

Supplemental Materials and Methods

Whole exome sequencing. Genomic DNA was extracted from whole blood from 567 early onset (age 0-18) IBD samples; 543 (95.8%) of these samples passed DNA QC. Libraries were prepared according to manufacturer instructions using 1 µg of input DNA per sample; whole exome capture was performed with the SureSelect Human All Exon 50-Mb Kit (Agilent Technologies). Libraries were validated with the KAPA Library Quantification Kit (KAPA Biosystems) and were then sequenced on the Illumina HiSeq platform according to standard protocols. Library preparation and sequencing was performed at Broad Institute's Genomics Platform, Cambridge, USA.

Filtering and validation of variants. Primers used for validation were designed using EmPrime or Primer3. M13 forward and reverse tags (Forward tag:TGTAAAACGACGGCCAGT; Reverse tag:CAGGAAACAGCTATGACC) were added to the primer sequence for easier Sanger downstream analysis. The PCR amplicons were purified using Promega, Wizard SV gel and PCR Clean-up System (Promega, Madison, WI) and sent to Genewiz, (South Plainfield, NJ) for sequencing. The Sanger sequencing results were analyzed using the online 4Peaks DNA sequence trace viewer software. The primers used for the validation are shown in Supplemental Table 2. Not all variants required Sanger validation since they were validated by either frequency, by cluster, or by 1000 genomes.

Circulating Neutrophil Purification and RNA Preparation. Neutrophils were purified using the MACexpress Neutrophil Isolation Kit according to the manufacturer's protocol (Miltenyi Biotec). After purification the neutrophils were centrifuged and re-suspended in RNAlater (Qiagen) and stored at -80°C until further processing. Neutrophil RNA was extracted using TRIzol LS reagent (Life Technologies) according to the manufacturer's protocol.

RNA Sequencing and Analysis. Following removal of barcodes and primers, raw sequences were aligned to the Hg19 human genome, with reference annotations provided by UCSC.

Alignment was performed under the following parameters: 1) minimum identity of 90%; 2) maximum gaps of 5%; 3) minimum aligned read length of 25; 4) one match to output per read; and 5) reads with >5 matches were ignored. Reads were aligned using a proprietary Burrow Wheeler Transform-based method, COBWeb. Using the Expectation-Maximization algorithm, reads per transcript per million (RPKM) were computed from aligned reads. RPKM were thresholded at 1, normalized using the DESeq algorithm, and baselined to the median of all samples (N=40448 transcripts). Transcripts with reasonable expression, >3 reads in 100% of samples in at least one of the three conditions (control, normal ROS Crohns, low ROS Crohns) were included in differential analyses (N=13355 transcripts).

Ontological Analysis. In ontological analyses of genes derived from comparing low and normal ROS CD neutrophils to controls, up/down genes included those shared between the low/normal ROS CD vs controls comparisons and those that were specific to low or normal ROS CD (see Venn diagram). In order to provide more granular focus on the transcriptomic impact of low or normal ROS production on glycolysis in the CD background, we performed candidate gene identification and prioritization through Toppgene. Using ‘glycolysis’ as the query term, we used GATACA (gataca.cchmc.org) and ToppGene to build a glycolysis-related gene set. Using 90 glycolysis genes as the training set, we identified low/normal ROS-related genes with significant functional overlap ($p<0.05$) with glycolytic functions, processes, and pathways.

Supplemental Table 1. Characteristics of 543 IBD Participants with Exome Sequencing Data.

Age at diagnosis	Range	0-18
	Median	8
	Mean	7.5
Gender	Female	226 (42%)
	Male	317 (58%)
Diagnosis	CD	416 (77%)
	UC	89 (16%)
	IBD-other	38 (7%)
Self-identified race	African-American	86 (16%)
	Caucasian	376 (69%)
	South/East Asian	15 (3%)
	Other/Not recorded	66 (12%)

Supplemental Table 2. Primers used for Sanger Sequencing of NADPH Oxidase Gene Variants.

Supplemental Table 3. Clinical and Demographic Characteristics of the Participants with Neutrophil Function Testing

	Age at Diagnosis	Age at Testing	Male	White	AA	L1	L2	L3
Control (n=26)	NA	14(6-19)	13(50)	21(81)	4(15)	NA	NA	NA
CD (n=129)	11(1-20)	15(4-23)	79(61)	115(89)	11(9)	13(10)	18(14)	98(76)

AA: African-American; L1: ileal location; L2: colon-only location, L3: ileo-colonic location; CD: Crohn Disease; NA: not applicable; one control & three CD subjects were Asian; age is shown as mean(range) in years; remaining variables are shown as n(%)

Supplemental Table 4. Missense Mutations in Core NADPH Oxidase Genes in European, African, and East/South Asian Ancestry.

The minor allele frequency for validated missense mutations in core NADPH oxidase genes identified in 543 early onset IBD patients is shown for the dbSNP and ExAC databases for the indicated ancestries. Novel mutations for a database are indicated by “-“ for the MAF.

Supplemental Table 5. Neutrophil Activation Markers and Functions in Patients Stratified by FMLP Induced ROS Production

	CD ROS Lo	CD ROS HI
FPR1	27(24,31)	28(25,32)
CD64 Index	1.5(1.1,2)	1.2(1,1.4)
CD11B	1(0.9,1.1)*	1.2(1.1,1.3)
Phagocytosis	6.6(6.1,7.1)	7.3(6.6,8)
Killing	85(82,88)	85(83,88)

ROS Lo was defined as FMLP induced MFI < 360; data are shown as mean (95thCI) MFI for FPR1, CD64 Index, and CD11B; as number of *Staph Aureus* engulfed per cell for phagocytosis; and as percentage of *Staph Aureus* engulfed per cell for killing;
 *p<0.05 vs CD ROS Hi

Supplemental Table 6. Disease Activity and Treatment Exposures at the Time of Neutrophil Function Measurements

	Disease Duration	Moderate- Severe Activity	Antibiotic	Cortico- steroid	5ASA	IMM	Anti-TNF
CD	60(0-156)	4(7)	3(5)	5(8)	10(16)	19(31)	37(61)
Low ROS (n=61)							
CD Normal ROS (n=68)	55(0-138)	6(9)	8(12)	7(10)	11(16)	27(40)	41(60)

Low ROS was defined as FMLP induced MFI < 360; data are shown as mean (range) in months for disease duration or n(%) for other factors; The mean (95thCI) time between neutrophil function measurements and time of surgery was 27(14,40) months. Disease activity was defined by Physician Global Assessment (PGA); 5ASA: mesalamine; IMM: immune modulator, 6-mercaptopurine or methotrexate. Differences between groups were tested by chi2 test.

Supplemental Table 7. Clinical and Demographic Characteristics of
CD Patients Stratified by Core *NADPH* Oxidase Gene Mutation Carriage

Supplemental Table 8. Core Neutrophil NADPH Oxidase Gene Expression in Normal and Low ROS CD Neutrophils.

Gene Symbol	Gene ID	CD ROS NI (raw)	CD ROS Lo (raw)	Fold-Change	p-value	Regulation
CYBA	1535	459.6597	443.3696	1.002125	0.984565	up
CYBB	1536	2075.979	2225.3076	1.113678	0.641644	up
FPR1	2357	4200.4673	4128.7485	1.021205	0.912778	up
NCF1	653361	943.92926	898.38	-1.01132	0.954754	down
NCF2	4688	8668.249	9555.354	1.14527	0.496052	up
NCF4	4689	1044.3026	1149.8049	1.143907	0.418135	up
RAC1	5879	1451.679	1787.6343	1.279384	0.048853	up
RAC2	5880	5833.94	5662.6714	1.008444	0.936435	up

ROS Lo was defined as FMLP induced MFI < 360

Supplemental Table 9. Differentially Expressed Genes in Normal and Low ROS CD Neutrophils and Control Neutrophils.

Differentially expressed genes for each pair-wise comparison are indicated in bold font, with genes also contained within the glycolysis gene training set underlined.

Supplemental Table 10. Glycolysis Trained Gene Sets for Differentially Expressed Genes in Normal and Low ROS CD Neutrophils and Control Neutrophils.

Supplemental Table 11. Biologic Pathways Enriched in Differentially Expressed Genes in Normal and Low ROS CD Neutrophils and Control Neutrophils.

Supplemental Table 12. Core Genes Distinguishing Low ROS CD Neutrophils.

Fold-change differences for each pairwise comparison are shown.

Supplemental Table 13. Potentially Damaging Mutations in Core Genes which Distinguish Low ROS CD Neutrophils.

The minor allele frequency for potentially damaging missense mutations in 50 genes whose expression distinguishes low ROS CD neutrophils identified in 543 early onset IBD patients is shown for the dbSNP and ExAC databases for the indicated ancestries. Novel mutations for a database are indicated by “-“ for the MAF.

Supplemental Figure 1. Neutrophil ROS Production in CD and CGD patients and Healthy Controls.

Neutrophil ROS production was determined in the CCHMC Clinical Immunology Lab and is shown as the median (IQR) for healthy controls (n=11), CD patients (n=17), autosomal recessive (AR) CGD patients (n=5) and X-linked CGD patients (n=6). Differences between groups were tested by ANOVA with Tukey's multiple comparison test. a:p=0.005 versus control; b:p<0.0001 versus AR-CGD and X-linked CGD; c:p<0.0001 versus control and CD.

Supplemental Figure 2. Flow Cytometry Measurement of Neutrophil Cell Surface Proteins.

Representative data are shown for flow cytometry measurement of A) FPR1, B) CD11b, and C) the neutrophil CD64 index.

Supplemental Figure 3. Analytic Pipeline for Gene Expression Data.

Two analytic pipelines were followed to identify transcriptomic and functional signatures of low ROS CD neutrophils in comparison to normal ROS CD neutrophils and control neutrophils. Beginning with all highly expressed transcripts (N=13355), Welch's t-tests were used to identify differentially expressed genes ($p<0.05$ and $fc>1.5$). The first pipeline compared normal ROS CD neutrophils vs controls, and low ROS CD neutrophils vs controls. The second pipeline compared low ROS CD neutrophils vs normal ROS CD neutrophils. These gene lists were submitted for ontological analysis; further, genes from these lists were ranked by functional importance using a glycolysis training set. Top ranked genes were submitted for further ontological analysis.

Supplemental Figure 4. Venn diagram Showing Shared and Unique Genes Differentially Expressed in CD Neutrophils with Low and Normal ROS Production.

In the first analytic pipeline, differentially regulated genes between normal ROS CD neutrophils vs control neutrophils ($N=618$) and low ROS CD neutrophils vs control neutrophils ($N=834$) were overlapped using a Venn diagram. We identified 272 consistently downregulated and 105 consistently upregulated genes in low and normal ROS CD compared to controls. Further, we identified 186 down and 271 upregulated genes specific to low ROS CD neutrophils, and 195 down and 46 upregulated genes specific to normal ROS CD neutrophils.

Supplemental Figure 5. Metabolic and Immune Functions Differentially Expressed in CD Neutrophils with Normal and Low ROS Production Compared to Control Neutrophils.

A) Upregulated genes between normal ROS CD neutrophils vs control neutrophils ($N=151$) and between low ROS CD neutrophils and control neutrophils ($N=376$) were submitted to ToppCluster for ontological analysis. Highly significant and informative ontologies were selected to identify common mechanisms disrupted in CD neutrophils, and to identify disrupted mechanisms specific to low- and normal-ROS CD neutrophils. B) The same process was repeated for the 467 and 458 genes downregulated in normal and low ROS CD neutrophils, respectively, when compared to control neutrophils.

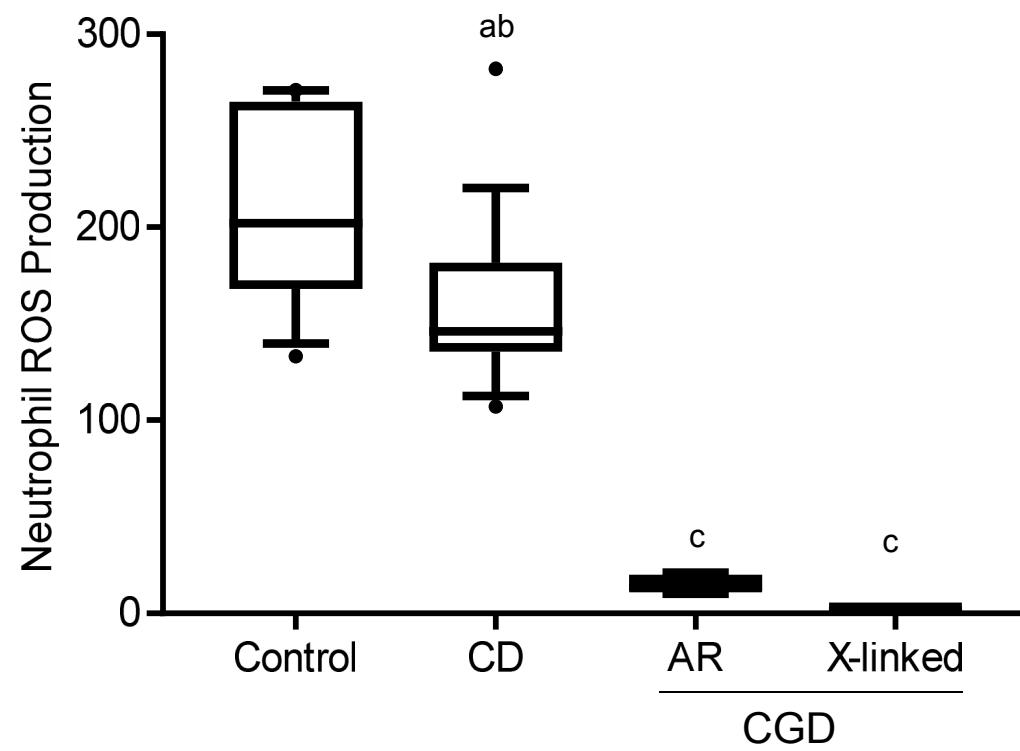
Supplemental Figure 6. Heat Map of Genes Differentially Expressed between CD Neutrophils with Normal or Low ROS Production and Control Neutrophils.

Candidate gene prioritization through functional enrichment analysis, using genes differentially regulated between normal (A) or low (B) ROS CD neutrophils and controls as the test set and a glycolysis gene list as the training set, ranked the test genes in order of importance in the context of glycolytic functions. Test genes with significant enrichment are included in the heatmap, where blue, black, and yellow correspond to expression below, at, and above the median, respectively.

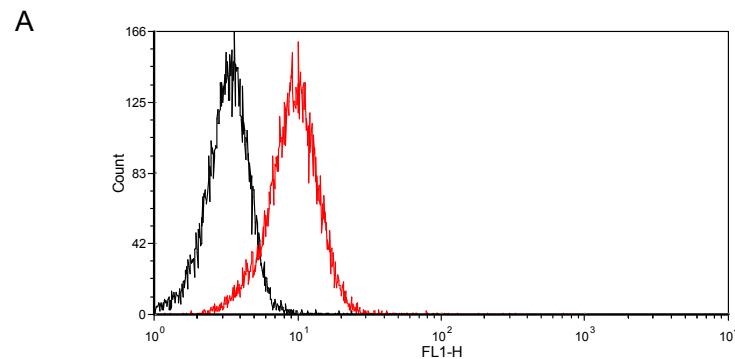
Supplemental Figure 7. Metabolic and Immune Functions Differentially Expressed between CD Neutrophils with Low versus Normal ROS Production.

In the second analytic pipeline, low ROS CD neutrophils were compared directly to normal ROS to identify 411 differentially regulated genes. Up and downregulated genes were submitted to Toppcluster to identify mechanisms and pathways enriched in the gene sets, where highly significant and informative ontologies were included for visualization.

