

Summary of Supplementary Data

Supplementary Table S1. Details of the data sources used in this study.

Supplementary Table S2. MAGMA analysis results-Gene list.

Supplementary Table S3. The SMR analysis was employed to analyze the association between eQTLGen's eQTL and vitiligo.

Supplementary Table S4. Primer sequences used for quantitative real-time PCR (qPCR)

Supplementary Figure S1. Sub-clustering and compositional analysis of epidermal antigen-presenting cells (APCs).

Supplementary Table S1 Details of the data sources used in this study.

Traits	Data source	Data type	Source
Vitiligo	FinnGen R12	GWAS	https://r12.finngen.fi/
eqtl	eQTLGen	GWAS	https://molgenis26.gcc.rug.nl/downloads/eqtngen/cis-eqtl/SMR_formatted/cis-eQTL-SMR_20191212.tar.gz
Vitiligo	GEO-GSE203262	scRNA-seq	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE203262

Supplementary Table S2 MAGMA analysis results-Gene list.

GENE	Ensembl ID	GENE	CHR	START	STOP	NSNPS	NPARAM	N	ZSTAT	P
ENSG00000002919		SNX11	17	46180719	46200436	23	5	466064	1.6971	0.04484
ENSG00000005001		PRSS22	16	2902728	2908171	37	6	466064	1.8876	0.02954
ENSG00000005448		WDR54	2	74648805	74652882	2	1	466064	1.865	0.03109
ENSG00000005812		FBXL3	13	77566740	77601330	98	14	466064	1.6707	0.04739
ENSG00000006047		YBX2	17	7191571	7197934	8	4	466064	1.8274	0.03382
ENSG00000007038		PRSS21	16	2867164	2876305	27	7	466064	1.8252	0.03398
ENSG00000007933		FMO3	1	1.71E+08	1.71E+08	87	12	466064	1.652	0.04927
ENSG00000008226		DLEC1	3	38080696	38165516	138	22	466064	2.6736	0.00375
ENSG00000008282		SYPL1	7	1.06E+08	1.06E+08	70	12	466064	2.9667	0.00151
ENSG00000009307		CSDE1	1	1.15E+08	1.15E+08	145	27	466064	1.8429	0.03267
ENSG00000009413		REV3L	6	1.12E+08	1.12E+08	559	36	466064	1.8715	0.03064
ENSG00000010292		NCAPD2	12	6602522	6641121	60	11	466064	1.7299	0.04183
ENSG00000011523		CEP68	2	65283500	65314138	73	16	466064	2.1516	0.01572
ENSG00000012223		LTF	3	46477136	46526724	113	13	466064	2.5241	0.0058
ENSG00000013288		MAN2B2	4	6576902	6625089	149	24	466064	2.1791	0.01466
ENSG00000013364		MVP	16	29831715	29859355	25	3	466064	2.0594	0.01973
ENSG00000013561		RNF14	5	1.41E+08	1.41E+08	68	13	466064	2.3495	0.0094
ENSG00000019169		MARCO	2	1.2E+08	1.2E+08	114	16	466064	1.8381	0.03302
ENSG00000020129		NCDN	1	36023074	36032875	18	6	466064	1.7437	0.04061
ENSG00000023330		ALAS1	3	52232102	52248343	32	8	466064	1.8156	0.03472
ENSG00000028277		POU2F2	19	42590263	42700737	169	9	466064	1.6472	0.04976
ENSG00000029534		ANK1	8	41510739	41754280	816	50	466064	1.8896	0.0294
ENSG00000031003		FAM13B	5	1.37E+08	1.37E+08	313	27	466064	2.8146	0.00244
ENSG00000033327		GAB2	11	77926343	78129394	724	32	466064	1.9856	0.02354
ENSG00000034053		APBA2	15	29129629	29410518	912	75	466064	1.8051	0.03553
