

Table S1. Sequencing statistics of WGBS.

Sample ID	Donor ID	Cell type	Sequencing method	Num. of reads after quality trimming	Mapping efficiency	Duplications removed	C methylated in CpG context	C methylated in non-CpG context
la01	01	Alveolar cell	WGBS single-end 100bp	133,365,228	52.4%	26.93%	68.0%	0.8%
la02	02	Alveolar cell	WGBS single-end 100bp	138,415,577	51.6%	21.91%	66.4%	0.8%
la03	03	Alveolar cell	WGBS single-end 100bp	197,599,683	54.1%	53.53%	64.8%	0.9%
la04	04	Alveolar cell	WGBS single-end 100bp	265,932,383	53.3%	46.95%	66.6%	0.8%
la05	05	Alveolar cell	WGBS single-end 100bp	256,708,034	56.4%	55.71%	66.6%	4.6%
la06	06	Alveolar cell	WGBS single-end 100bp	296,574,994	48.7%	52.53%	64.0%	0.8%
la07	07	Alveolar cell	WGBS single-end 100bp	338,301,178	42.5%	51.92%	68.2%	0.9%
la08	08	Alveolar cell	WGBS single-end 100bp	291,242,428	51.7%	37.14%	71.8%	0.7%
la09	09	Alveolar cell	WGBS single-end 100bp	185,932,397	53.1%	35.95%	67.0%	0.8%
la10	10	Alveolar cell	WGBS single-end 100bp	269,049,745	50.7%	74.44%	64.3%	1.1%
la11	11	Alveolar cell	WGBS single-end 100bp	259,913,667	53.3%	61.36%	67.6%	0.7%
la12	12	Alveolar cell	WGBS single-end 100bp	382,961,243	48.4%	54.07%	67.1%	0.7%
lb01	01	Bronchial cell	WGBS single-end 100bp	197,461,158	25.7%	33.48%	66.8%	0.9%
lb02	02	Bronchial cell	WGBS single-end 100bp	218,572,059	41.0%	63.56%	68.5%	1.2%
lb03	03	Bronchial cell	WGBS single-end 100bp	370,067,417	34.0%	55.47%	67.6%	2.0%
lb04	04	Bronchial cell	WGBS single-end 100bp	355,748,100	40.1%	52.23%	69.1%	1.0%
lb05	05	Bronchial cell	WGBS single-end 100bp	388,253,841	31.6%	50.77%	66.8%	0.9%
lb06	06	Bronchial cell	WGBS single-end 100bp	193,075,863	49.1%	23.81%	70.9%	0.8%
lb07	07	Bronchial cell	WGBS single-end 100bp	157,184,638	44.4%	20.72%	68.9%	0.8%
lb08	08	Bronchial cell	WGBS single-end 100bp	256,041,587	51.5%	70.26%	72.3%	0.8%
lb09	09	Bronchial cell	WGBS single-end 100bp	127,135,990	53.7%	57.69%	66.5%	1.0%
lb10	10	Bronchial cell	WGBS single-end 100bp	199,710,823	49.0%	77.41%	64.5%	0.9%
lb11	11	Bronchial cell	WGBS single-end 100bp	204,371,801	50.0%	67.36%	66.9%	1.0%
lb12	12	Bronchial cell	WGBS single-end 100bp	201,765,922	48.9%	29.82%	69.6%	0.8%
tc01	01	T lymphocytes	WGBS single-end 100bp	199,774,405	46.9%	15.34%	70.0%	1.0%
tc02	02	T lymphocytes	WGBS single-end 100bp	178,444,561	40.6%	11.24%	70.6%	1.4%
tc03	03	T lymphocytes	WGBS single-end 100bp	216,767,277	50.4%	17.49%	71.5%	0.8%
tc04	04	T lymphocytes	WGBS single-end 100bp	224,156,221	41.6%	13.74%	71.2%	1.3%
tc05	05	T lymphocytes	WGBS single-end 100bp	231,526,342	49.3%	17.80%	70.9%	0.9%
tc06	06	T lymphocytes	WGBS single-end 100bp	224,990,552	41.0%	17.16%	71.5%	1.4%
tc07	07	T lymphocytes	WGBS single-end 100bp	234,050,177	51.7%	20.07%	74.7%	1.0%
tc08	08	T lymphocytes	WGBS single-end 100bp	183,657,661	51.1%	17.99%	70.6%	0.9%
tc09	09	T lymphocytes	WGBS single-end 100bp	221,046,731	50.7%	15.45%	71.8%	1.1%
tc10	10	T lymphocytes	WGBS single-end 100bp	259,431,459	50.3%	17.79%	69.8%	1.0%
tc11	11	T lymphocytes	WGBS single-end 100bp	120,555,010	45.4%	10.58%	72.6%	1.4%
tc12	12	T lymphocytes	WGBS single-end 100bp	130,020,633	40.5%	6.69%	69.1%	1.4%

Table S2. Sequencing statistics of RNA-seq.

Sample ID	Subject ID	Cell type	Sequencing method	Raw read pairs	Aligned read pairs	Concordant pair alignment rate	Duplication removed
la01	01	Alveolar cell	RNA-seq paired-end 50bp	20,525,160	8,666,240	39.7%	17.9%
la02	02	Alveolar cell	RNA-seq paired-end 50bp	21,895,352	17,429,928	72.2%	3.5%
la03	03	Alveolar cell	RNA-seq paired-end 50bp	37,675,964	29,135,003	71.7%	6.7%
la04	04	Alveolar cell	RNA-seq paired-end 50bp	15,123,953	6,192,950	38.6%	17.5%
la05	05	Alveolar cell	RNA-seq paired-end 50bp	17,255,018	11,809,486	63.8%	9.9%
la06	06	Alveolar cell	RNA-seq paired-end 50bp	37,764,624	26,606,085	65.2%	8.6%
la07	07	Alveolar cell	RNA-seq paired-end 50bp	16,594,878	7,085,758	39.7%	12.9%
la08	08	Alveolar cell	RNA-seq paired-end 50bp	19,390,905	13,966,661	67.7%	12.0%
la09	09	Alveolar cell	RNA-seq paired-end 50bp	34,633,296	23,272,270	63.7%	12.0%
la10	10	Alveolar cell	RNA-seq paired-end 50bp	22,105,588	8,415,408	34.9%	16.0%
la11	11	Alveolar cell	RNA-seq paired-end 50bp	17,327,625	13,064,718	70.0%	5.9%
la12	12	Alveolar cell	RNA-seq paired-end 50bp	35,375,230	25,755,624	68.6%	14.2%
lb01	01	Bronchial cell	RNA-seq paired-end 50bp	18,128,260	11,854,702	63.4%	13.8%
lb02	02	Bronchial cell	RNA-seq paired-end 50bp	17,274,538	12,900,772	69.4%	5.7%
lb03	03	Bronchial cell	RNA-seq paired-end 50bp	37,495,354	28,786,632	70.8%	5.5%
lb04	04	Bronchial cell	RNA-seq paired-end 50bp	17,256,492	7,443,891	41.7%	19.5%
lb05	05	Bronchial cell	RNA-seq paired-end 50bp	17,711,249	12,798,808	67.2%	8.2%
lb06	06	Bronchial cell	RNA-seq paired-end 50bp	37,798,674	27,998,929	69.1%	7.0%
lb07	07	Bronchial cell	RNA-seq paired-end 50bp	22,476,567	16,309,164	66.7%	5.7%
lb08	08	Bronchial cell	RNA-seq paired-end 50bp	20,095,012	13,231,669	62.2%	12.4%
lb09	09	Bronchial cell	RNA-seq paired-end 50bp	39,143,660	29,175,790	70.0%	6.5%
lb10	10	Bronchial cell	RNA-seq paired-end 50bp	20,645,518	15,787,781	73.0%	7.6%
lb11	11	Bronchial cell	RNA-seq paired-end 50bp	17,632,022	13,950,927	73.6%	4.4%
lb12	12	Bronchial cell	RNA-seq paired-end 50bp	35,317,708	25,356,043	67.8%	10.6%
tc01	01	T lymphocytes	RNA-seq paired-end 50bp	19,360,549	13,584,187	66.7%	9.7%
tc02	02	T lymphocytes	RNA-seq paired-end 50bp	18,249,336	14,831,275	74.8%	6.1%
tc03	03	T lymphocytes	RNA-seq paired-end 50bp	19,345,431	13,994,159	67.7%	9.3%
tc04	04	T lymphocytes	RNA-seq paired-end 50bp	19,587,327	9,224,657	44.5%	16.2%
tc05	05	T lymphocytes	RNA-seq paired-end 50bp	18,609,091	15,170,606	77.7%	6.5%
tc06	06	T lymphocytes	RNA-seq paired-end 50bp	20,585,541	15,152,410	69.6%	10.5%
tc07	07	T lymphocytes	RNA-seq paired-end 50bp	21,491,747	16,504,481	71.3%	8.0%
tc08	08	T lymphocytes	RNA-seq paired-end 50bp	20,515,410	8,423,841	37.9%	17.7%
tc09	09	T lymphocytes	RNA-seq paired-end 50bp	21,464,734	16,637,497	71.8%	6.8%
tc10	10	T lymphocytes	RNA-seq paired-end 50bp	20,796,603	10,197,361	46.3%	18.6%
tc11	11	T lymphocytes	RNA-seq paired-end 50bp	19,073,004	9,273,361	46.1%	18.4%
tc12	12	T lymphocytes	RNA-seq paired-end 50bp	20,280,599	10,437,623	48.7%	21.2%

Table S3. Source of annotation of genomic features.

Feature	Resource
CpG island	http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database/
DNase hypersensitive areas	http://hgdownload.cse.ucsc.edu/goldenpath/hg19/encodeDCC/wgEncodeRegDnaseClustered/wgEncodeRegDnaseClusteredV3.bed.gz
Transcription factor (TF) binding regions	http://hgdownload.cse.ucsc.edu/goldenpath/hg19/encodeDCC/wgEncodeRegTfbsClustered/wgEncodeRegTfbsClusteredV3.bed.gz
Repeat (repeat masker)	http://www.repeatmasker.org/species/hg.html
Gene annotation (GRCh37.73 gtf format)	ftp.ensembl.org; /pub/release-73/gtf/homo_sapiens

Table S4. Promoter DMR genes.

Alveolar > Bronchial	Alveolar < Bronchial	Lung > T	Lung < T
A2ML1	A1BG	A1CF	A1BG
A3GALT2	ABCA1	ABCA2	A2M
A4GALT	ABCA8	ABCA8	A2ML1
AAAS	ABCB4	ABCA9	A3GALT2
AACS	ABCG2	ABCD2	A4GALT
AADAT	ABHD17A	ABHD17A	AAGAB
AAGAB	ABISBP	AC002451.1	AAMDC
AAK1	ABLM3	AC005358.1	AAMP
AAAT	AC006116.20	AC006449.1	AASDH
AATK	AC018816.3	AC007377.1	AATF
ABCA12	AC020952.1	AC008271.1	AATK
ABCA3	AC022210.1	AC008686.1	ABAT
ABCA5	AC037199.1	AC010547.9	ABCA3
ABCB1	AC037459.4	AC011294.3	ABCA5
ABCB6	AC069368.3	AC011484.1	ABCA7
ABCB9	AC083862.1	AC016251.1	ABCB6
ABCC10	AC087477.1	AC018445.1	ABCB8
ABCC12	AC087645.1	AC019206.1	ABCB9
ABCC3	AC090673.2	AC026202.1	ABCC1
ABCC5	AC091801.1	AC026461.1	ABCC10
ABCC8	AC092675.3	AC074091.13	ABCC3
ABCF1	AC112715.2	AC087477.1	ABCC5
ABCG1	AC135178.1	AC090673.2	ABCD4
ABCG4	ACOXL	AC096644.1	ABCF1
ABHD11	ACRBP	AC114494.1	ABHD12
ABHD12	ACSS3	AC131971.1	ABHD14A
ABHD12B	ACVRL1	ACSM2A	ABHD14A-ACY1
ABHD14A	ADAMTS10	ACTR3	ABHD14B
ABHD2	ADAMTS16	ACTR6	ABHD2
ABHD8	ADAMTS4	ADAMTS16	ABHD5
ABLM1	ADAMTS9	ADAMTS9	ABHD6
ABLM2	ADAMTSL1	ADCY2	ABHD8
AC000003.2	ADAMTSL4	ADCYAP1R1	ABII
AC005008.2	ADAP2	ADGB	ABLI
AC006547.14	ADCY2	ADRA1A	ABLM2
AC007952.5	ADGB	ADRBK1	ABR
AC007952.6	ADII	AD000662.92	ABRA
AC010646.3	ADM5	AGBL1	AC003101.1
AC011239.1	ADRBK1	AK4	AC004528.1
AC011298.1	AFAP1L1	AKR1E2	AC004824.2
AC011475.1	AFE3	AL136115.1	AC005008.2
AC012485.1	AGPAT1	AL136218.1	AC005606.1
AC016251.1	AGRN	AL158091.1	AC005609.1
AC016586.1	AGT	AL162424.1	AC006014.1
AC017028.1	AHSG	AL353354.2	AC006486.9
AC021218.2	AIM1	AL591806.1	AC007773.3
AC022498.1	AKAP12	ALDOC	AC007952.1
AC024580.1	AKAP8	ALOX5AP	AC007956.1
AC026310.1	AKNAD1	ALS2CL	AC009365.3
AC026740.1	AKR1B1	AMPD1	AC010441.1
AC051642.1	AKR1C1	AMZ2	AC010760.1
AC068533.7	ALOX5	ANKRD26	AC011500.1
AC073342.1	ALPK1	ANKRD66	AC011897.1
AC074091.13	ALPL	ANO1	AC012313.1
AC074389.6	ALPP	ANO2	AC012485.1
AC079210.1	ALS2CL	AP000295.9	AC016586.1
AC079354.1	ALX1	APLN	AC022498.1
AC079602.1	AMBRA1	POBEC3A	AC024580.1
AC092811.1	AMER2	POBEC3C	AC026369.1
AC093157.1	AMICA1	AQP2	AC037459.4
AC093323.1	ANAPC5	ARHGAP29	AC061992.1
AC093677.1	ANGPT2	ARHGAP30	AC069547.2
AC104534.3	ANGPTL2	ARHGAP32	AC079210.1
AC104667.3	ANKRD24	ARHGAP39	AC079354.1
AC104809.3	ANKRD44	ARHGDIIB	AC079602.1
AC106873.4	ANXA2R	ARHGEF11	AC090616.2
AC110619.2	AOAH	ARHGEF4	AC092811.1
AC119673.1	AOC3	ARPP19	AC092964.1
AC131097.4	AP000322.53	ASAP2	AC093157.1
AC131971.1	AP000679.2	ASB8	AC093677.1
AC138517.1	AP3B2	ASUN	AC104472.1
AC140061.12	APC	ASXL2	AC104667.3
AC144568.2	APLN	ASZ1	AC119673.1
AC174470.1	POB	ATG4D	AC127496.1
ACAA1	APOL1	ATM	AC131097.4
ACACA	APOL3	ATP13A5	AC140061.12
ACACB	APOLD1	ATP6V0D2	ACACB
ACAD10	AQP1	B2M	ACAD10
ACAN	ARAP3	B3GALT5	ACAD11
ACAP1	ARGLU1	B4GALT4	ACADL
ACAP3	ARHGAP17	B4GALT6	ACADVL
ACBD4	ARHGAP28	BATF	ACAP2
ACER3	ARHGAP40	BCL2L1	ACAP3
ACKR2	ARHGAP44	BICC1	ACAT1
ACKR3	ARHGDIIB	BIRC3	ACIN1
ACLY	ARID5A	BLID	ACKR2
ACOT11	ARL11	BLOC1S5-TXNDC5	ACKR3
ACOT7	ARN2T	BPI	ACLY
ACOX2	ARPP21	BRD1	ACO2
ACP1	ARRB1	BRDT	ACOT11
ACPL2	ART4	BST2	ACOX1
ACPP	ASF1B	BTBD16	ACOX2
ACSBG1	ASH2L	BTLA	ACOX3
ACSF2	ASTN1	BUB3	ACPI
ACSF3	ATG12	C10orf11	ACRBP
ACSL1	ATP6V0A1	C10orf13	ACSF2
ACSL3	ATP6V1E2	C10orf126	ACSL3
ACSL6	B2M	C10orf129	ACSM1
ACSM1	B4GALNT3	C11orf21	ACSM3
ACSM3	B4GALT6	C14orf37	ACSS1
ACSS1	BAALC	C15orf32	ACTA1
ACSS2	BANP	C15orf53	ACTA2
ACTA2	BARX1	C15orf59	ACTC1
ACTB	BATF2	C16orf54	ACTG1
ACTG1	BBX	C16orf97	ACTN1
ACTL6B	BCL6B	C17orf97	ACTR3C
ACTL7A	BDNF	C18orf32	ACTR5
ACTN4	BHLHE22	C19orf18	ACTR8
ACTR1A	BHMT2	C1GALT1	ACVR1
ACTR3C	BN3	C1orf162	ACVR1B
ACVR1B	BIVM	C1orf174	ACVR2A
ACY1	BMPR1A	C1orf186	ACVR2B
ACYP1	BNC1	C1orf200	ACVRL1
ACYP2	BOP1	C1orf226	ACY1
ADAM10	BRD7	C1orf95	ACYP1
ADAM12	BRE	C21orf88	ADA

ADAM15	BRINP2	C2CD48	ADAM19
ADAM28	BST2	C2CD5	ADAM30
ADAM8	BTN2A1	C3orf18	ADAM9
ADAMTS14	BTN3A1	C4orf45	ADAMTS10
ADAMTS8	BTN3A3	C5orf56	ADAMTS14
ADAMTSL5	BTNL9	C6	ADAMTS18
ADAT1	BUB1	C6orf106	ADAMTS20
ADAT3	BZRAP1	C6orf48	ADAMTS4
ADC	C10orf113	C7	ADAMTS7
ADCK2	C10orf90	C7orf63	ADAMTSL4
ADCK3	C11orf45	C8orf17	ADAMTSL5
ADCK4	C11orf58	C8orf44	ADARB1
ADCY4	C11orf89	C8orf56	ADAT3
ADCY5	C12orf43	C9orf170	ADC
ADCY6	C12orf79	C46	ADCK2
ADCY9	C14orf177	CADM1	ADCK3
ADD1	C14orf23	CAPZA1	ADCK4
ADH5	C14orf28	CASC10	ADCK5
ADHFE1	C14orf39	CASP10	ADCY3
ADIG	C16orf80	CASP8	ADCY4
ADIPQO	C17orf97	CASQ2	ADCY6
ADIPOR2	C1orf200	CASS4	ADCY9
ADIRF	C1orf53	CBX3	ADD1
ADORA1	C1orf68	CCDC110	ADD3
ADORA2A	C1QTNF3	CCDC129	ADH5
ADRA1B	C20orf197	CCDC167	ADH7
ADRM1	C20orf26	CCDC173	ADHFE1
ADSSL1	C2orf80	CCDC65	ADII
AEBP1	C4orf40	CCDC66	ADIG
AEBP2	C5orf38	CCL11	ADIPOR2
AEN	C5orf56	CCL13	ADIRF
AES	C5orf64	CCL21	ADK
AFF1	C6	CCL3	ADM2
AGA	C6orf118	CCL4	ADM5
AGAP2	C7	CCL5	ADNP
AGAP2-AS1	C7orf25	CCL7	ADNP2
AGAP3	C7orf54	CCM2	ADORA2B
AGBL4	CACNA1D	CCND3	ADPRHL1
AGBL5	CACNA2D4	CCNL1	ADRA1D
AGFG1	CACNG2	CCR4	ADRA2A
AGPAT5	CACCTN	CCR5	ADRB2
AGPAT6	CADM1	CCR6	ADRBK2
AGR2	CADM2	CCR7	AES
AHCY	CADM4	CCR8	AFAP1
AHCYL2	CADPS	CD160	AFF1
AHNAK	CALB2	CD1B	AGAP2-AS1
AHNAK2	CALCOCO2	CD1C	AGAP3
AHRR	CAMK2B	CD1E	AGBL4
AHSA2	CARD11	CD2	AGBL5
AICDA	CARD8	CD200R1	AGER
AIFM3	CARHSP1	CD226	AGK
AIG1	CASC10	CD27	AGL
AIM1L	CASKIN2	CD28	AGO2
AIP	CASP10	CD300LB	AGO4
AJUBA	CASP2	CD33	AGPAT1
AK2	CASP8	CD36	AGPAT2
AK3	CASR	CD3D	AGPAT4
AKAP1	CBFB	CD3G	AGPAT6
AKAP6	CBX1	CD48	AGTPBP1
AKAP7	CC2D1A	CD5	AHCYL1
AKR1A1	CCBE1	CD52	AHCYL2
AKR1B10	CCDC3	CD53	AHDC1
AKR1B15	CCDC64	CD58	AHNAK2
AKR1C2	CCDC64B	CD69	AHRR
AKR1C3	CCDC68	CD70	AHSA2
AKT1	CCDC69	CD72	AHSP
AKTIP	CCDC82	CD79B	AIF1
AL022328.1	CCDC88A	CD8A	AIF1L
AL031590.1	CCL14	CD96	AIFM3
AL031663.2	CCL8	CDCA7	AIM1L
AL031666.2	CCM2L	CDH17	AIRE
AL035252.1	CCND3	CDKN2B	AJUBA
AL035588.1	CCNDBP1	CEBPE	AK1
AL035681.1	CCNL2	CEBPG	AK3
AL049840.1	CCR2	CENPM	AK5
AL118506.1	CCR4	CHRM3	AK9
AL133318.1	CCR5	CHRM5	AKAP1
AL137002.1	CCRL2	CHRNA3	AKAP10
AL137026.1	CCRN4L	CHST12	AKAP5
AL139080.1	CD163L1	CKLF	AKAP8L
AL158147.2	CD1E	CKLF-CMTM1	AKR1A1
AL160175.1	CD244	CLCA4	AKR1B1
AL161784.1	CD300A	CLDN12	AKR7A3
AL162431.1	CD33	CLDND2	AKT1
AL163636.6	CD34	CLEC12A	AKT2
AL335583.1	CD53	CLEC19A	AL020996.1
AL335909.2	CD59	CLEC2D	AL031666.2
AL391421.1	CD93	CLEC4E	AL035252.1
AL590452.1	CD14A	CLEC5A	AL035406.1
AL591025.1	CD42EP1	CLEC1	AL035681.1
AL603965.1	CDH11	CLMP	AL049747.1
AL645608.1	CDH7	CLNK	AL049840.1
ALAS1	CDK2AP1	CLPP	AL118506.1
ALDH16A1	CDRT4	CNBD1	AL121761.2
ALDH1A1	CDX2	CNIH4	AL133318.1
ALDH1A3	CDYL2	CNOT6L	AL136376.1
ALDH1L1	CECR2	CNTNAP3	AL136531.1
ALDH1L2	CEP55	CNTNAP4	AL137002.1
ALDH3A1	CERKL	COBLL1	AL138815.2
ALDH3A2	CETP	COG4	AL139080.1
ALDH3B1	CFC1	COL12A1	AL139333.1
ALDH3B2	CHD7	COL13A1	AL161450.1
ALG1	CHIC2	COL6A5	AL163636.6
ALG1L	CHMP7	COL6A6	AL356356.1
ALG9	CHN1	COL9A1	AL365202.1
ALOX12	CIEBB	COLEC10	AL590452.1
ALOX12B	CINP	CORO1A	AL590822.1
ALOX15	CIRH1A	CPO	AL590822.2
ALPK2	CLCA4	CPSF1	AL645608.1
AMBP	CLCN1	CR2	AL807752.1
AMD1	CLDN14	CREM	ALAS1
AMH	CLDN15	CRHR2	ALDH1A3
AMN1	CLDN20	CRK	ALDH2
AMOTL1	CLEC14A	CST4	ALDH3A2
AMOTL2	CLEC19A	CST7	ALDH3B1
AMPD3	CLEC3B	CTB-133G6.1	ALDH3B2
AMT	CLUL1	CTD-2287016.3	ALDH4A1
ANG	CMSS1	CTD-2547L24.3	ALDH9A1

ANGEL1	CMTM2	CTD-2616J11.11	ALG1
ANK1	CNGA3	CTLA4	ALG12
ANK3	CNOT10	CTTNBP2	ALG9
ANKDD1A	CNR1	CXXC11	ALKBBH3
ANKDD1B	CNTLN	CYP2C19	ALLC
ANKFY1	CNTNAP2	CYP39A1	ALOX12
ANKH	COL12A1	CYP3A4	ALOX12B
ANKRD10	COL14A1	CYP46A1	ALOX5
ANKRD13B	COL1A2	CYP4A22	ALPK1
ANKRD2	COL22A1	CYP7A1	ALPK2
ANKRD22	COL24A1	CYTIP	ALPK3
ANKRD23	COL27A1	DAOA	ALS2CR11
ANKRD29	COL2A1	DAPL1	ALS2CR12
ANKRD39	COL3A1	DCSTAMP	AMBRA1
ANKRD46	COL6A3	DDAH1	AMDHD1
ANKRD62	COLEC10	DDC8	AMFR
ANKRD65	COLEC11	DDX39A	AMIGO2
ANKRD9	COLQ	DEFA4	AMIGO3
ANKS6	COPS8	DEFB133	AMMECR1L
ANKUB1	CORO2B	DGKA	AMN
ANLN	COX7A1	DHRS7C	AMN1
ANO1	CPA6	DIABLO	AMOTL2
ANO10	CPAMD8	DIP2A	AMT
ANO2	CPE	DKFZP761K2322	AMZ1
ANO7	CPED1	DNAH14	ANAPC1
ANP32D	CRBN	DNAJC22	ANAPC16
ANPEP	CRCP	DNTT	ANAPC2
ANXA11	CREB1	DOK2	ANAPC5
ANXA13	CRH	DOK6	ANG
ANXA2	CRLF1	DPH7	ANGEL2
ANXA3	CRMP1	DR1	ANGPT2
ANXA4	CRY1	DSCAM	ANGPT4
ANXA6	CSF2RB	DSCR8	ANGPTL2
ANXA8L2	CSF3	DSG1	ANGPTL4
ANXA9	CSMD2	DSPF	ANGPTL5
AOC1	CSMD3	DUSP2	ANHx
AP000304.12	CTB-133G6.1	DUSP22	ANK1
AP001055.1	CTB-186H2.3	DYSF	ANK3
AP001362.1	CTD-2014B16.3	EDEM1	ANKDD1A
AP001631.10	CTNNA3	EDIL3	ANKDD1B
AP002348.1	CTNND2	EEF1A1	ANKFY1
AP003068.23	CTSK	EEF1B2	ANKH
AP003733.1	CTTNBP2	EFCAB1	ANKK1
APIB1	CUL2	EIF3M	ANKMY1
APIG1	CYLD	ENPP6	ANKRA2
APIG2	CYP19A1	EPYC	ANKRD10
APIM2	CYP27C1	ERH	ANKRD13A
APIS3	CYP2A13	EV12A	ANKRD13B
AP2A1	CYP2A7	F11	ANKRD13D
AP2B1	CYTL1	FABP5	ANKRD16
AP2S1	DAAM2	FAM124B	ANKRD22
AP3M1	DACH1	FAM159A	ANKRD23
AP3S2	DCLK1	FAM173A	ANKRD24
AP4S1	DDO	FAM178A	ANKRD28
AP5B1	DDR2	FAM196A	ANKRD29
APBA1	DDX59	FAM198B	ANKRD30B
APBB1	DFNB59	FAM205A	ANKRD33
APBB1IP	DICER1	FAM78A	ANKRD35
APBB2	DIO2	FANK1	ANKRD37
APCDD1L	DKFZP434H0512	FASLG	ANKRD39
APLP2	DKK3	FBLIM1	ANKRD40
APOA1	DLGAP2	FBXO5	ANKRD42
APOA1BP	DLX4	FCRL6	ANKRD46
APOA4	DLX6	FCF12	ANKRD50
APOBEC3C	DMGDH	FHIT	ANKRD52
APOBEC3D	DMRT2	FILIP1	ANKRD53
APOBEC3H	DMTN	FSCB	ANKRD6
APOD	DNAH2	FSIP2	ANKRD62
APOL4	DNAH9	FUS	ANKRD63
APPL2	DNAJC11	FUT7	ANKRD65
AQP10	DNM2	FUT8	ANKRD9
AQP12B	DNTT	FYB	ANKS3
AQP3	DOCK10	GAD1	ANKUB1
AQP4	DOCK9	GALM	ANO4
AQP5	DOK3	GALNT14	ANO9
AQP6	DOK4	GAPT	ANP32A
AQP7	DPPA4	GAS2L3	ANPEP
AQPEP	DPT	GATA4	ANTXR2
ARFGEF1	DPYS	GATM	ANXA11
ARG2	DPYSL2	GBP4	ANXA2
ARHGAP15	DRD4	GCDH	ANXA2R
ARHGAP21	DSC2	GCN1L1	ANXA5
ARHGAP22	DSC3	GCNT1	AOC2
ARHGAP23	DTNBP1	GDF6	AOC3
ARHGAP24	DUSP16	GIMAP1	AOX1
ARHGAP26	DUSP5	GIMAP2	AP000688.1
ARHGDA	DVL3	GIMAP4	AP001024.1
ARHGDG	DYSF	GIMAP6	AP001362.1
ARHGEF11	E2F5	GIMAP7	AP001652.1
ARHGEF16	ECSCR	GIMAP8	AP003041.2
ARHGEF17	EDARADD	GIAR	AP003068.23
ARHGEF18	EDEM2	GLIPR1	AP005482.1
ARHGEF19	EDNRA	GLRX	APIB1
ARHGEF38	EEF1G	GNGT2	APIG2
ARHGEF39	EGFL7	GNLY	APIM1
ARHGEF40	EIF4E3	GNPDA1	APIM2
ARID1B	ELAVL4	GPBP1	AP2A1
ARID3A	ELTD1	GPM6A	AP2A2
ARID3B	EMID1	GPR107	AP2M1
ARID5B	EMILN1	GPR114	AP2S1
ARIH2	EML5	GPR128	AP3D1
ARL15	ENOX1	GPR171	AP3M1
ARL4D	ENPEP	GPR183	AP4E1
ARL8A	ENTPD1	GPR55	AP4M1
ARMC4	EOGT	GPR65	AP4S1
ARMC8	EPAS1	GPR68	APBB1IP
ARNT	EPG5	GPR98	APBB3
ARNTL	EPHB4	GPX5	APC2
ARPC1A	ERVFRD-1	GRID2	APCDD1
ARPC1B	ESAM	GSDMB	APEX1
ARPP19	ESPN	GTF3A	APH1B
ARRB2	ESYT1	GTPC	APIP
ARRDC1	ETS1	GZMA	APITD1
ARSA	EVIS	GZMB	APITD1-CORT
ARSG	EXD2	GZMM	APLP2
ARSJ	EXOC6	HAVCR2	APMAP
ARTN	EZH1	HCG27	APOA1
ARVCF	FABP5	HCST	APOA2

ASAH1	FAH	HELB	APOE
ASAP3	FAM105A	HESX1	APOL4
ASB13	FAM110B	HIST1H4I	APOPT1
ASB18	FAM110D	HIST2H2AA3	APPL1
ASB2	FAM124B	HIST4H4	APPL2
ASB3	FAM131B	HLA-B	APRT
ASB4	FAM13B	HLA-E	APTX
ASB6	FAM167B	HLA-F	AQP4
ASCC2	FAM170B	HMG A2	AQP6
ASCL4	FAM184A	HMHB1	AQP7
ASCL5	FAM188B	HNRNP A2B1	AQP8
ASH1L	FAM189A1	HNRNPC	ARAP1
ASL	FAM198B	HNRNPF	ARC
ASPDH	FAM19A3	HPSE2	AREL1
ASPG	FAM200B	hsa-mir-150	ARE5
ASPSCR1	FAM214B	HSF5	ARFIP1
ASS1	FAM231D	HSPA8	ARGLU1
ATAD3C	FAM26E	HSPD1	ARHGAP1
ATE1	FAM49A	HSPE1	ARHGAP18
ATF7	FAM65A	HTR2A	ARHGAP19
ATF7IP	FAM69B	ICOS	ARHGAP21
ATF7IP2	FAM78A	IFITM1	ARHGAP23
ATG13	FAM81B	IFITM2	ARHGAP42
ATG14	FAM89A	IFNAR2	ARHGAP5
ATG16L1	FBXL5	IGFL3	ARHGDIG
ATG16L2	FBXO15	IGFLR1	ARHGEF12
ATG2B	FBXO18	IGFN1	ARHGEF15
ATG3	FCGR2A	IGLL1	ARHGEF18
ATG4D	FCN3	IGSF5	ARHGEF19
ATG5	FCRL2	IKZF1	ARHGEF25
ATG9B	FES	IKZF3	ARHGEF37
ATHL1	FEZF1	IL10RA	ARHGEF39
ATL1	FGF17	IL12RB2	ARHGEF40
ATN1	FGF23	IL17RD	ARID1B
ATOH8	FGF5	IL18RAP	ARID2
ATP13A4	FHL3	IL19	ARID3C
ATP1A1	FLIP1	IL2RA	ARL10
ATP1B1	FLKBP15	IL32	ARL4A
ATP1B3	FLJ27365	IL4I1	ARL4D
ATP2A2	FMN2	INTS6	ARL9
ATP2A3	FMNL3	IPCEF1	ARMC2
ATP2B2	FOXA1	IQCG	ARMC9
ATP2C1	FOXA2	IRF2	ARNT
ATP5A1	FOX D2	IRF8	ARRDC1
ATP5D	FOX D4	ITGA4	ARRDC3
ATP5I	FPR1	KARS	ARSI
ATP5J2	FRAT1	KAT6A	ART3
ATP5S	FYN	KCNA4	ART5
ATP5SL	FZD5	KCND3	ARTN
ATP6V0A2	GABRA6	KCNJ13	ARVCF
ATP6V0D1	GABRB3	KCNK17	AS3MT
ATP6V0E2	GABRG3	KCTD5	ASAH1
ATP6V1B1	GABRR1	KDM4E	ASB1
ATP6V1H	GAREML	KDR	ASB16
ATP8B1	GBP5	KIAA0087	ASB4
ATP8B2	GBX1	KIF21B	ASCC1
ATP8B3	GDA	KIF2A	ASCC2
ATP9B	GDF3	KLF2	ASF1B
ATXN1	GDF6	KLHL14	ASGR1
ATXN10	GIMAP1	KLHL6	ASIC3
ATXN2L	GIMAP2	KLRD1	ASNS
ATXN7	GIMAP4	KLRG1	ASPA
ATXN7L1	GIMAP5	KLRP1	ASPDH
AUTS2	GIMAP6	KMO	ASPG
AVP1	GIMAP7	KRT1	ASPSCR1
AXIN1	GIMAP8	KRT78	ASTN2
AZGP1	GIPR	KRT79	ASXL3
AZIN1	GIT2	KRTAP12-3	ATAD3C
B3GAT3	GJA5	KRTAP12-4	ATF4
B3GNT5	GLB1L3	KRTAP13-3	ATF6B
B3GNTL1	GLRX	KRTAP16-1	ATF7
B4GALNT1	GM2A	KRTAP4-12	ATF7IP2
B4GALT1	GMFG	KRTAP5-1	ATG14
B4GALT2	GNB4	LAIR2	ATG3
B4GALT7	GNG11	LAMA1	ATG4C
B9D1	GNGT2	LAPTM5	ATG7
BACE2	GP1BB	LAT	ATL1
BACH1	GP6	LBH	ATN1
BACH2	GPN3	LCESA	ATP10D
BAG3	GPR52	LDLRAD2	ATP13A4
BAHD1	GPRC5C	LEF1	ATP1A2
BAI2	GPX3	LEPROTL1	ATP1A3
BAIAP2L1	GRB2	LGMN	ATP1B1
BAIAP2L2	GREM2	LILRA1	ATP1B2
BAIAP3	GRIA1	LILRA2	ATP2A1
BANF2	GRIK2	LILRB2	ATP2A3
BAP1	GRM8	LIMD2	ATP2B2
BATF	GSC	LIME1	ATP4A
BAZ1B	GSTM5	LMO2	ATP5D
BAZ2A	GYPE	LMX1A	ATP5H
BBG3	GZMA	LNPEP	ATP5J
BBS5	GZMB	LONRF2	ATP5L
BCAR3	H6PD	LPHN2	ATP5L2
BCCIP	HDAC7	LPXN	ATP5S
BCKDHA	HEATR6	LRRRC3B	ATP5SL
BCKDHB	HERC3	LRRRC43	ATP6V0A1
BCL11A	HEYL	LRRRC55	ATP6V0A4
BCL2L14	HHEX	LSAMP	ATP6V0C
BCL2L15	HIP1	LSM14A	ATP6V0D1
BCL2L2	HMHB1	LSMEM2	ATP6V1B2
BCL3	HORMAD2	LTA	ATP6V1E2
BCL6	HPCAL1	LTB	ATP6V1G2
BCL7A	HPSE2	LY86	ATP6V1G2-DDX39B
BCL7C	HRH2	LYL1	ATP8A2
BCL9	HS3ST3A1	MAK	ATP8B3
BCL9L	HS3ST5	MAML3	ATPAF1
BDH1	HSD11B1	MAN2A1	ATXN1
BDKRB1	HSPA12B	MAP1LC3B2	ATXN10
BDKRB2	HSPB2	MAP2	ATXN2
BEGAIN	HSPB2-C11orf52	MAP6	ATXN7L1
BEND5	HSPB3	MAPKAPK3	ATXN7L3
BEND7	HSPB8	MCHR2	AU1
BEST2	HTT	MED10	AVIL
BEST3	HYAL1	MED18	AVPI1
BFAR	HYAL2	MED7	AXL
BFBP1	HYPK	MEI	AZ1
BFBP2	ICAM2	MEOX1	AZU1
BGLAP	ICAM5	MFAP3L	B3GALNT1

BID	ID2	MGAT4A	B3GALNT2
BLCAP	ID3	MK167	B3GALT2
BLOC1S1	IFFO1	MKL1	B3GAT1
BLVRA	IFI27	MLLT11	B3GNT1
BMF	IFI44	MME	B3GNT2
BM11	IFI44L	MMP23B	B3GNT3
BMPR1B	IFT140	MMP8	B3GNT4
BNIP3	IGSF10	MMRN1	B3GNT5
BNIP3L	IHH	MORC2	B3GNT8
BNIP1	IKZF1	MPL	B3GNT9
BOC	IL18BP	MRPL10	B4GALNT1
BOD1	IL36RN	MS4A1	B4GALT1
BPIFB1	IL6	MS4A7	B4GALT2
BPIFB2	ILDR1	MSRA	B4GALT3
BRD3	INHBA	MT1M	B9D1
BRD4	INMT	MTHFS	BACE1
BRF1	INMT-FAM188B	MT01	BACH1
BRICD5	INO80	MTPN	BACH2
BRIP1	INPP5B	MUC3A	BAD
BRPF3	INPP5D	MVB12A	BAG3
BRSK1	INPP5K	MYEOV	BAG5
BRSK2	INTS3	MYF5	BAHD1
BRWD1	INTS8	MYF6	BAI1
BSG	INTS9	MYO1G	BAI2
BST1	IQCF2	MYO7B	BAIAP2
BTBD16	IQCK	MYRFL	BAIAP2L1
BTBD19	IRF5	MZB1	BAIAP2L2
BTBD3	IRX1	NAA16	BARD1
BTC	IRX2	NAA40	BARHL1
BTG1	IRX3	NABP1	BATF2
BTG3	IRX6	NAT2	BAZ2A
BTG4	ISL1	NBN	BBS2
BTNL8	ITFG3	NCL	BBX
BZW2	ITGA5	NCR2	BCAM
C10orf10	ITGBL1	NCR3	BCAN
C10orf35	ITI15	NDUFS1	BCAP29
C10orf55	ITPKA	NDUFV2	BCAR1
C10orf71	ITPRIP	NEBP	BCAS3
C10orf91	IZUMO4	NEGR1	BCCIP
C10orf99	JAK1	NEIL2	BCKDHA
C11orf1	JAKMIP2	NFE2	BCKDK
C11orf16	JAM2	NFKBID	BC12L12
C11orf35	JAM3	NKAIN2	BC12L15
C11orf49	JMJD1C	NKG7	BC12L2
C11orf52	JPH4	NLRP2	BC12L2-PABPN1
C11orf54	JRKL	NME6	BCL3
C11orf63	KANK4	NMT2	BCL6
C11orf80	KAT6B	NOP58	BCL6B
C11orf85	KCNA4	NOS1AP	BCL7A
C11orf88	KCNE3	NOX5	BCL7C
C11orf94	KCNH2	NPAT	BCL9
C12orf23	KCNJ8	NPHP4	BCO2
C12orf36	KCNMB1	NPR3	BCR
C12orf42	KCNMB3	NPY4R	BDH1
C12orf45	KCNQ2	NR2F1	BDH2
C12orf49	KCNQ3	NRG2	BDNF
C12orf54	KCNQ5	NRROS	BECN1
C12orf74	KCNS1	NSG1	BEGAIN
C12orf75	KCTD10	NSUN7	BEND5
C13orf45	KCTD13	NUB1	BEST2
C14orf139	KCTD16	NUDT5	BFAR
C14orf164	KCTD5	NUP210	BFSF1
C14orf166B	KIAA0226L	NUSAP1	BIHLHA15
C14orf180	KIAA0355	NUTM2F	BIHMT2
C14orf64	KIAA0922	NUTM2G	BICD1
C14orf80	KIAA1024L	OIP5	BLACE
C15orf38	KIAA1033	OR10J5	BLCAP
C15orf38-AP3S2	KIAA1199	OR10S1	BLM
C15orf39	KIF17	OR10T2	BLOC1S1
C15orf41	KLC3	OR2H2	BLVRA
C15orf54	KLF11	OR2K2	BMF
C15orf62	KLF6	OR4D11	BMP1
C16orf70	KLHDC3	OR51B5	BMP8B
C16orf74	KLHL14	OR51F1	BMPR1B
C16orf89	KLHL31	OR51J1	BMPR2
C16orf91	KLHL35	OR52D1	BNIP3L
C16orf96	KLHL6	OR56A4	BNIP1
C16orf98	KLK2	OR5A2	BOD1
C17orf107	KMO	OR5AU1	BOK
C17orf62	KRT1	OR8B12	BOLA1
C17orf75	KRT81	OR9G1	BOLA3
C17orf77	KRT83	ORAI1	BPHL
C17orf99	KRT9	ORC2	BPIFB3
C18orf63	KRTAP10-1	OSM	BPIFB4
C18orf64	KRTAP11-1	OSR1	BPTF
C19orf10	KRTAP12-3	OTOG	BRAF
C19orf33	KRTAP12-4	P2RX4	BRAT1
C19orf45	KRTAP16-1	P2RY11	BRCA1
C19orf48	KRTAP2-1	PAHA3	BRD3
C19orf54	KRTAP2-2	PAMR1	BRD4
C19orf55	KRTAP2-3	PAOX	BRD7
C19orf57	KRTAP4-11	PARK7	BRF1
C19orf59	KRTAP5-6	PARVA	BR13
C19orf60	KRTAP5-9	PATL2	BRICD5
C19orf67	LAIR1	PCED1B	BRSK1
C19orf82	LARP6	PCLO	BRSK2
C1orf105	LASP1	PDCD5	BRWD1
C1orf106	LAT	PDE10A	BSG
C1orf110	LBH	PDE7A	BST1
C1orf116	LCE1C	PDE8B	BTBD11
C1orf127	LELP1	PDLIM3	BTBD17
C1orf145	LGALS1	PECR	BTBD18
C1orf147	LGI1	PGAM1	BTBD19
C1orf167	LGI3	PGK2	BTBD3
C1orf168	LHFPL2	PIGX	BTBD6
C1orf170	LHX8	PIK3C3	BTBD9
C1orf172	LHX9	PILRB	BTG3
C1orf180	LILRB1	PIM1	BTN2A2
C1orf186	LILRB4	PITX2	BUB1B
C1orf194	LINTA	PKNOX2	BUD31
C1orf195	LINC00346	PLA2G7	BVES
C1orf21	LXIL	PLAC8	C10orf10
C1orf210	LMBR1	PLCD3	C10orf107
C1orf213	LMBR1L	PLEKH13	C10orf32
C1orf228	LMNL	PLEKH11	C10orf32-ASMT
C1orf229	LMOD3	PLEKHM3	C10orf35
C1orf56	LOXHD1	PLGRKT	C10orf67
C1orf63	LRAT	PLSCR2	C10orf71

C1orf74	LRBA	PMFBP1	C10orf95
C1orf86	LRCH1	PMS1	C11orf1
C1QTNF1-AS1	LRRC17	PNMAL2	C11orf35
C1QTNF6	LRRC32	PPAN	C11orf52
C1QTNF9	LRRJQ3	PPAN-P2RY11	C11orf54
C1R	LRRN4	PPME1	C11orf65
C1S	LRRTM4	PPP1CA	C11orf80
C2	LSM4	PPP5D1	C11orf82
C20orf112	LTB4R	PRDM9	C11orf91
C20orf166	LYL1	PRED62	C11orf94
C20orf85	LYRM4	PRF1	C11orf96
C21orf2	MIAP	PRKACG	C12orf23
C21orf58	MAB21L1	PRKCQ	C12orf4
C21orf67	MAB21L2	PRPF40A	C12orf45
C22orf26	MAP1S	PRPSA2	C12orf49
C22orf31	MAP2	PRR11	C12orf57
C22orf42	MAP3K10	PRR13	C12orf60
C2CD2	MAP3K7CL	PRR9	C12orf61
C2CD3	MAP4K2	PRSS12	C12orf71
C2orf50	MAP4K4	PRSS46	C13orf45
C2orf54	MAPK3	PRSS57	C14orf164
C2orf62	MAPKBP1	PSMB8	C14orf166
C2orf70	42795	PSMB9	C14orf180
C2orf82	42796	PTGER4	C14orf2
C3orf14	42795	PTMA	C15orf38
C3orf27	MARCO	PTPA2	C15orf38-AP3S2
C3orf49	MARK3	PTPN6	C15orf39
C3orf83	MAS1L	PTPN7	C15orf41
C4A	MASP1	PTPRCAP	C15orf52
C4B	MBD4	PTPRG	C15orf61
C4BPB	MCIDAS	PVRIG	C16orf11
C4orf19	MCOLN3	PYGL	C16orf45
C4orf36	MDGA2	RAB27B	C16orf47
C4orf47	MEAI	RAB3C	C16orf62
C4orf51	MED6	RAB3GAP1	C16orf74
C5	MEF2C	RAB8B	C16orf86
C5orf20	MEF2D	RAC2	C16orf89
C5orf22	MEGF10	RAD1	C16orf91
C5orf49	MEST	RAG2	C16orf95
C6orf15	MFIH1A5	RARRES3	C17orf61-PLSCR3
C6orf164	MGAT4A	RASSF1	C17orf67
C6orf229	MGST3	RBM27	C17orf72
C6orf25	MICALCL	RBM38	C17orf99
C6orf48	MIR3654	RBPI	C18orf42
C6orf99	MKL2	RCAN2	C18orf8
C7orf43	MKX	RCAN3	C19orf10
C8G	MLH3	RCSD1	C19orf24
C8orf59	MME	REEP5	C19orf33
C8orf74	MMP1	RFX3	C19orf40
C8orf86	MMRN1	RGCC	C19orf45
C9orf117	MNX1	RGL3	C19orf47
C9orf139	MPP4	RGL4	C19orf53
C9orf142	MPP7	RHBDD1	C19orf55
C9orf147	MPPED1	RHOA	C19orf57
C9orf152	MPPED2	RHOBTB1	C19orf67
C9orf169	MRGPRF	RNASE13	C19orf77
C9orf173	MRGPRX1	RNF113B	C19orf81
C9orf3	MS4A14	RNF125	C1D
C9orf64	MS4A18	RNF126	C1orf105
C9orf69	MS4A3	RNF133	C1orf106
C9orf92	MS4A4A	RNF148	C1orf115
C9orf96	MS4A7	RNF166	C1orf122
CA11	MSANTD2	RNF167	C1orf131
CA12	MSI1	RNF44	C1orf141
CA14	MSR1	RP1	C1orf147
CA4	MSRB3	RP11-108K14.8	C1orf167
CA9	MT1HL1	RP11-116D17.1	C1orf170
CAB39	MTSS1	RP11-187E13.1	C1orf172
CABIN1	MTURN	RP11-210M15.2	C1orf180
CABLES1	MTUS2	RP11-51F16.8	C1orf189
CABLES2	MVB12A	RP11-738G5.2	C1orf198
CACHD1	MYH14	RP11-849H4.2	C1orf213
CACNA1A	MYLK	RP11-998D10.1	C1orf220
CACNA1H	MYO16	RP3-468K18.5	C1ORF220
CACNA2D2	MYO1B	RP4-583P15.14	C1orf222
CACNB1	MYO1C	RPL13A	C1orf229
CACNB2	MYO3A	RPL22L1	C1orf233
CACUL1	MYO5B	RPL34	C1orf43
CALD1	MYOC	RPL35A	C1orf51
CALML3	MYOT	RPL4	C1orf52
CALML5	MYZAP	RPS11	C1orf54
CALML6	N4BP2L1	RPS18	C1orf61
CAMK2A	NAALAD2	RPS2	C1orf63
CAMKK1	NAT8	RPS3A	C1orf65
CAMP	NBEA	RPS6KB2	C1orf74
CAMSAPI	NCL	RTN4R	C1orf85
CAMTA1	NDUFS2	RVR2	C1orf86
CANT1	NEB	S100Z	C1orf94
CAP1	NEBL	SIPR1	C1QL3
CAPG	NECAB1	SAMM50	C1QTNF1
CAPN1	NEIL2	SAMSN1	C1QTNF1-AS1
CAPN11	NETO1	SAYSDF	C1QTNF6
CAPN12	NEU3	SCLY	C1QTNF7
CAPN2	NFASC	SCN11A	C1QTNF8
CAPN9	NFATC1	SCO1	C1QTNF9
CAPNS2	NFYC	SCRN1	C1QTNF9B
CAPRIN1	NGF	SCT	C1R
CAPS	NHSL1	SCTR	C20orf166
CAPZB	NID1	SEC16B	C20orf194
CARD10	NID2	SEL1L	C20orf201
CARD14	NINJ2	SELL	C21orf2
CARD6	NIPAL2	SELPLG	C21orf37
CARNS1	NTT2	SEMA3D	C21orf58
CARS2	NKD1	SEMA6D	C22orf23
CASD1	NKX1-2	SERPINA12	C22orf24
CASP7	NKX2-1	SETD6	C22orf26
CASQ1	NKX2-8	SH2B3	C2CD2
CATSPERG	NKX3-1	SH2D1B	C2CD2L
CAV2	NLR4	SH2D2A	C2CD3
CBFA2T2	NLRP3	SH3RF3	C2orf27A
CBFA2T3	NMRK1	SHCBP1L	C2orf40
CBLC	NMT2	SKLEC10	C2orf42
CBS	NMU	SIRPG	C2orf44
CBX7	NOL9	SIX1	C2orf50
CC2D2A	NOTCH1	SLAMF1	C2orf54
CCBL1	NPDC1	SLAMF7	C2orf62
CCBL2	NPPC	SLBP	C2orf71
CCDC104	NR1H3	SLC15A4	C2orf73

CCDC114	NR2F1	SLC1A1	C2orf81
CCDC12	NR3C1	SLC25A27	C2orf88
CCDC138	NR4A2	SLC25A44	C3orf20
CCDC14	NR4A3	SLC26A7	C3orf52
CCDC146	NRROS	SLC30A10	C3orf55
CCDC149	NRSN1	SLC44A1	C3orf58
CCDC154	NRXN1	SLC5A4	C3orf62
CCDC155	NTSDC4	SLC5A9	C3orf83
CCDC159	NTRK2	SLC6A1	C4BPA
CCDC175	NUB1	SLC6A2	C4orf51
CCDC180	NUBPL	SLC8A3	C5
CCDC183	NUDT1	SLC9A3	C5AR1
CCDC19	NUMB	SLC06A1	C5AR2
CCDC24	NUTM2B	SMARCA1	C5orf22
CCDC28B	NUTM2D	SMCO2	C5orf38
CCDC30	NXPH2	SMIM21	C5orf45
CCDC33	NXPH4	SMOC1	C5orf49
CCDC37	ODF2	SNX11	C6orf15
CCDC38	OFCC1	SNX20	C7orf49
CCDC57	OLFML1	SOBP	C7orf50
CCDC58	OLFML2A	SORCS2	C7orf61
CCDC60	ONECUT1	SP5	C8G
CCDC78	OPALIN	SPAM1	C8orf12
CCDC81	OPRK1	SPATA31D1	C8orf22
CCDC85C	OR11G2	SPEF2	C8orf31
CCDC88B	OR1G1	SPINT4	C8orf4
CCDC88C	OR1N2	SPN	C8orf46
CCDC92	OR2V1	SPP1	C8orf58
CCDC93	OR52I2	SRGN	C8orf88
CCDC96	OR9Q1	ST8S1A4	C9orf116
CCDC97	OSBPL10	STAB2	C9orf142
CCL1	OSM	STAC	C9orf147
CCL15	OSR1	STAMBP	C9orf156
CCL15-CCL14	OTX1	STAT5A	C9orf169
CCL22	PACRGL	STK17A	C9orf172
CCNB1IP1	PAD14	STK17B	C9orf3
CCND1	PAFAH1B2	STK4	C9orf47
CCND2	PAH	STT3B	C9orf66
CCNF	PALB1	SUB1	C9orf9
CCNG1	PALM	SUCLG2	C9orf96
CCN2	PALM2	SULT1A4	CA10
CCNJL	PAPPA2	SUN2	CA11
CCNY	PAPSS2	SUSD3	CA14
CCPG1	PARD3	SV2B	CA7
CCR10	PATL2	SYK	CA9
CCR3	PAX1	TAB2	CABLES1
CCS	PAX3	TAGAP	CABP1
CCT4	PAX6	TAP1	CACFD1
CCT7	PAX9	TAPBP1	CACNA1A
CCZ1	PCDH7	TAS2R16	CACNA1B
CCZ1B	PDLIM7	TAS2R40	CACNA1H
CD151	PDZRN3	TBATA	CACNB1
CD164L2	PEX11G	TBC1D10C	CACNB2
CD19	PGM1	TBC1D12	CACNG5
CD22	PGPEP1L	TBC1D9	CACUL1
CD2BP2	PIGX	TBPL2	CALB2
CD300LF	PIK3CG	TBX2	CALCA
CD300LG	PIK3R6	TCF7	CALCOCO1
CD55	PITPNA	TCF7L1	CALCOCO2
CD6	PITPNM2	TECTA	CALHM2
CD63	PITX1	TEK15	CALM2
CD82	PITX2	TENM4	CALM3
CD9	PKD2L2	TEX19	CALML4
CDAN1	PKHD1L1	TEX33	CALR
CDI23	PKN1	TFDP1	CALY
CDG42	PLAUR	TFPI2	CAMK1
CDG42BPA	PLCB1	TGFB1	CAMK1D
CDG42BPB	PLCD3	TGOLN2	CAMK1G
CDG42SE1	PLEKHG4B	THSD7A	CAMK2B
CDCA2	PLEKHJ1	THSD7B	CAMK2G
CDCA7L	PLEKHO1	TIFA	CAMKK1
CDCP2	PLEKHO2	TIPIN	CAMKK2
CDH26	PLIN5	TLK1	CAMKV
CDH3	PLVAP	TLL1	CAMSAP2
CDHR2	PLXDC1	TMEFF2	CAMSAP3
CDHR3	PLXND1	TMEM129	CAMTA1
CDK12	PM20D1	TMEM144	CAMTA2
CDK17	PNKD	TMEM229A	CAPN1
CDK18	PON2	TMEM232	CAPN2
CDK3	PPA2	TMEM66	CAPN9
CDK5	PPAP2A	TMIGD2	CAPS
CDK5RAP1	PPARG	TMPO	CAPZB
CDK5RAP2	PPCDC	TMPRSS2	CARD6
CDKAL1	PPEF2	TNF	CARHSP1
CDKN1A	PPFIBP1	TNFAIP8L2	CARM1
CDKN3	PPIL6	TNFRSF21	CARS
CDR2	PPP1R13L	TNFRSF25	CARTPT
CDRT1	PPP1R14A	TNFRSF4	CASC1
CDT1	PPP1R16B	TNFRSF9	CASC4
CDX1	PPP1R1A	TNFSF13B	CASKIN2
CDYL	PPP2R2B	TNFSF14	CASP4
CEACAM6	PPP2R4	TNFSF4	CASP6
CECR1	PPP4R2	TNNI1	CASP7
CECR5	PRDM1	TNRC6B	CASR
CEL	PRDM14	TOX3	CAST
CELA3A	PRDM8	TRABD	CATSPERG
CELA3B	PRED57	TRABD2A	CAV2
CELF1	PRED58	TRAF3IP3	CBFA2T2
CELF6	PRICKLE1	TRAF5	CBLB
CELSR1	PRKAR1B	TRAT1	CBLC
CELSR2	PRKD1	TREML2	CBLN1
CENPJ	PRMT1	TRIM10	CBLN2
CENPM	PRODH2	TRIM41	CBLN3
CENPP	PROK1	TRIML2	CBS
CEP104	PROK2	TRNT1	CBX7
CEP112	PROX1	TROVE2	CBX8
CEP152	PRPF40B	TSHZ1	CC2D1B
CEP170B	PRR14L	TSLP	CC2D2A
CEP250	PRSS16	TSSK1B	CCBL1
CEP68	PRSS3	TSSK4	CCDC102B
CEP85	PRX	TXLNB	CCDC105
CEP85L	PSD4	TXNDC8	CCDC106
CEP95	PSG1	TXNDR3	CCDC12
CEPT1	PSG4	UBASH3A	CCDC122
CERK	PSMB8	UBE2F	CCDC125
CERS1	PSMB9	UBE2H	CCDC126
CERS2	PTCH2	UBE2U	CCDC135
CERS4	PTDSS1	UBIAD1	CCDC136

CES3	PTGIR	UBQLN4	CCDC138
CES4A	PTPRB	UCHL1	CCDC14
CFB	PTPRD	UCP2	CCDC142
CFTR	PTPRH	UCP3	CCDC146
CGB1	PTPRQ	UGGT2	CCDC150
CGB5	PVRL3	UGT1A3	CCDC154
CGB8	PYURF	UGT1A5	CCDC155
CGNL1	QKI	ULK3	CCDC157
CHAD	RAB27B	UNC80	CCDC159
CHADL	RABL6	UNC93A	CCDC163P
CHCHD6	RALB	USP20	CCDC166
CHD2	RALYL	VAMP1	CCDC17
CHD3	RAMP3	VHL	CCDC181
CHD6	RANBP3	VPS16	CCDC183
CHEK2	RAPGEF2	VPS45	CCDC19
CHB1L1	RAPGEF4	VPS52	CCDC28B
CHB1L2	RASGEF1C	VPS54	CCDC36
CHID1	RASL12	VWF	CCDC41
CHIT1	RASSF2	WASF3	CCDC42B
CHKA	RASSF8	WBP2NL	CCDC64
CHMP1A	RAX	WDFY2	CCDC68
CHP1	RBM17	WDR70	CCDC78
CHRD12	RBMS2	WDR83	CCDC8
CHRM1	BBP4	WFDC1	CCDC80
CHRNA1	RCAN2	WFDC9	CCDC81
CHRNA10	RCBTB2	WIBG	CCDC85C
CHRNA2	RCSN1	WNT5A	CCDC89
CHRNA6	RDH13	XCL2	CCDC9
CHRNA9	RELL1	YWHAZ	CCDC92
CHST1	RERG	ZBTB25	CCDC93
CHST10	RFTN2	ZC3H12A	CCDC96
CHST5	RGCC	ZC3HAV1	CCER2
CHSY1	RLG3	ZFAT	CCL14
CHTF18	RGLS1	ZFPM2	CCL15
CIB2	RHOG	ZNF215	CCL15-CCL14
CIC	RHOJ	ZNF276	CCL23
CITTA	RTT2	ZNF334	CCM2L
CIRBP	RNF144A	ZNF407	CCNMB1P1
CTT	RNF166	ZNF462	CCND1
CKAP5	RNF207	ZNF691	CCND2
CKB	RNL5	ZNF704	CCNDBP1
CKMT2	ROBO2	ZNF784	CCNL2
CLASP1	ROBO3	ZNF788	CCNO
CLASRP	ROBO4	ZNF846	CCNT1
CLCNKA	RP11-101E3.5	ZP1	CCNYL1
CLCNKB	RP11-108SN6.3	ZSWIM5	CCPG1
CLDN11	RP11-1220K2.2		CCR10
CLDN18	RP11-366L20.2		CCR3
CLDN19	RP11-6L6.2		CCRL2
CLDN22	RP11-94B19.4		CCSAP
CLDN25	RPL22		CCT7
CLDN4	RREB1		CCT8
CLDN6	RSAD2		CCZ1B
CLDN7	RSPH6A		CD151
CLDN8	RTN1		CD1D
CLDN9	RTN4		CD248
CLEC16A	RUFY4		CD2BP2
CLEC1A	RUNX1T1		CD300LF
CLEC2A	RXRG		CD302
CLEC2B	S1PR1		CD320
CLEC4G	SALL2		CD40
CLGN	SAMM50		CD55
CLH1C1	SBSPOH		CD59
CLIC3	SCAND3		CD63
CLIC5	SCARB2		CD68
CLIP1	SCHIP1		CD9
CLIP4	SCIN		CDAN1
CLK3	SCN1B		CDI123
CLK4	SCTR		CDI25C
CLMN	SDCCAG8		CDI34
CLN6	SDK1		CDI42EP2
CLNK	SEC63		CDI42EP4
CLPTMIL	SEL1L2		CDI42EP5
CLRN2	SEMA6D		CDI42SE1
CLSTN1	42993		CDI42
CLTC	42983		CDI47L
CLTCL1	SERPINB2		CDI4P1
CLUAP1	SETD7		CDI4P2
CLVS1	SFTPC		CDI41
CLYBL	SH2B3		CDI415
CMBL	SH2D2A		CDI422
CMIP	SH3BP5		CDI423
CMKLR1	SH3PXD2B		CDI426
CMTM3	SHANK3		CDI43
CMTR1	SHE		CDI45
CNDP2	SHH		CDI49
CNGB1	SHISA2		CDI4R1
CNKSRI	SHISA6		CDI4R3
CNKSRI3	SHIAE		CDI4R4
CNN2	SIDT1		CDI410
CNN3	SKGLEC9		CDI411B
CNNM4	SIRPB2		CDI412
CNOT7	SIRT2		CDI415
CNP	SIX1		CDI418
CNPY4	SIX2		CDI42AP1
CNRIP1	SIX3		CDI45
CNTD1	SIX6		CDI45RAP2
CNTD2	SLAMF1		CDI48
CNTN4	SLC10A4		CDI4L1
CNTN6	SLC15A1		CDI4N2A
COA1	SLC15A4		CDI4N2C
COA5	SLC16A1		CDNF
COG1	SLC16A10		CDRT1
COG7	SLC19A2		CDRT4
COL17A1	SLC1A1		CDSN
COL18A1	SLC1A2		CDYL
COL20A1	SLC22A16		CEACAM6
COL23A1	SLC22A2		CEBPA
COL7A1	SLC24A1		CECR5
COL9A2	SLC24A5		CELF1
COL9A3	SLC25A13		CELF3
COLCA1	SLC25A25		CELF4
COLCA2	SLC26A4		CELF5
COMMD9	SLC2A3		CEND1
COMT	SLC30A8		CENPB
COPB2	SLC35G1		CENPK
COP56	SLC38A1		CENPP
COP57B	SLC38A4		CEP104