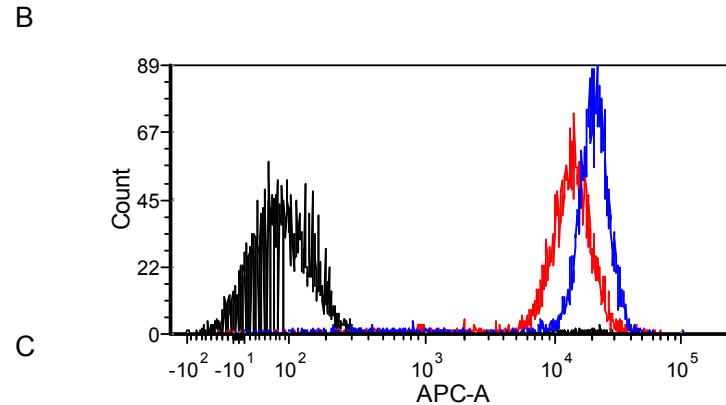
Supplemental Figure 1



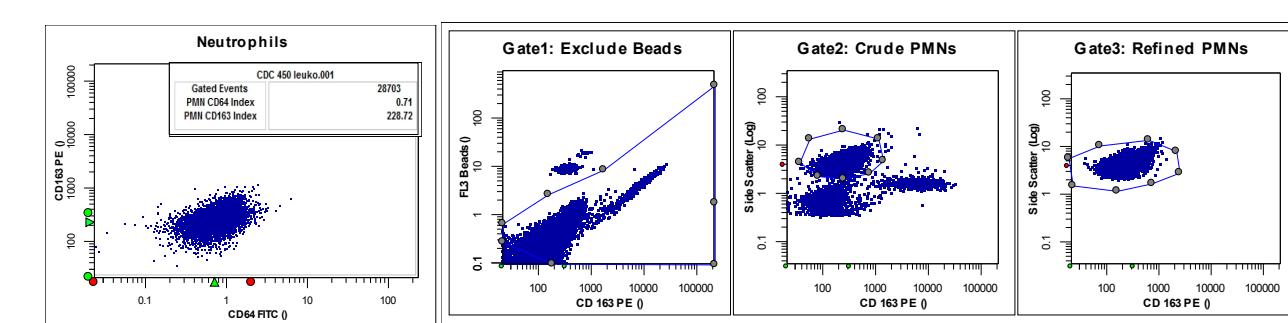
Supplemental Figure 2



Black isotype, red FPR1

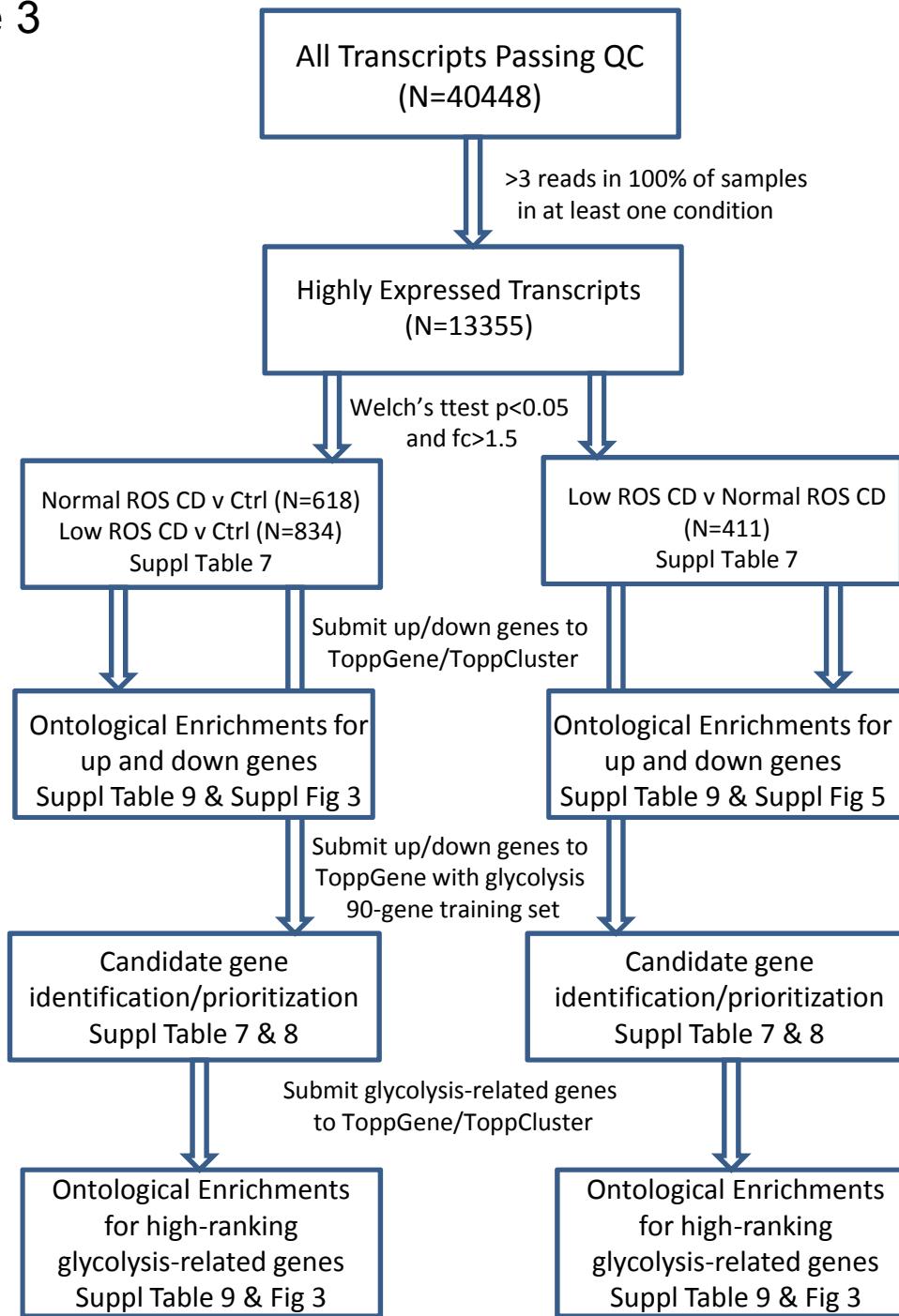


Black isotype,
Red low ROS CD CD11b
Blue high ROS CD CD11b

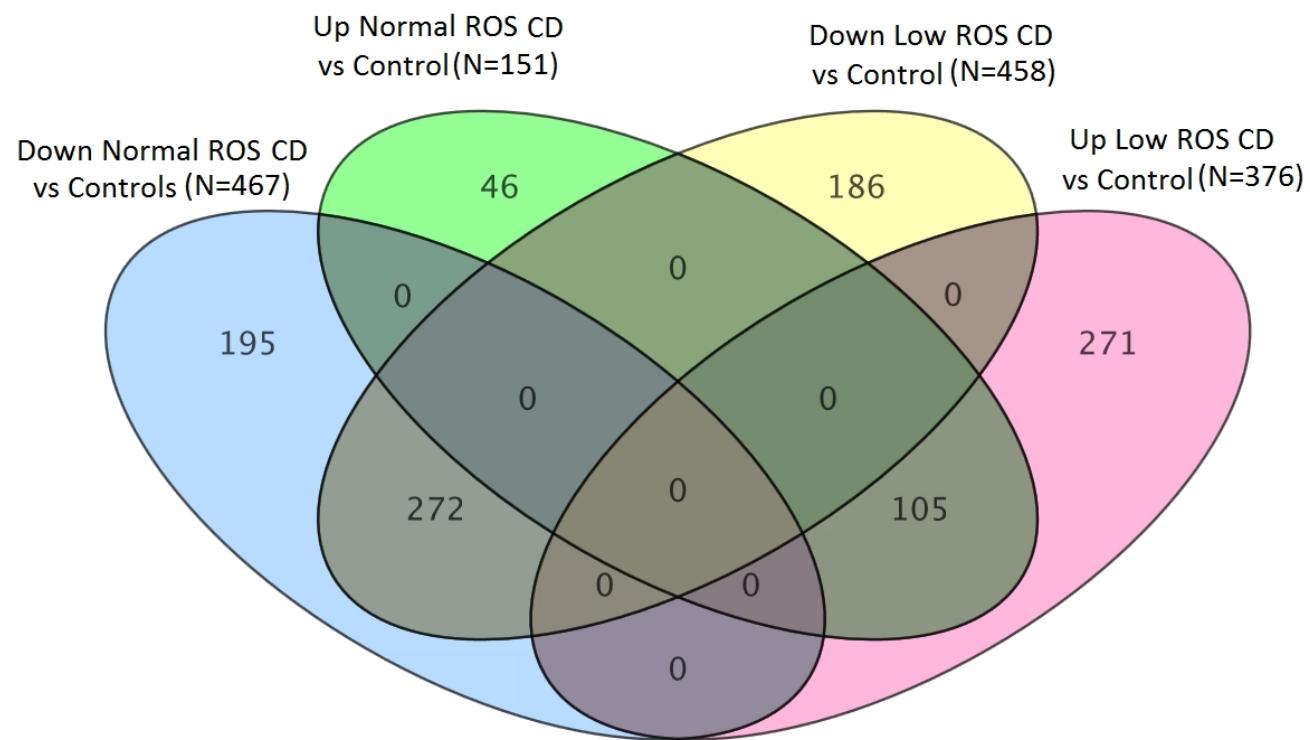


CD64 Index

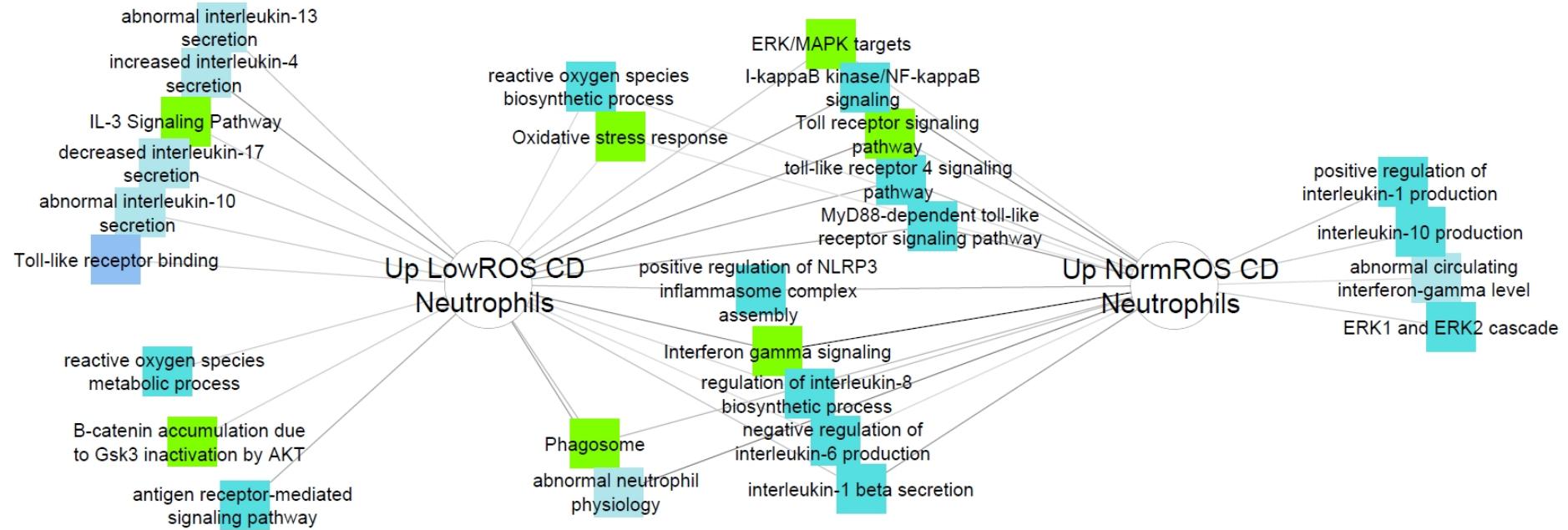
Supplemental Figure 3



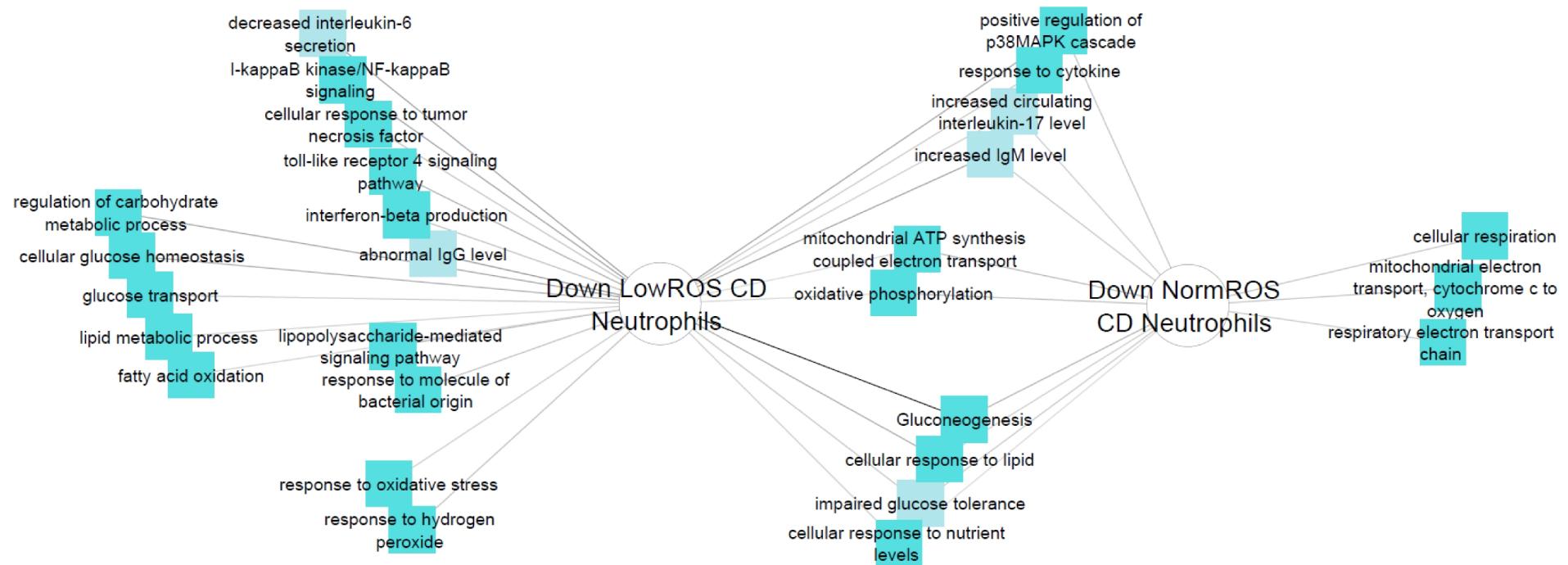
Supplemental Figure 4



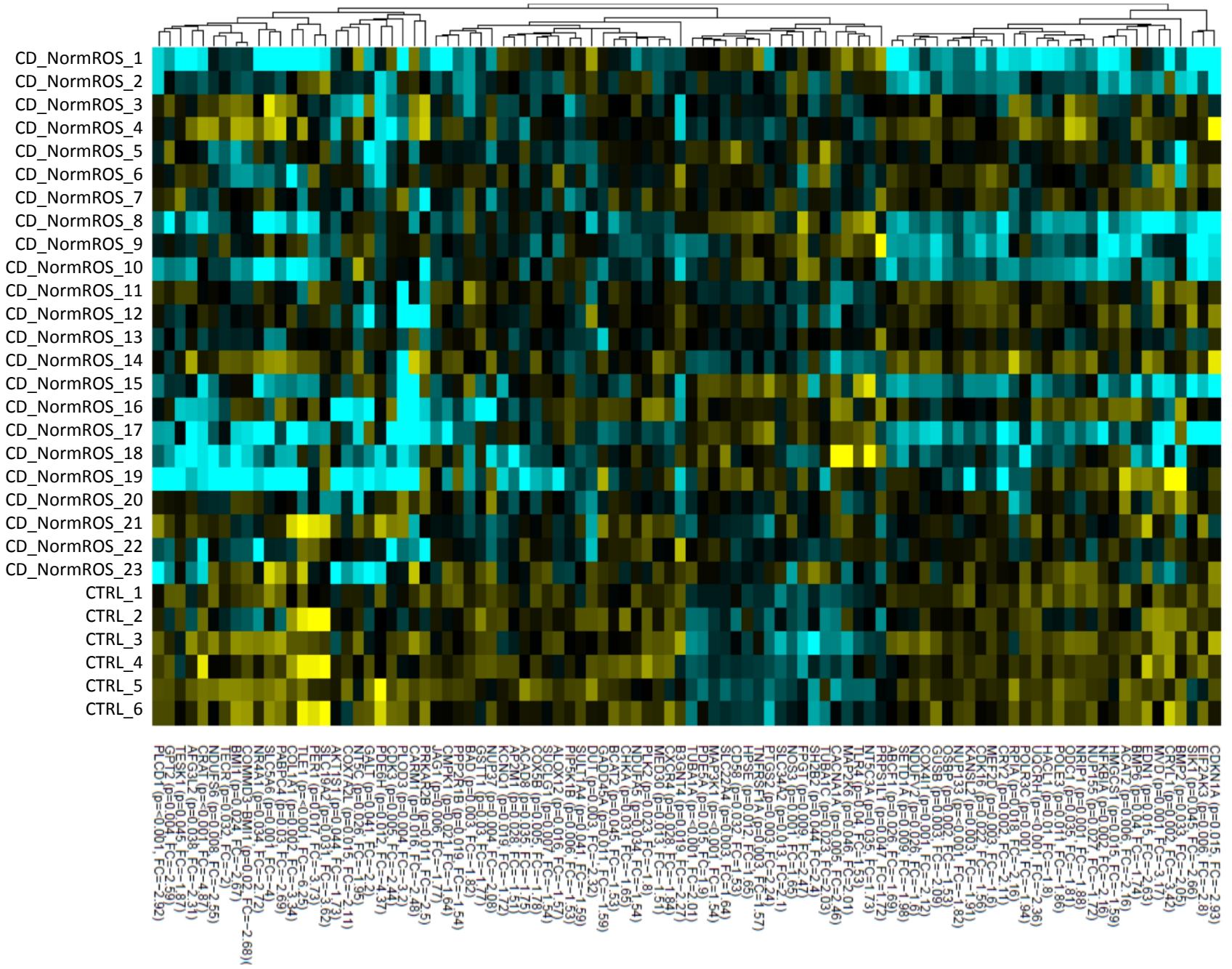
Supplemental Figure 5A



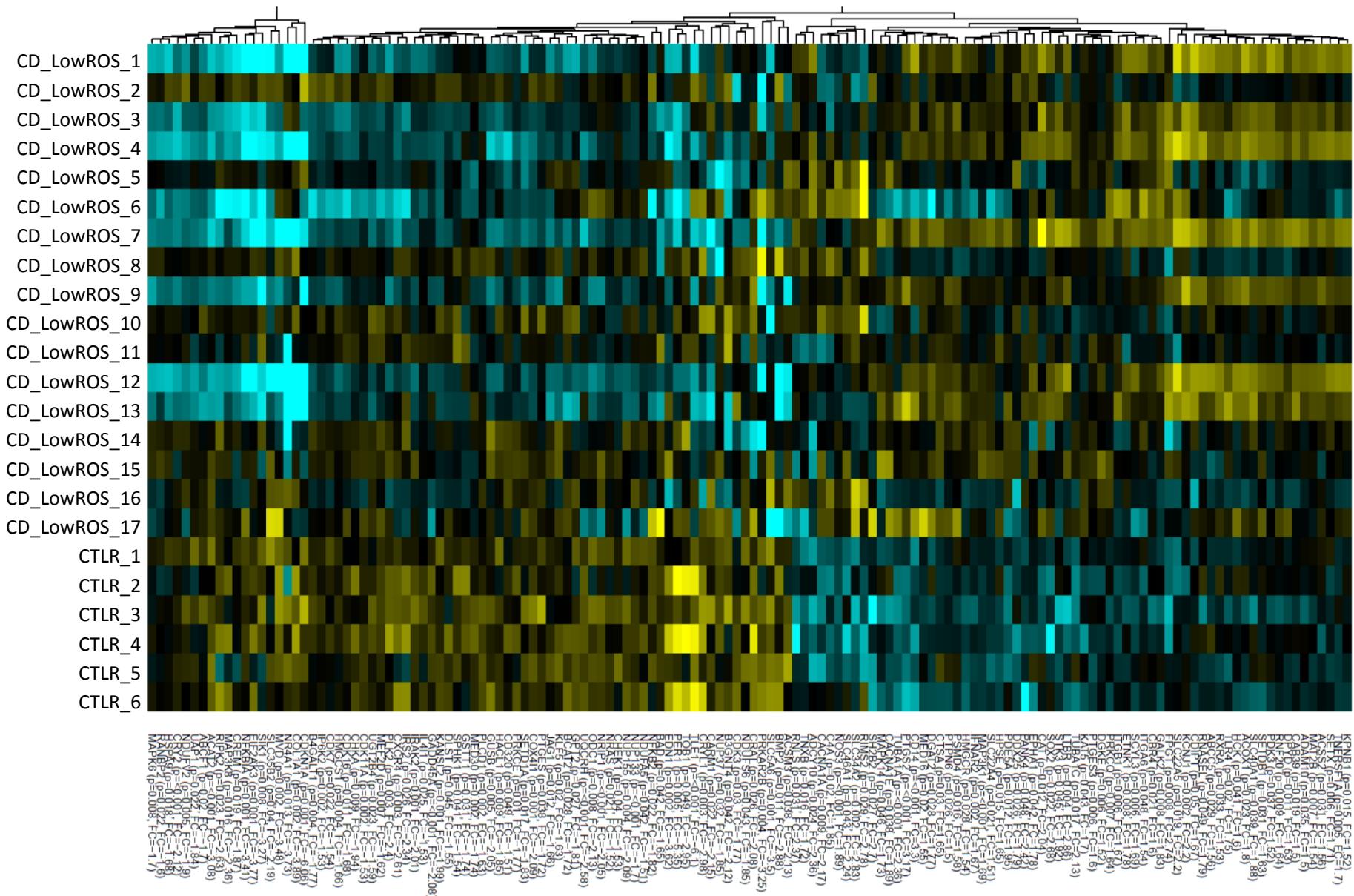
Supplemental Figure 5B



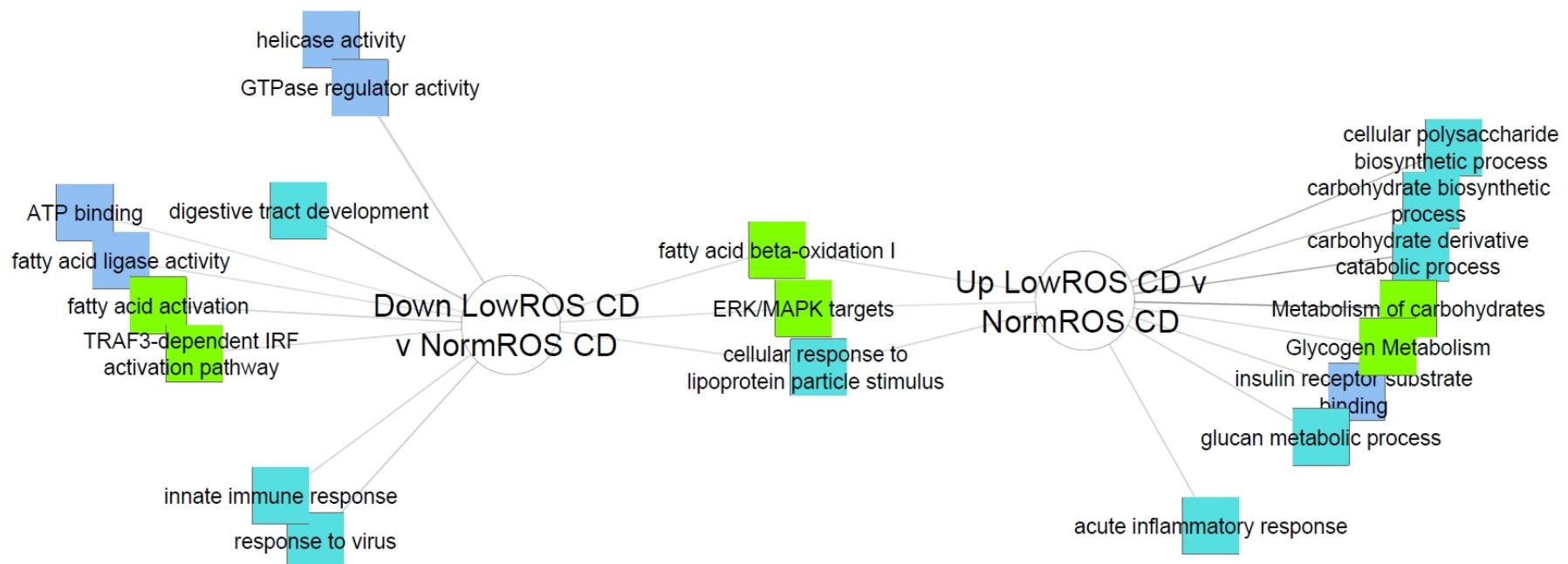
Supplemental Figure 6A



Supplemental Figure 6B



Supplemental Figure 7



Gene	chrom	pos	ref	alt	rsID	Sequencing Forward Primer (5'-3')	Sequencing Reverse Primer (5'-3')
CYBA	chr16	88643450	C	T	Novel	TGTAAAACGACGGCCAGTTCGCTGCATTATTGAGGT	CAGGAAACAGCTATGACCAGTGTCCACCACGGATCTTC
CYBA	chr16	88646184	C	T	rs779140893	TGTAAAACGACGGCCAGTGCAGTCATAACCAAACGAGGT	CAGGAAACAGCTATGACCAGAACACCCAGGACCGAACAA
CYBA	chr16	88646828	A	G	rs4673	TGTAAAACGACGGCCAGTGAACACTGAGGTAAGTGGGGG	CAGGAAACAGCTATGACCAGTGTCCAGACCTGTTGGAACC
CYBA	chr16	88647125	T	G	rs11547387	TGTAAAACGACGGCCAGTGAACACTGAGGTAAGTGGGGG	CAGGAAACAGCTATGACCAGTGTCCAGACCTGTTGGAACC
NCF1	chr7	74777318	C	T	rs782800778	TGTAAAACGACGGCCAGTAATCCAGGACAACCGCAAAGA	CAGGAAACAGCTATGACCAAACCACTAAAAGGCCGAGC
NCF1	chr7	74779274	G	A	rs139225348	TGTAAAACGACGGCCAGTTCTCGGGTTGACCTCATGTT	CAGGAAACAGCTATGACCTGAAGAAGTCGAGGAGGTGGG
NCF1	chr7	74779295	C	T	Novel	TGTAAAACGACGGCCAGTTCGGGCTTGACCTCATGTTCT	CAGGAAACAGCTATGACCTGAAGAAGTCGAGGAGGTGGG
NCF1	chr7	74779319	T	G	rs144018361	TGTAAAACGACGGCCAGTTCTCGGGCTTGACCTCATGTT	CAGGAAACAGCTATGACCTGAAGAAGTCGAGGAGGTGGG
NCF1	chr7	74779322	A	G	rs10614	TGTAAAACGACGGCCAGTTGGGTTGACCTCATGTTCT	CAGGAAACAGCTATGACCTGAAGAAGTCGAGGAGGTGGG
NCF1	chr7	74780830	C	A	Novel	TGTAAAACGACGGCCAGTTCTCTCAGGACAAAAAGCC	CAGGAAACAGCTATGACCTTCATTAGCCCAAACACTC
NCF2	chr1	183560204	G	A	rs55761650	TGTAAAACGACGGCCAGTACAGGGAAAGTCTGAGTGTCAAC	CAGGAAACAGCTATGACCTTCAGGGTGACCAAGGCTTTC
NCF2	chr1	183563531	T	A	rs147744729	TGTAAAACGACGGCCAGTCCTCATTGCACTCACCACTGTGT	CAGGAAACAGCTATGACCTGTGCCAATCACGAAACTGC
NCF2	chr1	183566954	A	G	rs35937854	TGTAAAACGACGGCCAGTCTCAACTTAGCACATCTGGGC	CAGGAAACAGCTATGACCTCATGTTCAACGGGCAGGTAT
NCF2	chr1	183590217	C	T	rs147415774	TGTAAAACGACGGCCAGTGACTIONGACAGCCTCACAAAGG	CAGGAAACAGCTATGACCAGGGTTATGAGTCAGTTGCCAAA
NCF4	chr22	36865055	C	A	rs112306225	TGTAAAACGACGGCCAGTTCTCCTTAGGTTTCGTACCG	CAGGAAACAGCTATGACCTAGAGTGTGTTGGGTGGAAGC

Gene	chrom	pos	ref	alt	rsID	AA change	Alt allele effect	cadd	dbSNP MAF	hg19 pos (for Exac)	ExAC freq	ExAC European MAF	ExAC African MAF	ExAC East/South Asian MAF
CYBA	chr16	88643450	C	T	Novel	R164H	nonsynonymous	35	-	88709858	-	-	-	-
CYBA	chr16	88646184	C	T	rs779140893	A101T	nonsynonymous	24.9	0.000009	88712592	-	-	-	-
CYBA	chr16	88646816	C	T	rs149344911	V76M	nonsynonymous	24	0.000795	88713224	0.00075381	1.37412E-05	0.006755453	0.000557014
CYBA	chr16	88646828	A	G	rs4673	Y72H	nonsynonymous	11.7	0.689776	88713236	0.690830215	0.684183071	0.54867684	0.729532978
CYBA	chr16	88647125	T	G	rs11547387	K60T	nonsynonymous	3.32	0.003791	88713533	0.003870922	0.00516692	0.001614292	0.000460675
CYBB	chrX	37798966	G	A	rs139670417	R229H	nonsynonymous	26.7	0.000788	37658219	0.000667671	0.000180837	0.004772902	0
CYBB	chrX	37804069	G	C	rs141756032	G364R	nonsynonymous	23	0.003901	37663322	0.004000732	0.006105822	0.000587475	0.001194815
NCF1	chr7	74777318	C	T	rs782800778	R42W	nonsynonymous	31	0.000062	74191664	6.16034E-05	7.17731E-05	0.000108085	4.33163E-05
NCF1	chr7	74779274	G	A	rs139225348	G83R	nonsynonymous	20.2	0.008833	74193620	0.009059	0.01331	0.002852	0.0016795
NCF1	chr7	74779295	C	T	Novel	R90C	nonsynonymous	31	-	74193641	-	-	-	-
NCF1	chr7	74779319	T	G	rs144018361	C98G	nonsynonymous	22.9	0.000712	74193665	0.0007298	0.001215	0.0002341	0
NCF1	chr7	74779322	A	G	rs17856077, rs17295741, rs10614	S99G	nonsynonymous	-	-	74193668	0.4984	0.47845	0.3351	0.5174
NCF1	chr7	74780830	C	A	Novel	A149E	nonsynonymous	-	-	74195176	-	-	-	-
NCF1	chr7	74783529	G	A	rs145360423	W193*	stopGain	36	0.000646	74197872	0.0006464	0.001093	0.0001114	0
NCF2	chr1	183560204	G	A	rs55761650	P454S	nonsynonymous	0.75	0.004066	183529339	0.004118345	0.005930309	0.000768787	0.000993404
NCF2	chr1	183563229	T	A	rs35012521	N419I	nonsynonymous	28.4	0.005324	183532364	0.005370675	0.00550814	0.001249279	0.00723198
NCF2	chr1	183563301	C	T	rs145229115	R395Q	nonsynonymous	23.4	0.001036	183532436	0.001062568	0.00155415	0.000480492	0
NCF2	chr1	183563302	G	A	rs13306575	R395W	nonsynonymous	34	0.015222	183532437	0.015108826	0.000136329	0.001729771	0.016180329
NCF2	chr1	183563455	C	T	rs147908264	R386Q	nonsynonymous	13.4	0.002271	183532590	0.002298832	0.000818331	0.000192345	0.008465146
NCF2	chr1	183563531	T	A	rs147744729	T361S	nonsynonymous	26.6	0.001892	183532666	0.001871177	0.002114655	0.000770861	0.001550326
NCF2	chr1	183566954	A	G	rs35937854	V297A	nonsynonymous	22.9	0.004115	183536089	0.003724211	0.000122743	0.040753556	0
NCF2	chr1	183574503	G	A	rs376994104	A162V	nonsynonymous	35	0.000025	183543638	2.47093E-05	2.7265E-05	9.60984E-05	0
NCF2	chr1	183590217	C	T	rs147415774	R38Q	nonsynonymous	34	0.001408	183559352	0.001449657	0.00226306	0.000384468	0
NCF4	chr22	36865055	C	A	rs112306225	T85N	nonsynonymous	7.59	0.002867	37261097	0.002869607	0.002720004	0.009452348	3.98565E-05
NCF4	chr22	36870523	C	T	rs150976323	R151C	nonsynonymous	35	0.000056	37266565	4.9843E-05	0	0.000489141	3.99616E-05
NCF4	chr22	36875672	C	T	rs146911421	T216M	nonsynonymous	33	0.000647	37271714	0.000649253	0.000965144	0.000197824	7.98021E-05

Mutation	ROS	Age (years)	Male	White	African-American	L1	L2	L3	p	Duration	B2	B3	Sx
	median(IQR)	median(range)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	median(range)	n(%)	n(%)	n(%)
No mutation (n=20)	571(301,1005)	9(1-17)	13(65)	17(85)	3(15)	1(5)	4(20)	15(75)	9(45)	83(36-130)	4(20)	2(10)	6(30)
CYBA Y72H Hom (n=16)	350(198,545)	9(2-15)	7(50)	12(86)	2(14)	1(7)	2(14)	11(79)	6(43)	74(35-137)	3(21)	1(7)	4(29)
NADPH oxidase mutation (n=10)	329(211,377)	9(7-12)	8(80)	9(90)	1(10)	1(10)	3(30)	6(60)	8(80)	95(55-156)	6(60)	2(20)	7(70)
CYBA Y72H Hom CYBA V76M NCF2 R38Q	189	9	1	0	1	0	1	0	1	133	1	1	1
CYBA Y72H Hom NCF2 T361S	353	12	1	1	0	0	0	1	0	85	0	0	0
CYBA Y72H Hom NCF2 T361S	346	8	1	1	0	0	1	0	0	62	0	0	0
CYBA A101T NCF1 S99G Hom NCF1 G83R	349	10	0	1	0	0	1	0	1	104	1	0	1
CYBA K60T	790	11	1	1	0	0	0	1	1	55	0	0	0
NCF1S99G Hom	238	7	1	1	0	0	0	1	1	125	1	0	1
NCF1S99G Hom	312	7	0	1	0	0	0	1	1	81	1	0	1
NCF2 N419I	218	9	1	1	0	0	0	1	1	110	1	1	1
NCF2 P454S	174	9	1	1	0	0	0	1	1	156	0	0	1
NCF4 T85N	448	10	1	1	0	1	0	0	1	71	1	0	1

Hom: homozygous carriage

Remainder are heterozygous

ROS: fMLP induced neutrophil ROS production

L1: ileal location

p:perianal disease

B2: stricturing behavior

L2: colon-only location

B3: internal penetrating behavior

L3: ileo-colonic location

Sx: surgery

Gene Symbol	LowROS CD v NormROS CD		NormROS CD v CTRL		LowROS CD v CTRL	
	P-value	FC	P-value	FC	P-value	FC
A1CF	0.729	-1.075	0.047	1.636	0.127	1.522
A2M	0.044	2.377	0.884	-1.132	0.389	2.099
AAAS	0.031	1.898	0.547	-1.326	0.407	1.432
AAR2	0.452	1.297	0.004	-3.029	0.011	-2.336
ABCB6	0.891	-1.027	0.017	-1.669	0.006	-1.714
ABCC5	0.037	1.593	0.929	-1.020	0.029	1.563
ABCF1	0.991	-1.003	0.026	-1.694	0.020	-1.699
ABCF3	0.443	1.153	0.007	-1.621	0.034	-1.406
ABHD10	0.041	1.846	0.270	-1.642	0.757	1.124
ABHD12	0.561	-1.226	0.029	-3.325	0.015	-4.075
ABHD17B	0.088	-1.227	0.161	-1.252	0.025	-1.536
ABI3	0.011	2.086	0.536	-1.318	0.301	1.582
ABT1	0.037	1.409	0.029	-2.069	0.184	-1.469
ABTB2	0.692	1.103	0.087	1.825	0.038	2.013
ACAD8	0.012	1.559	0.035	-1.747	0.599	-1.121
ACAT2	0.242	-1.425	0.006	-2.159	0.000	-3.076
ACD	0.039	2.182	0.098	-2.054	0.882	1.062
ACOX1	0.210	1.341	0.193	1.344	0.023	1.801
ACPP	0.031	1.555	0.908	1.023	0.029	1.590
ACSL3	0.015	-1.590	0.847	-1.076	0.186	-1.711
ACSM3	0.227	-1.429	0.200	-1.488	0.038	-2.127
ACSS2	0.018	1.616	0.869	-1.035	0.031	1.562
ACTG1P4	0.587	-1.148	0.000	3.276	0.001	2.854
ACTR3B	0.004	2.059	0.755	-1.173	0.271	1.756
ACTR3C	0.048	1.650	0.641	1.128	0.016	1.862
ACYP1	0.012	2.593	0.279	-1.636	0.365	1.584
ADAM10	0.113	1.260	0.308	1.192	0.035	1.502
ADCY10	0.458	1.227	0.074	1.922	0.024	2.357
ADNP2	0.145	-1.321	0.173	-1.333	0.009	-1.762
ADPRHL2	0.949	-1.021	0.024	-1.786	0.025	-1.824
AEN	0.755	-1.139	0.008	-3.246	0.001	-3.699
AFF1	0.530	-1.114	0.009	1.755	0.022	1.576
AFG3L2	0.593	1.211	0.038	-2.314	0.099	-1.911
AGL	0.019	1.535	0.980	-1.008	0.233	1.522
AGPAT6	0.154	-1.491	0.149	-1.541	0.013	-2.298
AK8	0.043	-1.501	0.565	-1.295	0.164	-1.943
AKAP10	0.134	1.346	0.315	1.172	0.016	1.578

AKAP14	0.881	-1.048	0.005	-2.810	0.005	-2.946
AKT1S1	0.018	1.805	0.044	-1.727	0.803	1.045
ALG1L2	0.022	1.725	0.650	-1.118	0.069	1.542
ALG6	0.055	1.391	0.639	1.091	0.047	1.518
ALKBH2	0.010	-2.613	0.936	1.044	0.109	-2.503
ALKBH5	0.546	1.111	0.006	-1.577	0.016	-1.420
ALOX12	0.548	1.112	0.016	-1.565	0.066	-1.408
AMICA1	0.204	1.461	0.240	1.444	0.029	2.110
AMMECR1L	0.027	1.562	0.824	-1.081	0.271	1.445
ANAPC5	0.130	1.411	0.030	-1.843	0.243	-1.306
ANGPTL2	0.046	1.871	0.663	-1.318	0.556	1.420
ANGPTL7	0.460	1.245	0.028	-1.823	0.169	-1.464
ANKK1	0.039	-1.577	0.156	1.893	0.660	1.200
ANKRD55	0.214	1.514	0.369	1.443	0.043	2.185
ANKRD61	0.238	1.510	0.000	-3.537	0.008	-2.343
ANKRD65	0.623	1.063	0.034	1.488	0.020	1.581
ANP32B	0.866	1.027	0.013	-1.838	0.015	-1.789
ANP32C	0.273	1.290	0.035	1.778	0.007	2.294
ANXA4	0.014	1.520	0.457	-1.280	0.602	1.188
ANXA9	0.017	2.312	0.964	1.026	0.141	2.373
AP1AR	0.034	-1.663	0.020	1.991	0.458	1.197
AP2M1	0.024	1.396	0.028	-1.506	0.599	-1.079
AP4M1	0.223	-1.134	0.006	-1.582	0.001	-1.794
AP5S1	0.672	1.067	0.003	-1.605	0.005	-1.504
APBA3	0.037	1.924	0.469	-1.428	0.526	1.347
API5	0.050	1.553	0.480	-1.252	0.463	1.241
APOL1	0.624	-1.076	0.004	1.823	0.007	1.694
APOL2	0.877	-1.034	0.007	1.927	0.010	1.864
APOL6	0.379	-1.240	0.006	2.176	0.023	1.754
APOM	0.083	-1.367	0.151	-1.320	0.013	-1.805
APTX	0.277	1.312	0.028	-1.728	0.053	-1.317
AQP9	0.726	-1.055	0.033	1.555	0.079	1.475
AREG	0.062	-1.854	0.144	-2.763	0.035	-5.122
ARHGAP26-AS1	0.951	1.014	0.000	1.752	0.011	1.776
ARL13A	0.012	2.404	0.774	1.124	0.043	2.701
ARMCX5-GPRASP2	0.038	1.911	0.550	-1.270	0.349	1.505
ARPC5	0.187	1.323	0.221	1.364	0.031	1.805
ARPC5L	0.469	-1.197	0.033	-1.670	0.010	-1.998
ARRDC2	0.315	-1.295	0.013	-2.240	0.002	-2.902