ENSG00000037757		MRI1	19	13875346	13885096	16	2	466064	1.801	0.03585
ENSG00000044574		HSPA5	9	1.28E+08	1.28E+08	14	5	466064	2.2717	0.01155
ENSG00000047457		CP	3	1.49E+08	1.49E+08	250	21	466064	2.3075	0.01051
ENSG00000048405		ZNF800	7	1.27E+08	1.27E+08	249	25	466064	1.8178	0.03455
ENSG00000049089		COL9A2	1	40766159	40783488	49	10	466064	2.4159	0.00785
ENSG00000049618		ARID1B	6	1.57E+08	1.58E+08	1124	82	466064	1.8423	0.03272
ENSG00000052723		SIKE1	1	1.15E+08	1.15E+08	35	8	466064	2.1933	0.01414
ENSG00000053918		KCNQ1	11	2465914	2870339	1180	158	466064	2.6021	0.00463
ENSG00000056972		TRAF3IP2	6	1.12E+08	1.12E+08	141	19	466064	1.7611	0.03911
ENSG00000060642		PIGV	1	27113963	27124889	11	5	466064	1.7384	0.04108
ENSG00000060709		RIMBP2	12	1.31E+08	1.31E+08	1234	99	466064	2.5405	0.00554
ENSG00000060971		ACAA1	3	38144620	38178733	40	11	466064	2.4493	0.00716
ENSG00000061455		PRDM6	5	1.22E+08	1.23E+08	239	26	466064	2.4947	0.0063
ENSG00000062282		DGAT2	11	75470557	75512579	108	14	466064	2.0035	0.02256
ENSG00000064225		ST3GAL6	3	98451080	98540045	205	30	466064	2.4011	0.00817
ENSG00000064300		NGFR	17	47572655	47592379	31	6	466064	2.6302	0.00427
ENSG00000064787		BCAS1	20	52553316	52687304	447	22	466064	2.2367	0.01265
ENSG00000065268		WDR18	19	983174	994569	68	8	466064	1.8222	0.03421
ENSG00000065534		MYLK	3	1.23E+08	1.24E+08	672	47	466064	2.4787	0.00659
ENSG00000065621		GSTO2	10	1.06E+08	1.06E+08	90	9	466064	2.8029	0.00253
ENSG00000065911		MTHFD2	2	74425689	74444692	18	5	466064	1.8928	0.02919
ENSG00000066044		ELAVL1	19	8023463	8070543	199	32	466064	2.6638	0.00386
ENSG00000067113		PPAP2A	5	54720682	54830878	389	30	466064	2.3985	0.00823
ENSG00000067798		NAV3	12	78224685	78606790	999	83	466064	1.8471	0.03237
ENSG00000067955		CBFB	16	67063019	67134961	72	9	466064	1.9178	0.02757
ENSG00000068001		HYAL2	3	50355221	50360337	5	3	466064	1.8765	0.03029
ENSG00000068912		ERLEC1	2	54014181	54045956	81	12	466064	1.9639	0.02477
ENSG00000069424		KCNAB2	1	6051526	6161253	349	41	466064	2.1743	0.01484
ENSG00000069696		DRD4	11	637293	640706	7	3	466064	2.3066	0.01054
ENSG00000069812		HES2	1	6472478	6484730	19	5	466064	2.1799	0.01463
ENSG00000070729		CNGB1	16	57917503	58005020	245	42	466064	1.9602	0.02499
ENSG00000070770		CSNK2A2	16	58191811	58231824	162	15	466064	2.8492	0.00219
ENSG00000071242		RPS6KA2	6	1.67E+08	1.67E+08	2101	85	466064	1.8813	0.02997
ENSG00000071243		ING3	7	1.21E+08	1.21E+08	64	8	466064	1.8816	0.02994
ENSG00000071539		TRIP13	5	892758	919472	63	5	466064	1.6517	0.04929
ENSG00000071564		TCF3	19	1609291	1652604	95	22	466064	2.197	0.01401
ENSG00000072121		ZFYVE26	14	68194091	68283307	141	13	466064	1.825	0.034
ENSG00000072657		TRHDE	12	72481046	73059422	1826	58	466064	1.8993	0.02877