COPZ1	SLC4A10	CEP152
COQ2	SLC52A3	CEP164
COQ4	SLC5A1	CEP170B
CORIN	SLC6A1	CEP55
CORO1C	SLC6A2	CEP68
CORO2A	SLC8A2	CEP70
CORO6	SLIT2	CEP76
CORO7	SMAD6	CEP95
COTL1	SMARCD2	CEPT1
COX19	SMOX	CERS2
COX20	SMYD3	CERS3
COX6A2	SNAI1	CERS4
CP	SNCG	CERS5
CPA5	SNRK	CES2
CPM	SNX10	CES4A
CPN1	SNX11	CFB
CPNE1	SNX20	CFDP1
CPNE3	SNX4	CFI
CPNE5	SNX6	CFL1
CPNE7	SNX8	CFTR
CPQ	SOBP	COB2
CPSF3L	SOCS2	CGNL1
CPSF4L	SOCS6	CH17-132F21.1
CPT1A	SOX18	CHAF1A
CPT1C	SOX6	CHAT
CPVL	SP140L	CHCHD3
CPXM2	SPA17	CHCHD4
CRABP1	SPAG17	CHD1L
CRADD	SPARC	CHD2
CRAMP1L	SPATA13	CHD3
CREBZF	SPATA18	CHD5
CRELD1	SPECC1	CHD9
CRELD2	SPEG	CHEK2
CREM	SPG7	CHFR
CRHBP	SPICE1	CHIA
CRHR2	SPINK4	CHIC2
CRIM1	SPIRE1	CHID1
CRIP1	SPIRE2	CHKA
CRLS1	SPPL2A	CHKBC-CPT1B
CRNKL1	SPTSSB	CHL1
CROCC	SRGAP1	CHML
CROT	SRGN	CHMP1A
CRTC1	SSBP3	CHMP2A
CRY2	ST18	CHMP3
CRYBA4	ST20	CHN1
CRYBB1	ST3GAL1	CHP1
CRYM	ST8SIA1	CHPT1
CSF1	STAMBPL1	CHRD12
CSF2	STARD13	CHRNA4
CSGALNACT1	STARD3	CHRNB4
CSNK1A1	STAT1	CHRNA4
CSNK1D	STC2	CHRNA4
CSNK2A2	STK10	CHRNA4
CSRNP1	STK32B	CHRNA4
CSRNP2	STK4	CHRNA4
CSTA	STON1-GTF2A1L	CHRNA4
CT62	STRN4	CHRNA4
CTB-102L5.4	STYK1	CHRNA4
CTB-96E2.2	SUB1	CHRNA4
CTBP2	SUCLG2	CHRNA4
CTBS	SULT1C4	CHRNA4
CTC-432M15.3	SVEP1	CHRNA4
CTC-487M23.8	SVOP	CHRNA4
CTCF	SYK	CHRNA4
CTD-2207O23.3	SYNDIG1	CHRNA4
CTD-2267D19.3	T	CHRNA4
CTD-2330K9.3	TACC1	CHRNA4
CTD-2410N18.5	TAOK2	CHRNA4
CTD-2545M3.6	TAP1	CHRNA4
CTD-2583A14.10	TBC1D24	CHRNA4
CTD-2600O9.1	TBC1D4	CHRNA4
CTD-3203P2.2	TBR1	CHRNA4
CTD-3214H19.16	TBX15	CHRNA4
CTDSPL	TBX2	CHRNA4
CTF1	TBXA2R	CHRNA4
CTHRC1	TCF12	CHRNA4
CTNNA1	TCF15	CHRNA4
CTNNA2	TCF21	CHRNA4
CTNNBIP1	TCL1A	CHRNA4
CTNNBL1	TEK	CHRNA4
CTR2	TENM4	CHRNA4
CTSB	TERT	CHRNA4
CTSD	TESPA1	CHRNA4
CTSE	TEX26	CHRNA4
CTSS	TEX33	CHRNA4
CTSW	TF	CHRNA4
CTXN3	TFAP2A	CHRNA4
CUBN	TFAP2B	CHRNA4
CUEDC1	TECP2L1	CHRNA4
CUL3	THBS2	CHRNA4
CUL9	THBS4	CHRNA4
CUX1	TLE1	CHRNA4
CUZD1	TMC3	CHRNA4
CX3CL1	TMCC3	CHRNA4
CXCL1	TMEM100	CHRNA4
CXCL16	TMEM121	CHRNA4
CXCL17	TMEM130	CHRNA4
CXXC5	TMEM140	CHRNA4
CYB561	TMEM145	CHRNA4
CYB5A	TMEM200C	CHRNA4
CYB5R1	TMEM204	CHRNA4
CYB5R2	TMEM219	CHRNA4
CYB5R3	TMEM38B	CHRNA4
CYFIP1	TMEM39B	CHRNA4
CYFIP2	TMEM59L	CHRNA4
CYHR1	TMEM88	CHRNA4
CYP1B1	TMPPRSS2	CHRNA4
CYP24A1	TMX3	CHRNA4
CYP27A1	TNFAIP8L3	CHRNA4
CYP2F1	TNFRSF1B	CHRNA4
CYP2R1	TNFSF4	CHRNA4
CYP2S1	TNP3	CHRNA4
CYP2W1	TNR	CHRNA4
CYP3A5	TNRC6C	CHRNA4
CYP4B1	TOX3	CHRNA4
CYP4F12	TRAF3IP3	CHRNA4
CYP4F3	TRAP	CHRNA4
CYP7B1	TRAK2	CHRNA4

CYP8B1	TRAPPC3L	CNEPIR1
CYR61	TRDMT1	CNGB1
CYTH1	TRIM25	CNIH2
D2HGDH	TRIM36	CNKSR3
DAAM1	TRIML1	CNN1
DAB2	TSFM	CNN3
DACT1	TSPEAR	CNNM1
DAG1	TTC22	CNNM2
DAGLB	TTC38	CNNM4
DALRD3	TTC6	CNOT10
DAP	TTL10	CNOT7
DAP3	TTYH3	CNP
DAPK1	TUSC3	CNRIP1
DAPP1	TUT1	CNTN1
DAW1	TYK2	CNTN2
DAZAP1	UBE2G1	CNTN6
DBNL	UNC5C	CNTNAP1
DCBLD2	USP19	CNTR0B
DCDC2B	USP41	COA5
DCHS1	USP44	COASY
DCLK2	UTP11L	COG7
DCLRE1C	UTRN	COL11A1
DCN	UTS2B	COL11A2
DCST1	VASH1	COL17A1
DCST2	VAT1	COL18A1
DCTN1	VIM	COL20A1
DCTN3	VPS45	COL5A1
DCUN1D2	WARS2	COL6A1
DCUN1D3	WASF3	COL6A2
DCUN1D4	WBP11	COL6A3
DDAH2	WDR1	COL8A2
DDBI	WDR7	COL9A2
DDC	WDR72	COL9A3
DDHD2	WDFC10B	COLCA2
DDI2	WNK4	COLGALT1
DDR1	WNT5A	COLO
DDT	WNT7A	COMMD4
DDX11	WNT7B	COMT
DDX31	WRNIP1	COP55
DDX42	XAF1	COP56
DDX46	XPOT	COP57B
DDX5	YWHAE	COP58
DEAF1	ZAP70	COQ2
DEF6	ZAR1	COQ5
DEF44	ZBTB16	CORO1C
DEFB134	ZBTB18	CORO2A
DEGS2	ZBTB20	CORO7-PAM16
DENND1A	ZBTB37	COX11
DENND1B	ZC3H11A	COX15
DENND1C	ZCCHC4	COX20
DENND2C	ZFHX3	COX4I2
DENND2D	ZFHX4	COX6A2
DENND3	ZFPM2	COX7A1
DENND5A	ZMAT4	COX7A2
DEPDC4	ZNF22	COX7A2L
DERA	ZNF277	CPA1
DERL3	ZNF334	CPA6
DFNB31	ZNF366	CPD
DGAT1	ZNF385B	CPEB1
DGAT2	ZNF512B	CPEB4
DGCR6	ZNF596	CPX1
DGKA	ZNF655	CPN1
DGUOK	ZNF71	CPNE3
DHCR24	ZNF710	CPNE5
DHODH	ZP2	CPNE6
DHRS12	ZRANB1	CPNE9
DHRS3		CPSF2
DHX32		CPSF4L
DHX35		CPT1A
DHX57		CPT1B
DIDO1		CPT1C
DIO1		CPT2
DIP2B		CPXM2
DIP2C		CR1L
DIRC3		CRABP1
DIS3L2		CRADD
DISC1		CRAMP1L
DIXDC1		CRB1
DKFZP434E1119		CRB2
DKFZP434O1614		CRB3
DKFZP761J1410		CREB3L1
DKK4		CREB3L4
DLEC1		CREBBP
DLG5		CREBZF
DLGAP4		CREG1
DLK2		CRH
DLST		CRHR1
DMAP1		CRIM1
DMC1		CRIP1
DMPK		CRISP2
DMXL1		CROCC
DNA2		CROT
DNAAF1		CRTAM
DNAH1		CRTAP
DNAH10		CRTC1
DNAH100S		CRX
DNAH11		CRY2
DNAH17		CRYBA4
DNAH17-AS1		CRYBB1
DNAH3		CRYGS
DNAH5		CRYZ
DNAH6		CRYZL1
DNAH7		CS
DNAH8		CSAD
DNAJA4		CSDC2
DNAJB1		CSF1
DNAJB12		CSF3
DNAJB13		CSF3R
DNAJB2		CSHL1
DNAJB5		CSNK1A1
DNAJC16		CSNK1D
DNAJC17		CSNK1E
DNAJC18		CSNK2A1
DNAJC5B		CSNK2A2
DNAJC7		CSNK2B-LY6G5B-1181
DNALI1		CSPG4
DNASE1		CSPG5
DNASE1L2		CSRNP1

DNMBP	CSRPI
DNMT1	CSTA
DNTTIP2	CSTF2T
DOC2B	CSTF3
DOCK2	CTAGES
DOCK4	CTB-50L17.14
DOCK7	CTB-96E2.2
DOCK8	CTBP2
DOK7	CTC-241N9.1
DOPEY2	CTC-260F20.3
DPCD	CTC-432M15.3
DPEP1	CTC-479C5.12
DPF1	CTC-487M23.8
DPF3	CTC-490E21.12
DPM2	CTCFL
DPP6	CTD-2132N18.3
DPP9	CTD-2144E22.5
DPY19L1	CTD-2162K18.4
DPY19L3	CTD-2192J16.22
DPYSL3	CTD-2207O23.10
DRAM1	CTD-2207O23.3
DRAM2	CTD-2228K2.5
DRC1	CTD-2330K9.3
DSCR3	CTD-2349B8.1
DSG4	CTD-2368P22.1
DSP	CTD-2545M3.6
DTNB	CTD-2583A14.10
DTX2	CTD-2587H24.4
DTX4	CTD-2600O9.1
DUOX1	CTD-3088G3.8
DUOXA1	CTD-3222D19.2
DUSP10	CTDSP1
DUSP13	CTDSP2
DUSP14	CTDSPL
DUSP15	CTDSPL2
DUSP2	CTF1
DUSP6	CTGF
DUSP7	CTHRC1
DUSP8	CTNNAL1
DUT	CTNNB1
DYM	CTNNBIP1
DYNCL1L2	CTNNBL1
DYNLT1	CTPS1
DYTN	CTRB1
DZIP1L	CTRL
E2F1	CTSA
E2F6	CTSB
E2F8	CTSK
E4F1	CTSS
EARS2	CTSZ
EBF1	CTTNBP2NL
EBNA1BP2	CTU1
ECE1	CTXN1
ECHDC1	CTXN2
ECT2L	CUBN
EDAR	CUL3
EDC4	CUL9
EDIL3	CUX1
EDN1	CUX2
EDN2	CWH43
EDRF1	CX3CL1
EED	CXCL1
EEFSEC	CXCL13
EFCAB1	CXCL17
EFCAB10	CXCR1
EFCAB2	CXCR4
EFCAB5	CXCC5
EFCAB6	CYB561
EFHB	CYB5A
EFNA1	CYB5D1
EFNA3	CYB5R1
EFNA4	CYB5R3
EFNB3	CYGB
EFR3B	CYHR1
EFTUD2	CYP1A1
EGFR	CYP27A1
EGLN2	CYP27B1
EGR1	CYP2E1
EGR2	CYP2R1
EHBP1	CYP2W1
EHBP1L1	CYP3A5
EHF	CYP4F11
EHMT2	CYP4F2
EIF1	CYP4F22
EIF2AK3	CYP51A1
EIF2AK4	CYR61
EIF3B	CYSTM1
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EIF3G	DAAM1
EIF3K	DACT1
EIF3L	DACT3
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EIF4E2	DAO
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EIF4G2	DAPK2
EIF4G3	DAPK3
EIF5B	DAXX
ELAC2	DAZAP1
ELF3	DBNDD2
ELF5	DBP
ELFN2	DBX1
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ELL2	DCAKD
ELL3	DCHS1
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ELMOD1	DCN
ELN	DCP1B
ELP2	DCPS
EMC8	DCTN1
EMG1	DCTN2
EML2	DCTN3
EML3	DCUN1D2
EML4	DCUN1D3
EML6	DCUN1D4
EMP1	DDAH2
EMP3	DDC
ENAH	DDIT3
ENC1	DDR1

ENO1	DDT
ENPP2	DDX11
ENPP3	DDX17
ENTPD3	DDX31
ENTPD6	DDX39B
ENTPD8	DDX47
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EPB41L4A	DEFB132
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EPCAM	DENND2A
EPHA2	DENND2C
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EPHB3	DENND4C
EPHX2	DENND6A
EPM2A	DEPDC1B
EPN2	DEPDC4
EPN3	DERA
EPS8	DES12
ERAP1	DFFB
ERBB2	DFNB31
ERBB2IP	DGAT1
ERBB3	DGKG
ERC1	DGKQ
ERCC4	DHCR24
ER12	DHH
ERMAP	DHODH
ERMARD	DHRS13
ERMN	DHRS3
ERN1	DHRS4L2
ERRFI1	DHRS7B
ERVW-1	DHRS9
ESM1	DHX16
ESR1	DHX57
ESKP1	DIAPH1
ESKP2	DICER1
ESYT3	DIDO1
ETFA	DIO1
ETHE1	DIO2
ETNK2	DIO3
ETS2	DIP2C
ETV4	DIRAS1
ETV6	DISC1
EVA1A	DISP1
EVA1B	DIXDC1
EVA1C	DKFZP434A062
EVISL	DKFZP434H0512
EVPL	DKFZP761J1410
EVPLL	DLEU7
EWSR1	DLG1
EXOC3	DLG4
EXOC3L2	DLG5
EXOC3L4	DLGAP2
EXOC7	DLGAP4
EXOSC1	DLK1
EXOSC10	DLK2
EXPH5	DLL4
EYA1	DLST
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F7	DNAAF1
FA2H	DNAAF3
FAAH	DNAH1
FABP6	DNAH12
FADS2	DNAH2
FADS3	DNAH3
FAF1	DNAJB11
FAF2	DNAJB13
FAM101A	DNAJB5
FAM105B	DNAJB6
FAM107B	DNAJC14
FAM110A	DNAJC18
FAM117A	DNAJC21
FAM120A	DNAJC4
FAM120B	DNAJCSB
FAM129A	DNALI1
FAM131A	DNASE1L2
FAM131C	DND1
FAM134B	DNER
FAM134C	DNHD1
FAM13C	DNLZ
FAM154A	DNM3
FAM160A1	DNMBP
FAM160B2	DNMT3A
FAM163B	DNMT3B
FAM166A	DNMT3L
FAM166B	DNPEP
FAM167A	DOCK2A
FAM171A2	DOCK7
FAM174B	DOCK9
FAM177B	DOK1
FAM178B	DOK4
FAM180A	DOK7
FAM181A	DOPEY1
FAM183A	DOPEY2
FAM188A	DPAGT1
FAM189A2	DPCD
FAM192A	DPEP1
FAM193A	DPH1
FAM193B	DPH3
FAM194A	DPH6
FAM195B	DPM2
FAM19A5	DPP4
FAM200A	DPP7
FAM208B	DPP8
FAM20A	DPP9
FAM210B	DPY19L1
FAM211B	DPY19L3
FAM213A	DPYSL2
FAM214A	DRAM1
FAM219A	DRAM2
FAM222A	DRC1
FAM228A	DRD3
FAM229A	DROSHA
FAM26D	DSCAML1
FAM3B	DSN1
FAM3D	DTNB
FAM49B	DTNBP1

FAM53A	DTWD2
FAM53B	DTX3
FAM57A	DTX4
FAM65C	DUOXA1
FAM69A	DUS1L
FAM71F1	DUSP13
FAM76B	DUSP14
FAM81A	DUSP15
FAM83A	DUSP16
FAM83B	DUSP4
FAM83E	DUSP5
FAM83G	DUSP6
FAM92A1	DUSP8
FAM92B	DVL1
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FANCD2	DYNC1H1
FARP1	DYNC1L2
FARP2	DYNLL1
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FASTK	E2F1
FASTKD5	E2F4
FAT3	E2F8
FAXC	E4F1
FAXDC2	EAPP
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FBLIM1	EBI3
FBLN1	ECD
FBLN5	ECE2
FBLN7	ECHDC1
FBN3	ECHDC2
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FBXL18	ECM2
FBXL22	ECT2L
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FBXO24	EDEM3
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FBXO34	EDNRB
FBXO39	EEF1A2
FBXO40	EEF1G
FBXO42	EEF2K
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FBXO47	EFCAB12
FBXO48	EFCAB14
FBXO9	EFCAB4A
FBXW11	EFCAB4B
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FBXW4	EFCC1
FBXW5	EFEMP2
FBXW7	EFHB
FCGRT	EFNA1
FCHO1	EFNA5
FCHSD1	EFNB3
FCRLB	EFS
FDFT1	EFTUD2
FDXACB1	EGFR
FECH	EGLN2
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FEZ1	EGR2
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FGD5	EHD2
FGD6	EHD3
FGF1	EHF
FGF22	EHMT1
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GFGR3	EIF2B5
GGGY	EIF3G
FHIT	EIF3H
FHL2	EIF3K
FHOD1	EIF3L
FHOD3	EIF4B
FKBP4	EIF4E1B
FLJ1	EIF4G1
FLJ1	EIF4G3
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FLJ00418	ELANE
FLNB	ELAVL2
FLNC	ELF3
FLT1	ELF5
FLT4	ELFN2
FLVCR2	ELK3
FLYWCH1	ELL2
FMNL1	ELL3
FMNL2	ELMO2
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FMOD	ELMOD2
FN1	ELOVL6
FNDC1	ELP6
FNIP1	EMC1
FNIP2	EMC3
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FOLH1	EMILIN1
FOLR1	EML2
FOSL2	EML3
FOXJ1	EML6
FOXJ2	EMP1
FOXN1	EMR2
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FOXP2	ENKD1
FOXP4	ENO1
FOXS1	ENO2
PGS	ENOSF1
FRAT2	ENPP5
FRK	ENTHD1
FRMD5	ENTPD2
FRMD6	ENTPD3
FRMPD2	ENTPD7
FRY	EOGT
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FSCN2	EPAS1
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FSD2	EPB41L2

FSIP1	EPB41L5
FTCD	EPC1
FTH1	EPC2
FTO	EPCAM
FURIN	EPHA2
FUS	EPHB3
FUT2	EPHB4
FUT3	EPHB6
FUT4	EPHX1
FUZ	EPM2A
FXR1	EPN1
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FXYD3	EPX
FXYD4	ERBB2
FXYD6	ERBB3
FXYD7	ERC1
FYCO1	ERF
FZD6	ERGIC1
FZR1	ER12
G3BP2	ER13
GAA	ERICH1
GABPB2	ERMAP
GABRA5	ERMARD
GABRP	ERMN
GAL3ST1	ERN2
GAL3ST2	ERP27
GALC	ERRF11
GALE	ESAM
GALK1	ESD
GALNT10	ESPL1
GALNT15	ESPNL
GALNT16	ESR1
GALNT7	ESRP2
GALNT8	ESYT3
GALR3	ETFDH
GAPVD1	ETHE1
GAREM	ETNK2
GARNL3	ETS2
GAS2L1	ETV2
GAS6	ETV4
GAS8	ETV6
GATSL3	EVA1B
GBAS	EVC
GCGR	EVC2
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GCNT3	EXD3
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GDE1	EXOC3L2
GDF1	EXOC4
GDF15	EXOC8
GDF5	EXOSC1
GDI2	EXOSC10
GDPD4	EXOSC3
GDPD5	EXOSC7
GEMIN4	EXPH5
GET4	EXT1
GFAP	EXT2
GF11B	EXTL1
GFPT2	EXTL3
GGA1	F10
GGA2	F11R
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GGCT	F3
GGH	F7
GGT1	FA2H
GGT5	FAAH
GGT6	FADS1
GGTLC1	FADS2
GHR	FADS6
GHRHR	FAF2
GINS2	FAHD2B
GINS4	FAM101A
GIPC1	FAM102A
GJB3	FAM102B
GJB5	FAM107A
GJB7	FAM109A
GLIPR2	FAM109B
GLMN	FAM110C
GLRX3	FAM110D
GLTPD2	FAM114A1
GLUL	FAM115A
GMEB2	FAM118B
GMP	FAM129B
GMNN	FAM131A
GMPPA	FAM132A
GNA13	FAM134C
GNA15	FAM136A
GNAI2	FAM13A
GNAL	FAM13B
GNAO1	FAM149A
GNAS	FAM154A
GNAT1	FAM161A
GNAZ	FAM166A
GNB1	FAM167A
GNB2L1	FAM167B
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GNL3	FAM177B
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GNPTAB	FAM179B
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GNS	FAM184B
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GOT1	FAM200B
GPATCH4	FAM204A
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GPR115	FAM221A
GPR126	FAM221B
GPR132	FAM222A
GPR133	FAM228A
GPR135	FAM228B
GPR137	FAM229A
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GPR157	FAM26E
GPR161	FAM3B
GPR162	FAM3C
GPR17	FAM53A
GPR176	FAM53B
GPR18	FAM53C
GPR55	FAM57A
GPR75	FAM60A
GPR75-ASB3	FAM64A
GPR87	FAM69B
GPRC5A	FAM69C
GPRC5B	FAM71E2
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GPSM2	FAM81A
GPT	FAM83B
GPT2	FAM83C
GPX2	FAM83E
GPX4	FAM84A
GRAMD1B	FAM84B
GRAMD1C	FAM92A1
GRAMD2	FAM96B
GRAMD3	FAN1
GRAMD4	FANCC
GRAP2	FANCD2OS
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GREB1	FANCG
GREB1L	FASTK
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GRIN2A	FBN3
GRIP1	FBXL14
GRK1	FBXL15
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GRN	FBXL20
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GSAP	FBXL3
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GSE1	FBXO2
GSN	FBXO21
GSPT1	FBXO24
GSTA4	FBXO27
GSTM4	FBXO3
GSTO2	FBXO31
GSTP1	FBXO32
GSTT2	FBXO34
GTF2F2	FBXO38
GTF2H3	FBXO39
GTF3A	FBXO40
GTF3C1	FBXO41
GTPBP1	FBXO42
GUCA2A	FBXO44
GULP1	FBXO6
GUSB	FBXO7
GXYLT2	FBXO9
GYG1	FBXW10
GYS1	FBXW11
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H2AFY	FBXW5
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HAAO	FCER2
HABP2	FCF1
HADH	FCGBP
HAGH	FCGR2A
HAMP	FCGRT
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HAS1	FCHSD2
HAUS4	FCN3
HAVCR1	FCRL4
HCAR1	FCRLB
HCAR2	FDFT1
HCAR3	FDPS
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HCLS1	FEM1B
HCRT	FER
HDAC1	FETUB
HDAC11	FEZ1
HDAC2	FEZ2
HDAC5	FFAR2
HDAC9	FFAR3
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HDGF	FGD2
HDGFRP2	FGD6
HDLBP	FGF1
HEATR5A	FGF17
HEATR5B	FGF20
HEG1	FGF8
HELZ	FGFBP1
HELZ2	FGFR1
HERC1	FGFR1OP
HERPUD1	FGFR4
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HGFAC	FHL3
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HHLA2	FIBCD1
HIC2	FIBIN
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HKDC1	FLNB
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HM13	FLVCR2
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HMGAI	FMO5
HMGB4	FNBP4
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HMOX2	FNDC3B
HMSD	FNDC7
HN1L	FNIP1
HN1A	FNIP2
HNFA	FOCAD
HNMT	FOLR1
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HOMEZ	FOXJ2
HOOK2	FOXJ3
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HR	FRMD5
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HRC1	FRRS1L
HS1BP3	FRS3
HS3ST1	FRY
HSBP1	FRYL
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HUNK	FZD1
HYAL4	FZD6
HY1	FZD9
HYLS1	FZR1
LARS	G0S2
ICA1L	G2E3
ICAM1	G3BP2
ICAM4	GAB2
ICT1	GABBR1
IDH2	GABRA2
IDUA	GABRA5
IER3IP1	GABRG1
IFFO2	GABRG3
IFI16	GAL3ST1
IFITM1	GAL3ST2
IFITM10	GAL3ST3
IFITM5	GALC
IFNGR1	GALE
IFT27	GALK1
IFT57	GALNT10
IFT80	GALNT11
IGDCC3	GALNT12
IGF1	GALNT18
IGF2	GALNT2
IGF2BP1	GALNT3
IGFALS	GALNT5
IGFBP2	GALNT9
IGFBP5	GALNTL5
IGFBP7	GALP
IGFL1	GALR3
IGFL4	GAMT
IGLON5	GANC
IGSF11	GAPDHS
IGSF21	GAPVD1
IGSF23	GAS2L1
IGSF9	GAS2L2
IGSF9B	GAS7
IKBBK	GAS8
IKBBKE	GATA2
IKZF4	GATA6
IKZF5	GATSL2
IL10RB	GATSL3
IL17B	GBAS
IL17RE	GBE1
IL17REL	GBT1
IL18	GBP6
	GBX2

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IL1F10	GCFC2
IL1R1	GCGR
IL1R2	GCK
IL1RL2	GCKR
IL20RA	GCLC
IL20RB	GCNT2
IL21R	GCOM1
IL22RA1	GDAP1
IL22RA2	GDE1
IL24	GDF11
IL33	GDF15
IL34	GDF2
IL36G	GDF5
IL37	GDPD3
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IL4R	GFOD1
IL5RA	GFPT1
IL6R	GFRA2
IMPA2	GFRA3
IMPG1	GGCT
INADL	GGH
INF2	GGT5
INH1	GGT6
INPP1	GH1
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INPP4B	GHRL
INPP5A	GIGYF1
INPP5F	GIGYF2
INPP5J	GINS2
INPPL1	GINS4
INS	GIPC3
INS-IGF2	GIPR
INSR	GIT1
INTS1	GJA4
INTS10	GJB3
INTS4	GJC2
INTU	GJD3
IPO11	GKAP1
IPO13	GLB1L3
IPO9	GLE1
IQCA1	GLI2
IOCJ	GLI4
IOCJ-SCHIP1	GLIS1
IQGAP1	GLIS2
IQGAP2	GLS
IQSEC1	GLT1D1
IREB2	GLT8D2
IRF2BP1	GLTPD2
IRF6	GLTSCR1L
IRF7	GLUL
IRF9	GLYR1
ISG20	GMEB2
ISG20L2	GMPR
ISLR	GNA11
ISLR2	GNA12
ISX	GNA13
ISYNA1	GNA14
ITGA2B	GNA15
ITGA3	GNA2
ITGA7	GNAS
ITGA8	GNB1
ITGA9	GNB2L1
ITGAL	GNE
ITGAM	GNG13
ITGB1	GNG4
ITGB1BP1	GNG8
ITGB3	GNL1
ITGB7	GNMT
ITIH2	GNPAT
ITIH4	GNPDA2
ITPA	GNPTAB
ITPK1	GNRH2
ITPKC	GNS
ITPR2	GOLGA1
ITPR3	GOLGA2
ITSN2	GOLGA6L6
IYD	GOLGA7
JAG1	GOLGA7B
JAG2	GOLGA8B
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JARID2	GORASP2
JDP2	GPAM
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JMJD7-PLA2G4B	GPBAR1
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JSRP1	GPD1L
JUP	GPD2
KALRN	GPFR1
KANK1	GPHN
KANK3	GPIHBP1
KANSL3	GPNI
KAT2A	GPR108
KAT7	GPR123
KAT8	GPR124
KATNAL2	GPR126
KAZN	GPR139
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LDLRAP1	HIST1H3E
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LEFTY1	HK1
LEFTY2	HK2
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LETM2	HKDC1
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MAG12	IFT122
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MAP4K5	IL1RAP
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MAPK12	ILDR1
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MARK2	ING2
MARK4	INHA
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MARVELD2	INHBE
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MDM2	IQCH
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MDS2	IQCK
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MECR	IQSEC1
MED12L	IQSEC3
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MED24	IRS1
MED26	IRX2
MED31	IRX5
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MICU2	KANK1
MIER1	KANK2
MIER2	KANSL3
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MITF	KAT8
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OPN3	LY6G5C
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OR2J2	LYPD3
OR52B4	LYPD4
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OR9Q2	LYPLAL1
ORAOV1	LYRM1
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OSER1	LYSMD3
OSGIN1	LYSMD4
OSMR	LYZL4
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OXR1	MAB21L3
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PAK7	MAP1LC3A
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PATZ1	MAPRE3
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PBX1	42797
PBX3	42801
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PCBP3	MARS

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PCOLCE2	MATN4
PCP4L1	MAU2
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PCSK6	MBD4
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PDZK1IP1	MED30
PDZRN4	MED31
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PECR	MED8
PEF1	MEF2B
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PER2	MEF2BNB-MEF2B
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PIAS3	MGRN1
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PIEZO2	MGST3
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PIK3R2	MICU2
PIK3R3	MIDN
PINLYP	MIEF1
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PIWIL4	MINK1
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PKNOX1	MKLN1
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PLA2G3	MLF1
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PLA2G4F	MLN
PLA2G6	MLNR
PLA2	MLTK
PLAC8	MLX
PLAC9	MLYCD

PLAT	MMAB
PLB1	MMACHC
PLCB4	MMD
PLCD1	MMD2
PLCH1	MMEL1
PLCL2	MMP11
PLCXD2	MMP14
PLD1	MMP15
PLD3	MMP19
PLD4	MMP26
PLD6	MMP9
PLEC	MMRN2
PLEKH44	MMS19
PLEKH45	MN1
PLEKH47	MNT
PLEKHF1	MOB2
PLEKHG1	MOB3C
PLEKHG3	MOBP
PLEKHG4	MOCS2
PLEKHG5	MON1A
PLEKHG6	MORN2
PLEKHH3	MOV10
PLEKHM1	MPG
PLEKHN1	MPHOSPH10
PLIN3	MPI
PLIN4	MPO
PLK5	MPP2
PLLP	MPP4
PLSCR4	MPPE1
PLTP	MPST
PLXNA1	MPV17
PLXNA2	MPZL2
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PLXNB2	MRC2
PLXNC1	MRFAP1
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PMS2	MRGPRG
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PNOC	MRPL23
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PNPLA2	MRPL34
PNPLA6	MRPL35
PNPLA7	MRPL38
PNPLA8	MRPL50
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PODNL1	MRPS18C
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POGK	MRPS23
POLA2	MRPS25
POLD1	MRPS31
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POLH	MS4A8
POLN	MSANTD3
POLR1D	MSANTD4
POLR2D	MSC
POLR2E	MSH5
POLR2F	MSH5-SAPCD1
POLR2J3	MSH6
POLR2M	MSL1
POLR3E	MSLN
POLRMT	MSLNL
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POU6F1	MT2A
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PPAPDC1B	MTA2
PPARGC1A	MTA3
PPARGC1B	MTAP
PPF1A4	MTCH1
PPL	MTCH2
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PPMIJ	MTFR1
PPMIK	MTFR1L
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PPP1R16A	MTHFD1L
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PPP1R32	MTHFSD
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PPP1R42	MTMR12
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PPP2CB	MTMR3
PPP2R1B	MTMR4
PPP2R2A	MTNR1A
PPP2R2C	MTNR1B
PPP2R5C	MTOR
PPP3CA	MTRNR2L1
PPP4R1	MTRNR2L12
PPP4R4	MTRNR2L8
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PPP6R1	MTURN
PPP6R2	MTX1
PPP6R3	MUC1
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PRAM1	MUC5B
PRCP	MUC6
PREP	MUS81
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PREX2	MVK
PRICKLE4	MX1
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PRKAG2	MXI1
PRKAG3	MXRA7
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PRKCD	MYADM2
PRKCE	MYBBP1A
PRKCZ	MYBPC2
PRLR	MYBPC3
PRM3	MYBPHL
PRMT2	MYH7

PRMT7	MYL2
PRMT8	MYL5
PROC	MYL6
PROCA1	MYL9
PRODH	MYLPF
PROM2	MYO15A
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PROSER2	MYO1C
PRPF4B	MYO1H
PRPH	MYO5A
PRK15L	MYO5C
PRK5L	MYOCD
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PRRC2C	MYOM3
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PRRT3	MYZAP
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PRSS36	NAA60
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PSD	NAB2
PSEN2	NACAD
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PSMD1	NADSYN1
PSMD5	NAGA
PSMD9	NAGK
PSME1	NAGPA
PSMG3	NANOG
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PTCH1	NAPRT1
PTGES	NARS
PTGFRN	NARS2
PTGR1	NAT14
PTGS2	NATNL
PTK6	NBAS
PTMS	NBEAL1
PTOV1	NBEAL2
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PTPN2	NCKAP5L
PTPN21	NCKIPSD
PTPN23	NCOA4
PTPN3	NCOA6
PTPRF	NCOA7
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PTPRM	NCS1
PTPRN2	NDE1
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PTTG2	NDN
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PUM2	NDUFA13
PUS1	NDUFA7
PUS7	NDUFA9
PUSL1	NDUFAF5
PVRL1	NDUFAF6
PVRL4	NDUFB7
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PXDN	NDUFC2-KCTD14
PXMP2	NDUFS2
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PYCR2	NEDD4
PYGB	NEFH
PYGM	NEIL1
PYROXD2	NEK2
QDPR	NEK3
QSOX2	NEK6
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R3HDM4	NET1
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RAB17	NFE2L3
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RAB20	NFIC
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RAB26	NFKBIA
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RAB36	NFRKB
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RABL2B	NINJ1
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RAD18	NIPAL3
RAD23A	NISCH
RAD51B	NTT1
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RAF1	NKIRAS1
RAI1	NKX1-1
RAI14	NKX2-1
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RALY	NLN
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RANGAP1	NLRP7
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RARA	NME5

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RASL11B	NOMO3
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RASSF7	NOTCH1
RASSF9	NOTCH2
RAX2	NOTCH2NL
RBBP8	NOTCH3
RBBP8NL	NOTCH4
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RBL2	NOVA1
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RBM47	NPEPPS
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RBMS3	NPIPB11
RBMXL1	NPIPB8
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RBPMS	NPPA
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RCBTB1	NPRL3
RCC1	NPTN
RCC2	NPTX2
RCL1	NPTXR
RCOR2	NQO1
KDH12	NR0B2
KDH16	NR1D1
KDH5	NR1H3
KDX	NR1I2
REC8	NR2C1
RECQL4	NR2C2
RECQL5	NR2C2AP
REEP1	NR2F6
REEP2	NR3C2
REEP6	NR4A1
RELN	NR5A1
REM2	NRAP
REPIN1	NRARP
REPS1	NRBP1
REST	NRF1
REV1	NRG4
REXO2	NRIP2
RFESD	NRN1L
RFPL3S	NRSN2
RFT1	NRTN
RFX2	NSD1
RFX4	NSFL1C
RFX8	NSMAF
RGMA	NSUN2
RGMB	NSUN4
RGPD8	NTSC1A
RGS14	NTSC2
RGS16	NTSDC2
RGS20	NTSDC3
RGS66	NTAN1
RGS7	NTF3
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RHBDF2	NTMT1
RHBDL1	NTNG2
RHCE	NTPCR
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RHOBTB3	NUDCD3
RHOD	NUDT1
RHOH	NUDT16L1
RHOT1	NUDT6
RHPN1	NUMA1
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RILPL1	NUMBL
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RIMBP3C	NUP205
RIMKLB	NUP37
RIN1	NUP43
RIN2	NUP54
RLTPR	NUP85
RMDN2	NUP98
RMI2	NUPL1
RMND5B	NUPR1
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RNASE4	NVL
RNASE6	NXF1
RNASE7	NXPE3
RND3	NXPH3
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RNF126	OAT
RNF130	OAZ2
RNF135	OBSL1
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RNF149	ODC1
RNF157	ODF2
RNF165	ODF2L
RNF175	ODF3B
RNF183	OGFOD2
RNF186	OLFML2A
RNF212	OLFML3
RNF213	OLR1
RNF215	OPA3
RNF222	OPRL1
RNF223	OR2B11
RNF224	OR4K15
RNF24	OR4M2
RNF39	OR4N4
RNF43	OR7A10
RNPC3	ORA13
RNPEP	ORAOV1
RNPEPL1	ORC6
ROGDI	OSBP2

ROM1	OSBPL2
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RORC	OSBPL5
RP1-102H19.8	OSBPL7
RP1-130H16.18	OSBPL9
RP1-170O19.20	OSER1
RP1-317E23.6	OSGEP
RP1-32H10.10	OSMR
RP1-4G17.5	OST4
RP1-66C13.4	OTOA
RP11-1055B8.7	OTOF
RP11-1070N10.3	OTOF3
RP11-162A12.2	OTOS
RP11-181C3.1	OTUB1
RP11-187E13.1	OTUB2
RP11-187E13.2	OVCA2
RP11-1C1.5	OVCHI-AS1
RP11-201K10.3	OVGP1
RP11-242G20.1	OXCT1
RP11-247C2.2	OXNAD1
RP11-257K9.8	P2RX2
RP11-276H1.3	P2RX3
RP11-295K3.1	P2RX5
RP11-295P9.3	P2RX5-TAXIBP3
RP11-296A16.1	P2RX6
RP11-297M9.1	P2RY14
RP11-315O6.2	P2RY2
RP11-342M21.2	P4HB
RP11-343C2.7	PABPC1L
RP11-351M8.1	PABPC4
RP11-382J12.1	PABPC4L
RP11-404P21.8	PACRGL
RP11-410N8.4	PACS2
RP11-426L16.10	PAC SIN1
RP11-477N12.3	PAC SIN2
RP11-47I22.3	PAC SIN3
RP11-47I22.4	PAF1
RP11-544M22.13	PAFAH1B2
RP11-552I3.12	PAK1
RP11-552I14.1	PAK4
RP11-574K11.31	PAK6
RP11-595B24.2	PAK7
RP11-613M10.9	PALM
RP11-618P17.4	PALM2
RP11-637O19.3	PALM3
RP11-644F5.10	PALMD
RP11-676J12.7	PAM16
RP11-680G10.1	PANK1
RP11-701P16.2	PANX2
RP11-762I7.5	PAPL
RP11-794P6.2	PAPOLG
RP11-872D17.8	PAQR6
RP11-87C12.2	PAQR7
RP11-93B14.6	PARK2
RP13-279N23.2	PARN
RP13-672B3.2	PARP1
RP1L1	PARP14
RP4-583P15.14	PARP2
RPA1	PARS2
RPA3	PATZ1
RPH3A	PAX2
RPL13	PAX5
RPL18	PBX3
RPL23A	PBX4
RPL31	PBXIP1
RPL36AL	PCBD1
RPL5	PCBP3
RPP25L	PCBP4
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RPRD2	PCCB
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RPS28	PCDH17
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RPS6KA4	PCDH8
RPS8	PCDHA1
RPSA	PCDHA10
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RSPH3	PCDHA4
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RSU1	PCDHA6
RTDR1	PCDHA7
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RUSC1	PCDHB13
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RXRA	PCDHB15
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SAMHD1	PCDHGB4
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SASH1	PCGF2
SBF1	PCGF3
SBF2	PCGF5
SBK3	PCK2
SBN02	PCOLCE
SBP1	PCOLCE2
SBSN	PCP2
SCAMP4	PCSK1
SCAP	PCSK4
SCAPER	PCSK9
SCARA3	PCYOX1
SCARF2	PDP1
SCEL	PDCD11
SCG5	PDCD6
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SCGB3A2	PDE4A
SCMH1	PDE4C
SCN2B	PDE6B
SCN4A	PDE6D
SCNN1A	PDE8A
SCNN1D	PDGFA
SCNN1G	PDGFB
SCOC	PDGFRB
SCRN2	PDHX
SCU/BE2	PDIA2
SCU/BE3	PDIA5
SDC2	PDIA6
SDC3	PDK2
SDHC	PDLM1
SDPR	PDLM2
SDR16C5	PDLM5
SDR9C7	PDLM7
SDS	PDP1
SDSL	PDPK1
SEC14L2	PDSS2
SEC14L3	PDXDC1
SEC22C	PDXK
SEC24C	PDZD3
SEC24D	PDZD7
SEC31B	PDZK1IP1
SECISBP2	PEA15
SECTM1	PEAR1
SELE	PEBP4
SELENBP1	PELP1
SELM	PEMT
SELPLG	PENK
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SESTD1	PHF20
SETBP1	PHF21A
SETD3	PHF23
SETD4	PHF3
SETD5	PHKB
SETD8	PHKG1
SF3B3	PHLDA1
SFN	PHLDA3
SFPQ	PHLDB2
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SFTA2	PHPT1
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SFTPD	PHYHIP
SFXN1	PHYHIPL
SGCA	PHYKPL
SGK1	PI4KA
SGK2	PI4KB
SGK223	PIANP
SGK3	PIAS3
SGMS2	PIAS4
SGPL1	PIBF1
SGPP1	PIDD
SGSM2	PIFO
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SH2D3A	PIGH
SH2D4A	PIGP
SH2D4B	PIGQ
SH2D6	PIGR
SH3BGR	PIGU
SH3BGR13	PIGY
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SH3BP4	PIK3C2B
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SH3D21	PIK3R2
SH3GL1	PIK3R3

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SH3RF3	PIP5KL1
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SHB	PITPNA
SHC2	PITRM1
SHD	PIWIL4
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SHISA5	PKDREJ
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SHROOM3	PKG
SHAH1	PKM
SHAH2	PKMYT1
SIDT2	PKP2
SIGLEC15	PKP4
SIK1	PLA2G12B
SIK2	PLA2G15
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SIT1	PLA2G4F
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SK1	PLA2R1
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SKP1	PLBD2
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SLC12A6	PLCXD3
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SLC15A2	PLEKHD1
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SLC1A4	PLIN5
SLC1A5	PLK2
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SLC20A2	PLSCR4
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SLC22A15	PLXDC1
SLC22A18AS	PLXNA1
SLC22A4	PLXNA4
SLC22A5	PLXNB1
SLC22A6	PLXNB2
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SLC24A4	PNMA1
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SLC25A42	POLB
SLC25A48	POLD1
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SLC26A10	POLDIP3
SLC26A9	POLE2
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SLC27A5	POLN
SLC27A6	POLQ
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SLC47A2	PPP1CC
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SLC4A2	PPP1R12B
SLC4A4	PPP1R12C
SLC4A5	PPP1R14B
SLC4A9	PPP1R15A
SLC51A	PPP1R16A
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SLC52A2	PPP1R1B
SLC5A10	PPP1R21
SLC5A2	PPP1R37
SLC6A11	PPP1R3D
SLC6A12	PPP1R3E
SLC6A19	PPP1R7
SLC6A3	PPP1R9B
SLC6A6	PPP2R1A
SLC6A9	PPP2R1B
SLC7A1	PPP2R2C
SLC7A5	PPP2R4
SLC7A6	PPP2R5B
SLC7A7	PPP3CA
SLC7A8	PPP4R1
SLC9A3R1	PPP4R4
SLC9A5	PPP5C
SLC9B1	PPP6R3
SLCO2B1	PPT1
SLCO3A1	PPT2
SLCO4A1	PPT2-EGFL8
SLFN12L	PPTC7
SLFN13	PPWD1
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SLIT3	PRAP1
SLMAP	PRCD
SLN	PRDM1
SLU7	PRDM10
SLURP1	PRDM11
SLX4IP	PRDM13
SMAD1	PRDM16
SMAD3	PREDS7
SMAD4	PRELP
SMARCA4	PREX1
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SMARCD1	PRKAB1
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SMC5	PRKAR1A
SMCO4	PRKCB
SMG5	PRKCD
SMIM22	PRKCDBP
SMIM4	PRKCI
SMIM6	PRKCSH
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SMO	PRKD3
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SMPD3	PRKRIR
SMPD4	PRLHR
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SMTNL1	PRND
SMTNL2	PROB1
SMURF2	PROCA1
SMYD2	PRODH
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SNAP23	PROK2
SNAP47	PROSER1
SND1	PROSER2
SNED1	PROX1
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SNX24	PRPF40B
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SORD	PRR5
SOS2	PRR5-ARHGAP8
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SOX10	PRRC2A
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SOX15	PRRT1
SOX8	PRRT2
SP1	PRRT3
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SP3	PRRX2
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SPEF1	PRTG
SPEF2	PRTN3
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SRK	PTPRJ
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STAR	QDPR
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STARD5	QRFP
STARD7	QSOX1
STAT4	QSOX2
STAT6	QTRTD1
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STRA6	RAB35
STRIP1	RAB36
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TEKT5	REM2
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TEPP	RESP18
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TEX36	RIFNG
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TIFA	RHOT1
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TMEM110	RNF212
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TMEM161B	RP1-32110.10

TMEM163	RP1-66C13.4
TMEM165	RP11-101E3.5
TMEM175	RP11-1026M7.2
TMEM180	RP11-1055B8.6
TMEM184B	RP11-1070N10.3
TMEM189	RP11-1099M24.7
TMEM19	RP11-111M22.2
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TMEM192	RP11-131H24.4
TMEM210	RP11-133K1.2
TMEM214	RP11-139J15.7
TMEM229B	RP11-1407O15.2
TMEM231	RP11-145E5.5
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TMEM237	RP11-162P23.2
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TNFSF13	RP11-637O19.3
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TNNT1	RP13-672B3.2
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TRAM1	RUSC2
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TRIM47	SI00A2
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TRIM7	SACS

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UCKL1	SERTAD4
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UEVLD	SETD2
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UNC13D	SF3B14
UNC5D	SF3B2
UNC93B1	SFMBT2
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UROS	SGCD
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USO1	SGOL1
USP10	SGSH
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USP35	SH3PXD2B
USP36	SH3RF1
USP40	SH3RF2
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USP43	SHARPIN
USP45	SHB
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UST	SHCBBP1
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VAC14	SHMT2
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VDAC2	SIK2
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VEZF1	SIRPA
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SPTBN4
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SREK1
SRGAP2
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SSBP3
SSC5D
SSFA2
SSH1
SSH2
SSH3
SSPN
SSR3
SST
SSTR3
SSTR5
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ST3GAL4
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ST6GALNAC2
ST6GALNAC4
ST7
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STARDD3
STARDD5
STAT4
STAT5B
STAT6
STK11
STK24
STK35
STK38L
STK39
STMN1
STOM
STPG1
STRIP1
STRN
STRN3
STRN4
STX16
STX19
STX1B
STX3
STX5
STX6

STXBP2
SUCLA2
SUGP2
SULF2
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SULT1A2
SULT4A1
SULT6B1
SUMF1
SUMF2
SUN1
SUN3
SUOX
SUTP4H1
SUTP5H
SUTP6H
SURF1
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SUV420H1
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SWI5
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SYCP2L
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SYDE2
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SYNE4
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SYNPO
SYNPO2
SYS1
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SYT3
SYT5
SYT8
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TAF2
TAF4
TAF4B
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TDRD9
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TECR
TEF
TEKT2
TEKT4
TELO2
TENC1
TEPP
TERT

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TESK2
TET3
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TEX2
TEX26
TEX35
TEX38
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TFAP4
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TLR6
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TM4SF4
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TM7SF3
TM9SF3
TM9SF4
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TMC4
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TMCC2
TMCO3
TMCO4
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TMED6
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TMEM139
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TMPRSS3
TMPRSS6
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TNFRSF1A
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TNFSF11
TNFSF13
TNFSF15
TNFSF18
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TNNC2
TNNI3
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TNRC6C
TNXB
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TOR4A
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TOX2
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TP53I3
TP53INP1
TP53INP2
TP53TG3D
TP53TG5
TP63
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TPGS2
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TPM2
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TPRN
TPSAB1
TPSG1
TPT1
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TRAF3IP2
TRAF4
TRAIIP
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TRAK2
TRAM1
TRAPPC12
TRAPPC2L
TRAPPC3L
TRAPPC9
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TREM1
TRERF1
TREN1
TRH
TRIB1
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TRIM74
TRIM8
TRIM9
TRIOBP
TRIP10
TRIP11
TRIP6

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TRPV4
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TSC22D4
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TSKU
TSN
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TSPAN3
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TSSC1
TSSK3
TSSK6
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TTC27
TTC3
TTC32
TTC34
TTC37
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TTC40
TTC9B
TTF2
TTLL4
TTLL5
TTLL8
TTPA
TTR
TTYH1
TUBG1
TUBG2
TULP1
TULP3
TUSC1
TUT1
TWIST2
TXNDC11
TXNDC5
TXNIP
TXNL4A
TXNRD1
TYRO3
TYROBP
TYW3
UAP1
UAP1L1
UBA5
UBA7
UBALD1
UBAP1
UBAP1L
UBASH3B
UBB
UBE2E1
UBE2G2
UBE2I
UBE2J2
UBE2M
UBE2N
UBE2Q1
UBE4B
UBL4B
UBL7
UBN1
UBOX5
UBQLN1
UBR5
UBXN1
UBXN6
UCK1
UCK2
UCKL1
UCN
UCN3
UFSF2
UGDH
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UGT3A1
UMC1
UNC13B
UNC45B
UNC50
UNC5B
UNC79
UNC93B1
UNKL
UPF1
UPK1B
UPK3A
UPK3B
UPP1
UQCC1
UQCC2
URAD
URGCP
UROS
USB1
USO1
USP19
USP2
USP22
USP3
USP31
USP33
USP35
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USP40
USP45
USP46
USP48
USP53
USP54
USP6
UTP11L
UTS2B
UTS2R
UVRAG
UVSSA
VAC14
VAMP3
VAMP8
VANGL2
VAPA
VARS2
VASH1
VASH2
VASN
VASP
VAT1
VAX1
VCAM1
VEGFA
VEGFB
VENTX
VEZF1
VEZT
VGLL4
VHLL
VIPR2
VIT
VMO1
VNN2
VPS13B
VPS13C
VPS29
VPS35
VPS37B
VPS41
VPS4B
VPS51
VPS53
VPS72
VRTN
VSG10
VSG10L
VSG2
VSTM2A
VSTM2L
VSX1
VTCN1
VTN
VWA1
VWA3A
VWA5B2
VWA7
VWA9
WAPAL
WARS
WASF2
WBP1L
WBP2
WBSCR27
WDR12
WDR18
WDR20
WDR24
WDR26
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WDR35
WDR45B
WDR46
WDR48
WDR5
WDR52
WDR54
WDR5B
WDR61
WDR74
WDR81
WDR88
WDR90
WDR91
WFDC3
WFDC5
WFKKN1
WFKKN2
WFS1
WHSC1
WIF1
WISP1
WISP2
WIZ
WNT10A
WNT10B
WNT2B
WNT3
WNT7A
WRAP53
WRB
WRNIP1
WSB1
WSB2
WT1
WWOX
WWP2
WWTR1
XBP1
XKR9
XPO7
XRCC2
XRCC3
YAF2
YBX3
YIPF1

YJEFN3
YKT6
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YPEL4
YPEL5
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YTHDC2
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YWHAH
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YY1AP1
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ZC3H18
ZC3H3
ZC3H4
ZC3H7A
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ZCCHC11
ZCCHC2
ZCCHC24
ZCCHC6
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ZDHHHC13
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ZDHHHC17
ZDHHHC19
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ZFAND4
ZFAND5
ZFAND6
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ZFYVE9
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ZIC4
ZIK1
ZKSCAN1
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ZMAT5
ZMIZ2
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ZNF77
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ZNF841
ZNF850
ZNF860
ZNF90
ZNF98
ZNRF1
ZNRF2
ZNRF3
ZSCAN1
ZSCAN10
ZSCAN18
ZSCAN21
ZSWIM4
ZUFSP
ZXDC
ZZEF1

Table S5. Enrichment of promoter DMR genes. P values after Benjamin's correction are provided.