ARSF	0.109	-1.342	0.075	-1.465	0.005	-1.966
ASAP1-IT1	0.103	1.304	0.140	1.495	0.026	1.949
ASB1	0.034	1.756	0.852	-1.074	0.204	1.635
ASF1B	0.028	1.974	0.566	1.384	0.098	2.732
ASNSD1	0.128	1.262	0.038	-1.651	0.205	-1.309
ASPH	0.020	1.562	0.996	1.002	0.309	1.565
ATF1	0.511	1.125	0.046	1.669	0.022	1.877
ATF4P4	0.282	-1.313	0.201	-1.360	0.044	-1.786
ATF6	0.166	1.264	0.219	1.278	0.037	1.615
ATG16L1	0.872	-1.034	0.023	-1.508	0.013	-1.559
ATG2A	0.387	-1.314	0.026	-1.686	0.013	-2.216
ATG9A	0.665	-1.070	0.015	-1.516	0.007	-1.622
ATL2	0.777	-1.050	0.003	-1.627	0.001	-1.709
ATP10D	0.539	1.243	0.068	1.878	0.008	2.334
ATP2C2	0.008	2.209	0.024	-2.755	0.569	-1.247
ATP8A2P3	0.718	1.204	0.026	-2.456	0.070	-2.040
ATPIF1	0.011	1.532	0.446	-1.180	0.219	1.298
ATXN2L	0.497	-1.116	0.067	-1.410	0.027	-1.573
ATXN7L3B	0.455	1.132	0.025	-1.626	0.075	-1.436
AUP1	0.239	1.281	0.049	-1.766	0.176	-1.379
AVL9	0.138	1.292	0.143	1.283	0.005	1.657
AZI1	0.687	-1.140	0.011	-2.332	0.007	-2.660
B3GNT4	0.841	1.069	0.019	-2.266	0.042	-2.121
B4GALT1	0.185	-1.281	0.041	-1.380	0.004	-1.769
BAD	0.726	1.105	0.003	-1.823	0.042	-1.650
BAGE2	0.983	-1.003	0.044	1.748	0.047	1.743
BAMBI	0.562	1.235	0.000	-8.125	0.000	-6.579
BARD1	0.046	2.079	0.265	-1.992	0.940	1.044
BBS1	0.381	1.303	0.090	2.766	0.040	3.605
BBS12	0.050	2.137	0.222	-1.952	0.873	1.095
BCAT2	0.538	-1.125	0.045	-1.527	0.028	-1.719
BCCIP	0.984	1.006	0.014	-2.195	0.007	-2.182
BCL11A	0.044	1.680	0.851	-1.102	0.424	1.525
BCL2L13	0.722	-1.047	0.041	1.603	0.062	1.531
BCL9L	0.192	-1.493	0.064	-2.221	0.010	-3.316
BCS1L	0.013	2.124	0.014	-2.650	0.503	-1.248
BEX1	0.578	1.267	0.001	-5.609	0.005	-4.426
BIRC3	0.152	-1.558	0.016	-1.852	0.001	-2.887
BLCAP	0.448	1.143	0.010	-1.689	0.064	-1.478

BLM	0.080	-1.558	0.083	-2.014	0.012	-3.137
BLOC1S1	0.024	1.997	0.323	1.685	0.036	3.363
BLOC1S4	0.282	1.476	0.049	-2.073	0.318	-1.404
BLVRA	0.449	-1.204	0.041	-1.677	0.014	-2.020
BMF	0.912	-1.028	0.022	-1.920	0.009	-1.974
BMI1	0.145	1.496	0.024	-2.674	0.132	-1.788
BMP2	0.424	-1.405	0.033	-2.053	0.011	-2.885
BMP2K	0.319	1.203	0.118	1.442	0.032	1.735
BMP6	0.551	1.158	0.040	-1.741	0.100	-1.503
BOD1	0.504	1.264	0.001	-2.961	0.003	-2.343
BRD9	0.080	1.517	0.039	-2.279	0.224	-1.502
BRF2	0.025	1.918	0.035	-1.912	0.988	1.003
BRI3BP	0.007	2.144	0.802	-1.150	0.278	1.865
BRMS1	0.282	-1.142	0.051	-1.656	0.020	-1.891
BRPF1	0.173	1.402	0.041	-1.770	0.142	-1.263
BSDC1	0.343	1.110	0.003	-1.632	0.013	-1.471
BTN3A3	0.272	1.394	0.169	1.612	0.011	2.248
BTRC	0.010	2.080	0.771	-1.195	0.364	1.740
C10orf105	0.529	-1.144	0.040	-1.315	0.040	-1.504
C10orf131	0.013	2.081	0.737	1.113	0.005	2.315
C10orf55	0.541	-1.423	0.002	-4.661	0.002	-6.630
C12orf61	0.171	-1.630	0.001	-3.853	0.000	-6.279
C14orf1	0.144	1.483	0.022	-2.165	0.160	-1.460
C16orf74	0.031	1.567	0.599	-1.285	0.689	1.220
C16orf93	0.024	1.762	0.348	1.678	0.068	2.957
C17orf102	0.591	1.146	0.003	3.800	0.002	4.356
C17orf96	0.018	-2.690	0.520	1.548	0.410	-1.738
C19orf25	0.043	1.859	0.273	1.398	0.010	2.598
C19orf47	0.007	1.580	0.457	-1.342	0.666	1.178
C19orf48	0.793	1.057	0.037	-1.879	0.040	-1.777
C1orf111	0.034	1.818	0.523	-1.367	0.589	1.330
C1orf141	0.113	-1.341	0.427	-1.164	0.046	-1.561
C1orf50	0.023	2.231	0.308	-1.587	0.448	1.405
C1orf56	0.310	-1.160	0.005	-1.652	0.001	-1.916
C1orf74	0.840	-1.075	0.002	-2.765	0.003	-2.973
C1QL3	0.025	2.300	0.739	-1.198	0.260	1.919
C20orf196	0.049	1.980	0.385	-1.521	0.592	1.302
C21orf67	0.010	2.141	0.314	-1.974	0.902	1.085
C21orf91	0.659	-1.088	0.020	1.563	0.089	1.437

C22orf26	0.033	2.072	0.203	-1.815	0.777	1.141
C22orf34	0.626	-1.099	0.049	2.201	0.075	2.003
C2orf47	0.769	-1.078	0.003	-2.246	0.004	-2.422
C2orf69	0.294	1.139	0.004	-1.519	0.038	-1.334
C4A	0.366	1.248	0.136	1.481	0.020	1.848
C5orf56	0.516	-1.109	0.026	1.552	0.075	1.399
C6orf203	0.211	1.643	0.043	-2.372	0.400	-1.444
C7orf10	0.043	2.014	0.581	-1.353	0.486	1.489
C7orf26	0.007	1.541	0.095	-1.465	0.794	1.051
C8orf76	0.623	1.107	0.049	-1.505	0.085	-1.359
C9orf50	0.031	-1.629	0.688	1.182	0.422	-1.378
CAAP1	0.116	-1.785	0.016	-2.159	0.001	-3.853
CAB39	0.274	1.208	0.121	1.246	0.019	1.505
CACNA1A	0.618	-1.131	0.005	2.458	0.009	2.174
CACNA1E	0.466	1.160	0.083	1.632	0.038	1.893
CAHM	0.012	2.018	0.906	1.046	0.054	2.110
CARHSP1	0.134	1.298	0.030	-1.717	0.198	-1.323
CARM1	0.723	1.151	0.016	-2.480	0.022	-2.155
CASP4	0.639	1.112	0.011	2.001	0.005	2.225
CAT	0.227	1.384	0.136	1.475	0.012	2.042
CBR4	0.156	1.187	0.108	1.349	0.021	1.602
CBWD2	0.840	1.041	0.052	1.507	0.046	1.569
CBWD3	0.361	1.227	0.137	1.428	0.034	1.751
CBWD4P	0.248	1.423	0.239	1.399	0.017	1.991
CBWD5	0.525	1.140	0.017	1.666	0.007	1.899
CBWD7	0.439	1.176	0.024	1.648	0.006	1.937
CBX4	0.203	-1.284	0.169	-1.359	0.027	-1.744
CCBL2	0.088	1.260	0.064	1.392	0.005	1.753
CCDC112	0.033	1.520	0.323	-1.389	0.769	1.094
CCDC117	0.580	-1.106	0.002	-1.576	0.000	-1.743
CCDC134	0.879	-1.075	0.001	-3.098	0.009	-3.331
CCDC138	0.495	1.194	0.005	-2.280	0.024	-1.910
CCDC157	0.031	2.086	0.335	-1.666	0.680	1.252
CCDC170	0.239	1.302	0.011	-1.642	0.300	-1.262
CCDC180	0.122	1.586	0.025	-2.010	0.382	-1.267
CCDC28A	0.287	-1.191	0.082	-1.347	0.018	-1.605
CCDC59	0.633	-1.103	0.040	-1.547	0.011	-1.705
CCDC96	0.029	1.782	0.153	2.308	0.031	4.113
CCL4	0.726	1.156	0.018	-2.845	0.038	-2.462

CCNB2	0.023	1.995	0.456	-1.402	0.388	1.423
CCNL2	0.197	1.157	0.004	-1.569	0.037	-1.356
CCR1	0.889	-1.045	0.004	4.319	0.005	4.132
CCR2	0.043	2.277	0.486	1.411	0.044	3.213
CCRL2	0.599	1.173	0.046	-1.833	0.113	-1.563
CCT2	0.294	-1.301	0.082	-1.801	0.018	-2.343
CCT4	0.413	1.226	0.015	-1.862	0.008	-1.518
CCT6B	0.650	-1.172	0.047	-2.042	0.015	-2.395
CD14	0.022	2.038	0.122	1.617	0.000	3.295
CD200R1	0.023	2.731	0.414	-1.699	0.491	1.607
CD274	0.140	-1.701	0.000	4.654	0.007	2.735
CD300A	0.439	1.192	0.107	1.506	0.038	1.796
CD300LF	0.458	1.167	0.095	1.371	0.019	1.600
CD320	0.289	-1.198	0.155	-1.260	0.049	-1.509
CD58	0.701	-1.049	0.032	1.531	0.055	1.459
CD7	0.193	-1.392	0.031	2.021	0.249	1.451
CD83	0.335	-1.618	0.029	-2.711	0.004	-4.386
CD9	0.006	3.315	0.735	-1.275	0.211	2.600
CDC20	0.036	1.830	0.950	-1.033	0.282	1.771
CDC42EP2	0.401	1.399	0.077	3.323	0.032	4.648
CDCA4	0.787	1.096	0.006	-3.600	0.013	-3.284
CDCA8	0.010	2.076	0.118	-2.217	0.882	-1.068
CDH13	0.019	2.195	0.925	-1.065	0.300	2.060
CDH17	0.464	-1.109	0.068	-1.399	0.024	-1.552
CDIP1	0.032	2.077	0.044	-2.063	0.980	1.007
CDIPT	0.189	1.596	0.880	1.047	0.050	1.671
CDK11A	0.873	-1.023	0.001	-1.493	0.002	-1.528
CDK16	0.730	-1.082	0.022	-1.556	0.011	-1.683
CDK2AP1	0.192	1.246	0.040	-2.080	0.123	-1.670
CDK2AP2	0.032	1.983	0.706	-1.178	0.218	1.683
CDK3	0.273	1.375	0.005	-2.436	0.030	-1.772
CDK7	0.244	-1.234	0.208	-1.245	0.022	-1.537
CDKN1A	0.191	-2.066	0.015	-2.934	0.001	-6.064
CEACAM21	0.016	2.275	0.753	-1.228	0.361	1.854
CEACAM3	0.220	1.274	0.195	1.305	0.024	1.663
CEBPE	0.030	2.006	0.639	-1.285	0.444	1.561
CEBPZ	0.338	-1.326	0.221	-1.456	0.039	-1.930
CENPC	0.575	-1.114	0.081	-1.395	0.012	-1.554
CFB	0.020	1.790	0.295	-1.389	0.342	1.289

CFD	0.361	1.534	0.037	4.297	0.011	6.593
CFH	0.044	2.513	0.371	-1.904	0.694	1.320
CGRRF1	0.163	-1.395	0.258	-1.295	0.018	-1.807
CHAC2	0.145	1.456	0.033	-2.056	0.190	-1.412
CHAF1A	0.888	-1.022	0.022	-1.555	0.017	-1.590
CHCHD10	0.513	1.260	0.013	-3.322	0.045	-2.637
CHEK1	0.186	-1.149	0.132	-1.331	0.040	-1.530
CHGA	0.225	1.439	0.122	2.014	0.026	2.898
CHKA	0.226	-1.178	0.031	-1.645	0.009	-1.938
CHST13	0.047	1.552	0.675	-1.133	0.341	1.370
CHTF18	0.019	2.166	0.472	1.646	0.090	3.564
CIAPIN1	0.121	1.571	0.000	-3.599	0.001	-2.291
CILP	0.048	2.125	0.809	-1.171	0.380	1.815
CIRBP	0.578	1.086	0.002	-1.567	0.006	-1.443
CIRH1A	0.559	-1.157	0.020	-1.886	0.010	-2.182
CISD1	0.354	1.364	0.108	2.648	0.041	3.613
CISH	0.699	1.107	0.054	3.278	0.040	3.628
CKLF-CMTM1	0.148	-2.598	0.081	-1.864	0.011	-4.844
CLC	0.744	1.145	0.021	-4.690	0.035	-4.094
CMPK1	0.138	1.332	0.021	-1.643	0.172	-1.234
CNGA1	0.444	-1.132	0.001	2.085	0.003	1.842
CNOT11	0.750	1.056	0.029	1.453	0.027	1.535
CNPY2	0.166	-1.478	0.250	-1.373	0.035	-2.030
CNR1	0.025	3.280	0.682	1.400	0.091	4.590
CNTF	0.081	-1.372	0.516	-1.105	0.040	-1.516
COL10A1	0.113	1.609	0.265	1.460	0.012	2.348
COL1A1	0.722	-1.167	0.002	-3.336	0.002	-3.891
COL23A1	0.016	2.043	0.598	-1.290	0.388	1.584
COL9A2	0.028	2.360	0.111	-3.307	0.628	-1.401
COMM3	0.291	1.423	0.004	-3.516	0.029	-2.471
COMM3-BMI1	0.101	1.515	0.020	-2.683	0.123	-1.772
COMT	0.044	1.836	0.361	-2.145	0.849	-1.168
COPS2	0.294	-1.192	0.101	-1.360	0.012	-1.621
COQ2	0.100	1.366	0.363	1.245	0.035	1.700
COQ9	0.048	2.016	0.418	-1.370	0.304	1.472
CORO1C	0.128	1.230	0.121	1.286	0.009	1.582
COX17	0.572	-1.113	0.045	-1.611	0.022	-1.794
COX4I1	0.940	1.014	0.001	-2.121	0.001	-2.091
COX5B	0.172	1.254	0.005	-1.782	0.069	-1.421

COX7A2L	0.008	1.936	0.015	-2.112	0.699	-1.091
CRAT	0.006	2.335	0.000	-4.868	0.026	-2.085
CREG1	0.032	-1.477	0.269	-1.281	0.013	-1.891
CRELD2	0.822	1.057	0.038	2.175	0.030	2.300
CREM	0.166	-1.522	0.439	-1.230	0.019	-1.872
CRISP3	0.007	2.111	0.551	-1.471	0.585	1.436
CRLF3	0.201	1.285	0.257	1.197	0.022	1.539
CRY2	0.987	-1.005	0.002	-2.109	0.000	-2.119
CRYL1	0.663	1.145	0.002	-3.418	0.003	-2.984
CSGALNACT1	0.005	1.656	0.161	-1.337	0.319	1.238
CSGALNACT2	0.466	-1.089	0.045	-1.439	0.020	-1.567
CTDSPL	0.031	2.186	0.001	-4.730	0.064	-2.164
CTGLF12P	0.023	1.760	0.340	-1.401	0.493	1.256
CTSA	0.163	1.270	0.230	1.303	0.030	1.654
CUL7	0.017	1.851	0.958	-1.021	0.137	1.813
CXCL1	0.068	1.441	0.194	1.398	0.020	2.015
CXCR1	0.289	1.345	0.080	1.821	0.019	2.449
CXCR3	0.043	-2.203	0.910	-1.101	0.309	-2.426
CXCR4	0.055	-1.416	0.028	-1.842	0.003	-2.608
CXorf40B	0.214	1.311	0.013	-2.236	0.050	-1.705
CYB561D2	0.665	1.151	0.023	-1.898	0.065	-1.649
DAOA-AS1	0.526	1.132	0.017	2.099	0.009	2.377
DAPP1	0.482	-1.161	0.004	1.976	0.013	1.701
DCAF7	0.146	1.348	0.389	1.166	0.041	1.572
DCHS2	0.812	1.073	0.031	3.704	0.025	3.976
DCTN6	0.149	-1.283	0.065	-1.441	0.004	-1.850
DDIT4	0.969	-1.010	0.020	-1.683	0.014	-1.699
DDT	0.024	1.629	0.180	-1.500	0.732	1.087
DDTL	0.030	1.647	0.759	-1.086	0.073	1.517
DDX24	0.726	-1.078	0.030	-1.747	0.010	-1.882
DDX25	0.485	-1.137	0.008	2.041	0.026	1.795
DDX27	0.975	-1.007	0.001	-1.904	0.001	-1.917
DDX28	0.088	1.621	0.009	-2.721	0.079	-1.679
DEFA4	0.033	2.514	0.878	-1.226	0.595	2.050
DENND2C	0.680	-1.080	0.035	-1.548	0.023	-1.671
DERA	0.039	1.729	0.737	-1.099	0.131	1.573
DGAT2	0.189	1.321	0.155	1.338	0.028	1.768
DGCR11	0.124	1.357	0.100	1.717	0.019	2.330
DGKE	0.899	1.018	0.012	1.492	0.006	1.518

DHRS12	0.197	1.330	0.076	1.885	0.020	2.507
DHRS7	0.029	1.550	0.355	-1.159	0.094	1.337
DHX40	0.454	-1.131	0.087	-1.339	0.028	-1.515
DIO2-AS1	0.219	-1.326	0.197	-1.353	0.043	-1.795
DIP2A-IT1	0.237	1.398	0.023	-2.486	0.130	-1.778
DISC1	0.896	1.024	0.053	1.480	0.036	1.516
DKK3	0.706	-1.094	0.004	-2.003	0.004	-2.191
DLG5	0.229	-1.449	0.152	-2.131	0.048	-3.088
DLGAP1-AS1	0.477	1.133	0.012	-1.724	0.031	-1.521
DLST	0.850	-1.027	0.062	-1.506	0.045	-1.546
DNAAF1	0.029	-2.080	0.142	-3.105	0.032	-6.460
DNAJA3	0.002	2.609	0.473	-1.630	0.475	1.601
DNAJB2	0.990	-1.003	0.048	-1.642	0.022	-1.647
DNAJB4	0.637	1.167	0.049	-2.188	0.114	-1.875
DNAJB7	0.125	1.297	0.008	-1.601	0.108	-1.234
DNAJB9	0.462	-1.210	0.114	-1.548	0.033	-1.873
DNAJC11	0.014	2.574	0.498	-1.578	0.464	1.631
DNAJC2	0.127	-1.233	0.208	-1.319	0.044	-1.626
DNASE1L1	0.003	1.687	0.473	1.321	0.066	2.228
DND1	0.064	1.545	0.492	1.200	0.011	1.854
DNMBP	0.604	-1.172	0.017	-2.545	0.007	-2.981
DPPA5	0.030	1.641	0.217	-1.601	0.949	1.025
DPRXP4	0.377	1.300	0.193	1.598	0.033	2.078
DPYD	0.427	1.133	0.046	1.347	0.011	1.527
DSTN	0.102	1.255	0.030	-1.523	0.254	-1.214
DTWD1	0.079	1.719	0.005	-3.177	0.105	-1.848
DUS2	0.015	1.987	0.282	-1.484	0.332	1.339
DUSP2	0.612	-1.279	0.126	-2.001	0.033	-2.559
DUSP23	0.003	2.620	0.088	-1.849	0.288	1.417
DUSP3	0.540	-1.100	0.009	2.220	0.017	2.018
DUSP4	0.021	-3.439	0.703	1.376	0.294	-2.500
DUSP6	0.150	1.264	0.030	1.668	0.004	2.109
DUT	0.151	1.436	0.003	-2.323	0.067	-1.618
E2F3	0.112	1.266	0.127	1.322	0.010	1.673
EDEM3	0.117	1.206	0.138	1.282	0.017	1.546
EDN1	0.329	-1.378	0.015	-2.628	0.002	-3.620
EFCAB10	0.821	1.053	0.004	-2.259	0.007	-2.145
EFCAB12	0.018	1.636	0.515	-1.221	0.290	1.340
EFEMP2	0.004	2.351	0.004	-2.266	0.875	1.038

EFNB2	0.696	1.166	0.035	-3.974	0.056	-3.407
EGFL8	0.041	1.548	0.244	1.668	0.049	2.582
EIF1B-AS1	0.017	2.104	0.966	-1.017	0.099	2.069
EIF2AK3	0.461	-1.346	0.006	-2.803	0.001	-3.773
EIF4E3	0.698	1.059	0.023	1.449	0.013	1.534
ELAC1	0.126	-1.227	0.001	-1.659	0.000	-2.035
ELL2	0.070	-1.609	0.051	-2.124	0.005	-3.417
ELL3	0.864	1.049	0.006	-2.213	0.010	-2.111
ELMO2	0.402	-1.175	0.036	-1.623	0.010	-1.906
ELP2	0.651	-1.143	0.016	-1.988	0.002	-2.272
EMC2	0.257	1.303	0.410	1.189	0.005	1.550
EMC8	0.072	1.446	0.016	-2.240	0.134	-1.549
EML6	0.213	1.153	0.027	1.391	0.004	1.604
EMR2	0.480	1.129	0.042	1.569	0.015	1.772
ENG	0.019	2.346	0.538	-1.624	0.644	1.444
ENKD1	0.019	2.128	0.643	-1.318	0.403	1.615
ENPP4	0.338	1.443	0.001	-4.979	0.005	-3.449
EPB41L4A-AS1	0.322	-1.527	0.180	-2.070	0.042	-3.160
EPB41L5	0.088	-1.440	0.028	2.751	0.114	1.910
EPHA1	0.176	1.245	0.163	1.426	0.042	1.776
EPHB4	0.027	2.022	0.866	-1.106	0.308	1.829
EPHX1	0.013	2.309	0.116	-2.050	0.773	1.126
EPHX3	0.018	2.265	0.536	1.253	0.016	2.838
EPPK1	0.038	1.957	0.353	-1.666	0.767	1.175
ERAP2	0.585	-1.142	0.021	1.774	0.038	1.553
EREG	0.020	-1.186	0.104	-1.292	0.017	-1.532
ERI1	0.970	1.009	0.029	2.013	0.033	2.030
ESRP2	0.145	1.466	0.024	2.417	0.003	3.543
ETNK1	0.099	1.381	0.157	1.292	0.008	1.784
EVI2A	0.751	1.057	0.025	1.604	0.019	1.695
EXOC5	0.171	1.232	0.209	1.302	0.041	1.604
EYS	0.556	1.134	0.039	1.465	0.017	1.662
EZH2	0.859	-1.066	0.064	-2.184	0.035	-2.327
F12	0.741	-1.102	0.022	-1.811	0.024	-1.997
F2RL1	0.228	1.271	0.015	1.702	0.002	2.163
F5	0.906	1.020	0.061	1.596	0.047	1.628
FABP3	0.307	-1.395	0.163	-1.996	0.043	-2.784
FADD	0.071	1.499	0.820	1.056	0.027	1.583
FADS3	0.411	1.292	0.000	-3.037	0.004	-2.350

FAM160A2	0.480	-1.098	0.067	-1.609	0.038	-1.767
FAM162A	0.216	1.423	0.015	-2.780	0.080	-1.953
FAM174B	0.004	2.325	0.668	1.230	0.055	2.859
FAM179A	0.114	-1.813	0.264	-1.467	0.015	-2.659
FAM184B	0.475	-1.085	0.005	-1.552	0.001	-1.684
FAM185A	0.554	1.124	0.058	1.494	0.016	1.679
FAM198B	0.021	2.784	0.468	1.569	0.042	4.368
FAM19A2	0.048	1.740	0.446	-1.433	0.678	1.215
FAM200A	0.006	2.326	0.512	-1.233	0.044	1.887
FAM209A	0.240	-1.320	0.252	-1.320	0.022	-1.742
FAM3A	0.585	1.180	0.033	-1.966	0.102	-1.666
FAM53B	0.165	1.270	0.002	-1.682	0.020	-1.324
FAM92B	0.212	1.168	0.027	1.486	0.005	1.736
FANCB	0.027	1.710	0.484	-1.243	0.258	1.376
FANK1	0.429	1.078	0.024	1.464	0.011	1.578
FAS-AS1	0.948	-1.016	0.032	-1.781	0.012	-1.809
FBXL14	0.069	1.781	0.418	1.425	0.036	2.539
FBXL5	0.612	1.086	0.005	1.517	0.005	1.648
FBXO22	0.596	-1.108	0.010	-1.705	0.008	-1.889
FBXO30	0.682	1.088	0.016	1.439	0.037	1.565
FBXO31	0.417	-1.421	0.009	-3.895	0.002	-5.535
FBXO38	0.671	1.064	0.030	1.415	0.023	1.506
FCGR1A	0.856	1.066	0.003	3.559	0.002	3.795
FCGR1B	0.949	1.019	0.000	3.933	0.000	4.008
FCGR1C	0.918	1.048	0.002	5.517	0.001	5.782
FCRLB	0.042	-1.619	0.025	1.890	0.496	1.167
FEM1B	0.057	1.222	0.030	-1.612	0.164	-1.319
FICD	0.029	2.192	0.012	-2.535	0.645	-1.157
FILIP1L	0.533	-1.362	0.010	-3.246	0.001	-4.422
FLJ10038	0.253	-1.191	0.007	-2.166	0.002	-2.580
FLJ14186	0.157	1.259	0.047	-1.761	0.203	-1.398
FLJ23867	0.299	-1.406	0.231	-1.373	0.026	-1.931
FLJ42393	0.108	1.341	0.096	2.782	0.045	3.731
FMNL2	0.723	-1.107	0.039	1.768	0.125	1.597
FNBP4	0.803	1.037	0.043	-1.563	0.055	-1.507
FOXC1	0.117	-1.943	0.003	-3.472	0.000	-6.746
FPGT	0.705	1.112	0.009	2.468	0.008	2.744
FUNDc2	0.859	1.051	0.004	-2.342	0.003	-2.228
FUT11	0.550	1.163	0.017	-1.876	0.092	-1.612

FUT7	0.179	1.396	0.118	2.395	0.043	3.345
FXR2	0.028	1.700	0.391	1.281	0.009	2.177
FYTTD1	0.154	-1.341	0.393	-1.228	0.029	-1.647
GAB3	0.100	1.409	0.359	1.155	0.018	1.628
GADD45A	0.123	-1.313	0.011	-1.587	0.000	-2.085
GADD45B	0.128	-1.719	0.108	-1.431	0.008	-2.461
GALK2	0.118	1.329	0.123	1.378	0.008	1.831
GALT	0.018	2.061	0.041	-2.201	0.840	-1.068
GATSL3	0.035	2.073	0.190	-2.101	0.981	-1.013
GBP1	0.485	-1.285	0.004	3.132	0.016	2.436
GBP1P1	0.414	-1.536	0.024	2.549	0.237	1.659
GBP2	0.504	-1.159	0.002	1.938	0.015	1.673
GBP3	0.231	-1.486	0.007	2.278	0.124	1.534
GBP4	0.413	-1.197	0.011	1.836	0.014	1.534
GBP5	0.477	-1.319	0.003	3.228	0.014	2.447
GEM	0.040	-1.607	0.028	1.682	0.779	1.047
GFOD1	0.893	-1.035	0.042	-3.349	0.038	-3.466
GGTA1P	0.009	2.741	0.510	-1.953	0.737	1.404
GHRLOS	0.931	-1.010	0.000	-1.668	0.000	-1.685
GIF	0.290	1.406	0.154	2.120	0.048	2.981
GIMAP4	0.980	1.009	0.053	2.753	0.048	2.777
GIMAP8	0.141	1.953	0.142	2.475	0.020	4.833
GINS3	0.017	1.681	0.574	-1.198	0.282	1.404
GJB2	0.537	1.296	0.033	-2.199	0.196	-1.697
GJB7	0.595	1.137	0.054	1.650	0.017	1.875
GLRX3	0.983	1.004	0.000	-2.190	0.001	-2.181
GMNN	0.071	1.659	0.252	1.539	0.014	2.553
GNG10	0.515	-1.138	0.018	1.803	0.055	1.584
GNRH1	0.198	1.365	0.428	1.201	0.025	1.639
GOLGA8T	0.047	1.567	0.092	-1.858	0.612	-1.186
GPN3	0.061	1.753	0.581	1.182	0.027	2.072
GPR155	0.617	1.071	0.021	1.420	0.005	1.520
GPR19	0.006	2.942	0.836	1.105	0.037	3.250
GPR85	0.927	-1.018	0.043	1.649	0.058	1.620
GPR98	0.335	1.163	0.040	1.503	0.013	1.747
GPT2	0.202	1.435	0.004	-2.594	0.027	-1.807
GRAMD1C	0.023	2.295	0.968	1.014	0.028	2.327
GRAMD4	0.049	1.974	0.710	-1.241	0.438	1.590
GRASP	0.135	-2.001	0.000	-7.821	0.000	-15.650