ENSG00000072736		NFATC3	16	68118654	68263162	222	13	466064	1.9033	0.0285
ENSG00000072786		STK10	5	1.71E+08	1.72E+08	473	65	466064	2.3037	0.01062
ENSG00000073067		CYP2W1	7	1022835	1029276	41	12	466064	1.6589	0.04857
ENSG00000073578		SDHA	5	218356	256815	275	5	466064	2.3399	0.00964
ENSG00000075043		KCNQ2	20	62037542	62103993	189	26	466064	1.8289	0.0337
ENSG00000075303		SLC25A40	7	87462883	87505672	124	11	466064	1.856	0.03173
ENSG00000076928		ARHGEF1	19	42387228	42434302	32	8	466064	2.6224	0.00437
ENSG00000076984		MAP2K7	19	7968728	7979363	26	7	466064	2.9427	0.00163

ENSG00000077157	PPP1R12B	1	2.02E+08	2.03E+08	347	19	466064	1.8348	0.03327
ENSG00000077380	DYNC112	2	1.73E+08	1.73E+08	190	17	466064	1.6556	0.0489
ENSG00000078328	RBFOX1	16	6069095	7763340	10284	455	466064	2.1759	0.01478
ENSG00000078369	GNB1	1	1716729	1822495	229	23	466064	2.2557	0.01204
ENSG00000078401	EDN1	6	12290596	12297427	25	8	466064	1.8861	0.02964
ENSG00000078795	PKD2L2	5	1.37E+08	1.37E+08	152	18	466064	1.9352	0.02648
ENSG00000078967	UBE2D4	7	43966037	43995735	70	13	466064	2.3082	0.01049
ENSG00000079101	CLUL1	18	596988	650334	185	37	466064	2.1897	0.01427
ENSG00000079689	SCGN	6	25652464	25702011	155	24	466064	2.425	0.00765
ENSG00000080200	CRYBG3	3	97595819	97663810	108	20	466064	1.7927	0.03651
ENSG00000080293	SCTR	2	1.2E+08	1.2E+08	225	16	466064	2.1526	0.01567
ENSG00000080644	CHRNA3	15	78885394	78913637	75	5	466064	1.6979	0.04476
ENSG00000081026	MAGI3	1	1.14E+08	1.14E+08	918	100	466064	2.0496	0.0202
ENSG00000081853	PCDHGA2	5	1.41E+08	1.41E+08	340	15	466064	1.7946	0.03636
ENSG00000082212	ME2	18	48405419	48474691	160	21	466064	1.9844	0.0236
ENSG00000082213	C5orf22	5	31532373	31555165	71	15	466064	1.7146	0.04321
ENSG00000083168	KAT6A	8	41786997	41909508	264	40	466064	1.8231	0.03414
ENSG00000084073	ZMPSTE24	1	40723779	40759856	88	11	466064	2.2361	0.01267
ENSG00000085365	SCAMP1	5	77656339	77776562	418	22	466064	2.0504	0.02016
ENSG00000086504	MRPL28	16	417384	420527	10	3	466064	2.0985	0.01793
ENSG00000086666	ZFAND6	15	80351910	80430735	360	30	466064	2.076	0.01895
ENSG00000087116	ADAMTS2	5	1.79E+08	1.79E+08	841	60	466064	2.0306	0.02115
ENSG00000087237	CETP	16	56995762	57017757	76	20	466064	1.6913	0.04539
ENSG00000088812	ATRN	20	3451687	3631769	458	19	466064	1.9998	0.02276
ENSG00000089101	C20orf26	20	20033158	20341346	979	59	466064	2.1739	0.01486
ENSG00000089169	RPH3A	12	1.13E+08	1.13E+08	919	46	466064	1.7353	0.04135
ENSG00000089486	CDIP1	16	4560676	4588829	53	10	466064	3.2521	0.00057
ENSG00000089847	ANKRD24	19	4183351	4224811	185	28	466064	1.7404	0.0409
ENSG00000090273	NUDC	1	27226729	27273353	68	11	466064	1.9194	0.02747
ENSG00000091164	TXNL1	18	54264439	54318831	175	12	466064	2.5831	0.0049