GO term of biological process	Alveolar > Bronchial	Alveolar < Bronchial	Lung > T	Lung < T
GO:0000041--transition metal ion transport	0.89	1.00	1.00	1.00
GO:0000082--G1/S transition of mitotic cell cycle	0.85	1.00	1.00	1.00
GO:0000122--negative regulation of transcription from RNA polymerase II promoter	0.75	0.40	1.00	0.02
GO:0000272--polysaccharide catabolic process	0.69	1.00	1.00	1.00
GO:0000902--cell morphogenesis	0.78	0.41	1.00	1.00
GO:0000904--cell morphogenesis involved in differentiation	0.75	0.26	1.00	1.00
GO:0001539--ciliary or flagellar motility	0.64	1.00	1.00	1.00
GO:0001558--regulation of cell growth	0.55	1.00	1.00	0.42
GO:0001666--response to hypoxia	0.74	1.00	1.00	0.62
GO:0001701--in utero embryonic development	0.60	1.00	1.00	0.35
GO:0001736--establishment of planar polarity	0.85	1.00	1.00	1.00
GO:0001890--placenta development	0.66	1.00	1.00	0.62
GO:0001932--regulation of protein amino acid phosphorylation	0.58	1.00	1.00	1.00
GO:0001936--regulation of endothelial cell proliferation	0.83	1.00	1.00	0.24
GO:0001938--positive regulation of endothelial cell proliferation	0.71	1.00	1.00	0.31
GO:0002455--humoral immune response mediated by circulating immunoglobulin	0.89	1.00	1.00	1.00
GO:0002685--regulation of leukocyte migration	0.80	1.00	1.00	1.00
GO:0002687--positive regulation of leukocyte migration	0.71	1.00	1.00	1.00
GO:0003009--skeletal muscle contraction	0.54	1.00	1.00	1.00
GO:0003012--muscle system process	0.80	1.00	1.00	0.80
GO:0003015--heart process	0.88	1.00	1.00	1.00
GO:0005976--polysaccharide metabolic process	0.75	1.00	1.00	0.47
GO:0005984--disaccharide metabolic process	0.85	1.00	1.00	1.00
GO:0006022--aminoglycan metabolic process	0.86	1.00	1.00	0.69
GO:0006026--aminoglycan catabolic process	0.84	1.00	1.00	1.00
GO:0006030--chitin metabolic process	0.52	1.00	1.00	1.00
GO:0006032--chitin catabolic process	0.52	1.00	1.00	1.00
GO:0006081--cellular aldehyde metabolic process	0.69	1.00	1.00	0.43
GO:0006110--regulation of glycolysis	0.88	1.00	1.00	1.00
GO:0006111--regulation of gluconeogenesis	0.85	1.00	1.00	1.00
GO:0006470--protein amino acid dephosphorylation	0.58	1.00	1.00	1.00
GO:0006631--fatty acid metabolic process	0.03	1.00	1.00	0.35
GO:0006633--fatty acid biosynthetic process	0.40	1.00	1.00	0.79
GO:0006636--unsaturated fatty acid biosynthetic process	0.64	1.00	1.00	0.75
GO:0006643--membrane lipid metabolic process	0.37	1.00	1.00	1.00
GO:0006664--glycolipid metabolic process	0.80	1.00	1.00	1.00
GO:0006665--sphingolipid metabolic process	0.40	1.00	1.00	1.00
GO:0006672--ceramide metabolic process	0.59	1.00	1.00	1.00
GO:0006687--glycosphingolipid metabolic process	0.86	1.00	1.00	1.00
GO:0006688--glycosphingolipid biosynthetic process	0.63	1.00	1.00	1.00
GO:0006690--icosanoid metabolic process	0.41	1.00	1.00	0.75
GO:0006691--leukotriene metabolic process	0.74	1.00	1.00	1.00
GO:0006692--prostanoid metabolic process	0.88	1.00	1.00	1.00
GO:0006693--prostaglandin metabolic process	0.88	1.00	1.00	1.00
GO:0006730--one-carbon metabolic process	0.87	1.00	1.00	1.00
GO:0006732--coenzyme metabolic process	0.86	1.00	1.00	0.31
GO:0006760--folic acid and derivative metabolic process	0.76	1.00	1.00	1.00
GO:0006767--water-soluble vitamin metabolic process	0.84	1.00	1.00	1.00
GO:0006778--porphyrin metabolic process	0.74	1.00	1.00	1.00
GO:0006787--porphyrin catabolic process	0.85	1.00	1.00	1.00
GO:0006793--phosphorus metabolic process	0.74	1.00	1.00	0.31
GO:0006796--phosphate metabolic process	0.74	1.00	1.00	0.31
GO:0006811--ion transport	0.84	0.12	1.00	0.41
GO:0006820--anion transport	0.58	0.43	1.00	1.00
GO:0006826--iron ion transport	0.85	1.00	1.00	1.00
GO:0006865--amino acid transport	0.74	1.00	1.00	0.52
GO:0006879--cellular iron ion homeostasis	0.80	1.00	1.00	1.00
GO:0006897--endocytosis	0.85	1.00	1.00	0.14
GO:0006914--autophagy	0.88	1.00	1.00	1.00
GO:0006915--apoptosis	0.03	1.00	0.06	0.66
GO:0006928--cell motion	0.53	0.01	1.00	1.00
GO:0006936--muscle contraction	0.71	1.00	1.00	0.79
GO:0006941--striated muscle contraction	0.55	1.00	1.00	1.00
GO:0006942--regulation of striated muscle contraction	0.86	1.00	0.65	1.00
GO:0006986--response to unfolded protein	0.84	1.00	1.00	1.00
GO:0007010--cytoskeleton organization	0.75	1.00	1.00	0.65
GO:0007090--regulation of S phase of mitotic cell cycle	0.76	1.00	1.00	1.00
GO:0007155--cell adhesion	0.67	0.01	0.01	0.02
GO:0007163--establishment or maintenance of cell polarity	0.86	1.00	1.00	1.00
GO:0007169--transmembrane receptor protein tyrosine kinase signaling pathway	0.85	1.00	1.00	0.78
GO:0007242--intracellular signaling cascade	0.37	0.57	0.13	0.00
GO:0007398--ectoderm development	0.71	0.16	1.00	1.00
GO:0007409--axonogenesis	0.88	0.14	1.00	1.00
GO:0007411--axon guidance	0.75	0.21	1.00	0.79
GO:0007565--female pregnancy	0.80	1.00	1.00	0.71
GO:0007584--response to nutrient	0.53	1.00	1.00	1.00
GO:0007585--respiratory gaseous exchange	0.58	1.00	1.00	1.00
GO:0007588--excretion	0.72	1.00	1.00	1.00
GO:0008104--protein localization	0.88	1.00	1.00	1.00
GO:0008202--steroid metabolic process	0.57	1.00	1.00	0.78
GO:0008203--cholesterol metabolic process	0.78	1.00	1.00	0.49
GO:0008219--cell death	0.02	1.00	0.09	0.42
GO:0008285--negative regulation of cell proliferation	0.65	0.56	1.00	0.71
GO:0008361--regulation of cell size	0.03	1.00	1.00	0.18
GO:0008544--epidermis development	0.60	0.30	1.00	1.00
GO:0008610--lipid biosynthetic process	0.09	1.00	1.00	0.42
GO:0008624--induction of apoptosis by extracellular signals	0.83	1.00	0.22	1.00
GO:0008630--DNA damage response, signal transduction resulting in induction of apoptosis	0.75	1.00	1.00	1.00
GO:0009108--coenzyme biosynthetic process	0.86	1.00	1.00	0.48
GO:0009247--glycolipid biosynthetic process	0.64	1.00	1.00	1.00
GO:0009395--phospholipid catabolic process	0.57	1.00	1.00	1.00
GO:0009411--response to UV	0.84	1.00	1.00	1.00
GO:0009719--response to endogenous stimulus	0.56	1.00	1.00	0.02
GO:0009725--response to hormone stimulus	0.67	1.00	1.00	0.02
GO:0009792--embryonic development ending in birth or egg hatching	0.58	0.16	1.00	0.23
GO:0009890--negative regulation of biosynthetic process	0.45	0.66	1.00	0.02
GO:0009894--regulation of catabolic process	0.78	1.00	1.00	0.70
GO:0009896--positive regulation of catabolic process	0.86	1.00	1.00	0.18
GO:0009967--positive regulation of signal transduction	0.88	1.00	0.45	0.34
GO:0009991--response to extracellular stimulus	0.76	1.00	1.00	0.31
GO:0010033--response to organic substance	0.54	1.00	1.00	0.01
GO:0010035--response to inorganic substance	0.74	1.00	1.00	0.77
GO:0010038--response to metal ion	0.54	1.00	1.00	1.00
GO:0010324--membrane invagination	0.85	1.00	1.00	0.14
GO:0010558--negative regulation of macromolecule biosynthetic process	0.53	1.00	1.00	0.02
GO:0010562--positive regulation of phosphorus metabolic process	0.89	1.00	1.00	1.00
GO:0010605--negative regulation of macromolecule metabolic process	0.41	1.00	1.00	0.19
GO:0010608--posttranscriptional regulation of gene expression	0.80	1.00	1.00	1.00
GO:0010627--regulation of protein kinase cascade	0.34	1.00	1.00	0.48
GO:0010629--negative regulation of gene expression	0.46	1.00	1.00	0.00
GO:0010647--positive regulation of cell communication	0.85	1.00	0.69	0.41

GO:0010675--regulation of cellular carbohydrate metabolic process	0.88	1.00	1.00	1.00
GO:0010676--positive regulation of cellular carbohydrate metabolic process	0.62	1.00	1.00	1.00
GO:0010740--positive regulation of protein kinase cascade	0.65	1.00	0.44	0.65
GO:0010906--regulation of glucose metabolic process	0.81	1.00	1.00	1.00
GO:0010907--positive regulation of glucose metabolic process	0.56	1.00	1.00	0.78
GO:0010941--regulation of cell death	0.87	1.00	0.09	0.71
GO:0012501--programmed cell death	0.03	1.00	0.07	0.75
GO:0015698--inorganic anion transport	0.79	0.64	1.00	0.61
GO:0015804--neutral amino acid transport	0.84	1.00	1.00	1.00
GO:0015837--amine transport	0.80	1.00	1.00	0.73
GO:0015849--organic acid transport	0.75	1.00	1.00	0.46
GO:0016042--lipid catabolic process	0.53	1.00	1.00	1.00
GO:0016044--membrane organization	0.69	1.00	1.00	0.23
GO:0016049--cell growth	0.40	1.00	1.00	0.53
GO:0016053--organic acid biosynthetic process	0.34	1.00	1.00	1.00
GO:0016125--sterol metabolic process	0.73	1.00	1.00	0.65
GO:0016192--vesicle-mediated transport	0.75	1.00	1.00	0.41
GO:0016265--death	0.02	1.00	0.10	0.47
GO:0016311--dephosphorylation	0.11	1.00	1.00	1.00
GO:0016331--morphogenesis of embryonic epithelium	0.88	0.53	1.00	1.00
GO:0016338--calcium-independent cell-cell adhesion	0.86	1.00	1.00	1.00
GO:0016481--negative regulation of transcription	0.59	1.00	1.00	0.00
GO:0016575--histone deacetylation	0.81	1.00	1.00	1.00
GO:0017157--regulation of exocytosis	0.88	1.00	1.00	1.00
GO:0019216--regulation of lipid metabolic process	0.87	1.00	1.00	1.00
GO:0019220--regulation of phosphate metabolic process	0.64	1.00	1.00	0.24
GO:0019370--leukotriene biosynthetic process	0.88	1.00	1.00	1.00
GO:0019400--alditol metabolic process	0.84	1.00	1.00	1.00
GO:0019725--cellular homeostasis	0.78	1.00	1.00	0.47
GO:0019751--polyol metabolic process	0.74	1.00	1.00	1.00
GO:0022610--biological adhesion	0.64	0.01	0.01	0.01
GO:0030029--actin filament-based process	0.71	1.00	1.00	0.19
GO:0030030--cell projection organization	0.54	0.39	1.00	0.66
GO:0030031--cell projection assembly	0.88	1.00	1.00	1.00
GO:0030036--actin cytoskeleton organization	0.60	1.00	1.00	0.18
GO:0030148--sphingolipid biosynthetic process	0.67	1.00	1.00	1.00
GO:0030155--regulation of cell adhesion	0.88	1.00	0.17	1.00
GO:0030198--extracellular matrix organization	0.84	0.44	1.00	0.45
GO:0030308--negative regulation of cell growth	0.70	1.00	1.00	0.77
GO:0030330--DNA damage response, signal transduction by p53 class mediator	0.86	1.00	1.00	1.00
GO:0030334--regulation of cell migration	0.61	0.56	1.00	0.47
GO:0030335--positive regulation of cell migration	0.62	1.00	1.00	0.78
GO:0030520--estrogen receptor signaling pathway	0.84	1.00	1.00	1.00
GO:0030522--intracellular receptor-mediated signaling pathway	0.84	1.00	1.00	0.69
GO:0030834--regulation of actin filament depolymerization	0.89	1.00	1.00	1.00
GO:0030835--negative regulation of actin filament depolymerization	0.81	1.00	1.00	1.00
GO:0030879--mammary gland development	0.83	1.00	0.59	1.00
GO:0031175--neuron projection development	0.89	0.18	1.00	1.00
GO:0031327--negative regulation of cellular biosynthetic process	0.53	0.61	1.00	0.01
GO:0031329--regulation of cellular catabolic process	0.86	1.00	1.00	0.66
GO:0031331--positive regulation of cellular catabolic process	0.84	1.00	1.00	0.41
GO:0031399--regulation of protein modification process	0.88	1.00	1.00	1.00
GO:0031589--cell-substrate adhesion	0.86	1.00	1.00	1.00
GO:0031667--response to nutrient levels	0.60	1.00	1.00	0.62
GO:0032147--activation of protein kinase activity	0.80	1.00	1.00	1.00
GO:0032148--activation of protein kinase B activity	0.68	1.00	1.00	1.00
GO:0032268--regulation of cellular protein metabolic process	0.78	1.00	1.00	1.00
GO:0032318--regulation of Ras GTPase activity	0.84	1.00	1.00	1.00
GO:0032446--protein modification by small protein conjugation	0.86	1.00	1.00	0.57
GO:0032526--response to retinoic acid	0.75	1.00	1.00	1.00
GO:0032535--regulation of cellular component size	0.06	1.00	1.00	0.34
GO:0032869--cellular response to insulin stimulus	0.85	1.00	1.00	0.78
GO:0032870--cellular response to hormone stimulus	0.88	1.00	1.00	0.42
GO:0032970--regulation of actin filament-based process	0.89	1.00	1.00	1.00
GO:0032989--cellular component morphogenesis	0.80	0.66	1.00	1.00
GO:0033013--tetrapyrrole metabolic process	0.74	1.00	1.00	1.00
GO:0033015--tetrapyrrole catabolic process	0.85	1.00	1.00	1.00
GO:0033189--response to vitamin A	0.88	1.00	1.00	1.00
GO:0033273--response to vitamin	0.74	1.00	1.00	1.00
GO:0033559--unsaturated fatty acid metabolic process	0.12	1.00	1.00	0.77
GO:0033674--positive regulation of kinase activity	0.53	1.00	1.00	0.35
GO:0034330--cell junction organization	0.86	1.00	1.00	1.00
GO:0034637--cellular carbohydrate biosynthetic process	0.86	1.00	1.00	0.23
GO:0035023--regulation of Rho protein signal transduction	0.03	1.00	1.00	1.00
GO:0040007--growth	0.84	1.00	1.00	0.76
GO:0040008--regulation of growth	0.84	1.00	1.00	0.34
GO:0040012--regulation of locomotion	0.84	0.37	1.00	0.41
GO:0040017--positive regulation of locomotion	0.81	1.00	1.00	1.00
GO:0040029--regulation of gene expression, epigenetic	0.54	1.00	1.00	0.42
GO:0042044--fluid transport	0.81	1.00	1.00	1.00
GO:0042127--regulation of cell proliferation	0.85	0.15	0.53	0.32
GO:0042168--heme metabolic process	0.74	1.00	1.00	1.00
GO:0042176--regulation of protein catabolic process	0.85	1.00	1.00	0.69
GO:0042325--regulation of phosphorylation	0.58	1.00	1.00	0.26
GO:0042493--response to drug	0.52	1.00	1.00	1.00
GO:0042592--homeostatic process	0.79	1.00	0.55	0.62
GO:0042771--DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis	0.86	1.00	1.00	1.00
GO:0042787--protein ubiquitination during ubiquitin-dependent protein catabolic process	0.81	1.00	1.00	0.66
GO:0042981--regulation of apoptosis	0.85	1.00	0.08	0.71
GO:0043009--chordate embryonic development	0.57	0.16	1.00	0.28
GO:0043067--regulation of programmed cell death	0.86	1.00	0.09	0.71
GO:0043087--regulation of GTPase activity	0.81	1.00	1.00	1.00
GO:0043122--regulation of I-kappaB kinase/NF-kappaB cascade	0.75	1.00	0.52	1.00
GO:0043123--positive regulation of I-kappaB kinase/NF-kappaB cascade	0.85	1.00	0.40	1.00
GO:0043242--negative regulation of protein complex disassembly	0.86	1.00	1.00	1.00
GO:0043393--regulation of protein binding	0.85	1.00	1.00	1.00
GO:0043449--cellular alkene metabolic process	0.61	1.00	1.00	1.00
GO:0043450--alkene biosynthetic process	0.88	1.00	1.00	1.00
GO:0043549--regulation of kinase activity	0.76	1.00	1.00	0.36
GO:0043567--regulation of insulin-like growth factor receptor signaling pathway	0.78	1.00	1.00	1.00
GO:0044057--regulation of system process	0.84	1.00	1.00	0.23
GO:0044093--positive regulation of molecular function	0.86	1.00	1.00	0.60
GO:0044270--nitrogen compound catabolic process	0.59	1.00	1.00	0.75
GO:0045749--negative regulation of S phase of mitotic cell cycle	0.71	1.00	1.00	1.00
GO:0045786--negative regulation of cell cycle	0.80	1.00	1.00	1.00
GO:0045792--negative regulation of cell size	0.54	1.00	1.00	0.59
GO:0045821--positive regulation of glycolysis	0.79	1.00	1.00	1.00
GO:0045859--regulation of protein kinase activity	0.84	1.00	1.00	0.32
GO:0045860--positive regulation of protein kinase activity	0.55	1.00	1.00	0.34
GO:0045892--negative regulation of transcription, DNA-dependent	0.85	0.41	1.00	0.00
GO:0045913--positive regulation of carbohydrate metabolic process	0.62	1.00	1.00	1.00
GO:0045926--negative regulation of growth	0.86	1.00	1.00	1.00
GO:0045930--negative regulation of mitotic cell cycle	0.57	1.00	1.00	1.00

GO:0045934--negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.56	0.67	1.00	0.02
GO:0045937--positive regulation of phosphate metabolic process	0.89	1.00	1.00	1.00
GO:0046394--carboxylic acid biosynthetic process	0.34	1.00	1.00	1.00
GO:0046465--icosanoid biosynthetic process	0.80	1.00	1.00	0.76
GO:0046467--membrane lipid biosynthetic process	0.64	1.00	1.00	1.00
GO:0046519--sphingoid metabolic process	0.58	1.00	1.00	1.00
GO:0046578--regulation of Ras protein signal transduction	0.02	1.00	1.00	1.00
GO:0046847--filopodium assembly	0.86	1.00	1.00	0.72
GO:0046903--secretion	0.86	0.33	1.00	1.00
GO:0046942--carboxylic acid transport	0.75	1.00	1.00	0.43
GO:0048146--positive regulation of fibroblast proliferation	0.86	1.00	1.00	1.00
GO:0048167--regulation of synaptic plasticity	0.56	1.00	1.00	1.00
GO:0048667--cell morphogenesis involved in neuron differentiation	0.84	0.21	1.00	1.00
GO:0048729--tissue morphogenesis	0.88	0.27	1.00	0.22
GO:0048812--neuron projection morphogenesis	0.86	0.16	1.00	1.00
GO:0048870--cell motility	0.78	0.07	1.00	1.00
GO:0050769--positive regulation of neurogenesis	0.89	0.54	1.00	1.00
GO:0050879--multicellular organismal movement	0.75	1.00	1.00	0.59
GO:0050881--musculoskeletal movement	0.75	1.00	1.00	0.59
GO:0051016--barbed-end actin filament capping	0.85	1.00	1.00	1.00
GO:0051056--regulation of small GTPase mediated signal transduction	0.02	1.00	1.00	0.71
GO:0051057--positive regulation of small GTPase mediated signal transduction	0.81	1.00	1.00	1.00
GO:0051098--regulation of binding	0.77	1.00	1.00	0.58
GO:0051172--negative regulation of nitrogen compound metabolic process	0.59	0.56	1.00	0.02
GO:0051173--positive regulation of nitrogen compound metabolic process	0.88	0.17	1.00	0.32
GO:0051174--regulation of phosphorus metabolic process	0.64	1.00	1.00	0.24
GO:0051186--cofactor metabolic process	0.64	1.00	1.00	0.30
GO:0051187--cofactor catabolic process	0.67	1.00	1.00	1.00
GO:0051188--cofactor biosynthetic process	0.80	1.00	1.00	0.43
GO:0051253--negative regulation of RNA metabolic process	0.83	0.45	1.00	0.01
GO:0051270--regulation of cell motion	0.54	0.53	1.00	0.17
GO:0051272--positive regulation of cell motion	0.57	1.00	1.00	0.57
GO:0051291--protein heterooligomerization	0.64	1.00	1.00	0.80
GO:0051336--regulation of hydrolase activity	0.81	1.00	1.00	1.00
GO:0051338--regulation of transferase activity	0.77	1.00	1.00	0.34
GO:0051347--positive regulation of transferase activity	0.52	1.00	1.00	0.32
GO:0051591--response to cAMP	0.88	1.00	1.00	1.00
GO:0051642--centrosome localization	0.85	1.00	1.00	1.00
GO:0051674--localization of cell	0.78	0.07	1.00	1.00
GO:0051693--actin filament capping	0.86	1.00	1.00	1.00
GO:0051899--membrane depolarization	0.59	1.00	1.00	1.00
GO:0055072--iron ion homeostasis	0.84	1.00	1.00	1.00
GO:0060047--heart contraction	0.88	1.00	1.00	1.00
GO:0060048--cardiac muscle contraction	0.88	1.00	1.00	0.78
GO:0060079--regulation of excitatory postsynaptic membrane potential	0.88	1.00	1.00	1.00
GO:0060341--regulation of cellular localization	0.89	0.10	0.05	0.52
GO:0060429--epithelium development	0.87	0.12	1.00	0.40
GO:0060627--regulation of vesicle-mediated transport	0.89	1.00	1.00	0.34
GO:0070482--response to oxygen levels	0.78	1.00	1.00	0.70
GO:0001501--skeletal system development	1.00	0.00	1.00	0.78
GO:0001503--ossification	1.00	0.58	1.00	1.00
GO:0001525--angiogenesis	1.00	0.00	1.00	0.18
GO:0001568--blood vessel development	1.00	0.00	1.00	0.41
GO:0001570--vasculogenesis	1.00	0.22	1.00	1.00
GO:0001654--eye development	1.00	0.31	1.00	1.00
GO:0001655--urogenital system development	1.00	0.02	1.00	1.00
GO:0001656--metanephros development	1.00	0.05	1.00	1.00
GO:0001657--ureteric bud development	1.00	0.27	1.00	1.00
GO:0001708--cell fate specification	1.00	0.61	1.00	1.00
GO:0001763--morphogenesis of a branching structure	1.00	0.06	1.00	0.75
GO:0001764--neuron migration	1.00	0.25	1.00	1.00
GO:0001775--cell activation	1.00	0.26	0.00	1.00
GO:0001817--regulation of cytokine production	1.00	0.55	0.02	1.00
GO:0001822--kidney development	1.00	0.07	1.00	1.00
GO:0001838--embryonic epithelial tube formation	1.00	0.45	1.00	1.00
GO:0001841--neural tube formation	1.00	0.62	1.00	1.00
GO:0001867--complement activation, lectin pathway	1.00	0.52	1.00	1.00
GO:0001889--liver development	1.00	0.64	1.00	0.20
GO:0001944--vasculature development	1.00	0.00	1.00	0.41
GO:0002009--morphogenesis of an epithelium	1.00	0.40	1.00	1.00
GO:0002040--sprouting angiogenesis	1.00	0.67	1.00	1.00
GO:0002520--immune system development	1.00	0.27	0.02	1.00
GO:0002521--leukocyte differentiation	1.00	0.21	0.03	1.00
GO:0003002--regionalization	1.00	0.16	1.00	0.55
GO:0006140--regulation of nucleotide metabolic process	1.00	0.59	1.00	1.00
GO:0006355--regulation of transcription, DNA-dependent	1.00	0.27	1.00	0.07
GO:0006357--regulation of transcription from RNA polymerase II promoter	1.00	0.00	1.00	0.02
GO:0006468--protein amino acid phosphorylation	1.00	0.58	1.00	0.27
GO:0006813--potassium ion transport	1.00	0.47	1.00	0.37
GO:0006869--lipid transport	1.00	0.45	1.00	1.00
GO:0006935--chemotaxis	1.00	0.33	0.03	1.00
GO:0006955--immune response	1.00	0.39	0.00	1.00
GO:0006959--humoral immune response	1.00	0.63	0.08	1.00
GO:0007158--neuron adhesion	1.00	0.58	1.00	1.00
GO:0007167--enzyme linked receptor protein signaling pathway	1.00	0.62	1.00	0.41
GO:0007194--negative regulation of adenylate cyclase activity	1.00	0.66	1.00	1.00
GO:0007243--protein kinase cascade	1.00	0.61	1.00	0.24
GO:0007259--JAK-STAT cascade	1.00	0.61	1.00	1.00
GO:0007265--Ras protein signal transduction	1.00	0.29	0.71	0.75
GO:0007266--Rho protein signal transduction	1.00	0.59	1.00	0.64
GO:0007267--cell-cell signaling	1.00	0.00	0.52	0.71
GO:0007268--synaptic transmission	1.00	0.18	1.00	0.34
GO:0007369--gastrulation	1.00	0.69	1.00	0.35
GO:0007389--pattern specification process	1.00	0.02	1.00	0.66
GO:0007423--sensory organ development	1.00	0.04	1.00	1.00
GO:0007431--salivary gland development	1.00	0.41	1.00	1.00
GO:0007492--endoderm development	1.00	0.31	1.00	1.00
GO:0007498--mesoderm development	1.00	0.23	1.00	1.00
GO:0007507--heart development	1.00	0.02	1.00	0.69
GO:0007517--muscle organ development	1.00	0.16	1.00	0.55
GO:0007548--sex differentiation	1.00	0.53	1.00	1.00
GO:0007596--blood coagulation	1.00	0.41	1.00	1.00
GO:0007599--hemostasis	1.00	0.51	1.00	1.00
GO:0007605--sensory perception of sound	1.00	0.68	1.00	1.00
GO:0007610--behavior	1.00	0.00	0.69	1.00
GO:0007611--learning or memory	1.00	0.37	1.00	1.00
GO:0007626--locomotory behavior	1.00	0.15	0.07	1.00
GO:0007631--feeding behavior	1.00	0.67	1.00	1.00
GO:0008284--positive regulation of cell proliferation	1.00	0.31	0.59	1.00
GO:0008340--determination of adult life span	1.00	0.58	1.00	1.00
GO:0008360--regulation of cell shape	1.00	0.44	1.00	1.00
GO:0009310--amine catabolic process	1.00	0.62	1.00	1.00
GO:0009611--response to wounding	1.00	0.18	0.06	1.00

GO:0009798--axis specification	1.00	0.39	1.00	1.00
GO:0009891--positive regulation of biosynthetic process	1.00	0.24	1.00	0.47
GO:0009950--dorsal/ventral axis specification	1.00	0.62	1.00	1.00
GO:0009952--anterior/posterior pattern formation	1.00	0.18	1.00	0.51
GO:0009953--dorsal/ventral pattern formation	1.00	0.20	1.00	1.00
GO:0009968--negative regulation of signal transduction	1.00	0.62	1.00	1.00
GO:0010259--multicellular organismal aging	1.00	0.41	1.00	1.00
GO:0010552--positive regulation of specific transcription from RNA polymerase II promoter	1.00	0.70	1.00	1.00
GO:0010557--positive regulation of macromolecule biosynthetic process	1.00	0.25	1.00	0.34
GO:0010604--positive regulation of macromolecule metabolic process	1.00	0.36	1.00	0.34
GO:0010628--positive regulation of gene expression	1.00	0.10	1.00	0.22
GO:0010648--negative regulation of cell communication	1.00	0.61	1.00	1.00
GO:0010720--positive regulation of cell development	1.00	0.67	1.00	1.00
GO:0010743--regulation of foam cell differentiation	1.00	0.12	1.00	1.00
GO:0010745--negative regulation of foam cell differentiation	1.00	0.41	1.00	1.00
GO:0010817--regulation of hormone levels	1.00	0.53	1.00	1.00
GO:0010876--lipid localization	1.00	0.58	1.00	1.00
GO:0010883--regulation of lipid storage	1.00	0.42	1.00	1.00
GO:0010885--regulation of cholesterol storage	1.00	0.13	1.00	1.00
GO:0010887--negative regulation of cholesterol storage	1.00	0.52	1.00	1.00
GO:0010942--positive regulation of cell death	1.00	0.62	0.05	1.00
GO:0014031--mesenchymal cell development	1.00	0.61	1.00	1.00
GO:0015672--monovalent inorganic cation transport	1.00	0.65	1.00	0.41
GO:0015711--organic anion transport	1.00	0.70	1.00	1.00
GO:0015800--acidic amino acid transport	1.00	0.26	1.00	1.00
GO:0015810--aspartate transport	1.00	0.58	1.00	1.00
GO:0015813--L-glutamate transport	1.00	0.52	1.00	1.00
GO:0015833--peptide transport	1.00	0.44	1.00	1.00
GO:0016055--Wnt receptor signaling pathway	1.00	0.62	1.00	0.42
GO:0016337--cell-cell adhesion	1.00	0.16	1.00	0.00
GO:0016477--cell migration	1.00	0.16	1.00	1.00
GO:0016485--protein processing	1.00	0.56	1.00	1.00
GO:0018108--peptidyl-tyrosine phosphorylation	1.00	0.16	1.00	1.00
GO:0018212--peptidyl-tyrosine modification	1.00	0.18	1.00	1.00
GO:0019226--transmission of nerve impulse	1.00	0.05	1.00	0.13
GO:0019439--aromatic compound catabolic process	1.00	0.70	1.00	1.00
GO:0019827--stem cell maintenance	1.00	0.56	1.00	1.00
GO:0019835--cytolysis	1.00	0.42	0.07	1.00
GO:0021532--neural tube patterning	1.00	0.42	1.00	1.00
GO:0021536--dienecephalon development	1.00	0.31	1.00	1.00
GO:0021537--telencephalon development	1.00	0.62	1.00	1.00
GO:0021871--forebrain regionalization	1.00	0.37	1.00	1.00
GO:0021904--dorsal/ventral neural tube patterning	1.00	0.52	1.00	1.00
GO:0021915--neural tube development	1.00	0.17	1.00	1.00
GO:0021983--pituitary gland development	1.00	0.62	1.00	1.00
GO:0022604--regulation of cell morphogenesis	1.00	0.45	1.00	0.54
GO:0030001--metal ion transport	1.00	0.68	1.00	0.34
GO:0030097--hemopoiesis	1.00	0.21	0.10	1.00
GO:0030098--lymphocyte differentiation	1.00	0.27	0.07	1.00
GO:0030099--myeloid cell differentiation	1.00	0.30	1.00	1.00
GO:0030111--regulation of Wnt receptor signaling pathway	1.00	0.28	1.00	1.00
GO:0030168--platelet activation	1.00	0.71	1.00	1.00
GO:0030178--negative regulation of Wnt receptor signaling pathway	1.00	0.39	1.00	1.00
GO:0030182--neuron differentiation	1.00	0.06	1.00	0.76
GO:0030199--collagen fibril organization	1.00	0.37	1.00	1.00
GO:0030212--hyaluronan metabolic process	1.00	0.67	1.00	1.00
GO:0030217--T cell differentiation	1.00	0.26	0.07	1.00
GO:0030278--regulation of ossification	1.00	0.27	1.00	1.00
GO:0030323--respiratory tube development	1.00	0.02	1.00	0.68
GO:0030324--lung development	1.00	0.02	1.00	0.69
GO:0030326--embryonic limb morphogenesis	1.00	0.39	1.00	1.00
GO:0030502--negative regulation of bone mineralization	1.00	0.52	1.00	1.00
GO:0030799--regulation of cyclic nucleotide metabolic process	1.00	0.56	1.00	1.00
GO:0030800--negative regulation of cyclic nucleotide metabolic process	1.00	0.24	1.00	1.00
GO:0030802--regulation of cyclic nucleotide biosynthetic process	1.00	0.53	1.00	1.00
GO:0030803--negative regulation of cyclic nucleotide biosynthetic process	1.00	0.24	1.00	1.00
GO:0030808--regulation of nucleotide biosynthetic process	1.00	0.53	1.00	1.00
GO:0030809--negative regulation of nucleotide biosynthetic process	1.00	0.24	1.00	1.00
GO:0030814--regulation of cAMP metabolic process	1.00	0.60	1.00	1.00
GO:0030815--negative regulation of cAMP metabolic process	1.00	0.19	1.00	1.00
GO:0030817--regulation of cAMP biosynthetic process	1.00	0.58	1.00	1.00
GO:0030818--negative regulation of cAMP biosynthetic process	1.00	0.19	1.00	1.00
GO:0030855--epithelial cell differentiation	1.00	0.17	1.00	0.52
GO:0030856--regulation of epithelial cell differentiation	1.00	0.64	1.00	1.00
GO:0030900--forebrain development	1.00	0.01	1.00	1.00
GO:0031016--pancreas development	1.00	0.14	1.00	1.00
GO:0031018--endocrine pancreas development	1.00	0.62	1.00	1.00
GO:0031279--regulation of cyclase activity	1.00	0.71	1.00	1.00
GO:0031280--negative regulation of cyclase activity	1.00	0.66	1.00	1.00
GO:0031328--positive regulation of cellular biosynthetic process	1.00	0.21	1.00	0.44
GO:0031644--regulation of neurological system process	1.00	0.67	1.00	0.72
GO:0032612--interleukin-1 production	1.00	0.33	1.00	1.00
GO:0032940--secretion by cell	1.00	0.39	1.00	1.00
GO:0032990--cell part morphogenesis	1.00	0.32	1.00	1.00
GO:0033363--secretory granule organization	1.00	0.62	1.00	1.00
GO:0034374--low-density lipoprotein particle remodeling	1.00	0.67	1.00	1.00
GO:0035107--appendage morphogenesis	1.00	0.16	1.00	1.00
GO:0035108--limb morphogenesis	1.00	0.16	1.00	1.00
GO:0035113--embryonic appendage morphogenesis	1.00	0.39	1.00	1.00
GO:0035116--embryonic hindlimb morphogenesis	1.00	0.31	1.00	1.00
GO:0035137--hindlimb morphogenesis	1.00	0.14	1.00	1.00
GO:0035148--tube lumen formation	1.00	0.47	1.00	1.00
GO:0035239--tube morphogenesis	1.00	0.02	1.00	1.00
GO:0035270--endocrine system development	1.00	0.02	1.00	1.00
GO:0035272--exocrine system development	1.00	0.67	1.00	1.00
GO:0035295--tube development	1.00	0.00	1.00	1.00
GO:0042060--wound healing	1.00	0.26	1.00	1.00
GO:0042110--T cell activation	1.00	0.55	0.00	1.00
GO:0042157--lipoprotein metabolic process	1.00	0.64	1.00	0.62
GO:0042330--taxi	1.00	0.33	0.03	1.00
GO:0042445--hormone metabolic process	1.00	0.47	1.00	1.00
GO:0042471--ear morphogenesis	1.00	0.26	1.00	1.00
GO:0042472--inner ear morphogenesis	1.00	0.27	1.00	1.00
GO:0042692--muscle cell differentiation	1.00	0.64	1.00	0.72
GO:0043010--camera-type eye development	1.00	0.21	1.00	1.00
GO:0043062--extracellular structure organization	1.00	0.12	1.00	0.07
GO:0043065--positive regulation of apoptosis	1.00	0.66	0.05	1.00
GO:0043068--positive regulation of programmed cell death	1.00	0.61	0.05	1.00
GO:0043090--amino acid import	1.00	0.24	1.00	1.00
GO:0043092--L-amino acid import	1.00	0.24	1.00	1.00
GO:0043583--ear development	1.00	0.13	1.00	1.00
GO:0043588--skin development	1.00	0.18	1.00	1.00
GO:0045137--development of primary sexual characteristics	1.00	0.70	1.00	1.00

GO:0045165--cell fate commitment	1.00	0.18	1.00	1.00
GO:0045321--leukocyte activation	1.00	0.66	0.00	1.00
GO:0045449--regulation of transcription	1.00	0.62	1.00	0.34
GO:0045577--regulation of B cell differentiation	1.00	0.58	1.00	1.00
GO:0045580--regulation of T cell differentiation	1.00	0.61	0.37	1.00
GO:0045582--positive regulation of T cell differentiation	1.00	0.71	0.56	1.00
GO:0045586--regulation of gamma-delta T cell differentiation	1.00	0.52	0.41	1.00
GO:0045588--positive regulation of gamma-delta T cell differentiation	1.00	0.52	0.41	1.00
GO:0045596--negative regulation of cell differentiation	1.00	0.07	1.00	1.00
GO:0045597--positive regulation of cell differentiation	1.00	0.00	1.00	0.75
GO:0045619--regulation of lymphocyte differentiation	1.00	0.39	0.34	1.00
GO:0045621--positive regulation of lymphocyte differentiation	1.00	0.53	0.31	1.00
GO:0045637--regulation of myeloid cell differentiation	1.00	0.69	1.00	1.00
GO:0045639--positive regulation of myeloid cell differentiation	1.00	0.47	1.00	0.71
GO:0045664--regulation of neuron differentiation	1.00	0.22	1.00	1.00
GO:0045666--positive regulation of neuron differentiation	1.00	0.53	1.00	1.00
GO:0045667--regulation of osteoblast differentiation	1.00	0.25	1.00	1.00
GO:0045669--positive regulation of osteoblast differentiation	1.00	0.56	1.00	1.00
GO:0045761--regulation of adenylate cyclase activity	1.00	0.67	1.00	1.00
GO:0045765--regulation of angiogenesis	1.00	0.39	1.00	0.61
GO:0045893--positive regulation of transcription, DNA-dependent	1.00	0.02	1.00	0.35
GO:0045935--positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.00	0.13	1.00	0.35
GO:0045941--positive regulation of transcription	1.00	0.09	1.00	0.25
GO:0045944--positive regulation of transcription from RNA polymerase II promoter	1.00	0.00	1.00	0.60
GO:0045980--negative regulation of nucleotide metabolic process	1.00	0.31	1.00	1.00
GO:0046631--alpha-beta T cell activation	1.00	0.64	1.00	1.00
GO:0046632--alpha-beta T cell differentiation	1.00	0.52	1.00	1.00
GO:0046634--regulation of alpha-beta T cell activation	1.00	0.55	1.00	1.00
GO:0046635--positive regulation of alpha-beta T cell activation	1.00	0.58	1.00	1.00
GO:0046637--regulation of alpha-beta T cell differentiation	1.00	0.27	1.00	1.00
GO:0046638--positive regulation of alpha-beta T cell differentiation	1.00	0.39	1.00	1.00
GO:0046643--regulation of gamma-delta T cell activation	1.00	0.52	0.41	1.00
GO:0046645--positive regulation of gamma-delta T cell activation	1.00	0.52	0.41	1.00
GO:0046649--lymphocyte activation	1.00	0.57	0.00	1.00
GO:0046883--regulation of hormone secretion	1.00	0.64	1.00	1.00
GO:0048469--cell maturation	1.00	0.58	1.00	1.00
GO:0048514--blood vessel morphogenesis	1.00	0.00	1.00	0.42
GO:0048534--hemopoietic or lymphoid organ development	1.00	0.19	0.03	1.00
GO:0048562--embryonic organ morphogenesis	1.00	0.22	1.00	0.68
GO:0048568--embryonic organ development	1.00	0.02	1.00	0.53
GO:0048584--positive regulation of response to stimulus	1.00	0.39	0.02	1.00
GO:0048598--embryonic morphogenesis	1.00	0.01	1.00	0.07
GO:0048608--reproductive structure development	1.00	0.26	1.00	1.00
GO:0048663--neuron fate commitment	1.00	0.24	1.00	1.00
GO:0048666--neuron development	1.00	0.24	1.00	0.71
GO:0048704--embryonic skeletal system morphogenesis	1.00	0.70	1.00	0.51
GO:0048705--skeletal system morphogenesis	1.00	0.69	1.00	0.49
GO:0048706--embryonic skeletal system development	1.00	0.61	1.00	0.53
GO:0048730--epidermis morphogenesis	1.00	0.56	1.00	1.00
GO:0048732--gland development	1.00	0.09	1.00	1.00
GO:0048736--appendage development	1.00	0.11	1.00	1.00
GO:0048754--branching morphogenesis of a tube	1.00	0.07	1.00	0.78
GO:0048762--mesenchymal cell differentiation	1.00	0.61	1.00	1.00
GO:0048839--inner ear development	1.00	0.27	1.00	1.00
GO:0048858--cell projection morphogenesis	1.00	0.26	1.00	1.00
GO:0048863--stem cell differentiation	1.00	0.71	1.00	1.00
GO:0048864--stem cell development	1.00	0.58	1.00	1.00
GO:0050663--cytokine secretion	1.00	0.58	1.00	1.00
GO:0050678--regulation of epithelial cell proliferation	1.00	0.53	1.00	1.00
GO:0050701--interleukin-1 secretion	1.00	0.25	1.00	1.00
GO:0050707--regulation of cytokine secretion	1.00	0.66	0.21	1.00
GO:0050708--regulation of protein secretion	1.00	0.53	0.26	1.00
GO:0050714--positive regulation of protein secretion	1.00	0.64	0.20	1.00
GO:0050727--regulation of inflammatory response	1.00	0.60	1.00	1.00
GO:0050767--regulation of neurogenesis	1.00	0.27	1.00	1.00
GO:0050804--regulation of synaptic transmission	1.00	0.64	1.00	1.00
GO:0050808--synapse organization	1.00	0.57	1.00	0.42
GO:0050817--coagulation	1.00	0.41	1.00	1.00
GO:0050877--neurological system process	1.00	0.47	1.00	1.00
GO:0050878--regulation of body fluid levels	1.00	0.56	1.00	1.00
GO:0050954--sensory perception of mechanical stimulus	1.00	0.60	1.00	1.00
GO:0051023--regulation of immunoglobulin secretion	1.00	0.67	0.59	1.00
GO:0051024--positive regulation of immunoglobulin secretion	1.00	0.43	1.00	1.00
GO:0051046--regulation of secretion	1.00	0.04	0.10	1.00
GO:0051047--positive regulation of secretion	1.00	0.34	0.34	1.00
GO:0051050--positive regulation of transport	1.00	0.21	0.20	0.52
GO:0051090--regulation of transcription factor activity	1.00	0.60	1.00	1.00
GO:0051094--positive regulation of developmental process	1.00	0.00	1.00	0.40
GO:0051101--regulation of DNA binding	1.00	0.64	1.00	0.72
GO:0051222--positive regulation of protein transport	1.00	0.65	0.01	1.00
GO:0051240--positive regulation of multicellular organismal process	1.00	0.26	1.00	1.00
GO:0051241--negative regulation of multicellular organismal process	1.00	0.26	1.00	1.00
GO:0051252--regulation of RNA metabolic process	1.00	0.33	1.00	0.16
GO:0051254--positive regulation of RNA metabolic process	1.00	0.02	1.00	0.41
GO:0051350--negative regulation of lyase activity	1.00	0.66	1.00	1.00
GO:0051588--regulation of neurotransmitter transport	1.00	0.58	1.00	1.00
GO:0051604--protein maturation	1.00	0.65	1.00	1.00
GO:0051605--protein maturation by peptide bond cleavage	1.00	0.56	1.00	1.00
GO:0051607--defense response to virus	1.00	0.70	1.00	1.00
GO:0051938--L-glutamate import	1.00	0.52	1.00	1.00
GO:0051960--regulation of nervous system development	1.00	0.26	1.00	1.00
GO:0051969--regulation of transmission of nerve impulse	1.00	0.62	1.00	1.00
GO:0060041--retina development in camera-type eye	1.00	0.14	1.00	1.00
GO:0060042--retina morphogenesis in camera-type eye	1.00	0.56	1.00	1.00
GO:0060173--limb development	1.00	0.11	1.00	1.00
GO:0060284--regulation of cell development	1.00	0.26	1.00	1.00
GO:0060348--bone development	1.00	0.52	1.00	1.00
GO:0060485--mesenchyme development	1.00	0.62	1.00	1.00
GO:0060541--respiratory system development	1.00	0.02	0.74	0.66
GO:0060562--epithelial tube morphogenesis	1.00	0.27	1.00	1.00
GO:0070168--negative regulation of biomineral formation	1.00	0.52	1.00	1.00
GO:0000075--cell cycle checkpoint	1.00	1.00	0.75	1.00
GO:0001756--somitogenesis	1.00	1.00	0.60	1.00
GO:0001776--leukocyte homeostasis	1.00	1.00	0.04	1.00
GO:0001816--cytokine production	1.00	1.00	0.10	1.00
GO:0001894--tissue homeostasis	1.00	1.00	0.59	1.00
GO:0001906--cell killing	1.00	1.00	0.34	1.00
GO:0001909--leukocyte mediated cytotoxicity	1.00	1.00	0.65	1.00
GO:0001910--regulation of leukocyte mediated cytotoxicity	1.00	1.00	0.03	1.00
GO:0001912--positive regulation of leukocyte mediated cytotoxicity	1.00	1.00	0.02	1.00
GO:0002036--regulation of L-glutamate transport	1.00	1.00	0.33	1.00
GO:0002037--negative regulation of L-glutamate transport	1.00	1.00	0.24	1.00
GO:0002250--adaptive immune response	1.00	1.00	0.55	1.00

GO:0002252-immune effector process	1.00	1.00	0.07	1.00
GO:0002260-lymphocyte homeostasis	1.00	1.00	0.02	1.00
GO:0002443-leukocyte mediated immunity	1.00	1.00	0.05	1.00
GO:0002449-lymphocyte mediated immunity	1.00	1.00	0.10	1.00
GO:0002460-adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	1.00	1.00	0.55	1.00
GO:0002474-antigen processing and presentation of peptide antigen via MHC class I	1.00	1.00	0.15	1.00
GO:0002573-myeloid leukocyte differentiation	1.00	1.00	0.60	1.00
GO:0002637-regulation of immunoglobulin production	1.00	1.00	0.76	1.00
GO:0002683-negative regulation of immune system process	1.00	1.00	0.65	1.00
GO:0002684-positive regulation of immune system process	1.00	1.00	0.00	1.00
GO:0002694-regulation of leukocyte activation	1.00	1.00	0.00	1.00
GO:0002695-negative regulation of leukocyte activation	1.00	1.00	0.48	1.00
GO:0002696-positive regulation of leukocyte activation	1.00	1.00	0.00	1.00
GO:0002697-regulation of immune effector process	1.00	1.00	0.01	1.00
GO:0002699-positive regulation of immune effector process	1.00	1.00	0.03	1.00
GO:0002700-regulation of production of molecular mediator of immune response	1.00	1.00	0.76	1.00
GO:0002703-regulation of leukocyte mediated immunity	1.00	1.00	0.02	1.00
GO:0002705-positive regulation of leukocyte mediated immunity	1.00	1.00	0.03	1.00
GO:0002706-regulation of lymphocyte mediated immunity	1.00	1.00	0.03	1.00
GO:0002708-positive regulation of lymphocyte mediated immunity	1.00	1.00	0.03	1.00
GO:0002715-regulation of natural killer cell mediated immunity	1.00	1.00	0.03	1.00
GO:0002717-positive regulation of natural killer cell mediated immunity	1.00	1.00	0.03	1.00
GO:0002819-regulation of adaptive immune response	1.00	1.00	0.46	1.00
GO:0002821-positive regulation of adaptive immune response	1.00	1.00	0.53	1.00
GO:0002822-regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	1.00	1.00	0.45	1.00
GO:0002824-positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	1.00	1.00	0.51	1.00
GO:0005996-monosaccharide metabolic process	1.00	1.00	0.60	0.69
GO:0006414-translational elongation	1.00	1.00	0.45	1.00
GO:0006486-protein amino acid glycosylation	1.00	1.00	0.76	1.00
GO:0006487-protein amino acid N-linked glycosylation	1.00	1.00	0.51	1.00
GO:0006491-N-glycan processing	1.00	1.00	0.16	1.00
GO:0006707-cholesterol catabolic process	1.00	1.00	0.65	1.00
GO:0006874-cellular calcium ion homeostasis	1.00	1.00	0.59	1.00
GO:0006875-cellular metal ion homeostasis	1.00	1.00	0.53	1.00
GO:0006917-induction of apoptosis	1.00	1.00	0.01	1.00
GO:0006952-defense response	1.00	1.00	0.00	1.00
GO:0006954-inflammatory response	1.00	1.00	0.04	1.00
GO:0006968-cellular defense response	1.00	1.00	0.00	1.00
GO:0007088-regulation of mitosis	1.00	1.00	0.74	1.00
GO:0007093-mitotic cell cycle checkpoint	1.00	1.00	0.49	1.00
GO:0007166-cell surface receptor linked signal transduction	1.00	1.00	0.13	1.00
GO:0007213-muscarinic acetylcholine receptor signaling pathway	1.00	1.00	0.70	1.00
GO:0007346-regulation of mitotic cell cycle	1.00	1.00	0.28	1.00
GO:0008037-cell recognition	1.00	1.00	0.73	1.00
GO:0008283-cell proliferation	1.00	1.00	0.20	1.00
GO:0009617-response to bacterium	1.00	1.00	0.68	1.00
GO:0010564-regulation of cell cycle process	1.00	1.00	0.24	1.00
GO:0010638-positive regulation of organelle organization	1.00	1.00	0.22	1.00
GO:0010829-negative regulation of glucose transport	1.00	1.00	0.65	1.00
GO:0012502-induction of programmed cell death	1.00	1.00	0.01	1.00
GO:0015844-monoamine transport	1.00	1.00	0.48	1.00
GO:0015850-organic alcohol transport	1.00	1.00	0.74	1.00
GO:0016052-carbohydrate catabolic process	1.00	1.00	0.76	1.00
GO:0016064-immunoglobulin mediated immune response	1.00	1.00	0.71	1.00
GO:0016127-sterol catabolic process	1.00	1.00	0.65	1.00
GO:0019321-pentose metabolic process	1.00	1.00	0.70	1.00
GO:0019722-calcium-mediated signaling	1.00	1.00	0.36	1.00
GO:0019724-B cell mediated immunity	1.00	1.00	0.74	1.00
GO:0019882-antigen processing and presentation	1.00	1.00	0.10	1.00
GO:0019932-second-messenger-mediated signaling	1.00	1.00	0.27	0.53
GO:0030101-natural killer cell activation	1.00	1.00	0.25	1.00
GO:0031294-lymphocyte costimulation	1.00	1.00	0.02	1.00
GO:0031295-T cell costimulation	1.00	1.00	0.02	1.00
GO:0031341-regulation of cell killing	1.00	1.00	0.05	1.00
GO:0031343-positive regulation of cell killing	1.00	1.00	0.03	1.00
GO:0031349-positive regulation of defense response	1.00	1.00	0.27	1.00
GO:0031575-G1/S transition checkpoint	1.00	1.00	0.48	1.00
GO:0032101-regulation of response to external stimulus	1.00	1.00	0.53	1.00
GO:0032103-positive regulation of response to external stimulus	1.00	1.00	0.60	1.00
GO:0032386-regulation of intracellular transport	1.00	1.00	0.47	0.77
GO:0032388-positive regulation of intracellular transport	1.00	1.00	0.21	1.00
GO:0032880-regulation of protein localization	1.00	1.00	0.31	0.41
GO:0032890-regulation of organic acid transport	1.00	1.00	0.48	1.00
GO:0032891-negative regulation of organic acid transport	1.00	1.00	0.65	1.00
GO:0032943-mononuclear cell proliferation	1.00	1.00	0.24	1.00
GO:0032944-regulation of mononuclear cell proliferation	1.00	1.00	0.02	1.00
GO:0032945-negative regulation of mononuclear cell proliferation	1.00	1.00	0.56	1.00
GO:0032946-positive regulation of mononuclear cell proliferation	1.00	1.00	0.09	1.00
GO:0033043-regulation of organelle organization	1.00	1.00	0.41	1.00
GO:0033157-regulation of intracellular protein transport	1.00	1.00	0.69	1.00
GO:0035282-segmentation	1.00	1.00	0.59	1.00
GO:0042035-regulation of cytokine biosynthetic process	1.00	1.00	0.51	1.00
GO:0042102-positive regulation of T cell proliferation	1.00	1.00	0.06	1.00
GO:0042108-positive regulation of cytokine biosynthetic process	1.00	1.00	0.13	1.00
GO:0042113-B cell activation	1.00	1.00	0.15	1.00
GO:0042129-regulation of T cell proliferation	1.00	1.00	0.02	1.00
GO:0042130-negative regulation of T cell proliferation	1.00	1.00	0.44	1.00
GO:0042269-regulation of natural killer cell mediated cytotoxicity	1.00	1.00	0.03	1.00
GO:0042306-regulation of protein import into nucleus	1.00	1.00	0.51	1.00
GO:0042307-positive regulation of protein import into nucleus	1.00	1.00	0.15	1.00
GO:0042345-regulation of NF-kappaB import into nucleus	1.00	1.00	0.18	1.00
GO:0042346-positive regulation of NF-kappaB import into nucleus	1.00	1.00	0.03	1.00
GO:0042990-regulation of transcription factor import into nucleus	1.00	1.00	0.51	1.00
GO:0042993-positive regulation of transcription factor import into nucleus	1.00	1.00	0.07	1.00
GO:0043029-T cell homeostasis	1.00	1.00	0.02	1.00
GO:0043269-regulation of ion transport	1.00	1.00	0.24	1.00
GO:0043271-negative regulation of ion transport	1.00	1.00	0.31	1.00
GO:0043413-biopolymer glycosylation	1.00	1.00	0.76	1.00
GO:0043525-positive regulation of neuron apoptosis	1.00	1.00	0.65	1.00
GO:0044070-regulation of anion transport	1.00	1.00	0.41	1.00
GO:0044275-cellular carbohydrate catabolic process	1.00	1.00	0.45	1.00
GO:0045066-regulatory T cell differentiation	1.00	1.00	0.72	1.00
GO:0045069-regulation of viral genome replication	1.00	1.00	0.36	1.00
GO:0045088-regulation of innate immune response	1.00	1.00	0.44	1.00
GO:0045089-positive regulation of innate immune response	1.00	1.00	0.28	1.00
GO:0045428-regulation of nitric oxide biosynthetic process	1.00	1.00	0.44	1.00
GO:0045429-positive regulation of nitric oxide biosynthetic process	1.00	1.00	0.61	1.00
GO:0045576-mast cell activation	1.00	1.00	0.53	1.00
GO:0045579-positive regulation of B cell differentiation	1.00	1.00	0.47	1.00
GO:0045787-positive regulation of cell cycle	1.00	1.00	0.24	0.51
GO:0045840-positive regulation of mitosis	1.00	1.00	0.37	1.00
GO:0045954-positive regulation of natural killer cell mediated cytotoxicity	1.00	1.00	0.03	1.00
GO:0046164-alcohol catabolic process	1.00	1.00	0.61	1.00

GO:0046325--negative regulation of glucose import	1.00	1.00	0.59	1.00
GO:0046365--monosaccharide catabolic process	1.00	1.00	0.47	1.00
GO:0046651--lymphocyte proliferation	1.00	1.00	0.47	1.00
GO:0046785--microtubule polymerization	1.00	1.00	0.53	1.00
GO:0046824--positive regulation of nucleocytoplasmic transport	1.00	1.00	0.28	1.00
GO:0048002--antigen processing and presentation of peptide antigen	1.00	1.00	0.46	1.00
GO:0048535--lymph node development	1.00	1.00	0.20	1.00
GO:0048871--multicellular organismal homeostasis	1.00	1.00	0.45	1.00
GO:0048872--homeostasis of number of cells	1.00	1.00	0.25	1.00
GO:0050670--regulation of lymphocyte proliferation	1.00	1.00	0.02	1.00
GO:0050671--positive regulation of lymphocyte proliferation	1.00	1.00	0.09	1.00
GO:0050672--negative regulation of lymphocyte proliferation	1.00	1.00	0.56	1.00
GO:0050709--negative regulation of protein secretion	1.00	1.00	0.45	1.00
GO:0050710--negative regulation of cytokine secretion	1.00	1.00	0.20	1.00
GO:0050778--positive regulation of immune response	1.00	1.00	0.23	1.00
GO:0050792--regulation of viral reproduction	1.00	1.00	0.61	1.00
GO:0050848--regulation of calcium-mediated signaling	1.00	1.00	0.59	1.00
GO:0050850--positive regulation of calcium-mediated signaling	1.00	1.00	0.48	1.00
GO:0050863--regulation of T cell activation	1.00	1.00	0.00	1.00
GO:0050864--regulation of B cell activation	1.00	1.00	0.37	1.00
GO:0050865--regulation of cell activation	1.00	1.00	0.00	1.00
GO:0050866--negative regulation of cell activation	1.00	1.00	0.55	1.00
GO:0050867--positive regulation of cell activation	1.00	1.00	0.00	1.00
GO:0050868--negative regulation of T cell activation	1.00	1.00	0.47	1.00
GO:0050870--positive regulation of T cell activation	1.00	1.00	0.00	1.00
GO:0050871--positive regulation of B cell activation	1.00	1.00	0.27	1.00
GO:0050900--leukocyte migration	1.00	1.00	0.76	1.00
GO:0051048--negative regulation of secretion	1.00	1.00	0.73	0.79
GO:0051051--negative regulation of transport	1.00	1.00	0.65	0.22
GO:0051223--regulation of protein transport	1.00	1.00	0.11	0.45
GO:0051249--regulation of lymphocyte activation	1.00	1.00	0.00	1.00
GO:0051250--negative regulation of lymphocyte activation	1.00	1.00	0.71	1.00
GO:0051251--positive regulation of lymphocyte activation	1.00	1.00	0.00	1.00
GO:0051726--regulation of cell cycle	1.00	1.00	0.70	1.00
GO:0051783--regulation of nuclear division	1.00	1.00	0.74	1.00
GO:0051785--positive regulation of nuclear division	1.00	1.00	0.37	1.00
GO:0051937--catecholamine transport	1.00	1.00	0.59	1.00
GO:0051952--regulation of amine transport	1.00	1.00	0.27	1.00
GO:0051953--negative regulation of amine transport	1.00	1.00	0.53	1.00
GO:0051955--regulation of amino acid transport	1.00	1.00	0.65	1.00
GO:0051956--negative regulation of amino acid transport	1.00	1.00	0.41	1.00
GO:0055066--metal ion homeostasis	1.00	1.00	0.46	1.00
GO:0055066--di-, tri-valent inorganic cation homeostasis	1.00	1.00	0.74	0.73
GO:0055074--calcium ion homeostasis	1.00	1.00	0.47	1.00
GO:0070085--glycosylation	1.00	1.00	0.76	1.00
GO:0070201--regulation of establishment of protein localization	1.00	1.00	0.16	0.27
GO:0070661--leukocyte proliferation	1.00	1.00	0.24	1.00
GO:0070663--regulation of leukocyte proliferation	1.00	1.00	0.02	1.00
GO:0070664--negative regulation of leukocyte proliferation	1.00	1.00	0.56	1.00
GO:0070665--positive regulation of leukocyte proliferation	1.00	1.00	0.09	1.00
GO:0000165--MAPKKK cascade	1.00	1.00	1.00	0.22
GO:0000187--activation of MAPK activity	1.00	1.00	1.00	0.59
GO:0000271--polysaccharide biosynthetic process	1.00	1.00	1.00	0.41
GO:0001101--response to acid	1.00	1.00	1.00	0.72
GO:0001569--patterning of blood vessels	1.00	1.00	1.00	0.73
GO:0001678--cellular glucose homeostasis	1.00	1.00	1.00	0.47
GO:0001702--gastrulation with mouth forming second	1.00	1.00	1.00	0.73
GO:0001704--formation of primary germ layer	1.00	1.00	1.00	0.59
GO:0001707--mesoderm formation	1.00	1.00	1.00	0.70
GO:0001818--negative regulation of cytokine production	1.00	1.00	1.00	0.78
GO:0002011--morphogenesis of an epithelial sheet	1.00	1.00	1.00	0.76
GO:0002027--regulation of heart rate	1.00	1.00	1.00	0.78
GO:0005977--glycogen metabolic process	1.00	1.00	1.00	0.78
GO:0005978--glycogen biosynthetic process	1.00	1.00	1.00	0.62
GO:0006112--energy reserve metabolic process	1.00	1.00	1.00	0.58
GO:0006350--transcription	1.00	1.00	1.00	0.51
GO:0006471--protein amino acid ADP-ribosylation	1.00	1.00	1.00	0.78
GO:0006497--protein amino acid lipidation	1.00	1.00	1.00	0.72
GO:0006575--cellular amino acid derivative metabolic process	1.00	1.00	1.00	0.41
GO:0006675--biogenic amine metabolic process	1.00	1.00	1.00	0.80
GO:0006635--fatty acid beta-oxidation	1.00	1.00	1.00	0.77
GO:0006644--phospholipid metabolic process	1.00	1.00	1.00	0.48
GO:0006650--glycerophospholipid metabolic process	1.00	1.00	1.00	0.35
GO:0006656--phosphatidylcholine biosynthetic process	1.00	1.00	1.00	0.64
GO:0006720--isoprenoid metabolic process	1.00	1.00	1.00	0.62
GO:0006733--oxidoreduction coenzyme metabolic process	1.00	1.00	1.00	0.80
GO:0006739--NADP metabolic process	1.00	1.00	1.00	0.58
GO:0006766--vitamin metabolic process	1.00	1.00	1.00	0.78
GO:0006769--nicotinamide metabolic process	1.00	1.00	1.00	0.73
GO:0006790--sulfur metabolic process	1.00	1.00	1.00	0.57
GO:0006812--cation transport	1.00	1.00	1.00	0.41
GO:0006835--dicarboxylic acid transport	1.00	1.00	1.00	0.72
GO:0006873--cellular ion homeostasis	1.00	1.00	1.00	0.49
GO:0006916--anti-apoptosis	1.00	1.00	1.00	0.59
GO:0006937--regulation of muscle contraction	1.00	1.00	1.00	0.23
GO:0006940--regulation of smooth muscle contraction	1.00	1.00	1.00	0.49
GO:0006972--hyperosmotic response	1.00	1.00	1.00	0.79
GO:0007050--cell cycle arrest	1.00	1.00	1.00	0.52
GO:0007156--homophilic cell adhesion	1.00	1.00	1.00	0.00
GO:0007160--cell-matrix adhesion	1.00	1.00	1.00	0.78
GO:0007178--transmembrane receptor protein serine/threonine kinase signaling pathway	1.00	1.00	1.00	0.35
GO:0007179--transforming growth factor beta receptor signaling pathway	1.00	1.00	1.00	0.31
GO:0007219--Notch signaling pathway	1.00	1.00	1.00	0.69
GO:0007264--small GTPase mediated signal transduction	1.00	1.00	1.00	0.47
GO:0007272--ensheathment of neurons	1.00	1.00	1.00	0.53
GO:0007416--synaptogenesis	1.00	1.00	1.00	0.48
GO:0007422--peripheral nervous system development	1.00	1.00	1.00	0.70
GO:0007622--rhythmic behavior	1.00	1.00	1.00	0.58
GO:0007623--circadian rhythm	1.00	1.00	1.00	0.44
GO:0008045--motor axon guidance	1.00	1.00	1.00	0.79
GO:0008272--sulfate transport	1.00	1.00	1.00	0.72
GO:0008277--regulation of G-protein coupled receptor protein signaling pathway	1.00	1.00	1.00	0.41
GO:0008344--adult locomotory behavior	1.00	1.00	1.00	0.64
GO:0008366--axon ensheathment	1.00	1.00	1.00	0.53
GO:0008654--phospholipid biosynthetic process	1.00	1.00	1.00	0.27
GO:0009062--fatty acid catabolic process	1.00	1.00	1.00	0.70
GO:0009100--glycoprotein metabolic process	1.00	1.00	1.00	0.71
GO:0009116--nucleoside metabolic process	1.00	1.00	1.00	0.53
GO:0009119--ribonucleoside metabolic process	1.00	1.00	1.00	0.44
GO:0009141--nucleoside triphosphate metabolic process	1.00	1.00	1.00	0.78
GO:0009144--purine nucleoside triphosphate metabolic process	1.00	1.00	1.00	0.66
GO:0009166--nucleotide catabolic process	1.00	1.00	1.00	0.65
GO:0009199--ribonucleoside triphosphate metabolic process	1.00	1.00	1.00	0.80

