10	1	Loss	1.47	Loss
cAL11	1	Loss	1.74	Loss

[1] As estimated by Control-FreeC using WGS data. [2] Assessed using QX200 ddPCR system (Bio-Rad).

Supplementary Table S20. Genes affected by genetic alterations in pcALCL and involved in signaling via the PI-3-K/AKT pathway, MAPK pathway or G-proteins.

Patient	Genes
cAL1	DGKI, GRM8, MET
cAL2	RET, RGS7
cAL3	GPS2, MAP3K1, RASA1, TNK1, MAP3K20
cAL4	GPS2, PDPK1, TNK1
cAL5	PIK3R1, STK24
cAL6	None
cAL7	None
cAL8	PDGFD, PPM1L, PTPRK, STK24
cAL9	CREB3L1, PIK3R1
cAL10	CREBBP, ERBB4, DRD5, PDPK1, PIK3C2B, RGS11, RGS12, SND1, STK24, WNK2
cAL11	None
cAL12	ERBB2IP, GPR56