ENSG00000091317	CMTM6	3	32522804	32544900	39	10	466064	1.8442	0.03258
ENSG00000091704	CPA1	7	1.3E+08	1.3E+08	24	3	466064	2.6767	0.00372
ENSG00000092208	GEMIN2	14	39583427	39606177	60	10	466064	1.7657	0.03872
ENSG00000092531	SNAP23	15	42783431	42837547	57	14	466064	1.9566	0.0252
ENSG00000095713	CRTAC1	10	99624757	99790585	328	18	466064	1.733	0.04155
ENSG00000095794	CREM	10	35415719	35501886	111	15	466064	1.9862	0.02351
ENSG00000096384	HSP90AB1	6	44214824	44221620	18	5	466064	2.9422	0.00163
ENSG00000097021	ACOT7	1	6324329	6454451	430	23	466064	1.7144	0.04323
ENSG00000100129	EIF3L	22	38244875	38285414	122	19	466064	1.7667	0.03864
ENSG00000100284	TOM1	22	35695268	35743985	221	18	466064	1.8397	0.03291
ENSG00000100320	RBFOX2	22	36134783	36424473	1268	89	466064	2.3397	0.00965
ENSG00000100359	SGSM3	22	40766595	40806293	46	5	466064	1.7449	0.0405
ENSG00000100362	PVALB	22	37196728	37215523	60	11	466064	1.6942	0.04512
ENSG00000100372	SLC25A17	22	41165634	41215403	110	9	466064	1.7034	0.04425
ENSG00000100380	ST13	22	41220539	41253026	57	9	466064	2.1262	0.01674
ENSG00000100412	ACO2	22	41865129	41924993	120	12	466064	1.822	0.03423
ENSG00000100554	ATP6V1D	14	67761088	67826982	167	12	466064	1.7588	0.0393
ENSG00000100596	SPTLC2	14	77972340	78083116	355	28	466064	1.8303	0.0336
ENSG00000100813	ACIN1	14	23527773	23564823	54	16	466064	1.6828	0.04621
ENSG00000101004	NINL	20	25433341	25566153	302	18	466064	1.6745	0.04702
ENSG00000101084	C20orf24	20	35234137	35240960	4	2	466064	1.6875	0.04576
ENSG00000101132	PFDN4	20	52824386	52844591	38	9	466064	2.3912	0.0084
ENSG00000101150	TPD5L2	20	62496596	62522898	52	9	466064	1.8876	0.02954
ENSG00000101152	DNAJC5	20	62526518	62567384	123	16	466064	2.2339	0.01274
ENSG00000101162	TUBB1	20	57594309	57601709	26	6	466064	2.1133	0.01729
ENSG00000102452	NALCN	13	1.02E+08	1.02E+08	979	69	466064	2.1782	0.01469
ENSG00000102755	FLT1	13	28874489	29069265	587	45	466064	1.8688	0.03083
ENSG00000102871	TRADD	16	67188083	67194201	6	2	466064	1.8552	0.03178
ENSG00000102878	HSF4	16	67197288	67203848	12	3	466064	2.1166	0.01715
ENSG00000102981	PAR6A	16	67694849	67696681	2	1	466064	2.3032	0.01063
ENSG00000102996	MMP15	16	58059470	58080805	74	6	466064	1.957	0.02517
ENSG00000103089	FA2H	16	74746853	74808729	218	27	466064	1.6901	0.04551
ENSG00000103248	MTHFSD	16	86563782	86588841	95	15	466064	1.6904	0.04548
ENSG00000103260	METRNL	16	765115	769655	21	5	466064	1.8618	0.03132
ENSG00000103335	PIEZO1	16	88781751	88851619	372	28	466064	1.6499	0.04948
ENSG00000103381	CPPED1	16	12756919	12897874	615	42	466064	1.7629	0.03896
ENSG00000103415	HMOX2	16	4524691	4560348	92	11	466064	3.7782	7.90E-05
ENSG00000103423	DNAJA3	16	4475806	4506776	93	8	466064	3.9444	4.00E-05