GO:0009205--purine ribonucleoside triphosphate metabolic process	1.00	1.00	1.00	0.78
GO:0009250--glucan biosynthetic process	1.00	1.00	1.00	0.62
GO:0009743--response to carbohydrate stimulus	1.00	1.00	1.00	0.41
GO:0009746--response to hexose stimulus	1.00	1.00	1.00	0.62
GO:0009749--response to glucose stimulus	1.00	1.00	1.00	0.52
GO:0009820--alkaloid metabolic process	1.00	1.00	1.00	0.77
GO:0010001--glial cell differentiation	1.00	1.00	1.00	0.72
GO:0010563--negative regulation of phosphorus metabolic process	1.00	1.00	1.00	0.78
GO:0010594--regulation of endothelial cell migration	1.00	1.00	1.00	0.60
GO:0010717--regulation of epithelial to mesenchymal transition	1.00	1.00	1.00	0.40
GO:0010718--positive regulation of epithelial to mesenchymal transition	1.00	1.00	1.00	0.76
GO:0010769--regulation of cell morphogenesis involved in differentiation	1.00	1.00	1.00	0.74
GO:0010770--positive regulation of cell morphogenesis involved in differentiation	1.00	1.00	1.00	0.76
GO:0010923--negative regulation of phosphatase activity	1.00	1.00	1.00	0.69
GO:0014037--Schwann cell differentiation	1.00	1.00	1.00	0.40
GO:0014065--phosphoinositide 3-kinase cascade	1.00	1.00	1.00	0.76
GO:0014075--response to amine stimulus	1.00	1.00	1.00	0.69
GO:0014706--striated muscle tissue development	1.00	1.00	1.00	0.67
GO:0016051--carbohydrate biosynthetic process	1.00	1.00	1.00	0.13
GO:0016246--RNA interference	1.00	1.00	1.00	0.63
GO:0016310--phosphorylation	1.00	1.00	1.00	0.24
GO:0016339--calcium-dependent cell-cell adhesion	1.00	1.00	1.00	0.02
GO:0016441--posttranscriptional gene silencing	1.00	1.00	1.00	0.73
GO:0016458--gene silencing	1.00	1.00	1.00	0.59
GO:0016540--protein autoprocessing	1.00	1.00	1.00	0.57
GO:0016567--protein ubiquitination	1.00	1.00	1.00	0.49
GO:0018130--heterocycle biosynthetic process	1.00	1.00	1.00	0.71
GO:0018210--peptidyl-threonine modification	1.00	1.00	1.00	0.73
GO:0019318--hexose metabolic process	1.00	1.00	1.00	0.72
GO:0019362--pyridine nucleotide metabolic process	1.00	1.00	1.00	0.80
GO:0019395--fatty acid oxidation	1.00	1.00	1.00	0.69
GO:0019637--organophosphate metabolic process	1.00	1.00	1.00	0.35
GO:0019748--secondary metabolic process	1.00	1.00	1.00	0.60
GO:0021546--rhomomere development	1.00	1.00	1.00	0.43
GO:0021569--rhomomere 3 development	1.00	1.00	1.00	0.69
GO:0021604--cranial nerve structural organization	1.00	1.00	1.00	0.69
GO:0021610--facial nerve morphogenesis	1.00	1.00	1.00	0.69
GO:0021612--facial nerve structural organization	1.00	1.00	1.00	0.69
GO:0021675--nerve development	1.00	1.00	1.00	0.78
GO:0021696--cerebellar cortex morphogenesis	1.00	1.00	1.00	0.78
GO:0022410--circadian sleep/wake cycle process	1.00	1.00	1.00	0.62
GO:0022602--ovulation cycle process	1.00	1.00	1.00	0.79
GO:0030003--cellular cation homeostasis	1.00	1.00	1.00	0.79
GO:0030005--cellular di-, tri-valent inorganic cation homeostasis	1.00	1.00	1.00	0.72
GO:0030035--microspike assembly	1.00	1.00	1.00	0.78
GO:0030100--regulation of endocytosis	1.00	1.00	1.00	0.18
GO:0030239--myofibril assembly	1.00	1.00	1.00	0.53
GO:0030258--lipid modification	1.00	1.00	1.00	0.59
GO:0030518--steroid hormone receptor signaling pathway	1.00	1.00	1.00	0.34
GO:0030534--adult behavior	1.00	1.00	1.00	0.41
GO:0030866--cortical actin cytoskeleton organization	1.00	1.00	1.00	0.79
GO:0031032--actomyosin structure organization	1.00	1.00	1.00	0.32
GO:0031344--regulation of cell projection organization	1.00	1.00	1.00	0.78
GO:0031346--positive regulation of cell projection organization	1.00	1.00	1.00	0.75
GO:0031647--regulation of protein stability	1.00	1.00	1.00	0.80
GO:0031668--cellular response to extracellular stimulus	1.00	1.00	1.00	0.53
GO:0032355--response to estradiol stimulus	1.00	1.00	1.00	0.76
GO:0032387--negative regulation of intracellular transport	1.00	1.00	1.00	0.60
GO:0032436--positive regulation of proteasomal ubiquitin-dependent protein catabolic process	1.00	1.00	1.00	0.76
GO:0032680--regulation of tumor necrosis factor production	1.00	1.00	1.00	0.60
GO:0032856--activation of Ras GTPase activity	1.00	1.00	1.00	0.69
GO:0032862--activation of Rho GTPase activity	1.00	1.00	1.00	0.69
GO:0032868--response to insulin stimulus	1.00	1.00	1.00	0.43
GO:0032925--regulation of activin receptor signaling pathway	1.00	1.00	1.00	0.29
GO:0033628--regulation of cell adhesion mediated by integrin	1.00	1.00	1.00	0.76
GO:0033692--cellular polysaccharide biosynthetic process	1.00	1.00	1.00	0.48
GO:0034284--response to monosaccharide stimulus	1.00	1.00	1.00	0.62
GO:0034440--lipid oxidation	1.00	1.00	1.00	0.69
GO:0035051--cardiac cell differentiation	1.00	1.00	1.00	0.59
GO:0035194--posttranscriptional gene silencing by RNA	1.00	1.00	1.00	0.73
GO:0040013--negative regulation of locomotion	1.00	1.00	1.00	0.77
GO:0040014--regulation of multicellular organism growth	1.00	1.00	1.00	0.66
GO:0040018--positive regulation of multicellular organism growth	1.00	1.00	1.00	0.42
GO:0042063--gliogenesis	1.00	1.00	1.00	0.69
GO:0042158--lipoprotein biosynthetic process	1.00	1.00	1.00	0.54
GO:0042278--purine nucleoside metabolic process	1.00	1.00	1.00	0.34
GO:0042308--negative regulation of protein import into nucleus	1.00	1.00	1.00	0.78
GO:0042439--ethanolamine and derivative metabolic process	1.00	1.00	1.00	0.60
GO:0042552--myelination	1.00	1.00	1.00	0.49
GO:0042594--response to starvation	1.00	1.00	1.00	0.80
GO:0042745--circadian sleep/wake cycle	1.00	1.00	1.00	0.71
GO:0042749--regulation of circadian sleep/wake cycle	1.00	1.00	1.00	0.62
GO:0043085--positive regulation of catalytic activity	1.00	1.00	1.00	0.72
GO:0043200--response to amino acid stimulus	1.00	1.00	1.00	0.66
GO:0043392--negative regulation of DNA binding	1.00	1.00	1.00	0.77
GO:0043405--regulation of MAP kinase activity	1.00	1.00	1.00	0.18
GO:0043406--positive regulation of MAP kinase activity	1.00	1.00	1.00	0.34
GO:0043408--regulation of MAPKKK cascade	1.00	1.00	1.00	0.69
GO:0043410--positive regulation of MAPKKK cascade	1.00	1.00	1.00	0.52
GO:0043523--regulation of neuron apoptosis	1.00	1.00	1.00	0.72
GO:0043547--positive regulation of GTPase activity	1.00	1.00	1.00	0.60
GO:0043627--response to estrogen stimulus	1.00	1.00	1.00	0.21
GO:0043691--reverse cholesterol transport	1.00	1.00	1.00	0.78
GO:0044092--negative regulation of molecular function	1.00	1.00	1.00	0.78
GO:0044242--cellular lipid catabolic process	1.00	1.00	1.00	0.80
GO:0044264--cellular polysaccharide metabolic process	1.00	1.00	1.00	0.60
GO:0045017--glycerolipid biosynthetic process	1.00	1.00	1.00	0.27
GO:0045187--regulation of circadian sleep/wake cycle, sleep	1.00	1.00	1.00	0.62
GO:0045444--fat cell differentiation	1.00	1.00	1.00	0.72
GO:0045600--positive regulation of fat cell differentiation	1.00	1.00	1.00	0.63
GO:0045682--regulation of epidermis development	1.00	1.00	1.00	0.60
GO:0045684--positive regulation of epidermis development	1.00	1.00	1.00	0.69
GO:0045732--positive regulation of protein catabolic process	1.00	1.00	1.00	0.26
GO:0045785--positive regulation of cell adhesion	1.00	1.00	1.00	0.74
GO:0045807--positive regulation of endocytosis	1.00	1.00	1.00	0.49
GO:0045927--positive regulation of growth	1.00	1.00	1.00	0.52
GO:0045931--positive regulation of mitotic cell cycle	1.00	1.00	1.00	0.71
GO:0045933--positive regulation of muscle contraction	1.00	1.00	1.00	0.53
GO:0045936--negative regulation of phosphate metabolic process	1.00	1.00	1.00	0.78
GO:0045987--positive regulation of smooth muscle contraction	1.00	1.00	1.00	0.52
GO:0046128--purine ribonucleoside metabolic process	1.00	1.00	1.00	0.34
GO:0046165--alcohol biosynthetic process	1.00	1.00	1.00	0.62
GO:0046320--regulation of fatty acid oxidation	1.00	1.00	1.00	0.77

GO:0046364--monosaccharide biosynthetic process	1.00	1.00	1.00	0.74
GO:0046470--phosphatidylcholine metabolic process	1.00	1.00	1.00	0.53
GO:0046473--phosphatidic acid metabolic process	1.00	1.00	1.00	0.76
GO:0046474--glycerophospholipid biosynthetic process	1.00	1.00	1.00	0.20
GO:0046486--glycerolipid metabolic process	1.00	1.00	1.00	0.54
GO:0046489--phosphoinositide biosynthetic process	1.00	1.00	1.00	0.73
GO:0046496--nicotinamide nucleotide metabolic process	1.00	1.00	1.00	0.73
GO:0046498--S-adenosylhomocysteine metabolic process	1.00	1.00	1.00	0.63
GO:0046579--positive regulation of Ras protein signal transduction	1.00	1.00	1.00	0.78
GO:0046777--protein amino acid autophosphorylation	1.00	1.00	1.00	0.58
GO:0046822--regulation of nucleocytoplasmic transport	1.00	1.00	1.00	0.78
GO:0046823--negative regulation of nucleocytoplasmic transport	1.00	1.00	1.00	0.52
GO:0048008--platelet-derived growth factor receptor signaling pathway	1.00	1.00	1.00	0.78
GO:0048332--mesoderm morphogenesis	1.00	1.00	1.00	0.78
GO:0048483--autonomic nervous system development	1.00	1.00	1.00	0.13
GO:0048511--rhythmic process	1.00	1.00	1.00	0.35
GO:0048545--response to steroid hormone stimulus	1.00	1.00	1.00	0.30
GO:0048593--camera-type eye morphogenesis	1.00	1.00	1.00	0.62
GO:0048738--cardiac muscle tissue development	1.00	1.00	1.00	0.63
GO:0048745--smooth muscle tissue development	1.00	1.00	1.00	0.20
GO:0048857--neural nucleus development	1.00	1.00	1.00	0.57
GO:0048878--chemical homeostasis	1.00	1.00	1.00	0.63
GO:0050764--regulation of phagocytosis	1.00	1.00	1.00	0.78
GO:0050766--positive regulation of phagocytosis	1.00	1.00	1.00	0.71
GO:0050795--regulation of behavior	1.00	1.00	1.00	0.44
GO:0050801--ion homeostasis	1.00	1.00	1.00	0.52
GO:0050999--regulation of nitric-oxide synthase activity	1.00	1.00	1.00	0.78
GO:0051100--negative regulation of binding	1.00	1.00	1.00	0.71
GO:0051129--negative regulation of cellular component organization	1.00	1.00	1.00	0.78
GO:0051130--positive regulation of cellular component organization	1.00	1.00	1.00	0.51
GO:0051146--striated muscle cell differentiation	1.00	1.00	1.00	0.57
GO:0051180--vitamin transport	1.00	1.00	1.00	0.72
GO:0051224--negative regulation of protein transport	1.00	1.00	1.00	0.43
GO:0051346--negative regulation of hydrolase activity	1.00	1.00	1.00	0.66
GO:0051651--maintenance of location in cell	1.00	1.00	1.00	0.78
GO:0051789--response to protein stimulus	1.00	1.00	1.00	0.72
GO:0051896--regulation of protein kinase B signaling cascade	1.00	1.00	1.00	0.66
GO:0055002--striated muscle cell development	1.00	1.00	1.00	0.69
GO:0055008--cardiac muscle tissue morphogenesis	1.00	1.00	1.00	0.39
GO:0055010--ventricular cardiac muscle morphogenesis	1.00	1.00	1.00	0.41
GO:0055082--cellular chemical homeostasis	1.00	1.00	1.00	0.34
GO:0055085--transmembrane transport	1.00	1.00	1.00	0.39
GO:0060415--muscle tissue morphogenesis	1.00	1.00	1.00	0.39
GO:0060491--regulation of cell projection assembly	1.00	1.00	1.00	0.73
GO:0060537--muscle tissue development	1.00	1.00	1.00	0.34
GO:0070302--regulation of stress-activated protein kinase signaling pathway	1.00	1.00	1.00	0.80
GO:0070423--nucleotide-binding oligomerization domain containing signaling pathway	1.00	1.00	1.00	0.69
GO:0070431--nucleotide-binding oligomerization domain containing 2 signaling pathway	1.00	1.00	1.00	0.69
GO:0070647--protein modification by small protein conjugation or removal	1.00	1.00	1.00	0.58
GO:0090003--regulation of establishment of protein localization to plasma membrane	1.00	1.00	1.00	0.76

Table S6. DEGs.

Alveolar > Bronchial	Alveolar < Bronchial	Lung > T	Lung < T
FGR	TSPAN6	TSPAN6	Clorf112
MAD1L1	SCYL3	CFH	FGR
CASP10	GCLC	FUCA2	NIPAL3
TFPI	STPG1	SEMA3F	MAD1L1
PLXND1	ENPP4	HS3ST1	SARM1
HSPB6	HS3ST1	TMEM176A	CAMKK1
PKD4	KLHL13	ICA1	RECQL
SKAP2	ALS2	TFPI	ARHGAP33
FAM214B	SLC7A2	HSPB6	DVL2
COFZ2	CD38	PKD4	CCDC109B
ITGAL	ZMYND10	ST7	DHX33
ITGA3	ARX	PRKAR2B	ITGAL
MAP3K14	PRSS22	ITGA3	ZFX
CX3CL1	BZRAP1	TMEM98	OSBPL7
TNFRSF12A	WDR54	CX3CL1	MAP3K14
RALA	CROT	TNFRSF12A	MAP3K9
ETV1	CRLF1	BAIAP2L1	JHDM1D
IFRD1	BAIAP2L1	ALDH3B1	PHTF2
ADIPOR2	ALDH3B1	GTTF2IRD1	DBF4
CEACAM21	TTC22	ARHGAP44	IFRD1
MATK	USH1C	ARSD	MARK4
RHBDF1	PNPLA4	RHBDF1	CEACAM21
CACNA2D2	CDKL3	TEAD3	PAFAH1B1
CDKL5	PROM1	FMO3	TRAPPC6A
CDK11A	DNAH9	SYPL1	MATK
CYTH3	BAIAP3	MGST1	CD79B
SPAG9	DLEC1	NFIX	TKTL1
AASS	CYB561	ETV7	RPUSD1
ST3GAL1	PLEKHG6	CD9	CRAMP1L
IL32	VTAI	STAB1	MYLIP
RHOBTB2	GIPR	KAL1	E2F2
TRAF3IP3	FUZ	DCN	JARID2
IFFO1	LRRC23	LTF	CELSR3
STAB1	MKS1	HEBP1	ST3GAL1
FYN	LTF	GPRC5A	MMP25
MRC2	CCDC88C	ACBP	IL32
TSPAN9	IL20RA	MTMR11	TRAF3IP3
ABHD5	GLT8D1	CHDH	ZNF207
PLAUR	CYP24A1	IL20RA	IFFO1
DCN	ZFP64	VWTR1	NISCH
TYROBP	MNAT1	VSIG2	IDS
CD22	MRE11A	PHLDB1	ZNF200
SEMA3B	PLEKHB1	MARCO	FYN
ALOX5	NRXN3	SNAI2	HIVEP2
CLDN11	SLC45A4	CD74	APBA3
HEBP1	GCLM	NRXN3	AKAP8L
GPRC5A	RRAGD	ALAS1	MBTD1
CD6	HSF2	DERA	RNF216
TACC3	TOMM34	EHD2	QPCTL
YAF2	MIPEP	HSD17B6	MAN2B2
WAS	HMGB3	TYMP	NUB1
IGF1	IKZF2	GRN	CLK1
SLC38A5	IFT88	VCAN	CD6
SLC11A1	EFCAB1	CDH1	TACC3
PHLDB1	ADSS	RAI14	ZC3H3
MARCO	USP2	TNC	CCDC88C
SNAI2	CDH1	CAPG	WAS
HGF	DNAH5	ADRB1	ZRANB1
SAMD4A	C6	CTNNA1	RUNX3
RUNX3	TDP1	DSG2	SPAST
CSB	SPATA7	GPM6B	OSBPL5
PHL1	ADAM28	CC2D2A	DEF6
PLEKH01	BARX2	LMO3	RTEL1-TNFRSF6B
EHD2	TRT1	KITLG	SLAMF7
HSD17B6	CUL7	LTBP1	BTN3A1
NR1H3	CTPS2	RCN1	PRKCH
TYMP	CP	ELN	SH2D2A
VIM	KIAA0556	NEDD4L	TNFRSF1B
CD44	USP28	DKK3	POU2F2
PRKCH	CC2D2A	LIMA1	BCLAF1
TNFRSF1B	COL9A2	BCAR1	BAK1
GRN	EPN3	HOMER3	CHPF2
FAM13B	PPP1R3F	PRSS8	SLC4A7
ARHGAP31	SLC4A8	FNIP2	APBA2
ARID4A	PLEKHA5	MSMO1	ASTE1
PNPLA6	AKR7A2	LAMA3	STAP1
GAB2	ANAPC4	TRAF3IP2	MYOM2
ATP6V0A1	LY75	DCBLD2	ZZZ3
TMSB10	HHAT	LAMC2	MRII
VCL	FOXC1	CDK14	PHLPP2
DAPK2	ATP9A	YBX3	INPP4A
TIMP2	GYG2	PRDM6	MED17
TUBG2	PKP2	NCKAP1	PHF15
FLT4	LAMC2	DGAT2	LCP2
TRIO	ALDH18A1	ISOC2	WDR37
VCAN	PSD	GPC1	YTHDC2
MSR1	PIGV	LIMCH1	USP28
FAM65A	PTPRU	SPA17	TSPAN17
CAPG	SPAG4	WISP2	UTS2
AP2S1	CDH3	ST3GAL6	TNFRSF9
LCP2	ZNF112	ATP2C2	FOXP3
CNTLN	SLC6A16	SNX24	MPHOSPH9
PREX2	SPA17	ANKS1A	FOXN3
WWC3	EYA2	SLC9A3R2	NRIP2
ARHGAP6	SNCAIP	NTHL1	FAM168A
MAP4	BTBD1	ERBB3	RELT
ROS1	BCAS1	PDIA5	NOP58
CELF2	NTN1	MYLK	CYFIP2
PER3	TBC1D22B	GSTO2	TAB2
LTBP1	GSTO2	ME1	USP36
ELN	ZMYND12	CLDN18	ZNF280C
HEXB	NGEF	FGFR2	TRAF1
DKK3	PFKP	EML1	RC3H2
LAMC3	TP53BP1	EVIS	PRDM1
BCAR1	FGFR3	PRKCZ	ATP11B
HOMER3	REEP1	ROGD1	FLYWCH1
SIKE1	KIF2A	HYAL2	UNKL
LAMA3	PITX1	PLEKHH3	TARBP1
OPN3	VPS35	REEP1	MXD1
MCOLN3	NUCB2	LAPTM4A	CDK17
CCDC35A	PFN2	MAST4	SLC2A3
PRDM1	PTPN3	GPR116	CTDP1
TMCC3	DAPP1	MAOB	OGFR
USP13	ST6GALNAC1	PLA2G10	QSER1
PPP1R12A	WIP1	LRP6	TNK2
RASGRF1	AP3M2	PFN2	ELMO2

ATP2B4	ST6GALNAC2	PTPN3	GLTSCR1
DGKG	C16orf80	NDST1	SPHK2
FLYWCH1	OSBPL3	ST6GALNAC2	MTMR1
TBXAS1	TRIP13	PTPN21	RNF4
MXD1	LNX1	RPS6KA2	CASP8
SLC2A3	ACAP1	LMCD1	ASUN
BCAT1	XRCC1	CYBRD1	TSPAN32
HDAC7	MCM2	EPN2	MEF2BNB-MEF2B
PRDM6	TP63	ALDH3A2	LPAR2
GUCY1B3	NSF	RHOBTB1	CNN2
LIMCH1	CLASP1	P4HA2	PMS1
TSPAN32	ATP2A3	TMEM38A	TAF11
WISP2	SRI	FERMT2	ZNF76
SLC12A2	SEMA3C	DHRS9	UHRF1BP1
ABCA7	CELSR1	IGF3BP2	DGKA
CHIBL2	ATP12A	MAP3K13	TMEM206
CALCR1	KIFAP3	GLI2	CYB5R4
SLC9A3R2	TRAF4	NOTCH3	SEC61A2
TRAM2	RARB	TEAD2	PRKCQ
ANKRD44	UBE2T	MGLL	FAM107B
MYLK	DNAJC10	NTN4	CDK13
PRKCQ	SPAG6	PTPLAD1	MTHFD2
TBC1D1	N4BP2	ARHGEF10L	FOXJ2
YBX1	TULP3	SEMA3C	CD84
TIE1	ADCY2	ACAT1	ZBTB11
CD84	ZCWPW1	CELSR1	THUMPDI
SP11	TP73	RASAL2	ID11
CLDN18	OSBPL6	PLXNA2	KLF6
ATXN3	LNX	GPC4	CACNB1
MYO9A	CDC14A	RAP1GAP	ZFY
KLF6	RABL2B	CTTNBP2	PDZD4
PPAP2A	RFX3	RARB	CBFB
TNFRSF1A	SLC4A4	FBLN1	RASSF1
HYAL2	SESN1	LAMP3	OTUD5
RASSF1	PHI1D3	NEBL	TBC1D25
IFB5	MOK	EDN1	POLR1A
TFE3	HSP90AA1	SLC1A3	RASGRP2
ACSL4	ARG2	LNX	KCNAB2
ATP11A	HSPB11	TNS1	CLCC2D
RASGRP2	PHLPP1	OPHN1	KORA
PPP2R5B	ATP8B1	EPB41L2	KIAA1107
GPR116	DLG3	MOXD1	PHRF1
ABCC9	SERTAD4	STX7	FGF22
TGFBFR3	ULK2	SLC4A4	RNF126
ATP1B3	GRHL2	MOK	MNT
FSTL3	ZNF446	CXCL2	JMJD6
PTPN21	NOA1	MEF2C	ASNS
ATP2B1	GSTP1	CADPS2	PABPC1
MGAT4A	AGBL5	ATP8B1	TCOF1
ARHGAP10	MAPRE3	SMARCD3	CDC42
RPS6KA2	SCAMP1	COBLL1	NCK2
LMCD1	WDR47	SERTAD4	MGAT4A
SEL1L	TTC39A	ITGB5	RPL31
TRIB2	IPO11	FAT1	ING3
MBD3	HSD17B2	GSTP1	TCF3
CYBRD1	TXLNG	APLP2	TRIB2
PRKACA	MTMR2	COL16A1	DAZAP1
LIMS2	MT3	CD59	MARK2
TFRC	GMCL1	MECOM	CHFR
FCGR2B	TFAP2C	CTTN	NFATC3
STK10	RFX2	TTC39A	STK10
CRMP1	METTTL2A	MGST2	ACAP1
MRV11	TGDS	USP40	SIDT1
PVR	TMEM40	CHMP5	RP3-402G11.5
SCARB1	KIF9	EPDR1	TBX21
PDE4A	SLC4A11	CEACAM6	EED
FERMT2	DYNLL1	TRIP6	ATP2A3
PTGS2	ANAPC5	MMP2	IPCEF1
FRY	DZANK1	LPCAT2	ZZEF1
PICALM	C20orf26	PIR	ANO8
NOTCH3	TASP1	AAMDC	TXK
TEAD2	FXYD3	SULT2B1	TTC38
MGLL	LAG3	GNA11	SLC25A40
NUAK1	NUDC	ASAP3	VPS9D1
ZNF532	CERS4	EPB41L1	MARK3
SCARF1	NAT14	KIF9	FOSL2
ARHGEF10L	DTX2	DYNLL1	SEC31B
TXK	ILSRA	FXYD3	ARHGAP15
FRYL	TF	BLVRB	ARHGAP15
FSCN1	NLRP1	LYZ	MCM6
ARHGAP15	RGS17	LAMB1	ICAM3
RBMS2	PHGDH	ABCC6	ARHGEF1
ACACB	EZR	MLTK	MAP2K7
PAG1	TEKT2	TMEM101	DGKD
MCAM	VNN3	CCDC80	NFKB2
DGKD	MSH2	DPYSL2	GTF3C1
NFKB2	EPB41L4B	COMT	IL4R
APBB1IP	NANS	GABRP	APBB1IP
FGFR1	DFNB31	FM02	LRCH4
FBLN1	CRISP3	EPB41L4B	FAM76B
ITGA8	EFHC1	NANS	SIRT6
CST7	HSP90AB1	CRTAC1	CST7
MAP2	DSP	BAMBI	PIAS2
LAMP3	IFT74	TREM2	N4BP2
ACER3	H2AFY2	PGC	SYNU2
C12orf5	MZF1	EFHC1	PPP2R5C
EDN1	OCEL1	DSP	P2RY10
ITM2A	MISP	TMED1	TNRC6C
RUNX1T1	SLC7A4	NRP1	PKD2L2
FKBP7	SEC14L3	PALMD	MYH7B
SLC1A3	GCAT	TSPAN15	THOC1
TNS1	ANKRD54	MISP	SP140
REXO1	CENPM	DERL3	CDC14A
RAPGEF3	SLC5A1	SUSD2	SENP1
CIC	CBY1	GGT5	LIPE
LRRRC16A	RTDR1	PRODH	KIF22
PGM1	XPB1	LGALS2	RAB21
EPB41L2	RAB36	TRIOBP	CPOX
MOXD1	DNAL4	KDELR3	CLDN1
SCTR	TTL1	CBY1	RBL1
RAB21	BIK	TIMP3	IGSF9B
CPB2	MCAT	MCAT	AP4E1
CLDN1	IFT27	RBF1OX2	RSBN1
CXCL2	PRMT5	APOL4	TCF7
COL4A4	ATP6V1D	CHADL	PTPRC
OSTM1	SAMD15	PMN1	STK17B
MEF2C	AHSA1	PYGL	ZNF510
PTPRC	SDX4	GSTZ1	DUSP12

FYB	CEP128	LGMN	IL12RB2
EPB41L3	RPS6KA5	ZFYVE21	FYB
COBLL1	REC8	PSMB5	TRAF5
KAT6A	TM9SF1	TM9SF1	GSK3B
PLOD1	UQCC	NFATC4	P2RX5
BCORL1	IFT52	PLTP	DIS3
FCN1	TCFL5	CD40	NUFIP1
PILRA	DIDO1	PLCB4	CYLD
SNX10	SPEF1	MYL9	ZNF586
LAT2	SEC23B	MANBAL	ZNF264
HSD17B14	FERMT1	JAG1	SMAP2
FTL	KIF3B	PXM4	KIF3C
ADAMTS2	WFDK2	CST3	MYNN
MMP2	EPPN	WFDK2	OVGP1
SH3BP2	PIGU	MAP1LC3A	ATG16L1
NID2	METTL4	RBBP8	MAST2
AURKA	PSMD10	PGRCM1	NME8
CASS4	MID1	MID1	ERO1LB
REM1	NXT2	PLS3	PPP1R15A
DOCK9	PRPS2	SMARCA1	SRRT
ARHGAP28	MOSPD1	ASB9	BAX
SMOX	WDR13	TIMP1	ATXN7L3
SIGLEC1	SLC25A14	GABRE	UIMC1
FKBP1A	SLC35A2	NDFIP2	GNAO1
F11	PCSK1N	KLF5	SH3BP2
TESC	CDK16	UGGT2	L2HGDH
P2RX7	PCYT1B	TSC22D1	CASS4
SLC24A6	FGF14	MSLN	CNOT3
TBX5	NDFIP2	ELMO3	PTPN4
FXYD5	KLF5	PLL	KHSRP
HEPH	MRPS31	CCL17	C3orf18
CDIP1	ELMO3	ESRP2	ATRN
GMP	LYRM1	WFDK1	MAVS
RCOR1	TSNAXIP1	CRYM	SIRPG
LTPB4	CCDC113	SYT17	MAPKAPK5
SLC9A1	PRSS54	TMC5	SLC24A6
PCBP4	SETD6	CORO2B	PXN
KGSI	SMIPD3	RASL12	FUS
ICAM1	FA2H	CTSH	FXYD5
LYZ	HSDL1	TTC23	GMP
LEPREL1	USP10	CD276	BIRC5
FLT3LG	HAGHL	HOMER2	LAG3
MCOLN1	METRN	DMXL2	ZBTB25
EFNB1	RHBDL1	LAPTM4B	ARHGAP4
PTPNM2	CRYM	STK3	CCNK
NLR4	CLUAP1	EMC2	PCBP4
NRCAM	TOX3	ESRP1	RGS1
LAMB1	RPGRIP1L	ZC2HC1A	FLT3LG
ITGA6	CCP110	SQLE	PDP
RAPGEF4	IQCH	SH2D4A	GLG1
MLTK	CORO2B	PPP2CB	RBM27
CDV3	ACSBG1	TUSC3	CDV3
APOH	HOMER2	ASAH1	ORC6
ANGPT2	RHOV	FCGRT	G2E3
CD200	MYEF2	PPP1R13L	HNRNPC
SEMA6A	CSPP1	PEX11G	TRPM7
UNC13D	RP1	EPHX3	WDR76
DPYSL2	EYA1	MYH14	AGO1
PTGS1	ESRP1	ICAM4	RFFL
SH2D3C	IL7	CEACAM5	UNC13D
TBC1D2	SPAG1	KDELR1	MAP3K1
SORBS1	PYCRL	TMEM205	NUP188
CRTAC1	ANXA13	FAM83E	CWF19L1
TPSD1	SQLE	TPP2	IKZF5
TREM2	GSR	PON3	CREM
FKBP5	TUSC3	PON2	FKBP5
PGC	PEX11G	PTN	ZNF184
ITPR3	MED25	DFNA5	SIRT1
ACOT7	VRK3	CAV2	IL12RB1
SCD	EPHX3	CAV1	ABL1
NRP1	DYRK1B	MET	CDC7
MYO9B	CNTD2	TSPAN12	ERMP1
KCNK6	TJP3	CPVL	FAM21A
HSD3B7	PLIN3	GRB10	MAST3
42796	CNFN	COBL	SETD1A
GADD45B	CCDC114	FAM188B	CIRBP
PALM	CAPS	HSPB1	IZUMO4
ZDHHC8	FAM83E	WASL	GADD45B
LZTR1	PIK3R2	SFRP4	TRMT2A
SUSD2	ISYNA1	TSPAN13	ZDHHC8
SPECC1L	TMEM59L	RARRES2	KLHL22
GGT1	PBX4	AGR2	MED15
PPM1F	C7orf63	TMEM176B	CRKL
CYTH4	DUS4L	GLI3	LZTR1
MFNG	DNAH11	BLVRA	DDTL
LGALS1	TTC26	SLC1A1	OSM
TTC28	MET	PRUNE2	TBC1D10A
JOSD1	RNF32	ASPN	SF3A1
TIMP3	IQCE	PTGR1	PPIL2
SUN2	TAX1BP1	AK1	YPPL1
HMOX1	ABHD11	MPDZ	CYTH4
TSPO	FAM188B	PP5K1B	MFNG
PDGFB	ZKSCAN1	GLIS3	HIRA
MYH9	PTPRZ1	SHB	SH3BP1
NCF4	RPA3	PDLIM1	PIK3BP1
CSF2RB	CEP41	CXCL12	TCF20
IL2RB	ANKMY2	ACTA2	JOSD1
DESI1	ACTR3C	TBC1D12	GTPBP1
CTSG	AGR2	CCDC47	PPP6R2
GZMH	POLD2	ALDH3A1	SBF1
GZMB	SPATA6L	B9D1	SUN2
POLE2	FSD1L	LGALS3BP	CHKB
SOS2	PRUNE2	CCL2	APOBEC3H
RIN3	CORO2A	SGCA	TTL12
LGMN	PTGR1	MRPL27	CBX7
ITPK1	RLN2	ABCC3	RPL3
PAPLN	NCS1	DUSP3	CACNA1I
PCK2	GLIS3	FAM20A	GRAP2
NFKBIA	DNMBP	YWHA	FAM118A
SEC23A	ERLIN1	DHRS7B	KCTD17
PROCR	TRDMT1	TMEM97	IL2RB
CD40	DNAJC12	PMF22	EP300
STK4	PBLD	RAB34	RANGAP1
CTSZ	KRT23	MAPK10	ZC3H7B
SLC04A1	RNF43	NDUFC1	TRMU
C20orf27	TRIM37	TBC1D9	CERK
CDC25B	DHX40	CPE	BRD1
RASSF2	RECQL5	WFS1	ZBED4

SIRPB1	ALDH3A1	AADAT	MLC1
CCM2L	B9D1	SOD3	HDAC10
MYL9	C17orf75	SLC2A9	KHNYN
HCK	DLX4	SH3D19	GZMH
SNTA1	RND2	GLRB	GZMB
SMAD7	PRKAR1A	BST1	METTL21D
RNF125	EFNB3	FAM149A	SOS2
CHRD1L	SLC9A3R1	CRYAB	NIN
SRPX	CWH43	VWA5A	GNPNAT1
PLS3	MAPK10	DTX4	CGRRF1
RENBP	GALNT7	UNC93B1	TMED8
TAZ	TRIM2	MS4A6A	RIN3
UBI4A	TBC1D19	CCND1	PPM1A
EEA1	GLRB	FOI1	HIF1A
KLF8	LRP2BP	ARHGEF17	SRSF5
TNFSF13B	FAM149A	GALNT18	TELO2
ACP5	UGDH	SLC15A3	PCNX
FLT1	CCDC34	MDK	SMEK1
RGCC	C11orf63	SOX6	NFKBIA
MSLN	HSPA8	EXPH5	SLA2
HSF4	VWA5A	CORO1C	NFATC2
CORO1A	UNC93B1	TSPAN11	PABPC1L
MAPK3	CHORDC1	MLEC	STK4
GDPD3	KIAA1377	KRT18	SLMO2
N4BP1	HIPK3	TENC1	GMEB2
PLLP	MDK	WNT5B	CDC25B
ZNF423	SLC22A18	MANSC1	SNPH
MMP15	CALCA	ALDH2	TLDC2
NDRG4	PITPNM1	SCNN1A	SAMHD1
TANGO6	EXPH5	LTBR	NOP56
PLA2G15	POU2AF1	CDK2AP1	ACTR5
HCFC1R1	PRPF40B	MGP	PPP1R16B
WFDC1	PTGES3	GPR133	ADNP2
COTL1	BCL7A	COP87A	METTL4
CRISPLD2	PPM1H	DSE	SMCHD1
NME4	ELK3	TMEM14C	CEP76
FOXF1	WNT5B	FAM184A	CEP192
FAM173A	TRPV4	TPD52L1	RNF125
CAPN15	PRMT8	NCOA7	MB1
PIEZO1	AKAP3	SASH1	VSG1
QPRT	OGFOD2	CAP2	ALG13
PYCARD	GTF2H3	RAB23	AMMECR1
STX4	MDM1	PERP	SUV39H1
SYT17	UHRF1BP1L	KIAA1244	ATP11C
AQP9	SUDS3	GPR126	ABCD1
LACTB	ST8SIA1	SMOC2	ELF4
CSK	C2CD5	PTK7	MTMR8
HERC1	FRK	VEGFA	PIM2
RASL12	RSPH4A	SLC29A1	EMD
FAH	MAK	LAMA4	TAZ
TJP1	GCNT2	CLIC5	RP2
CA2	HINT3	PRSS16	CD40LG
LAPTM4B	FAM65B	NUDT12	RBM3
PLAT	STK38	SPARC	SUPT20H
NDRG1	ICK	PDE8B	SLC25A15
SLC39A14	RBM24	RNF130	VWA8
ARHGEF10	CAP2	C5orf15	INTS6
MAN2B1	ALDH5A1	LIFR	TRADD
NUCB1	VNN2	WWC1	CORO1A
RELB	GMNN	DPYSL3	CENPT
CLASRP	PERP	BCL6	ACD
DOT1L	KIAA1244	ARL6	ZNF821
CD37	PACRG	AMOTL2	SLC7A6OS
SF3A2	C6orf118	BBP1	SLC7A6
LYL1	DNPH1	BCHIE	AXIN1
RETN	ENPP5	WNT5A	TAF1C
DMPK	NME5	HES1	NAGPA
LILRB1	IK	C3orf14	ABCC1
SNAPC2	MSH3	IFT57	SLC7A5
IL27RA	POLR3G	FRMD4B	CAPN15
OLFM2	ST8SIA4	ATP6V1A	GSPT1
RASAL3	C5orf15	PLSCR4	RBL2
SYDE1	HMGXB3	AADAC	MAZ
PLD3	EHHADH	ARHGEF26	IL21R
PRX	CNTN3	TNNC1	CSK
TGFB1	HGD	RTKN	MTFMT
DENND3	CLDN16	SLC35F5	SLC30A4
NKG7	ARL6	EPB41L5	TRIM35
CD33	CEP70	TP53B	RIPK2
MEIS3	SERPIN2	TANC1	SNX16
PTPRS	FGF12	ITGB6	EEF1D
CLEC11A	PRKAR2A	GCA	LEPROTL1
CARD8	IFT57	SPTBN1	TNFRSF10A
PLA2G4C	HHLA2	ACADL	NEFM
DBP	IQCG	EVA1A	KLHDC4
RASIP1	ROPN1B	EFEMP1	KCNN4
ARRDC2	PODXL2	FN1	MAP4K1
HPN	KIAA1257	UNC50	NFKB1B
SMG9	NEK11	IGFBP2	TUBB4A
NAMPT	ACVR2B	IGFBP5	CLASRP
PIK3CG	ABCC5	EFHD1	ARHGEF18
PON2	AADAC	IL1R1	DOT1L
WDR91	PLCH1	FHL2	CD37
PTN	DNAH1	MLPH	SF3A2
TFEC	NEK4	HDLBP	TRMT1
CAV2	STEAP3	QPCT	CCDC130
CAV1	STAM2	SDC1	AES
WNT2	ACVR1	KYNU	KIR3DX1
HOXA5	REEP6	RND3	LILRB1
CPED1	PCSK4	EPAS1	IL27RA
CPVL	GALNT3	SPR	PPP6R1
GRB10	DNAH6	PARD3B	MED26
CYP3A5	IGFBP2	DHCR24	RASAL3
SNX8	OTX1	QSOX1	AKAP8
PCOLCE	CHST10	ERRFI1	ZNF419
IMPDH1	ABCB6	RHO	CCNE1
SERPINE1	STK16	NCF2	URI1
MEST	PPP1R7	PLA2G4A	RP516
MEOX2	SLC25A12	WLS	FBL
TSPAN13	SLC1A4	OLFML3	FSDI
RARRES2	THADA	TMEM9	PRKD2
GIMAP2	C2orf42	OSCP1	CACTIN
GLI3	CD207	LPHN2	CCDC9
AEBP1	GRIN3B	MFAP2	HNRNPU1
LIMK1	MSH6	CDK18	FZR1
SLC1A1	SPR	HMGCL	BBC3
MEGF9	BCL9	GALE	TGFB1
TGFB1	MORN1	CD46	LIM2

OGN	RALGPS2	AKR1A1	RPS19
ASPN	TMEM59	PRDX1	GLTSCR2
ECM2	ICMT	PIK3R3	NGG7
ENG	KIAA1324	TSPAN1	TYK2
DOCK8	WDR77	CNN3	ATP1A3
TESK1	FBXO2	F3	CARD8
TYRP1	DNAJC6	IRF6	ZNF175
NPDC1	PHTF1	42796	DBP
PTGDS	OSCP1	CTSD	TNPO2
DVL1	MYCL	NRP2	JAK3
GATA3	ACADM	FILIP1	RPL18A
RASSF4	UAP1	PLAGL1	ARRDC2
CXCL12	SSX2IP	RAB32	ELL
PLEKH1A1	SLC2A1	CTGF	CRTC1
PALD1	CDC20	TCF21	ETV2
UNC5B	TSPAN1	PKD2	ZNF14
C10orf54	CCDC181	RARRES1	PBX4
SPOCK2	FAAH	MFS1	AVL9
CCSER2	MROH9	PPL	RASA4
ACTA2	ABCD3	PCDH17	PIK3CG
LZTS2	IRF6	TJP2	SP4
KAZALD1	RCAN3	C2orf40	CBLL1
FBXW4	SLC35A3	C1orf198	ZC3HAV1
SH3PXD2A	NEK2	CTNNA1	ADAP1
MAP3K8	MUC5B	WDR34	LFNG
ZMZ1	IFT46	NEK6	BRAT1
TSPAN14	CASC1	BSPRY	VIPR2
RG89	HMGN3	HSDL2	STX1A
42982	UBE3D	PGF	EPHB6
GALK1	ADGB	IFT43	CASP2
CAMTA2	MYB	NPC2	USP42
HOXB6	ARMC2	LTBP2	C1GALT1
SLC6A4	RARRES1	FKBP1B	CLDN15
BLMH	WDR35	EPCAM	NRF1
ICAM2	DNAH7	AVP1	EZH2
CCL2	GTF3C3	LRP11	GIMAP2
ABI3	C2orf40	MYCT1	URGCP
PPP1R9B	FAM206A	CYSTM1	LIMK1
COL1A1	WDR34	KIAA1217	AKNA
SGCA	CNTRL	TGFB1	TNFSF8
VAT1	TRIM32	SIL1	RLN1
HLF	BSPRY	PLS1	KIAA1432
MMD	GALNT12	CLU	KDM4C
RANGRF	FCF1	SCPEP1	TESK1
WSB1	CCDC176	PLBD1	RGP1
TMEM104	ACYP1	CSTA	RAPGEF1
TNFAIP1	IFT43	CAT	CCNJ
CDR2L	DNAL1	TNFSF10	GATA3
PMP22	TTL5	CPXM2	SPOCK2
ODAM	PPP4R4	TMEM54	C10orf2
GAB1	ZC2HC1C	FMOD	SUFU
CPE	BCL11A	FAM213A	C10orf137
SOD3	EPCAM	ZNF205	MTPAP
SH3D19	TCTN3	INHBA	NEURL
BST1	CCDC147	FKBP9	OBFC1
RAPGEF2	MSX2	RAMP3	MAP3K8
CRYAB	LRP11	CLTA	UBE2S
ZBTB16	CCDC170	CALD1	NUFIP2
SNX15	TP53AIP1	SFTPA1	RPL19
LPXN	HSPH1	PLAU	TUBD1
EHD1	SERP1	CISD1	INTS2
MS4A6A	PLS1	IFT81	CAMTA2
MS4A4A	DUSP4	RASSF8	MED13
ST3GAL4	CLU	BHLHE41	PEN1
TMEM109	CRISPLD1	SSPN	CHRNA
FOI3	SCPEP1	PRDX4	DDX5
ARHGEF17	CEP89	EBP1	CYTH1
IL10RA	ZSCAN18	LRP1	CNTNAP1
GALNT18	TRMT1L	BAZ2B	ALOX12
COMMD9	B4GALT4	G0S2	SLC16A6
SLC15A3	MAPK8IP1	PFKFB2	MAP2K6
CD5	PAEP	C4BPA	SLC9A3R1
CD81	ODF2L	OBSL1	UNC119
AIP	PTGFR	ENKD1	PHF12
VWF	BBS9	SNX21	NFKB1
PPFIBP1	WIPF3	SLP1	INPP4B
CD69	DNAI1	SDC4	RPL34
CLEC2B	BICC1	PMEP1	GRPEL1
SELPLG	IFT81	C2orf85	FBXW7
CORO1C	KBTBD4	IQSEC2	KLF3
KCTD10	MORF4L2	F13A1	CRTAM
CAMKK2	FAM199X	SERPINB6	LPXN
BIN2	TTC21B	MOCS1	ATG2A
LIN7A	B9D2	TREM1	EHD1
TENC1	DAW1	COL21A1	CPT1A
LTA4H	ENKD1	SOX4	IL10RA
SH2B3	PI3	RAB17	BIRC2
OAS3	SLP1	MT1G	DDX6
ARHGDB1B	WFD3	DOK4	CB1
GPR133	CDH26	EFNB2	CD5
CHD4	MOCS3	BMP4	AMBRA1
ATN1	C2orf85	SOX9	MADD
PTPN6	BCAS4	C3	SLC35F2
LPCAT3	FASTKD3	TRIP10	C11orf21
CLEC4A	PAIP2B	RTN2	TCIRG1
COL12A1	POF1B	SDCBP2	CD69
BTN3A3	CRISP2	FOXA2	PRDM4
NEDD9	SIRT5	NRSN2	CLEC2B
ADTRP	PEX6	RRBP1	SELPLG
MAN1A1	ZNF391	FLRT3	CAPRN2
SERINC1	SPDEF	OVOL2	CSRNP2
SASH1	TCP11	DSTN	BIN2
UST	GNGMT	NECAB3	IL23A
PHACTR1	RPP40	ID1	RSRC2
CD83	CXCL6	TMEM115	PARP11
BMP5	SCGB2A1	TMEM53	SH2B3
BAG2	TMT4	PRDX5	DUSP16
FHL5	TM9SF2	ASL	CDKN1B
KHDRBS2	PTGER2	IF6	ARHGDB1B
B3GAT2	SOX9	OMG	DDX55
HECA	TEKT3	WDR60	SLC38A1
GPR126	H3ST3B1	ARMCX1	STX2
QKI	C2orf195	ATP13A4	IFNG
MDFI	POLR1B	TSPAN8	TIMELESS
TFEB	TGM3	TNFRSF19	NOP2
CCND3	OVOL2	GNG11	USP5
SRF	ERGIC3	POR	GOLT1B
VEGFA	BPIFB1	STEAP4	RAB35

LAMA4	AMOT	GNAI1	PHC1
CLIC5	PDCD2L	SGCE	FGFR1OP2
LY86	PRDX5	KDR	KLRB1
MAN2A1	TRAP1	YWHAH	BTN3A3
SEMA5A	PCNXL4	A4GALT	CEP85L
C7	SIX1	CDC42EP1	ADTRP
HBEGF	PZP	MPST	RNGTT
GZMK	OMG	TST	FAM65B
APBB3	TSPAN8	DOCK4	FANCE
SPARC	RAB3IP	PODXL	STK38
ITK	LRRC61	FOXP2	SRSF3
ARSB	FBXL16	RABL5	MDN1
CDH6	TNFRSF19	CALU	BACH2
NPR3	RNF6	MYO1B	E2F3
PCDH12	STYXL1	TWSG1	AIM1
NR3C1	PPAT	EIF2AK4	RPS12
LJFR	C22orf23	MYO5C	C6orf62
DPYSL3	APOBEC3F	FAM63B	B3GAT2
PDGFRB	RIBC2	KNSTRN	ZBTB24
DBN1	KRT17	CALML4	HECA
CD86	CDHR3	ISLR	CCR6
AMOTL2	FOXP2	ANAPC13	PHF1
RBP2	RABL5	PALLD	CCND3
RBP1	LRRC4	CD68	GLTSCR1L
BCHE	TTBK2	TXNDC17	PPP2R5D
ACAP2	ELL3	AP1M2	SRF
GNAI2	CALML4	MTUS1	EXOC2
HYAL1	THAP10	KLK10	BTN2A1
FRMD4B	BBOX1	AJUBA	FBRSL1
EFCC1	E2F8	FOXA1	MAN2A1
PLSCR4	SOX15	RNASE1	MRPS30
CISH	LRRC6	EPB41L4A	GZMK
MAPKAPK3	AP1M2	FGF13	HAVCR1
ARHGEF26	KLK14	CDKN1C	ITK
VIPR1	KLK10	SAT1	RASGRF2
TNNC1	FOXA1	SH3BP4	CCNG1
TTL	EGLN3	DOCK6	LMNB1
EPB41L5	EPB41L4A	CNN1	LNPEP
TFCP2L1	FOXJ1	PVR12	NUP155
TP53B	LPPR3	APOE	ACTR8
CYTIP	HDHD1	APOC1	TBCCD1
TANC1	EFCA4B	PLVAP	NPR12
ITGB6	RSPH3	MLLT4	CBLB
ITGA4	MLLT1	GDF15	KLHL18
SPTBN1	STK33	TRPM4	KLHL24
LOXL3	CACNG6	CRB3	CLCN2
CCDC88A	SSBP4	OLFM1	INO80D
ACADL	CAMSAP1	LAMA5	EEF1B2
EVA1A	UBAC1	ASS1	ADAM23
FN1	TNNT3	YIPF2	MOB1A
GLS	TUBGCP2	SMPDL3B	PIKFYVE
GNLY	NPAS1	LRP3	ZAP70
IL1R2	ARHGEF16	CASZ1	CYTIP
IL1RL1	ATPIF1	RGN	ITGA4
IL18R1	SLC6A8	COX4I2	IFIH1
MLPH	TTL19	ACS2	MOGS
CNPPD1	ZNF341	NAPSA	PAPOLG
ID2	GFAP	PDLIM4	COQ10B
HPCAL1	PRR7	TUBG1	GNLY
PRKD3	RAB11FIP4	VPS25	ZNF142
QPCT	RLIM	RAMP2	IL18RAP
WIPF1	HACL1	MAP1B	PASK
ORC2	PDLIM4	IL13RA1	ID2
PLEK	KIF3A	PPP1R1B	ODC1
AAK1	NPHP4	KHDRBS3	NOL10
PCYOX1	MAP1B	PEX11B	STRN
EPAS1	PIAS3	FMO5	DCAF17
ARID3A	ZSCAN5A	RAI2	DLX2
EPHA4	ZNF132	LGALS3	SRSF7
PRRX1	RHPN2	SPATA6	PLCL1
ANGPTL1	ABHD12B	IQCA1	WIPF1
QSOX1	FBXW9	RAMP1	PNO1
RAP1A	ZNF20	SERPINF1	PLEK
ARHGEF2	SPATA6	ITGB4	KISS1R
MEF2D	CCT6B	TRIM47	PLEKHA3
SRM	ARFIP2	CLEC10A	FAM20B
PRG4	CNGA4	BTBD3	AMPD2
MIIP	IQCA1	RIN2	KCNC4
RGS2	SERPINF1	RAB25	HDAC1
OLFML3	UBE2G1	CH3L1	TRIM62
PLEKHM2	COQ3	POSTN	DLGAP3
CD2	FIGNL1	STARD13	MEF2D
MAP7D1	UNK	RNF128	SWT1
RRAGC	RG522	TCEAL4	SLC35D1
NID1	ANKEF1	MACROD1	GADD45A
KMO	BTBD3	RTN3	BCAS2
AKT3	ACY3	MYH11	AGMAT
ST6GALNAC5	ALDH3B2	LRR1Q1	TFAP2E
CD48	MTL5	SFTPD	CD2
LPHN2	RBM38	SWAP70	TTF2
MFAP2	VSTM2L	HSD17B4	KIF21B
KIF17	RSG1	PEBP4	EXOC8
RAB7L1	SLC41A1	CNTN6	TSNAX
CD160	CCNA1	CHL1	HPCAL4
ID3	COG6	MEIS2	MTR
LEPRE1	STOML3	SORT1	RLF
VAMP4	PDE6B	PTGFRN	ETV3
PTBP2	HSPBP1	SPIRE1	SLAMF1
HSD11B1	HRASLS2	FST	CD48
MAN1C1	FAM83F	ECHDC3	SSX2IP
SLC5A9	LRR1Q1	EMP1	ZNHIT6
TREH	DYDC2	SOX5	RBBP5
KPTN	TMEM254	ACP2	GPR89A
TNNT2	LRRCC1	DTNA	RAB7L1
CAMSAP2	E2F5	SLC43A3	CD160
KLF7	AMPD3	COL4A2	NSUN4
C1orf54	TMEM66	ADAMTS8	DR1
SGIP1	TTC9	CTSL	FASLG
PLAGL1	CCNB1	FAM189A2	RCAN3
RAB32	CDK7	CCNJL	C1orf63
SGK1	VTCN1	TMEM60	ESYT2
TCF21	GRHL1	LMO2	STK11
ABCG2	SAI2	EHF	RPS25
CCND2	CRB1	ELF5	CREB1
KLP9	ERN2	CD63	CA14
C1orf98	GRP	KRT7	LRMP
PHF19	ANKRD16	MAP7	USP35
SLC46A2	KCTD1	NHSL1	ELOVL4

CSF3R	SOX5	AHI1	CASP8AP2
IFI27L2	HOOK1	CPM	TNFAIP3
NPC2	CYP2J2	DYNC1L2	SLC16A7
ACOT2	RNF138	KCNK1	ZNF430
LTBP2	FHOD3	CAPN9	DCLRE1B
FLVCR2	TCN1	GLUL	KLF12
GPR68	CLDN10	LAMC1	CCND2
RHOQ	DZIP1	CYP27A1	SENP5
ATAD2B	ARHGAP32	ARMC9	FBXW2
FKBP1B	RFK	DRAM1	PHF19
LGALS1	GOLM1	FLNB	DCAF4
CNRIP1	CCDC146	SUCLA2	FCF1
OGRL1	RINT1	LMO7	NEK9
FAM178A	KIAA1009	SPRY2	IRF2BP1
IFT13	MRAP2	TNS3	GPR68
IFT2	LCA5	GNMNB	DNMT3A
PPP1R3C	EHF	RAPGEF5	YPEL5
GNA13	PRRG4	RAC1	GPAM
HOXB5	GLS2	KDELR2	PYROXD2
TEK	PPP1R1A	NKX2-1	C10orf76
MOB3B	ACVR1B	ABHD17C	GNA13
CD274	KCNH3	GALNT5	DUSP1
MTHFD1L	MAP7	KCTD3	WDR55
ARAP3	CD164	IL1RN	CENPL
PLXDC2	LACE1	NIPSNAP3A	GORAB
IQSEC3	HEY2	RALGPS1	MSANTD2
WBP4	PKIB	FAM129B	MASTL
SMAD9	SMPD2	STXBP1	EPC1
TGFB1	REPS1	SLC31A1	MTRF1
GLT8D2	CCDC102A	ENPP2	PROSER1
SOC3	KCNK1	IL33	ELF1
PDLIM2	TSGA10	CCL21	FAM53C
TBX2	ARHGEF4	KIF13A	TMPO
TBX4	APPL2	GMPR	APAF1
ADCY7	VILL	YIPF3	TNFRSF10B
PLBD1	FLNB	LRRC1	PTK2B
KCNX8	SCRN1	TLR2	PPP3CC
PDZRN3	CIDEB	SLC02B1	UBIAD1
CSTA	TTC5	GGH	FAM117A
FABP3	ZFXD2	SULF1	NCAPH
ACKR5	MYCBPAP	TRPC6	KIAA0922
POLR3GL	ODF2	MMP7	PAPD5
CXCR4	WDR38	YAP1	ADCY7
SASH3	SPAG8	TRIM29	PYROXD1
FMOD	PPIL1	RDX	PSPC1
FAM126A	TFAP2A	C11orf1	ZNF549
HOXA7	KIAA0319	FXYD6	ZNF211
INHBA	SLC22A23	THBS1	KIF18A
RAMP3	BPHL	LRRC49	DEPDC7
RECK	VARS2	UACA	PILRB
CALD1	FAM8A1	DUOX1	ZMYM2
SFTPA1	C6orf52	BCAR3	GJB6
PLAU	TTC29	TLL1	ZNF639
SRGN	ANKRD42	FNBP1L	TMEM156
EGR2	NEK1	ARHGAP29	CXCR4
HVCN1	TMPPRSS4	DYNC2L1	RPL21
RASSF8	MMP7	CYP11B1	GTFA3A
ITPR2	C11orf70	MYOF	SASH3
NECAB1	TRIM29	TACC2	LAX1
PKN1	BTG4	ARL3	CD244
SPRYD7	POU2F3	RBP4	LY9
ITIH5	PPP2R1B	IDH1	RBBP6
ARHGAP9	LRRRC49	ITGAV	ZC3H7A
NCKAP1L	PAK6	SLC40A1	RPL5
MMP19	GIPC2	DIRC2	RWDD3
SPATS2	CLCA2	MNS1	RPAP2
NR4A1	DBT	SECISBP2L	ZMIZ2
LRP1	IFT172	ARHGAP24	HERPUD2
NFE2	DYNC2L1	CXCL9	CCZ1
TNFAIP6	CYP2C8	FRAS1	POLM
BATE3	LOXL4	SCARB2	SLC25A51
G0S2	ARL3	CDKL2	RECK
RAP2C	GPR87	SHROOM3	DCAF10
C4BPA	NAB1	ANXA3	TRIM24
CKS2	MDH1B	PAPSS1	SRGN
PREX1	ABH2	ERP27	SLC25A16
PLCG1	DIRC2	CPNE8	CCDC91
TOX2	MNS1	FGD4	WWP1
PTGIS	VWA9	LRIG3	DDX39A
PMEPA1	FAM13A	LUM	PKN1
ATP8A1	BBS7	MMAB	CD97
HIF3A	BMPR1B	SUOX	CENPK
F13A1	HADH	RAB20	ARHGAP9
MOCS1	PAPSS1	GRTP1	AMD1
TREM1	ERP27	RTN1	USP45
KCNK17	KIF21A	JDP2	ACVR1C
NRN1	FAM60A	FBLN5	SLC36A1
MYRF	LRIG3	WARS	RAP2C
AHNAK	C12orf52	DUOXA1	EXOSC9
DOK4	CCDC65	TSPAN3	AGO2
RAP2A	GALNT6	TPM1	FAM209A
EFNB2	TMBIM6	ARRDC4	TTPAL
PPP1R12C	MORN3	SH3GL3	PREX1
SLC2A4RG	GRTF1	TGFB1I1	PLCG1
INSIG2	TTC6	IGSF6	SRSF6
TRIP10	REM2	MARVELD3	ZNF831
TNFSF14	NOVA1	ZFXH3	RAB22A
FOSB	EFCAB11	CPNE2	SNAI1
RTN2	AK7	GCSH	STX16
VASP	FAM181A	CDH11	ZBP1
GPCPD1	C14orf79	NOL3	LYPD3
CD93	SORD	GFOD2	TRERF1
BMP2	SLC27A2	TOM1L1	PACSN1
LRRN4	TSPAN3	G6PC3	HIST1H1D
SIPR4	DNAJA4	IMP2	AARS2
NCLN	BBS4	OSBPL1A	HIST1H1A
CHURC1-FNTB	CCDC33	GATA6	RPS10
MMP24	WDR93	ERBB2	TBCC
ID1	FTO	GRB7	RIOK1
ST3GAL3	MARVELD3	IGFBP4	NUP153
HECTD3	KATNB1	NFIC	RUNX2
F10	NUDT7	IFTM3	WNT1
IGF1R1	GALNS	COL6A1	SH3TC1
HCTST	GAS8	APP	GPR18
RRAS	GFOD2	EPHA2	IRF1
SBD5	PRPSAP2	PGD	RNF113A
GLIS2	TOM1L1	EVA1B	42984
RHOJ	TOB1	FCN3	PTGER2