GRB10	<u>0.004</u>	<u>2.029</u>	0.339	-1.573	0.576	1.290
GRIP1	0.540	-1.239	<u>0.038</u>	<u>3.269</u>	0.085	2.638
GRIP2	0.095	1.314	<u>0.048</u>	<u>1.673</u>	<u>0.006</u>	<u>2.199</u>
GRPEL2	<u>0.011</u>	<u>2.110</u>	<u>0.016</u>	<u>-2.229</u>	0.842	-1.057
GSTT1	0.906	1.020	<u>0.030</u>	<u>-1.775</u>	<u>0.031</u>	<u>-1.741</u>
GTF2E2	0.089	1.355	0.519	1.162	<u>0.048</u>	<u>1.573</u>
GTF2I	0.707	-1.064	<u>0.023</u>	-1.458	<u>0.030</u>	<u>-1.552</u>
GTF3C2	<u>0.002</u>	<u>1.549</u>	0.199	-1.287	0.321	1.203
GTF3C4	0.603	-1.116	0.095	-1.550	<u>0.021</u>	<u>-1.729</u>
GTPBP4	0.548	1.229	<u>0.000</u>	<u>-3.472</u>	<u>0.000</u>	<u>-2.825</u>
GUSB	0.937	1.020	<u>0.003</u>	<u>-2.090</u>	<u>0.005</u>	<u>-2.050</u>
GVINP1	0.951	1.012	0.052	1.490	<u>0.015</u>	<u>1.508</u>
GYG2P1	<u>0.002</u>	<u>-1.723</u>	0.556	-1.120	<u>0.008</u>	<u>-1.930</u>
GYS1	<u>0.022</u>	<u>1.626</u>	0.904	1.063	0.291	1.727
HAAO	<u>0.004</u>	<u>2.817</u>	0.515	-1.418	0.232	1.986
HACL1	0.912	-1.023	<u>0.010</u>	<u>-1.804</u>	<u>0.009</u>	<u>-1.846</u>
HADH	<u>0.048</u>	<u>2.039</u>	0.830	-1.171	0.468	1.740
HCAR2	0.949	-1.013	<u>0.041</u>	<u>1.509</u>	0.060	1.489
HCAR3	0.611	-1.132	<u>0.022</u>	<u>1.636</u>	0.137	1.445
HCK	0.125	1.406	0.516	1.137	<u>0.041</u>	<u>1.599</u>
HCRTR1	<u>0.027</u>	<u>1.643</u>	0.526	1.351	0.115	2.219
HEATR1	0.058	1.860	<u>0.006</u>	<u>-2.414</u>	0.212	-1.298
HEXA	<u>0.046</u>	<u>1.643</u>	0.488	-1.474	0.836	1.115
HEXA-AS1	0.661	1.060	0.063	1.448	<u>0.041</u>	<u>1.535</u>
HIST1H1C	<u>0.003</u>	<u>1.668</u>	0.097	-1.612	0.884	1.035
HIST1H2AL	<u>0.034</u>	<u>2.127</u>	0.719	-1.365	0.600	1.558
HIST1H2BJ	0.638	-1.128	<u>0.029</u>	<u>1.665</u>	0.189	1.476
HIST2H2BF	0.685	1.139	<u>0.037</u>	<u>1.879</u>	<u>0.001</u>	<u>2.141</u>
HLA-DQA1	0.672	1.127	<u>0.042</u>	<u>1.819</u>	<u>0.009</u>	<u>2.049</u>
HLX	0.832	1.037	<u>0.030</u>	<u>1.647</u>	<u>0.023</u>	<u>1.708</u>
HMG20A	<u>0.003</u>	<u>1.950</u>	0.618	-1.161	0.096	1.679
HMGCR	0.782	1.033	<u>0.032</u>	1.494	<u>0.028</u>	<u>1.543</u>
HMGCS1	0.846	-1.043	<u>0.015</u>	<u>-1.587</u>	<u>0.004</u>	<u>-1.656</u>
HN1	0.082	1.264	0.227	1.313	<u>0.044</u>	<u>1.659</u>
HPRT1	<u>0.026</u>	<u>1.817</u>	0.688	-1.225	0.431	1.483
HPS4	0.133	-1.175	<u>0.000</u>	-1.458	<u>0.000</u>	<u>-1.713</u>
HPSE	0.979	1.004	<u>0.012</u>	<u>1.647</u>	<u>0.015</u>	<u>1.653</u>
HRH2	<u>0.041</u>	<u>1.783</u>	0.643	1.181	0.051	2.105
HSBP1L1	0.967	-1.012	<u>0.045</u>	<u>-2.972</u>	<u>0.041</u>	<u>-3.007</u>

HSD17B10	0.013	2.391	0.040	-3.191	0.567	-1.335
HSDL1	0.595	-1.098	0.063	-2.341	0.044	-2.570
HSPA13	0.479	-1.222	0.129	-1.493	0.007	-1.824
HSPA9	0.887	-1.041	0.065	-1.612	0.018	-1.679
HYAL2	0.026	1.616	0.596	1.256	0.123	2.029
HYI	0.002	2.021	0.394	-1.313	0.159	1.539
HYKK	0.480	-1.103	0.037	1.926	0.064	1.746
ICOSLG	0.313	-1.636	0.046	-2.576	0.007	-4.214
IER5	0.701	-1.136	0.005	-2.257	0.003	-2.563
IFI16	0.516	-1.148	0.043	1.781	0.107	1.551
IFI27L2	0.043	-1.742	0.580	1.238	0.382	-1.407
IFI44	0.020	-2.283	0.714	1.240	0.299	-1.842
IFI6	0.033	-2.131	0.994	1.004	0.179	-2.123
IFIH1	0.046	-1.607	0.470	1.209	0.227	-1.329
IFIT1B	0.597	-1.161	0.005	5.854	0.008	5.044
IFIT5	0.048	-1.663	0.572	1.295	0.570	-1.285
IFNAR2	0.381	1.132	0.009	1.472	0.002	1.665
IFNK	0.859	1.064	0.032	-2.847	0.053	-2.675
IFT122	0.021	1.704	0.042	-1.736	0.917	-1.018
IGSF8	0.026	2.295	0.294	-1.554	0.352	1.477
IL10RA	0.178	-1.298	0.042	-1.628	0.004	-2.113
IL21R	0.036	-1.364	0.230	-1.281	0.011	-1.748
IL4I1	0.054	-1.248	0.228	-1.225	0.025	-1.528
ILF2	0.658	1.125	0.049	-1.831	0.068	-1.628
ILF3	0.550	-1.168	0.038	-1.828	0.006	-2.134
ILKAP	0.672	1.083	0.000	-2.066	0.000	-1.908
IMP3	0.058	-2.142	0.267	-1.471	0.011	-3.150
INHBC	0.039	2.644	0.838	1.148	0.138	3.035
INO80B	0.061	1.346	0.000	-1.858	0.022	-1.380
INSR	0.028	1.579	0.286	-1.331	0.527	1.186
IP6K2	0.383	-1.129	0.005	-1.356	0.002	-1.531
IPO11	0.309	1.399	0.031	-2.083	0.210	-1.489
IPO8	0.285	1.214	0.146	1.330	0.031	1.615
IRAK1BP1	0.080	1.283	0.042	1.580	0.005	2.027
IRAK2	0.067	-1.383	0.045	-1.453	0.001	-2.010
IRF2BP1	0.042	1.983	0.715	-1.091	0.066	1.818
IRF2BP2	0.378	-1.265	0.167	-1.475	0.033	-1.866
IRF5	0.119	-1.426	0.028	-1.927	0.002	-2.748
IRS2	0.208	-1.325	0.103	-1.768	0.026	-2.342

ISCA1	0.164	-1.418	0.127	-1.431	0.008	-2.029
ITFG1	0.003	1.545	0.815	-1.038	0.014	1.488
ITGA6	0.217	1.263	0.334	1.216	0.048	1.536
ITGB1	0.264	1.230	0.052	1.359	0.006	1.672
ITGB1BP1	0.204	1.429	0.020	-1.749	0.406	-1.224
ITPA	0.022	2.099	0.383	-1.560	0.580	1.346
IWS1	0.069	1.312	0.171	1.205	0.007	1.582
JAG1	0.789	1.061	0.006	-1.766	0.012	-1.664
JAKMIP3	0.044	2.037	0.735	1.123	0.017	2.287
JMY	0.549	-1.265	0.020	-2.770	0.004	-3.503
JOSD1	0.804	-1.052	0.015	-1.664	0.010	-1.750
KANSL2	0.834	-1.041	0.003	-1.909	0.001	-1.988
KAT5	0.007	1.335	0.297	1.273	0.043	1.698
KBTBD11	0.005	2.443	0.056	-2.607	0.871	-1.067
KBTBD4	0.068	1.603	0.036	-1.932	0.428	-1.205
KCNE1	0.039	1.971	0.680	1.415	0.235	2.788
KCNH3	0.030	2.016	0.186	-2.268	0.829	-1.125
KCNJ1	0.013	2.506	0.702	-1.140	0.002	2.198
KCNJ15	0.922	1.022	0.015	2.265	0.012	2.315
KCNK17	0.039	2.026	0.454	-1.559	0.666	1.300
KCNQ1	0.161	1.347	0.019	-1.718	0.311	-1.275
KCNRG	0.448	1.321	0.081	1.676	0.023	2.214
KCTD10	0.707	-1.070	0.012	-1.661	0.005	-1.777
KCTD15	0.015	2.687	0.576	-1.329	0.182	2.021
KCTD2	0.011	1.444	0.018	-1.502	0.796	-1.040
KCTD4	0.586	1.085	0.001	-1.690	0.009	-1.557
KCTD5	0.413	1.214	0.033	-1.689	0.173	-1.391
KCTD6	0.031	2.014	0.758	-1.189	0.342	1.694
KDELR1	0.010	1.621	0.118	-1.672	0.918	-1.032
KIAA0040	0.524	1.151	0.067	1.533	0.019	1.764
KIAA1407	0.005	1.746	0.085	-1.377	0.136	1.268
KIAA1737	0.312	1.107	0.001	-1.549	0.007	-1.399
KIAA1984-AS1	0.044	2.081	0.180	-1.576	0.409	1.320
KIF24	0.077	1.335	0.188	1.390	0.023	1.856
KLF10	0.678	-1.211	0.053	-2.176	0.020	-2.635
KLF2	0.229	1.264	0.170	1.423	0.043	1.799
KLF5	0.507	-1.150	0.086	-1.418	0.020	-1.630
KLF9	0.948	-1.021	0.000	-3.642	0.000	-3.717
KLHDC10	0.001	1.506	0.591	-1.074	0.017	1.403

KLHDC2	0.925	1.013	0.021	-1.504	0.032	-1.485
KLHL11	0.503	1.143	0.042	-1.775	0.078	-1.553
KLHL21	0.849	1.025	0.001	-1.515	0.006	-1.479
KLHL22	0.007	2.138	0.066	-2.076	0.929	1.030
KLRAP1	0.847	1.032	0.049	-1.517	0.058	-1.470
KPNB1	0.588	1.112	0.061	1.366	0.015	1.519
KRI1	0.387	1.151	0.041	-1.721	0.095	-1.494
KRT23	0.133	1.652	0.021	-1.957	0.445	-1.185
KRT8	0.889	-1.019	0.047	-1.508	0.046	-1.537
KRT8P12	0.586	-1.088	0.060	-1.514	0.036	-1.647
KY	0.225	1.238	0.191	1.326	0.036	1.641
LACTB	0.146	-1.453	0.291	-1.246	0.010	-1.810
LAMP3	0.031	-1.701	0.067	1.581	0.583	-1.076
LEMD2	0.197	1.323	0.019	-1.671	0.021	-1.263
LGALS12	0.048	2.099	0.402	-1.685	0.717	1.246
LGALS8	0.255	-1.253	0.000	2.069	0.002	1.651
LILRA1	0.031	1.576	0.724	-1.101	0.189	1.431
LILRA5	0.550	-1.109	0.039	1.600	0.108	1.443
LINC00152	0.403	1.133	0.087	1.453	0.031	1.646
LINC00202-1	0.040	1.504	0.520	-1.153	0.263	1.305
LINC00266-1	0.683	1.093	0.069	1.810	0.048	1.979
LINC00282	0.428	1.199	0.019	3.041	0.010	3.646
LINC00324	0.032	1.640	0.651	1.306	0.211	2.143
LINC00537	0.311	1.263	0.079	1.578	0.006	1.993
LINC00582	0.041	1.907	0.752	1.122	0.090	2.140
LINC00593	0.036	1.960	0.194	2.047	0.025	4.011
LINC00629	0.698	-1.047	0.030	1.527	0.048	1.458
LINC00649	0.423	1.100	0.103	1.388	0.046	1.527
LINC00654	0.010	2.177	0.896	-1.051	0.058	2.072
LINC00667	0.986	-1.003	0.008	-2.193	0.008	-2.199
LINC00854	0.018	2.269	0.832	1.140	0.138	2.587
LINC00948	0.472	-1.186	0.084	-1.694	0.036	-2.009
LINC00960	0.144	1.352	0.600	1.122	0.048	1.517
LINC00987	0.010	2.393	0.307	-1.474	0.196	1.623
LINS	0.272	1.332	0.410	1.275	0.037	1.698
LLPH	0.229	-2.168	0.036	-2.624	0.002	-5.690
LOC100127888	0.004	-2.214	0.615	-1.461	0.147	-3.233
LOC100127974	0.817	-1.059	0.022	-1.548	0.027	-1.640
LOC100129518	0.284	-1.457	0.017	-2.547	0.003	-3.711

LOC100129726	0.296	-1.360	0.002	-2.651	0.000	-3.605
LOC100130093	0.016	1.502	0.501	1.036	0.009	1.556
LOC100130476	0.254	-1.548	0.001	-3.560	0.000	-5.510
LOC100133445	0.400	1.346	0.043	-2.386	0.180	-1.773
LOC100133985	0.007	2.144	0.191	1.997	0.019	4.282
LOC100287036	0.953	-1.013	0.004	-1.781	0.002	-1.804
LOC100287177	0.801	1.063	0.027	-1.542	0.081	-1.450
LOC100288846	0.032	1.702	0.203	-1.485	0.603	1.146
LOC100288897	0.965	-1.009	0.031	1.792	0.035	1.776
LOC100289473	0.037	1.572	0.170	-1.362	0.479	1.155
LOC100294362	0.277	-1.208	0.013	1.986	0.046	1.644
LOC100505549	0.193	1.290	0.289	1.262	0.038	1.627
LOC100505702	0.702	1.084	0.071	1.775	0.047	1.924
LOC100506207	0.296	-1.340	0.195	-1.428	0.042	-1.914
LOC100506241	0.394	1.259	0.095	1.630	0.010	2.052
LOC100506639	0.243	1.236	0.022	-1.758	0.100	-1.422
LOC100506655	0.884	-1.053	0.024	-2.087	0.035	-2.197
LOC100527964	0.037	2.197	0.580	1.457	0.104	3.202
LOC101927045	0.215	1.163	0.038	1.391	0.005	1.617
LOC101927069	0.085	1.582	0.043	-1.989	0.437	-1.257
LOC101927272	0.542	1.171	0.050	2.491	0.023	2.918
LOC101927865	0.010	2.518	0.047	-2.424	0.929	1.039
LOC101927902	0.150	-1.293	0.053	-1.531	0.005	-1.980
LOC101927939	0.009	1.542	0.952	1.014	0.085	1.563
LOC101928047	0.048	1.872	0.661	-1.357	0.638	1.380
LOC101928133	0.544	-1.135	0.003	-1.744	0.000	-1.979
LOC101928324	0.040	1.783	0.138	-1.773	0.987	1.006
LOC101928403	0.976	-1.011	0.043	-1.796	0.057	-1.816
LOC101928476	0.032	-1.733	0.960	1.017	0.181	-1.705
LOC101928527	0.123	1.292	0.146	1.577	0.035	2.038
LOC101928537	0.318	-1.191	0.049	1.756	0.126	1.474
LOC101928668	0.049	1.856	0.763	1.198	0.211	2.224
LOC101929736	0.033	1.605	0.112	-1.826	0.726	-1.138
LOC150381	0.039	1.882	0.834	1.123	0.191	2.115
LOC150776	0.698	1.087	0.037	-1.969	0.054	-1.812
LOC257358	0.334	1.309	0.006	-2.593	0.041	-1.981
LOC283922	0.391	1.146	0.016	-1.752	0.051	-1.529
LOC285389	0.439	-1.220	0.028	1.582	0.252	1.297
LOC285889	0.029	1.818	0.826	-1.046	0.067	1.737

LOC286367	0.253	1.236	0.137	1.531	0.041	1.891
LOC441009	0.207	1.359	0.100	2.448	0.038	3.327
LOC441124	0.583	1.130	0.042	-1.988	0.084	-1.759
LOC442075	0.310	-1.130	0.002	-1.441	0.000	-1.628
LOC494141	0.092	-1.343	0.002	-1.759	0.000	-2.362
LOC541473	0.050	1.512	0.093	-1.759	0.611	-1.163
LOC641776	0.029	1.593	0.154	1.665	0.018	2.653
LOC642846	0.510	1.356	0.034	-4.855	0.079	-3.579
LOC643733	0.607	-1.121	0.014	2.282	0.033	2.035
LOC644090	0.750	-1.063	0.032	-1.804	0.021	-1.918
LOC653712	0.966	-1.008	0.032	2.046	0.034	2.031
LOC727896	0.820	-1.040	0.033	1.516	0.032	1.458
LOC728323	0.368	1.204	0.031	1.541	0.008	1.855
LOC728431	0.029	-2.097	0.745	1.148	0.164	-1.827
LOC729739	0.070	1.236	0.080	1.406	0.012	1.739
LOC730668	0.421	1.144	0.074	1.387	0.019	1.586
LOXL4	0.205	1.275	0.227	1.315	0.028	1.677
LPAR6	0.339	1.234	0.118	1.529	0.028	1.887
LPCAT4	0.009	2.325	0.617	-1.426	0.474	1.631
LRP5L	0.067	-1.533	0.014	-1.555	0.000	-2.384
LRRC17	0.437	-1.185	0.040	3.665	0.063	3.093
LRRC34	0.012	1.621	0.758	-1.176	0.545	1.378
LRRC41	0.394	1.304	0.001	-3.027	0.001	-2.322
LSG1	0.260	-1.217	0.139	-1.264	0.013	-1.538
LTB4R2	0.023	1.842	0.059	1.726	0.001	3.178
LTBR	0.030	1.619	0.078	1.768	0.004	2.863
LUCAT1	0.514	1.131	0.001	1.704	0.001	1.928
LY6E	0.023	-2.928	0.732	1.437	0.511	-2.038
LYG1	0.037	2.250	0.590	-1.312	0.316	1.715
LYPD4	0.011	1.833	0.123	3.081	0.034	5.645
MACF1	0.219	1.215	0.167	1.310	0.023	1.592
MAD2L1BP	0.202	-1.318	0.112	-1.545	0.019	-2.037
MAGIX	0.168	1.422	0.369	1.319	0.033	1.876
MAGOH2	0.024	1.880	0.585	-1.285	0.426	1.462
MAK16	0.296	1.235	0.002	-2.130	0.011	-1.725
MAP2K6	0.774	-1.061	0.046	2.009	0.055	1.893
MAP3K1	0.398	1.097	0.000	1.536	0.000	1.686
MAP3K8	0.090	-1.530	0.158	-1.546	0.016	-2.364
MAPK14	0.664	1.086	0.069	1.594	0.046	1.732

MAPK6	0.230	-1.317	0.154	-1.289	0.008	-1.698
MAT2B	0.187	1.231	0.143	1.254	0.007	1.544
MBOAT4	0.645	1.169	0.020	-2.276	0.070	-1.947
MBP	0.264	1.264	0.242	1.242	0.047	1.569
MBTPS1	0.680	-1.058	0.002	-1.696	0.000	-1.795
MCM2	0.296	1.513	0.049	-3.225	0.187	-2.131
MCM3AP	0.048	1.661	0.233	-1.371	0.198	1.212
MCM3AP-AS1	0.266	1.439	0.015	-2.145	0.190	-1.490
MCM4	0.290	1.151	0.042	-1.716	0.112	-1.491
MCM7	0.080	1.748	0.039	-2.115	0.421	-1.210
MCTP2	0.226	1.215	0.128	1.285	0.016	1.562
MCU	0.002	1.607	0.316	-1.260	0.271	1.275
MEA1	0.015	1.516	0.563	-1.113	0.067	1.362
MED16	0.206	1.311	0.359	1.183	0.020	1.551
MED22	0.014	1.637	0.575	-1.152	0.113	1.421
MED26	0.793	-1.055	0.037	-1.446	0.008	-1.525
MED28	0.590	1.065	0.006	-1.527	0.012	-1.434
MED30	0.300	-1.153	0.013	-1.505	0.002	-1.736
MED4-AS1	0.395	-1.155	0.061	-1.371	0.020	-1.584
MEF2D	0.968	-1.008	0.003	-1.603	0.007	-1.616
MEI1	0.414	-1.167	0.074	-1.287	0.023	-1.502
MERTK	0.006	2.173	0.648	1.274	0.088	2.768
METRNL	0.270	-1.282	0.126	-1.381	0.035	-1.770
MGC12916	0.426	-1.345	0.119	-1.534	0.033	-2.063
MIA-RAB4B	0.008	2.537	0.775	1.214	0.110	3.080
MICB	0.602	1.128	0.189	1.379	0.038	1.555
MIER3	0.808	-1.051	0.021	-1.515	0.021	-1.592
MIF4GD	0.036	1.985	0.388	-1.756	0.847	1.130
MIR181A2HG	0.159	1.337	0.141	1.665	0.033	2.226
MIR3198-1	0.597	-1.144	0.089	-1.375	0.036	-1.573
MIR4435-1HG	0.102	1.344	0.184	1.397	0.027	1.877
MIR4742	0.032	1.689	0.392	1.410	0.058	2.382
MIS18BP1	0.766	1.045	0.006	-1.594	0.018	-1.525
MKKS	0.030	2.034	0.603	1.343	0.091	2.732
MLEC	0.033	1.507	0.410	-1.339	0.739	1.126
MLLT11	0.064	1.541	0.000	-2.746	0.002	-1.781
MMP14	0.045	2.341	0.067	2.420	0.002	5.665
MNDA	0.333	1.307	0.170	1.555	0.034	2.032
MOGS	0.149	1.329	0.000	-2.291	0.008	-1.724

MOSPD2	0.195	1.481	0.119	1.504	0.006	2.227
MOV10	0.030	-1.727	0.427	1.235	0.158	-1.399
MPP1	0.990	1.002	0.042	1.524	0.044	1.527
MRGBP	0.969	1.010	0.040	-1.812	0.062	-1.795
MRPL18	0.848	-1.058	0.079	-1.548	0.028	-1.637
MRPL4	0.440	1.201	0.015	-2.200	0.038	-1.832
MRPL51	0.049	1.759	0.769	1.138	0.115	2.001
MRPL55	0.013	2.037	0.001	-2.912	0.147	-1.430
MRS2	0.045	2.195	0.123	-2.247	0.963	-1.023
MRVI1-AS1	0.065	1.789	0.213	1.431	0.001	2.560
MSMP	0.116	1.498	0.001	-2.332	0.063	-1.557
MSRB1	0.471	1.215	0.076	1.797	0.030	2.184
MT2A	0.017	-2.767	0.179	-2.454	0.014	-6.789
MTERFD2	0.264	1.245	0.010	-1.696	0.012	-1.362
MTRNR2L5	0.288	1.820	0.114	1.866	0.018	3.396
MTRNR2L7	0.959	-1.013	0.015	2.168	0.018	2.141
MUL1	0.334	1.227	0.048	-1.729	0.177	-1.409
MVD	0.817	-1.098	0.001	-3.170	0.002	-3.480
MXD3	0.248	1.134	0.037	1.335	0.008	1.514
MXD4	0.615	1.110	0.011	-1.936	0.025	-1.744
MXI1	0.947	-1.014	0.011	-1.707	0.008	-1.730
MYBPH	0.038	2.460	0.096	-2.096	0.685	1.173
MYCBP2-AS1	0.026	1.556	0.369	-1.258	0.356	1.237
MYEF2	0.764	-1.047	0.013	-1.460	0.015	-1.528
MYEOV2	0.044	1.916	0.036	-1.783	0.776	1.075
MLYL12B	0.042	1.262	0.120	1.263	0.007	1.594
MYL7	0.028	1.528	0.779	-1.046	0.105	1.461
MYO16-AS1	0.371	1.372	0.032	-2.494	0.156	-1.818
MYO7B	0.023	2.102	0.913	-1.056	0.147	1.991
MZF1	0.019	1.861	0.549	1.384	0.106	2.576
MZT1	0.581	1.178	0.011	-2.117	0.040	-1.797
N4BP3	0.462	-1.434	0.079	-2.776	0.030	-3.982
NAA10	0.006	1.520	0.191	1.406	0.013	2.138
NABP1	0.698	-1.063	0.017	1.596	0.051	1.502
NAGLU	0.035	1.802	0.740	-1.213	0.503	1.486
NAT9	0.003	1.700	0.909	-1.031	0.080	1.648
NBPF14	0.023	1.698	0.696	-1.177	0.404	1.443
NBPF3	0.125	1.230	0.019	-1.795	0.093	-1.459
NBPF9	0.907	-1.069	0.026	-3.376	0.037	-3.609

NCBP2	0.346	-1.168	0.069	-1.510	0.017	-1.764
NCBP2-AS2	0.273	1.267	0.017	-2.857	0.049	-2.254
NDC80	0.953	1.012	0.041	-1.685	0.032	-1.664
NDUFA5	0.863	1.021	0.034	-1.542	0.042	-1.511
NDUFAF1	0.376	1.204	0.126	1.532	0.046	1.845
NDUFB7	0.020	1.910	0.854	-1.130	0.436	1.690
NDUFS6	0.223	1.378	0.008	-2.547	0.043	-1.848
NDUFV2	0.445	-1.187	0.026	-1.596	0.005	-1.895
NEDD8-MDP1	0.001	2.015	0.206	-1.455	0.230	1.385
NEIL1	0.750	-1.113	0.183	-1.660	0.047	-1.848
NELFA	0.155	1.467	0.010	-1.997	0.138	-1.362
NET1	0.528	-1.277	0.022	-2.324	0.006	-2.968
NFE2	0.176	1.512	0.162	1.496	0.009	2.263
NFKB2	0.399	-1.222	0.057	-1.490	0.022	-1.821
NFKBIA	0.239	-1.579	0.002	-2.158	0.001	-3.406
NFKBIE	0.342	-1.473	0.032	-2.008	0.006	-2.958
NFU1	0.134	1.419	0.029	-1.981	0.187	-1.396
NFXL1	0.086	-1.471	0.017	1.906	0.297	1.296
NHLH1	0.049	1.743	0.913	1.037	0.036	1.807
NHP2	0.190	-1.542	0.008	-2.996	0.001	-4.620
NIF3L1	0.028	1.614	0.484	1.343	0.085	2.166
NISCH	0.099	1.422	0.030	-1.716	0.279	-1.207
NKRF	0.772	-1.064	0.056	-1.645	0.031	-1.751
NLGN4Y	0.311	-1.155	0.044	2.045	0.088	1.770
NLRP7	0.023	2.021	0.218	1.790	0.020	3.617
NMRAL1	0.010	2.237	0.822	-1.167	0.347	1.917
NNT	0.030	1.833	0.407	-1.494	0.648	1.227
NOP56	0.722	1.100	0.025	-1.839	0.015	-1.672
NOS3	0.388	1.142	0.001	1.655	0.000	1.889
NPRL3	0.515	-1.173	0.016	-1.752	0.004	-2.056
NPSR1-AS1	0.404	1.187	0.061	1.702	0.015	2.021
NR1H4	0.311	-1.362	0.133	-1.537	0.029	-2.094
NR4A1	0.478	-1.370	0.034	-2.721	0.013	-3.727
NR4A2	0.362	-1.312	0.053	-1.828	0.002	-2.398
NR4A3	0.331	-1.734	0.025	-2.836	0.001	-4.917
NRAS	0.454	-1.104	0.084	-1.377	0.021	-1.520
NRDE2	0.002	1.639	0.076	-1.464	0.575	1.119
NRIP1	0.684	-1.089	0.001	-1.881	0.000	-2.048
NRROS	0.500	1.229	0.035	-2.134	0.111	-1.737