ENSG00000103426	CORO7-PAM16	16	4390252	4470495	195	18	466064	2.5484	0.00541
ENSG00000103449	SALL1	16	51169886	51185278	22	7	466064	2.9896	0.0014
ENSG00000103495	MAZ	16	29817427	29823649	10	2	466064	1.9404	0.02617
ENSG00000104064	GABPB1	15	50569389	50647605	207	17	466064	1.6553	0.04893
ENSG00000104140	RHOV	15	41164412	41166487	8	2	466064	1.689	0.04561

ENSG00000104313	EYA1	8	72109668	72274467	601	34	466064	2.0744	0.01902
ENSG00000104450	SPAG1	8	1.01E+08	1.01E+08	240	28	466064	2.038	0.02078
ENSG00000104613	INTS10	8	19674651	19709594	182	26	466064	1.9361	0.02643
ENSG00000104626	ERI1	8	8859657	8974256	555	43	466064	2.5779	0.00497
ENSG00000104731	KLHDC4	16	87730091	87799598	260	24	466064	1.773	0.03811
ENSG00000104755	ADAM2	8	39601254	39695808	161	20	466064	2.3887	0.00845
ENSG00000104921	FCER2	19	7753644	7767032	48	9	466064	2.0119	0.02211
ENSG00000104938	CLEC4M	19	7828035	7834491	16	6	466064	2.5734	0.00504
ENSG00000104976	SNAPC2	19	7985201	7988135	4	2	466064	1.7353	0.04134
ENSG00000104979	C19orf53	19	13884982	13889276	22	3	466064	1.7129	0.04336
ENSG00000105131	EPHX3	19	15337730	15344246	8	4	466064	1.7161	0.04307
ENSG00000105278	ZFR2	19	3804022	3869030	221	28	466064	1.7169	0.043
ENSG00000105369	CD79A	19	42381190	42385439	11	1	466064	2.7413	0.00306
ENSG00000105372	RPS19	19	42363988	42376994	12	3	466064	2.7402	0.00307
ENSG00000105404	RABAC1	19	42460833	42463542	1	1	466064	1.8453	0.0325
ENSG00000105409	ATP1A3	19	42470734	42501649	23	6	466064	1.9809	0.0238
ENSG00000105426	PTPRS	19	5158506	5340814	638	82	466064	1.9969	0.02292
ENSG00000105507	CABP5	19	48533210	48547310	50	9	466064	1.7639	0.03887
ENSG00000105609	LILRB5	19	54754263	54761164	15	6	466064	3.0513	0.00114
ENSG00000105737	GRIK5	19	42502473	42573650	60	8	466064	1.7112	0.04353
ENSG00000105784	RUNDC3B	7	87256864	87461611	484	36	466064	1.919	0.0275
ENSG00000105793	GTPBP10	7	89964537	90020769	314	20	466064	1.8378	0.03305
ENSG00000106066	CPVL	7	29034847	29235067	673	78	466064	2.8523	0.00217
ENSG00000106069	CHN2	7	29161890	29553944	1353	106	466064	1.9679	0.02454
ENSG00000106100	NOD1	7	30464143	30518400	164	24	466064	1.914	0.02781
ENSG00000106436	MYL10	7	1.01E+08	1.01E+08	96	3	466064	2.3042	0.01061
ENSG00000106477	CEP41	7	1.3E+08	1.3E+08	92	19	466064	2.2814	0.01126
ENSG00000106538	RARRS2	7	1.5E+08	1.5E+08	2	1	466064	1.6911	0.04541
ENSG00000106608	URGCP	7	43915493	43966010	143	18	466064	2.3472	0.00946
ENSG00000106633	GCK	7	44183872	44237769	153	20	466064	2.0873	0.01843
ENSG00000106948	AKNA	9	1.17E+08	1.17E+08	201	33	466064	1.9553	0.02527
ENSG00000107185	RGP1	9	35749203	35758572	15	5	466064	1.7474	0.04029
ENSG00000107521	HPS1	10	1E+08	1E+08	65	10	466064	1.8056	0.03549
ENSG00000107731	UNC5B	10	72972327	73062621	143	10	466064	1.677	0.04677