HSPA2	LRRC46	HSPG2	HS3ST3B1
SGPPP1	BCAS3	CYR61	GGA3
EV12A	SS18	TINAGL1	C1orf61
AIF1L	SLC39A6	PTPRF	GTFC34
FAM78A	WRAP53	CYP4B1	KIR2DL1
NUP214	CCDC40	SLC44A3	SLC2A4RG
TMEM35	ZNF750	CTTNBP2NL	PSD4
FGD3	WDR45B	ATP1B1	TNFSF9
MASP1	FBXO15	CREG1	CD70
PTPRB	hsa-mir-1199	DPT	SH2D3A
PLA2G5	PPAP2C	MGST3	TNFSF14
HP1BP3	URB1	RGS5	FOSB
SIN3B	CBLC	RGL1	EMI2
KLF2	ZNF473	RORC	STK35
MACF1	FAM71E1	CGN	MCM8
TUBA4A	C1orf222	SELENBP1	S1PR4
GNG11	FHAD1	RAB13	HNRNP3R
HIP1	CNKSR1	S100A8	MAX
PTPN12	SYTL1	SLC39A1	LRFN3
FGL2	ADC	CREB3L4	IGFLR1
KDR	PTPRF	KCNN3	HCST
GAL3ST1	BEST4	SCCPDH	CCR7
ADORA2A	CYP4B1	CDC42BPA	FRMD8
ATF4	TMEM61	MBOAT2	IRF3
CDC42EP1	SLC44A3	PSEN2	PRR12
APOL3	NME7	EPHX1	STAT5A
TPST2	MPC2	OSR1	AHDC1
APOL2	PVRL4	CALM2	ZNF384
RAC2	UFC1	MEIS1	ELK1
DOCK4	PPOX	NPHP1	ATG14
PODXL	USP21	MALL	ZBTB1
MYO1B	XPR1	THNSL2	PLEKHG3
CHN1	RORC	PKP4	EV12A
WDFY4	GOLPH3L	GULP1	FAM78A
CGNL1	DYRK3	NBEAL1	SLC10A3
DL14	SMYD2	SPAG16	TIMM8A
ISLR	SUSD4	ACKR3	ZNF484
PALLD	DUSP10	RBM53	FGD3
SPCS3	CREB3L4	OSBP10	HIVEP3
CD68	KCNN3	ITGA9	BCL11B
KIF1C	SCCPDH	CTDSP1	HELB
SIGLEC9	ETNK2	COL8A1	RAP1B
ADCY4	CALM2	TMEM108	DYRK2
BC12L2	WDPCP	NCEH1	FBXL12
CDO1	ANKRD53	ILDR1	HP1BP3
SEC14L1	NPHP1	SLIT2	EMR2
RHBDF2	THNSL2	SNCA	KLF2
MAP7D3	RABL2A	SFRP2	SYNGR3
CDKN1C	ZC3H8	PDGFC	WDR24
SHC2	GULP1	NKD2	FBXL16
ABHD17A	KANSL1L	MYO10	CHTF18
STARD8	SPAG16	OSMR	KDM4B
DOCK6	HES6	LHFPL2	TUBA4A
CNN1	ANKMY1	PAM	RBM48
EXOC3L2	SHQ1	FAM50B	ZNF780B
APOE	TMF1	TNFRSF21	LRFN1
APOC1	LRIG1	CYP39A1	SPINK2
PLVAP	TAGLN3	ARHGAP18	PPAT
BST2	ALDH1L1	AIG1	TUBGCP6
USHBP1	AMT	SLC22A3	DGCR8
COLGALT1	CCDC39	CREB5	ASPHD2
ARPC1B	ILDR1	EGFR	ADORA2A
FCHO1	MUC4	IGFBP3	APOL3
PXDN	PLAC8	TMEM47	TPST2
PGPEP1	TRMT10A	SLC16A2	RAC2
OLFM1	CAMK2D	GPC3	APOBEC3F
LSP1	NAF1	NSDHL	POT1
TNNI2	ROPN1L	ZNF185	DNAJB9
COL5A1	SRD5A1	CETN2	CCDC136
GMFG	FAM50B	MRPS28	OSGEP11
THEMIS2	DCDC2	LACTB2	TMOD2
MPP1	KAAG1	SYBU	CCNT1
ZNF331	TNFRSF21	MAL2	KRI1
LRP3	LGSN	SLC39A4	CDKN2D
PRRG1	TCTE1	VLDLR	DTD2
RGN	CYP39A1	NFIB	NRL
AKAP12	TPBG	CDKN2B	RHBDF2
LILRB2	ARHGAP18	C9orf3	ARHGEF6
COX4I2	SLC18B1	ZNF462	SGOL1
HIGD1B	DYNLT1	GSN	KLF16
IDO1	GBAS	LCN2	TMEM8A
SH3BP5	PSPH	MSRB2	ABHD17A
RFTN1	ZC3HAV1L	PARD3	EFCAB4B
NAPSA	PRPS1	FAM13C	GNL3L
MGAT1	CXorf57	C10orf11	ATP8B3
GFPT2	CETN2	ADIRF	GTPBP3
AOC3	BIN3	TCF7L2	TULP4
RAMP2	PPAPDC1B	SCCB1A1	FCHO1
ACAP3	TRIM55	SYT8	KLHDC7B
ANO1	SYBU	HSD17B12	JUND
TMEM204	FAM83A	TNKS1BP1	ZNF557
STARD3	ARHGAP39	SERPING1	HELZ2
RARA	C9orf72	C11orf89	SAMD10
PPP1R1B	CEP78	SERPINH1	LSP1
KHDRBS3	UGCG	C11orf52	PNPLA7
RAI2	ASTN2	ST14	CEP85
NR0B2	WDR31	FADS1	TAF4
MATN3	PTGES	EI24	ATG4D
PPARG	LCN2	MPZL2	EIF2S3
EMILIN2	INPP5E	TAGLN	GMFG
PTPRE	PLEKHS1	TM7SF2	MAP3K10
INPP5K	LRRC27	CTF1	LRRC47
DDC	CNNM2	N6AMT2	SESN2
IGJ	SCGB1A1	HNMT	HIP1R
XAF1	SYT8	LYPD1	ZNF317
MATN2	ZNF214	DOCK1	PPAN
HSPA12B	C11orf49	DIXDC1	ANGPTL6
NES	CCDC81	IL18	C19orf66
ARHGEF11	PAK1	CRIM1	PLXNA3
SYT11	TTC12	THRB	ZNF331
ZBED3	C11orf52	DIP2C	C12orf65
KANK4	GLB1L2	MAGI1	UBE4B
XPO4	ST14	AKAP6	ULBP2
ALOX5AP	DAK	MIPOL1	LATS1
WASF3	TM7SF2	KCTD14	RBM49
CHRM3	DOC2A	CCDC3	ZNF341
MYH10	CNTN5	EPS8	ARHGEF9
MPRIIP	MXK	AKR1C2	NFATC1

CHI3L1	TMEM218	ACSL1	RLIM
CHIT1	CTAGE5	SLC25A4	TRAF3
EPSTI1	LYPD6B	SERP2	NR1H2
STARD13	PDCD4	DST	DIAPH1
PRAM1	ADRA2A	SCHIP1	UBE2D2
MYH11	SPATA4	TMEM56	ACAP3
PDZD2	FSIP1	PTPN14	C1orf159
GIMAP6	FAM173B	HSPB8	THOC6
GIMAP4	DIXDC1	TMEM178A	CA6
SFTPD	DLAT	TCF7L1	WDR44
LYVE1	PHI1D2	CCDC50	LLGL1
SBF2	C2orf50	IGSF10	C19orf12
MCAL2	ENKUR	SPARCL1	GCH1
LOXL2	IPMK	GIA1	ZSWIM4
PEBP4	AKAP6	FARP1	DCAF15
CTIF	NUBPL	BMP3	CC2D1A
CAMK1	C4orf33	PTPRK	NUP210
GSTM5	TEX9	MARVELD2	PRKAA1
GSTM3	MFSDB	PIOD2	RAP1GAP2
PSRC1	TMEM45B	GPR125	CLUH
PTPN22	CCDC122	ACOXL	RPA1
CD101	CCDC74B	BMP6	TBC1D14
SPIRE1	UHMK1	C16orf89	H3F3B
SLC38A2	RPP38	FBXL2	KDM6B
KIDINS220	ZSCAN1	LURAP1L	DLG4
IL6ST	TMEM123	CNKSR3	TERF2
FST	SPEF2	PID1	NXT1
NAV1	CAPSL	DDAH1	KIAA0907
IL15RA	CCNO	THY1	FCRL2
DOCK2	SLC30A6	AB3BP	SYT11
EMP1	GPR180	CEP112	TOE1
RERG	TCTEX1D1	ABCA6	MUTYH
KLRD1	WDR78	UCHL1	RBM38
KLRC1	BMP3	ENAH	OSER1
FAM127A	IFLTD1	SH3RF1	DMGDH
SPOCD1	MARVELD2	PDLM3	FBXO44
DSC2	CLGN	SORBS2	ZMYM5
DTNA	CCDC148	CXADR	USPL1
APLR	GPR110	PPAR4	XPO4
FADS2	FAM81B	APCDD1	LGR6
PDGFRA	ING1	PIEZO2	RFXAP
COL4A2	ADPRHL1	SLC7A7	SUV420H2
ADAMTS8	FBXL2	VSIG4	ZNF414
ETS1	FAM92B	TMEM237	CSNK1G2
NREP	KCNJ16	DEPTOR	MED10
TMEM2	FBXO36	RRAGA	BTG1
HAVCR2	ZNF599	MICU3	C12orf29
TAOK3	ANKFN1	PSD3	CCDC59
TBX3	MSI2	MCU	ARNTL
OASL	GDDPD1	GNA14	CATSPERB
CD36	C6orf57	WIF1	IRAK2
TESPA1	CHST9	KCNMA1	VHL
STX11	DNAAF1	ADAMTSL3	PRPF38B
RAB11FIP5	ABCA5	TSPAN7	TSPAN2
DYSF	C4orf19	PCDH1	PTPN22
KCNMB4	CCDC173	NPTN	AP4B1
CPM	FAM69A	RAB11FIP1	FKBP11
FHOD1	CXADR	RBPMS	LPIN1
NPL	SLFN13	NRG1	RPS15A
LAMC1	PLCL2	CLDN12	IL2RA
DOCK10	USP43	FZD1	CCNH
SLC19A3	CYP2U1	MYO1E	DOCK2
CYP27A1	RSPH10B	AFAP1L1	KLRD1
DRAM1	PROM2	KCNJ15	KLRC1
TBC1D4	AK9	ETS2	RAB33A
THSD1	PTPRN2	CREB3L1	MST4
LRCH1	AZIN1	SLC34A2	CDC48
SCEL	AGPAT5	FMNL2	AGO4
EDNRB	GRAMD3	RADIL	RNF138
LCP1	LRGUK	KRTCAP3	DHX34
TNS3	RBM45	MRPL17	ETS1
GPNMB	PDIA4	DZIP1L	WDR36
RAPGEF5	ALS2CR12	FAIM	C9orf40
AOAH	TMEM237	FAM46B	AGTPBP1
CCM2	SPAG17	SLC13A3	RNFT2
MYO1G	FMN2	TSPAN33	CCDC64
TTYH3	TTC18	CD1C	DTX1
TM6SF1	GNA14	CD1E	PNPLA8
LIMD2	C8orf37	PPP1R9A	MDFIC
GALNT5	C15orf26	NBL1	MTO1
SCN7A	N6AMT1	F11R	PRR5L
HILX	CLDN8	IFNGR2	DNAJC14
IL1RN	RPGR	LAD1	GDF11
BIN1	CDK20	CSRP1	TESPA1
GYPC	FBXO32	C1QC	AGAP2
KLF4	GALK2	CCDC24	HNRNP1
TMOD1	MPV17L	CBR1	MCAL1
DAB2IP	LRP8	PTMS	EGR4
ANGPTL2	CLDN12	CYB5R1	RAB11FIP5
SLC31A2	C1orf158	CIR	CCDC142
TLR4	HYDIN	CHCHD6	USP15
USP20	ZNF19	LRRC36	KLHL36
GARNL3	FAM81A	TPP3	FBXL8
ENPP2	LCASL	ZDHHC1	URB2
NOV	C9orf43	ATP6V0D1	EGLN1
IL11RA	WDR19	RGS12	TAF5L
RNF38	DRC1	CPAMD8	RC3H1
TLN1	RAB28	NR2F6	DOCK10
CCL21	FAM213B	TFF3	WNT10A
SIT1	KRTCAP3	CBS	MFSD9
DNAJB5	WDR66	PDXK	EDAR
PIM1	UBXN11	CSTB	TGFBRAP1
TMEM63B	RHPN1	CACFD1	EPC2
IRF4	LRRC43	LMNA	CKAP2
FOXF2	DZIP1L	AZGP1	TBC1D4
NRM	FAIM	PTGER1	BORA
FGFBP2	RHBDL2	C5orf45	COG3
FHDC1	HIST1H2BD	SCGB3A1	RCBTB2
FCHSD2	RIBC1	DMKN	LCP1
ARRB1	C2orf62	COX7A1	SETDB2
SLCO2B1	CNOT11	CYGB	AOAH
IL18BP	FAM86C1	ZNF385A	TBRG4
RAB30	DNAH3	AQP5	HUS1
LRRC32	NPM2	CXCL16	MYO1G
PRCP	CACHD1	TNFSF13	RSAD1
TRPC6	C21orf59	CCDC64B	LIMD2
RDX	CLIC6	LRP5	BRIP1
FXYD6	CCDC24	PDZK1IP1	TRA2B

CASP1	RUNX1	PPAP2B	ERMN
THBS1	C2orf81	RBP7	BLK
NUSAP1	CHAF1B	PDPN	CBWD2
PAQR5	HLCS	KIAA1522	SMPD4
UACA	CCDC17	ALPL	SAP130
SMAD6	CCDC135	WNT4	BIN1
PLCB2	CHCHD6	DIRAS3	UGGT1
SEMA6D	TPPP3	NFIA	C9orf78
GCOM1	ZDHHC1	DNAJB4	FPGS
IFI44L	PIP	SNX7	USP20
ARHGAP29	NPR2	HAAO	TEX10
ADCY3	GNE	PIGR	MYC
THUMP2	IQCC	ACTG2	POLR1E
EMILIN1	TFF3	VSNL1	SIT1
TMEM180	TMPPRSS3	NOSTRIN	RPS6
CALHM2	RSPH1	PCDP1	PIM1
ENTPD1	WDR4	S100A11	FTSJD2
PLCE1	C21orf58	S100A9	FRS3
RBP4	C9orf116	CLDN1	IRF4
STAT4	C9orf117	COL6A3	TUBB2A
HECW2	TMEM190	SLC15A2	RIPK1
SSFA2	MPZL3	FSTL1	TCF19
TMOD3	TLCD1	ELF3	MDC1
HERC5	LRRRC71	IGFBP7	TPMT
PDE5A	PPP1R16A	FBLN2	FGFBP2
42989	ORAI2	GLB1L	PRKRIR
ANXA3	LRWD1	NFASC	RAB30
ENPEP	FBXL13	MNDA	TGS1
PPP3CA	SCGB3A1	CDS1	SORL1
SLC39A8	DMKN	WDFY3	ALKBH8
RGS3	BDH1	PTPN13	CTDSP12
GUCD1	LRRRC56	PRICKLE2	MAPKBP1
PARVG	FDXR	SMIM14	HAUS2
GABARAPL1	AQP5	ABHD6	PARP6
PRICKLE1	RAVER1	DNASE1L3	PLCB2
CLSTN3	ALOX15	RBM47	RSL24D1
CD27	ZNF653	APBB2	EPT1
AMIGO2	WDR90	CXCL3	ACTR2
GLIPR1	CCDC78	CXCL1	SLC5A6
PHLDA1	HS3ST6	CPA3	SLC3A1
DUSP6	CCDC64B	CDCP1	STAMBPL1
LUM	ZG16B	CLEC3B	CUZD1
SYCP3	SHANK2	DNALI1	DUSP5
SDSL	PPP1R32	LIPH	KIF20B
ACVRL1	PARS2	HEYL	DBR1
ITGB7	KIAA1522	PRKCD	ZNF365
LMBR1L	UBXN10	SGMS2	TET1
LPAR6	WNT4	PLXNB1	STAT4
RHOF	TTL10	SPRY1	FASTKD1
SSTR1	C1orf87	INTU	FAM117B
FRMD6	NFIA	ANXA5	PARP16
GPR65	OMA1	GUCY1A3	HERC5
FBLN5	LRR1Q3	EDIL3	C4orf21
FGF7	SNX7	RNF180	HNRNPD
HDC	WDR63	CMBL	RAP1GDS1
TLE3	KLHDC9	SCGB3A2	G3BP2
PSTPIP1	C1orf74	RHOBTB3	CNOT6L
BCL2A1	AXDND1	GPX8	LEF1
MESDC1	SPATA17	FOXQ1	MAPK8IP3
PML	PIGR	SHROOM1	ALG10
MFGE8	TRIM17	HEY1	CLSTN3
FURN	CAPN13	ZNF704	KLRG1
CRIC3	FAM84A	FABP5	VAMP1
ITGAX	CLHC1	COL1A2	CD27
TGFB1I1	CCDC104	CHMP4C	42803
CDR2	CCDC138	CTSB	GLIPR1
IGSF6	CCDC74A	DLC1	NEDD1
ARHGAP17	TEKT4	ALDH7A1	TDG
NLRCS	SPATA18	BAALC	GIT2
CMTM3	PCDP1	FZD6	FAM222A
CDH11	SGPP2	CTHRC1	SLC7A1
NOL3	INHBB	MAMDC2	NPFF
CDH13	BBS5	C8orf34	NABP2
OSGIN1	ANKRD23	ALDH1A1	N4BP2L1
IRF8	PACRGL	RASEF	CELA1
GID4	BNIP1	FBP1	KANSL2
MYOCD	DHX57	TMEM246	ITGB7
PCTP	TGFA	WBSR27	ZNF740
SKAP1	C1orf189	CLDN3	HNRNPA1L2
SSH2	FAM175A	C10orf10	SETD1B
ABCA8	CLDN1	BEND7	VPS33A
NPC1	HIPK1	VSTM4	RHOF
SLC14A1	SLC15A2	PRDX3	DENR
ARRB2	ELF3	NDRG2	SLAIN1
ZMYND15	STK36	UBTD1	NAA30
ASGR1	NEK10	ARHGAP42	DCAF5
PIK3R5	ANKZF1	PACIN3	RAB15
ARHGDI1A	GLB1L	IFE27	WDR89
TM66	SERPNI1	CLMN	GPR65
TTYH2	NUAK2	SMCO4	SLC12A6
SECTM1	EFHB	HTRA1	BAHD1
IGFBP4	ICA1L	SPRED1	CDAN1
BRD4	SPICE1	SPINT1	TLE3
IFITM3	KIAA1407	CKB	PSTPIP1
COL6A1	CDS1	DPCD	PIF1
COL6A2	C3orf67	LARP6	USP3
EMP3	RBM47	PCBD1	LINS
RNPEPL1	PRRT3	C2	ULK3
MYO1F	LZTFL1	CYB5A	HAPLN3
SLC47A1	YEATS2	USP54	POLG
RGN3	DNALI1	C11orf74	CRTC3
SH3BGR13	CCDC37	CYB5R2	ARMC5
C1orf216	IFT122	ST5	CDR2
EVA1B	SFMBT1	TMEM130	TXNL4B
MAP3K6	SLC51A	MFAP4	NLRCS
FCN3	S100P	CCDC68	CMTM3
HSPG2	INTU	RRAD	MAP1LC3B
CYR61	HSPA4L	NGFRAP1	RHOT2
PRKACB	POC1A	NNMT	RPS2
TINAGL1	PRSS12	LDHD	ZNF287
CTTNBP2NL	SAP30	ANPEP	CTRL
C1orf162	MAD2L1	SCNN1G	TOB1
CD3	MAP9	NAV2	SGSM2
ITGA10	CEP44	C15orf48	SKAP1
GPA33	TMEM144	MSA1A5	ARSG
RXRG	FAM160A1	TEF	TAF4B
DPT	ZNF474	ACSF2	ESCO1
FCGR2A	F2RL1	PRRX2	C18orf8

RGS5	SCGB3A2	PRR15L	ARRB2
RGS16	CDC20B	GPRC5B	MINK1
HMCN1	GPX8	MYO5B	PIK3R5
ECM1	GFM2	GPX4	TP53
ADAMTSL4	GJB7	CYP2S1	TMC6
MCL1	GRIK2	TMC4	TTYH2
CTSK	KIAA0895	CDC42EP5	RPTOR
VASH2	KIF6	PPP1R14A	TRIM65
S100A8	SLC29A4	SPINT2	RNF157
SLC27A3	MIOS	C19orf33	CBX4
RIT1	SYTL3	NXN	RNF165
DEGS1	IQUB	FAM57A	ZCCHC2
ITPKB	CHMP4C	SLC43A2	PMAIP1
ARL8A	SLC13A4	RILP	FAM134C
OSR1	C8orf58	SERPINF2	PRDM15
RHOB	C7orf57	CYB5D2	VAV1
EMIL4	HNFB4G	GGT6	DUS3L
MEIS1	HEATR2	KLK11	DPP9
AFF3	OXR1	IGFBP6	ZFP14
GALNT13	FZD6	NUDT8	ATHL1
ZNF385B	TP53INP1	HID1	SIK1
NBEAL1	TMEM67	EVPL	NTN5
CTDSP1	C9orf24	TK1	ADAMTS10
CSRNPI	C8orf34	ECI1	RNPEPL1
STAC	ALDH1A1	BSC12	CAPN10
PTPRG	KIF27	TTC21A	MYO1F
COL8A1	TMEM246	CTNNB1	EVISL
PHLDB2	CXorf22	BATF2	SIGLEC10
PLA1A	WBSCR27	SCARA3	RPL13A
ADPRH	KIAA1958	UBTD2	NOSIP
AGTR1	RNF183	NTSDC2	ZNF614
TMEM44	STRBP	ACOX2	ARHGEF19
SLIT2	CLDN3	FAM107A	EFHD2
ATP10D	WNK2	MFS2A	PLK4
SNCA	PIGO	SCNN1B	PRKACB
ANK2	ARMC3	RAB31	MTF2
USP53	CCDC67	SFTPC	CD53
SETD7	LRRC18	SDPR	GPA33
42795	PGM2L1	SERINC2	XCUL1
NKD2	DNAAF2	COL3A1	XCL2
FAM105A	TTC8	ADAM9	NUF2
GZMA	FAAH2	PKIG	NR1B3
PIK3R1	ENOX2	NPNT	ISG20L2
LHFPL2	AK8	ATOH8	ZNF687
ARHGAP26	C9orf9	SFTPB	SETDB1
C1QTNF2	STOX1	ZNF608	ANP32E
KCNMB1	BMS1	PPIC	GABPB2
GFOD1	PPP1R36	STXBP6	INTS7
DOK3	AGBL2	PXDC1	DUSP10
PPP1R18	CLMN	MFS2A	TP53BP2
HMGCLL1	CKB	PARM1	ATP8B2
FGD2	BTRC	EFNA1	TPM3
RSP03	DPCD	B3GALNT1	GATAD2B
GNA12	SENPH	ARL13B	TTC13
CREB5	GABRB3	PTK2	SDE2
TMEM140	C16orf71	PTAFR	FBXO28
EPHA1	FAM227B	SDC2	ITPKB
DENND2A	C11orf65	CLIC4	LBR
TMEM47	CYB5A	MUC15	PTPN7
MSN	C11orf74	GJB1	RPS27A
CXorf36	IDH3A	ANTXR1	SLC20A1
IL2RG	C16orf46	AGPAT2	FBLN7
CSGALNACT1	WEE1	MTT1E	POLR2D
ATP6V1B2	IQCD	LDHB	AMMECR1L
DOK2	RRAD	PCDH7	SLC4A10
TACC1	WDR16	REPS2	KIAA1715
RSP02	BLCAP	TPST1	CDCA7
PLIN2	ATF7IP2	TM4SF1	FANCD2
CDKN2B	PLEKHA7	ALCAM	EAF1
NTRK2	ACSM1	SLC16A5	CSRNPI
SHC3	PEX11A	FAXDC2	IQSEC1
LPPR1	SCNN1G	CMTM8	RPL32
SNX30	CHP2	GABARAP	NFKBIZ
SLC25A25	PIP4K2C	FABP4	NXPE3
NOTCH1	DIS3L	SMAD1	KIAA0226
ST8SIA6	MS4A8	SEMA3E	TM4SF19
ZEB1	MAP1A	GPRC5C	DGKQ
CAMK2G	EVA1C	KRT8	FIP1L1
ADIRF	DUSP18	CD14	LYAR
ANKRD1	TTC16	KRT4	CENPC
FUOM	COQ4	IRX2	PYURF
GSTO1	CCDC103	TMEM133	TIFA
ITPRIP	ENDOG	SOC56	SPATA5
RGS10	UGT1A6	KCNS3	CCNA2
ADM	COQ7	SDR16C5	NAF1
DGKZ	KATNAL2	HTRA3	RPS3A
TNKS1BP1	MYO5B	GSTA4	CYP4V2
SERPING1	TRIM68	ZNF415	SKP2
SLC43A1	ZNF23	PRKCDBP	GZMA
SERPINH1	PPP2R3B	FEZ2	PIK3R1
ATM	SPATA33	INSR	IQGAP2
GGTLC1	RHEBL1	PRKCE	TNFAIP8
EML3	TUBA1A	C1GALT1C1	N4BP3
FEZ1	ZNF610	TMEM37	CDKAL1
ESAM	CYP2S1	LRG1	FAM193B
SIDT2	TMC4	KRT19	RNF44
TAGLN	SPINT2	GLOD5	PPP1R18
FERMT3	DNAAF3	MAP6	NFKBIE
CDC42EP2	PSCA	SPSB1	MMS22L
TAOK2	FAM57A	P2RY6	PNRC1
KLRF1	WDR81	TMEM51	PM20D2
CLEC1A	HSD11B1L	GATM	SCML4
ITGB1	GGT6	AQP4	ABRACL
FCGR1A	KLK11	TLN2	MTFR2
LATS2	KLK13	SYNPO	WTAP
GP6M6A	KRT80	LAMB2	C7orf26
VEGFC	ZNF232	CCL11	PURB
CCDC102B	TEKT1	ID4	POMZP3
DLG2	TMEM68	TPSAB1	ZNF92
RGS18	TMEM99	NEGR1	ATXN7L1
PPP1R1C	RAB26	MACROD2	C7orf43
PIP4K2A	BSC12	COPRS	GIGYF1
CACNA1C	HRASLS5	ALG14	TMEM209
TMEM86A	TTC21A	GNG12	SH3KBP1
PLBD2	ENTPD3	GGGY	CASK
CCDC3	ULK4	TCEAL1	KDM6A
FRMD4A	TTC39C	C2orf54	ZNF182
PTPRO	BMI1	CHCHD1	CHST7

QDPR	MOBP	SMPDL3A	KRBOX4
EDNRA	DEGS2	EFEMP2	ZNF41
INPP1	BDKRB2	CCL19	ZMYM3
ASAP2	COG7	EGFL7	GPR174
ADAM17	SCNN1B	MRGPRF	CCDC120
FLII	FEN1	RHOD	IL2RG
WWC2	SERINC2	CKS1B	ACRC
ZNF385D	DYNLRB2	DMRT2	DOCK11
DST	ZSWIM1	SNCG	RPL10
KCNE4	VWA3B	STOX2	CSGALNACT1
TMEM163	LDLRAD4	TRIB1	DOK2
GPATCH11	CXXC4	CIQB	CHMP7
HSPB8	TCTN2	CIQA	GIN54
PKK1	CEP120	NDNF	RPL7
PDE3B	ZBBX	AGR3	UHRF2
TCF7L1	AR	CCDC106	HAUS6
PLEKHH2	ARMC4	JUP	ZCCHC7
SPARCL1	RGS14	PIFO	CEP78
GJA1	C22orf5	GNCG	POLE3
PELO	RASSF6	CD34	MED22
HHEX	MUC15	MSRB3	ASB6
UTRN	LRRRC45	FAM174A	CIZ1
CARHSP1	NRG4	PHLDA3	FAM73B
BANK1	HNRNPf	SLC16A11	C9orf42
DAB2	SYAP1	MFS4	DPH7
ACOXL	TPST1	IQCK	NOTCH1
RASSF3	ZNF764	SLC2A1	NACC2
FAM49B	TIGD4	B3GNT1	ADD3
ASAP1	TMEM154	SH3PXD2B	TAF5
LPCAT1	ALCAM	BTC	RGS10
CD8A	SERPINA6	DES	DGKZ
PID1	SLC16A5	CSRP2	PTPRJ
DGKE	FABP6	TP53I1	SESN3
ZUFSP	FAM161A	APITD1	RPS3
GRAP	C14orf42	DOLK	NCAM1
ANKRD29	CDK1	PHYHD1	NPAT
THY1	FRMPD2	CST6	ATM
UBASH3B	SEMA3E	GRAMD2	MTA2
ROBO4	SLC30A1	SCUBE2	ROM1
NRGN	KRT8	MCTP1	PLCH2
AB1BP	ADORA2B	KCNE3	CPSF7
ANGPT1	SPATA24	P2RY2	B3GAT3
PTPNC1	KRT4	C1orf72	LSM14B
ABCA6	SLC23A1	NR2F1	CABLES2
ABCA10	NPAS2	SFN	FERMT3
DISP1	HSD17B13	BAIAP2	VPS51
TNIK	EMB	A2M	CNKSR2
FAM167A	SOC56	TUBB6	KLRF1
PGM5	TTL6	NUPR1	C10orf68
CCSAP	POLH	CLEC14A	TIRAP
GBP5	DYDC1	PLA2G16	CD226
PDLIM3	PAQR8	B3GNT5	TEX12
LY96	DCCD1	NCKAP5	PIP4K2A
PDE1C	HS6ST2	BASP1	PIP4K2A
JAM2	INSR	IRX5	DHX37
ADAMTS1	RBK5	PXMP2	CCR4L
FGD5	LRG1	C8orf4	CACNA2D4
PIEZO2	ZNF440	MUC20	BTBD11
TMEM55A	KRT19	SIX5	CSNK1G3
SLC25A28	KRT15	SCN4B	SCLT1
SAMSN1	NAT1	EPS8L2	VPS26B
RHOC	DLK2	CHD9	QTRTD1
DBI	ZNF561	PAWR	MMAA
SLC7A7	PPID	PTRF	NR3C2
GRIA1	LPAR3	IRX3	ADAM8
PIK3AP1	MAP6	EFCAB4A	RNF144A
TTN	ZNF584	NAALADL2	FLJ1
VSIG4	DNAI2	CD151	MLF1IP
FZD7	SPSB1	FAM20C	SACS
PPARGC1B	C20orf201	ODF3B	CCL28
ELMO1	LRRRC34	MLF1	PARP8
SLC26A2	KND1C	NDUFAF3	PSTPIP2
SLA	TTC40	STAP2	PKK1
CLIC2	PWWP2B	PDE4DIP	PDE3B
ELMSAN1	CYP4F11	CTXN1	JMY
WIF1	LRRRC48	ERBB4	ZNF773
KCNMA1	ZNF57	KCTD12	ZNF256
ADAMTSL3	SNTB1	GRINA	SUV39H2
MAP3K7CL	MBOAT1	THBD	NMT2
BACH1	AZU1	STX19	USP12
TSPAN7	CERS6	RIIAD1	CAMK4
ANKRD9	COPRS	TMEM139	ZFP36L2
FGF18	CCDC11	EXOSC4	MBNL1
NTAN1	C2CD2L	HY1	PRDM8
ZFYVE9	RSPH9	SEPW1	HNRNPDL
FZD1	MUCL1	MRFAP1	JAKMIP1
SUSD3	ZFAND4	C10orf67	CENPH
ST3GAL2	EFCAB12	FUCA1	BCL2L11
IL34	CES4A	TMEM125	ANAPC1
CACNA1D	CES2	HLA-DQB1	RASSF3
KIT	NBEA	VWA1	HNRNPNU
AFAP1L1	ADH6	CDC42EP4	RANBP2
TSC22D3	CAKAD	FCER1A	AHCTF1
KCNJ15	TADA2B	BBS10	NR4A2
ERG	CCDC96	ZNF771	CD96
TSPAN18	RHOD	TDRP	FAM49B
ZNF618	VANGL1	C7orf41	UBP1
SNX22	IQCB1	MCFD2	CD8A
TMSB15A	SAA1	KCNE1	RPIA
MRAS	AGR3	ARSJ	GT2F2E1
ESYT3	C2orf70	CUEDC1	C7orf31
FAM46B	CCDC41	NQO1	JAZF1
COLEC12	NUDT4	RPH3AL	MCOLN2
GPR153	APOBEC4	PENK	CHD1
SHROOM4	42804	TMEM45A	HS2ST1
AHCYL2	NET1	RNF135	NUS1
CD1D	SPTBN2	YIPF6	GRAP
NCF1	RBM4B	CLDN7	AK5
GDPD5	PIFO	CCDC149	ANKH
SLAMF8	LRRRC63	CHST15	CDH12
RNF166	CEP19	WRB	GPR15
NBL1	FAM174A	BACE2	PTPNC1
ITLN2	GSTA3	UBIE2E2	TRIM11
FCER1G	C12orf66	CIS	GBP5
STC1	ZNHIT2	BGN	BUB3
CSRP1	TNK1	NDN	SRSF12
CIQC	SLC16A11	NTM	PSMA8
RCAN1	BBS1	TSKU	C21orf91

SCUBE1	ZNF497	ANXA2	WNT7A
PTMS	IQCK	HCAR2	OXNAD1
HK2	WDR49	C1orf116	PLCL2
C1R	BTC	CRIP2	CXXC1
ACE	DNAH12	VMO1	SKA1
ZYX	CNIH2	CADM1	ZNF18
ABR	CATSPERD	C19orf59	FBXL18
PTGIR	KCTD13	GAS6	GOLGA7B
ZBTB8A	CD164L2	PTTG1IP	HSPA13
CPAMD8	ABO	C10orf107	SAMSN1
ABCG1	FAM182B	TNFAIP8L3	USP25
ITGB2	FAM131A	GKN2	C16orf87
ZNF761	VWASA	LHFP	SLC16A1
GPSM1	APTD1	CMTM4	HEATR3
SHKBP1	LIPF2	MACC1	C9orf85
PKN3	UCP2	KREMEN1	PK3AP1
AMICA1	P2RY2	FAM162B	C10orf12
PCSK7	TEX26	NUDT14	FAM126B
CD3G	C1orf172	FAM3B	SLA
ANO10	RUVBL1	COA3	RAB39B
PTH1R	BAIAP2	TMPRSS2	C9orf41
FGFR4	WBSCR28	ADAP2	BATF
HK3	PLEKHF2	CLDN5	CDK
PTGER1	UNC119B	GOLGA6L4	WHAMM
ZNF333	C11orf16	OAF	TIAM1
U2AF1L4	MBLAC2	TACSTD2	SFXN2
COX7A1	GPX2	PRKD1	PPP2R2B
ZNF577	SMIM19	SLIT3	RPL30
ITGA5	PRR18	PKP3	SUPV3L1
CD300LG	DMRTA1	CSF1	FAM122B
FMNL3	EID2B	PROS1	EEF1A1
GRASP	PRR15	42983	TYSDN1
CXCL16	CNTD1	ZBTB7C	PHF6
SCIMP	B3GNT5	TNFAIP2	SAMD8
RNASEK-C17orf49	MAP3K19	WBP5	UTP14A
BCL6B	MYO1D	PPIL6	TBC1D31
TNFSF13	CCDC121	SFTPA2	ATAD2
ASRGL1	PFN4	TCN2	FBXO32
LRP5	BASP1	GAS2L1	FBX5
TPC2	IRX5	METTL7A	SASS6
PDZK1IP1	PNMA1	FAM174B	BRPF1
ZYG11B	FUT2	ROR1	TATDN2
PPAP2B	MUC20	MUC1	PAXIP1
RBP7	LY6H	NR2F2	SUSD3
FBLIM1	ZDHHC13	TLCD2	ST3GAL2
PDPN	WDR73	FAM212A	RNF111
LAPTM5	SMCR7	PBX1	TSC22D3
SDC3	C8orf47	NDUFA4L2	DSCR3
CAMK2N1	ZBTB33	IFT11	TAB3
ALPL	RPRM	KLHDC8B	C9orf91
MXRA8	EFCAB4A	ZNRF1	BRAF
MEGF6	C12orf68	SLC51B	SKI
NEXN	ODF3B	42795	LDLRAP1
ELTD1	DPY19L2	CYP4X1	DUSP2
NTNG1	C2orf73	C5orf38	XKR8
HENMT1	MLF1	42988	EYA3
GBP2	GRAMD1C	TEAD1	MITD1
GBP4	STAP2	MITF	SPATA2
ARPC5	PDE4DIP	AKR1C1	CPA5
DDR2	PPP1R42	KIAA1598	ZC3H18
PEA15	DALRD3	SESTD1	GDPD5
OLFML2B	NT5DC1	BCAM	PPP1R15B
FCGR3B	P4HTM	MAG2	AGPAT6
IERS	DTX3	GJA4	ZSCAN12
C1orf115	CTNX1	TLR5	ELK4
PKDCC	CA8	THSD4	RNF166
HAAO	ZNF713	C1orf168	SPATA2L
MAPKAPK2	KCTD12	MORN2	ZNF276
FRZB	DHFR1	COL4A5	FAM160B2
NOSTRIN	STX19	AGRN	TOMM40L
HPGDS	RIAD1	HES4	CDC42SE2
C1QTNF7	C1orf173	PLSCR1	EPB41
TNFAIP8L2	RMII	FAM92A1	FBXW5
ARHGAP25	TMEM107	RALGAP2	MRPL10
S100A9	RRS1	S100A16	IGF2BP1
TDRD10	CCDC89	ZDHHC9	MORC3
CCNYL1	C10orf67	PRELP	ARHGAP27
FZD5	NSUN7	C9orf152	ADPGK
COL6A3	C1orf101	APOD	PADI4
LMOD1	GEMIN4	H1FO	ATP13A2
CCDC141	FJX1	PLAC9	BTG2
TGFB2	PLD6	CLDN4	THEM4
TRAT1	FAM216B	FAM47E	RGL4
MNDA	SERTAD2	S100A13	GPR114
PYHIN1	ABCA13	MAOA	TEPP
ADAMTS9	C1orf194	S100A14	SPON2
DNASE1L3	B3GNT3	KAZN	CTBP1
APBB2	ANKRD18A	KIAA0408	ZFYVE28
PCOLCE2	TDRP	CXCL17	ZFYVE28
CXCL3	RCI1	HLA-DRB1	RLTPR
PPBP	ZNF816	SERPINA3	ZNF230
PF4	ZNF609	SPATS2L	ATAD3B
TM4SF18	GLIPR1L2	CTSE	UBASH3A
ZDHHC3	KCNE1	SFTA2	RRP1B
CLEC3B	HIST1H2AC	CD55	TRAPPC10
CCR1	HIST1H2BC	EPHB4	GAB3
HEYL	SLC36A4	PPP1R26	AIRE
BAP1	ZDHHC20	MYL6B	ITGB2
ARHGEF3	ZFP3	SULT1A1	RALGDS
EMCN	CAPS2	SLC6A9	SPATC1L
CAMP	OXTR	PLXNB2	MCM3AP
SPRY1	BBS12	MYO6	DIP2A
DUSP7	NQO1	ADH1B	S100B
PPM1M	MAPK15	TCF4	SLC2A6
GUCY1A3	MUC16	DAPK1	SHKBP1
HPGD	HIST3H2A	HLA-DQA1	DEDD2
IL15	NME9	S100A2	SIK3
HHIP	CCDC108	KIAA1211L	NEK8
EDIL3	SYNE4	LAMB3	CD3G
STARD4	SOX2	ARHGEF12	ZBTB7B
ESM1	TMEM45A	SRGAP1	NLRX1
RICTOR	GPR135	ANXA4	IL6R
EBF1	ATG9B	MAFG	UBE2Q1
CSF2	C5orf30	SRC	CRTC2
42986	PNMAL1	FAM110D	NBEAL2
SHROOM1	WRB	SERPINA1	PPP1R35
MB21D1	TMEM30B	TPSB2	FCRL3
CITID2	RAD51B	KANK2	IER2

SAMD3	CYB5D1	SVIL	ZNF394
GALNT10	BACE2	VEPH1	RECQL4
BMPER	AC079354.1	PDGFA	LRRC14
KIAA1324L	CEP97	SLC2A10	FOXH1
HEY1	FAM104B	NMB	CELF5
TAGAP	SATB1	PARVA	MFSD12
COL1A2	TRAK1	FAM114A1	YDJC
BR13	SLC25A10	TXNRD3	ZNF382
SOX17	FANCF	CFD	PLXDC1
DLC1	CHST6	OCLN	IKZF3
TNFRSF11B	RUVBL2	MYO1C	DBF4B
SBSPO1	CTD-3193O13.9	S100A6	RAVER1
GPR146	CCDC60	MPZL1	LEMMD2
GPER	CCDC125	LPAR1	RPL26
CA3	JRK1	HBCH	SPSB3
BAALC	C10orf107	HMGNS	CCNF
CTHRC1	GBP6	SLC29A3	NEU3
DCSTAMP	RIPK4	ASPH	TAF6L
GEM	EP400	SPRED2	NXF1
ABCA1	FAM46C	TPM2	SLC25A45
MAMDC2	TNFAIP8L3	SH3BGR12	RP56KA4
SVEP1	SFXN4	HLA-DRB5	SLC1A7
FBP1	DGCR6	ITGBL1	C1orf77
CYBB	C11orf88	CTNND1	USP24
MID1IP1	EFHC2	TUSC1	NOL9
FIGF	CMTM4	PAPSS2	KLHL21
SPTSSA	ASCL2	UNC13B	ZSWIM5
42802	ANKRD45	PPP1R14C	GMEB1
CFI2	MAATS1	MSRB1	JAK1
ZCCHC24	GPR39	CDC42BPB	CTRC
FOLR2	DNAH2	EGFL6	DRAXIN
PKNOX2	EIF3C	GK	LAPTM5
C10orf10	LRTOMT	CES1	SCNN1D
VSTM4	ALDH1A3	SHISA4	HENMT1
COMTD1	TACSTD2	NOS1AP	ATXN7L2
ZNF503	ZDHHC23	DMD	ZNF326
NSD1	MAP7D2	NAGA	GFH1
TMEM52B	WDR27	KIAA1279	SLC30A7
FAM69B	SLTRK6	TGM2	SLAMF6
KIAA1462	NELL2	CAPN8	FCRLB
ARIHGEF40	HIST2H2BE	C1orf53	FCGR3B
ZNF219	42983	FAM229B	FLVCR1
BTNL9	LRRRC26	FANK1	RBM15
TTCT7B	ZBTB7C	DDO	DENND2D
IFI27L1	APOO	FAM127B	IER5
IFI27	SDR42E1	GPRIN2	CNST
CACNB2	FAM227A	HLA-DOA	B3GALNT2
PTPLA	TMEM121	HLA-DMA	IL24
SMCO4	CIB1	HLA-DRA	FAIM3
AMOTL1	EFCAB10	NOTCH4	DISC1
HTRA1	ADSSL1	ERICH2	MEMO1
SPRED1	PPIL6	LAYN	FBXO41
RAB8B	KIAA0825	HSPA1A	ANKRD23
IKBIP	CDNF	DDR1	ARHGAP25
FBN1	NUPR1L	TBC1D8	DCAF16
CYYR1	TNFAIP8L1	RANBP17	GPR155
C2	SMYD3	TCTN1	PBXIP1
TMEM100	METTL7A	AARD	EIF4E3
SMPD1	AHNAK2	TRIQK	PROK2
ILK	LMLN	MTIM	TMEM183A
TPP1	MORN5	CFI	TRIM46
KIAA0355	C6orf201	C2CD4B	KIAA1524
MFA4P4	PCYT2	RGL3	EOMES
CCDC68	C1orf110	ITSN1	TRAT1
CLEC4E	THBSL1	GPX3	NUAK2
NDEL1	KRT5	FAM127C	PYHIN1
NGFRAP1	AGBL4	DARC	EIF5A2
NNMT	EDARADD	KLHL23	PPM1L
AGBL1	SLC51B	LTC4S	CTL44
XRCC6BP1	CYP4F12	LEPROT	ICOS
MSA7	ZNF749	EMP2	CD200R1
MSA14	KLHL32	UBD	COX18
MSA15	TMEM212	TAX1BP3	PPM1K
MAPRE2	CYP4X1	TSPAN4	GMPS
MEI1	CCDC30	ANG	TIPARP
GNGT2	AKAP14	C11orf93	CCNL1
TBC1D2B	KLK12	PLIN5	RPL9
SNX20	ZNF396	STARD10	TOPBP1
DPEP2	FAM86B1	ARHGEF28	UCN
CD3D	KIF24	C5orf49	ZNF513
CA4	C17orf58	IFB3	KIAA1143
TPM4	BCDIN3D	NBP1	WDR43
GPDI	CCDC42B	AP4M1	DTX3L
AXL	TMEM17	CEBPD	ZC3H12A
NFKBID	TMEM232	C1QTNF5	SNIP1
LAIR1	FAM183A	APOC4-APOC2	UVSSA
CDC42EP5	EFCAB6	NTF4	FAM208A
PPP1R14A	ESPN	SFTA3	ARHGEF3
DAPK3	TMEM216	HSDP1	RNF168
RILP	AKR1C1	HLA-DPA1	SLC9B1
ANGPTL4	TSPYL4	HLA-DQB2	SLC9B2
CD300C	DVNC2H1	GPX1	ZNF589
CD300A	WDR86	ANKRD65	ATRIIP
TMEM88	CDHR4	SMIM1	C4orf29
TMC8	PLEKHG7	ARHGEF38	RAD54L2
ABCA3	IFT140	HLA-DQA2	WDR82
SLC3A2	TLR5	TXNDC5	HMGB2
ATG16L2	C17orf97	AQP1	PRMT10
NAALADL1	VMAC	KRBOX1	LMBRD2
BATF2	RP11-72304.6	YAE1D1	SERINC5
VASN	DNAJB13	CD302	ERAP2
FAM107A	ZFP69	ARHGAP8	PAPD4
CX3CR1	HIST1H1C	INMT	UTP15
FILIP1L	CCDC157	ARPC1A	ACSL6
MFSD2A	C1orf168	PEG10	MB21D1
MLKL	AC002472.13	C15orf38	CITED2
RHOH	DNER	HLA-DMB	CREBRF
RAB31	MORN2	GNG10	SFXN1
TNXB	NWD1	UPK3B	SAMD3
LG13	WN17B	CFB	STXBPF5
SFTPC	C6orf132	GSTA1	ANKRD55
BMP1	FAM166A	DBNDD2	STK17A
SDPR	HEPACAM2	ETV5	TRA2A
CHRM1	TUBB4B	SCARF2	RPS14
COL3A1	ENO4	PCP4L1	C7orf60
AXIN2	FOCAD	ECSCR	RELL2
SLC16A4	TCTEX1D4	ECSCR	ZNF12
IL7R	CERKL	GPR162	TAGAP

NPNT	C9orf171	IQCI-SCHIP1	LMTK2
ATOH8	C12orf55	SEPP1	SLC4A2
TNIP2	FAM154B	C1orf210	FASTK
VAMP5	RHCE	TRNP1	YWHAZ
PLA2G4F	FAM221A	CLDN23	SLC25A32
SLC35G2	NOXA1	BRK1	TMEM65
INPP5D	SNTN	DYX1C1	LETM2
STXBP6	ZDHHC11	HP	FXN
LGALS9	GJB3	FNTB	TMEM71
PXDC1	PTPLAD2	RNASE4	ATP7A
SIGLEC7	C1orf192	SMIM6	ZNF367
COL4A3	ANKDD1B	CCPG1	TRMT10B
MAP2K1	APOD	FXVD1	BRWD3
PARM1	CLDN4	SMIM22	FBXO33
FAM110B	FAM47E	FBXO17	DDX26B
CXCL10	ZNF33A	F11R	GTF2A1
NPIP3	GJB5	FAM47E	INPPL1
CXCL11	FAM179A		PCF11
ADRB2	ALG1L		ARF6
B3GALNT1	CXCL17		TAF3
SHE	PTPRT		QSOX2
PTAFR	SPOCK3		SNAPC4
NPR1	C16orf93		SDCCAG3
SCN9A	AKR1C3		DDX21
SDC2	KIF19		NSMF
CD52	SRGAP3		FRAT1
PLEKHA2	FAM217B		TC2N
CLIC4	LCOR		MOAP1
GPR183	ADH7		C1QL3
ZEB2	NOXO1		KIAA1731
CLIC3	ZNF569		R3HCC1L
ANTXR1	ZNF775		LIPC
LUZP1	ZNF799		GLB1L3
FASN	C20orf96		RAB8B
LDB2	ESRRG		ZNF319
ITGAM	IPO4		COP52
TM4SF1	SLC6A9		ARH1
KLF13	PLXNB2		ZNF202
ZFPF2	TTC30B		CUL5
SIK2	ERI2		PLEKHFI
CRTAP	ZNF33B		KIAA0355
HSPB2	FAM150A		RPL27A
FABP4	S100A2		CENPN
DENND5B	KIAA1211L		ATMIN
CD14	HIST3H2BB		MAPK7
MZB1	KPNA5		PRKCB
PFKFB3	ANXA4		NDST2
SERPINB9	WDR5B		B2M
KCNS3	DTHD1		ZNF592
AKAP13	KIAA1671		CATSPER2
HTRA3	SLC25A29		FAM111A
FOXP2	LRRRC8B		TMEM170A
USP32	NEK5		C18orf54
PLA2G1B	GPR123		STAT6
GSTA4	C9orf169		PATL1
OSCAR	SLC22A4		TSC22D4
TANC2	ZNF165		EPB42
PRKCDBP	SLC22A5		SMAD3
SIPR1	IPP		MAPRE2
PKIA	CYP2F1		MBD6
FPR2	SLC2A10		NUDT21
FPR1	TTC30A		MEI1
SOX7	BCO2		FAM102A
GIMAP8	KCNMB2		SP2
NETO2	DNAH10		NOD2
TMEM37	CR1L		SNX20
SOSTDC1	WDR96		RNF214
GAA	CCDC180		ENGASE
KCNK3	C4orf22		CD3D
APLN	MEIG1		ENTHD2
HOPX	LEKR1		STIM1
LRRRC8C	PCDH20		IRGQ
PTGER4	CCDC151		PPP2R3B
FGG	ZNF273		ZNF668
PTCRA	NUP62CL		ZNF646
GPR34	MB		FAM129C
RGS19	ZNF607		KLHL26
SLFNL1	BPIFA1		GATAD2A
NINJ2	TMEM116		MVD
C3AR1	GFPT1		PROCA1
AQP4	MTIF		RPL13
SYNPO	ZNF69		ZNF641
MAL	SH3BGRL2		DHRS13
EPHX4	C1orf228		TP53I13
LAMB2	ZNF627		ZNF701
KLF11	KCNRG		LENG8
CD8B	LRBA		LAIR2
SLFN12	FAM3D		ZNF526
ID4	CALM1		KIR3DL1
TPSAB1	CEP290		TMKGID2
CLEC7A	FAM179B		CHAF1A
SPTLC3	DLL1		KIFC2
CLEC12A	ECI2		KRT1
RCAN2	PPP1R14C		ACER1
IL16	RASSF9		CD300A
SYNPO2	PAX9		TMC8
GTPBP2	RUNDC1		ZNF598
IL17D	KIAA1737		CASKIN1
CTSW	DZIP3		ZNF597
SMPDL3A	KIAA0753		NLRC3
EFEMP2	EFCAB2		C11orf84
SLFN11	ECT2L		ATG16L2
EGFL7	FAM229B		RPSA
MRGPRF	FANK1		SF1
MYD88	HIST2H2BF		MAP4K2
BNC2	CCDC160		CCDC88B
LRRN3	C1orf141		DDIT4
RAPH1	EFCAB7		PTGDR
CYSLTR1	LDLRAD1		TTC39C
ABLIM3	LRRRC73		GLYCTK
GLRX	TRAF3IP1		KIF5C
SNCG	SMIM5		MGAT2
MMRN2	ERCC12		HISTH1IE
MAP3K11	NELFE		CXCR1
CIOB	SLC44A4		ING5
CIOA	HSPA1B		ATG4B
OLR1	VWA7		RFWD3
CCDC36	LY6G5C		RHOH

EHBP1L1	APOM	ATXN2L
PTPRM	CCHCR1	HEXIM2
VEGFB	DDR1	CDKN2AIP
PEAK1	TRIM39	SNRNP48
TNFRSF10D	RNF39	AXIN2
NABP1	TBC1D8	IL7R
SLC19A1	CASC10	SEMA4C
HSPB7	C9orf135	CNNM3
HEG1	TTC25	ABHD15
CD7	TCTN1	ZNF507
PLK3	LRRC10B	NSG1
GOLIM4	TMEM1231	ZBTB49
HOXB2	C4orf47	ANKRD49
CIQTNF1	PSENEN	INPP5D
CD34	ZBTB10	TMEM129
MSRB3	LGR4	JMID7-PLA2G4B
SELP	MUC12	FEM1B
ZHX3	DENND6B	MECP2
PHLDA3	TTC23L	SLC25A6
PODN	HN1L	XPO6
GOLT1A	SERPINB5	RP11-231C14.4
CMKLR1	RP11-503N18.1	RGS14
SLCO2A1	ANKUB1	TBC1D10B
KIAA1551	WDR52	CASB
C4orf32	DIO1	NPIP3
FZD4	FGFR1OP	ZRSR2
CD248	CCDC19	CD52
EMR1	TCTEX1D2	PLEKHA2
DENND6A	ZNF625-ZNF20	GPR183
GLMN	TMEM110	DFFB
C3orf55	ADAT3	APLF
PTDSS2	KCTD11	BOLA2B
P2RY14	UBD	HIC2
CHST2	LTB4R2	HEXDC
ZDHHIC14	CLDN9	DUS1L
CSRP2	FBXO16	CSGALNACT2
DDIT3	MYCBP	ITGAM
CATSPER1	C12orf74	IFFO2
LPL	C11orf93	CHD3
TBC1D10C	BBIP1	KCNAB3
POLD4	FAM187A	ZNF778
LRRC25	PLIN5	GPR25
LONRF3	PPME1	USP38
CCDC85B	CPEB1	ADPRM
NR2F1	EML6	ZNF282
MSRA	COL28A1	FOS
A2M	FAM166B	FAM115C
ARL4D	C5orf49	NFXL1
TUBB6	TSTD1	RALGAPB
NUPR1	TTC34	WIBG
TPRN	SYCE3	KRT72
ZNF683	C5orf54	SERPINB9
SPHK1	FAM200A	EMB
HSD11B2	DCDC2B	IRF2BP1
CLEC14A	AC011242.6	TRABD
BDNF	C17orf72	ZNF296
BOK	C3orf83	CDCA4
NCKAP5	SCAMP4	FOXX2
VSIG10	LINC00948	BFSF2
METRNL	PATL2	KBTBD2
WSB2	ANKRD66	RNF139
C8orf4	ANKRD18B	PDGF
FIBIN	STMND1	TSNARE1
RHOG	TSPAN19	ATP6V0E2
ANO6	PINLYP	SOC55
KCNA3	MCIDAS	ZNF692
CASKIN2	ANKRD65	NAIF1
HIC1	C12orf75	JUNB
PPF1A3	ARHGEF38	CHST11
SAMD9L	B3GNT9	ASXL1
NIM1	RNF103	ZNF318
GPR4	GATS	LRRC8C
PTRF	SMKR1	RSL1D1
ZBED2	PNMA2	LRRC8D
CD163	PDXP	PTGER4
CD163L1	AF011889.5	NMUR1
CD151	C2orf15	PIK3CD
FAM20C	AMACR	SLC25A33
PVRL3	WFDC6	ZIK1
MYOZ1	AP000322.53	ATF7IP
GRB2	CFB	RGS19
FAM211B	ZNF487	BCL2
ALS2CL	WDR92	RHNO1
KDEL2	WDR65	ZNF570
MAF	TUBA4B	MLLT3
CTNNBIP1	GSTA1	ZNF217
RPP25	GSTA2	CYP4F22
THBD	CCDC13	C20orf196
TMEM139	ADH1C	MAL
MSC	PCP4L1	RAB33B
APOLD1	CCDC153	ORMDL3
EXOC3L1	HAUS5	SMN1
GIMAP7	TMEM150C	MOB3A
HLA-DQB1	RP11-503N18.3	CYCS
GATA2	SPATS1	CD8B
GPC5	MRPS17	MALT1
ALOX15B	KIAA1456	ISG20
PCED1B	FAM218A	IL16
FOXS1	GPR162	DNAJB7
CDH5	ZNF550	CARNS1
MYADM	APITD1-CORT	PPP1CA
42979	TRNP1	CTSW
FZD2	ATXN7L3B	RASGRP1
HCLS1	SY51-DBNDD2	RAD9A
SERTM1	SAA2-SAA4	FAM21C
GAS1	CYP2A6	ZMAT3
HMHA1	DYX1C1	THEMIS
PRF1	NHLRC4	MUS81
TMEM64	GALNT4	NAA16
SHISA2	RP11-192H23.4	RAB43
KCTD2	RP5-102I20.4	RAB37
FCRL6	SMIM6	SNX32
F2R	RP3-369A17.5	KRT2
PJA1	C15orf65	DMXL1
CCL13	MIA	ZNF621
DDX60L	C21ORF59	NADSYN1
AATK	SMIM22	ANKRD13D
ZNF467	C6ORF165	OXSRI

RAP2B	ADRBK1
C6orf223	KDM2A
SLC9A9	ESRRA
LSM10	PARP15
IBA57	ABCD2
RTKN2	KIAA1919
TNRC18	ZNF483
NOP10	SLC2A14
FAM89A	ZBTB21
UNC5C	DAB1
UBA7	THAP2
MOB2	SMARCC1
UBE2E2	CHD2
SYNM	SULT1B1
API52	RCE1
CIS	CXorf23
KBTBD3	STAT5B
PLCXD1	CD7
CAPN12	EIF1
BGN	PHOSPHO1
FES	ZNF791
MXRA7	NRROS
CSF1R	KLHL15
LCK	FBXO45
COL18A1	SLC25A30
TCEAL7	LEMD3
GJC1	CYB561D1
CADM1	C12orf66
SPNS2	ZNF80
C19orf59	TNK1
SLC8A1	GTF2IRD2B
LYSMD4	GCSAM
GAS6	IL20RB
TMEM119	MSL2
CCBE1	ANGEL2
FHL3	ZNF266
GKN2	SLC29A2
FAM167B	KIAA1551
FAM101B	FGFBP3
UPP1	NR1D2
LHFP	PCP2
OLFML1	CEP135
FAM162B	DENND6A
KIRREL	PDE12
SH2D1A	NLRP6
SMTN	C3orf33
ST6GALNAC3	KCTD13
DENND5A	GPR171
ADAP2	DHX36
CLDN5	CHST2
TSPYL2	GK5
PCDH9	VCPIP1
ACOT1	TRAF6
CDR1	ZNF654
SLIT3	PACS1
CSF1	DDIT3
PTP4A3	ZNF408
TMEM255B	ARHGAP1
DUSP8	GOLGA8A
PDE4B	CCNE2
SNN	NRIP3
ATL3	EIF3F
SMIM10	RFESD
PRR16	TBC1D10C
FMNL1	RPS6KB2
F8	ZNF169
FAM43A	UBE2O
NRBP2	JAKMIP2
IFITM2	ZNF683
WBP5	MYPOP
IL3RA	ATAD5
SFTPA2	CRLF3
ARL15	SYNE3
SOC51	CLK2
TCN2	LPCAT4
GPRIN3	ZNF575
ROR1	KBTBD11
C17orf70	LMNB2
PRKG1	MEX3C
LSAMP	CDK5R1
OLFML2A	LRRCC37A3
FAM212A	TCEANC
NDUFA4L2	C8G
C16orf52	GCNT4
IKZF1	NFATC2IP
GNB1L	DPP7
EVI2B	SMCR8
LAMP1	MTX3
KLHDC8B	ULK1
IRS2	RPS6KA3
ZNF529	PUS1
AIDA	KCNA3
CD300LF	NAP1L5
PIPSK1C	NR2C2
42795	ARH2
BACE1	SLC25A22
GLDN	PIDD
GNG2	JUN
BTN3A2	IL17RA
C5orf38	MBOAT4
ARHGAP30	ANXA2R
ARAP1	SOX12
PDE2A	HNRNPA0
LILRB4	ZNF620
TNFRSF4	ZBTB41
TRABD2A	RPS27
KANK3	GPR150
EMID1	TSSK6
FPR3	SH2B1
C11orf96	ZC3H12D
COL4A1	ZNF543
GJA4	ZNF354B
ISG15	ZFAND2A
SPRY4	KLHL11
TRPV2	SLC25A20
NHEJ1	CD28
PEAR1	GTPBP6
SOWAHD	ERN1

PLSCR3	GPR35
DMBT1	PARP10
COL14A1	SUZ12
TPRG1	ZHX2
S100A3	TRIM73
RILPL1	ZBTB7A
ARL4C	CTC1
MAPK12	SNX18
SMTNL2	RRS1
PRKAR1B	C12orf42
DCUN1D3	PER1
SELL	SPTY2D1
HBA2	CLK3
PARVB	ARID3B
PRELP	KLHL28
KLRG2	ZBTB18
MSL1	GCC1
LRRK2	ZFPM1
KCTD21	PCED1B
PLAC9	AKAP5
HN1	ZNF154
PCDH18	ZNF784
FAM150B	CCR8
KIAA0408	TSHZ1
IL1RAP	PSTK
HLA-DRB1	ZNF48
S100A4	TMEM86B
MPHOSPH8	42979
TUBB	MYLPF
SFTA2	HCLS1
GIMAP5	ATP5EP2
ZNF34	HARB1
PTPN1	HMHA1
EPHB4	FUT7
TSC22D2	ZNF594
NCOR2	PCGF5
MAN2A2	PRF1
MME	SIPR5
SULF2	ZDHHC20
LAMA2	MAP3K15
ADH1B	MAP6D1
TCF4	CXCR2
HRH1	GREM2
ZNF431	ZNF792
HLA-DQA1	D2HGDH
GM2A	LSMEM1
ADA	AEN
ARID5A	SLC25A42
PDLIM7	FCRL6
FLNA	NPM1
FUT11	ZNF746
SERTAD1	XXyac-YRM2039.2
ANXA6	RAP2B
IGF2R	ZBTB2
SULT1A2	FANCB
FAM110D	SETD2
TPSB2	TMIE
KANK2	ZFP41
SVIL	ATG9B
FBXL22	SLAH2
DACT3	RFX7
ADARB1	TGIT
VEPH1	ZNF101
STMN3	TMEM259
PDGFA	ZNF708
COL13A1	P2RY8
SPN	TSEN54
C5orf56	UBA7
GZMM	FAM159A
HOXA4	C22orf26
ZNF615	FBXL6
DPP4	PGBD4
PDCD1LG2	NPLC4
S100A10	TSHZ2
CFD	KPNA2
MAP1LC3C	RNASE10
FAM49A	SPNS3
MYO1C	SATB1
DNM3	ACTL10
SIRPA	C16orf72
GRK6	LCK
SULT1C4	ZNF721
CSF2RA	HMGNA
FKBP1C	SPATA13
FAM109A	GPR19
SPRED2	ABHD16B
FAM115A	PLGLB1
TPM2	ZNF623
HLA-DRB5	C19orf71
PLN	NPIP1A
ITGBL1	TRIM61
PAPSS2	GT2H2C
EGFL6	ASB7
RCS1	TREX2
TMEM184B	GPR132
ZNF521	MX2
ZNF358	KLRC4
CD247	TANGO2
DENND4B	HIST2H3D
ARHGEF15	ZNF530
CD3E	KLHL25
RUSC2	FAM19A1
GRK5	FAM101B
SFMBT2	NOG
MAP3K3	UPP1
TGM2	TRIM52
INF2	ASCL2
FCGR3A	NPIP5
SOX18	CCR4
MAFB	UTY
NHSL2	AC138969.4
ZDHHC18	SH2D1A
C10orf128	SDR42E2
GPRIN2	PRKX
SYT15	PP2D1
BMPR2	PTP4A2
HLA-DMA	FAM120C
COL5A2	PPP1R2

TAP2	TSPYL2
HLA-DRA	C22orf46
NOTCH4	IRAK1
AGER	HIST2H2AC
CARD16	HIST2H2AB
PRRC2A	HIST1H1B
AIF1	PLA2G6
LST1	SS18L1
PSORS1C1	CCR10
LILRB3	FOXO4
HLA-E	ZFP1
GABBR1	XPOT
PKHD1L1	FDX4B
MT1A	SNN
MT1M	42987
SAMD9	ZBTB40
TMSB4X	APOBR
CYS1	UBE2G2
DOK6	H1FX
HBA1	FMNL1
ATP10A	NTSC1B
COL6A6	UBOX5
VGLL3	ANO9
GPX3	NDNL2
SLC48A1	LRRRC37B
FAM127C	DDX51
GIMAP1	NOMO2
DNLZ	PRSS57
LTC4S	ZNF74
LCAT	UBALD2
PTPRCAP	ZBTB37
PVRIG	CCDC137
SIPA1	SOC51
LBH	ATP6V0A2
GPSM3	SP140L
LAT	IFNLR1
NCKIPSD	GPRIN3
DDAH2	C17orf70
KLRK1	IRF7
EMP2	POU3F1
ITGA1	SNA3
TSPAN4	EP400NL
PRCD	MYBL1
SOGA3	CXorf38
ZSWIM8	ADAMTSL5
IFI30	WDR53
VAMP2	DMWD
FADS3	SLC52A2
HLA-DPB1	IKZF1
C1QTNF5	ARL17A
ATXN1L	GNB1L
APOC4-APOC2	EVI2B
TMEM233	IFITM1
ORM1	LAMP1
HLA-DPA1	C16orf54
HLA-DQB2	PTCH1
TWIST2	ZNF267
HLA-DQA2	IRS2
GATSL3	C7orf61
TNFSF12	RASA3
LY6G5B	ZNF566
PCDHGC3	ZNF529
AQP1	ZNF284
PLCXD2	KRT73
HLA-DOB	CYP2R1
CD302	PIPSK1C
INMT	BCL9L
PLEKHO2	BLOCI54
C8orf58	BTLA
AKAP2	ZNF17
HLA-DMB	GPAT2
STON1	PPP1CC
UPK3B	ZNF75D
MUSTN1	NKRF
ETV5	KPNA4
LILRA6	NAP1L2
HBB	GNG2
NAIP	BTN3A2
ECSCR	ARHGAP30
ECSCR	PRR5
SEPP1	CCDC73
RP11-122A3.2	BCR
TMEM200B	SPIN2B
PCDHGB7	CXCR3
IGLL5	HEXIM1
INMT-FAM188B	TRABD2A
EBLN2	POFUT2
HP	TNFRSF18
PRR24	PPARA
RP11-718G2.3	RHD
SLC22A31	GPR141
HOXB7	CMC1
OVCA2	SPATA21
MYZAP	RNF220
RP11-599B13.6	TSPYL4
FXYD1	FNBP1
LIN37	HSPA14
FBXO17	SIRT7
CTD-3214H19.16	PLEKHN1
MILR1	B3GALT.L
	FANCA
	SEMA4D
	FANCM
	ZFP69
	PLSCR3
	TTC24
	KLHL17
	RINL
	ZNF490
	ARL4C
	ZC3H6
	ZNF383
	ZNF669
	C19orf35
	C3orf62
	ZNF559
	SBK1
	PRR19

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DUSP28
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RBM34
ZNF548
CNR2
SLX4
ZNF563
FBF1
CTD-3088G3.8
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HUS1B
LITAF
BLOC1S3
ZNF527
ZNF600
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PNRC2
ZKSCAN3
LIN54
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SLC35E2B
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PLEKHG4
ZNF681
TMEM63A
ZNF766
ZNF107
ZNF836
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POM121
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FUT4
ZNF781
EVL
ZNF765
ZNF124
TSC22D2
YRDC
ZNF777
ZNF775
ZNF605
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TPK1
AFAP1
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ZNF136
ZKSCAN5
TECP2
HSH2D
ZNF512B
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ZNF700
HIST1H2AG
ADA
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PPTC7
HIST1H2AD
CBWD3
NOP9
SLC39A10
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ZNF470
ZNF100
ZSCAN25
ANXA6
ZNF420
ZMYM1
ARRDC1
IGF2R
ZGPAT
ZNF682
PCNXL3
ABCB8
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HIST1H4J
SYNGAP1
BLM
PELI1
ZNF655
UAP1L1
ZNF786
ZNF517
ZNF675
HIST1H3D
MAP3K5
STMN3
SPN
ZNF628
MIB2
GZMM
TOPORS
ZNF841
CXorf40A
CDC42SE1
DPP4
ZNF460
RPS26
EME2

TAF13
ATAD3A
ZNF461
SLC9A8
HIST4H4
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SGTB
ZNF790
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ERO1L
FCHSD1
ZNF71
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HOXC4
PIM3
ZNF26
MGEA5
ZXDB
ZNF808
ZNF789
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MDM4
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SLC9A6
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OPA1
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TYW1
ITPR1PL1
MAP3K3
C1orf74
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RPL39
GPRASP1
TBKBP1
MAGEE1
CCDC167
L3MBTL3
ZNF525
COX20
CHML
SPRN
HIST2H2BF
LIME1
CHIC1
AGAP6
TIMM23B
ZDHHHC18
CXorf65
RING1
RXRB
BRD2
TAP2
PBX2
DOM3Z
VARS
C6orf47
NCR3
ZNF551
ZNF805
HLA-F
ZNF783
SLFN12L
ZBTB10
C4orf46
PDE7A
SAP25
GPR56
TECPR1
SAMD9
CNEP1R1
CPT1B
SMN2
C17orf107
DENND1C
KLRC2
KLRC3
ZNF316
CEMP1
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COLQ
PRR22

TAS2R14
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GIMAP1
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RPS29
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KLRK1
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LTB4R
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VAMP2
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PLXNA4
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FAM229A
ERCC6
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LTB
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MTFP1
AP5Z1
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PGBD3
KCTD7
NAT6
KIR2DL3
APOBEC3D
P2RY11
RBM12
APOBEC3C
CEBPA
PGAM5
MARS2
INSL3
RP1-130H16.18
RP11-514O12.4
ZNF324B
AP000295.9
RNF103-CHMP3
ARPC4-TTL3
TAP2
ATP6V1E2
GLI4
ZNF550
CTC-534A2.2
CCDC71L
NPIPBI1
LRRC24
CHKB-CPT1B
RP11-466P24.2
STX16-NPEPL1
CHMP1B
EID3
RP11-196G11.1
MIR3654
POLR2M
FDXACB1
NKG2-E

KLRC4-KLRK1
ZNF10
DND1
PDLG2
RP11-286N22.8
KIAA1147
LSM14A
RP11-48B14.2
RP11-347C12.3
RP11-644F5.10
RTEL1
ZNF578
DCAF8
KIAA0391
MCIR
UBE2F-SCLY
POC1B-GALNT4
RP11-468E2.4
C16orf95
SULT1A3
ZNF865
TEN1-CDK3
RP11-345J4.5
CTC-479C5.12
CORO7
LA16c-306E5.2
CTB-133G6.1
RPL17
FSBP
AD000671.6
RP11-793H13.10
UPK3BL
RP11-552F3.12
ZNF224
CTD-2207O23.3
MTRNR2L12
ARHGAP19-SLIT1
MINOS1-NBL1
BIVM-ERCC5
ZMYM6
RP11-302M6.4
WBP7
RP11-438J1.1

Table S7. Enrichment of DEGs. P values after Benjamin's correction are provided.