NSUN5	0.414	1.184	0.002	-2.052	0.003	-1.733
NT5C	0.331	1.403	0.026	-1.949	0.292	-1.389
NT5C3A	0.305	-1.280	0.035	1.727	0.159	1.350
NUDT13	0.191	-1.320	0.039	-1.510	0.001	-1.993
NUDT17	0.265	-1.131	0.012	-1.454	0.002	-1.644
NUDT22	0.005	2.025	0.698	-1.227	0.342	1.650
NUDT3	0.001	1.707	0.669	-1.115	0.112	1.531
NUFIP1	0.902	1.053	0.023	-2.290	0.042	-2.174
NUMA1	0.126	1.182	0.013	-1.509	0.092	-1.277
NUP133	0.642	1.066	0.000	-1.817	0.000	-1.704
NUP155	0.301	-1.216	0.027	-1.720	0.004	-2.092
NUP37	0.709	1.121	0.004	-2.079	0.032	-1.854
NUTM2A	0.688	1.068	0.059	1.602	0.032	1.711
NXF1	0.469	1.092	0.004	-1.530	0.024	-1.401
OBFC1	0.403	1.169	0.004	1.801	0.000	2.106
OCEL1	0.001	2.735	0.217	-2.013	0.553	1.359
OCM	0.013	2.199	0.352	-1.575	0.514	1.396
OCRL	0.012	2.115	0.444	-1.514	0.520	1.397
ODC1	0.470	-1.179	0.035	-1.808	0.008	-2.131
OGFOD2	0.552	1.167	0.017	3.849	0.010	4.491
OGFR	0.140	1.416	0.011	-2.033	0.097	-1.435
OGFR-AS1	0.702	1.135	0.010	-4.199	0.017	-3.701
OR10V2P	0.006	2.624	0.247	-2.132	0.737	1.231
OR2A4	0.020	1.831	0.794	1.062	0.024	1.946
OR2A7	0.006	1.928	0.572	-1.134	0.073	1.699
OR52K1	0.311	1.416	0.165	1.965	0.041	2.782
OR52K2	0.143	1.599	0.225	1.560	0.009	2.494
OR7E5P	0.077	1.391	0.175	1.581	0.039	2.200
OR9A2	0.012	2.368	0.668	1.075	0.006	2.545
ORC5	0.490	1.299	0.034	-2.802	0.115	-2.157
ORM1	0.030	2.015	0.127	-2.094	0.929	-1.039
ORM2	0.008	1.975	0.631	-1.269	0.373	1.556
OSBP	0.925	1.015	0.002	-1.532	0.002	-1.510
OSBPL11	0.276	1.196	0.009	1.345	0.003	1.609
OSGEP	0.034	2.182	0.106	-2.370	0.849	-1.086
OSGIN2	0.010	-1.389	0.245	-1.237	0.015	-1.718
OTUD6B	0.844	-1.043	0.048	-1.512	0.054	-1.577
OVCH1-AS1	0.029	1.955	0.039	1.663	0.000	3.250
P2RY10	0.378	1.438	0.044	-2.287	0.234	-1.591

PABPC4	0.288	1.382	<u>0.030</u>	<u>-2.689</u>	0.102	-1.946
PAGR1	0.046	1.633	0.659	1.172	0.075	1.914
PANK4	0.490	1.154	0.090	2.095	<u>0.048</u>	<u>2.418</u>
PAPD5	0.081	-1.405	0.588	-1.127	<u>0.039</u>	<u>-1.583</u>
PAPSS2	<u>0.033</u>	<u>1.668</u>	0.364	1.698	0.101	2.833
PARP16	0.026	1.538	0.796	-1.070	0.213	1.437
PARP3	0.759	-1.058	<u>0.038</u>	<u>1.684</u>	0.072	1.591
PARP9	0.396	-1.177	<u>0.018</u>	<u>1.673</u>	0.097	1.421
PASK	<u>0.007</u>	<u>-1.523</u>	0.164	1.307	0.417	-1.165
PATE2	0.905	1.016	<u>0.035</u>	<u>1.538</u>	<u>0.035</u>	<u>1.563</u>
PATL2	0.145	1.249	<u>0.038</u>	<u>-1.501</u>	0.266	-1.202
PBDC1	0.018	2.266	0.388	-1.649	0.581	1.374
PCDH45	0.018	1.638	0.467	-1.181	0.250	1.387
PCYT2	0.531	1.210	<u>0.010</u>	<u>-3.640</u>	<u>0.023</u>	<u>-3.009</u>
PDCD7	0.188	-1.196	0.144	-1.471	<u>0.049</u>	<u>-1.759</u>
PDCL3	0.341	-1.457	0.154	-1.953	<u>0.031</u>	<u>-2.846</u>
PDE5A	0.847	1.029	<u>0.015</u>	<u>1.900</u>	<u>0.012</u>	<u>1.955</u>
PDE6D	0.000	1.882	0.393	-1.382	0.397	1.363
PDE6H	<u>0.014</u>	<u>2.414</u>	<u>0.012</u>	<u>-4.370</u>	0.253	-1.810
PDE9A	<u>0.036</u>	<u>1.972</u>	0.265	-1.859	0.912	1.060
PDHA1	0.430	1.089	<u>0.037</u>	<u>-1.610</u>	0.073	-1.479
PDK3	0.412	1.155	0.117	1.315	<u>0.037</u>	<u>1.519</u>
PDRG1	0.042	-2.097	0.227	2.389	0.854	1.140
PECAM1	0.035	1.400	0.505	1.159	<u>0.047</u>	<u>1.623</u>
PER1	0.252	-1.434	<u>0.017</u>	<u>-3.730</u>	<u>0.005</u>	<u>-5.349</u>
PEX1	0.044	1.633	0.193	-1.381	0.280	1.182
PEX11B	0.108	1.240	<u>0.006</u>	<u>-1.688</u>	0.067	-1.361
PFKFB2	0.295	-1.223	0.073	-1.796	<u>0.025</u>	<u>-2.197</u>
PFN2	0.652	1.149	0.077	1.762	<u>0.038</u>	<u>2.025</u>
PGM5	<u>0.019</u>	<u>2.177</u>	0.323	-1.421	0.212	1.532
PGM5-AS1	0.005	2.418	0.614	-1.321	0.302	1.830
PGP	0.016	1.820	0.110	-1.805	0.977	1.009
PGPEP1L	0.040	1.722	0.713	-1.251	0.596	1.377
PHF1	0.723	-1.114	0.064	-1.556	<u>0.033</u>	<u>-1.734</u>
PHF15	0.082	-1.170	<u>0.015</u>	<u>-1.521</u>	<u>0.003</u>	<u>-1.779</u>
PIAS2	0.340	1.273	<u>0.022</u>	<u>-1.631</u>	0.273	-1.281
PIAS3	0.312	-1.201	<u>0.003</u>	<u>-1.684</u>	<u>0.000</u>	<u>-2.022</u>
PICALM	0.517	1.103	<u>0.009</u>	<u>1.509</u>	<u>0.006</u>	<u>1.664</u>
PIGK	<u>0.031</u>	<u>1.770</u>	0.790	-1.088	0.088	1.628

PIGO	0.079	-1.180	0.018	-1.281	0.001	-1.511
PIGV	0.993	1.003	0.048	-1.884	0.044	-1.879
PIH1D2	0.040	1.823	0.926	1.041	0.199	1.898
PIK3AP1	0.755	-1.047	0.010	1.594	0.012	1.522
PIM2	0.133	-1.389	0.180	-1.253	0.010	-1.741
PIN1	0.018	1.867	0.500	-1.379	0.509	1.354
PINX1	0.227	-1.213	0.208	-1.237	0.035	-1.500
PIP5K1B	0.034	1.429	0.006	-1.526	0.632	-1.068
PITHD1	0.481	1.109	0.008	-1.617	0.014	-1.457
PITRM1-AS1	0.743	1.116	0.036	-2.080	0.052	-1.863
PKDREJ	0.748	-1.149	0.037	-2.497	0.026	-2.870
PKI55	0.023	2.070	0.981	1.011	0.108	2.093
PKN3	0.017	2.071	0.210	-1.552	0.353	1.334
PKP4	0.034	1.531	0.622	-1.202	0.512	1.273
PLAU	0.346	-1.803	0.022	-3.351	0.005	-6.043
PLAUR	0.234	-1.351	0.141	-1.314	0.021	-1.776
PLCB1	0.046	1.523	0.125	-1.470	0.878	1.036
PLCD1	0.017	1.793	0.000	-2.924	0.002	-1.630
PLCD3	0.754	1.048	0.041	1.472	0.039	1.542
PLCL2	0.117	1.222	0.075	1.251	0.002	1.528
PLK2	0.121	-1.332	0.023	-1.801	0.003	-2.400
PLK3	0.921	-1.028	0.017	-1.586	0.070	-1.631
PLK4	0.118	2.141	0.046	-3.962	0.344	-1.850
PLOD3	0.009	2.324	0.004	-3.200	0.282	-1.377
PNMA1	0.386	1.322	0.012	-2.945	0.034	-2.227
POC5	0.032	2.081	0.891	-1.047	0.036	1.988
PODNL1	0.381	-1.175	0.028	-1.761	0.009	-2.070
POFUT2	0.544	-1.132	0.078	-1.373	0.016	-1.554
POLD3	0.382	1.158	0.095	1.412	0.030	1.634
POLE	0.035	1.896	0.323	-1.821	0.943	1.041
POLE3	0.898	1.026	0.011	-1.864	0.012	-1.816
POLE4	0.003	2.705	0.408	-1.569	0.300	1.724
POLI	0.045	1.241	0.244	1.213	0.026	1.504
POLR1C	0.805	1.096	0.011	-3.435	0.015	-3.135
POLR2G	0.018	2.208	0.165	-2.139	0.949	1.032
POLR2H	0.030	2.109	0.248	-2.224	0.934	-1.055
POLR2J3	0.532	-1.080	0.022	-1.445	0.009	-1.560
POLR3B	0.026	1.528	0.092	-1.604	0.847	-1.050
POLR3C	0.970	1.009	0.001	-1.943	0.003	-1.926

POLR3E	0.257	-1.466	0.039	-1.708	0.005	-2.504
PON3	0.424	1.097	0.063	1.478	0.028	1.621
POT1	0.103	1.297	0.091	1.219	0.003	1.581
POTEF	0.015	1.355	0.159	1.339	0.015	1.815
POTEI	0.181	1.291	0.242	1.291	0.032	1.667
PPDPF	0.135	-1.587	0.239	-1.532	0.035	-2.432
PPIAP30	0.046	1.352	0.038	1.504	0.002	2.034
PPIH	0.604	-1.211	0.048	-2.962	0.023	-3.588
PPM1M	0.164	1.257	0.179	1.323	0.025	1.663
PPP1R15A	0.828	-1.052	0.047	-1.569	0.066	-1.651
PPP1R15B	0.535	-1.110	0.045	-1.370	0.021	-1.521
PPP1R37	0.031	1.913	0.116	-1.932	0.980	-1.010
PPP1R7	0.036	1.569	0.691	1.160	0.128	1.820
PPP2R1B	0.542	1.096	0.019	-1.537	0.050	-1.402
PPP2R5D	0.020	1.869	0.210	-1.487	0.328	1.257
PRDM1	0.011	-1.534	0.237	-1.740	0.059	-2.668
PRDM8	0.795	1.040	0.057	2.505	0.050	2.605
PRKAR2B	0.523	-1.297	0.011	-2.504	0.004	-3.248
PRKCE	0.568	-1.125	0.070	-1.572	0.010	-1.769
PRKCQ	0.078	1.286	0.151	1.277	0.007	1.642
PRMT1	0.032	1.703	0.673	1.243	0.170	2.116
PRMT10	0.587	-1.120	0.030	-1.766	0.010	-1.979
PROK2	0.375	1.242	0.053	1.895	0.019	2.353
PRPS1L1	0.375	-1.249	0.047	1.725	0.210	1.381
PRR12	0.182	1.521	0.049	-2.012	0.267	-1.323
PRR24	0.031	1.654	0.608	-1.161	0.178	1.424
PRSS12	0.219	1.474	0.018	-2.644	0.068	-1.795
PSEN2	0.032	2.038	0.571	1.361	0.089	2.774
PSMD11	0.316	1.187	0.003	-1.775	0.004	-1.495
PSMD4	0.011	1.583	0.990	-1.002	0.016	1.580
PSMD5	0.374	-1.121	0.017	-1.466	0.004	-1.643
PSMD5-AS1	0.375	1.153	0.013	-1.529	0.112	-1.326
PSME1	0.390	1.122	0.118	1.344	0.042	1.507
PSMG1	0.462	1.331	0.034	-3.169	0.094	-2.380
PTER	0.011	1.701	0.696	1.114	0.040	1.895
PTGES	0.128	-1.206	0.134	-1.429	0.038	-1.724
PTGES3	0.549	1.071	0.017	1.496	0.006	1.602
PTGS2	0.087	1.418	0.003	2.235	0.000	3.169
PTMA	0.818	1.049	0.031	-1.934	0.033	-1.844

PTPMT1	0.345	1.208	0.011	-2.224	0.030	-1.840
PTPN6	0.184	1.205	0.172	1.248	0.026	1.504
PTPN9	0.002	2.257	0.376	-1.449	0.257	1.557
PTPRJ	0.295	1.153	0.094	1.343	0.020	1.547
PVRL2	0.026	-2.164	0.975	-1.019	0.169	-2.204
PZP	0.039	2.358	0.938	-1.051	0.225	2.244
QSOX1	0.364	-1.270	0.217	-1.292	0.042	-1.642
RAB11B-AS1	0.038	-1.605	0.953	-1.025	0.244	-1.646
RAB27A	0.270	1.169	0.084	1.335	0.015	1.560
RAB39A	0.041	-1.791	0.022	2.525	0.353	1.410
RAB41	0.030	1.857	0.868	-1.072	0.253	1.732
RAB4B-EGLN2	0.273	1.195	0.076	1.505	0.025	1.798
RABAC1	0.344	1.198	0.116	1.465	0.032	1.754
RABGGTB	0.554	-1.132	0.006	-1.839	0.001	-2.082
RAD21-AS1	0.929	1.011	0.022	1.571	0.021	1.588
RAD23A	0.550	-1.237	0.129	-1.832	0.047	-2.265
RANBP2	0.345	-1.248	0.196	-1.285	0.022	-1.603
RANBP9	0.282	-1.106	0.013	-1.410	0.003	-1.559
RANGAP1	0.016	-1.559	0.735	1.054	0.038	-1.479
RBM24	0.038	-1.933	0.477	-2.004	0.190	-3.872
RBM38	0.823	-1.067	0.113	-1.677	0.028	-1.790
RBMY2FP	0.013	-1.897	0.491	1.421	0.587	-1.335
RBPMS	0.232	1.446	0.146	1.437	0.032	2.078
RCOR2	0.285	1.448	0.050	2.570	0.008	3.722
RFC4	0.109	-1.269	0.270	-1.186	0.023	-1.506
RFX2	0.043	1.543	0.337	-1.361	0.672	1.134
RFXAP	0.826	1.079	0.023	-2.513	0.050	-2.329
RGPD3	0.566	-1.139	0.070	-1.467	0.015	-1.671
RGPD5	0.442	-1.178	0.034	-1.835	0.007	-2.161
RGPD6	0.418	-1.210	0.033	-1.792	0.004	-2.169
RGPD8	0.621	1.090	0.003	-1.574	0.019	-1.444
RGR	0.976	-1.004	0.013	1.668	0.016	1.662
RGS13	0.007	-2.088	0.004	2.365	0.555	1.133
RGS2	0.381	1.129	0.020	1.779	0.008	2.009
RGS6	0.171	1.417	0.112	1.765	0.019	2.502
RGS7	0.045	-2.266	0.116	2.216	0.964	-1.022
RGS9	0.313	1.305	0.121	1.461	0.020	1.906
RHOB	0.118	1.684	0.481	1.191	0.039	2.006
RILP	0.172	-1.354	0.002	1.750	0.259	1.293

RILPL2	0.339	-1.152	0.012	-1.595	0.003	-1.839
RIMS2	0.458	1.318	0.094	2.113	0.029	2.784
RIN2	0.807	-1.066	0.046	1.758	0.039	1.649
RIOK1	0.420	-1.248	0.009	-2.107	0.000	-2.629
RIPK2	0.067	-1.681	0.229	-1.566	0.023	-2.633
RIPK4	0.026	2.404	0.668	-1.384	0.466	1.738
RMDN2	0.070	1.337	0.303	1.215	0.013	1.624
RNASE6	0.692	-1.178	0.031	-2.424	0.030	-2.856
RNASEL	0.231	1.299	0.264	1.380	0.049	1.792
RNASET2	0.361	1.195	0.152	1.360	0.047	1.626
RNF122	0.221	1.277	0.049	-1.657	0.299	-1.298
RNF144A-AS1	0.021	-1.588	0.092	1.682	0.838	1.060
RNF146	0.264	1.253	0.026	1.710	0.005	2.142
RNF181	0.385	1.220	0.022	-1.737	0.038	-1.424
RNF20	0.044	1.402	0.378	1.168	0.009	1.637
RNF214	0.013	1.613	0.933	-1.023	0.126	1.577
RNH1	0.427	1.256	0.006	-2.964	0.022	-2.359
RNLS	0.604	1.122	0.056	2.114	0.031	2.372
RNMT	0.950	-1.018	0.038	-1.998	0.023	-2.035
RNPEP	0.004	1.872	0.953	-1.014	0.013	1.846
RPA3-AS1	0.183	1.382	0.058	1.526	0.001	2.109
RPIA	0.087	1.547	0.018	-2.165	0.250	-1.399
RPL21P44	0.476	1.184	0.039	1.758	0.011	2.080
RPL23AP53	0.394	1.165	0.099	1.436	0.035	1.673
RPL23AP7	0.579	1.069	0.018	1.580	0.010	1.688
RPL23AP82	0.203	1.155	0.060	1.349	0.015	1.557
RPRD1B	0.887	-1.025	0.024	-1.662	0.021	-1.703
RPS10P7	0.044	1.365	0.286	1.332	0.042	1.817
RPS26P11	0.516	-1.201	0.111	-1.558	0.031	-1.871
RPS6KA2	0.029	1.715	0.430	-1.307	0.398	1.312
RRN3P2	0.037	1.582	0.046	-1.756	0.683	-1.110
RSBN1	0.119	-1.288	0.353	-1.197	0.045	-1.542
RSRC1	0.080	1.404	0.642	1.086	0.013	1.525
RTCB	0.046	2.061	0.400	-1.835	0.867	1.123
RXRA	0.104	1.343	0.471	1.142	0.033	1.533
S100Z	0.001	3.434	0.739	-1.122	0.004	3.060
SAMD9L	0.732	-1.104	0.018	2.047	0.012	1.854
SAMHD1	0.587	-1.163	0.012	1.951	0.020	1.677
SAP30	0.460	-1.126	0.076	-1.504	0.034	-1.694

SART1	0.410	1.165	0.014	-1.528	0.056	-1.311
SCAND1	0.835	1.077	0.026	-2.186	0.014	-2.030
SCARNA14	0.615	-1.158	0.001	-4.439	0.001	-5.139
SCARNA5	0.284	1.379	0.035	-1.807	0.115	-1.311
SCLY	0.000	2.659	0.788	1.135	0.048	3.017
SCML1	0.451	-1.284	0.110	-1.978	0.026	-2.541
SCRN3	0.775	1.049	0.025	1.528	0.012	1.603
SCRT2	0.043	1.654	0.776	1.117	0.130	1.848
SCYL3	0.254	1.259	0.108	1.341	0.006	1.689
SDC2	0.042	2.018	0.237	-1.409	0.209	1.432
SDF4	0.013	2.048	0.934	1.030	0.037	2.110
SEC11C	0.132	-1.216	0.144	-1.488	0.042	-1.809
SEC61B	0.999	1.000	0.036	-1.639	0.037	-1.639
SECTM1	0.911	1.026	0.048	2.060	0.048	2.113
SEL1L3	0.034	1.746	0.476	-1.231	0.199	1.418
SELPLG	0.076	1.764	0.629	1.185	0.030	2.090
SEMA4B	0.714	1.086	0.056	1.495	0.031	1.625
SENP3	0.009	1.610	0.507	-1.253	0.448	1.285
SEPSECS	0.560	-1.101	0.063	-1.432	0.035	-1.576
SEPT14	0.761	1.060	0.001	1.694	0.003	1.795
SERHL2	0.030	1.522	0.742	1.120	0.158	1.705
SERPIND1	0.441	1.332	0.011	-2.071	0.139	-1.555
SERPINE2	0.045	1.907	0.276	-1.848	0.954	1.032
SERTAD2	0.756	-1.065	0.012	-1.535	0.005	-1.634
SESN1	0.807	-1.053	0.016	-2.119	0.011	-2.232
SESN2	0.233	-1.459	0.215	-1.375	0.045	-2.007
SETD1A	0.760	1.080	0.009	-1.978	0.017	-1.832
SETD6	0.880	1.038	0.032	1.679	0.046	1.743
SETD8	0.513	-1.129	0.058	-1.645	0.029	-1.858
SETDB1	0.042	1.443	0.553	1.130	0.031	1.630
SETX	0.187	1.249	0.075	1.366	0.006	1.707
SF3B5	0.369	1.200	0.004	-1.795	0.065	-1.496
SFI1	0.008	1.649	0.595	-1.141	0.137	1.446
SFT2D3	0.199	1.353	0.020	-1.745	0.110	-1.290
SGOL2	0.024	1.967	0.277	-1.582	0.579	1.243
SH2B2	0.522	1.125	0.044	2.397	0.027	2.697
SH2D4A	0.008	2.396	0.871	-1.106	0.248	2.165
SH3BP5L	0.056	1.332	0.057	1.380	0.001	1.838
SH3D19	0.407	-1.223	0.120	-1.425	0.017	-1.742

SHB	0.572	-1.324	0.026	-3.471	0.009	-4.596
SHROOM3	0.822	1.055	0.023	1.844	0.020	1.946
SIAH3	0.804	-1.041	0.044	-1.902	0.036	-1.980
SIGLEC15	0.039	-1.808	0.931	1.046	0.297	-1.729
SIGMAR1	0.021	1.795	0.431	-1.329	0.382	1.351
SIK1	0.679	-1.227	0.045	-2.662	0.008	-3.266
SIRPD	0.149	1.317	0.151	1.629	0.043	2.146
SLAMF7	0.504	-1.155	0.009	1.623	0.110	1.406
SLC16A14	0.635	1.192	0.017	-2.666	0.058	-2.236
SLC19A2	0.955	-1.012	0.031	-3.618	0.030	-3.661
SLC1A5	0.883	-1.060	0.001	-5.420	0.001	-5.747
SLC22A25	0.144	1.248	0.174	1.326	0.029	1.654
SLC22A4	0.627	-1.081	0.003	1.635	0.021	1.512
SLC22A5	0.383	1.329	0.088	1.658	0.019	2.204
SLC25A11	0.018	2.118	0.341	-1.504	0.396	1.408
SLC25A29	0.046	1.979	0.139	-1.749	0.736	1.131
SLC25A3	0.497	-1.126	0.009	-1.523	0.003	-1.714
SLC25A36	0.781	-1.087	0.004	-2.156	0.001	-2.344
SLC25A51	0.318	-1.209	0.040	-1.772	0.012	-2.143
SLC2A5	0.009	3.120	0.537	-1.720	0.511	1.814
SLC34A2	0.154	1.349	0.013	2.096	0.002	2.827
SLC35A5	0.132	1.449	0.416	1.194	0.005	1.730
SLC35B2	0.420	-1.341	0.139	-1.631	0.040	-2.188
SLC35D1	0.720	-1.056	0.057	-1.558	0.033	-1.645
SLC36A4	0.466	1.137	0.000	-1.774	0.004	-1.560
SLC3A2	0.786	1.078	0.048	-1.727	0.020	-1.602
SLC40A1	0.276	1.320	0.248	1.425	0.039	1.881
SLC46A1	0.469	1.142	0.078	1.963	0.043	2.241
SLC46A2	0.033	1.915	0.966	1.022	0.195	1.956
SLC4A2	0.025	-1.894	0.498	1.493	0.683	-1.269
SLC5A6	0.758	1.144	0.001	-4.002	0.001	-3.500
SLC7A5	0.226	-1.754	0.022	-3.078	0.002	-5.399
SLIRP	0.829	-1.054	0.022	-1.876	0.031	-1.977
SMARCB1	0.017	1.508	0.297	-1.324	0.632	1.139
SMIM3	0.354	1.269	0.031	-2.475	0.084	-1.951
SMTNL1	0.749	-1.103	0.029	1.835	0.065	1.663
SMURF1	0.461	-1.182	0.170	-1.293	0.042	-1.528
SNAPC4	0.084	1.454	0.665	1.112	0.050	1.617
SNED1	0.044	1.764	0.015	-2.044	0.468	-1.159

SNHG1	0.735	-1.083	0.000	-2.673	0.000	-2.895
SNHG11	0.093	1.779	0.006	-3.085	0.097	-1.734
SNHG17	0.492	-1.166	0.007	-1.954	0.001	-2.279
SNHG3	0.238	-1.164	0.010	-1.510	0.001	-1.758
SNHG5	0.875	1.021	0.046	-1.637	0.050	-1.604
SNHG9	0.545	1.223	0.005	-2.757	0.019	-2.255
SNORA48	0.326	-1.210	0.137	-1.375	0.027	-1.663
SNORA63	0.406	-1.132	0.013	-1.479	0.002	-1.675
SNORA70G	0.443	-1.109	0.012	-1.468	0.002	-1.629
SNORA79	0.401	-1.237	0.137	-1.424	0.042	-1.762
SNORD97	0.774	-1.093	0.011	-1.719	0.035	-1.880
SNUPN	0.441	1.086	0.026	-1.514	0.070	-1.395
SNX17	0.002	1.979	0.017	-1.831	0.665	1.080
SNX20	0.950	1.008	0.028	1.497	0.024	1.509
SNX30	0.586	1.070	0.008	-1.606	0.019	-1.501
SNX9	0.995	1.003	0.056	-2.835	0.034	-2.826
SOX2	0.047	1.397	0.090	1.921	0.022	2.684
SPAG5-AS1	0.591	1.121	0.010	-1.827	0.038	-1.630
SPHK1	0.506	-1.123	0.137	-1.372	0.041	-1.541
SPRY1	0.343	-1.500	0.001	-3.574	0.000	-5.363
SPRYD3	0.097	1.753	0.390	1.444	0.041	2.531
SPSB3	0.049	1.615	0.021	-1.806	0.493	-1.119
SPTB	0.010	1.637	0.705	1.077	0.010	1.764
SPTY2D1-AS1	0.827	1.097	0.017	2.822	0.027	3.094
SRSF2	0.364	-1.136	0.031	-1.412	0.004	-1.605
SRSF6	0.622	1.077	0.007	-1.651	0.009	-1.532
SSBP4	0.041	-1.642	0.963	1.024	0.376	-1.603
SSSCA1	0.722	-1.083	0.050	-1.554	0.012	-1.683
ST3GAL4	0.179	-1.310	0.006	1.553	0.409	1.186
ST6GALNAC3	0.072	1.624	0.007	-1.955	0.436	-1.204
STAG3L2	0.940	1.008	0.002	-1.600	0.002	-1.588
STAG3L3	0.603	1.063	0.007	-1.776	0.013	-1.671
STK11IP	0.044	1.387	0.225	1.312	0.012	1.820
STK25	0.019	1.936	0.880	1.080	0.171	2.092
STK3	0.345	1.222	0.143	1.574	0.045	1.924
STRA13	0.018	1.841	0.409	-1.502	0.682	1.226
STRAP	0.494	-1.157	0.206	-1.310	0.042	-1.515
STRIP1	0.758	1.051	0.002	-1.611	0.007	-1.533
STX11	0.089	-1.439	0.037	1.570	0.652	1.091

STX7	0.310	1.250	0.148	1.329	0.039	1.661
STX8	0.017	1.987	0.976	-1.015	0.181	1.958
SUCLG1	0.565	1.066	0.007	-1.537	0.015	-1.443
SUCO	0.563	-1.137	0.022	-1.543	0.002	-1.754
SULT1A4	0.762	1.051	0.041	-1.593	0.082	-1.515
SUMO1P3	0.196	-1.321	0.126	-1.329	0.010	-1.755
SUPT5H	0.799	-1.053	0.015	-1.514	0.011	-1.594
SYNE4	0.039	1.691	0.612	-1.205	0.408	1.404
SYT2	0.169	1.484	0.061	1.793	0.005	2.662
SYTL1	0.032	1.679	0.113	-1.536	0.595	1.093
SYVN1	0.151	1.330	0.010	-1.740	0.189	-1.308
TAF1C	0.293	-1.240	0.003	-3.243	0.001	-4.021
TAF5	0.476	1.181	0.000	-2.112	0.003	-1.788
TAGAP	0.410	-1.124	0.017	1.584	0.053	1.409
TAPSAR1	0.493	1.143	0.038	1.459	0.015	1.668
TARP	0.050	2.182	0.880	-1.143	0.461	1.908
TAS1R1	0.040	2.000	0.594	-1.342	0.467	1.491
TATDN1	0.718	-1.044	0.007	1.603	0.010	1.536
TATDN2	0.895	-1.016	0.001	-1.555	0.001	-1.580
TBC1D10A	0.012	1.947	0.076	-2.069	0.870	-1.063
TBC1D17	0.006	1.944	0.203	-1.355	0.049	1.435
TBCE	0.006	1.585	0.987	-1.005	0.154	1.577
TCAIM	0.368	1.239	0.098	1.555	0.026	1.927
TCEB2	0.093	1.392	0.002	-1.872	0.085	-1.344
TCHP	0.048	1.607	0.850	-1.047	0.052	1.535
TCOF1	0.725	-1.110	0.150	-1.540	0.048	-1.709
TCP1	0.603	-1.061	0.033	-1.500	0.018	-1.591
TCTN3	0.434	-1.342	0.146	-1.751	0.037	-2.350
TDP1	0.173	1.258	0.022	-1.538	0.165	-1.223
TECR	0.114	1.487	0.032	-1.999	0.225	-1.344
TESK1	0.379	1.289	0.045	-1.874	0.160	-1.454
TFCP2	0.023	1.691	0.962	-1.010	0.009	1.674
TFIP11	0.266	1.228	0.000	-1.809	0.010	-1.473
TFPI	0.744	-1.047	0.003	1.533	0.009	1.465
TGIF1	0.098	-1.377	0.059	-1.548	0.003	-2.132
TGM3	0.495	1.189	0.048	2.869	0.027	3.410
TGM4	0.018	1.939	0.315	-1.378	0.246	1.408
THOC1	0.529	-1.214	0.018	-2.050	0.003	-2.489
THOC6	0.046	1.960	0.803	1.055	0.053	2.067