ENSG00000107779	BMPR1A	10	88516407	88692595	305	31	466064	2.4819	0.00653
ENSG00000107890	ANKRD26	10	27280843	27389421	455	37	466064	2.2696	0.01162
ENSG00000107984	DKK1	10	54074056	54077802	13	4	466064	2.1874	0.01436
ENSG00000108094	CUL2	10	35297479	35379570	86	12	466064	1.9129	0.02788
ENSG00000108306	FBXL20	17	37415384	37558776	318	22	466064	2.1929	0.01416
ENSG00000108352	RAPGEFL1	17	38333263	38351908	38	9	466064	1.658	0.04866
ENSG00000108379	WNT3	17	44839872	44910520	200	20	466064	1.8551	0.03179
ENSG00000108384	RAD51C	17	56769934	56811703	122	12	466064	2.953	0.00157
ENSG00000108511	HOXB6	17	46671639	46682354	2	1	466064	1.875	0.0304
ENSG00000108798	ABI3	17	47287589	47300587	42	10	466064	2.2082	0.01361
ENSG00000109132	PHOX2B	4	41746099	41750987	7	2	466064	1.7208	0.04264
ENSG00000109184	DCUN1D4	4	52709166	52783003	155	15	466064	2.3481	0.00944
ENSG00000109189	USP46	4	53457138	53525502	198	20	466064	2.3663	0.00898
ENSG00000109220	CHIC2	4	54875956	54930857	119	16	466064	1.6832	0.04617
ENSG00000109445	ZNF330	4	1.42E+08	1.42E+08	33	6	466064	1.6478	0.04969
ENSG00000109586	GALNT7	4	1.74E+08	1.74E+08	482	69	466064	2.9455	0.00161
ENSG00000109680	TBC1D19	4	26578059	26756973	216	13	466064	2.1671	0.01511
ENSG00000109787	KLF3	4	38665817	38702663	98	22	466064	1.6546	0.04901
ENSG00000110169	HPX	11	6452279	6463847	25	8	466064	1.9502	0.02557
ENSG00000110400	PVRL1	11	1.19E+08	1.2E+08	313	17	466064	2.6512	0.00401
ENSG00000110422	HIPK3	11	33278218	33378569	213	29	466064	1.9653	0.02469
ENSG00000111262	KCNA1	12	5019071	5040527	85	16	466064	1.799	0.03601
ENSG00000111321	LTBR	12	6484211	6500733	73	5	466064	1.7146	0.04321
ENSG00000111339	ART4	12	14978503	14996429	79	10	466064	1.9907	0.02326
ENSG00000111450	STX2	12	1.31E+08	1.31E+08	177	23	466064	1.9769	0.02402
ENSG00000111731	C2CD5	12	22601517	22697480	167	16	466064	1.9962	0.02296
ENSG00000111860	CEP85L	6	1.19E+08	1.19E+08	779	27	466064	2.1388	0.01623
ENSG00000112029	FBXO5	6	1.53E+08	1.53E+08	74	8	466064	2.1415	0.01612
ENSG00000112033	PPARD	6	35310335	35395968	173	18	466064	1.7005	0.04452
ENSG00000112096	SOD2	6	1.6E+08	1.6E+08	236	42	466064	2.2064	0.01368
ENSG00000112200	ZNF451	6	56951642	57035105	155	10	466064	2.1554	0.01557
ENSG00000112208	BAG2	6	57037124	57054631	24	6	466064	2.4651	0.00685
ENSG00000112210	RAB23	6	57053607	57087078	38	8	466064	2.1441	0.01601
ENSG00000112234	FBXL4	6	99316420	99395849	251	23	466064	2.3382	0.00969
ENSG00000112294	ALDH5A1	6	24495080	24537435	168	23	466064	1.6941	0.04513
ENSG00000112378	PERP	6	1.38E+08	1.38E+08	45	11	466064	1.9864	0.0235
ENSG00000112511	PHF1	6	33378176	33384230	14	6	466064	2.3802	0.00865
ENSG00000112706	IMPG1	6	76630832	76782395	525	41	466064	1.9041	0.02845