GO term of biological process	Alveolar > Bronchial	Alveolar < Bronchial	Lung > T	Lung < T
GO:0000122-negative regulation of transcription from RNA polymerase II promoter	0.323780297	1	1	0.015850199
GO:0000165-MAPK cascade	0.005421604	1	1	1
GO:0000186-activation of MAPKK activity	0.060850365	1	1	0.898353109
GO:0000187-activation of MAPK activity	0.042512433	1	1	1
GO:0000188-inactivation of MAPK activity	0.681616274	1	1	1
GO:0000226-microtubule cytoskeleton organization	0.489688564	0.759949831	0.418575827	1
GO:0000902-cell morphogenesis	0.237053067	1	1	1
GO:0001501-skeletal system development	0.020277606	1	0.246166313	1
GO:0001503-ossification	0.222375945	1	0.809183512	1
GO:0001516-prostaglandin biosynthetic process	0.323538799	1	1	1
GO:0001525-angiogenesis	7.24E-16	1	3.92E-08	1
GO:0001558-regulation of cell growth	3.11E-05	1	0.01664093	1
GO:0001568-blood vessel development	0.003594002	1	0.639246056	1
GO:0001569-patterning of blood vessels	0.002486344	1	0.273009037	1
GO:0001570-vasculogenesis	7.45E-10	1	0.454493419	1
GO:0001574-ganglioside biosynthetic process	0.270583565	1	1	1
GO:0001657-ureteric bud development	0.095448561	1	0.009418569	1
GO:0001666-response to hypoxia	2.26E-05	1	0.031096756	1
GO:0001701-in utero embryonic development	0.011181561	1	0.820682913	1
GO:0001763-morphogenesis of a branching structure	0.200847708	1	1	1
GO:0001764-neuron migration	0.066410654	1	0.274401586	1
GO:0001766-membrane raft polarization	0.648372779	1	0.512374186	1
GO:0001771-immunological synapse formation	0.096149473	1	1	0.721069893
GO:0001816-cytokine production	0.367992782	1	1	0.080967413
GO:0001821-histamine secretion	0.708382741	1	1	1
GO:0001822-kidney development	0.357262352	1	0.237554341	1
GO:0001837-epithelial to mesenchymal transition	0.042541615	1	0.767144415	1
GO:0001845-phagolysosome assembly	0.708382741	1	1	1
GO:0001886-endothelial cell morphogenesis	0.027766761	1	0.316891387	1
GO:0001889-liver development	0.76654764	1	0.70239463	1
GO:0001892-embryonic placenta development	0.726242179	1	1	1
GO:0001932-regulation of protein phosphorylation	0.786503933	1	1	0.891935653
GO:0001933-negative regulation of protein phosphorylation	0.107270692	1	1	1
GO:0001934-positive regulation of protein phosphorylation	4.41E-05	1	0.139349641	1
GO:0001935-endothelial cell proliferation	0.614018159	1	1	1
GO:0001937-negative regulation of endothelial cell proliferation	0.00344018	1	0.128299316	1
GO:0001938-positive regulation of endothelial cell proliferation	0.000224	1	0.024012771	1
GO:0001945-lymph vessel development	0.648372779	1	1	1
GO:0001946-lymphangiogenesis	0.141856906	1	1	1
GO:0001947-heart looping	0.597251653	0.189006831	1	1
GO:0001954-positive regulation of cell-matrix adhesion	0.020358273	1	1	1
GO:0001955-blood vessel maturation	0.003780973	1	1	1
GO:0001957-intramembranous ossification	0.071889736	1	1	1
GO:0001958-endochondral ossification	0.420718574	1	1	1
GO:0001960-negative regulation of cytokine-mediated signaling pathway	0.283325756	1	1	1
GO:0001974-blood vessel remodeling	0.081013648	1	0.703699402	1
GO:0002003-angiotensin maturation	0.467558262	1	1	1
GO:0002040-sprouting angiogenesis	0.000762	1	0.73403992	1
GO:0002042-cell migration involved in sprouting angiogenesis	0.006273284	1	0.243221083	1
GO:0002053-positive regulation of mesenchymal cell proliferation	0.064182752	1	0.212345899	1
GO:0002062-chondrocyte differentiation	0.256922401	1	1	1
GO:0002250-adaptive immune response	0.002485604	1	1	0.000179255
GO:0002291-T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	0.520976287	1	1	1
GO:0002376-immune system process	0.580310907	1	1	1
GO:0002407-dendritic cell chemotaxis	0.540711528	1	1	0.86867831
GO:0002456-T cell mediated immunity	0.648372779	1	1	0.51216384
GO:0002467-germinal center formation	0.648372779	1	1	1
GO:0002503-peptide antigen assembly with MHC class II protein complex	0.267572994	1	0.216664163	1
GO:0002504-antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	5.48E-05	1	0.000108	1
GO:0002523-leukocyte migration involved in inflammatory response	0.141856906	1	0.744070672	1
GO:0002544-chronic inflammatory response	0.734893417	1	0.606714584	1
GO:0002576-platelet degranulation	5.44E-10	1	5.59E-06	1
GO:0002666-positive regulation of T cell tolerance induction	0.708382741	1	1	1
GO:0002690-positive regulation of leukocyte chemotaxis	0.614018159	1	1	1
GO:0002693-positive regulation of cellular extravasation	0.520976287	1	1	1
GO:0003006-developmental process involved in reproduction	0.708382741	1	0.626086653	1
GO:0003007-heart morphogenesis	0.71955975	1	1	1
GO:0003091-renal water homeostasis	0.71955975	1	1	1
GO:0003104-positive regulation of glomerular filtration	0.708382741	1	1	1
GO:0003148-outflow tract septum morphogenesis	0.571048734	1	1	1
GO:0003151-outflow tract morphogenesis	0.008285127	1	0.639410753	1
GO:0003158-endothelium development	0.398460486	1	0.053520005	1
GO:0003181-atrioventricular valve morphogenesis	0.027766761	1	1	1
GO:0003197-endocardial cushion development	0.375218128	1	1	1
GO:0003198-epithelial to mesenchymal transition involved in endocardial cushion formation	0.259373999	1	0.841717012	1
GO:0003203-endocardial cushion morphogenesis	0.171691347	1	1	1
GO:0003208-cardiac ventricle morphogenesis	0.283325756	1	1	1
GO:0003209-cardiac atrium morphogenesis	0.130978038	1	1	1
GO:0003222-ventricular trabecula myocardium morphogenesis	0.468510825	1	1	1
GO:0003273-cell migration involved in endocardial cushion formation	0.708382741	1	1	1
GO:0003281-ventricular septum development	0.526544545	1	1	1
GO:0006171-cAMP biosynthetic process	0.064697892	1	1	1
GO:0006461-protein complex assembly	0.431862978	1	0.788560264	1
GO:0006468-protein phosphorylation	0.003234414	1	1	2.50E-05
GO:0006469-negative regulation of protein kinase activity	0.003455491	1	0.311152997	1
GO:0006508-proteolysis	0.68254723	1	0.838484627	1
GO:0006629-lipid metabolic process	0.699638729	1	1	1
GO:0006644-phospholipid metabolic process	0.784234117	1	0.831818544	1
GO:0006691-leukotriene metabolic process	0.395738669	1	1	1
GO:0006693-prostaglandin metabolic process	0.646931558	1	1	1
GO:0006812-cation transport	0.634286649	1	1	1
GO:0006816-calcium ion transport	0.441464706	1	1	1
GO:0006821-chloride transport	0.770314718	1	1	1
GO:0006869-lipid transport	0.076268617	1	0.548144103	1
GO:0006874-cellular calcium ion homeostasis	0.719736682	1	1	1
GO:0006897-endocytosis	0.083061647	1	1	1
GO:0006898-receptor-mediated endocytosis	0.005702355	1	0.808788106	1
GO:0006909-phagocytosis	0.001445472	1	1	1
GO:0006911-phagocytosis, engulfment	0.31522468	1	1	1
GO:0006915-apoptotic process	0.071782355	1	0.651461291	0.003313254
GO:0006919-activation of cysteine-type endopeptidase activity involved in apoptotic process	0.649241004	1	1	0.46811346

GO:0006928--movement of cell or subcellular component	0.000121	1	1	1
GO:0006935--chemotaxis	0.000119	1	0.273408509	1
GO:0006936--muscle contraction	0.002324072	1	0.104010261	1
GO:0006937--regulation of muscle contraction	0.323538799	1	1	1
GO:0006939--smooth muscle contraction	0.270583565	1	1	1
GO:0006952--defense response	0.109236941	1	1	1
GO:0006954--inflammatory response	1.04E-12	1	0.195016735	0.682949175
GO:0006955--immune response	9.60E-16	1	0.731833276	0.005115741
GO:0006959--humoral immune response	0.263411338	1	1	0.880189513
GO:0006968--cellular defense response	0.056441946	1	1	0.039339827
GO:0007010--cytoskeleton organization	0.034402708	1	0.050654407	0.911419634
GO:0007015--actin filament organization	3.14E-06	1	0.450065252	1
GO:0007043--cell-cell junction assembly	0.021124825	1	1	1
GO:0007044--cell-substrate junction assembly	0.071889736	1	1	1
GO:0007155--cell adhesion	1.63E-20	1	1.04E-11	1
GO:0007159--leukocyte cell-cell adhesion	0.150315599	1	1	1
GO:0007160--cell-matrix adhesion	3.04E-06	1	0.023480089	1
GO:0007162--negative regulation of cell adhesion	0.009435242	1	0.607971324	1
GO:0007165--signal transduction	3.26E-18	1	0.000432	0.014317824
GO:0007166--cell surface receptor signaling pathway	7.14E-06	1	0.787254666	0.385066509
GO:0007169--transmembrane receptor protein tyrosine kinase signaling pathway	3.75E-06	1	0.416031249	0.354977246
GO:0007173--epidermal growth factor receptor signaling pathway	0.236877584	1	0.454493419	0.866503052
GO:0007179--transforming growth factor beta receptor signaling pathway	0.001166146	1	0.057583891	1
GO:0007182--common-partner SMAD protein phosphorylation	0.398460486	1	1	1
GO:0007184--SMAD protein import into nucleus	0.734893417	1	1	1
GO:0007188--adenylate cyclase-modulating G-protein coupled receptor signaling pathway	0.192655842	1	1	1
GO:0007189--adenylate cyclase-activating G-protein coupled receptor signaling pathway	0.236401639	1	1	1
GO:0007200--phospholipase C-activating G-protein coupled receptor signaling pathway	0.738810138	1	1	1
GO:0007204--positive regulation of cytosolic calcium ion concentration	0.02879768	1	1	0.903578962
GO:0007205--protein kinase C-activating G-protein coupled receptor signaling pathway	0.020646747	1	1	1
GO:0007219--Notch signaling pathway	0.726272785	0.970713192	0.621051899	1
GO:0007229--integrin-mediated signaling pathway	4.96E-08	1	0.054442749	1
GO:0007263--nitric oxide mediated signal transduction	0.675503878	1	1	1
GO:0007264--small GTPase mediated signal transduction	0.012003368	1	0.594756259	0.657274412
GO:0007265--Ras protein signal transduction	0.152127223	1	1	0.404849089
GO:0007266--Rho protein signal transduction	0.002351649	1	0.142006441	1
GO:0007267--cell-cell signaling	0.057237363	1	0.076083782	1
GO:0007399--nervous system development	0.723845963	1	0.614550896	1
GO:0007411--axon guidance	0.14282666	1	0.023274122	1
GO:0007507--heart development	3.40E-06	1	0.11330979	1
GO:0007517--muscle organ development	0.160402185	1	0.805492296	1
GO:0007519--skeletal muscle tissue development	0.263171689	1	0.31323088	1
GO:0007528--neuromuscular junction development	0.258682523	1	1	1
GO:0007565--female pregnancy	0.781109132	1	1	1
GO:0007568--aging	0.135022597	1	0.17260625	1
GO:0007569--cell aging	0.681616274	1	1	1
GO:0007584--response to nutrient	0.76654764	1	1	1
GO:0007585--respiratory gaseous exchange	0.119876694	1	0.247365371	1
GO:0007596--blood coagulation	0.00130266	1	1	1
GO:0007597--blood coagulation, intrinsic pathway	0.0871	1	1	1
GO:0008015--blood circulation	0.000152	1	1	1
GO:0008016--regulation of heart contraction	0.389520696	1	1	1
GO:0008037--cell recognition	0.510173804	1	1	1
GO:0008217--regulation of blood pressure	0.006523398	1	1	1
GO:0008277--regulation of G-protein coupled receptor protein signaling pathway	0.014627559	1	1	1
GO:0008283--cell proliferation	0.007252199	1	0.309592501	0.927757165
GO:0008284--positive regulation of cell proliferation	0.000652	1	0.104037354	1
GO:0008285--negative regulation of cell proliferation	0.002309147	1	0.130483074	1
GO:0008354--germ cell migration	0.734893417	1	1	1
GO:0008360--regulation of cell shape	2.10E-10	1	0.000777	0.820486733
GO:0008630--intrinsic apoptotic signaling pathway in response to DNA damage	0.323714876	1	1	0.184963745
GO:0009190--cyclic nucleotide biosynthetic process	0.194496511	1	1	1
GO:0009268--response to pH	0.558114413	1	1	1
GO:0009306--protein secretion	0.71955975	1	1	1
GO:0009311--oligosaccharide metabolic process	0.681616274	1	1	1
GO:0009611--response to wounding	0.001651281	1	0.247646541	1
GO:0009612--response to mechanical stimulus	0.034646039	0.854184746	0.081990422	1
GO:0009615--response to virus	0.770479098	1	1	0.572625048
GO:0009749--response to glucose	0.609540691	1	1	1
GO:0009887--organ morphogenesis	0.210615022	1	0.702587042	1
GO:0009966--regulation of signal transduction	0.148104106	1	1	1
GO:0009967--positive regulation of signal transduction	0.047717403	1	1	0.005947038
GO:0009968--negative regulation of signal transduction	0.275198978	1	1	1
GO:0010506--regulation of autophagy	0.113411908	1	1	1
GO:0010518--positive regulation of phospholipase activity	0.648372779	1	1	1
GO:0010544--negative regulation of platelet activation	0.034188435	1	1	1
GO:0010572--positive regulation of platelet activation	0.520976287	1	1	1
GO:0010575--positive regulation of vascular endothelial growth factor production	0.472648075	1	1	1
GO:0010595--positive regulation of endothelial cell migration	0.000217	1	0.013016879	1
GO:0010596--negative regulation of endothelial cell migration	0.021124825	1	0.747530223	1
GO:0010628--positive regulation of gene expression	3.45E-05	1	0.010279585	1
GO:0010629--negative regulation of gene expression	0.010754164	1	1	0.761743891
GO:0010634--positive regulation of epithelial cell migration	0.754595823	1	0.223894229	1
GO:0010715--regulation of extracellular matrix disassembly	0.267572994	1	1	1
GO:0010718--positive regulation of epithelial to mesenchymal transition	0.03434578	1	1	1
GO:0010719--negative regulation of epithelial to mesenchymal transition	0.510173804	1	0.605917815	1
GO:0010744--positive regulation of macrophage derived foam cell differentiation	0.009806953	1	1	1
GO:0010745--negative regulation of macrophage derived foam cell differentiation	0.646931558	1	1	1
GO:0010759--positive regulation of macrophage chemotaxis	0.141856906	1	0.316891387	1
GO:0010811--positive regulation of cell-substrate adhesion	0.001090139	1	0.000114	1
GO:0010812--negative regulation of cell-substrate adhesion	0.095930534	1	1	1
GO:0010818--T cell chemotaxis	0.200847708	1	1	0.899155198
GO:0010863--positive regulation of phospholipase C activity	0.060720545	1	1	1
GO:0010873--positive regulation of cholesterol esterification	0.734893417	1	1	1
GO:0010875--positive regulation of cholesterol efflux	0.095930534	1	1	1
GO:0010881--regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	0.115601188	1	1	1
GO:0010886--positive regulation of cholesterol storage	0.130978038	1	1	1
GO:0010887--negative regulation of cholesterol storage	0.398460486	1	1	1
GO:0010952--positive regulation of peptidase activity	0.259373999	1	0.457581505	1
GO:0010976--positive regulation of neuron projection development	0.020092134	1	0.639456051	1
GO:0010977--negative regulation of neuron projection development	0.687761494	1	1	1
GO:0014002--astrocyte development	0.171691347	1	1	1
GO:0014065--phosphatidylinositol 3-kinase signaling	0.472648075	1	1	1

GO:0014066--regulation of phosphatidylinositol 3-kinase signaling	0.009445273	1	0.778237621	1
GO:0014068--positive regulation of phosphatidylinositol 3-kinase signaling	0.000262	1	0.479653097	1
GO:0014909--smooth muscle cell migration	0.648372779	1	1	1
GO:0014911--positive regulation of smooth muscle cell migration	0.726242179	1	1	1
GO:0014912--negative regulation of smooth muscle cell migration	0.323538799	1	0.53228888	1
GO:0015758--glucose transport	0.754595823	1	1	1
GO:0015884--folic acid transport	0.648372779	1	1	1
GO:0016049--cell growth	0.421989624	1	1	1
GO:0016055--Wnt signaling pathway	0.149444719	1	0.310479404	0.842181446
GO:0016337--single organismal cell-cell adhesion	0.009992462	1	0.030342183	1
GO:0016477--cell migration	2.26E-05	1	5.01E-06	0.893237206
GO:0016485--protein processing	0.719187297	1	1	1
GO:0016525--negative regulation of angiogenesis	2.08E-06	1	0.227531297	1
GO:0017015--regulation of transforming growth factor beta receptor signaling pathway	0.1483938	1	1	1
GO:0017121--phospholipid scrambling	0.528830825	1	1	1
GO:0018105--peptidyl-serine phosphorylation	0.330232873	1	1	0.356671885
GO:0018108--peptidyl-tyrosine phosphorylation	0.00111602	1	1	1
GO:0018146--keratan sulfate biosynthetic process	0.258682523	1	1	1
GO:0019221--cytokine-mediated signaling pathway	0.071394823	1	1	1
GO:0019370--leukotriene biosynthetic process	0.1483938	1	0.826136625	1
GO:0019371--cyclooxygenase pathway	0.096149473	1	1	1
GO:0019372--lipoxygenase pathway	0.259373999	1	1	1
GO:0019722--calcium-mediated signaling	0.263171689	1	1	1
GO:0019835--cytolysis	0.014740852	1	1	0.824177195
GO:0019882--antigen processing and presentation	0.212674226	1	0.022362063	1
GO:0019886--antigen processing and presentation of exogenous peptide antigen via MHC class II	0.342225815	1	0.000776	1
GO:0019933--cAMP-mediated signaling	0.43841433	1	1	1
GO:0019934--cGMP-mediated signaling	0.200847708	1	1	1
GO:0022617--extracellular matrix disassembly	0.002810577	1	0.004264983	1
GO:0030011--maintenance of cell polarity	0.267572994	1	1	1
GO:0030032--lamellipodium assembly	0.389520696	1	1	1
GO:0030033--microvillus assembly	0.064697892	1	1	0.86867831
GO:0030036--actin cytoskeleton organization	8.15E-09	1	0.16454748	1
GO:0030041--actin filament polymerization	0.725353792	1	0.212345899	1
GO:0030048--actin filament-based movement	0.540711528	1	1	1
GO:0030097--hemopoiesis	0.171023773	1	1	1
GO:0030099--myeloid cell differentiation	0.633878665	1	1	1
GO:0030154--cell differentiation	0.432122257	1	1	1
GO:0030155--regulation of cell adhesion	0.089359309	1	1	1
GO:0030168--platelet activation	6.32E-09	1	0.776636544	0.553083923
GO:0030178--negative regulation of Wnt signaling pathway	0.728442318	1	0.082218915	1
GO:0030185--nitric oxide transport	0.520976287	1	1	1
GO:0030194--positive regulation of blood coagulation	0.323538799	1	1	1
GO:0030195--negative regulation of blood coagulation	0.194496511	1	0.116858364	1
GO:0030198--extracellular matrix organization	1.95E-26	1	3.09E-15	1
GO:0030199--collagen fibril organization	0.00142487	1	0.206099252	1
GO:0030203--glycosaminoglycan metabolic process	0.580310907	1	0.012813794	1
GO:0030207--chondroitin sulfate catabolic process	0.323538799	1	1	1
GO:0030212--hyaluronan metabolic process	0.558114413	1	1	1
GO:0030214--hyaluronan catabolic process	0.133105577	1	1	1
GO:0030217--T cell differentiation	0.148104106	1	1	0.012110216
GO:0030224--monocyte differentiation	0.22010917	1	0.703338764	1
GO:0030282--bone mineralization	0.119876694	1	1	1
GO:0030301--cholesterol transport	0.468510825	1	1	1
GO:0030308--negative regulation of cell growth	0.000657	1	0.849955361	1
GO:0030316--osteoclast differentiation	0.267744687	1	1	1
GO:0030318--melanocyte differentiation	0.726242179	1	1	1
GO:0030324--lung development	0.006948704	1	0.009805458	1
GO:0030334--regulation of cell migration	0.011782998	1	0.171234892	1
GO:0030335--positive regulation of cell migration	1.58E-12	1	0.004062983	1
GO:0030336--negative regulation of cell migration	1.02E-05	1	0.142472094	1
GO:0030501--positive regulation of bone mineralization	0.017629857	1	0.536129021	1
GO:0030511--positive regulation of transforming growth factor beta receptor signaling pathway	0.010038652	1	0.693094364	1
GO:0030512--negative regulation of transforming growth factor beta receptor signaling pathway	0.151551207	1	0.668641465	1
GO:0030514--negative regulation of BMP signaling pathway	0.261862462	1	0.827961245	0.880826469
GO:0030516--regulation of axon extension	0.259373999	1	0.841717012	1
GO:0030574--collagen catabolic process	5.98E-05	1	0.453719017	1
GO:0030593--neutrophil chemotaxis	0.018263082	1	0.511779307	1
GO:0030595--leukocyte chemotaxis	0.044012199	1	1	1
GO:0030819--positive regulation of cAMP biosynthetic process	0.770314718	1	1	1
GO:0030833--regulation of actin filament polymerization	0.715673044	1	1	1
GO:0030838--positive regulation of actin filament polymerization	0.050356852	1	0.07938153	1
GO:0030866--cortical actin cytoskeleton organization	0.123460886	1	0.693094364	1
GO:0030889--negative regulation of B cell proliferation	0.323538799	1	1	0.332444112
GO:0030890--positive regulation of B cell proliferation	0.014627559	1	1	0.250472357
GO:0030947--regulation of vascular endothelial growth factor receptor signaling pathway	0.708382741	1	1	1
GO:0030948--negative regulation of vascular endothelial growth factor receptor signaling pathway	0.528830825	1	1	1
GO:0030949--positive regulation of vascular endothelial growth factor receptor signaling pathway	0.468510825	1	1	1
GO:0031032--actomyosin structure organization	0.21902112	1	0.001815775	1
GO:0031077--post-embryonic camera-type eye development	0.708382741	1	1	1
GO:0031100--organ regeneration	0.01011663	1	1	1
GO:0031274--positive regulation of pseudopodium assembly	0.646931558	1	0.841717012	1
GO:0031295--T cell costimulation	1.12E-10	1	0.394540655	0.000543805
GO:0031397--negative regulation of protein ubiquitination	0.801388373	1	1	1
GO:0031532--actin cytoskeleton reorganization	0.003478411	1	0.417818413	1
GO:0031547--brain-derived neurotrophic factor receptor signaling pathway	0.708382741	1	1	1
GO:0031581--hemidesmosome assembly	0.558114413	1	0.024512463	1
GO:0031589--cell-substrate adhesion	0.014839308	1	1	1
GO:0031623--receptor internalization	7.50E-05	1	0.785508437	1
GO:0031639--plasminogen activation	0.734893417	1	1	1
GO:0031663--lipopolysaccharide-mediated signaling pathway	0.008358702	1	1	0.836813384
GO:0031668--cellular response to extracellular stimulus	0.614018159	1	1	1
GO:0031954--positive regulation of protein autophosphorylation	0.058129724	1	0.247509815	1
GO:0032020--ISG15-protein conjugation	0.398460486	1	1	1
GO:0032060--bleb assembly	0.015884421	1	0.254325324	1
GO:0032091--negative regulation of protein binding	0.263411338	1	1	1
GO:0032092--positive regulation of protein binding	0.786558391	1	1	1
GO:0032233--positive regulation of actin filament bundle assembly	0.467558262	1	0.744070672	1
GO:0032270--positive regulation of cellular protein metabolic process	0.133105577	1	1	1
GO:0032332--positive regulation of chondrocyte differentiation	0.675503878	1	0.448031082	1
GO:0032348--negative regulation of aldosterone biosynthetic process	0.708382741	1	1	1
GO:0032355--response to estradiol	0.674605087	1	0.011499776	1
GO:0032367--intracellular cholesterol transport	0.398460486	1	1	1

GO:0032374--regulation of cholesterol transport	0.708382741	1	1	1
GO:0032486--Rap protein signal transduction	0.096149473	1	1	1
GO:0032496--response to lipopolysaccharide	2.74E-07	1	0.103039888	0.137192577
GO:0032497--detection of lipopolysaccharide	0.148729878	1	1	1
GO:0032570--response to progesterone	0.481454003	1	0.669255271	1
GO:0032673--regulation of interleukin-4 production	0.708382741	1	1	1
GO:0032689--negative regulation of interferon-gamma production	0.002486344	1	1	1
GO:0032715--negative regulation of interleukin-6 production	0.100201	1	1	0.179500074
GO:0032720--negative regulation of tumor necrosis factor production	0.034844195	1	1	0.649678174
GO:0032729--positive regulation of interferon-gamma production	0.008285127	1	1	0.159937507
GO:0032753--positive regulation of interleukin-4 production	0.1483938	1	1	0.463808445
GO:0032760--positive regulation of tumor necrosis factor production	0.027875738	1	1	0.572019542
GO:0032825--positive regulation of natural killer cell differentiation	0.200847708	1	1	0.899155198
GO:0032835--glomerulus development	0.283325756	1	1	1
GO:0032836--glomerular basement membrane development	0.734893417	1	1	1
GO:0032956--regulation of actin cytoskeleton organization	0.16220626	1	0.224418336	1
GO:0032964--collagen biosynthetic process	0.398460486	1	1	1
GO:0033138--positive regulation of peptidyl-serine phosphorylation	0.459349089	1	0.794983661	0.404849089
GO:0033280--response to vitamin D	0.614018159	1	1	1
GO:0033344--cholesterol efflux	0.367992782	1	1	1
GO:0033622--integrin activation	0.130978038	1	0.41522544	1
GO:0033627--cell adhesion mediated by integrin	0.03142065	1	1	1
GO:0033631--cell-cell adhesion mediated by integrin	0.708382741	1	1	1
GO:0033632--regulation of cell-cell adhesion mediated by integrin	0.520976287	1	1	0.811409165
GO:0033690--positive regulation of osteoblast proliferation	0.467558262	1	0.316891387	1
GO:0033700--phospholipid efflux	0.715673044	1	1	1
GO:0033993--response to lipid	0.648372779	1	1	1
GO:0034097--response to cytokine	0.003540672	1	0.79244369	1
GO:0034113--heterotypic cell-cell adhesion	0.005063357	1	1	1
GO:0034138--toll-like receptor 3 signaling pathway	0.200847708	1	1	1
GO:0034142--toll-like receptor 4 signaling pathway	0.0871	1	1	0.652505564
GO:0034199--activation of protein kinase A activity	0.270583565	1	1	1
GO:0034260--negative regulation of GTPase activity	0.397531928	1	0.785508437	1
GO:0034329--cell junction assembly	0.194496511	1	1	1
GO:0034333--adherens junction assembly	0.734893417	1	1	1
GO:0034341--response to interferon-gamma	0.633878665	1	1	1
GO:0034375--high-density lipoprotein particle remodeling	0.769096237	1	1	1
GO:0034383--low-density lipoprotein particle clearance	0.648372779	1	1	1
GO:0034392--negative regulation of smooth muscle cell apoptotic process	0.267572994	1	1	1
GO:0034394--protein localization to cell surface	0.223798822	1	1	1
GO:0034405--response to fluid shear stress	0.283325756	1	1	1
GO:0034446--substrate adhesion-dependent cell spreading	0.001090139	1	0.025480678	1
GO:0034616--response to laminar fluid shear stress	0.130978038	1	1	1
GO:0034765--regulation of ion transmembrane transport	0.650165651	1	1	1
GO:0035023--regulation of Rho protein signal transduction	0.002687896	1	1	0.877789556
GO:0035024--negative regulation of Rho protein signal transduction	0.769096237	1	1	1
GO:0035025--positive regulation of Rho protein signal transduction	0.420718574	1	1	1
GO:0035050--embryonic heart tube development	0.769096237	1	1	1
GO:0035148--tube formation	0.648372779	1	1	1
GO:0035162--embryonic hemopoiesis	0.468510825	1	1	1
GO:0035313--wound healing, spreading of epidermal cells	0.283325756	1	1	1
GO:0035335--peptidyl-tyrosine dephosphorylation	0.351744933	0.982613621	1	1
GO:0035385--Roundabout signaling pathway	0.558114413	1	1	1
GO:0035414--negative regulation of catenin import into nucleus	0.375218128	1	1	1
GO:0035456--response to interferon-beta	0.734893417	1	1	1
GO:0035457--cellular response to interferon-alpha	0.283325756	1	1	1
GO:0035556--intracellular signal transduction	3.70E-06	1	0.826064818	0.050157665
GO:0035690--cellular response to drug	0.029800836	1	1	1
GO:0035767--endothelial cell chemotaxis	0.734893417	1	1	1
GO:0035793--positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway	0.520976287	1	1	1
GO:0035810--positive regulation of urine volume	0.066618767	1	1	1
GO:0035855--megakaryocyte development	0.468510825	1	1	1
GO:0035904--aorta development	0.614018159	1	1	1
GO:0035912--dorsal aorta morphogenesis	0.200847708	1	1	1
GO:0035914--skeletal muscle cell differentiation	0.397012454	1	1	0.836828984
GO:0035924--cellular response to vascular endothelial growth factor stimulus	0.001673608	1	0.320192172	1
GO:0035987--endodermal cell differentiation	0.001714598	1	0.001815775	1
GO:0036006--cellular response to macrophage colony-stimulating factor stimulus	0.398460486	1	1	1
GO:0036120--cellular response to platelet-derived growth factor stimulus	0.614018159	1	0.747530223	0.903800975
GO:0036151--phosphatidylcholine acyl-chain remodeling	0.472648075	1	0.796071244	1
GO:0038063--collagen-activated tyrosine kinase receptor signaling pathway	0.398460486	1	0.825044341	1
GO:0038083--peptidyl-tyrosine autophosphorylation	0.133612331	1	1	0.019433715
GO:0038091--positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor signaling pathway	0.520976287	1	1	1
GO:0038096--Fc-gamma receptor signaling pathway involved in phagocytosis	0.68162702	1	1	1
GO:0038180--nerve growth factor signaling pathway	0.648372779	1	1	1
GO:0042058--regulation of epidermal growth factor receptor signaling pathway	0.648372779	1	1	1
GO:0042060--wound healing	0.560072201	1	5.05E-06	1
GO:0042098--T cell proliferation	0.115660188	1	1	0.384972428
GO:0042102--positive regulation of T cell proliferation	0.000249	1	1	0.27750252
GO:0042110--T cell activation	7.19E-05	1	1	8.92E-07
GO:0042116--macrophage activation	0.375218128	1	1	1
GO:0042118--endothelial cell activation	0.375218128	1	1	1
GO:0042127--regulation of cell proliferation	0.005153579	1	0.412660836	0.015709496
GO:0042130--negative regulation of T cell proliferation	0.002783865	1	0.154515629	1
GO:0042157--lipoprotein metabolic process	0.001090139	1	1	1
GO:0042311--vasodilation	0.715673044	1	1	1
GO:0042327--positive regulation of phosphorylation	0.150315599	1	1	1
GO:0042340--keratan sulfate catabolic process	0.558114413	1	1	1
GO:0042346--positive regulation of NF-kappaB import into nucleus	0.773018316	1	1	1
GO:0042476--odontogenesis	0.767880198	1	0.027964446	1
GO:0042482--positive regulation of odontogenesis	0.148729878	1	1	1
GO:0042493--response to drug	0.026406708	1	0.272059536	1
GO:0042535--positive regulation of tumor necrosis factor biosynthetic process	0.467558262	1	1	1
GO:0042542--response to hydrogen peroxide	0.703893935	1	0.548783232	1
GO:0042552--myelination	0.517110023	1	0.396005051	1
GO:0042632--cholesterol homeostasis	0.28448765	1	0.668641465	1
GO:0042692--muscle cell differentiation	0.769096237	1	1	0.764991873
GO:0042730--fibrinolysis	0.447576246	1	1	1
GO:0042789--mRNA transcription from RNA polymerase II promoter	0.540711528	1	1	1
GO:0042832--defense response to protozoan	0.32649162	1	1	1
GO:0042981--regulation of apoptotic process	0.395871813	1	1	0.538170426
GO:0043011--myeloid dendritic cell differentiation	0.007155893	1	1	1
GO:0043029--T cell homeostasis	0.472648075	1	1	0.015924331

GO:0043065--positive regulation of apoptotic process	7.60E-05	1	0.743424581	0.080345556
GO:0043085--positive regulation of catalytic activity	0.766064701	1	1	1
GO:0043087--regulation of GTPase activity	0.170897719	1	1	1
GO:0043113--receptor clustering	0.39059725	1	1	1
GO:0043116--negative regulation of vascular permeability	0.044012199	1	1	1
GO:0043123--positive regulation of I-kappaB kinase/NF-kappaB signaling	0.641816127	1	0.461608477	0.006654607
GO:0043129--surfactant homeostasis	0.200847708	1	0.139504271	1
GO:0043149--stress fiber assembly	0.03142065	1	1	1
GO:0043154--negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.066464372	1	0.010098729	1
GO:0043206--extracellular fibril organization	0.044012199	1	0.394534467	1
GO:0043277--apoptotic cell clearance	0.03142065	1	0.243221083	1
GO:0043303--mast cell degranulation	0.646931558	1	1	1
GO:0043305--negative regulation of mast cell degranulation	0.130978038	1	1	1
GO:0043372--positive regulation of CD4-positive, alpha-beta T cell differentiation	0.708382741	1	1	1
GO:0043393--regulation of protein binding	0.675503878	1	1	1
GO:0043406--positive regulation of MAP kinase activity	0.014299484	1	0.318684384	1
GO:0043407--negative regulation of MAP kinase activity	0.065548472	1	0.573587049	1
GO:0043410--positive regulation of MAPK cascade	0.014860161	1	1	1
GO:0043433--negative regulation of sequence-specific DNA binding transcription factor activity	0.190829701	1	0.778535118	0.822467723
GO:0043491--protein kinase B signaling	0.482572536	1	1	1
GO:0043507--positive regulation of JUN kinase activity	0.174867522	1	1	1
GO:0043517--positive regulation of DNA damage response, signal transduction by p53 class mediator	0.558114413	1	1	1
GO:0043524--negative regulation of neuron apoptotic process	0.769451893	1	1	1
GO:0043534--blood vessel endothelial cell migration	0.375218128	1	1	1
GO:0043536--positive regulation of blood vessel endothelial cell migration	0.115601188	1	1	1
GO:0043537--negative regulation of blood vessel endothelial cell migration	0.323538799	1	1	1
GO:0043542--endothelial cell migration	0.297929643	1	1	1
GO:0043547--positive regulation of GTPase activity	3.87E-16	1	0.029366801	0.034272924
GO:0043552--positive regulation of phosphatidylinositol 3-kinase activity	0.389520696	1	0.667357744	1
GO:0043627--response to estrogen	0.083682677	1	1	1
GO:0043654--recognition of apoptotic cell	0.528830825	1	1	1
GO:0043950--positive regulation of cAMP-mediated signaling	0.558114413	1	1	1
GO:0044267--cellular protein metabolic process	0.209777748	1	0.010101612	1
GO:0044344--cellular response to fibroblast growth factor stimulus	0.341213124	1	1	1
GO:0044351--macropinocytosis	0.648372779	1	1	1
GO:0045019--negative regulation of nitric oxide biosynthetic process	0.066618767	1	1	1
GO:0045059--positive thymic T cell selection	0.648372779	1	1	0.138340604
GO:0045086--positive regulation of interleukin-2 biosynthetic process	0.558114413	1	1	0.525118461
GO:0045087--innate immune response	0.018064444	1	1	0.02055799
GO:0045332--phospholipid translocation	0.510173804	1	1	1
GO:0045429--positive regulation of nitric oxide biosynthetic process	0.397531928	1	0.548891614	1
GO:0045446--endothelial cell differentiation	0.467558262	1	1	1
GO:0045576--mast cell activation	0.200847708	1	1	1
GO:0045600--positive regulation of fat cell differentiation	0.07078417	1	0.001548394	1
GO:0045648--positive regulation of erythrocyte differentiation	0.633878665	1	1	1
GO:0045651--positive regulation of macrophage differentiation	0.646931558	1	1	1
GO:0045657--positive regulation of monocyte differentiation	0.528830825	1	1	1
GO:0045666--positive regulation of neuron differentiation	0.502131755	1	0.061728466	1
GO:0045668--negative regulation of osteoblast differentiation	0.736195224	1	1	0.684403903
GO:0045669--positive regulation of osteoblast differentiation	0.006714787	1	0.000613	1
GO:0045671--negative regulation of osteoclast differentiation	0.123460886	1	1	1
GO:0045746--negative regulation of Notch signaling pathway	0.580310907	1	1	1
GO:0045765--regulation of angiogenesis	0.389520696	1	0.022202997	1
GO:0045766--positive regulation of angiogenesis	6.32E-09	1	0.029012035	1
GO:0045773--positive regulation of axon extension	0.341213124	1	1	1
GO:0045779--negative regulation of bone resorption	0.194496511	1	1	1
GO:0045780--positive regulation of bone resorption	0.646931558	1	1	1
GO:0045785--positive regulation of cell adhesion	0.652806625	1	0.548891614	1
GO:0045786--negative regulation of cell cycle	0.000768	1	1	1
GO:0045840--positive regulation of mitotic nuclear division	0.420718574	1	1	1
GO:0045859--regulation of protein kinase activity	0.786503933	1	1	1
GO:0045860--positive regulation of protein kinase activity	0.16220626	1	0.668268496	1
GO:0045893--positive regulation of transcription, DNA-templated	0.170223246	1	1	0.019898885
GO:0045906--negative regulation of vasoconstriction	0.708382741	1	1	1
GO:0045907--positive regulation of vasoconstriction	0.434104376	1	1	1
GO:0045944--positive regulation of transcription from RNA polymerase II promoter	0.041507841	1	1	0.009910137
GO:0045953--negative regulation of natural killer cell mediated cytotoxicity	0.708382741	1	1	1
GO:0045986--negative regulation of smooth muscle contraction	0.708382741	1	1	1
GO:0045987--positive regulation of smooth muscle contraction	0.058129724	1	1	1
GO:0045995--regulation of embryonic development	0.646931558	1	0.841717012	1
GO:0046007--negative regulation of activated T cell proliferation	0.734893417	1	1	1
GO:0046326--positive regulation of glucose import	0.634286649	1	1	1
GO:0046330--positive regulation of JNK cascade	0.718521043	1	1	0.065499904
GO:0046627--negative regulation of insulin receptor signaling pathway	0.297929643	1	1	1
GO:0046677--response to antibiotic	0.71955975	1	1	1
GO:0046718--viral entry into host cell	0.061145985	1	0.147238944	1
GO:0046777--protein autophosphorylation	0.000264	1	1	0.021496578
GO:0046834--lipid phosphorylation	0.558114413	1	1	0.525118461
GO:0046847--filopodium assembly	0.540711528	1	1	1
GO:0046854--phosphatidylinositol phosphorylation	0.008566153	1	1	1
GO:0048008--platelet-derived growth factor receptor signaling pathway	0.123305615	1	1	1
GO:0048010--vascular endothelial growth factor receptor signaling pathway	0.003463394	1	0.001934151	1
GO:0048012--hepatocyte growth factor receptor signaling pathway	0.734893417	1	0.606714584	1
GO:0048014--Tie signaling pathway	0.520976287	1	1	1
GO:0048015--phosphatidylinositol-mediated signaling	0.037860315	1	1	1
GO:0048016--inositol phosphate-mediated signaling	0.467558262	1	1	1
GO:0048146--positive regulation of fibroblast proliferation	0.03750874	1	0.103636927	1
GO:0048246--macrophage chemotaxis	0.646931558	1	0.841717012	1
GO:0048251--elastic fiber assembly	0.528830825	1	0.41522544	1
GO:0048286--lung alveolus development	0.000247	1	0.103411136	1
GO:0048469--cell maturation	0.021969626	1	1	1
GO:0048557--embryonic digestive tract morphogenesis	0.614018159	1	1	1
GO:0048565--digestive tract development	0.31522468	1	1	1
GO:0048596--embryonic camera-type eye morphogenesis	0.558114413	1	1	1
GO:0048661--positive regulation of smooth muscle cell proliferation	0.00247875	1	0.778535118	1
GO:0048662--negative regulation of smooth muscle cell proliferation	0.012305627	1	0.597604598	1
GO:0048704--embryonic skeletal system morphogenesis	0.481454003	1	1	1
GO:0048705--skeletal system morphogenesis	0.71955975	1	1	1
GO:0048711--positive regulation of astrocyte differentiation	0.467558262	1	1	1
GO:0048738--cardiac muscle tissue development	0.064697892	1	1	1
GO:0048739--cardiac muscle fiber development	0.648372779	1	1	1
GO:0048813--dendrite morphogenesis	0.666449638	1	0.842642922	1
GO:0048821--erythrocyte development	0.769096237	1	1	1

GO:0048839--inner ear development	0.324130907	1	1	1
GO:0048842--positive regulation of axon extension involved in axon guidance	0.130978038	1	1	1
GO:0048844--artery morphogenesis	0.014740852	1	1	1
GO:0048845--venous blood vessel morphogenesis	0.071889736	1	1	1
GO:0048846--axon extension involved in axon guidance	0.558114413	1	0.024512463	1
GO:0048870--cell motility	0.037346446	1	0.049909163	1
GO:0048873--homeostasis of number of cells within a tissue	0.580310907	1	1	1
GO:0050679--positive regulation of epithelial cell proliferation	0.765716057	1	0.090030017	1
GO:0050690--regulation of defense response to virus by virus	0.258682523	1	1	0.880242747
GO:0050702--interleukin-1 beta secretion	0.200847708	1	1	1
GO:0050715--positive regulation of cytokine secretion	0.681616274	1	1	1
GO:0050727--regulation of inflammatory response	0.662109429	1	1	1
GO:0050728--negative regulation of inflammatory response	0.004660462	1	1	0.526146445
GO:0050729--positive regulation of inflammatory response	0.109673474	1	0.280555493	1
GO:0050731--positive regulation of peptidyl-tyrosine phosphorylation	0.016890295	1	1	1
GO:0050766--positive regulation of phagocytosis	0.123305615	1	1	1
GO:0050770--regulation of axonogenesis	0.571048734	1	1	1
GO:0050774--negative regulation of dendrite morphogenesis	0.734893417	1	0.606714584	1
GO:0050776--regulation of immune response	5.27E-07	1	1	0.000409903
GO:0050790--regulation of catalytic activity	0.738810138	1	1	1
GO:0050821--protein stabilization	0.416461469	1	1	1
GO:0050850--positive regulation of calcium-mediated signaling	0.726242179	1	1	1
GO:0050852--T cell receptor signaling pathway	0.000564	1	1	7.01E-05
GO:0050853--B cell receptor signaling pathway	0.784234117	1	1	1
GO:0050859--negative regulation of B cell receptor signaling pathway	0.708382741	1	1	0.913221894
GO:0050862--positive regulation of T cell receptor signaling pathway	0.648372779	1	1	0.020213788
GO:0050870--positive regulation of T cell activation	0.270583565	1	1	0.903800975
GO:0050873--brown fat cell differentiation	0.71955975	1	1	1
GO:0050885--neuromuscular process controlling balance	0.751525045	1	1	1
GO:0050900--leukocyte migration	6.23E-16	1	0.41698216	0.711622209
GO:0050918--positive chemotaxis	0.142519025	1	0.792982671	1
GO:0050921--positive regulation of chemotaxis	0.007765558	1	0.794828701	1
GO:0050930--induction of positive chemotaxis	0.395738669	1	1	1
GO:0051017--actin filament bundle assembly	0.634286649	1	0.004659733	1
GO:0051056--regulation of small GTPase mediated signal transduction	5.28E-10	1	0.317485879	0.3133401
GO:0051150--regulation of smooth muscle cell differentiation	0.398460486	1	1	1
GO:0051209--release of sequestered calcium ion into cytosol	0.324130907	1	1	1
GO:0051216--cartilage development	0.171023773	1	0.318684384	1
GO:0051260--protein homooligomerization	0.663523883	1	1	1
GO:0051272--positive regulation of cellular component movement	0.375218128	1	1	1
GO:0051280--negative regulation of release of sequestered calcium ion into cytosol	0.708382741	1	1	1
GO:0051384--response to glucocorticoid	0.718521043	1	0.149091081	1
GO:0051450--myoblast proliferation	0.708382741	1	1	1
GO:0051482--positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	0.526544545	1	1	1
GO:0051491--positive regulation of filopodium assembly	0.018365903	1	1	1
GO:0051493--regulation of cytoskeleton organization	0.675503878	1	0.789089062	1
GO:0051496--positive regulation of stress fiber assembly	0.176444548	1	0.512503098	1
GO:0051497--negative regulation of stress fiber assembly	0.22010917	1	1	1
GO:0051607--defense response to virus	0.307920041	1	1	0.33299458
GO:0051764--actin crosslink formation	0.467558262	1	0.084474142	1
GO:0051781--positive regulation of cell division	0.779105796	1	0.417818413	1
GO:0051894--positive regulation of focal adhesion assembly	0.773018316	1	0.247509815	1
GO:0051895--negative regulation of focal adhesion assembly	0.468510825	1	0.648117011	1
GO:0051897--positive regulation of protein kinase B signaling	0.004355895	1	0.004683414	1
GO:0051898--negative regulation of protein kinase B signaling	0.666449638	1	1	1
GO:0051918--negative regulation of fibrinolysis	0.375218128	1	1	1
GO:0051924--regulation of calcium ion transport	0.633878665	1	1	1
GO:0051926--negative regulation of calcium ion transport	0.066618767	1	1	1
GO:0051928--positive regulation of calcium ion transport	0.181767647	1	1	1
GO:0055003--cardiac myofibril assembly	0.558114413	1	1	1
GO:0060021--palate development	0.015964273	1	1	1
GO:0060033--anatomical structure regression	0.708382741	1	1	1
GO:0060039--pericardium development	0.734893417	1	1	1
GO:0060045--positive regulation of cardiac muscle cell proliferation	0.223798822	1	1	1
GO:0060055--angiogenesis involved in wound healing	0.375218128	1	1	1
GO:0060100--positive regulation of phagocytosis, engulfment	0.200847708	1	1	1
GO:0060135--maternal process involved in female pregnancy	0.367992782	1	0.73403992	1
GO:0060317--cardiac epithelial to mesenchymal transition	0.012910246	1	1	1
GO:0060325--face morphogenesis	0.634286649	1	1	1
GO:0060326--cell chemotaxis	1.35E-06	1	0.28116569	1
GO:0060333--interferon-gamma-mediated signaling pathway	0.001100981	1	0.246932417	1
GO:0060337--type I interferon signaling pathway	0.28448765	1	1	1
GO:0060347--heart trabecula formation	0.095930534	1	1	1
GO:0060348--bone development	0.614810512	1	0.75942267	1
GO:0060389--pathway-restricted SMAD protein phosphorylation	0.259373999	1	1	1
GO:0060412--ventricular septum morphogenesis	0.041487582	1	1	1
GO:0060441--epithelial tube branching involved in lung morphogenesis	0.769096237	1	0.243221083	1
GO:0060665--regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	0.708382741	1	1	1
GO:0060670--branching involved in labyrinthine layer morphogenesis	0.734893417	1	1	1
GO:0060840--artery development	0.528830825	1	1	1
GO:0060841--venous blood vessel development	0.708382741	1	1	1
GO:0060842--arterial endothelial cell differentiation	0.708382741	1	1	1
GO:0060976--coronary vasculature development	0.681616274	1	1	1
GO:0060982--coronary artery morphogenesis	0.528830825	1	1	1
GO:0061028--establishment of endothelial barrier	0.009806953	1	1	1
GO:0061298--retina vasculature development in camera-type eye	0.528830825	1	1	1
GO:0061299--retina vasculature morphogenesis in camera-type eye	0.071889736	1	1	1
GO:0061304--retinal blood vessel morphogenesis	0.708382741	1	1	1
GO:0061384--heart trabecula morphogenesis	0.648372779	1	1	1
GO:0070098--chemokine-mediated signaling pathway	0.489688564	1	0.631605621	1
GO:0070208--protein heterotrimerization	0.323538799	1	1	1
GO:0070233--negative regulation of T cell apoptotic process	0.130978038	1	1	1
GO:0070373--negative regulation of ERK1 and ERK2 cascade	0.713474302	1	0.514149989	1
GO:0070374--positive regulation of ERK1 and ERK2 cascade	2.93E-07	1	0.013114773	1
GO:0070527--platelet aggregation	0.000702	1	1	1
GO:0070588--calcium ion transmembrane transport	0.667275023	1	1	1
GO:0071222--cellular response to lipopolysaccharide	6.08E-05	1	1	0.654200886
GO:0071223--cellular response to lipoteichoic acid	0.734893417	1	1	1
GO:0071230--cellular response to amino acid stimulus	0.557837214	1	0.417818413	1
GO:0071260--cellular response to mechanical stimulus	0.017203881	1	1	0.9107496
GO:0071300--cellular response to retinoic acid	0.459349089	1	0.399492126	1
GO:0071320--cellular response to cAMP	0.504960554	1	1	1
GO:0071333--cellular response to glucose stimulus	0.504960554	1	1	1