THUMPD3	0.652	-1.087	0.012	-1.528	0.002	-1.661
THYN1	0.346	1.378	0.050	-2.146	0.228	-1.557
TIA1	0.250	1.200	0.058	1.575	0.016	1.890
TICAM1	0.120	-1.590	0.263	-1.272	0.011	-2.022
TICAM2	0.174	1.577	0.275	1.508	0.014	2.378
TIFA	0.263	-1.267	0.010	2.032	0.054	1.603
TIGD2	0.022	1.790	0.588	-1.243	0.393	1.440
TIMM17A	0.714	-1.102	0.030	-1.730	0.014	-1.907
TIMM8B	0.003	1.661	0.118	-1.599	0.881	1.039
TIMMDC1	0.049	1.751	0.442	-1.206	0.046	1.452
TINAGL1	0.046	-1.238	0.036	-1.315	0.002	-1.627
TLE1	0.951	1.025	0.000	-6.252	0.000	-6.101
TLR1	0.464	1.134	0.003	1.630	0.002	1.848
TLR4	0.518	1.142	0.040	1.530	0.020	1.746
TLR8	0.929	-1.017	0.017	1.883	0.023	1.852
TM2D2	0.483	-1.116	0.042	-1.424	0.011	-1.590
TMC3	0.043	1.795	0.325	-1.588	0.785	1.131
TMCO3	0.332	-1.205	0.130	-1.406	0.038	-1.695
TMCO6	0.150	1.249	0.135	1.308	0.008	1.634
TMED8	0.037	1.697	0.466	-1.342	0.524	1.265
TMEM132D	0.074	1.432	0.632	1.085	0.008	1.553
TMEM134	0.043	-1.729	0.073	1.653	0.864	-1.046
TMEM141	0.021	1.809	0.453	-1.450	0.661	1.248
TMEM185A	0.928	1.029	0.030	-2.010	0.029	-1.953
TMEM187	0.019	2.109	0.962	-1.022	0.173	2.063
TMEM189	0.854	-1.060	0.025	-2.197	0.013	-2.329
TMEM198B	0.224	1.399	0.042	-2.247	0.211	-1.605
TMEM214	0.016	1.480	0.039	-1.554	0.789	-1.050
TMEM216	0.023	1.835	0.846	-1.136	0.469	1.615
TMEM231	0.029	1.522	0.199	-1.426	0.798	1.067
TMEM249	0.048	-1.649	0.023	1.728	0.751	1.048
TMEM258	0.037	1.683	0.239	-1.309	0.204	1.286
TMEM39A	0.590	-1.107	0.078	-1.487	0.039	-1.647
TMEM44-AS1	0.122	1.366	0.333	1.320	0.049	1.803
TMEM51-AS1	0.147	1.313	0.307	1.214	0.033	1.595
TMEM65	0.400	1.110	0.012	1.516	0.004	1.682
TMEM72-AS1	0.137	1.141	0.053	1.362	0.011	1.555
TMOD2	0.370	1.258	0.269	1.272	0.038	1.600
TMPRSS11BNL	0.920	-1.015	0.041	1.637	0.052	1.613

TMUB1	0.016	2.382	0.192	1.530	0.002	3.644
TMX2	0.251	1.253	0.000	-2.187	0.003	-1.745
TNC	0.081	1.328	0.365	1.201	0.030	1.595
TNFAIP3	0.089	-2.084	0.001	-3.316	0.000	-6.910
TNFAIP8L2	0.193	1.746	0.088	2.399	0.009	4.188
TNFRSF10A	0.418	-1.081	0.084	-1.456	0.046	-1.574
TNFRSF1A	0.633	1.085	0.003	1.571	0.005	1.705
TNFRSF25	0.048	-1.197	0.090	-1.254	0.007	-1.502
TNFRSF8	0.047	1.893	0.108	2.549	0.016	4.826
TNFSF10	0.598	-1.151	0.001	2.735	0.001	2.376
TNXB	0.419	1.164	0.059	1.477	0.016	1.719
TOB1	0.835	-1.051	0.058	-2.812	0.049	-2.954
TOLLIP	0.121	1.355	0.118	1.747	0.027	2.367
TOMM20	0.581	-1.120	0.028	-1.531	0.006	-1.715
TOMM7	0.956	1.013	0.061	-1.709	0.043	-1.688
TOP1MT	0.546	1.227	0.001	-3.438	0.004	-2.801
TOP3B	0.252	1.346	0.034	-1.668	0.217	-1.239
TP53BP2	0.314	-1.192	0.013	-1.378	0.001	-1.643
TPM4	0.429	-1.143	0.009	1.766	0.042	1.545
TPPP3	0.028	2.008	0.390	1.163	0.010	2.335
TPST1	0.163	1.386	0.021	-2.368	0.120	-1.709
TPST2	0.019	1.644	0.388	1.302	0.023	2.140
TRAFD1	0.539	-1.118	0.012	1.560	0.043	1.395
TRANK1	0.475	1.201	0.264	1.279	0.038	1.536
TRAPPC1	0.012	1.698	0.674	-1.120	0.123	1.517
TRAPPC8	0.264	1.186	0.130	1.292	0.025	1.531
TREML1	0.497	1.181	0.172	1.498	0.041	1.769
TREML2	0.418	1.135	0.077	1.421	0.035	1.613
TRIM21	0.706	1.117	0.254	1.372	0.040	1.533
TRIM35	0.259	1.488	0.016	-2.519	0.146	-1.693
TRIM41	0.019	1.439	0.380	1.206	0.019	1.736
TRIM61	0.047	-1.436	0.130	-1.306	0.003	-1.876
TRIM6-TRIM34	0.344	1.307	0.153	1.885	0.044	2.465
TRIM9	0.022	2.218	0.812	1.082	0.000	2.400
TRMT13	0.347	1.224	0.142	1.396	0.033	1.709
TRMU	0.097	1.599	0.016	-2.034	0.286	-1.272
TRNAS6	0.944	1.020	0.049	-3.589	0.052	-3.519
TSC22D2	0.276	-1.236	0.228	-1.236	0.016	-1.527
TSHZ1	0.045	-1.550	0.444	-1.329	0.079	-2.060

TSN	0.874	1.025	0.019	-1.570	0.022	-1.532
TSNAX-DISC1	0.710	1.074	0.079	1.518	0.040	1.631
TSPYL2	0.136	-1.599	0.016	-2.059	0.000	-3.293
TSPYL4	0.477	1.087	0.033	-1.624	0.060	-1.495
TTC13	0.091	1.481	0.768	1.058	0.015	1.567
TTC31	0.027	1.754	0.121	-1.782	0.961	-1.016
TTC38	0.470	-1.266	0.031	-2.450	0.009	-3.103
TTLL12	0.020	1.874	0.751	1.230	0.222	2.304
TUBA1A	0.330	1.173	0.000	2.008	0.000	2.355
TUBA1B	0.056	1.320	0.086	1.642	0.017	2.168
TUBA1C	0.751	1.053	0.023	2.027	0.017	2.134
TUBB1	0.724	1.076	0.025	-1.915	0.043	-1.780
TULP2	0.845	-1.060	0.038	-2.129	0.031	-2.257
TWISTNB	0.471	-1.186	0.008	-1.801	0.003	-2.136
TXLNG	0.759	-1.071	0.012	-1.816	0.001	-1.946
TXNDC11	0.466	-1.205	0.083	-1.489	0.014	-1.795
UAP1	0.526	-1.148	0.082	-1.606	0.022	-1.844
UBE2MP1	0.046	1.587	0.556	1.222	0.084	1.940
UBE2O	0.576	1.105	0.028	-1.618	0.074	-1.465
UBE2W	0.503	1.129	0.020	1.426	0.007	1.611
UBL4A	0.002	3.011	0.523	-1.489	0.252	2.023
UBTD1	0.047	1.908	0.858	-1.111	0.381	1.718
UBTD2	0.031	2.028	0.742	-1.166	0.223	1.740
UG0898H09	0.122	1.227	0.188	1.319	0.039	1.619
UGCG	0.812	1.049	0.006	-1.653	0.020	-1.576
UGT2B4	0.492	-1.128	0.048	-1.414	0.023	-1.594
UHRF1BP1	0.102	-1.259	0.073	-1.570	0.015	-1.976
ULK4P3	0.020	1.854	0.118	-2.472	0.590	-1.333
UNC45A	0.021	2.102	0.415	-1.448	0.323	1.452
UPRT	0.562	1.212	0.001	-2.855	0.019	-2.355
UQCRH	0.696	-1.092	0.000	-2.360	0.000	-2.578
USP14	0.262	-1.274	0.036	-1.565	0.003	-1.994
USP36	0.476	-1.367	0.092	-2.096	0.023	-2.866
USP42	0.331	-1.236	0.214	-1.276	0.023	-1.577
USP47	0.327	-1.202	0.229	-1.266	0.029	-1.522
USPL1	0.141	-1.430	0.277	-1.353	0.030	-1.935
UTP14C	0.006	1.782	0.471	-1.194	0.065	1.491
UTP20	0.310	-1.160	0.010	-1.437	0.002	-1.667
UTS2B	0.621	1.091	0.043	1.982	0.028	2.163

VAMP8	0.020	2.568	0.922	1.073	0.193	2.755
VBP1	0.176	1.329	0.422	1.165	0.003	1.549
VDAC2	0.813	-1.040	0.030	-1.453	0.018	-1.512
VILL	0.508	-1.274	0.124	-1.805	0.049	-2.299
VIMP	0.271	1.272	0.005	-2.060	0.020	-1.620
VPS11	0.036	1.383	0.028	-1.741	0.287	-1.258
VPS25	0.043	-1.426	0.168	-1.398	0.012	-1.994
VPS26B	0.016	1.616	0.007	-1.717	0.609	-1.062
VPS45	0.510	1.316	0.044	-2.621	0.154	-1.992
VPS72	0.061	1.645	0.346	1.294	0.008	2.128
VPS9D1-AS1	0.536	-1.165	0.018	2.227	0.053	1.911
VWF	0.009	2.862	0.740	-1.194	0.119	2.397
WASH5P	0.036	1.934	0.075	-2.005	0.917	-1.036
WASIR2	0.001	-1.292	0.192	-1.163	0.005	-1.502
WBP11	0.713	-1.071	0.028	-1.498	0.007	-1.604
WDFY3-AS2	0.028	2.036	0.489	-1.397	0.416	1.457
WDR12	0.280	-1.160	0.019	-1.896	0.007	-2.200
WDR43	0.401	-1.389	0.002	-2.816	0.000	-3.911
WDR45B	0.996	-1.001	0.002	-1.715	0.011	-1.717
WDR52	0.028	1.834	0.730	-1.163	0.321	1.577
WDR59	0.011	1.892	0.015	-2.017	0.786	-1.066
WDR6	0.034	1.805	0.226	-1.567	0.635	1.152
WDR77	0.340	1.265	0.008	-1.877	0.050	-1.485
WDSUB1	0.870	1.046	0.002	-2.063	0.014	-1.973
WDYHV1	0.058	1.901	0.007	-3.760	0.121	-1.977
WHAMM	0.203	-1.282	0.061	-1.458	0.003	-1.869
WNT4	0.177	1.209	0.042	1.933	0.015	2.337
WSB1	0.747	1.073	0.006	1.715	0.004	1.841
WSB2	0.528	1.081	0.009	1.467	0.002	1.586
XAB2	0.934	-1.021	0.017	-1.640	0.016	-1.674
XPNPEP1	0.648	-1.108	0.060	-1.710	0.027	-1.895
XPO5	0.353	1.390	0.044	-2.509	0.125	-1.805
XRRA1	0.425	1.112	0.029	1.439	0.006	1.600
YAP1	0.008	1.955	0.344	1.831	0.073	3.580
YBX2	0.026	2.202	0.797	-1.106	0.134	1.991
YEATS4	0.941	1.025	0.041	-2.256	0.053	-2.202
YTHDF3-AS1	0.005	2.153	0.904	1.069	0.172	2.301
YWHAH	0.014	2.168	0.336	-1.509	0.357	1.437
ZBED4	0.069	1.312	0.038	-1.686	0.266	-1.285

ZBTB1	0.564	-1.130	0.012	-1.690	0.005	-1.909
ZBTB10	0.998	-1.001	0.071	-2.245	0.039	-2.247
ZBTB25	0.878	-1.028	0.009	-1.724	0.010	-1.773
ZBTB5	0.507	-1.279	0.131	-1.614	0.018	-2.065
ZC3H12A	0.224	-1.639	0.030	-1.977	0.003	-3.241
ZCCHC12	0.035	1.726	0.107	-2.723	0.436	-1.578
ZCCHC18	0.791	-1.106	0.040	-3.339	0.029	-3.693
ZDHHC13	0.035	1.770	0.037	-1.649	0.681	1.073
ZDHHC7	0.702	-1.057	0.011	-1.473	0.009	-1.556
ZFAND5	0.143	-1.190	0.077	-2.758	0.048	-3.281
ZFAS1	0.312	-1.153	0.051	-1.596	0.020	-1.840
ZFP36L2	0.220	-1.253	0.007	-2.469	0.002	-3.092
ZHX1-C8ORF76	0.855	1.049	0.035	-1.717	0.019	-1.637
ZHX2	0.223	1.181	0.145	1.365	0.040	1.613
ZNF134	0.513	1.142	0.045	-1.612	0.083	-1.412
ZNF14	0.677	1.067	0.042	-1.548	0.081	-1.450
ZNF140	0.143	1.499	0.230	1.511	0.026	2.266
ZNF165	0.462	-1.359	0.015	-2.873	0.004	-3.905
ZNF197	0.006	1.347	0.236	1.138	0.001	1.533
ZNF200	0.313	1.217	0.024	1.816	0.007	2.210
ZNF212	0.044	1.750	0.022	-1.974	0.624	-1.128
ZNF217	0.355	1.213	0.089	1.425	0.025	1.729
ZNF281	0.270	-1.183	0.103	-1.476	0.033	-1.746
ZNF322	0.033	1.968	0.974	-1.011	0.044	1.948
ZNF326	0.684	-1.114	0.020	-1.668	0.010	-1.858
ZNF331	0.237	-1.331	0.173	-1.616	0.039	-2.151
ZNF34	0.161	1.527	0.011	-2.858	0.072	-1.872
ZNF41	0.100	1.794	0.636	1.170	0.027	2.098
ZNF415	0.018	1.883	0.044	-2.190	0.652	-1.163
ZNF418	0.005	2.167	0.822	1.102	0.061	2.388
ZNF433	0.936	1.021	0.043	-1.762	0.044	-1.726
ZNF438	0.720	1.077	0.086	1.650	0.047	1.777
ZNF441	0.088	1.475	0.096	1.485	0.008	2.190
ZNF443	0.073	1.765	0.032	-2.172	0.471	-1.231
ZNF496	0.111	-1.519	0.542	-1.187	0.039	-1.804
ZNF511	0.024	1.899	0.122	-1.988	0.910	-1.047
ZNF561	0.309	1.147	0.008	-1.571	0.061	-1.369
ZNF581	0.897	1.029	0.039	-1.544	0.018	-1.501
ZNF582	0.048	1.847	0.237	-2.148	0.811	-1.163

ZNF583	0.017	2.584	0.366	1.612	0.021	4.164
ZNF589	0.047	1.586	0.668	-1.162	0.372	1.366
ZNF600	0.029	1.947	0.995	-1.004	0.313	1.939
ZNF606	0.027	1.690	0.705	1.183	0.147	1.999
ZNF613	0.916	-1.029	0.007	1.944	0.028	1.889
ZNF624	0.022	2.195	0.567	1.464	0.101	3.213
ZNF629	0.004	2.052	0.157	-1.595	0.368	1.287
ZNF638	0.247	1.270	0.076	1.351	0.012	1.716
ZNF641	0.024	1.697	0.525	1.134	0.002	1.924
ZNF66	0.012	2.031	0.959	1.021	0.123	2.074
ZNF660	0.043	2.134	0.779	-1.206	0.415	1.770
ZNF667-AS1	0.096	1.708	0.870	-1.040	0.034	1.642
ZNF668	0.067	1.775	0.000	-3.557	0.001	-2.004
ZNF706	0.714	1.080	0.001	-2.171	0.003	-2.010
ZNF720	0.390	1.092	0.002	1.432	0.000	1.564
ZNF767	0.125	1.482	0.331	1.420	0.043	2.104
ZNF784	0.024	2.268	0.046	-2.154	0.858	1.053
ZNF805	0.061	-1.239	0.268	-1.212	0.033	-1.502
ZNF821	0.760	-1.084	0.025	-1.680	0.006	-1.822
ZNHIT3	0.445	-1.089	0.044	-1.468	0.019	-1.599
ZSCAN32	0.885	1.025	0.004	1.775	0.005	1.819
ZSCAN4	0.045	-1.580	0.314	1.263	0.377	-1.250

Gene Symbol	Norm ROS CD v Ctrl		Low ROS CD v Ctrl	
	P-value	FC	P-value	FC
ABCC5	-	-	0.029	1.563
ABCF1	0.026	-1.694	0.020	1.699
ACAD8	0.035	-1.747	-	-
ACAT2	0.006	-2.159	0.000	3.076
ACOX1	-	-	0.023	1.801
ACSM3	-	-	0.038	2.127
ACSS2	-	-	0.031	1.562
ADAM10	-	-	0.035	1.502
ADCY10	-	-	0.024	2.357
AFG3L2	0.038	-2.314	-	-
AKT1S1	0.044	-1.727	-	-
ALOX12	0.016	-1.565	-	-
AP2M1	0.028	-1.506	-	-
B3GNT4	0.019	-2.266	0.042	2.121
B4GALT1	-	-	0.004	1.769
BAD	0.003	-1.823	0.042	1.650
BCAT2	0.045	-1.527	0.028	1.719
BMI1	0.024	-2.674	-	-
BMP2	0.033	-2.053	0.011	2.885
BMP6	0.040	-1.741	-	-
C4A	-	-	0.020	1.848
CAB39	-	-	0.019	1.505
CACNA1A	0.005	2.458	0.009	2.174
CACNA1E	-	-	0.038	1.893
CARM1	0.016	-2.480	0.022	2.155
CAT	-	-	0.012	2.042
CBR4	-	-	0.021	1.602
CD14	-	-	0.000	3.295
CD320	-	-	0.049	1.509
CD58	0.032	1.531	-	-
CDIPT	-	-	0.050	1.671
CDK11A	-	-	0.002	1.528
CDK16	0.022	-1.556	0.011	1.683
CDK3	0.005	-2.436	0.030	1.772
CDK7	-	-	0.022	1.537
CDKN1A	0.015	-2.934	0.001	6.064
CHEK1	-	-	0.040	1.530
CHKA	0.031	-1.645	0.009	1.938
CMPK1	0.021	-1.643	-	-
COL1A1	0.002	-3.336	0.002	3.891
COMMD3-BMI1	0.020	-2.683	-	-
COX4I1	0.001	-2.121	0.001	2.091
COX5B	0.005	-1.782	-	-
COX7A2L	0.015	-2.112	-	-
CRAT	0.000	-4.868	0.026	2.085
CREM	-	-	0.019	1.872
CRY2	0.002	-2.109	0.000	2.119
CRYL1	0.002	-3.418	0.003	2.984

CTSA	-	-	0.030	1.654
CXCR4	0.028	-1.842	0.003	2.608
DDX25	-	-	0.026	1.795
DGAT2	-	-	0.028	1.768
DGKE	-	-	0.006	1.518
DLST	-	-	0.045	1.546
DPYD	-	-	0.011	1.527
DUT	0.003	-2.323	-	-
EDN1	0.015	-2.628	0.002	3.620
EIF2AK3	0.006	-2.803	0.001	3.773
EPHA1	-	-	0.042	1.776
ETNK1	-	-	0.008	1.784
FPGT	0.009	2.468	0.008	2.744
GADD45A	0.011	-1.587	0.000	2.085
GALK2	-	-	0.008	1.831
GALT	0.041	-2.201	-	-
GPT2	0.004	-2.594	0.027	1.807
GSTT1	0.030	-1.775	0.031	1.741
GUSB	0.003	-2.090	0.005	2.050
HACL1	0.010	-1.804	0.009	1.846
HCK	-	-	0.041	1.599
HMGCR	-	-	0.028	1.543
HMGCS1	0.015	-1.587	0.004	1.656
HPSE	0.012	1.647	0.015	1.653
HSPA9	-	-	0.018	1.679
IFNAR2	-	-	0.002	1.665
IL4I1	-	-	0.025	1.528
IP6K2	-	-	0.002	1.531
IRAK2	-	-	0.001	2.010
IRS2	-	-	0.026	2.342
ITGA6	-	-	0.048	1.536
ITGB1	-	-	0.006	1.672
JAG1	0.006	-1.766	0.012	1.664
KANSL2	0.003	-1.909	0.001	1.988
KAT5	-	-	0.043	1.698
KCNJ1	-	-	0.002	2.198
KCNQ1	0.019	-1.718	-	-
KLF5	-	-	0.020	1.630
KPNB1	-	-	0.015	1.519
LTBR	-	-	0.004	2.863
MAP2K6	0.046	2.009	-	-
MAP3K1	0.000	1.536	0.000	1.686
MAP3K8	-	-	0.016	2.364
MAPK14	-	-	0.046	1.732
MAPK6	-	-	0.008	1.698
MAT2B	-	-	0.007	1.544
MED16	-	-	0.020	1.551
MED30	0.013	-1.505	0.002	1.736
MEF2D	0.003	-1.603	0.007	1.616
MVD	0.001	-3.170	0.002	3.480

NDUFA5	0.034	-1.542	0.042	1.511
NDUFS6	0.008	-2.547	0.043	1.848
NDUFV2	0.026	-1.596	0.005	1.895
NFKB2	-	-	0.022	1.821
NFKBIA	0.002	-2.158	0.001	3.406
NOS3	0.001	1.655	0.000	1.889
NR4A1	0.034	-2.721	0.013	3.727
NRAS	-	-	0.021	1.520
NRIP1	0.001	-1.881	0.000	2.048
NT5C	0.026	-1.949	-	-
NT5C3A	0.035	1.727	-	-
NUP133	0.000	-1.817	0.000	1.704
NUP155	0.027	-1.720	0.004	2.092
NUP37	0.004	-2.079	0.032	1.854
ODC1	0.035	-1.808	0.008	2.131
OSBP	0.002	-1.532	-	-
PABPC4	0.030	-2.689	-	-
PANK4	-	-	0.048	2.418
PDE5A	0.015	1.900	0.012	1.955
PDE6H	0.012	-4.370	-	-
PDK3	-	-	0.037	1.519
PER1	0.017	-3.730	0.005	5.349
PIP5K1B	0.006	-1.526	-	-
PLCD1	0.000	-2.924	0.002	1.630
PLK2	0.023	-1.801	0.003	2.400
PLOD3	0.004	-3.200	-	-
POLE3	0.011	-1.864	-	-
POLR3C	0.001	-1.943	-	-
PPP2R1B	0.019	-1.537	-	-
PRKAR2B	0.011	-2.504	0.004	3.248
PRKCE	-	-	0.010	1.769
PRKCQ	-	-	0.007	1.642
PRPS1L1	0.047	1.725	-	-
PSMD4	-	-	0.016	1.580
PTGES	-	-	0.038	1.724
PTGES3	-	-	0.006	1.602
PTGS2	0.003	2.235	0.000	3.169
PTPN6	-	-	0.026	1.504
RANBP2	-	-	0.022	1.603
RIMS2	-	-	0.029	2.784
RIPK2	-	-	0.023	2.633
RNASEL	-	-	0.049	1.792
RNF20	-	-	0.009	1.637
RNLS	-	-	0.031	2.372
RPIA	0.018	-2.165	-	-
RXRA	-	-	0.033	1.533
SCYL3	-	-	0.006	1.689
SETD1A	0.009	-1.978	0.017	1.832
SETDB1	-	-	0.031	1.630
SETX	-	-	0.006	1.707

SH2B2	0.044	2.397	0.027	2.697
SIK1	0.045	-2.662	0.008	3.266
SLC19A2	0.031	-3.618	-	-
SLC22A4	0.003	1.635	0.021	1.512
SLC22A5	-	-	0.019	2.204
SLC34A2	0.013	2.096	0.002	2.827
SLC35B2	-	-	0.040	2.188
SLC40A1	-	-	0.039	1.881
SLC46A1	-	-	0.043	2.241
SLC5A6	0.001	-4.002	0.001	3.500
SOX2	-	-	0.022	2.684
SPHK1	-	-	0.041	1.541
STK3	-	-	0.045	1.924
SUCLG1	0.007	-1.537	-	-
SULT1A4	0.041	-1.593	-	-
TECR	0.032	-1.999	-	-
TESK1	0.045	-1.874	-	-
TLE1	0.000	-6.252	0.000	6.101
TLR4	0.040	1.530	0.020	1.746
TNFRSF1A	0.003	1.571	0.005	1.705
TNXB	-	-	0.016	1.719
TOB1	-	-	0.049	2.954
TUBA1A	0.000	2.008	0.000	2.355
TUBA1C	0.023	2.027	0.017	2.134
UAP1	-	-	0.022	1.844
UGT2B4	-	-	0.023	1.594
UQCRH	0.000	-2.360	0.000	2.578

Ontology	Up LowROS CD v CTRL	Down LowROS CD v CTRL	Up NormROS CD v CTRL	Down NormROS CD v CTRL	Up LowROS CD v NormROS CD
ATP binding	P=2.05E-8: ADCY10,STK3,MAPK14,SETX,GALK2,RNASEL,PDK3,KCNI1,N1,SLC22A4,SLC22A5,SCYL3,PANK4,DDX5,ARCCS5,ETNK1,DGKE,PRKCQ,ACSS2,HCK,MAP3K1,EPHA1	P=4.72E-7:CDK16,PLK2,ABCFL1,ACSM3,SPHK1,MAP3K8,RIPK2,IRAK2,CDK11A,SIK1,PRKCE,CHEK1,PFKFB2,MAPK6,CHKA,EIF2AK3,HSPA9,MVD,IP6K2,CDK3,CDK7	-	P=1.97E-2:CDK16,CMPK1,PLK2,ABCFL1,AFG3L2,PIP5K1B,SIK1,CHKA,TESK1,EIF2AK3,MVD,CDK3	P=5.91E-4:EPHB4,MKK5,ACSL3,DNAJA3,PASK,KCNJ1,RP56K2,ABCC5,RIPK4,MERTK,ACSS2,PAPSS2,PKN3,STK25
Carbohydrate metabolism	-	P=9.11E-7:B3GN4,DDIT4,RANBP2,BAD,SIK1,PRKCE,IRS2,PLCD1,PFKFB2,B4GALT1	-	P=0.021:B3GN4,CRY1,GAUT,PDHA1,GUSB,BAD,SIK1,PLCD1	P=5.64E-6:HEXA,PASK,GALT,AGL,GYS1,GRB10,SLC25A11,PLCD1,CSGALNACT1,HYAL2,SLC2A5,PGM5,DERA
Carboxylic acid metabolic process	P=1.24E-9:CBR4,CACNA1A,DPYD,MAPK14,DGAT2,PDK3,ACOX1,SLC22A4,SLC22A5,TLR4,KYAT3,PSMD4,SLC46A1,TNFRSF1A,ACSS2,PTGES3,TNXB,NOS3,PTGS2	P=9.11E-11:CRYL1,DDIT4,ACSM3,SPHK1,SLC5A6,PTGES,UGT2B4,PRKAR2B,AR2B,BCAT2,PRKCE,HACL1,DLST,IRS2,PFKFB2,ODC1,GPT2,LR4L1,CRAT,EIF2AK3,CREM,EDN1,NDUF56	2.47E-4:CACNA1A,NOS3,PTGS2,SLC22A4,TLR4,TNFRSF1A	P=7.37E-7:CRYL1,ACAD8,GALT,PDHA1,SLC5A6,TECR,PRKAR2B,BCAT2,HACL1,ODC1,SLC5A6,TECR,PRKAR2B,B,CRAT,EIF2AK3,ALOX12,EDN1,NDUF56	-
Fatty Acid Metabolism	P=9.36E-8:CBR4,MAPK14,DGAT2,PDK3,ACOX1,TLR4,TNFRSF1A,ACSS2,PTGES3,TNXB,PTGS2	P=9.37E-8:CRYL1,ACSM3,SPHK1,PTGES,PRKAR2B,HACL1,IRS2,CRAT,EIF2AK3,CREM,EDN1,NDUF56	P=0.005:PTGS2,TLR4,TNFRSF1A	P=0.042:ACAT2,TECR	-
Fatty Acid Oxidation	P=0.005:MAPK14,DGAT2,ACOX1	P=0.008:HACL1,IRS2,CRAT	-	P=8.06E-4:ACAD8,HACL1,CRAT,ALOX12	P=0.005:ACAD8,HADH,CRAT
Galactose Metabolism	P=0.045:GALK2	-	-	-	P=0.53E-4:GALT,PGM5
Glucose Transport/import	P=0.009:MAPK14,RNASEL,SHZB2	P=7.34E-5:RANBP2,NUP155,NUP37,NUP133,IRS2,EDN1	-	P=2.56E-3:NUP155,NUP37,NUP133	-
Glycogen biosynthesis	-	-	-	-	P=0.0012:PPP2R5D,AGL,GYS1
Insulin secretion	P=0.009:CACNA1A,CACNA1E,HMGCR,RIMS2	P=4.26E-4:CDK16,BAD,PRKCE,IRS2,PFKFB2,EIF2AK3	P=0.001:NOS3,TLR4	P=0.016:CDK16,BAD,KCNQ1,EIF2AK3	-
Lipopolysaccharide-mediated signaling	P=1.65E-6:MAPK14,CD14,TLR4,NOS3,HCK	P=9.01E-5:NFKBIA,IP6K2,IRAK2,PRKCE	-	-	-
Oxidation-reduction process	P=1.89E-4:CBR4,DPYD,MAPK14,RNLS,DGAT2,ACOX1,CAT,HMGCR,ACSS2,PTGES3,NOS3,PTGS2	-	-	-	P=3.1E-7:PASK,PLD3,ACAD8,AGL,GYS1,ASPH,GRB10,HAAO,COX7A2L,HSO17810,HADH,ACSS2,CRAT,NDUF87,NNT,PGM5
Oxidative phosphorylation	-	P=2.8E-5:COX4I1,NDUF5,UCRH,NDUF56,NDUFV2	-	P=0.008:NDUF5,NDUF56,NDUFV2	-
Reactive oxygen species biosynthesis	P=3.47E-4:MAPK14,PDK3,TLR4,CAT,NOS3,PTGS2	-	P=1.27E-4:NOS3,PTGS2,TLR4	-	-
Response to glucose	P=8.05E-4:CACNA1E,MAPK14,PDK3,PRKCQ,HMGCR	P=0.002:CDK16,BAD,PRKCE,IRS2,PFKFB2	-	-	-