ENSG00000112759	SLC29A1	6	44187242	44201888	38	11	466064	1.6454	0.04994

ENSG00000112964	GHR	5	42423879	42721979	580	32	466064	1.6672	0.04774
ENSG00000112984	KIF20A	5	1.38E+08	1.38E+08	11	4	466064	1.8229	0.03416
ENSG00000113161	HMGCR	5	74632154	74657929	88	15	466064	1.9267	0.02701
ENSG00000113391	FAM172A	5	92953775	93447404	939	56	466064	2.4479	0.00718
ENSG00000113552	GNPDA1	5	1.41E+08	1.41E+08	51	9	466064	2.5203	0.00586
ENSG00000113658	SMAD5	5	1.35E+08	1.36E+08	154	24	466064	2.0814	0.0187
ENSG00000113966	ARL6	3	97483365	97519953	30	11	466064	2.3049	0.01059
ENSG00000114125	RNF7	3	1.41E+08	1.41E+08	25	4	466064	2.5755	0.005
ENSG00000114383	TUSC2	3	50357458	50365682	11	5	466064	1.6803	0.04645
ENSG00000114439	BBX	3	1.07E+08	1.08E+08	804	51	466064	2.2666	0.01171
ENSG00000114450	GNB4	3	1.79E+08	1.79E+08	120	18	466064	2.0852	0.01853
ENSG00000114767	RRP9	3	51967446	51975957	4	2	466064	2.3389	0.00967
ENSG00000114933	INO80D	2	2.07E+08	2.07E+08	313	23	466064	2.9725	0.00148
ENSG00000114982	KANSL3	2	97258907	97308524	2	1	466064	2.4116	0.00794
ENSG00000115073	ACTR1B	2	98272431	98280570	44	5	466064	1.9106	0.02803
ENSG00000115085	ZAP70	2	98330023	98356325	84	15	466064	2.0224	0.02157
ENSG00000115163	CENPA	2	26987157	27023935	43	5	466064	2.7816	0.0027
ENSG00000115165	CYTIP	2	1.58E+08	1.58E+08	328	26	466064	1.9431	0.026
ENSG00000115239	GPR75-ASB3	2	53759810	54087170	891	29	466064	1.7855	0.03709
ENSG00000115274	INO80B	2	74682150	74688011	9	2	466064	2.4702	0.00675
ENSG00000115275	MOGS	2	74688184	74692537	10	2	466064	2.4481	0.00718
ENSG00000115282	TTC31	2	74710200	74722013	14	3	466064	2.719	0.00327
ENSG00000115289	PCGF1	2	74732170	74735707	5	2	466064	2.9306	0.00169
ENSG00000115318	LOXL3	2	74759541	74782817	78	8	466064	1.8278	0.03379
ENSG00000115325	DOK1	2	74776153	74784681	25	5	466064	1.9587	0.02507
ENSG00000115414	FN1	2	2.16E+08	2.16E+08	200	21	466064	1.8207	0.03433
ENSG00000115507	OTX1	2	63277192	63284971	16	2	466064	1.7528	0.03982
ENSG00000115514	TXNDC9	2	99935445	99957165	48	7	466064	1.9974	0.02289
ENSG00000115592	PRKAG3	2	2.2E+08	2.2E+08	27	5	466064	2.0358	0.02088
ENSG00000115593	SMYD1	2	88367299	88412906	128	17	466064	2.0353	0.02091
ENSG00000115594	IL1R1	2	1.03E+08	1.03E+08	295	25	466064	2.4851	0.00648
ENSG00000115598	IL1RL2	2	1.03E+08	1.03E+08	54	15	466064	1.6862	0.04588
ENSG00000115685	PPP1R7	2	2.42E+08	2.42E+08	79	7	466064	1.6991	0.04465
ENSG00000115738	ID2	2	8818975	8824583	6	3	466064	1.689	0.04561
ENSG00000116030	SUMO1	2	2.03E+08	2.03E+08	41	10	466064	2.1995	0.01392
ENSG00000116191	RALGPS2	1	1.79E+08	1.79E+08	440	29	466064	1.6689	0.04757
ENSG00000116194	ANGPTL1	1	1.79E+08	1.79E+08	50	9	466064	1.7972	0.03615
ENSG00000116237	ICMT	1	6281253	6296032	40	7	466064	1.9669	0.0246