GO:0071345~cellular response to cytokine stimulus	0.020358273	1	1	0.599530806
GO:0071347~cellular response to interleukin-1	0.30471151	1	0.631605621	1
GO:0071354~cellular response to interleukin-6	0.715673044	1	1	1
GO:0071356~cellular response to tumor necrosis factor	0.030378291	1	0.354570918	1
GO:0071361~cellular response to ethanol	0.715673044	1	1	1
GO:0071363~cellular response to growth factor stimulus	0.719614283	1	1	1
GO:0071364~cellular response to epidermal growth factor stimulus	0.482572536	1	0.739078566	1
GO:0071404~cellular response to low-density lipoprotein particle stimulus	0.060720545	1	1	1
GO:0071407~cellular response to organic cyclic compound	0.171023773	1	1	0.913962257
GO:0071456~cellular response to hypoxia	0.284479773	1	1	1
GO:0071461~cellular response to redox state	0.520976287	1	1	1
GO:0071493~cellular response to UV-B	0.648372779	1	1	1
GO:0071526~semaphorin-plexin signaling pathway	0.754595823	1	0.223894229	1
GO:0071560~cellular response to transforming growth factor beta stimulus	0.001821403	1	0.022887208	0.836828984
GO:0071803~positive regulation of podosome assembly	0.375218128	1	1	1
GO:0071872~cellular response to epinephrine stimulus	0.558114413	1	1	1
GO:0071901~negative regulation of protein serine/threonine kinase activity	0.614018159	1	0.142352669	1
GO:0072012~glomerulus vasculature development	0.708382741	1	1	1
GO:0072144~glomerular mesangial cell development	0.708382741	1	1	1
GO:0072277~metanephric glomerular capillary formation	0.520976287	1	1	1
GO:0072659~protein localization to plasma membrane	0.261712559	1	0.057315924	1
GO:0072661~protein targeting to plasma membrane	0.420718574	1	0.768090777	1
GO:0086064~cell communication by electrical coupling involved in cardiac conduction	0.646931558	1	1	1
GO:0090004~positive regulation of establishment of protein localization to plasma membrane	0.148104106	1	1	1
GO:0090023~positive regulation of neutrophil chemotaxis	0.510173804	1	0.281232591	1
GO:0090026~positive regulation of monocyte chemotaxis	0.171691347	1	1	1
GO:0090051~negative regulation of cell migration involved in sprouting angiogenesis	0.141856906	1	1	1
GO:0090090~negative regulation of canonical Wnt signaling pathway	0.531624907	1	0.154186426	1
GO:0090197~positive regulation of chemokine secretion	0.283325756	1	1	1
GO:0090271~positive regulation of fibroblast growth factor production	0.520976287	1	1	1
GO:0090280~positive regulation of calcium ion import	0.468510825	1	1	1
GO:0090398~cellular senescence	0.571048734	1	1	1
GO:0090557~establishment of endothelial intestinal barrier	0.467558262	1	1	1
GO:0090630~activation of GTPase activity	0.719639472	1	1	1
GO:0097028~dendritic cell differentiation	0.194496511	1	1	1
GO:0097190~apoptotic signaling pathway	0.017203881	1	1	0.035557417
GO:0097191~extrinsic apoptotic signaling pathway	0.614810512	1	1	0.075913265
GO:0097421~liver regeneration	0.580310907	1	1	0.905254664
GO:0097503~sialylation	0.39059725	1	1	1
GO:1900027~regulation of ruffle assembly	0.283325756	1	1	1
GO:1900165~negative regulation of interleukin-6 secretion	0.648372779	1	1	1
GO:1901653~cellular response to peptide	0.467558262	1	1	1
GO:1901660~calcium ion export	0.520976287	1	1	1
GO:1902042~negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	0.754595823	1	1	0.86889835
GO:1902895~positive regulation of pri-miRNA transcription from RNA polymerase II promoter	0.726242179	1	1	1
GO:1903779~regulation of cardiac conduction	0.236877584	1	1	1
GO:2000065~negative regulation of cortisol biosynthetic process	0.708382741	1	1	1
GO:2000249~regulation of actin cytoskeleton reorganization	0.0871	1	1	1
GO:2000279~negative regulation of DNA biosynthetic process	0.558114413	1	1	1
GO:2000352~negative regulation of endothelial cell apoptotic process	0.009402577	1	1	1
GO:2000353~positive regulation of endothelial cell apoptotic process	0.095930534	1	1	1
GO:2000379~positive regulation of reactive oxygen species metabolic process	0.341213124	1	1	1
GO:2000406~positive regulation of T cell migration	0.096149473	1	1	1
GO:2000484~positive regulation of interleukin-8 secretion	0.066618767	1	1	1
GO:2000573~positive regulation of DNA biosynthetic process	0.259373999	1	1	1
GO:2000643~positive regulation of early endosome to late endosome transport	0.648372779	1	1	1
GO:2000669~negative regulation of dendritic cell apoptotic process	0.520976287	1	1	1
GO:2000721~positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation	0.520976287	1	1	1
GO:2000727~positive regulation of cardiac muscle cell differentiation	0.375218128	1	1	1
GO:2000810~regulation of bicellular tight junction assembly	0.060720545	1	1	1
GO:2000811~negative regulation of anoikis	0.064697892	1	0.332694236	1
GO:2001181~positive regulation of interleukin-10 secretion	0.708382741	1	1	1
GO:2001202~negative regulation of transforming growth factor-beta secretion	0.520976287	1	1	1
GO:2001205~negative regulation of osteoclast development	0.708382741	1	1	1
GO:2001214~positive regulation of vasculogenesis	0.015884421	1	1	1
GO:2001238~positive regulation of extrinsic apoptotic signaling pathway	0.725353792	1	0.768090777	1
GO:2001300~lipoxin metabolic process	0.267572994	1	1	1
GO:0000086~G2/M transition of mitotic cell cycle	1	0.088103505	1	1
GO:0000710~meiotic mismatch repair	1	0.985316909	1	1
GO:0001736~establishment of planar polarity	1	0.036549505	1	1
GO:0001843~neural tube closure	1	0.425950978	0.222656913	1
GO:0001890~placenta development	1	0.980234582	1	1
GO:0001895~retina homeostasis	1	0.95226369	1	1
GO:0001951~intestinal D-glucose absorption	1	0.918284268	1	1
GO:0002934~desmosome organization	1	0.96852244	0.743728515	1
GO:0003341~cilium movement	1	3.00E-09	1	1
GO:0003351~epithelial cilium movement	1	2.46E-06	1	1
GO:0003356~regulation of cilium beat frequency	1	0.04311721	1	1
GO:0006047~UDP-N-acetylglucosamine metabolic process	1	0.753465204	1	1
GO:0006068~ethanol catabolic process	1	0.96852244	1	1
GO:0006069~ethanol oxidation	1	0.981733806	0.794828701	1
GO:0006081~cellular aldehyde metabolic process	1	0.969949362	0.084474142	1
GO:0006165~nucleoside diphosphate phosphorylation	1	0.968179413	1	1
GO:0006167~AMP biosynthetic process	1	0.41550189	1	1
GO:0006464~cellular protein modification process	1	0.968470353	1	1
GO:0006486~protein glycosylation	1	0.96627079	1	1
GO:0006536~glutamate metabolic process	1	0.988298472	1	1
GO:0006541~glutamine metabolic process	1	0.833587973	1	1
GO:0006805~xenobiotic metabolic process	1	0.109523411	0.005064163	1
GO:0006809~nitric oxide biosynthetic process	1	0.988298472	1	1
GO:0007009~plasma membrane organization	1	0.988298472	0.841717012	1
GO:0007017~microtubule-based process	1	0.883061922	1	1
GO:0007018~microtubule-based movement	1	0.008943728	1	1
GO:0007088~regulation of mitotic nuclear division	1	0.94912968	1	1
GO:0007131~reciprocal meiotic recombination	1	0.647386159	1	1
GO:0007163~establishment or maintenance of cell polarity	1	0.989646026	0.302892451	1
GO:0007224~smoothed signaling pathway	1	2.83E-06	0.778106877	1
GO:0007283~spermatogenesis	1	0.096215061	1	1
GO:0007286~spermatid development	1	0.208476728	1	1
GO:0007340~acrosome reaction	1	0.930940736	1	1
GO:0007368~determination of left/right symmetry	1	3.47E-09	1	1
GO:0007588~excretion	1	0.988129464	1	1
GO:0007605~sensory perception of sound	1	0.779933705	0.615109705	1

GO:0008544--epidermis development	1	0.41839885	0.55447721	1
GO:0008589--regulation of smoothened signaling pathway	1	0.09807613	0.789089062	1
GO:0009116--nucleoside metabolic process	1	0.784098046		1
GO:0009165--nucleotide biosynthetic process	1	0.902811727		1
GO:0009437--carnitine metabolic process	1	0.985316909		1
GO:010880--regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	1	0.968179413	0.747530223	1
GO:0010951--negative regulation of endopeptidase activity	1	0.956696429	0.006078847	1
GO:0015893--drug transport	1	0.96852244		1
GO:0016266--O-glycan processing	1	0.070860149		1
GO:0016310--phosphorylation	1	0.984369747		1
GO:0016338--calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	1	0.166281287	0.084348265	1
GO:0018095--protein polyglutamylation	1	0.900951185		1
GO:0019373--epoxygenase P450 pathway	1	0.968179413		1
GO:0019852--L-ascorbic acid metabolic process	1	0.396040955		1
GO:0021532--neural tube patterning	1	0.616248836		1
GO:0021591--ventricular system development	1	0.01365358		1
GO:0023014--signal transduction by protein phosphorylation	1	0.633583206		1
GO:0030030--cell projection organization	1	0.002232539		1
GO:0030317--sperm motility	1	0.000447		1
GO:0030517--negative regulation of axon extension	1	0.969949362		1
GO:0030953--astral microtubule organization	1	0.985316909		1
GO:0032465--regulation of cytokinesis	1	0.906829286		1
GO:0032516--positive regulation of phosphoprotein phosphatase activity	1	0.988298472		1
GO:0032869--cellular response to insulin stimulus	1	0.968149141		1
GO:0035058--nonmotile primary cilium assembly	1	0.001667931		1
GO:0035082--axoneme assembly	1	5.52E-06		1
GO:0035469--determination of pancreatic left/right asymmetry	1	0.96852244		1
GO:0035721--intraciliary retrograde transport	1	1.39E-06		1
GO:0035735--intraciliary transport involved in cilium morphogenesis	1	0.182159683		1
GO:0035845--photoreceptor cell outer segment organization	1	0.900951185		1
GO:0036158--outer dynein arm assembly	1	1.54E-05		1
GO:0036159--inner dynein arm assembly	1	4.26E-05		1
GO:0042073--intraciliary transport	1	4.14E-09		1
GO:0042384--cilium assembly	1	6.00E-38	0.61877916	1
GO:0042574--retinal metabolic process	1	0.981733806		1
GO:0042733--embryonic digit morphogenesis	1	0.947159248	0.454493419	1
GO:0043508--negative regulation of JUN kinase activity	1	0.404789073		1
GO:0043570--maintenance of DNA repeat elements	1	0.96852244		1
GO:0044458--motile cilium assembly	1	1.54E-05		1
GO:0045216--cell-cell junction organization	1	0.968179413	0.396111694	1
GO:0045494--photoreceptor cell maintenance	1	0.191138852		1
GO:0045617--negative regulation of keratinocyte differentiation	1	0.838710558		1
GO:0045724--positive regulation of cilium assembly	1	0.505584002		1
GO:0045880--positive regulation of smoothened signaling pathway	1	0.94912968		1
GO:0045910--negative regulation of DNA recombination	1	0.96852244		1
GO:0046328--regulation of JNK cascade	1	0.930940736		1
GO:0046907--intracellular transport	1	0.6954636		1
GO:0050678--regulation of epithelial cell proliferation	1	0.981733806		1
GO:0050680--negative regulation of epithelial cell proliferation	1	0.779627537	0.02370753	1
GO:0050891--multicellular organismal water homeostasis	1	0.838710558	0.139504271	1
GO:0050896--response to stimulus	1	0.982434544		1
GO:0051096--positive regulation of helicase activity	1	0.985316909		1
GO:0051131--chaperone-mediated protein complex assembly	1	0.988298472		1
GO:0051301--cell division	1	0.980998789	0.561929756	1
GO:0055114--oxidation-reduction process	1	0.181472068	1.20E-05	1
GO:0060041--retina development in camera-type eye	1	0.833413273		1
GO:0060271--cilium morphogenesis	1	1.64E-38	0.143470926	1
GO:0060285--cilium-dependent cell motility	1	0.001996855		1
GO:0060287--epithelial cilium movement involved in determination of left/right asymmetry	1	0.037406554		1
GO:0060294--cilium movement involved in cell motility	1	0.616248836		1
GO:0060487--lung epithelial cell differentiation	1	0.945824576		1
GO:0060672--epithelial cell morphogenesis involved in placental branching	1	0.794705235		1
GO:0060972--left/right pattern formation	1	0.272636876		1
GO:0061055--myotome development	1	0.794705235		1
GO:0061512--protein localization to cilium	1	0.001645714		1
GO:0070286--axonemal dynein complex assembly	1	1.39E-06		1
GO:0070986--left/right axis specification	1	0.988298472	0.841717012	1
GO:0071907--determination of digestive tract left/right asymmetry	1	0.616248836		1
GO:0071910--determination of liver left/right asymmetry	1	0.985316909		1
GO:0090307--mitotic spindle assembly	1	0.983787394		1
GO:1901844--regulation of cell communication by electrical coupling involved in cardiac conduction	1	0.838710558		1
GO:1902017--regulation of cilium assembly	1	0.903087451		1
GO:1903251--multi-ciliated epithelial cell differentiation	1	0.96852244		1
GO:1903830--magnesium ion transmembrane transport	1	0.930940736		1
GO:1903887--motile primary cilium assembly	1	0.41550189		1
GO:1904491--protein localization to ciliary transition zone	1	0.918284268		1
GO:0000302--response to reactive oxygen species	1		0.029051913	1
GO:0001523--retinoid metabolic process	1		0.046595358	1
GO:0001649--osteoblast differentiation	1		0.004693144	1
GO:0001658--branching involved in ureteric bud morphogenesis	1		0.051845689	1
GO:0001755--neural crest cell migration	1		0.827961245	1
GO:0001775--cell activation	1		0.316891387	1
GO:0001942--hair follicle development	1		0.074440373	1
GO:0002381--immunoglobulin production involved in immunoglobulin mediated immune response	1		0.743728515	1
GO:0003184--pulmonary valve morphogenesis	1		0.677074124	1
GO:0003215--cardiac right ventricle morphogenesis	1		0.457581505	1
GO:0003334--keratinocyte development	1		0.677074124	1
GO:0003382--epithelial cell morphogenesis	1		0.53228888	1
GO:0006024--glycosaminoglycan biosynthetic process	1		0.128449209	1
GO:0006027--glycosaminoglycan catabolic process	1		0.023056466	1
GO:0006605--protein targeting	1		0.669255271	1
GO:0006641--triglyceride metabolic process	1		0.792982671	1
GO:0006725--cellular aromatic compound metabolic process	1		0.459353413	1
GO:0006749--glutathione metabolic process	1		0.128947014	1
GO:0006886--intracellular protein transport	1		0.706921631	1
GO:0006953--acute-phase response	1		0.669255271	1
GO:0006957--complement activation, alternative pathway	1		0.457581505	1
GO:0006979--response to oxidative stress	1		0.07460035	1
GO:0007016--cytoskeletal anchoring at plasma membrane	1		0.744070672	1
GO:0007154--cell communication	1		0.639246056	1
GO:0007422--peripheral nervous system development	1		0.693094364	1
GO:0007442--hindgut morphogenesis	1		0.626086653	1
GO:0008152--metabolic process	1		0.579404278	1

GO:0008210--estrogen metabolic process	1	1	0.744070672	1
GO:0008344--adult locomotory behavior	1	1	0.79244369	1
GO:0008584--male gonad development	1	1	0.738201014	1
GO:0009404--toxin metabolic process	1	1	0.825044341	1
GO:0009617--response to bacterium	1	1	0.648354124	1
GO:0009636--response to toxic substance	1	1	0.222378121	1
GO:0009650--UV protection	1	1	0.794828701	1
GO:0009653--anatomical structure morphogenesis	1	1	0.702587042	1
GO:0009725--response to hormone	1	1	0.75942267	1
GO:0010033--response to organic substance	1	1	0.826138446	1
GO:0010193--response to ozone	1	1	0.626086653	1
GO:0010243--response to organonitrogen compound	1	1	0.53228888	1
GO:0010632--regulation of epithelial cell migration	1	1	0.743728515	1
GO:0010801--negative regulation of peptidyl-threonine phosphorylation	1	1	0.53228888	1
GO:0010837--regulation of keratinocyte proliferation	1	1	0.512374186	1
GO:0010839--negative regulation of keratinocyte proliferation	1	1	0.53228888	1
GO:0010906--regulation of glucose metabolic process	1	1	0.605917815	1
GO:0014032--neural crest cell development	1	1	0.841717012	1
GO:0016050--vesicle organization	1	1	0.826138446	1
GO:0016126--sterol biosynthetic process	1	1	0.057916239	1
GO:0016139--glycoside catabolic process	1	1	0.743728515	1
GO:0019439--aromatic compound catabolic process	1	1	0.743728515	1
GO:0019800--peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan	1	1	0.825044341	1
GO:0021762--substantia nigra development	1	1	0.725468831	1
GO:0021795--cerebral cortex cell migration	1	1	0.606714584	1
GO:0022408--negative regulation of cell-cell adhesion	1	1	0.596572908	1
GO:0030091--protein repair	1	1	0.825044341	1
GO:0030208--dermatan sulfate biosynthetic process	1	1	0.794828701	1
GO:0030216--keratinocyte differentiation	1	1	0.741146287	1
GO:0030325--adrenal gland development	1	1	0.448031082	1
GO:0030449--regulation of complement activation	1	1	0.053371558	1
GO:0030513--positive regulation of BMP signaling pathway	1	1	0.667357744	1
GO:0030855--epithelial cell differentiation	1	1	0.000458	1
GO:0030857--negative regulation of epithelial cell differentiation	1	1	0.316891387	1
GO:0030900--forebrain development	1	1	0.848298304	1
GO:0030902--hindbrain development	1	1	0.332694236	1
GO:0030903--notochord development	1	1	0.606714584	1
GO:0031016--pancreas development	1	1	0.554813833	1
GO:0032024--positive regulation of insulin secretion	1	1	0.734514881	1
GO:0032026--response to magnesium ion	1	1	0.457581505	1
GO:0032148--activation of protein kinase B activity	1	1	0.212345899	1
GO:0032331--negative regulation of chondrocyte differentiation	1	1	0.029064386	1
GO:0032410--negative regulation of transporter activity	1	1	0.743728515	1
GO:0032463--negative regulation of protein homooligomerization	1	1	0.825044341	1
GO:0032534--regulation of microvillus assembly	1	1	0.743728515	1
GO:0032613--interleukin-10 production	1	1	0.459353413	1
GO:0032914--positive regulation of transforming growth factor beta1 production	1	1	0.825044341	1
GO:0032967--positive regulation of collagen biosynthetic process	1	1	0.320192172	1
GO:0033197--response to vitamin E	1	1	0.744070672	1
GO:0033591--response to L-ascorbic acid	1	1	0.743728515	1
GO:0033628--regulation of cell adhesion mediated by integrin	1	1	0.744070672	1
GO:0034332--adherens junction organization	1	1	0.334261279	1
GO:0034447--very-low-density lipoprotein particle clearance	1	1	0.459353413	1
GO:0034613--cellular protein localization	1	1	0.548891614	1
GO:0034614--cellular response to reactive oxygen species	1	1	0.507425435	1
GO:0035329--hippo signaling	1	1	0.02796446	1
GO:0035567--non-canonical Wnt signaling pathway	1	1	0.703338764	1
GO:0036486--ventral trunk neural crest cell migration	1	1	0.626086653	1
GO:0038033--positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway	1	1	0.216664163	1
GO:0038128--ERBB2 signaling pathway	1	1	0.639246056	1
GO:0040007--growth	1	1	0.826138446	1
GO:0040037--negative regulation of fibroblast growth factor receptor signaling pathway	1	1	0.010021411	1
GO:0042092--type 2 immune response	1	1	0.743728515	1
GO:0042117--monocyte activation	1	1	0.512374186	1
GO:0042326--negative regulation of phosphorylation	1	1	0.507425435	1
GO:0042420--dopamine catabolic process	1	1	0.743728515	1
GO:0042475--odontogenesis of dentin-containing tooth	1	1	0.656835645	1
GO:0042572--retinol metabolic process	1	1	0.632391998	1
GO:0042744--hydrogen peroxide catabolic process	1	1	0.215743711	1
GO:0043066--negative regulation of apoptotic process	1	1	0.187503653	1
GO:0043086--negative regulation of catalytic activity	1	1	0.723790483	1
GO:0043434--response to peptide hormone	1	1	0.578537629	1
GO:0043567--regulation of insulin-like growth factor receptor signaling pathway	1	1	0.41522544	1
GO:0043588--skin development	1	1	0.767144415	1
GO:0045056--transcytosis	1	1	0.139504271	1
GO:0045444--fat cell differentiation	1	1	0.844801176	1
GO:0045454--cell redox homeostasis	1	1	0.760882474	1
GO:0045603--positive regulation of endothelial cell differentiation	1	1	0.744070672	1
GO:0045665--negative regulation of neuron differentiation	1	1	0.454493419	1
GO:0045740--positive regulation of DNA replication	1	1	0.75942267	1
GO:0045807--positive regulation of endocytosis	1	1	0.142352669	1
GO:0045926--negative regulation of growth	1	1	0.789089062	1
GO:0048013--ephrin receptor signaling pathway	1	1	0.392774894	1
GO:0048041--focal adhesion assembly	1	1	0.049909163	1
GO:0048247--lymphocyte chemotaxis	1	1	0.826138446	1
GO:0048333--mesodermal cell differentiation	1	1	0.744070672	1
GO:0048514--blood vessel morphogenesis	1	1	0.703338764	1
GO:0048667--cell morphogenesis involved in neuron differentiation	1	1	0.825044341	1
GO:0048754--branching morphogenesis of an epithelial tube	1	1	0.648354124	1
GO:0050730--regulation of peptidyl-tyrosine phosphorylation	1	1	0.457581505	1
GO:0050919--negative chemotaxis	1	1	0.247365371	1
GO:0050999--regulation of nitric-oxide synthase activity	1	1	0.075421674	1
GO:0051016--barbed-end actin filament capping	1	1	0.53228888	1
GO:0051045--negative regulation of membrane protein ectodomain proteolysis	1	1	0.825044341	1
GO:0051145--smooth muscle cell differentiation	1	1	0.457581505	1
GO:0051414--response to cortisol	1	1	0.626086653	1
GO:0051592--response to calcium ion	1	1	0.514149989	1
GO:0051639--actin filament network formation	1	1	0.677074124	1
GO:0051770--positive regulation of nitric-oxide synthase biosynthetic process	1	1	0.841717012	1
GO:0055012--ventricular cardiac muscle cell differentiation	1	1	0.825044341	1
GO:0055074--calcium ion homeostasis	1	1	0.605917815	1
GO:0060009--Sertoli cell development	1	1	0.677074124	1
GO:0060056--mammary gland involution	1	1	0.825044341	1

GO:0060070~canonical Wnt signaling pathway	1	1	0.513665287	1
GO:0060137~maternal process involved in parturition	1	1	0.825044341	1
GO:0060174~limb bud formation	1	1	0.254325324	1
GO:0060306~regulation of membrane repolarization	1	1	0.794828701	1
GO:0060426~lung vasculature development	1	1	0.825044341	1
GO:0060444~branching involved in mammary gland duct morphogenesis	1	1	0.116858364	1
GO:0060445~branching involved in salivary gland morphogenesis	1	1	0.744070672	1
GO:0060449~bud elongation involved in lung branching	1	1	0.090675578	1
GO:0060486~Clara cell differentiation	1	1	0.626086653	1
GO:0060510~Type II pneumocyte differentiation	1	1	0.743728515	1
GO:0060548~negative regulation of cell death	1	1	0.239031697	1
GO:0060686~negative regulation of prostatic bud formation	1	1	0.626086653	1
GO:0060706~cell differentiation involved in embryonic placenta development	1	1	0.825044341	1
GO:0060716~labyrinthine layer blood vessel development	1	1	0.789089062	1
GO:0060754~positive regulation of mast cell chemotaxis	1	1	0.825044341	1
GO:0061024~membrane organization	1	1	0.416116384	1
GO:0061036~positive regulation of cartilage development	1	1	0.090580992	1
GO:0061549~sympathetic ganglion development	1	1	0.606714584	1
GO:0070372~regulation of ERK1 and ERK2 cascade	1	1	0.73403992	1
GO:0070542~response to fatty acid	1	1	0.703338764	1
GO:0070830~bicellular tight junction assembly	1	1	0.024704057	1
GO:0070836~caveola assembly	1	1	0.743728515	1
GO:0070848~response to growth factor	1	1	0.648117011	1
GO:0070886~positive regulation of calcineurin-NFAT signaling cascade	1	1	0.606714584	1
GO:0071280~cellular response to copper ion	1	1	0.825044341	1
GO:0071346~cellular response to interferon-gamma	1	1	0.274611831	1
GO:0071425~hematopoietic stem cell proliferation	1	1	0.53228888	1
GO:0071474~cellular hyperosmotic response	1	1	0.825044341	1
GO:0071498~cellular response to fluid shear stress	1	1	0.794828701	1
GO:0071636~positive regulation of transforming growth factor beta production	1	1	0.825044341	1
GO:0071681~cellular response to indole-3-methanol	1	1	0.216664163	1
GO:0071801~regulation of podosome assembly	1	1	0.743728515	1
GO:0071902~positive regulation of protein serine/threonine kinase activity	1	1	0.536129021	1
GO:0072015~glomerular visceral epithelial cell development	1	1	0.254325324	1
GO:0072162~metanephric mesenchymal cell differentiation	1	1	0.743728515	1
GO:0072201~negative regulation of mesenchymal cell proliferation	1	1	0.743728515	1
GO:0072657~protein localization to membrane	1	1	0.841717012	1
GO:0086073~bundle of His cell-Purkinje myocyte adhesion involved in cell communication	1	1	0.825044341	1
GO:0086091~regulation of heart rate by cardiac conduction	1	1	0.273934664	1
GO:0090002~establishment of protein localization to plasma membrane	1	1	0.272906733	1
GO:0090009~primitive streak formation	1	1	0.677074124	1
GO:0090103~cochlea morphogenesis	1	1	0.605917815	1
GO:0090179~planar cell polarity pathway involved in neural tube closure	1	1	0.394534467	1
GO:0090263~positive regulation of canonical Wnt signaling pathway	1	1	0.839262022	1
GO:0090382~phagosome maturation	1	1	0.825044341	1
GO:0097062~dendritic spine maintenance	1	1	0.825044341	1
GO:0097067~cellular response to thyroid hormone stimulus	1	1	0.116858364	1
GO:0097284~hepatocyte apoptotic process	1	1	0.841717012	1
GO:0097490~sympathetic neuron projection extension	1	1	0.626086653	1
GO:0097491~sympathetic neuron projection guidance	1	1	0.626086653	1
GO:0098609~cell-cell adhesion	1	1	4.72E-05	1
GO:0098869~cellular oxidant detoxification	1	1	2.16E-06	1
GO:0098911~regulation of ventricular cardiac muscle cell action potential	1	1	0.316891387	1
GO:1900025~negative regulation of substrate adhesion-dependent cell spreading	1	1	0.841717012	1
GO:1901166~neural crest cell migration involved in autonomic nervous system development	1	1	0.743728515	1
GO:1901687~glutathione derivative biosynthetic process	1	1	0.029105573	1
GO:1902230~negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	1	1	0.53228888	1
GO:1902285~semaphorin-plexin signaling pathway involved in neuron projection guidance	1	1	0.626086653	1
GO:1902287~semaphorin-plexin signaling pathway involved in axon guidance	1	1	0.394534467	1
GO:1904953~Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation	1	1	0.825044341	1
GO:1990138~neuron projection extension	1	1	0.448031082	1
GO:2000009~negative regulation of protein localization to cell surface	1	1	0.677074124	1
GO:2000049~positive regulation of cell-cell adhesion mediated by cadherin	1	1	0.41522544	1
GO:2000107~negative regulation of leukocyte apoptotic process	1	1	0.825044341	1
GO:2000145~regulation of cell motility	1	1	0.551168658	1
GO:2000146~negative regulation of cell motility	1	1	0.606714584	1
GO:2000647~negative regulation of stem cell proliferation	1	1	0.743728515	1
GO:2000649~regulation of sodium ion transmembrane transporter activity	1	1	0.648117011	1
GO:2000741~positive regulation of mesenchymal stem cell differentiation	1	1	0.626086653	1
GO:2000987~positive regulation of behavioral fear response	1	1	0.743728515	1
GO:2001028~positive regulation of endothelial cell chemotaxis	1	1	0.743728515	1
GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	1	1	0.009418569	1
GO:0000027~ribosomal large subunit assembly	1	1	0.539404269	1
GO:0000077~DNA damage checkpoint	1	1	0.505242439	1
GO:0000079~regulation of cyclin-dependent protein serine/threonine kinase activity	1	1	0.684403903	1
GO:0000082~G1/S transition of mitotic cell cycle	1	1	0.522749796	1
GO:0000154~rRNA modification	1	1	0.913221894	1
GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	1	1	6.98E-05	1
GO:0000185~activation of MAPKKK activity	1	1	0.81113004	1
GO:0000209~protein polyubiquitination	1	1	0.459615944	1
GO:0000288~nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	1	1	0.899155198	1
GO:0000320~re-entry into mitotic cell cycle	1	1	0.913221894	1
GO:0000723~telomere maintenance	1	1	0.781846011	1
GO:0001706~endoderm formation	1	1	0.867335616	1
GO:0001779~natural killer cell differentiation	1	1	0.525118461	1
GO:0001782~B cell homeostasis	1	1	0.331682113	1
GO:0001783~B cell apoptotic process	1	1	0.83568948	1
GO:0001787~natural killer cell proliferation	1	1	0.811409165	1
GO:0001817~regulation of cytokine production	1	1	0.907197548	1
GO:0001829~trophoblast cell differentiation	1	1	0.607715718	1
GO:0001844~protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	1	1	0.36806295	1
GO:0001916~positive regulation of T cell mediated cytotoxicity	1	1	0.907197548	1
GO:0001922~B-1 B cell homeostasis	1	1	0.913221894	1
GO:0002230~positive regulation of defense response to virus by host	1	1	0.315088712	1
GO:0002262~myeloid cell homeostasis	1	1	0.51216384	1
GO:0002437~inflammatory response to antigenic stimulus	1	1	0.764991873	1
GO:0002725~negative regulation of T cell cytokine production	1	1	0.913221894	1
GO:0002726~positive regulation of T cell cytokine production	1	1	0.721069893	1
GO:0002755~MyD88-dependent toll-like receptor signaling pathway	1	1	0.654959827	1
GO:0002819~regulation of adaptive immune response	1	1	0.721357228	1
GO:0006260~DNA replication	1	1	0.363557769	1
GO:0006281~DNA repair	1	1	0.691012899	1
GO:0006306~DNA methylation	1	1	0.765043203	1

GO:0006325~chromatin organization	1	1	1	0.387914793
GO:0006334~nucleosome assembly	1	1	1	0.358257393
GO:0006351~transcription, DNA-templated	1	1	1	1.61E-23
GO:0006355~regulation of transcription, DNA-templated	1	1	1	1.09E-18
GO:0006357~regulation of transcription from RNA polymerase II promoter	1	1	1	0.025944176
GO:0006364~rRNA processing	1	1	1	1.50E-06
GO:0006366~transcription from RNA polymerase II promoter	1	1	1	0.043059379
GO:0006367~transcription initiation from RNA polymerase II promoter	1	1	1	0.811495712
GO:0006396~RNA processing	1	1	1	0.837190321
GO:0006397~mRNA processing	1	1	1	0.722515038
GO:0006402~mRNA catabolic process	1	1	1	0.903800975
GO:0006405~RNA export from nucleus	1	1	1	0.841207628
GO:0006412~translation	1	1	1	0.037135312
GO:0006413~translational initiation	1	1	1	6.34E-05
GO:0006470~protein dephosphorylation	1	1	1	0.378234992
GO:0006511~ubiquitin-dependent protein catabolic process	1	1	1	0.920468916
GO:0006517~protein deglycosylation	1	1	1	0.721069893
GO:0006614~SRP-dependent cotranslational protein targeting to membrane	1	1	1	4.30E-06
GO:0006661~phosphatidylinositol biosynthetic process	1	1	1	0.570125426
GO:0006974~cellular response to DNA damage stimulus	1	1	1	1.66E-05
GO:0006977~DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	1	1	1	0.33096367
GO:0006987~activation of signaling protein activity involved in unfolded protein response	1	1	1	0.899155198
GO:0007049~cell cycle	1	1	1	0.202720249
GO:0007050~cell cycle arrest	1	1	1	0.453771333
GO:0007062~sister chromatid cohesion	1	1	1	0.694905866
GO:0007067~mitotic nuclear division	1	1	1	0.913672441
GO:0007077~mitotic nuclear envelope disassembly	1	1	1	0.857870122
GO:0007095~mitotic G2 DNA damage checkpoint	1	1	1	0.764991873
GO:0007172~signal complex assembly	1	1	1	0.899155198
GO:0007175~negative regulation of epidermal growth factor-activated receptor activity	1	1	1	0.81113004
GO:0007212~dopamine receptor signaling pathway	1	1	1	0.907197548
GO:0007223~Wnt signaling pathway, calcium modulating pathway	1	1	1	0.876176211
GO:0007249~I-kappaB kinase/NF-kappaB signaling	1	1	1	0.27750252
GO:0007250~activation of NF-kappaB-inducing kinase activity	1	1	1	0.903800975
GO:0007254~JNK cascade	1	1	1	0.002397239
GO:0007257~activation of JUN kinase activity	1	1	1	0.081165679
GO:0008625~extrinsic apoptotic signaling pathway via death domain receptors	1	1	1	0.032542311
GO:0008626~granzyme-mediated apoptotic signaling pathway	1	1	1	0.913221894
GO:0009416~response to light stimulus	1	1	1	0.57060218
GO:0009791~post-embryonic development	1	1	1	0.840760779
GO:0010212~response to ionizing radiation	1	1	1	0.117539529
GO:0010332~response to gamma radiation	1	1	1	0.315046587
GO:0010467~gene expression	1	1	1	0.811501173
GO:0010468~regulation of gene expression	1	1	1	0.881229404
GO:0010501~RNA secondary structure unwinding	1	1	1	0.857870122
GO:0010508~positive regulation of autophagy	1	1	1	0.720443307
GO:0010529~negative regulation of transposition	1	1	1	0.51216384
GO:0010803~regulation of tumor necrosis factor-mediated signaling pathway	1	1	1	0.505242439
GO:0010939~regulation of necrotic cell death	1	1	1	0.867335616
GO:0010941~regulation of cell death	1	1	1	0.81113004
GO:0010957~negative regulation of vitamin D biosynthetic process	1	1	1	0.913221894
GO:0016032~viral process	1	1	1	0.315656995
GO:0016567~protein ubiquitination	1	1	1	0.000753474
GO:0016569~covalent chromatin modification	1	1	1	0.654200886
GO:0016579~protein deubiquitination	1	1	1	0.866494251
GO:0016925~protein sumoylation	1	1	1	0.319024714
GO:0016926~protein desumoylation	1	1	1	0.899155198
GO:0019083~viral transcription	1	1	1	7.83E-07
GO:0019885~antigen processing and presentation of endogenous peptide antigen via MHC class I	1	1	1	0.83568948
GO:0030101~natural killer cell activation	1	1	1	0.061504386
GO:0030225~macrophage differentiation	1	1	1	0.903800975
GO:0030307~positive regulation of cell growth	1	1	1	0.668611833
GO:0031064~negative regulation of histone deacetylation	1	1	1	0.913221894
GO:0031065~positive regulation of histone deacetylation	1	1	1	0.81113004
GO:0031573~intra-S DNA damage checkpoint	1	1	1	0.68830365
GO:0032088~negative regulation of NF-kappaB transcription factor activity	1	1	1	0.447580843
GO:0032211~negative regulation of telomere maintenance via telomerase	1	1	1	0.525118461
GO:0032388~positive regulation of intracellular transport	1	1	1	0.811409165
GO:0032436~positive regulation of proteasomal ubiquitin-dependent protein catabolic process	1	1	1	0.900447702
GO:0032471~negative regulation of endoplasmic reticulum calcium ion concentration	1	1	1	0.899155198
GO:0032480~negative regulation of type I interferon production	1	1	1	0.035020474
GO:0032481~positive regulation of type I interferon production	1	1	1	0.720205818
GO:0032508~DNA duplex unwinding	1	1	1	0.25040689
GO:0032609~interferon-gamma production	1	1	1	0.83568948
GO:0032648~regulation of interferon-beta production	1	1	1	0.913221894
GO:0032703~negative regulation of interleukin-2 production	1	1	1	0.81113004
GO:0032727~positive regulation of interferon-alpha production	1	1	1	0.525118461
GO:0032728~positive regulation of interferon-beta production	1	1	1	0.606916417
GO:0032733~positive regulation of interleukin-10 production	1	1	1	0.662567363
GO:0032740~positive regulation of interleukin-17 production	1	1	1	0.607715718
GO:0032743~positive regulation of interleukin-2 production	1	1	1	0.68830365
GO:0033077~T cell differentiation in thymus	1	1	1	0.606916417
GO:0033089~positive regulation of T cell differentiation in thymus	1	1	1	0.721069893
GO:0033209~tumor necrosis factor-mediated signaling pathway	1	1	1	0.761298682
GO:0033962~cytoplasmic mRNA processing body assembly	1	1	1	0.907197548
GO:0034122~negative regulation of toll-like receptor signaling pathway	1	1	1	0.907197548
GO:0035194~posttranscriptional gene silencing by RNA	1	1	1	0.83568948
GO:0035196~production of miRNAs involved in gene silencing by miRNA	1	1	1	0.899155198
GO:0035666~TRIF-dependent toll-like receptor signaling pathway	1	1	1	0.880242747
GO:0035771~interleukin-4-mediated signaling pathway	1	1	1	0.383338563
GO:0036297~interstrand cross-link repair	1	1	1	0.836828984
GO:0038110~interleukin-2-mediated signaling pathway	1	1	1	0.383338563
GO:0039530~MDA-5 signaling pathway	1	1	1	0.811409165
GO:0042104~positive regulation of activated T cell proliferation	1	1	1	0.850305558
GO:0042149~cellular response to glucose starvation	1	1	1	0.711816314
GO:0042752~regulation of circadian rhythm	1	1	1	0.651813286
GO:0042771~intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	1	1	1	0.553155704
GO:0042795~snRNA transcription from RNA polymerase II promoter	1	1	1	0.404849089
GO:0043124~negative regulation of I-kappaB kinase/NF-kappaB signaling	1	1	1	0.019433715
GO:0043153~entrainment of circadian clock by photoperiod	1	1	1	0.768340192
GO:0043280~positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	1	1	1	0.897889354
GO:0043368~positive T cell selection	1	1	1	0.811409165
GO:0043484~regulation of RNA splicing	1	1	1	0.905254664

GO:0043497--regulation of protein heterodimerization activity	1	1	1	0.899155198
GO:0043525--positive regulation of neuron apoptotic process	1	1	1	0.387914793
GO:0043620--regulation of DNA-templated transcription in response to stress	1	1	1	0.721357228
GO:0043923--positive regulation by host of viral transcription	1	1	1	0.332444112
GO:0043966--histone H3 acetylation	1	1	1	0.833819234
GO:0045060--negative thymic T cell selection	1	1	1	0.121875722
GO:0045071--negative regulation of viral genome replication	1	1	1	0.720443307
GO:0045084--positive regulation of interleukin-12 biosynthetic process	1	1	1	0.721357228
GO:0045088--regulation of innate immune response	1	1	1	0.607715718
GO:0045579--positive regulation of B cell differentiation	1	1	1	0.68830365
GO:0045589--regulation of regulatory T cell differentiation	1	1	1	0.913221894
GO:0045599--negative regulation of fat cell differentiation	1	1	1	0.184320825
GO:0045737--positive regulation of cyclin-dependent protein serine/threonine kinase activity	1	1	1	0.918190408
GO:0045814--negative regulation of gene expression, epigenetic	1	1	1	0.287683953
GO:0045869--negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	1	1	1	0.83568948
GO:0045892--negative regulation of transcription, DNA-templated	1	1	1	0.248623895
GO:0045930--negative regulation of mitotic cell cycle	1	1	1	0.551603818
GO:0045954--positive regulation of natural killer cell mediated cytotoxicity	1	1	1	0.00098071
GO:0046632--alpha-beta T cell differentiation	1	1	1	0.721357228
GO:0048147--negative regulation of fibroblast proliferation	1	1	1	0.315046587
GO:0048304--positive regulation of isotype switching to IgG isotypes	1	1	1	0.51216384
GO:0048535--lymph node development	1	1	1	0.86867831
GO:0048536--spleen development	1	1	1	0.142429952
GO:0048538--thymus development	1	1	1	0.387914793
GO:0050650--chondroitin sulfate proteoglycan biosynthetic process	1	1	1	0.899155198
GO:0050651--dermatan sulfate proteoglycan biosynthetic process	1	1	1	0.811409165
GO:0050688--regulation of defense response to virus	1	1	1	0.721357228
GO:0050777--negative regulation of immune response	1	1	1	0.867335616
GO:0050798--activated T cell proliferation	1	1	1	0.071808909
GO:0050856--regulation of T cell receptor signaling pathway	1	1	1	0.721357228
GO:0050861--positive regulation of B cell receptor signaling pathway	1	1	1	0.36806295
GO:0050868--negative regulation of T cell activation	1	1	1	0.81113004
GO:0050869--negative regulation of B cell activation	1	1	1	0.83568948
GO:0051028--mRNA transport	1	1	1	0.572019542
GO:0051092--positive regulation of NF-kappaB transcription factor activity	1	1	1	0.111067213
GO:0051259--protein oligomerization	1	1	1	0.763764436
GO:0051534--negative regulation of NFAT protein import into nucleus	1	1	1	0.575262305
GO:0051568--histone H3-K4 methylation	1	1	1	0.768340192
GO:0051591--response to cAMP	1	1	1	0.898353109
GO:0051726--regulation of cell cycle	1	1	1	0.023329716
GO:0060213--positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	1	1	1	0.81113004
GO:0060340--positive regulation of type I interferon-mediated signaling pathway	1	1	1	0.626934743
GO:0061014--positive regulation of mRNA catabolic process	1	1	1	0.18540169
GO:0061087--positive regulation of histone H3-K27 methylation	1	1	1	0.575262305
GO:0061158--3'-UTR-mediated mRNA destabilization	1	1	1	0.525118461
GO:0061470--T follicular helper cell differentiation	1	1	1	0.913221894
GO:0070059--intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	1	1	1	0.192960671
GO:0070266--necroptotic process	1	1	1	0.903800975
GO:0070301--cellular response to hydrogen peroxide	1	1	1	0.337818357
GO:0070383--DNA cytosine deamination	1	1	1	0.83568948
GO:0070423--nucleotide-binding oligomerization domain containing signaling pathway	1	1	1	0.025867435
GO:0071277--cellular response to calcium ion	1	1	1	0.880340345
GO:0071353--cellular response to interleukin-4	1	1	1	0.918190408
GO:0071479--cellular response to ionizing radiation	1	1	1	0.553155704
GO:0071550--death-inducing signaling complex assembly	1	1	1	0.899155198
GO:0071663--positive regulation of granzyme B production	1	1	1	0.811409165
GO:0072332--intrinsic apoptotic signaling pathway by p53 class mediator	1	1	1	0.850305558
GO:0072540--T-helper 17 cell lineage commitment	1	1	1	0.575262305
GO:0072643--interferon-gamma secretion	1	1	1	0.83568948
GO:0072676--lymphocyte migration	1	1	1	0.913221894
GO:0072678--T cell migration	1	1	1	0.36806295
GO:0090200--positive regulation of release of cytochrome c from mitochondria	1	1	1	0.659738046
GO:0090625--mRNA cleavage involved in gene silencing by siRNA	1	1	1	0.913221894
GO:0097193--intrinsic apoptotic signaling pathway	1	1	1	0.761685884
GO:0097296--activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	1	1	1	0.066190439
GO:1900017--positive regulation of cytokine production involved in inflammatory response	1	1	1	0.626934743
GO:1900103--positive regulation of endoplasmic reticulum unfolded protein response	1	1	1	0.575262305
GO:1900740--positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	1	1	1	0.264405413
GO:1901216--positive regulation of neuron death	1	1	1	0.57060218
GO:1901224--positive regulation of NIK/NF-kappaB signaling	1	1	1	0.68830365
GO:1901741--positive regulation of myoblast fusion	1	1	1	0.68667831
GO:1901796--regulation of signal transduction by p53 class mediator	1	1	1	0.041900619
GO:1902041--regulation of extrinsic apoptotic signaling pathway via death domain receptors	1	1	1	0.07778262
GO:1902237--positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	1	1	1	0.322039585
GO:1902263--apoptotic process involved in embryonic digit morphogenesis	1	1	1	0.811409165
GO:1902715--positive regulation of interferon-gamma secretion	1	1	1	0.138340604
GO:1903896--positive regulation of IRE1-mediated unfolded protein response	1	1	1	0.899155198
GO:1904628--cellular response to phorbol 13-acetate 12-myristate	1	1	1	0.83568948
GO:1904837--beta-catenin-TCF complex assembly	1	1	1	0.833819234
GO:1990314--cellular response to insulin-like growth factor stimulus	1	1	1	0.575262305
GO:2000271--positive regulation of fibroblast apoptotic process	1	1	1	0.721357228
GO:2000785--regulation of autophagosome assembly	1	1	1	0.86867831
GO:2001244--positive regulation of intrinsic apoptotic signaling pathway	1	1	1	0.654959827

Table S8. Network centrality scores of genes in DEG-DMR or DEG regulatory network. Sorted according to the rank of DEGs (last column).

Gene	DEG-DMR network			DEG network			DEG	DMR	Average rank of the three centrality scores	
	Degree	Betweenness	Eigenvector	Degree	Betweenness	Eigenvector			DEG-DMR	DEG
ETS1	115	12111.21	0.64	69	1104.13	0.77	A+	B+	4.7	2.7
TFAP2A	170	6059.49	0.65	104	760.7	0.76	B+	B+	6.3	3
SP11	71	14036.08	0.29	62	1743.58	0.56	A+	-	9	3.3
AR	133	5556.89	0.77	76	273.52	1	B+	-	6.7	3.7
RARA	65	6587.42	0.49	37	1345.08	0.69	A+	A+	9.3	4
MYB	91	10384.09	0.47	48	759.48	0.52	B+	A+	8	5.7
PPARG	67	6964.04	0.42	36	422.02	0.48	A+	B+	10.3	7
RARB	34	1412.98	0.22	18	30.5	0.34	B+	A+	23.3	10.3
RUNX1	14	10408.35	0.15	6	824.5	0.21	B+	A+	30	13.3
RXRG	38	397.11	0.13	20	42	0.17	A+	B+	38.7	14.7
FLI1	27	497.37	0.21	16	79.2	0.16	A+	A+	30.3	15.7
PTGS2	16	0	0.24	8	0	0.28	A+	A+	48.3	17.3
VEGFA	12	0	0.23	7	0	0.27	A+	A+	54	18.3
NOL3	16	0	0.29	6	0	0.27	A+	A+	47.3	19
PML	6	24.33	0.09	5	18.08	0.21	A+	-	92.7	20.3
CDH13	9	0	0.14	5	0	0.24	A+	-	65	22
S100A9	6	0	0.1	5	0	0.22	A+	-	90.7	22.3
SERPINE1	14	0	0.27	5	0	0.22	A+	-	50.3	22.7
MMP2	7	0	0.13	5	0	0.17	A+	A+	70	26.3
PLAT	6	0	0.11	4	0	0.2	A+	A+	84.7	26.7
TBXAS1	5	0	0.1	4	0	0.18	A+	A+	105.3	27
ICAM1	8	0	0.1	4	0	0.18	A+	A+	80.3	27.3
CD36	5	0	0.09	4	0	0.17	A+	-	111.3	28.7
ANGPTL4	8	0	0.13	4	0	0.17	A+	-	68.3	29.7
SCD	6	0	0.09	4	0	0.17	A+	-	100.7	29.7
CD40	5	0	0.07	4	0	0.15	A+	-	128.7	31.3
HMOX1	9	0	0.15	5	0	0.13	A+	-	64	32
PLAU	8	0	0.18	3	0	0.17	A+	-	62.7	32.3
HOXA4	3	0	0.08	3	0	0.17	A+	-	152.7	32.7
SMPD1	3	0	0.08	3	0	0.17	A+	A+	152.7	32.7
CCND2	11	0	0.13	6	0	0.12	A+	A+	65	33.7
MAPK3	11	6.64	0.14	4	0	0.13	A+	B+	58	35.3
APOE	5	0	0.11	3	0	0.16	A+	-	96	35.3
ERG	17	2793.6	0.12	11	50.2	0.1	A+	-	39	35.7
GADD45B	6	0	0.13	3	0	0.15	A+	-	78.3	35.7
TCN2	4	0	0.12	3	0	0.15	A+	-	106.3	36.3
SCARB1	4	0	0.11	3	0	0.14	A+	-	110	36.7
KRT19	5	0	0.13	3	0	0.14	B+	A+	90.3	37
GSTP1	5	0	0.08	3	0	0.14	B+	A+	117.3	37
FGFR1	5	0	0.07	3	0	0.14	A+	-	133.7	37
KLF5	4	0	0.07	3	0	0.14	B+	A+	147.7	37
S100A8	4	0	0.07	3	0	0.14	A+	-	147.7	37
SERPINF1	4	0	0.07	3	0	0.14	B+	A+	147.7	37
MNDA	4	0	0.1	3	0	0.13	A+	-	113.7	39
WAS	3	0	0.06	3	0	0.13	A+	-	180.3	39
TGFB1	11	0	0.21	3	0	0.12	A+	-	56.7	40.7
TGFBR2	12	0	0.14	4	0	0.11	A+	-	60	41.3
CYP27A1	6	0	0.11	3	0	0.12	A+	A+	84.3	44
DBI	4	0	0.06	3	0	0.12	A+	-	156.3	44
LPL	4	0	0.06	3	0	0.12	A+	-	156.3	44
NR1H3	4	0	0.06	3	0	0.12	A+	B+	156.3	44
VEGFB	7	0	0.14	3	0	0.11	A+	A+	69	45.3
VEGFC	5	0	0.08	3	0	0.11	A+	A+	125.7	45.3
EPAS1	21	85.08	0.07	13	0	0.08	A+	B+	94	46
MMP7	5	0	0.08	3	0	0.11	B+	-	125	46.7
NFKBIA	15	545.46	0.05	5	68	0.08	A+	-	115.3	47.3
CCNA1	7	0	0.12	4	0	0.1	B+	-	73.7	48
TP73	12	218.94	0.14	5	25	0.07	B+	A+	50.7	49.3
PDGFRB	3	0	0.05	3	0	0.11	A+	-	201.3	49.3
LCP1	2	0	0.06	2	0	0.13	A+	-	214	50.7
MUC4	5	0	0.12	2	0	0.12	B+	-	93	51.3
HOXA7	4	1.68	0.1	2	0	0.12	A+	A+	114	51.3
NCOR2	4	493.93	0.06	2	0	0.12	A+	-	149.7	51.3
CD38	2	0	0.05	2	0	0.12	B+	-	222	51.3
CDK7	2	0	0.05	2	0	0.12	B+	-	222	51.3
NEDD9	2	0	0.05	2	0	0.12	A+	-	222	51.3
TMSB10	2	0	0.05	2	0	0.12	A+	-	222	51.3
TNFRSF1B	2	0	0.05	2	0	0.12	A+	B+	222	51.3
PPBP	2	0	0.05	2	0	0.11	A+	-	242.7	56.7
LTC4S	6	0	0.13	2	0	0.11	A+	-	80.3	57.3
IL2RB	4	0	0.12	2	0	0.11	A+	-	107	57.3

KIT	4	0	0.1	2	0	0.11	A+	-	115.3	57.3
SLC19A1	3	0	0.07	2	0	0.11	A+	A+	171	57.3
ATP2A3	2	0	0.06	2	0	0.11	B+	A+	219	57.3
ENG	2	0	0.06	2	0	0.11	A+	-	219.3	57.3
RUNX1T1	4	0.34	0.03	3	0	0.08	A+	B+	218.3	58
PTGS1	3	0	0.07	2	0	0.11	A+	-	173	59.3
EDN1	8	0	0.13	2	0	0.1	A+	A+	67.3	60
CD83	4	0	0.1	2	0	0.1	A+	-	114.3	60
GATA3	4	0	0.08	2	0	0.1	A+	-	135.7	60
TNFRSF11B	4	0	0.08	2	0	0.1	A+	A+	137.3	60
PTGER2	3	0	0.07	2	0	0.1	B+	-	163.3	60
RETN	3	0	0.06	2	0	0.1	A+	-	173.7	60
ADAM28	2	0	0.05	2	0	0.1	B+	A+	227.7	60
ADIPOR2	2	0	0.05	2	0	0.1	A+	A+	227.7	60
UCP2	2	0	0.05	2	0	0.1	B+	-	227.7	60
TNNC1	7	0	0.13	3	0	0.07	A+	A+	71.3	61
LTF	4	0	0.1	2	0	0.09	B+	A+	113	63.7
ITGAX	4	0	0.09	2	0	0.09	A+	-	126	64
MME	3	0	0.08	2	0	0.09	A+	B+	151	64
CSF3R	3	0	0.05	2	0	0.09	A+	-	191.3	64
MSR1	3	0	0.05	2	0	0.09	A+	B+	191.7	64
CD53	2	0	0.04	2	0	0.09	A+	B+	259.3	64
TLR4	2	0	0.04	2	0	0.09	A+	-	259.3	64
FLT1	8	0	0.09	3	0	0.07	A+	A+	90.3	65
CSF1R	4	0	0.02	3	0	0.06	A+	-	256	65.7
ITGB1	5	0	0.11	2	0	0.09	A+	A+	97.7	66
CD22	4	0	0.09	2	0	0.09	A+	A+	125.3	66
SLC11A1	3	0	0.05	2	0	0.09	A+	A+	199	66
CD5	3	0	0.09	2	0	0.09	A+	-	144	67
LCK	2	0	0.05	2	0	0.09	A+	-	240	67
KCNMB1	2	0	0.05	2	0	0.09	A+	B+	240	67.7
CLU	2	0	0.05	2	0	0.09	B+	-	238	68
FABP3	3	0	0.04	2	0	0.08	A+	-	209.3	68.7
FADS2	3	0	0.04	2	0	0.08	A+	A+	209.3	69
PTCRA	3	0	0.03	2	0	0.08	A+	-	233.3	69.7
KCNMA1	4	0	0.08	2	0	0.08	A+	-	126.7	70
CSF1	3	0	0.04	2	0	0.08	A+	A+	221	70
PIGR	2	0	0.03	2	0	0.07	B+	A+	267.3	71.7
VWF	4	0	0.05	2	0	0.06	A+	-	171	75.7
FIGF	4	0	0.05	2	0	0.06	A+	-	182.7	76.3
KDR	4	0	0.04	2	0	0.06	A+	-	197.7	76.3
TGFA	4	0	0.06	2	0	0.06	B+	A+	156	77
HPGD	4	0	0.05	2	0	0.06	A+	-	175.7	77.3
SOCS1	5	0	0.05	2	0	0.06	A+	-	167.3	77.7
MET	7	0	0.09	2	0	0.06	B+	A+	89.3	78
PIM1	4	0	0.04	2	0	0.06	A+	-	206	78.3
FASN	5	0	0.09	2	0	0.05	A+	A+	111.7	78.7
NR3C1	6	0	0.1	2	0	0.05	A+	B+	91.7	85
CSTA	2	0	0.03	2	0	0.05	A+	A+	278.3	85
IL6ST	2	0	0.04	1	0	0.07	A+	-	255	97.3
PGC	2	0	0.08	1	0	0.07	A+	A+	195	97.7
CITED2	1	0	0.03	1	0	0.07	A+	-	328	97.7
ECM1	1	0	0.03	1	0	0.07	A+	-	328	97.7
FOXA1	1	0	0.03	1	0	0.07	B+	B+	328	97.7
HSD11B1	1	0	0.03	1	0	0.07	A+	B+	328	97.7
HSP90AA1	1	0	0.03	1	0	0.07	B+	A+	328	97.7
HSP90AB1	1	0	0.03	1	0	0.07	B+	A+	328	97.7
KLK14	1	0	0.03	1	0	0.07	B+	A+	328	97.7
ZMIZ1	1	0	0.03	1	0	0.07	A+	-	328	97.7
ATF4	18	48	0.01	12	20	0.03	A+	-	298.3	98.7
NFKB2	14	476.35	0.08	6	37	0.03	A+	-	71.3	100
SMAD9	14	1088.49	0.08	10	18	0.01	A+	-	65.7	102.3
STAT4	17	71.67	0.04	9	7	0.02	A+	A+	151.7	102.3
TCF7L1	15	1009.49	0.1	7	8	0.02	A+	-	55.7	103
SMAD7	13	702.57	0.08	6	8	0.01	A+	-	75.3	104.3
CSF2	5	0	0.04	1	0	0.05	A+	A+	185.3	104.3
TFRC	3	0	0.05	1	0	0.05	A+	-	196.3	104.3
FGL2	2	0	0.07	1	0	0.05	A+	-	203	104.3
TNFSF14	2	0	0.07	1	0	0.05	A+	-	203	104.3
CD8A	2	0	0.04	1	0	0.05	A+	-	258.3	104.3
CDK11A	2	0	0.04	1	0	0.05	A+	-	258.3	104.3
ANGPT2	2	0	0.04	1	0	0.05	A+	B+	261.3	104.3
THBD	2	0	0.04	1	0	0.05	A+	-	261.3	104.3
F13A1	2	0	0.03	1	0	0.05	A+	-	266.3	104.3

ITGA5	2	0	0.03	1	0	0.05	A+	B+	280	104.3
LYZ	1	0	0.03	1	0	0.05	A+	-	361	104.3
SH2D1A	1	0	0.03	1	0	0.05	A+	-	361	104.3
AXL	1	0	0.03	1	0	0.05	A+	-	361.7	104.3
GZMB	1	0	0.03	1	0	0.05	A+	B+	361.7	104.3
IER5	1	0	0.03	1	0	0.05	A+	-	361.7	104.3
ITGA4	1	0	0.03	1	0	0.05	A+	-	361.7	104.3
NRP1	1	0	0.03	1	0	0.05	A+	A+	361.7	104.3
PF4	1	0	0.03	1	0	0.05	A+	-	361.7	104.3
RELB	11	19	0.03	7	0	0.02	A+	-	207.3	104.7
SRF	2	0	0.02	2	0	0.05	A+	-	315.7	107.7
COL1A1	6	0	0.09	2	0	0.05	A+	-	97	108
PCK2	6	0	0.05	2	0	0.05	A+	A+	154.7	108.3
ACSL4	3	0	0.03	2	0	0.05	A+	-	247	108.3
FABP4	3	0	0.03	2	0	0.05	A+	-	247	108.3
OLR1	3	0	0.03	2	0	0.05	A+	A+	247	108.3
SORBS1	3	0	0.03	2	0	0.05	A+	-	247	108.3
VIM	5	0	0.09	2	0	0.04	A+	B+	112.7	110
SOS2	7	0	0.02	6	0	0.01	A+	A+	235.7	110
ITGAM	3	0	0.06	2	0	0.04	A+	A+	183.3	110.3
TIMP2	5	0	0.11	1	0	0.05	A+	A+	98.3	111
PLAUR	4	0	0.1	1	0	0.05	A+	B+	115.7	111
ADH6	4	0	0.1	1	0	0.05	B+	-	117.3	111
BST1	4	0	0.09	1	0	0.05	A+	A+	120.7	111
SCNN1G	4	0	0.09	1	0	0.05	B+	A+	126.3	111
HK2	4	0	0.08	1	0	0.05	A+	-	132.7	111
OXTR	3	0	0.09	1	0	0.05	B+	-	142.3	111
KIF2A	3	0	0.08	1	0	0.05	B+	-	154.7	111
LRP8	3	0	0.08	1	0	0.05	B+	A+	156	111
NRGN	3	0	0.08	1	0	0.05	A+	-	156	111
KRT17	3	0	0.08	1	0	0.05	B+	A+	158.3	111
MIPEP	3	0	0.06	1	0	0.05	B+	-	183	111
CCNB1	2	0	0.07	1	0	0.05	B+	-	199	111
CD7	2	0	0.07	1	0	0.05	A+	-	199	111
GALNS	2	0	0.07	1	0	0.05	B+	-	199	111
HSPA8	2	0	0.07	1	0	0.05	B+	-	199	111
IGFBP2	2	0	0.07	1	0	0.05	B+	A+	199	111
KRT5	2	0	0.07	1	0	0.05	B+	A+	199	111
SLPI	2	0	0.07	1	0	0.05	B+	-	199	111
ELN	3	0	0.05	1	0	0.05	A+	A+	204.7	111
POLD2	3	0	0.05	1	0	0.05	B+	-	204.7	111
FGFR3	3	0	0.05	1	0	0.05	B+	A+	206.3	111
PFKFB3	3	0	0.04	1	0	0.05	A+	-	208.7	111
FBLN1	2	0	0.05	1	0	0.05	A+	A+	234.3	111
ALOX5AP	2	0	0.05	1	0	0.05	A+	-	236.7	111
MT1A	2	0	0.05	1	0	0.05	A+	-	236.7	111
CELSR1	2	0	0.04	1	0	0.05	B+	A+	256	111
SLC6A4	2	0	0.04	1	0	0.05	A+	-	256	111
SRM	2	0	0.04	1	0	0.05	A+	-	256	111
ADM	2	0	0.04	1	0	0.05	A+	-	263.3	111
F2R	2	0	0.04	1	0	0.05	A+	-	264.3	111
GFAP	2	0	0.04	1	0	0.05	B+	A+	265.3	111
HIP1	2	0	0.03	1	0	0.05	A+	B+	279	111
AKR1C1	1	0	0.03	1	0	0.05	B+	B+	343.7	111
ALOX15	1	0	0.03	1	0	0.05	B+	A+	343.7	111
ARSB	1	0	0.03	1	0	0.05	A+	-	343.7	111
ATP10A	1	0	0.03	1	0	0.05	A+	-	343.7	111
ATP12A	1	0	0.03	1	0	0.05	B+	-	343.7	111
ATP6V1B2	1	0	0.03	1	0	0.05	A+	-	343.7	111
C1QTNF1	1	0	0.03	1	0	0.05	A+	-	343.7	111
CHRM3	1	0	0.03	1	0	0.05	A+	-	343.7	111
COL6A2	1	0	0.03	1	0	0.05	A+	-	343.7	111
GAA	1	0	0.03	1	0	0.05	A+	A+	343.7	111
GALNT3	1	0	0.03	1	0	0.05	B+	-	343.7	111
GCLC	1	0	0.03	1	0	0.05	B+	A+	343.7	111
GM2A	1	0	0.03	1	0	0.05	A+	B+	343.7	111
GNAI2	1	0	0.03	1	0	0.05	A+	A+	343.7	111
HCK	1	0	0.03	1	0	0.05	A+	-	343.7	111
HEXB	1	0	0.03	1	0	0.05	A+	-	343.7	111
HPGDS	1	0	0.03	1	0	0.05	A+	-	343.7	111
HRH1	1	0	0.03	1	0	0.05	A+	-	343.7	111
HSD17B2	1	0	0.03	1	0	0.05	B+	A+	343.7	111
KRT4	1	0	0.03	1	0	0.05	B+	A+	343.7	111
LAMB1	1	0	0.03	1	0	0.05	A+	A+	343.7	111