Gene	Low ROS CD vs	Normal ROS CD vs	Low ROS CD vs
	Normal ROS CD	Control	Control
ACTR3B	1.77	-1.01	1.76
ACYP1	2.71	-1.71	1.58
AMPD3	1.67	-1.08	1.55
BRI3BP	2.23	-1.20	1.86
CD9	3.50	-1.35	2.60
CRISP3	2.07	-1.44	1.44
CSGALNACT	1.74	-1.41	1.24
CTXN2	3.43	-4.67	-1.36
DACH1	1.60	-1.05	1.51
DNAJA3	2.45	-1.53	1.60
DNAJC1	-1.59	1.39	-1.15
DNASE1L1	1.77	1.26	2.23
DUSP23	2.35	-1.66	1.42
EFCAB12	1.52	-1.13	1.34
EFEMP2	2.16	-2.08	1.04
GRB10	2.04	-1.59	1.29
GTF3C2	1.59	-1.32	1.20
GYG2P1	-1.72	-1.12	-1.93
HAAO	3.18	-1.60	1.99
HYI	1.86	-1.21	1.54
ITFG1	1.50	-1.01	1.49
KBTBD11	1.90	-2.03	-1.07
LINC00654	2.42	-1.17	2.07
NC1001278	-2.58	-1.25	-3.23
NC1019279	1.68	-1.08	1.56
LRRC34	1.83	-1.32	1.38
MCU	1.52	-1.19	1.28
MYCBP2-AS	1.68	-1.36	1.24
NAA10	1.53	1.39	2.14
NAT9	1.65	-1.00	1.65
NDUFB7	2.03	-1.20	1.69
IEDD8-MDP	1.87	-1.35	1.38
NRDE2	1.56	-1.39	1.12
NUDT3	1.55	-1.01	1.53
OCEL1	2.70	-1.99	1.36
OCRL	2.38	-1.71	1.40
OR2A7	1.88	-1.11	1.70
ORM2	1.84	-1.18	1.56
PBDC1	2.63	-1.92	1.37
PDE6D	1.65	-1.21	1.36
POLE4	2.66	-1.54	1.72
PSMD4	1.61	-1.02	1.58
PTPN9	2.10	-1.35	1.56
PYCR1	-1.81	1.59	-1.14
RANGAP1	-1.66	1.12	-1.48
RAP2B	1.57	-1.36	1.16
RAPGEFL1	1.55	-1.09	1.43
RBMY2FP	-2.00	1.50	-1.34

RGS13	-1.81	2.04	1.13
RNPEP	1.83	1.01	1.85
S100Z	3.23	-1.06	3.06
SCLY	2.47	1.22	3.02
SLC46A2	2.27	-1.16	1.96
SNX17	1.71	-1.58	1.08
SPECC1L	1.52	-1.32	1.15
TBC1D17	1.74	-1.21	1.44
TIMM8B	1.60	-1.54	1.04
UBL4A	3.02	-1.49	2.02
ZNF629	1.81	-1.41	1.29

Gene	chrom	pos	ref	alt	rsID	AA change	Alt allele effect	cadd	dbSNP MAF	hg19 pos	ExAC freq	ExAC European MAF	ExAC African MAF	ExAC East Asian MAF	ExAC South Asian MAF	Validation
ACTR3B	chr7	152800645	A	G	Novel	Y72C	nonSynonymous	25.2	-	152497730	-	-	-	-	-	-
ACTR3B	chr7	152801700	G	A	Novel	R102Q	nonSynonymous	34	-	152498785	-	-	-	-	-	-
ACTR3B	chr7	152823439	C	T	rs149559061	A261V	nonSynonymous	20.3	0.000514	152520524	0.0005271	0.000809207	0.000288351	0	0.000181686	byCluster,byFrequency,by1000G
ACTR3B	chr7	152823405	C	T	rs140327402	R250W	nonSynonymous	23.5	0.049862	152520490	0.05	0.052101826	0.014148219	0.003929727	0.09446472	byCluster,byFrequency,by1000G
ACTR3B	chr7	152820410	G	C	rs781547923	E218Q	nonSynonymous	26.2	0.000013	152517495	0.00000824	0	0.000130548	0	0 unknown	
AMPD3	chr11	10493490	G	A	rs75286033	G361S	nonSynonymous	13.8	0.003524	10515037	0.003278	0	0.035521236	0.000115875	0	0 byCluster,byFrequency,by1000G
AMPD3	chr11	10487341	C	T	rs76836360	R306W	nonSynonymous	35	0.000032	10508888	0.0006342	0	0.00644228	0	0.000242336	byCluster,byFrequency,by1000G
AMPD3	chr11	10493476	G	A	rs61388455	R356Q	nonSynonymous	21.4	0.001784	10515023	0.00159	6.01287E-05	0.016968762	0	0 byCluster,byFrequency,by1000G	
AMPD3	chr11	10495666	T	C	rs36003153	Y455H	nonSynonymous	16.5	0.007748	10517213	0.007083	0.000135131	0.075595129	0.000115714	0 byCluster,byFrequency,by1000G	
AMPD3	chr11	10496826	C	T	rs144107914	S482L	nonSynonymous	20.7	0.000008	10518373	0.000313	0.000554407	0	0	0 byCluster,byFrequency	
AMPD3	chr11	10478587	G	A	rs149433198	D95N	nonSynonymous	28.9	0.000668	10500134	0.0006671	0.001215669	0	0	0 byCluster,byFrequency	
AMPD3	chr11	10493383	A	G	rs147246880	N325S	nonSynonymous	16.4	0.001061	10514930	0.001095	0.001665266	0	0	0.000242248	byCluster,byFrequency,by1000G
AMPD3	chr11	10500097	T	G	rs146000615	F523L	nonSynonymous	21.6	0.00133	10516444	0.001367	0.002113753	0.000480862	0	0 byCluster,byFrequency,by1000G	
AMPD3	chr11	10487356	G	T	rs117706710	V311L	nonSynonymous	27.4	0.000008	10508903	0.00733	0.011290032	0.001637765	0	0.002544529	byCluster,byFrequency,by1000G
AMPD3	chr11	10482189	C	T	rs11042836	R185W	nonSynonymous	21.7	0.000008	10503736	0.054	0.07738295	0.013084853	0.000116306	0.016545455	byCluster,byFrequency,byHapMap,by1000G
AMPD3	chr11	10493425	C	T	rs201115705	T339M	nonSynonymous	26.4	0.000437	10519472	0.0004365	0.000645045	0	0.000115687	0 byCluster,byFrequency	
AMPD3	chr11	10461608	G	A	rs373716662	R30Q	nonSynonymous	23.7	0.000087	10483155	0.00008236	1.49876E-05	0	0.000808875	0.000121124	byCluster,byFrequency,by1000G
AMPD3	chr11	10482160	G	A	rs762205591	R175Q	nonSynonymous	27.2	0.000066	10503707	0.00006589	3.02179E-05	0	0.00023218	0.000121124	byCluster,byFrequency
BRI3BP	chr12	124993909	G	C	Novel	G40A	nonSynonymous	11.5	-	125478455	-	-	-	-	-	-
BRI3BP	chr12	124993933	G	C	Novel	R48P	nonSynonymous	28.6	-	125478479	-	-	-	-	-	-
BRI3BP	chr12	124993947	T	G	Novel	F53V	nonSynonymous	11.8	-	125478493	-	-	-	-	-	-
BRI3BP	chr12	124993948	T	G	Novel	F53C	nonSynonymous	25.3	-	125478494	-	-	-	-	-	-
BRI3BP	chr12	124993954	A	C	Novel	Q55P	nonSynonymous	24.4	-	125478500	-	-	-	-	-	-
BRI3BP	chr12	124993955	G	C	Novel	Q55H	nonSynonymous	25.3	-	125478501	-	-	-	-	-	-
BRI3BP	chr12	124993962	A	C	Novel	S58R	nonSynonymous	24.4	-	125478508	-	-	-	-	-	-
BRI3BP	chr12	125025038	C	T	rs367895302	P122S	nonSynonymous	27.3	0.000058	125509584	0.00005766	9.02609E-05	0	0	6.0687E-05	byCluster,byFrequency
BRI3BP	chr12	125025105	G	C	rs369500614	G144A	nonSynonymous	25.3	0.000165	125509651	0.0001647	0.000269833	0.000192234	0	0 byCluster,byFrequency	
BRI3BP	chr12	124993932	C	A	rs686801899	R48S	nonSynonymous	26.7	-	125478478	-	-	-	-	unknown	
CD9	chr12	6236255	A	G	rs150663369	I201V	nonSynonymous	23.4	0.000538	6345421	0.0005518	0.000869878	0	0	0 byCluster,byFrequency,by1000G	
CD9	chr12	6235299	G	A	rs35799798	R140Q	nonSynonymous	27.4	0.000609	6344465	0.000626	0.000884187	0	0.000115554	0.00060562	byCluster,byFrequency,by1000G
CD9	chr12	6236250	T	G	rs770637195	V199G	nonSynonymous	28.2	0.000008	6345416	0.000008236	1.49966E-05	0	0	0 unknown	
CRISP3	chr6	49733839	C	T	rs149267211	C109Y	nonSynonymous	25.6	0.000066	49701552	0.00006589	0.000120243	0	0	0 byCluster,byFrequency	
CRISP3	chr6	49733743	C	G	rs75675396	G141A	nonSynonymous	23.8	0.000008	49701456	0.004555	0.001874007	0.000192197	0.007973192	0.000484555	byCluster,byFrequency,by1000G
CRISP3	chr6	49733726	C	A	rs1864312	A147S	nonSynonymous	10.6	0.000008	49701439	0.426	0.448097924	0.28830994	0.293179191	0.336423119	byCluster,byFrequency,byHapMap,by1000G
CRISP3	chr6	49737414	C	T	rs371866465	G18S	nonSynonymous	13.5	0.000092	49705127	0.0000906	0.000168252	0	0	0 byCluster,byFrequency	
CRISP3	chr6	49731165	C	A	rs757797049	C216F	nonSynonymous	32	0.000008	49698878	0.000008236	1.50177E-05	0	0	0 unknown	
CSGALNACT1	chr8	19505704	G	A	-	A44V	nonSynonymous	12.3	-	19363215	-	-	-	-	-	-
CSGALNACT1	chr8	19458601	G	A	rs147069782	L226F	nonSynonymous	27.9	0.000617	19316112	0.0005683	1.49835E-05	0.0060542	0	6.0562E-05	byCluster,byFrequency,by1000G
CSGALNACT1	chr8	19405929	C	T	rs139076756	E484K	nonSynonymous	28	0.000008	19263440	0.00001647	2.99706E-05	0	0	0 byCluster,byFrequency	
CSGALNACT1	chr8	19405940	C	T	rs144253363	R480H	nonSynonymous	23.1	0.001092	19263451	0.001062	4.49573E-05	0.011147415	0	0 byCluster,byFrequency,by1000G	
CSGALNACT1	chr8	19505795	G	A	rs117494579	R14W	nonSynonymous	28.7	0.000024	19363306	0.002331	6.054E-05	0.00029615	0.030891645	0.00036483	byCluster,byFrequency,by1000G
CSGALNACT1	chr8	19405961	A	T	rs17128366	F473Y	nonSynonymous	27.3	0.004913	19263472	0.004538	0.000119883	0.049875072	0	0.000121124	byCluster,byFrequency,byHapMap,by1000G
CSGALNACT1	chr8	19505246	C	T	rs17128518	V137I	nonSynonymous	11.2	0.002801	19362937	0.002537	0.000120337	0.027772383	0	6.05987E-05	byCluster,byFrequency,byHapMap,by1000G
CSGALNACT1	chr8	19458495	G	A	rs35868450	T261M	nonSynonymous	22.8	0.001202	19316006	0.001211	0.001348557	0.000288295	0.000115554	0.001332364	byCluster,byFrequency,by1000G
CSGALNACT1	chr8	19405817	C	G	rs61910741	R521P	nonSynonymous	34	0.000008	19263328	0.004126	0.00660502	0.001544998	0	0.00090843	byCluster,byFrequency,by1000G
CSGALNACT1	chr8	19405797	G	A	rs369428087	T467M	nonSynonymous	25.4	0.000641	19263490	0.0006589	0.000644349	0	0	0.00181686	byCluster,byFrequency,by1000G
CSGALNACT1	chr8	19458535	T	C	rs372233360	I248V	nonSynonymous	12.6	0.000033	19316046	0.00003295	4.49506E-05	9.60984E-05	0	0 byCluster,byFrequency	
CSGALNACT1	chr8	19420366	T	C	rs745646945	N369S	nonSynonymous	22.8	0.000041	19277877	0.00004118	4.49532E-05	9.61354E-05	0	6.0562E-05	byFrequency
CSGALNACT1	chr8	19505630	G	A	rs755710398	R69C	nonSynonymous	33	0.000017	19363141	0.00001647	1.5024E-05	0	0.000115929	0 byFrequency	
CSGALNACT1	chr8	19406037	C	T	rs779435105	G448R	nonSynonymous	34	0.000015	19263548	0.0001153	0.000104897	0	0	0.000363372	byFrequency
CTXN2	chr15	48201542	C	T	rs190880430	A81V	nonSynonymous	31	0.016279	48493739	0.017	0.006740776	0	0	0.037778905	byCluster,byFrequency,by1000G
DACH1	chr13	71866195	T	C	Novel	D192G	nonSynonymous	23.5	-	72440327	-	-	-	-	-	-
DACH1	chr13	71866222	G	T	Novel	P183H	nonSynonymous	23.5	-	72440354	-	-	-	-	-	-
DACH1	chr13	71866235	C	A	Novel	V179L	nonSynonymous	21.6	-	72440367	-	-	-	-	-	-
DACH1	chr13	71866237	G	C	Novel	P178R	nonSynonymous	22.8	-	72440369	-	-	-	-	-	-
DACH1	chr13	71866238	G	A	Novel	P178S	nonSynonymous	16.5	-	72440370	-	-	-	-	-	-
DACH1	chr13	71866249	G	A	Novel	S174L	nonSynonymous	22.3	-	72440381	-	-	-	-	-	-
DACH1	chr13	71866268	G	A	Novel	P168S	nonSynonymous	14	-	72440400	-	-	-	-	-	-
DACH1	chr13	71866270	A	G	Novel	L167P	nonSynonymous	23.3	-	72440402	-	-	-	-	-	-
DACH1	chr13	71866278	G	C	Novel	C164W	nonSynonymous	23.4	-	72440410	-	-	-	-	-	-
DACH1	chr13	71866279	C	A	Novel	C164F	nonSynonymous	16.8	-	72440411	-	-	-	-	-	-
DACH1	chr13	71866280	A	G	Novel	C164R	nonSynonymous	10.7	-	72440412	-	-	-	-	-	-
DACH1	chr13	71866649	C	G	Novel	A41P	nonSynonymous	16.3	-	72440787	-	-	-	-	-	-
DACH1	chr13	71866667	A	G	Novel	S35P	nonSynonymous	17.2	-	72440805	-	-	-	-	-	-
DACH1	chr13	71866676	A	G	Novel	S32P	nonSynonymous	19.8	-	72440814	-	-	-	-	-	-
DACH1	chr13	71866687	C	G	Novel	G28A	nonSynonymous	13.3	-	72440825	-	-	-	-	-	-
DACH1	chr13	71866690	G	A	Novel	S27F	nonSynonymous	21	-	72440828	-	-	-	-	-	-
DACH1	chr13	71866703	A													

DACH1	chr13	71866726	G	C	Novel	P15R	nonSynonymous	14.8	-	72440864	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71866727	G	C	Novel	P15A	nonSynonymous	10.6	-	72440865	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71866732	A	C	Novel	L13R	nonSynonymous	17.9	-	72440870	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71866734	C	G	Novel	Q12H	nonSynonymous	15.9	-	72440872	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71866746	G	C	Novel	I8M	nonSynonymous	13.6	-	72440884	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71866748	T	G	Novel	I8L	nonSynonymous	18.5	-	72440886	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71866753	G	T	Novel	A6D	nonSynonymous	16.8	-	72440891	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71630562	T	A	Novel	S374C	nonSynonymous	24	-	72204694	-	-	-	-	-	-	-	-	-	
DACH1	chr13	71489056	A	G	rs199546133	S55P	nonSynonymous	23.2	0.000787	72063188	0.000786	0.00097463	0.00010202	0	0.00109038	byCluster,byFrequency				
DACH1	chr13	71475180	G	A	rs200697835	R682C	nonSynonymous	27.1	0.000639	72049312	0.0006374	0.00103501	0.000102166	0	0.00012133	byCluster,byFrequency				
DACH1	chr13	71866706	T	A	rs367942830	T22S	nonSynonymous	15.5	0.00001	72440844	0.000008283	1.7301E-05	0	0	0	byCluster				
DACH1	chr13	71557102	C	T	rs374225059	V49I	nonSynonymous	21	0.00008	72131234	0.00005792	0	0.000714286	0	0	byCluster,byFrequency				
DACH1	chr13	71866742	G	T	rs573485179	P10T	nonSynonymous	14.5	0.00002	72440880	0.000008295	0	0.00013217	0	0	0 by1000G				
DACH1	chr13	71866714	G	C	rs750752070	P19R	nonSynonymous	16.2	0.00001	72440852	0.000008285	0	0.000126358	0	0	0 unknown				
DACH1	chr13	71866715	G	T	rs750752070	P19T	nonSynonymous	14.8	0.00001	72440853	0.000008285	0	0.000126358	0	0	0 unknown				
DACH1	chr13	71866218	C	G	rs753279642	Q184H	nonSynonymous	14	0.000052	72440350	0.00004962	7.8284E-05	0	0	0	0 byFrequency				
DACH1	chr13	71866225	G	C	rs754515488	T182S	nonSynonymous	12.4	0.00009	72440357	0.000008271	1.63484E-05	0	0	0	0 unknown				
DACH1	chr13	71866718	G	C	rs761619897	P18A	nonSynonymous	10.8	0.00001	72440856	0.000008287	1.72897E-05	0	0	0	0 unknown				
DACH1	chr13	71866351	C	G	rs766978855	S140T	nonSynonymous	11.1	-	72440483	0.00006668	0.000186637	0	0	0	0.000503145	unknown			
DACH1	chr13	71866724	G	C	rs767294898	P16A	nonSynonymous	10.6	0.00001	72440862	0.000008287	0	0	0	0	0 unknown				
DACH1	chr13	71866184	C	A	rs767389322	A196S	nonSynonymous	23.8	0.000033	72440316	0.000003308	0	0	0	0	0 byFrequency				
DACH1	chr13	71866277	C	G	rs772936864	G165R	nonSynonymous	23.8	0.000019	72440409	0.000008384	3.66274E-05	0	0	0	0 byFrequency				
DACH1	chr13	71866285	C	A	rs774654405	S162I	nonSynonymous	12	0.000022	72440417	0.000008461	4.22083E-05	0	0	0	0 unknown				
DACH1	chr13	71866234	C	A	rs778381328	V179G	nonSynonymous	13.8	0.00009	72440366	0.000008271	0	0	0	0	0 -				
DNAJA3	chr16	4454869	C	T	rs35375112	D466D	synonymous	17.9	0.000435	4504870	0.0004118	1.52161E-05	0.004521329	0	0	0 byCluster,byFrequency,by1000G				
DNAJA3	chr16	4448739	C	G	rs147164370	P378A	nonSynonymous	13.2	0.000311	4498740	0.0002553	1.59023E-05	0.002972399	0	0	0 byCluster,byFrequency,by1000G				
DNAJA3	chr16	4443141	G	A	rs141734527	R303Q	nonSynonymous	23.1	0.000375	4493142	0.0003459	3.01332E-05	0.003872967	0	0	0 byCluster,byFrequency,by1000G				
DNAJA3	chr16	4447013	C	T	rs143480833	T375M	nonSynonymous	22.1	0.000723	4497014	0.000733	0.000811444	0	0	0	0.002160761	byCluster,byFrequency,by1000G			
DNAJA3	chr16	4425933	C	T	rs201593669	R18W	nonSynonymous	23.5	0.000565	4475934	0.0002091	0	0.007082153	0	0	0 byCluster,byFrequency,by1000G				
DNAJA3	chr16	4425895	G	T	rs374995696	C5F	nonSynonymous	15.5	0.00014	4475896	0.00004952	0.000403226	0	0	0	0 byCluster,byFrequency				
DNAJA3	chr16	4448766	C	T	rs750067919	R387W	nonSynonymous	35	0.00008	4498767	0.000008236	1.52835E-05	0	0	0	0 unknown				
DNAJC1	chr10	21919916	C	A	-	S184I	nonSynonymous	31	-	22208845	-	-	-	-	-	-	-	-	-	
DNAJC1	chr10	21919903	T	A	Novel	R188S	nonSynonymous	24.7	-	22208832	-	-	-	-	-	-	-	-	-	
DNAJC1	chr10	21919911	T	G	Novel	K186Q	nonSynonymous	24	-	22208840	-	-	-	-	-	-	-	-	-	
DNAJC1	chr10	21919914	T	A	Novel	R185*	stopGain	39	-	22208843	-	-	-	-	-	-	-	-	-	
DNAJC1	chr10	21919929	C	T	Novel	D180N	nonSynonymous	25.6	-	22208858	-	-	-	-	-	-	-	-	-	
DNAJC1	chr10	21920956	C	T	rs149825372	D127N	nonSynonymous	24.1	0.000727	22209885	0.0007413	0.001116038	0.000195465	0	0	0.000499002	byCluster,byFrequency,by1000G			
DNAJC1	chr10	21919926	C	T	rs533121915	E181K	nonSynonymous	23.9	0.0002	22208855	-	0	0	0	0	by1000G				
DNAJC1	chr10	22003352	C	T	rs575609970	R28Q	nonSynonymous	12.3	0.00177	22292281	0.0007691	0	0	0	0	0.004712747	byCluster,byFrequency,by1000G			
DNAJC1	chr10	21759183	G	A	rs776269885	P528L	nonSynonymous	30	0.00008	22048112	0.000008236	1.51071E-05	0	0	0	0 byFrequency				
DNASE1L1	chrX	154405439	C	T	Novel	V44I	nonSynonymous	23.5	-	153633780	-	-	-	-	-	-	-	-	-	
DNASE1L1	chrX	154405447	T	C	Novel	D41G	nonSynonymous	16.8	-	153633788	-	-	-	-	-	-	-	-	-	
DNASE1L1	chrX	154405448	C	A	Novel	D41Y	nonSynonymous	29.2	-	153633789	-	-	-	-	-	-	-	-	-	
DUSP23	chr1	159781314	G	A	rs148687167	D72N	nonSynonymous	11.5	0.003349	159751104	0.0007519	0	0.036480687	0	0	0 byCluster,byFrequency,by1000G				
DUSP23	chr1	159782256	C	A	rs15144443	E124V	nonSynonymous	25.1	0.005103	159752046	0.00522	0.007942931	0.000480492	0	0	0.004118217	byCluster,byFrequency,byHapMap,by1000G			
DUSP23	chr1	159782276	G	A	rs1129923	G131S	nonSynonymous	34	0.084226	159752066	0.085	0.098785789	0.014033064	0.003467406	0.128422583	byCluster,byFrequency,byOtherPop,byHapMap,by1000G				
DUSP23	chr1	159781200	C	G	rs199665962	L34V	nonSynonymous	10.8	0.00057	159750950	0.0006973	0.004067107	0	0	0	0.00167806	byCluster,byFrequency,by1000G			
DUSP23	chr1	159782226	G	A	rs200750638	R114Q	nonSynonymous	14.1	0.000166	159752016	0.0001647	0.000239787	0	0	0	0.00242277	byCluster,byFrequency,by1000G			
EFCAB12	chr3	129401780	A	G	rs114112678	L511P	nonSynonymous	29.9	0.01627	129120623	0.001132	0	0.016441262	0	0	0.000157654	byCluster,byFrequency,by1000G			
EFCAB12	chr3	129411181	G	A	rs139410166	R338C	nonSynonymous	27.6	0.000099	129130024	0.00004133	0	0.000186986	0.000915751	0	0	0 byFrequency,by1000G			
EFCAB12	chr3	129411180	C	T	rs80141922	R338H	nonSynonymous	29.9	0.004619	129130023	0.002398	0	0.043890178	0	0	0.000180538	byCluster,byFrequency,by1000G			
EFCAB12	chr3	129411228	G	A	rs73865436	T322M	nonSynonymous	23.3	0.004848	129130071	0.00436	0.000140397	0.050127714	0.000971817	0.000125329	byCluster,byFrequency,by1000G				
EFCAB12	chr3	129421683	C	T	rs78778285	R57Q	nonSynonymous	25.3	0.001482	129140526	0.001349	0.00058804	0.014119753	0	0	6.09779E-05	byCluster,byFrequency,by1000G			
EFCAB12	chr3	129411175	G	A	rs73202271	R340W	nonSynonymous	26.3	0.146756	129130018	0.075	0.167828987	0.149083594	0.053789731	0.147633646	byCluster,byFrequency,by1000G				
EFCAB12	chr3	129401738	C	T	rs376335610	R525Q	nonSynonymous	21.4	0.000131	129120581	0.00006611	8.83236E-05	0	0	0.000382044	byCluster,byFrequency				
EFCAB12	chr3	129401661	G	A	rs551533324	P551S	nonSynonymous	28.3	0.000097	129120504	0.0003809	0	0	0	0.003690888	byCluster,byFrequency,by1000G				
EFCAB12	chr3	129402551	G	A	rs574254518	R478C	nonSynonymous	20.5	0.000076	129123194	0.00006619	5.36615E-05	0.000121921	0	0	0.000215363	byCluster,byFrequency,by1000G			
EFCAB12	chr3	129401610	C	T	rs755969961	V568M	nonSynonymous	24.4	0.000049	129120453	0.000008365	8.86997E-05	0	0	0	0 unknown				
EFEEMP2	chr11	65870174	C	T	rs143662598	R185H	nonSynonymous	22.4	0.000017	65637645	0.00001647	3.05344E-05	0	0	0	0 byCluster,byFrequency				
EFEEMP2	chr11	65870222	C	T	rs141310608	R169H	nonSynonymous	31	0.000083	65637693	0.00008237	0.000121884	9.80392E-05	0	0	6.05767E-05	byCluster,byFrequency			
EFEEMP2	chr11	65871247	C	T	rs2234462	G93S	nonSynonymous	14.1	0.002788	65638718	0.002875	0.003572501	0.001058507	0	0	0.000968992	byCluster,byFrequency,by1000G			
EFEEMP2	chr11	65867027	G	A	rs761729008	P408L	nonSynonymous	32	0.000008	65634498	0.000008									

NRDE2	chr14	90289033	C	T	rs777908634	C781Y	nonSynonymous	19.2	0.000016	90755377	0.00001647	2.99742E-05	0	0	0 byFrequency
NRDE2	chr14	90304342	T	A	rs781502472	K200*	stopGain	35	0.000017	90770686	0.00003295	6.03482E-05	0	0	0 byFrequency
NUDT3	chr6	3439285	G	T	rs146760187	F26L	nonSynonymous	19.3	0.001166	34360062	0.0008475	0.000291341	0.010138889	0	0 byCluster,byFrequency,by1000G
OCEL1	chr19	17227932	A	C	rs144196323	E182A	nonSynonymous	24.4	0.000578	17338741	0.0005024	0	0.005775895	0	0 byCluster,byFrequency,by1000G
OCEL1	chr19	17227118	C	T	rs144461877	A124V	nonSynonymous	13.3	0.000256	17337927	0.0002142	0	0.002523292	0	0 byCluster,byFrequency,by1000G
OCEL1	chr19	17228887	G	A	rs142863081	D253N	nonSynonymous	14.4	0.000778	17339696	0.0007495	9.0356E-05	0.007152523	0	0.000485201 byCluster,byFrequency,by1000G
OCEL1	chr19	17226748	G	T	rs10425488	R42L	nonSynonymous	23.1	0.091126	17337557	0.066	0.09580885	0.144380275	0	0.124835248 byCluster,byFrequency,by1000G
OCEL1	chr19	17227073	C	G	rs891203	A109G	nonSynonymous	11.4	0.17403	17337882	0.171	0.110112224	0.281461434	0.248145573	0.221905588 byCluster,byFrequency,by2Hit2Allele,byHapMap,by1000G
OCRL	chrX	129565818	G	A	rs137884245	D431N	nonSynonymous	23.1	0.00057	128699795	0.0005024	0	0.005226895	0	0 byCluster,byFrequency,by1000G
OCRL	chrX	129561251	G	A	rs138260625	M299I	nonSynonymous	17.4	0.005847	128695228	0.005436	2.08385E-05	0.000117523	0	0 byCluster,byFrequency,by1000G
OCRL	chrX	129504745	C	T	rs61752970	T14I	nonSynonymous	20.8	0.005202	128674722	0.005617	0.007225687	0.000949104	0	0.002174988 byCluster,byFrequency,by1000G
OCRL	chrX	129545013	A	G	rs747129019	N59D	nonSynonymous	25.1	0.000012	128678990	0.000008237	2.10859E-05	0	0	0 unknown
OCRL	chrX	129569323	A	C	rs770155745	N509T	nonSynonymous	10.4	0.000023	128703300	0.00003295	0	0	0.000301296	0 byFrequency
OCRL	chrX	129558999	G	A	rs781782723	R207Q	nonSynonymous	27	0.000033	128692876	0.00002471	0	0	0	9.87752E-05 byCluster,byFrequency,by1000G
OR2A7	chr7	144259214	C	A	Novel	V139F	nonSynonymous	11.5	-	143956307	-	-	-	-	-
OR2A7	chr7	144258913	G	C	rs200085936	T239S	nonSynonymous	21.3	0.017871	143956006	0.018	0.025689448	0.004036909	0.000115607	0.014356676 byCluster,byFrequency,by1000G
OR2A7	chr7	144258791	A	C	rs201738556	F280V	nonSynonymous	17.2	0.003047	143955884	0.028	0.012227629	0.059678094	0.127607362	0.026048127 byCluster,byFrequency,by1000G
OR2A7	chr7	144259402	G	A	rs3687586678	T76M	nonSynonymous	22.9	0.000891	143956495	0.0005172	0.001597132	0	0	0.000329164 byCluster,byFrequency,by1000G
OR2A7	chr7	144258730	A	T	rs531173389	L300*	stopGain	36	0.000304	143955823	0.000281	0	0.003727866	0	0 byFrequency,by1000G
OR2A7	chr7	144259393	C	T	rs747912287	R79Q	nonSynonymous	10.8	0.000124	143956486	0.00006863	0	0.001651255	0	0.000123946 byFrequency
OR2A7	chr7	144259339	T	A	rs765364621	M97K	nonSynonymous	10.5	0.017131	143956432	0.002317	0.026816945	0.005208333	0	0.001428571 byFrequency
ORM2	chr9	114331879	G	A	rs148221879	D164N	nonSynonymous	16	0.000063	117094159	0.0008895	2.99814E-05	0.009645062	0.00011558	0.000181818 byCluster,byFrequency,by1000G
ORM2	chr9	114331627	T	G	rs151073288	F130C	nonSynonymous	22	0.000008	117093907	0.0000906	0.000134884	9.61354E-05	0	0 byCluster,byFrequency
ORM2	chr9	114330557	C	G	rs112596931	L80V	nonSynonymous	13.4	0.006559	117092837	0.006319	0.000194932	0.068944602	0	0.000363945 byCluster,byFrequency,by1000G
ORM2	chr9	114330830	T	C	rs2636889	V99A	nonSynonymous	22.6	0.030213	117093110	0.027	0.000494723	0.300865385	0	0.00036346 byCluster,byFrequency,by2Hit2Allele,byHapMap,by1000G
ORM2	chr9	114329923	C	T	rs143336597	L7F	nonSynonymous	11.4	0.009442	117092203	0.003122	0.013714286	0.009313155	0	0.00280112 byCluster,byFrequency,by1000G
ORM2	chr9	114331841	C	T	rs368086091	T151M	nonSynonymous	23.6	0.000238	117094121	0.0002306	0.000180337	0.000582411	0	0 byCluster,byFrequency,by1000G
PBDC1	chrX	76173586	T	A	Novel	V11D	nonSynonymous	24	-	75393421	-	-	-	-	-
PBDC1	chrX	76173589	C	G	Novel	S12C	nonSynonymous	23.3	-	75393424	-	-	-	-	-
PBDC1	chrX	76173594	G	A	Novel	E14K	nonSynonymous	25.4	-	75393429	-	-	-	-	-
PBDC1	chrX	76173597	T	A	Novel	L15M	nonSynonymous	11.7	-	75393432	-	-	-	-	-
PBDC1	chrX	76173600	G	C	Novel	V16L	nonSynonymous	10.6	-	75393435	-	-	-	-	-
PBDC1	chrX	76173607	T	G	Novel	V18G	nonSynonymous	20.5	-	75393442	-	-	-	-	-
PBDC1	chrX	76173614	T	A	Novel	H20Q	nonSynonymous	17	-	75393449	-	-	-	-	-
PBDC1	chrX	76173627	C	A	Novel	P25T	nonSynonymous	25.3	-	75393462	-	-	-	-	-
PBDC1	chrX	76173628	C	G	Novel	P25R	nonSynonymous	26.4	-	75393463	-	-	-	-	-
PBDC1	chrX	76173635	G	T	Novel	E27D	nonSynonymous	14.6	-	75393470	-	-	-	-	-
PBDC1	chrX	76173637	C	G	Novel	S28W	nonSynonymous	32	-	75393472	-	-	-	-	-
PBDC1	chrX	76177619	C	T	Novel	P138S	nonSynonymous	26.9	-	75397454	-	-	-	-	-
PBDC1	chrX	76177632	C	T	Novel	S142F	nonSynonymous	13.7	-	75397467	-	-	-	-	-
PBDC1	chrX	76177643	A	T	Novel	K146*	stopGain	32	-	75397478	-	-	-	-	-
PBDC1	chrX	76173606	G	C	rs781867907	V18L	nonSynonymous	19.5	0.000013	75393441	0.00000824	0	0	0	0 unknown
PBDC1	chrX	76173592	G	A	rs782161107	G13E	nonSynonymous	24.4	0.000013	75393427	0.000008241	0	0	0.000153894	0 unknown
PBDC1	chrX	76173622	T	C	rs782545649	S23F	nonSynonymous	24.8	0.000013	75393457	0.00001648	2.2478E-05	0	0	0 unknown
PBDC1	chrX	76177658	G	T	rs782709186	G151W	nonSynonymous	34	0.000068	75397493	0.00005766	4.2461E-05	0.000119789	0.000302343	0 byCluster,byFrequency,by1000G
PDE6D	chr2	231732999	C	T	rs142298615	D136N	nonSynonymous	23.4	0.000514	232597709	0.000486	0.000284747	0.0075246	0	6.05767E-05 byCluster,byFrequency,by1000G
PDE6D	chr2	231732996	T	C	rs146510084	D137N	nonSynonymous	23.6	0.000934	232597706	0.0008484	0.000284747	0.0075246	0	6.05767E-05 byCluster,byFrequency,by1000G
POLE4	chr2	74958840	C	G	Novel	P54R	nonSynonymous	29.5	-	75185967	-	-	-	-	-
POLE4	chr2	74958729	G	T	rs12366	G17V	nonSynonymous	23.3	0.396426	75185856	0.204	0.499827824	0.404100529	0.470588235	0.340281856 byCluster,byFrequency,by2Hit2Allele,byHapMap,by1000G
PSMD4	chr1	151266017	C	T	Novel	S223F	nonSynonymous	32	-	151238493	-	-	-	-	-
PSMD4	chr1	151266059	G	A	Novel	R237Q	nonSynonymous	24.4	-	151238535	-	-	-	-	-
PSMD4	chr1	151266113	G	A	Novel	G255D	nonSynonymous	28.4	-	151238589	-	-	-	-	-
PSMD4	chr1	151266358	T	C	rs181572831	R275C	nonSynonymous	24.6	0.000055	151238834	0.00004942	1.49835E-05	9.60984E-05	0	0.000121124 byCluster,byFrequency,by1000G
PTPN9	chr15	75524213	A	G	rs50017042	I98T	nonSynonymous	26.6	0.000088	75816554	0.00008236	0	9.61354E-05	0	0 byCluster
PTPN9	chr15	75473746	C	T	rs186045366	R384H	nonSynonymous	14.7	0.000873	75760087	0.0008566	0	0.00048506	0	0 byCluster,byFrequency,by1000G
PTPN9	chr15	75505708	T	C	rs146356869	R312H	nonSynonymous	23.8	0.000016	75798049	0.0001153	0.000195219	9.61169E-05	0	0 byCluster,byFrequency
PTPN9	chr15	75470703	T	C	rs150528240	A464A	nonSynonymous	11.1	0.000486	75763044	0.0004859	0.000839228	0.000288351	0	0 byCluster,byFrequency
PTPN9	chr15	75505702	T	A	rs149279759	N314I	nonSynonymous	19.9	0.000659	75798043	0.0006671	0.001082316	0.000192308	0	6.1237E-05 byCluster,byFrequency,by1000G
PYCR1	chr17	81936151	A	C	rs138792258	M37R	nonSynonymous	12.6	0.000141	79894027	0.00014	0.000257576	0	0	0 byCluster,byFrequency
PYCR1	chr17	81935479	G	A	rs150227130	T59M	nonSynonymous	25.8	0.000267	79893355	0.0002227	0.000435353	0	0	7.00574E-05 byCluster,byFrequency,by1000G
PYCR1	chr17	81934958	C	T	rs199585131	V170I	nonSynonymous	20.9	0.000145	79892834	0.0001402	0.000248927	0	0	0 byCluster,byFrequency
RANGAP1	chr22	41256754	A	T	-	V282D	nonSynonymous	18.3	-	41652758	-	-	-	-	-
RANGAP1	chr22	41256076	G	C	rs12167166	Q340E	nonSynonymous	13.2	0.000429	41652080	0.0003706	0	0.004273504	0	0 byCluster,byFrequency,by1000G
RANGAP1	chr22	41264743	G	A	rs148292488	A134V	nonSynonymous	22	0.000222	41660747	0.0001977	0	0.00230858	0	0 byCluster,byFrequency,by1000G
RANGAP1	chr22	41256749	T	C	rs148624391	B284V	nonSynonymous	23.3	0.000091	41652753	0.0000906	0.000120941	0	0	0.000181906 byCluster,byFrequency
RANGAP1	chr22	41256253	G	C	rs114673061	A309G	nonSynonymous	22.6	0.001836	41652257	0.00168	0.000314928	0.016454965	0	0 byCluster,byFrequency,by1000G
RANGAP1	chr22	41264747	C	G	rs2229752	E133Q	nonSynonymous	25.4	0.00004	41660751	-	-	-	-	byCluster,byFrequency,by1000G
RANGAP1	chr22	41256733	T	C	rs374322211	R289H	nonSynonymous	20.1	0.0001	41652737	0.0000984	0.000105964	0	0	0.000303398 byCluster,byFrequency
RANGAP1	chr22	412													

RANGAP1	chr22	41254375	G	A	rs777615097	P398L	nonSynonymous	10.3	0.000008	41650379	0.000008236	0	0	0.000115607	0 unknown
RANGAP1	chr22	41264755	T	A	rs780709524	Q130L	nonSynonymous	18	0.000008	41660759	0.000008236	1.50047E-05	0	0	0 unknown
RAPGEFL1	chr17	40184583	T	A	Novel	D95E	nonSynonymous	10.1	-	38340835	-	-	-	-	-
RAPGEFL1	chr17	40193768	C	G	rs143788634	L506V	nonSynonymous	23.8	0.000157	38350020	0.0001565	0	0.001730104	0	0 byCluster,byFrequency
RAPGEFL1	chr17	40191625	A	T	rs372662080	M369L	nonSynonymous	21.7	0.000102	38347877	0.00007415	0	0.001101591	0	0 byCluster,byFrequency,by1000G
RAPGEFL1	chr17	40188916	G	A	rs763119373	R144H	nonSynonymous	28.6	0.000025	38345168	0.00002471	0	0.000290529	0	0 byCluster,byFrequency
RAPGEFL1	chr17	40193408	C	T	rs767817765	R468W	nonSynonymous	27.8	0.000025	38349660	0.00002471	1.49849E-05	0.000192271	0	0 byFrequency
RAPGEFL1	chr17	40189243	G	A	rs768709613	V177M	nonSynonymous	25.4	0.000008	38345495	0.000008236	0	0	0	6.0562E-05 unknown
RGS13	chr1	192659493	G	C	rs16834603	L150F	nonSynonymous	17.3	0.013914	192628623	0.012	0.000113078	0.139133102	0	0.000190452 byCluster,byFrequency,byHapMap,by1000G
RGS13	chr1	192644342	G	A	rs768361269	R3K	nonSynonymous	14.9	0.000017	192613472	0.00001647	3.00661E-05	0	0	0 byFrequency
RNPEP	chr1	201983051	C	G	Novel	P129A	nonSynonymous	12.6	-	201952179	-	-	-	-	-
RNPEP	chr1	201983058	G	C	Novel	R131P	nonSynonymous	16.2	-	201952186	-	-	-	-	-
RNPEP	chr1	201983060	G	C	Novel	A132P	nonSynonymous	12.1	-	201952188	-	-	-	-	-
RNPEP	chr1	201983063	G	C	Novel	A133P	nonSynonymous	19.4	-	201952191	-	-	-	-	-
RNPEP	chr1	201983066	G	C	Novel	E134Q	nonSynonymous	12.6	-	201952194	-	-	-	-	-
RNPEP	chr1	201983077	G	C	Novel	Q137H	nonSynonymous	23.2	-	201952205	-	-	-	-	-
RNPEP	chr1	201983079	T	G	Novel	V138G	nonSynonymous	25.5	-	201952207	-	-	-	-	-
RNPEP	chr1	201983087	A	C	Novel	T141P	nonSynonymous	15.7	-	201952215	-	-	-	-	-
RNPEP	chr1	201983090	T	G	Novel	Y142D	nonSynonymous	31	-	201952218	-	-	-	-	-
RNPEP	chr1	201983091	A	C	Novel	Y142S	nonSynonymous	28.8	-	201952219	-	-	-	-	-
RNPEP	chr1	201983105	G	C	Novel	G147R	nonSynonymous	31	-	201952233	-	-	-	-	-
RNPEP	chr1	201997413	C	T	rs79980228	R317C	nonSynonymous	34	0.006233	201966541	0.005807	0.00014984	0.063328849	0	6.0562E-05 byCluster,byFrequency,by1000G
RNPEP	chr1	202005604	G	T	rs190562495	G614V	nonSynonymous	29.6	0.000127	201974732	0.0001235	0.000179813	0	0	0 byCluster,byFrequency,by1000G
RNPEP	chr1	202001659	G	C	rs143039696	A440P	nonSynonymous	24.1	0.000499	201970787	0.0004777	0.000809401	9.61538E-05	0	0 byCluster,byFrequency,by1000G
RNPEP	chr1	202005651	G	A	rs148685424	A630T	nonSynonymous	14.3	0.000016	201974779	0.001408	0.001798022	0	0	0.002785853 byCluster,byFrequency,by1000G
RNPEP	chr1	201996189	G	T	rs74710742	K260N	nonSynonymous	20.7	0.000008	201965317	0.011	0.015496673	0.003843936	0	0.00660126 byCluster,byFrequency,by1000G
RNPEP	chr1	202003320	G	C	rs146663755	P504A	nonSynonymous	22.6	0.000799	201972448	0.0001402	4.50E-05	0.001155	0.0001156	0 byCluster,byFrequency,by1000G
RNPEP	chr1	201989500	G	A	rs201047350	G236R	nonSynonymous	34	0.000058	201958628	0.00005765	2.99787E-05	0.000384394	0.000115554	0 byCluster,byFrequency
RNPEP	chr1	201983040	C	T	rs201819747	S125F	nonSynonymous	19.3	0.000782	201952168	0.0002353	0.002619325	0	0	0 byCluster,byFrequency
RNPEP	chr1	201997416	T	A	rs374485540	S318T	nonSynonymous	24	0.000033	201966544	0.00003295	0	0.000288295	0	0 byCluster,byFrequency
RNPEP	chr1	202004437	G	A	rs3820439	V579I	nonSynonymous	13.9	0.000008	201973565	0.325	0.279537132	0.252552495	0.377842227	0.496183669 byCluster,byFrequency,by2Hit2Allele,byHapMap,by1000G
RNPEP	chr1	20289256	G	T	rs549263851	R97L	nonSynonymous	12.9	0.000668	201952084	0.000293	0.000996016	0	0	0.000841184 byFrequency,by1000G
RNPEP	chr1	201983054	T	G	rs557054580	C130G	nonSynonymous	14.1	0.001254	201952182	0.0002764	0	0.0215311	0	0 byCluster,byFrequency,by1000G
RNPEP	chr1	201996214	G	T	rs575051595	E269*	stopGain	41	0.000099	201965342	0.00009884	7.49356E-05	0	0.000808875	0 byCluster,byFrequency
RNPEP	chr1	202003375	T	C	rs749095534	I522T	nonSynonymous	20.3	0.000149	201972503	0.0001483	0.000271035	0	0	0 byFrequency
RNPEP	chr1	201999113	A	T	rs750504839	T368S	nonSynonymous	12.4	0.000017	201969041	0.0001647	0	0.000200441	0	0 byFrequency
RNPEP	chr1	201983096	G	C	rs758926508	V144L	nonSynonymous	25.3	0.000009	201952224	0.000008978	0	0	0	0 unknown
RNPEP	chr1	202003449	C	T	rs760016335	P547S	nonSynonymous	25.6	0.000009	201972577	0.000008237	1.69848E-05	0	0	0 unknown
S100Z	chr5	76875477	C	T	rs148288662	R40*	stopGain	37	0.000648	76171302	0.0008686	0.001415876	0.000102103	0	0 byCluster,byFrequency,by1000G
S100Z	chr5	76875472	A	C	rs1320308	E23A	nonSynonymous	23.1	0.385973	76171252	0.616	0.678840215	0.57377551	0.568688982	0.352296135 byCluster,byFrequency,byOtherPop,by2Hit2Allele,byHapMap,by1000G
SCLY	chr2	238083338	T	C	rs143511249	R298W	nonSynonymous	22.3	0.000066	23899179	0.00006589	5.99502E-05	9.61723E-05	0	0.001211513 byCluster,byFrequency
SCLY	chr2	238082165	G	A	rs145727476	V253M	nonSynonymous	33	0.000052	238990806	0.0004942	7.9159E-05	0.000100402	0	0 byCluster,byFrequency
SCLY	chr2	238098333	C	T	rs148012854	A447V	nonSynonymous	19.3	0.000061	239006974	0.00048	0.000784071	0.000519076	0.000271813	0.000294291 byCluster,byFrequency
SCLY	chr2	238081747	G	A	rs3104000	A183T	nonSynonymous	14.3	0.353028	238990388	0.357	0.432884822	0.082564398	0.211667826	0.224978774 byCluster,byFrequency,byHapMap,by1000G
SLC46A2	chr9	112886572	C	T	rs146664615	V420M	nonSynonymous	28.2	0.000124	115648852	0.0001235	1.4984E-05	0.001153181	0	0.0562E-05 byCluster,byFrequency
SLC46A2	chr9	112889585	G	A	rs169171454	A366V	nonSynonymous	23.2	0.001687	115651865	0.001499	3.01468E-05	0.016082435	0	0.000127828 byCluster,byFrequency,byHapMap,by1000G
SLC46A2	chr9	112890656	C	T	rs145291738	R9Q	nonSynonymous	14.2	0.000868	115652936	0.0008087	9.63639E-05	0.009214032	0	0 byCluster,byFrequency,by1000G
SLC46A2	chr9	112879815	C	T	rs74339125	V459M	nonSynonymous	25.1	0.003584	115642095	0.00369	0.00594917	0.000960984	0	0.000423985 byCluster,byFrequency,by1000G
SLC46A2	chr9	112889913	C	T	rs112054166	D257N	nonSynonymous	22.7	0.006124	115652193	0.006293	0.00978717	0.001249279	0.000115554	0.00121124 byCluster,byFrequency,by1000G
SLC46A2	chr9	112889792	G	T	rs756996058	V297A	nonSynonymous	17.4	0.000016	115652072	0.0001647	1.49885E-05	0	0	0 byFrequency
SLC46A2	chr9	112890051	A	C	rs757764932	C211G	nonSynonymous	23.7	0.000025	115652331	0.00002471	4.56649E-05	0	0	0 byFrequency
SNX17	chr2	27374354	A	C	-	K178Q	nonSynonymous	23.9	-	27597221	-	-	-	-	-
SNX17	chr2	27374721	T	C	rs142888525	M215T	nonSynonymous	23	0.000099	27597588	0.00009884	0.00019488	0.000192197	0	0 byCluster,byFrequency
SNX17	chr2	27374730	G	A	rs145463878	R218Q	nonSynonymous	23.5	0.00015	27597597	0.0001483	0.00239808	0	0	0 byCluster,byFrequency,by1000G
SNX17	chr2	27373276	G	A	rs78946094	E96K	nonSynonymous	24.1	0.003254	27596143	0.003311	0.005533063	0.000770713	0	0.000181818 byCluster,byFrequency,by1000G
SNX17	chr2	27373275	C	A	rs1477404391	N24H	nonSynonymous	26.6	0.0005152	27594142	0.0005271	0.00784503	0.001066098	0.000115929	0.000484731 byCluster,byFrequency,by1000G
SNX17	chr2	27375882	C	T	rs377585045	R339W	nonSynonymous	26.3	0.000008	27598749	0.000014	0	0.001057896	0.00023116	0.000121403 byCluster,byFrequency
SNX17	chr2	27376335	G	A	rs747235132	G402D	nonSynonymous	23	0.000008	27599202	0.000008236	1.50693E-05	0	0	0 unknown
SNX17	chr2	27376320	G	A	rs751199615	R397H	nonSynonymous	24.7	0.00000167	27599187	0.00001647	0	0	0	0.00012444 byCluster,byFrequency
SNX17	chr2	27375112	C	T	rs770828684	R245W	nonSynonymous	27.2	0.000082	27597979	0.00008236	4.49775E-05	0	0	6.05767E-05 byFrequency
SPECC1L	chr22	24347122	C	T	rs148229290	P897S	nonSynonymous	22.7	0.001498	24743090	0.001359	1.49858E-05	0.000480492	0.017679686	0.000181686 byCluster,byFrequency,by1000G
SPECC1L	chr22	24365533	C	T	rs190313411	S962L	nonSynonymous	25.4	0.000047	24761501	0.00004118	2.99742E-05	0	0.000231107	6.0562E-05 byCluster,byFrequency,by1000G
SPECC1L	chr22	24328848	A	G	rs6004132	T717A	nonSynonymous	14.8	0.0000512	24724816	0.0004859	3.15696E-05	0.004540967	0	0 byCluster,byFrequency,byHapMap,by1000G
SPECC1L	chr22	24334453	G	A	rs139167350	V814I	nonSynonymous	25.9	0.000247	24730421	0.0002471	0.000419551	0	0	0 byCluster,byFrequency
SPECC1L	chr22	24365530	C	T	rs599694	A961V	nonSynonymous	22.8	0.002073	24761498	0.00215	0.001633546	0	0.000231107	6.0562E-05 byCluster,byFrequency,by1000G
SPECC1L	chr22	24313452	C	T	rs3										

SPECC1L	chr22	24365499	G	A	rs204718	V951M	nonSynonymous	17.8	0.000071	24761467	1	1	1	0.999075358	1 byCluster,byFrequency,byHapMap,by1000G
SPECC1L	chr22	24321476	A	G	rs199673620	M166V	nonSynonymous	20.9	0.000617	24717444	0.000626	0.00107891	0.000288406	0	0 byCluster,byFrequency,by1000G
SPECC1L	chr22	24313419	C	T	rs199815517	S87F	nonSynonymous	24.1	0.00008	24709387	0.00008236	1.49858E-05	0	0	0 byCluster
SPECC1L	chr22	24321450	G	A	rs201337978	R157Q	nonSynonymous	17.8	0.000362	24717418	0.0003624	0.000449559	0	0	0.000848074 byCluster,byFrequency
TBC1D17	chr19	49884676	G	T	-	E454D	nonSynonymous	31	-	50387933	-	-	-	-	- -
TBC1D17	chr19	49888574	A	G	Novel	S633G	nonSynonymous	27.3	-	50391831	-	-	-	-	- -
TBC1D17	chr19	49884690	T	C	rs142816596	M459T	nonSynonymous	26.1	0.000318	50387947	0.0002883	0	0	0.003816794	6.05767E-05 byCluster,byFrequency,by1000G
TBC1D17	chr19	49882111	C	T	rs151237175	H200Y	nonSynonymous	21.5	0.000198	50385368	0.0001977	0.000299724	0	0	6.0562E-05 byCluster,byFrequency,by1000G
TBC1D17	chr19	49882046	C	T	rs146631204	P178L	nonSynonymous	34	0.000008	50385303	0.001038	0.001590636	9.61908E-05	0	0.00096911 byCluster,byFrequency
TBC1D17	chr19	49887746	A	G	rs149454222	N524S	nonSynonymous	23.3	0.001283	50391003	0.001244	0.002235279	0.000106406	0	0.000128551 byCluster,byFrequency,by1000G
TBC1D17	chr19	49882878	C	T	rs144381223	R305W	nonSynonymous	27.6	0.00134	50386135	0.001351	0.002268002	0.000103263	0	0.000521921 byCluster,byFrequency,by1000G
TBC1D17	chr19	49882362	G	C	rs200460228	D254H	nonSynonymous	23.9	0.00004	5038619	0.00004118	0	0.000292227	0	0 byCluster,byFrequency,by1000G
TBC1D17	chr19	49887766	T	G	rs371659502	C531G	nonSynonymous	27	0.000046	50391023	0.00004119	8.33806E-05	0	0	0 byCluster,byFrequency
TBC1D17	chr19	49880388	C	T	rs371768869	S102L	nonSynonymous	12.6	0.000116	50383645	0.0001153	0.00021234	0	0	0 byCluster,byFrequency
TBC1D17	chr19	49888509	C	T	rs376165198	P611L	nonSynonymous	23.7	0.000294	50391766	0.0001477	0	0.003117693	0	0 byCluster,byFrequency,by1000G
TBC1D17	chr19	49887728	C	T	rs763562597	T518I	nonSynonymous	32	0.000009	50390985	0.000008239	1.56769E-05	0	0	0 unknown
TMM6B	chr11	112086719	G	A	rs368516346	A17V	nonSynonymous	22.9	0.000008	111957443	0.00005768	0.000121755	0	0	0 byCluster,byFrequency
UBL4A	chrX	154485830	C	A	rs781866836	V102F	nonSynonymous	26.8	0.0000012	153714169	0.00000826	0	0	0	0.000161734 unknown
ZNF629	chr16	30784410	C	A	Novel	G25C	nonSynonymous	30	-	30795731	-	-	-	-	- -
ZNF629	chr16	30781848	T	A	rs61741652	H827L	nonSynonymous	11.1	0.004595	30793169	0.003923	0.000184695	0.044731405	0	0 byCluster,byFrequency,by1000G
ZNF629	chr16	30784160	C	G	rs199766404	K56N	nonSynonymous	25.6	0.000713	30795481	0.000597	0.001159299	0	0	0 byCluster,byFrequency
ZNF629	chr16	30784473	C	T	rs374972176	E4K	nonSynonymous	23.7	0.000091	30795794	0.00003468	0.000205508	0	0	0 byCluster,byFrequency
ZNF629	chr16	30784224	G	T	rs748667104	P35H	nonSynonymous	22.6	0.000012	30795545	0.00002484	4.35161E-05	0	0.000166058	0 byFrequency
ZNF629	chr16	30782776	C	T	rs766764636	D518N	nonSynonymous	26.8	0.000008	30794097	0.000008239	0	0	0	6.05767E-05 unknown