MAN2B1	1	0	0.03	1	0	0.05	A+	A+	343.7	111
NPR1	1	0	0.03	1	0	0.05	A+	-	343.7	111
NQO1	1	0	0.03	1	0	0.05	B+	-	343.7	111
PDE5A	1	0	0.03	1	0	0.05	A+	A+	343.7	111
RAD51B	1	0	0.03	1	0	0.05	B+	A+	343.7	111
SEL1L	1	0	0.03	1	0	0.05	A+	-	343.7	111
SLC13A4	1	0	0.03	1	0	0.05	B+	A+	343.7	111
SPHK1	1	0	0.03	1	0	0.05	A+	-	343.7	111
VIPR1	1	0	0.03	1	0	0.05	A+	-	343.7	111
CCND3	8	0	0.04	4	0	0.01	A+	B+	173.7	112
DDIT3	7	50	0	5	14	0	A+	-	378	115.3
SOCS2	6	0	0.07	2	0	0.04	A+	B+	118	117.3
EGR2	7	0	0.02	3	0	0.01	A+	A+	235.3	120.3
GLI3	27	0	0.01	14	0	0	A+	-	345.3	120.3
PRKACA	6	0	0.03	4	0	0	A+	-	187.7	123
PRKACB	5	0	0.01	4	0	0	A+	-	340.7	123
BTRC	7	0	0.06	3	0	0.01	B+	-	123.3	123.3
PIAS3	7	1052.5	0.03	3	1	0	B+	A+	200.3	125
PER3	17	6.95	0	6	1	0	A+	-	355	125
ID2	6	0	0.06	2	0	0.01	A+	B+	134.3	127.7
BACE1	1	0	0.03	1	0	0.05	A+	-	343.7	132
NID1	1	0	0.03	1	0	0.05	A+	B+	343.7	132
PTGDS	1	0	0.03	1	0	0.05	A+	-	343.7	132
NPAS2	13	1.5	0	4	1	0	B+	-	376	132
MAP3K14	4	0	0.03	2	0	0	A+	-	251.3	136
DAB2	1	0	0.01	1	0	0.04	A+	A+	477.7	136
CD163	3	0	0.07	1	0	0.04	A+	-	171.7	136.3
CD33	2	0	0.06	1	0	0.04	A+	B+	220	136.3
FES	2	0	0.06	1	0	0.04	A+	B+	220	136.3
IL3RA	2	0	0.06	1	0	0.04	A+	-	220	136.3
TFEC	2	0	0.02	1	0	0.04	A+	-	309.7	136.3
ITGB2	2	0	0.02	1	0	0.04	A+	-	313	136.3
CH13L1	2	0	0.02	1	0	0.04	A+	A+	321.7	136.3
FCGR1A	2	0	0.02	1	0	0.04	A+	-	322.7	136.3
ACP5	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
CD68	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
CSF2RA	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
CTSK	1	0	0.01	1	0	0.04	A+	B+	477.7	136.3
CYBB	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
IGJ	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
IL1RN	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
LSP1	1	0	0.01	1	0	0.04	A+	A+	477.7	136.3
NCF1	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
NCF4	1	0	0.01	1	0	0.04	A+	A+	477.7	136.3
TYROBP	1	0	0.01	1	0	0.04	A+	-	477.7	136.3
RUVBL1	4	2.96	0.02	2	0	0	B+	A+	250.3	136.7
SOX17	4	2.96	0.02	2	0	0	A+	-	250.3	136.7
SMAD6	11	707.41	0.11	2	0	0	A+	B+	55.3	140.7
ADA	5	0	0.1	1	0	0.04	A+	-	104	143
CDK1	4	0	0.1	1	0	0.04	B+	-	119.3	143
ALOX5	3	0	0.08	1	0	0.04	A+	B+	155.7	143
MCAM	3	0	0.08	1	0	0.04	A+	-	161	143
TF	4	0	0.05	1	0	0.04	B+	B+	175.3	143
TSC22D3	3	0	0.05	1	0	0.04	A+	-	187	143
IGF1	2	0	0.04	1	0	0.04	A+	A+	254.7	143
PTPRC	2	0	0.04	1	0	0.04	A+	-	257.7	143
CD34	2	0	0.03	1	0	0.04	A+	B+	274	143
ATP2B1	1	0	0.02	1	0	0.04	A+	-	453.7	143
CSRP1	1	0	0.02	1	0	0.04	A+	-	453.7	143
EPCAM	1	0	0.02	1	0	0.04	B+	A+	453.7	143
GATA2	1	0	0.02	1	0	0.04	A+	-	453.7	143
GTF2H3	1	0	0.02	1	0	0.04	B+	A+	453.7	143
HHEX	1	0	0.02	1	0	0.04	A+	B+	453.7	143
MAD2L1	1	0	0.02	1	0	0.04	B+	-	453.7	143
PDE4DIP	1	0	0.02	1	0	0.04	B+	-	453.7	143
PPP1R7	1	0	0.02	1	0	0.04	B+	-	453.7	143
SH2D3C	1	0	0.02	1	0	0.04	A+	-	453.7	143
SLC39A14	1	0	0.02	1	0	0.04	A+	-	453.7	143
TRAP1	1	0	0.02	1	0	0.04	B+	-	453.7	143
XBP1	3	3	0	2	0	0	B+	A+	461	146
CREB3L4	3	0	0	2	0	0	B+	-	431.3	146.7
CREB5	2	0	0	2	0	0	A+	-	470	147
MAPK12	6	8	0	2	0	0	A+	A+	380	147.3
PRRG1	1	0	0.01	1	0	0.02	A+	-	496	150.7

EHHADH	3	0	0.02	1	0	0.01	B+	-	373.3	153.3
ACADL	2	0	0.01	1	0	0.01	A+	-	427.3	153.3
ACADM	2	0	0.01	1	0	0.01	B+	-	427.3	153.3
ILK	2	0	0.01	1	0	0.01	A+	-	427.3	153.3
LYL1	1	0	0.01	1	0	0.01	A+	B+	499.7	154.7
UPP1	1	0	0.01	1	0	0.01	A+	-	499.7	154.7
SLA	1	0	0.01	1	0	0.01	A+	A+	500.3	154.7
SNAI2	1	0	0.01	1	0	0.01	A+	-	514.3	156.3
ZBTB16	2	0	0.01	1	0	0.01	A+	B+	427	156.7
CDH5	3	0	0.03	1	0	0.01	A+	-	233	157
ICAM2	1	0	0.01	1	0	0.01	A+	B+	519.3	157.3
PDGFB	5	0	0.08	1	0	0.01	A+	A+	120	157.7
EGLN3	3	0	0.02	1	0	0.01	B+	-	278	157.7
SLC2A1	2	0	0.01	1	0	0.01	B+	A+	417.3	157.7
TEK	1	0	0	1	0	0.01	A+	B+	526.3	157.7
AKT3	4	0	0	1	0	0.01	A+	-	405.7	159.3
THBS1	2	0	0.02	1	0	0.01	A+	-	311.3	159.7
NBL1	1	0	0.01	1	0	0.01	A+	A+	515	159.7
TFAP2C	3	39.25	0.04	1	0	0	B+	-	201.3	160.3
NFIA	1	0	0	1	0	0	B+	-	521.7	160.3
SELP	2	0	0	1	0	0	A+	-	460.3	162.7
TRAF4	1	0	0	1	0	0	B+	A+	524	162.7
MAPKAPK3	1	0	0	1	0	0	A+	-	540.7	164
CAMK2G	1	0	0	1	0	0	A+	-	541	164
RPS6KA5	1	0	0	1	0	0	B+	-	543.3	164
MAPKAPK2	1	0	0	1	0	0	A+	-	541	165
RPS6KA2	1	0	0	1	0	0	A+	-	541	165
CAMK2D	1	0	0	1	0	0	B+	-	543.3	165
CISH	3	0	0.01	1	0	0	A+	-	390.3	166.3
PRF1	2	0	0.01	1	0	0	A+	-	435.7	166.3
CD14	3	0	0.05	1	0	0	A+	-	192	167
TGFBR1	5	0	0.05	1	0	0	A+	-	172.3	167.3
ACVR1B	1	0	0	1	0	0	B+	A+	525	167.7
ID4	3	0	0.03	1	0	0	A+	-	243	168
ID1	3	0	0.03	1	0	0	A+	-	243	168.3
BMPR1B	2	0	0.01	1	0	0	B+	A+	437.3	168.3
ID3	4	0	0.05	1	0	0	A+	B+	174.7	169
SPRY4	1	0	0	1	0	0	A+	-	539	169.7
SPRED2	1	0	0	1	0	0	A+	A+	539.7	169.7
SPRED1	1	0	0	1	0	0	A+	-	538.7	170.3
SPRY1	1	0	0	1	0	0	A+	A+	539	170.3
HOXB2	1	0	0	1	0	0	A+	-	538.3	171
CDKN2B	7	0	0.1	1	0	0	A+	-	87	173
HHIP	1	0	0	1	0	0	A+	-	552.3	173.7
PVR	1	0	0	1	0	0	A+	-	552.3	174
WNT7B	1	0	0	1	0	0	B+	B+	556	174.3
WNT2	1	0	0	1	0	0	A+	-	551.3	174.7
BMP2	1	0	0	1	0	0	A+	-	556	175
WNT5B	1	0	0	1	0	0	B+	-	554.7	175.3
BMP5	1	0	0	1	0	0	A+	-	552.3	175.7
STK36	1	0	0	1	0	0	B+	-	552.3	176
WNT4	1	0	0	1	0	0	B+	A+	552.3	176.3
MEF2C	1	0	0	1	0	0	A+	B+	557.3	176.7
RORC	3	0.14	0	1	0	0	B+	A+	462.3	177
SP1	180	16798.58	1	NA	NA	NA	-	A+	1.7	-
E2F1	272	14537.93	0.48	NA	NA	NA	-	A+	4	-
ESR1	65	17430.87	0.49	NA	NA	NA	-	A+	5.3	-
SMAD4	52	11444.65	0.49	NA	NA	NA	-	A+	9.7	-
CREB1	92	8185.37	0.3	NA	NA	NA	-	B+	10	-
SMAD3	50	4914.74	0.44	NA	NA	NA	-	A+	14.7	-
EGR1	53	3092.56	0.4	NA	NA	NA	-	A+	15.7	-
HIF1A	62	4410.85	0.23	NA	NA	NA	-	A+	17.7	-
STAT1	62	5499.92	0.19	NA	NA	NA	-	B+	19	-
LEF1	29	1597.15	0.19	NA	NA	NA	-	A+	25.3	-
ETV4	40	568.1	0.21	NA	NA	NA	-	A+	26	-
SP3	43	615.35	0.19	NA	NA	NA	-	A+	26.3	-
ETS2	37	345.3	0.29	NA	NA	NA	-	A+	27.7	-
SMAD1	29	505.71	0.13	NA	NA	NA	-	A+	38.7	-
CCND1	27	0	0.31	NA	NA	NA	-	A+	41.3	-
NFIC	55	0	0.17	NA	NA	NA	-	A+	44	-
CDKN1A	18	0	0.28	NA	NA	NA	-	A+	44.7	-
RXRA	37	229.75	0.11	NA	NA	NA	-	A+	48	-
NR3C2	14	484.33	0.12	NA	NA	NA	-	A+	48.7	-
RARG	22	0.14	0.15	NA	NA	NA	-	A+	49.7	-

CIITA	10	9020.98	0.1	NA	NA	NA	-	A+	52	-
RBL2	11	1043.85	0.11	NA	NA	NA	-	A+	52.3	-
EGFR	11	0	0.22	NA	NA	NA	-	A+	56	-
JUP	10	12.48	0.13	NA	NA	NA	-	A+	62	-
ABCB1	8	0	0.18	NA	NA	NA	-	A+	63	-
CYP19A1	7	0	0.16	NA	NA	NA	-	B+	66	-
CETP	7	0	0.14	NA	NA	NA	-	B+	68	-
AKR1B1	6	0	0.15	NA	NA	NA	-	B+	73.7	-
IL6	7	0	0.11	NA	NA	NA	-	B+	77.7	-
APOA1	7	0	0.11	NA	NA	NA	-	A+	79	-
FLII	6	0	0.12	NA	NA	NA	-	A+	83.3	-
JAK3	7	0	0.1	NA	NA	NA	-	A+	84	-
HSD17B1	5	0	0.13	NA	NA	NA	-	A+	88	-
TERT	6	0	0.1	NA	NA	NA	-	B+	89	-
PSG1	5	0	0.12	NA	NA	NA	-	B+	91.7	-
PCSK6	5	0	0.12	NA	NA	NA	-	A+	92.7	-
AMH	5	0	0.11	NA	NA	NA	-	A+	94.3	-
CPT1A	6	0	0.09	NA	NA	NA	-	A+	96.3	-
HNF4A	5	0	0.11	NA	NA	NA	-	A+	97.3	-
NKX2-1	6	0	0.09	NA	NA	NA	-	B+	98	-
ADIPOQ	5	0	0.1	NA	NA	NA	-	A+	99.7	-
TNC	6	0	0.09	NA	NA	NA	-	A+	100.3	-
E2F5	6	0	0.09	NA	NA	NA	B+	B+	101.7	-
INS	6	0	0.08	NA	NA	NA	-	A+	104.3	-
ERBB2	5	0	0.1	NA	NA	NA	-	A+	105	-
APOB	5	0	0.1	NA	NA	NA	-	B+	105.7	-
AKT1	7	0	0.08	NA	NA	NA	-	A+	107.7	-
NCOA1	5	0	0.09	NA	NA	NA	-	A+	108.7	-
NCOR1	5	0	0.09	NA	NA	NA	-	A+	109	-
MUC5AC	4	0	0.11	NA	NA	NA	-	A+	111.7	-
SMURF2	17	230.43	0.05	NA	NA	NA	-	A+	112	-
POU2F2	11	0	0.07	NA	NA	NA	-	A+	114	-
HSPB1	4	0	0.1	NA	NA	NA	-	A+	116.3	-
TG	5	0	0.08	NA	NA	NA	-	A+	117.3	-
ACSL1	5	0	0.08	NA	NA	NA	-	A+	119	-
ATP2A2	4	0	0.1	NA	NA	NA	-	A+	119	-
CCL2	4	0	0.09	NA	NA	NA	A+	-	122.3	-
SFTPB	5	0	0.08	NA	NA	NA	-	A+	124.7	-
TGM1	5	0	0.07	NA	NA	NA	-	A+	127.7	-
ANPEP	5	0	0.07	NA	NA	NA	-	A+	128	-
FN1	4	0	0.08	NA	NA	NA	A+	A+	136	-
MDM2	5	0	0.07	NA	NA	NA	-	A+	137.7	-
POLA2	4	0	0.08	NA	NA	NA	-	A+	139.3	-
MUC1	4	0	0.08	NA	NA	NA	-	A+	140.3	-
ALPP	4	0	0.07	NA	NA	NA	-	B+	147.7	-
LIPE	3	0	0.08	NA	NA	NA	-	A+	149.3	-
DDX5	3	0	0.08	NA	NA	NA	-	A+	149.7	-
IFNGR1	3	0	0.08	NA	NA	NA	-	A+	149.7	-
CTF1	3	0	0.08	NA	NA	NA	-	A+	150.3	-
SERPINB2	3	0	0.08	NA	NA	NA	-	B+	150.3	-
COL7A1	3	0	0.08	NA	NA	NA	-	A+	151.3	-
KRT18	3	0	0.08	NA	NA	NA	-	A+	152.3	-
HNF1A	4	63.53	0.06	NA	NA	NA	-	A+	152.7	-
HOOK2	3	0	0.08	NA	NA	NA	-	A+	154.7	-
NTRK1	4	0	0.06	NA	NA	NA	-	A+	155	-
ARNT	5	628.65	0.05	NA	NA	NA	-	A+	155.3	-
MAP4K2	4	0	0.06	NA	NA	NA	-	B+	155.3	-
MMP14	3	0	0.08	NA	NA	NA	-	A+	155.3	-
MADCAM1	3	0	0.08	NA	NA	NA	-	A+	156	-
ACAA1	4	0	0.06	NA	NA	NA	-	A+	156.3	-
KRT16	3	0	0.08	NA	NA	NA	-	A+	157.7	-
EXOC3	3	0	0.08	NA	NA	NA	-	A+	158	-
STAT6	15	8.17	0.04	NA	NA	NA	-	A+	159.3	-
PARP1	3	0	0.08	NA	NA	NA	-	A+	161.3	-
PPARGC1A	4	19.22	0.05	NA	NA	NA	-	A+	162	-
ACSL3	4	0	0.06	NA	NA	NA	-	A+	162.3	-
MMP1	4	0	0.06	NA	NA	NA	-	B+	162.7	-
UTRN	3	0	0.07	NA	NA	NA	A+	B+	163.7	-
MAT2A	3	0	0.07	NA	NA	NA	-	A+	164	-
ATP1A1	4	0	0.05	NA	NA	NA	-	A+	169.7	-
CBS	3	0	0.07	NA	NA	NA	-	A+	170.3	-
NCL	3	0	0.07	NA	NA	NA	-	B+	170.3	-
COL2A1	3	0	0.07	NA	NA	NA	-	B+	171.3	-
CD19	3	0	0.07	NA	NA	NA	-	A+	173.3	-

HTT	9	327.83	0.03	NA	NA	NA	-	B+	173.7	-
PAX6	6	0	0.04	NA	NA	NA	-	B+	176	-
POLD1	3	0	0.06	NA	NA	NA	-	A+	177	-
MITF	7	72.5	0.03	NA	NA	NA	-	A+	177.3	-
CA9	4	0	0.05	NA	NA	NA	-	A+	178.7	-
FOXO1	7	114.63	0.03	NA	NA	NA	-	A+	178.7	-
GOT1	3	0	0.06	NA	NA	NA	-	A+	180	-
AGTR1	3	0	0.06	NA	NA	NA	A+	-	180.7	-
PPP2R2C	3	0	0.06	NA	NA	NA	-	A+	182.3	-
PGF	4	0	0.05	NA	NA	NA	-	A+	182.7	-
CYR61	3	0	0.05	NA	NA	NA	A+	A+	186.7	-
APC	6	247.14	0.03	NA	NA	NA	-	B+	190	-
CXCL1	3	0	0.05	NA	NA	NA	-	A+	192.7	-
ADD1	2	0	0.07	NA	NA	NA	-	A+	199	-
GUCA2A	2	0	0.07	NA	NA	NA	-	A+	199	-
HTR4	2	0	0.07	NA	NA	NA	-	A+	199	-
RGL3	2	0	0.07	NA	NA	NA	-	B+	199	-
MGAT5B	3	0	0.05	NA	NA	NA	-	A+	200.3	-
HDAC1	7	5094.27	0.02	NA	NA	NA	-	A+	200.7	-
ITGB3	3	0	0.05	NA	NA	NA	-	A+	200.7	-
ITGA2B	3	0	0.05	NA	NA	NA	-	A+	201	-
B3GAT3	3	0	0.05	NA	NA	NA	-	A+	203.7	-
IKBKB	16	308.09	0.02	NA	NA	NA	-	A+	204	-
BCL3	5	0	0.03	NA	NA	NA	-	A+	208.3	-
CAV1	2	0	0.06	NA	NA	NA	A+	-	208.7	-
IL1A	2	0	0.06	NA	NA	NA	-	A+	209	-
ACOX2	3	0	0.04	NA	NA	NA	-	A+	209.3	-
ITGAL	2	0	0.06	NA	NA	NA	A+	A+	209.3	-
SCARF1	2	0	0.06	NA	NA	NA	A+	-	209.3	-
CIB2	2	0	0.06	NA	NA	NA	-	A+	210.3	-
HHLA1	2	0	0.06	NA	NA	NA	-	A+	210.3	-
IRF9	6	1046.5	0.02	NA	NA	NA	-	A+	213	-
FGFBP1	2	0	0.06	NA	NA	NA	-	A+	214	-
CD44	2	0	0.06	NA	NA	NA	A+	-	215.7	-
CD9	2	0	0.06	NA	NA	NA	-	A+	215.7	-
SLC1A4	2	0	0.06	NA	NA	NA	B+	A+	215.7	-
VAMP2	2	0	0.06	NA	NA	NA	A+	-	215.7	-
ANKRD1	3	0	0.04	NA	NA	NA	A+	-	219.3	-
NNAT	2	0	0.06	NA	NA	NA	-	A+	219.3	-
ASB2	2	0	0.05	NA	NA	NA	-	A+	222	-
STRA6	2	0	0.05	NA	NA	NA	-	A+	222	-
TNFAIP2	2	0	0.05	NA	NA	NA	-	A+	222	-
IL4	3	0	0.04	NA	NA	NA	-	A+	224.3	-
IGFBP5	2	0	0.05	NA	NA	NA	-	A+	225.3	-
ADAMTS4	2	0	0.05	NA	NA	NA	-	B+	227.7	-
NCOA6	2	0	0.05	NA	NA	NA	-	A+	227.7	-
HOXB7	2	0	0.05	NA	NA	NA	A+	A+	229.3	-
LCAT	2	0	0.05	NA	NA	NA	A+	-	229.3	-
MUC2	2	0	0.05	NA	NA	NA	-	A+	229.3	-
NFYC	3	440.88	0.03	NA	NA	NA	-	B+	230.3	-
AGT	2	0	0.05	NA	NA	NA	-	B+	232	-
ARID4A	2	0	0.05	NA	NA	NA	A+	-	232	-
COL18A1	2	0	0.05	NA	NA	NA	A+	A+	232	-
INSR	2	0	0.05	NA	NA	NA	B+	A+	232	-
RBP1	2	0	0.05	NA	NA	NA	A+	-	232	-
ARNT2	4	498.71	0.03	NA	NA	NA	-	B+	235.7	-
GALC	2	0	0.05	NA	NA	NA	-	A+	236.7	-
GPX4	2	0	0.05	NA	NA	NA	-	A+	236.7	-
BCL6	3	33.8	0.03	NA	NA	NA	-	A+	237.7	-
COL3A1	3	0	0.03	NA	NA	NA	A+	B+	240	-
PPP2R4	2	0	0.05	NA	NA	NA	-	B+	240	-
KAT7	2	0	0.05	NA	NA	NA	-	A+	241.7	-
CASP8	3	0	0.03	NA	NA	NA	-	B+	242	-
PNOC	2	0	0.05	NA	NA	NA	-	A+	242.3	-
IGF2	2	0	0.05	NA	NA	NA	-	A+	243	-
ACACB	2	0	0.04	NA	NA	NA	A+	A+	245	-
ACSL6	3	0	0.03	NA	NA	NA	-	A+	247	-
AQP7	3	0	0.03	NA	NA	NA	-	A+	247	-
CPT1C	3	0	0.03	NA	NA	NA	-	A+	247	-
SLC27A1	3	0	0.03	NA	NA	NA	-	A+	247	-
PSEN2	4	0	0.03	NA	NA	NA	-	A+	250.3	-
BCKDHA	2	0	0.04	NA	NA	NA	-	A+	256	-
CFTR	2	0	0.04	NA	NA	NA	-	A+	256	-
HSPD1	2	0	0.04	NA	NA	NA	-	A+	257.7	-

ABCB4	2	0	0.04	NA	NA	NA	-	B+	259.3	-
ART4	2	0	0.04	NA	NA	NA	-	B+	260.3	-
FSTL3	2	0	0.04	NA	NA	NA	A+	-	260.3	-
PITX2	2	0	0.04	NA	NA	NA	-	B+	260.3	-
DUSP4	2	0	0.04	NA	NA	NA	B+	-	263.7	-
ECE1	2	0	0.04	NA	NA	NA	-	A+	264	-
GP6	2	0	0.04	NA	NA	NA	-	B+	264.7	-
CTSB	2	0	0.04	NA	NA	NA	-	A+	265	-
HSPA1A	2	0	0.04	NA	NA	NA	-	A+	265.3	-
OAT	2	0	0.04	NA	NA	NA	-	A+	265.3	-
JAG2	3	0	0.03	NA	NA	NA	-	A+	266	-
CSNK2A2	2	0	0.03	NA	NA	NA	-	A+	266.3	-
CXCR4	2	0	0.03	NA	NA	NA	A+	-	268.3	-
SP4	3	0	0.03	NA	NA	NA	-	A+	273.3	-
NAE1	2	0	0.03	NA	NA	NA	-	A+	274	-
PAX3	2	0	0.03	NA	NA	NA	-	B+	275	-
CXCL12	2	0	0.03	NA	NA	NA	A+	-	276	-
GPX3	2	0	0.03	NA	NA	NA	A+	B+	277	-
CDK5	2	0	0.03	NA	NA	NA	-	A+	278.7	-
HOXA2	2	0	0.03	NA	NA	NA	-	A+	280.3	-
BSG	2	0	0.03	NA	NA	NA	-	A+	280.7	-
ABCA1	2	0	0.03	NA	NA	NA	A+	B+	281	-
HBA2	2	0	0.03	NA	NA	NA	A+	-	301	-
POLE2	2	0	0.03	NA	NA	NA	A+	-	301	-
ABCG1	1	0	0.04	NA	NA	NA	A+	A+	304.7	-
ACAN	1	0	0.04	NA	NA	NA	-	A+	304.7	-
ALDH3A1	1	0	0.04	NA	NA	NA	B+	A+	304.7	-
ALOX15B	1	0	0.04	NA	NA	NA	A+	-	304.7	-
APBB1	1	0	0.04	NA	NA	NA	-	A+	304.7	-
BDKRB2	1	0	0.04	NA	NA	NA	B+	A+	304.7	-
C8G	1	0	0.04	NA	NA	NA	-	A+	304.7	-
CDH3	1	0	0.04	NA	NA	NA	B+	A+	304.7	-
COL4A1	1	0	0.04	NA	NA	NA	A+	-	304.7	-
COL4A2	1	0	0.04	NA	NA	NA	A+	-	304.7	-
COX7A1	1	0	0.04	NA	NA	NA	A+	B+	304.7	-
EDNRB	1	0	0.04	NA	NA	NA	A+	-	304.7	-
FURIN	1	0	0.04	NA	NA	NA	A+	A+	304.7	-
GJA1	1	0	0.04	NA	NA	NA	A+	-	304.7	-
GYPC	1	0	0.04	NA	NA	NA	A+	B+	304.7	-
MMP28	1	0	0.04	NA	NA	NA	-	A+	304.7	-
NQO2	1	0	0.04	NA	NA	NA	-	A+	304.7	-
PTN	1	0	0.04	NA	NA	NA	A+	-	304.7	-
RBPJ	16	4874.16	0.01	NA	NA	NA	-	A+	304.7	-
SIAH1	1	0	0.04	NA	NA	NA	-	A+	304.7	-
SLC19A3	1	0	0.04	NA	NA	NA	A+	A+	304.7	-
SLC5A1	1	0	0.04	NA	NA	NA	B+	B+	304.7	-
SPN	1	0	0.04	NA	NA	NA	A+	-	304.7	-
STAR	1	0	0.04	NA	NA	NA	-	A+	304.7	-
STARD3	1	0	0.04	NA	NA	NA	A+	B+	304.7	-
TP11	1	0	0.04	NA	NA	NA	-	A+	304.7	-
HOXA10	2	4.5	0.02	NA	NA	NA	-	A+	307.7	-
PDE7A	2	0	0.03	NA	NA	NA	-	A+	308.3	-
HDAC2	6	3066.3	0.01	NA	NA	NA	-	A+	308.7	-
TIMP3	2	0	0.03	NA	NA	NA	A+	-	308.7	-
HSD11B2	2	0	0.02	NA	NA	NA	A+	-	310	-
POU2AF1	2	0	0.02	NA	NA	NA	B+	-	310.7	-
GDF15	2	0	0.02	NA	NA	NA	-	A+	312.3	-
SELE	2	0	0.02	NA	NA	NA	-	A+	313.3	-
BDKRB1	2	0	0.02	NA	NA	NA	-	A+	313.7	-
CLTC	2	0	0.02	NA	NA	NA	-	A+	314	-
PRDM1	2	0	0.02	NA	NA	NA	A+	B+	314.3	-
SERPINB5	2	0	0.02	NA	NA	NA	B+	A+	314.7	-
WNT7A	2	0	0.02	NA	NA	NA	-	B+	315	-
CASP10	2	0	0.02	NA	NA	NA	A+	B+	315.3	-
FOXA2	2	0	0.02	NA	NA	NA	-	B+	321.3	-
ACPP	1	0	0.03	NA	NA	NA	-	A+	328	-
CCNG1	1	0	0.03	NA	NA	NA	-	A+	328	-
FHL2	1	0	0.03	NA	NA	NA	-	A+	328	-
KLK2	1	0	0.03	NA	NA	NA	-	B+	328	-
PKD1	1	0	0.03	NA	NA	NA	-	A+	328	-
TRPS1	1	0	0.03	NA	NA	NA	-	A+	328	-
UCP3	1	0	0.03	NA	NA	NA	-	A+	328	-
CTBP2	5	0	0.02	NA	NA	NA	-	A+	334.7	-
NFATC4	7	0	0.01	NA	NA	NA	-	A+	337.3	-

AGA	1	0	0.03	NA	NA	NA	-	A+	343.7	-
ALDH3A2	1	0	0.03	NA	NA	NA	-	A+	343.7	-
BFSP2	1	0	0.03	NA	NA	NA	-	A+	343.7	-
CALB2	1	0	0.03	NA	NA	NA	-	B+	343.7	-
CTSD	1	0	0.03	NA	NA	NA	-	A+	343.7	-
ERVW-1	1	0	0.03	NA	NA	NA	-	A+	343.7	-
GUSB	1	0	0.03	NA	NA	NA	-	A+	343.7	-
GYG1	1	0	0.03	NA	NA	NA	-	A+	343.7	-
IMPA2	1	0	0.03	NA	NA	NA	-	A+	343.7	-
MAPT	1	0	0.03	NA	NA	NA	-	A+	343.7	-
MBTPS1	1	0	0.03	NA	NA	NA	-	A+	343.7	-
MGAT3	1	0	0.03	NA	NA	NA	-	A+	343.7	-
NTRK3	1	0	0.03	NA	NA	NA	-	A+	343.7	-
PPL	1	0	0.03	NA	NA	NA	-	A+	343.7	-
RECQL4	1	0	0.03	NA	NA	NA	-	A+	343.7	-
TALDO1	1	0	0.03	NA	NA	NA	-	A+	343.7	-
NFAT5	6	0	0.01	NA	NA	NA	-	A+	345	-
NFATC1	6	0	0.01	NA	NA	NA	-	B+	345	-
NOTCH3	18	380.87	0	NA	NA	NA	A+	-	347	-
NOTCH4	18	380.87	0	NA	NA	NA	A+	-	347.3	-
PER2	17	6.95	0	NA	NA	NA	-	A+	354.7	-
SREBF1	6	0	0.01	NA	NA	NA	-	A+	356.7	-
BID	1	0	0.03	NA	NA	NA	-	A+	361.7	-
DNTT	1	0	0.03	NA	NA	NA	-	B+	361.7	-
EIF4G1	1	0	0.03	NA	NA	NA	-	A+	361.7	-
ICAM4	1	0	0.03	NA	NA	NA	-	A+	361.7	-
NTHL1	1	0	0.03	NA	NA	NA	-	A+	361.7	-
TOM1	1	0	0.03	NA	NA	NA	-	A+	361.7	-
ARNTL	14	10.5	0	NA	NA	NA	-	A+	369.3	-
SKP1	3	0	0.02	NA	NA	NA	-	A+	369.3	-
CCR5	3	0	0.02	NA	NA	NA	-	B+	369.7	-
MECOM	6	64.67	0	NA	NA	NA	-	A+	374.7	-
CRY1	14	0.95	0	NA	NA	NA	-	B+	375	-
TP63	3	0	0.01	NA	NA	NA	B+	A+	375.3	-
CAV2	1	0	0.02	NA	NA	NA	A+	A+	375.7	-
CDH1	1	0	0.02	NA	NA	NA	B+	-	375.7	-
CRHBP	1	0	0.02	NA	NA	NA	-	A+	375.7	-
CYP1B1	1	0	0.02	NA	NA	NA	-	A+	375.7	-
MACROD1	1	0	0.02	NA	NA	NA	-	A+	375.7	-
NR0B2	1	0	0.02	NA	NA	NA	A+	A+	375.7	-
PTPRG	1	0	0.02	NA	NA	NA	A+	-	375.7	-
SERPINB9	1	0	0.02	NA	NA	NA	A+	-	375.7	-
TAC3	1	0	0.02	NA	NA	NA	-	A+	375.7	-
TFF1	1	0	0.02	NA	NA	NA	-	A+	375.7	-
TIMP4	1	0	0.02	NA	NA	NA	-	A+	375.7	-
WISP2	1	0	0.02	NA	NA	NA	A+	A+	375.7	-
BGN	1	0	0.02	NA	NA	NA	A+	-	379.7	-
DACH1	1	0	0.02	NA	NA	NA	-	B+	379.7	-
IHH	1	0	0.02	NA	NA	NA	-	B+	379.7	-
ADAM8	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ADAMTS1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
ADAMTS14	1	0	0.02	NA	NA	NA	-	A+	382.3	-
AGER	1	0	0.02	NA	NA	NA	A+	-	382.3	-
AK3	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ALDH1A1	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
AMPD3	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
ANKRD16	1	0	0.02	NA	NA	NA	B+	-	382.3	-
ANXA13	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
AP1B1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ARHGEF17	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
ARMC4	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
ARMC8	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ASCC2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
B9D1	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
BDH1	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
BEND7	1	0	0.02	NA	NA	NA	-	A+	382.3	-
BIK	1	0	0.02	NA	NA	NA	B+	-	382.3	-
BLVRA	1	0	0.02	NA	NA	NA	-	A+	382.3	-
BTG4	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
BTN3A3	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
C11orf54	1	0	0.02	NA	NA	NA	-	A+	382.3	-
C1orf180	1	0	0.02	NA	NA	NA	-	A+	382.3	-
C1S	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
C4orf36	1	0	0.02	NA	NA	NA	-	A+	382.3	-

CALM1	1	0	0.02	NA	NA	NA	B+	-	382.3	-
CARHSP1	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
CASR	1	0	0.02	NA	NA	NA	-	B+	382.3	-
CCDC113	1	0	0.02	NA	NA	NA	B+	-	382.3	-
CCDC93	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CCP110	1	0	0.02	NA	NA	NA	B+	-	382.3	-
CD6	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
CECR1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CEL	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CELF1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CEP89	1	0	0.02	NA	NA	NA	B+	-	382.3	-
CHKA	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CLDN5	1	0	0.02	NA	NA	NA	A+	-	382.3	-
CLIP1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
COQ2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
COX6A2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CTBS	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CUZD1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
CX3CL1	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
CXorf57	1	0	0.02	NA	NA	NA	B+	-	382.3	-
CYYR1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
DCLRE1C	1	0	0.02	NA	NA	NA	-	A+	382.3	-
DCTN3	1	0	0.02	NA	NA	NA	-	A+	382.3	-
DDO	1	0	0.02	NA	NA	NA	-	B+	382.3	-
DNAAF2	1	0	0.02	NA	NA	NA	B+	-	382.3	-
DNER	1	0	0.02	NA	NA	NA	B+	-	382.3	-
DOCK10	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
DOCK9	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
DPCD	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
DUT	1	0	0.02	NA	NA	NA	-	A+	382.3	-
DYNC2H1	1	0	0.02	NA	NA	NA	B+	-	382.3	-
EDARADD	1	0	0.02	NA	NA	NA	B+	B+	382.3	-
EDIL3	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
EMR1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
ENAH	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ENPEP	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
ESYT3	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
FAIM	1	0	0.02	NA	NA	NA	B+	-	382.3	-
FAM107B	1	0	0.02	NA	NA	NA	-	A+	382.3	-
FAM184A	1	0	0.02	NA	NA	NA	-	B+	382.3	-
FBLIM1	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
FEN1	1	0	0.02	NA	NA	NA	B+	-	382.3	-
FGG	1	0	0.02	NA	NA	NA	A+	-	382.3	-
FHIT	1	0	0.02	NA	NA	NA	-	A+	382.3	-
FPR1	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
GALK2	1	0	0.02	NA	NA	NA	B+	-	382.3	-
GCHFR	1	0	0.02	NA	NA	NA	-	A+	382.3	-
GCLM	1	0	0.02	NA	NA	NA	B+	-	382.3	-
GDI2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
GGT5	1	0	0.02	NA	NA	NA	-	A+	382.3	-
GJC1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
GLIPR2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
GNL3	1	0	0.02	NA	NA	NA	-	A+	382.3	-
GPX2	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
GRAMD4	1	0	0.02	NA	NA	NA	-	A+	382.3	-
HERPUD1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
HPS4	1	0	0.02	NA	NA	NA	-	A+	382.3	-
HUNK	1	0	0.02	NA	NA	NA	-	A+	382.3	-
IFT80	1	0	0.02	NA	NA	NA	-	A+	382.3	-
IKZF1	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
IQCK	1	0	0.02	NA	NA	NA	B+	B+	382.3	-
KCNG4	1	0	0.02	NA	NA	NA	-	A+	382.3	-
KCNJ16	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
KIF24	1	0	0.02	NA	NA	NA	B+	-	382.3	-
KLHL29	1	0	0.02	NA	NA	NA	-	A+	382.3	-
KRT75	1	0	0.02	NA	NA	NA	-	A+	382.3	-
LIPC	1	0	0.02	NA	NA	NA	-	A+	382.3	-
LOXL1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
LPAR2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MAP1A	1	0	0.02	NA	NA	NA	B+	-	382.3	-
MAP2K6	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MAP4K5	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MAPK6	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MED17	1	0	0.02	NA	NA	NA	-	A+	382.3	-

MKX	1	0	0.02	NA	NA	NA	B+	B+	382.3	-
MMP15	1	0	0.02	NA	NA	NA	A+	-	382.3	-
MPPED2	1	0	0.02	NA	NA	NA	-	B+	382.3	-
MPST	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MRAS	1	0	0.02	NA	NA	NA	A+	-	382.3	-
MRPS23	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MSH2	1	0	0.02	NA	NA	NA	B+	-	382.3	-
MT1X	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MTHFD1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
MXI1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
N4BP1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
N4BP2L1	1	0	0.02	NA	NA	NA	-	B+	382.3	-
NAGK	1	0	0.02	NA	NA	NA	-	A+	382.3	-
NAIP	1	0	0.02	NA	NA	NA	A+	-	382.3	-
NDRG4	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
NDUFA7	1	0	0.02	NA	NA	NA	-	A+	382.3	-
NDUFAF6	1	0	0.02	NA	NA	NA	-	A+	382.3	-
NEK2	1	0	0.02	NA	NA	NA	B+	-	382.3	-
NEK4	1	0	0.02	NA	NA	NA	B+	-	382.3	-
NIPSNAP1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
NOL9	1	0	0.02	NA	NA	NA	-	B+	382.3	-
NUDT4	1	0	0.02	NA	NA	NA	B+	-	382.3	-
NUPR1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
OLFML1	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
OLFML3	1	0	0.02	NA	NA	NA	A+	-	382.3	-
OPN3	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
OSR1	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
PAK7	1	0	0.02	NA	NA	NA	-	A+	382.3	-
PBX4	1	0	0.02	NA	NA	NA	B+	-	382.3	-
PCOLCE	1	0	0.02	NA	NA	NA	A+	-	382.3	-
PDE8A	1	0	0.02	NA	NA	NA	A+	-	382.3	-
PDPN	1	0	0.02	NA	NA	NA	A+	-	382.3	-
PDXK	1	0	0.02	NA	NA	NA	-	A+	382.3	-
PDZK1IP1	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
PEF1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
PES1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
PEAS	1	0	0.02	NA	NA	NA	-	A+	382.3	-
PFN2	1	0	0.02	NA	NA	NA	B+	-	382.3	-
PHLDB1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
PIGU	1	0	0.02	NA	NA	NA	B+	-	382.3	-
PIK3R5	1	0	0.02	NA	NA	NA	A+	-	382.3	-
PLEKHB1	1	0	0.02	NA	NA	NA	B+	-	382.3	-
PLEKHF2	1	0	0.02	NA	NA	NA	B+	-	382.3	-
PPAT	1	0	0.02	NA	NA	NA	B+	-	382.3	-
PPM1J	1	0	0.02	NA	NA	NA	-	A+	382.3	-
PPP1R3E	1	0	0.02	NA	NA	NA	-	A+	382.3	-
PRKAR1A	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
PTPN6	1	0	0.02	NA	NA	NA	A+	-	382.3	-
RAB40C	1	0	0.02	NA	NA	NA	-	A+	382.3	-
RAD18	1	0	0.02	NA	NA	NA	-	A+	382.3	-
RALGDS	1	0	0.02	NA	NA	NA	-	A+	382.3	-
RANGRF	1	0	0.02	NA	NA	NA	A+	-	382.3	-
RASSF8	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
RDH16	1	0	0.02	NA	NA	NA	-	A+	382.3	-
RECK	1	0	0.02	NA	NA	NA	A+	-	382.3	-
RPA3	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
RPL31	1	0	0.02	NA	NA	NA	-	A+	382.3	-
RTN2	1	0	0.02	NA	NA	NA	A+	-	382.3	-
RTN4	1	0	0.02	NA	NA	NA	-	B+	382.3	-
RUVBL2	1	0	0.02	NA	NA	NA	B+	-	382.3	-
SAA2	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
SAFB2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SEC63	1	0	0.02	NA	NA	NA	-	B+	382.3	-
SECISBP2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SEPHS1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SERF2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SGK223	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SIRPA	1	0	0.02	NA	NA	NA	A+	-	382.3	-
SLC15A1	1	0	0.02	NA	NA	NA	-	B+	382.3	-
SLC22A16	1	0	0.02	NA	NA	NA	-	B+	382.3	-
SLC2A3	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
SLC35G1	1	0	0.02	NA	NA	NA	-	B+	382.3	-
SLC3A2	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
SLC43A2	1	0	0.02	NA	NA	NA	-	A+	382.3	-

SLC6A19	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SSFA2	1	0	0.02	NA	NA	NA	A+	-	382.3	-
SSTR1	1	0	0.02	NA	NA	NA	A+	-	382.3	-
ST13	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ST6GALNAC	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
STARD13	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
STK4	1	0	0.02	NA	NA	NA	A+	B+	382.3	-
STX11	1	0	0.02	NA	NA	NA	A+	-	382.3	-
STX3	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SUCLG1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
SULF2	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
SULT1A2	1	0	0.02	NA	NA	NA	A+	-	382.3	-
SYCP3	1	0	0.02	NA	NA	NA	A+	A+	382.3	-
SYNE2	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TAF6	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TBC1D16	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TBCC	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TFIP11	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TMBIM1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TMEM105	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TMEM132A	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TMEM47	1	0	0.02	NA	NA	NA	A+	-	382.3	-
TMOD3	1	0	0.02	NA	NA	NA	A+	-	382.3	-
TRIT1	1	0	0.02	NA	NA	NA	B+	A+	382.3	-
TSC1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TSNARE1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TSPAN6	1	0	0.02	NA	NA	NA	B+	-	382.3	-
TST	1	0	0.02	NA	NA	NA	-	A+	382.3	-
TTC6	1	0	0.02	NA	NA	NA	B+	B+	382.3	-
TUBA4A	1	0	0.02	NA	NA	NA	A+	-	382.3	-
TXNL1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
UBN1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
VMP1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
WAPAL	1	0	0.02	NA	NA	NA	-	A+	382.3	-
WBP4	1	0	0.02	NA	NA	NA	A+	-	382.3	-
WDR25	1	0	0.02	NA	NA	NA	-	A+	382.3	-
XPNPEP1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
YIPF1	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ZC3H7A	1	0	0.02	NA	NA	NA	-	A+	382.3	-
ZNF165	1	0	0.02	NA	NA	NA	B+	-	382.3	-
ZNF778	1	0	0.02	NA	NA	NA	-	A+	382.3	-
JAK1	3	0	0.01	NA	NA	NA	-	B+	390.3	-
SOCS7	3	0	0.01	NA	NA	NA	-	A+	390.3	-
TYK2	3	0	0.01	NA	NA	NA	-	B+	390.3	-
SNAI1	3	0	0.01	NA	NA	NA	-	B+	391.7	-
CRY2	7	0	0	NA	NA	NA	-	A+	394	-
CSNK1D	6	0	0	NA	NA	NA	-	A+	398.3	-
IRF7	3	126	0.01	NA	NA	NA	-	A+	400	-
TINAGL1	2	0	0.02	NA	NA	NA	A+	A+	403.3	-
SPINT1	2	0	0.02	NA	NA	NA	-	A+	406.7	-
DLL1	3	0	0.01	NA	NA	NA	B+	-	407.3	-
HLA-DOB	2	0	0.02	NA	NA	NA	A+	A+	408.3	-
HLA-DRA	2	0	0.02	NA	NA	NA	A+	-	408.3	-
FBXW11	4	0	0	NA	NA	NA	-	A+	410.7	-
DVL1	4	0	0	NA	NA	NA	A+	-	415.7	-
DVL3	4	0	0	NA	NA	NA	-	B+	415.7	-
CUL2	2	0	0.01	NA	NA	NA	-	B+	417.3	-
EGLN2	2	0	0.01	NA	NA	NA	-	A+	417.3	-
TRAF2	3	0	0.01	NA	NA	NA	-	A+	420	-
CYP8B1	2	0	0.01	NA	NA	NA	-	A+	427.3	-
ME1	2	0	0.01	NA	NA	NA	-	A+	427.3	-
PDPK1	2	0	0.01	NA	NA	NA	-	A+	427.3	-
PLTP	2	0	0.01	NA	NA	NA	-	A+	427.3	-
UBC	2	0	0.01	NA	NA	NA	-	A+	427.3	-
CHP1	3	0	0	NA	NA	NA	-	A+	436	-
CHP2	3	0	0	NA	NA	NA	B+	-	436	-
PPP3CA	3	0	0	NA	NA	NA	A+	A+	436	-
TFDP2	2	0	0.01	NA	NA	NA	-	A+	437	-
BMPRI1A	2	0	0.01	NA	NA	NA	-	B+	437.3	-
NFE2L2	4	6	0	NA	NA	NA	-	A+	437.7	-
ACACA	2	0	0.01	NA	NA	NA	-	A+	441.3	-
MDM4	2	0	0.01	NA	NA	NA	-	A+	441.7	-
DAP3	1	0	0.02	NA	NA	NA	-	A+	453.7	-
EBNA1BP2	1	0	0.02	NA	NA	NA	-	A+	453.7	-

EED	1	0	0.02	NA	NA	NA	-	A+	453.7	-
EMG1	1	0	0.02	NA	NA	NA	-	A+	453.7	-
HSPA9	1	0	0.02	NA	NA	NA	-	A+	453.7	-
MRPL38	1	0	0.02	NA	NA	NA	-	A+	453.7	-
MYBBP1A	1	0	0.02	NA	NA	NA	-	A+	453.7	-
NMU	1	0	0.02	NA	NA	NA	-	B+	453.7	-
NPM1	1	0	0.02	NA	NA	NA	-	A+	453.7	-
PLA2G6	1	0	0.02	NA	NA	NA	-	A+	453.7	-
RNF144A	1	0	0.02	NA	NA	NA	-	B+	453.7	-
SPIB	1	0	0.02	NA	NA	NA	-	A+	453.7	-
TERF2	1	0	0.02	NA	NA	NA	-	A+	453.7	-
TXNDC5	1	0	0.02	NA	NA	NA	-	A+	453.7	-
VAV1	1	0	0.02	NA	NA	NA	-	A+	453.7	-
COL6A1	1	0	0.02	NA	NA	NA	A+	-	464	-
ACVR1	1	0	0.02	NA	NA	NA	B+	-	464.3	-
COL6A3	1	0	0.02	NA	NA	NA	A+	B+	464.3	-
LAMC1	1	0	0.02	NA	NA	NA	A+	-	464.3	-
PAX1	3	0	0	NA	NA	NA	-	B+	464.3	-
PEX6	1	0	0.02	NA	NA	NA	B+	-	464.3	-
ZFYVE9	1	0	0.02	NA	NA	NA	A+	-	464.3	-
NKX3-1	2	0	0	NA	NA	NA	-	B+	465.3	-
ACE	1	0	0.02	NA	NA	NA	A+	-	466.3	-
CD69	1	0	0.02	NA	NA	NA	A+	-	466.3	-
PTGES	1	0	0.02	NA	NA	NA	B+	A+	466.3	-
TAB2	2	0	0	NA	NA	NA	-	A+	466.3	-
REST	2	0	0	NA	NA	NA	-	A+	467.3	-
PDGFRA	2	0	0	NA	NA	NA	A+	-	468	-
EIF2AK3	2	0	0	NA	NA	NA	-	A+	469	-
EIF2AK4	2	0	0	NA	NA	NA	-	A+	469	-
ADRB2	1	0	0.01	NA	NA	NA	A+	-	469.7	-
AQP3	1	0	0.01	NA	NA	NA	-	A+	469.7	-
CALCA	1	0	0.01	NA	NA	NA	B+	-	469.7	-
CD55	1	0	0.01	NA	NA	NA	-	A+	469.7	-
DIO2	1	0	0.01	NA	NA	NA	-	B+	469.7	-
HLA-DQB1	1	0	0.01	NA	NA	NA	A+	-	469.7	-
IL5RA	1	0	0.01	NA	NA	NA	B+	A+	469.7	-
INHBA	1	0	0.01	NA	NA	NA	A+	B+	469.7	-
KCNN3	1	0	0.01	NA	NA	NA	B+	A+	469.7	-
MYH10	1	0	0.01	NA	NA	NA	A+	-	469.7	-
NFE2	1	0	0.01	NA	NA	NA	A+	-	469.7	-
NPC1	1	0	0.01	NA	NA	NA	A+	-	469.7	-
NR4A2	1	0	0.01	NA	NA	NA	-	B+	469.7	-
NR4A3	1	0	0.01	NA	NA	NA	-	B+	469.7	-
PDE4D	1	0	0.01	NA	NA	NA	-	A+	469.7	-
PMP22	1	0	0.01	NA	NA	NA	A+	-	469.7	-
PXMP2	1	0	0.01	NA	NA	NA	-	A+	469.7	-
SFTPA2	1	0	0.01	NA	NA	NA	A+	-	469.7	-
SLC20A1	1	0	0.01	NA	NA	NA	-	A+	469.7	-
SLC9A1	1	0	0.01	NA	NA	NA	A+	-	469.7	-
ST3GAL5	1	0	0.01	NA	NA	NA	-	A+	469.7	-
MAML3	2	0	0	NA	NA	NA	-	A+	477.3	-
B2M	1	0	0.01	NA	NA	NA	-	B+	477.7	-
FOLR1	1	0	0.01	NA	NA	NA	-	A+	477.7	-
SCARB2	1	0	0.01	NA	NA	NA	-	B+	477.7	-
MAPK10	2	0	0	NA	NA	NA	B+	A+	481	-
FGF1	1	0	0.01	NA	NA	NA	-	A+	482.7	-
HBEGF	1	0	0.01	NA	NA	NA	A+	-	482.7	-
LFNG	2	0	0	NA	NA	NA	-	A+	487.7	-
ADAM17	2	0	0	NA	NA	NA	A+	-	488	-
DTX2	2	0	0	NA	NA	NA	B+	A+	488	-
DTX3	2	0	0	NA	NA	NA	B+	-	488	-
NUMB	2	0	0	NA	NA	NA	-	B+	488	-
NUMBL	2	0	0	NA	NA	NA	-	A+	488	-
B4GALT1	1	0	0.01	NA	NA	NA	-	A+	489.3	-
BNIP3	1	0	0.01	NA	NA	NA	-	A+	489.7	-
DTX4	2	0	0	NA	NA	NA	-	A+	489.7	-
EDN2	1	0	0.01	NA	NA	NA	-	A+	489.7	-
ENO1	1	0	0.01	NA	NA	NA	-	A+	489.7	-
ERRFI1	1	0	0.01	NA	NA	NA	-	A+	489.7	-
HOOK1	1	0	0.01	NA	NA	NA	B+	-	489.7	-
KCNA4	1	0	0.01	NA	NA	NA	-	B+	489.7	-
MDK	1	0	0.01	NA	NA	NA	B+	A+	489.7	-
MTOR	1	0	0.01	NA	NA	NA	-	A+	489.7	-
NR4A1	1	0	0.01	NA	NA	NA	A+	-	489.7	-

P4HTM	1	0	0.01	NA	NA	NA	B+	A+	489.7	-
PFKFB4	1	0	0.01	NA	NA	NA	-	A+	489.7	-
PFKL	1	0	0.01	NA	NA	NA	-	A+	489.7	-
PLIN2	1	0	0.01	NA	NA	NA	A+	-	489.7	-
PLSCR4	1	0	0.01	NA	NA	NA	A+	A+	489.7	-
PSENE1	2	0	0	NA	NA	NA	B+	-	489.7	-
TAC4	1	0	0.01	NA	NA	NA	-	A+	489.7	-
TFF3	1	0	0.01	NA	NA	NA	B+	A+	489.7	-
DLL4	2	0	0	NA	NA	NA	A+	-	490.3	-
JAG1	2	0	0	NA	NA	NA	-	A+	490.3	-
MFNG	2	0	0	NA	NA	NA	A+	-	491	-
KRT1	1	0	0.01	NA	NA	NA	-	B+	495.7	-
AMD1	1	0	0.01	NA	NA	NA	-	A+	497.3	-
APOH	1	0	0.01	NA	NA	NA	A+	-	497.3	-
MMP19	1	0	0.01	NA	NA	NA	A+	-	497.3	-
PSG4	1	0	0.01	NA	NA	NA	-	B+	497.3	-
SFTPD	1	0	0.01	NA	NA	NA	A+	A+	497.3	-
SLC6A6	1	0	0.01	NA	NA	NA	-	A+	497.3	-
NKD2	2	0	0	NA	NA	NA	A+	-	498.3	-
BCHE	1	0	0.01	NA	NA	NA	A+	-	499.3	-
MAP3K12	1	0	0.01	NA	NA	NA	-	A+	501.7	-
MSH6	1	0	0.01	NA	NA	NA	B+	A+	501.7	-
NPR2	1	0	0.01	NA	NA	NA	B+	-	501.7	-
PFKP	1	0	0.01	NA	NA	NA	B+	A+	501.7	-
SLC1A3	1	0	0.01	NA	NA	NA	A+	-	501.7	-
CD1D	1	0	0.01	NA	NA	NA	A+	-	503.3	-
MARK4	1	0	0.01	NA	NA	NA	-	A+	503.3	-
NRCAM	1	0	0.01	NA	NA	NA	A+	-	503.3	-
TCF3	1	0	0.01	NA	NA	NA	-	A+	503.3	-
A2M	1	0	0.01	NA	NA	NA	A+	-	505	-
CXCL10	1	0	0.01	NA	NA	NA	A+	-	505	-
CXCL11	1	0	0.01	NA	NA	NA	A+	-	505	-
FCGR3A	1	0	0.01	NA	NA	NA	A+	-	505	-
PPP2CA	1	0	0.01	NA	NA	NA	-	A+	505	-
PPP2CB	1	0	0.01	NA	NA	NA	-	A+	505	-
PPP2R1B	1	0	0.01	NA	NA	NA	B+	A+	505	-
PPP2R2A	1	0	0.01	NA	NA	NA	-	A+	505	-
PPP2R2B	1	0	0.01	NA	NA	NA	-	B+	505	-
PSMB9	1	0	0.01	NA	NA	NA	-	B+	505	-
PTGFR	1	0	0.01	NA	NA	NA	B+	-	505	-
TAP1	1	0	0.01	NA	NA	NA	-	B+	505	-
AHSG	1	0	0.01	NA	NA	NA	-	B+	509.3	-
ALAS1	1	0	0.01	NA	NA	NA	-	A+	509.3	-
C4A	1	0	0.01	NA	NA	NA	-	A+	509.3	-
C4BPB	1	0	0.01	NA	NA	NA	-	A+	509.3	-
DDB1	1	0	0.01	NA	NA	NA	-	A+	509.3	-
GTF3C1	1	0	0.01	NA	NA	NA	-	A+	509.3	-
GUCY1B3	1	0	0.01	NA	NA	NA	A+	-	509.3	-
HNRNP1A1	1	0	0.01	NA	NA	NA	-	A+	509.3	-
RGN	1	0	0.01	NA	NA	NA	A+	-	509.3	-
SFTPC	1	0	0.01	NA	NA	NA	A+	B+	509.3	-
STMN1	1	0	0.01	NA	NA	NA	-	A+	509.3	-
TRIM26	1	0	0.01	NA	NA	NA	-	A+	509.3	-
PROC	1	0	0.01	NA	NA	NA	-	A+	513.3	-
UROS	1	0	0.01	NA	NA	NA	-	A+	513.3	-
ETV6	1	0	0.01	NA	NA	NA	-	A+	514.3	-
CABLES1	1	0	0.01	NA	NA	NA	-	A+	515	-
FLNA	1	0	0.01	NA	NA	NA	A+	-	515.7	-
TGFBI	1	0	0.01	NA	NA	NA	A+	A+	515.7	-
ZEB1	1	0	0.01	NA	NA	NA	A+	-	515.7	-
ZEB2	1	0	0.01	NA	NA	NA	A+	-	515.7	-
ATP1B1	1	0	0.01	NA	NA	NA	-	A+	517	-
ATP1B3	1	0	0.01	NA	NA	NA	A+	A+	517	-
FXVD2	1	0	0.01	NA	NA	NA	-	A+	517	-
FXVD4	1	0	0.01	NA	NA	NA	-	A+	517	-
SCNN1A	1	0	0.01	NA	NA	NA	-	A+	517	-
SCNN1B	1	0	0.01	NA	NA	NA	B+	-	517	-
SGK1	1	0	0.01	NA	NA	NA	A+	A+	517	-
IRF5	1	0	0	NA	NA	NA	-	B+	520.7	-
CREM	1	0	0	NA	NA	NA	-	A+	521.3	-
ZBTB17	1	0	0	NA	NA	NA	-	A+	522	-
HOXB3	1	0	0	NA	NA	NA	-	A+	523.3	-
TRAF3	1	0	0	NA	NA	NA	-	A+	524	-
HNF4G	1	0	0	NA	NA	NA	B+	-	527	-

ERBB3	1	0	0	NA	NA	NA	-	A+	527.7	-
FGFR4	1	0	0	NA	NA	NA	A+	-	527.7	-
TRADD	1	0	0	NA	NA	NA	-	A+	529	-
AICDA	1	0	0	NA	NA	NA	-	A+	529.7	-
TYRP1	1	0	0	NA	NA	NA	A+	-	532.7	-
FBP1	1	0	0	NA	NA	NA	A+	-	533.3	-
AP2A1	1	0	0	NA	NA	NA	-	A+	533.7	-
AP2B1	1	0	0	NA	NA	NA	-	A+	533.7	-
AP2S1	1	0	0	NA	NA	NA	A+	A+	533.7	-
CLTCL1	1	0	0	NA	NA	NA	-	A+	533.7	-
FYN	1	0	0	NA	NA	NA	A+	B+	535	-
ARHGEF4	1	0	0	NA	NA	NA	B+	-	535.3	-
AXIN1	1	0	0	NA	NA	NA	-	A+	535.3	-
AXIN2	1	0	0	NA	NA	NA	A+	-	535.3	-
PDE6B	1	0	0	NA	NA	NA	B+	-	536.3	-
PRKCQ	1	0	0	NA	NA	NA	A+	-	537.3	-
IRS2	1	0	0	NA	NA	NA	A+	-	537.7	-
MAP3K8	1	0	0	NA	NA	NA	A+	-	537.7	-
CAMK2A	1	0	0	NA	NA	NA	-	A+	541	-
DISC1	1	0	0	NA	NA	NA	-	A+	541	-
MKNK2	1	0	0	NA	NA	NA	-	A+	541	-
RPS6KA4	1	0	0	NA	NA	NA	-	A+	541	-
CAMK2B	1	0	0	NA	NA	NA	-	B+	543.3	-
RPS6KA1	1	0	0	NA	NA	NA	-	A+	543.3	-
S100A2	1	0	0	NA	NA	NA	B+	A+	544.7	-
KAT2A	1	0	0	NA	NA	NA	-	A+	545	-
NOTCH1	1	0	0	NA	NA	NA	A+	B+	545.3	-
HK3	1	0	0	NA	NA	NA	A+	A+	545.7	-
PRKCZ	1	0	0	NA	NA	NA	-	A+	545.7	-
ZBP1	1	0	0	NA	NA	NA	-	A+	546.3	-
IKBKE	1	0	0	NA	NA	NA	-	A+	546.7	-
WNT2B	1	0	0	NA	NA	NA	-	A+	550.7	-
WNT3	1	0	0	NA	NA	NA	-	A+	551	-
PTCH2	1	0	0	NA	NA	NA	-	B+	551.3	-
WNT9B	1	0	0	NA	NA	NA	-	A+	551.3	-
CSNK1A1	1	0	0	NA	NA	NA	-	A+	552.3	-
SHH	1	0	0	NA	NA	NA	-	B+	552.3	-
MTSS1	1	0	0	NA	NA	NA	-	B+	554.7	-
PTCH1	1	0	0	NA	NA	NA	-	A+	554.7	-
WNT5A	1	0	0	NA	NA	NA	-	B+	554.7	-
ERN1	1	0	0	NA	NA	NA	-	A+	558.7	-
SLC22A8	1	0	0	NA	NA	NA	-	A+	559	-
SLC22A6	1	0	0	NA	NA	NA	-	A+	559.3	-