ENSG00000116299	KIAA1324	1	1.1E+08	1.1E+08	191	34	466064	1.8462	0.03244
ENSG00000116688	MFN2	1	12040238	12073571	73	14	466064	1.7217	0.04256
ENSG00000116819	TFAP2E	1	36038971	36060929	12	4	466064	2.2084	0.01361
ENSG00000117000	RLF	1	40627045	40706593	195	23	466064	2.0362	0.02087
ENSG00000117122	MFAP2	1	17300997	17307330	54	5	466064	1.752	0.03989
ENSG00000117298	ECE1	1	21543740	21671997	509	52	466064	1.9573	0.02515
ENSG00000117505	DR1	1	93811445	93835055	84	9	466064	2.0917	0.01823
ENSG00000117616	C1orf63	1	25568728	25664704	94	19	466064	1.6847	0.04602
ENSG00000117640	MTRF1L	1	26145131	26159432	36	7	466064	1.7758	0.03788
ENSG00000117697	NSL1	1	2.13E+08	2.13E+08	231	33	466064	1.8826	0.02988
ENSG00000117859	OSBPL9	1	52042851	52254889	292	20	466064	1.8436	0.03262
ENSG00000118402	ELOVL4	6	80624529	80657297	141	19	466064	2.0356	0.0209
ENSG00000118473	SGIP1	1	66999066	67213982	694	42	466064	1.7939	0.03641
ENSG00000118491	ZC2HC1B	6	1.44E+08	1.44E+08	160	19	466064	2.6676	0.00382
ENSG00000118518	RNF146	6	1.28E+08	1.28E+08	57	7	466064	1.8386	0.03299
ENSG00000118816	CCNI	4	77968311	77997158	100	7	466064	2.8249	0.00236
ENSG00000118894	FAM86A	16	5134305	5147809	110	15	466064	2.2109	0.01352
ENSG00000118972	FGF23	12	4477393	4488894	23	5	466064	1.7548	0.03965
ENSG00000119139	TJP2	9	71736209	71870124	297	18	466064	1.8256	0.03395
ENSG00000119314	PTBP3	9	1.15E+08	1.15E+08	374	35	466064	2.2876	0.01108
ENSG00000119321	FKBP15	9	1.16E+08	1.16E+08	226	34	466064	1.8642	0.03115
ENSG00000119457	SLC46A2	9	1.16E+08	1.16E+08	39	11	466064	2.1241	0.01683
ENSG00000119487	MAPKAP1	9	1.28E+08	1.28E+08	571	42	466064	1.7534	0.03977
ENSG00000119535	CSF3R	1	36931644	36948879	51	14	466064	1.8396	0.03291
ENSG00000119640	ACYP1	14	75519924	75536186	41	8	466064	1.8271	0.03384
ENSG00000119729	RHOQ	2	46768945	46810260	194	27	466064	1.9733	0.02423
ENSG00000119771	KLHL29	2	23608088	23931481	1032	42	466064	1.7862	0.03704
ENSG00000119778	ATAD2B	2	23971534	24149984	540	25	466064	2.5596	0.00524
ENSG00000119943	PYROXD2	10	1E+08	1E+08	70	10	466064	2.0114	0.02214
ENSG00000120093	HOXB3	17	46626232	46682274	2	1	466064	1.875	0.0304
ENSG00000120235	IFNA6	9	21349834	21351377	5	2	466064	2.1227	0.01689
ENSG00000120329	SLC25A2	5	1.41E+08	1.41E+08	2	1	466064	1.7607	0.03914
ENSG00000120686	UFM1	13	38923986	38937140	49	12	466064	3.3129	0.00046
ENSG00000120708	TGFB1	5	1.35E+08	1.35E+08	47	9	466064	1.8	0.03593
ENSG00000120729	MYOT	5	1.37E+08	1.37E+08	62	8	466064	1.9192	0.02748

ENSG00000120798	NR2C1	12	95414005	95467479	262	15	466064	1.9671	0.02458
ENSG00000120889	TNFRSF10B	8	22877646	22926692	184	37	466064	3.3152	0.00046
ENSG00000120925	RNF170	8	42704780	42752433	211	8	466064	1.9054	0.02837
ENSG00000121067	SPOP	17	47676246	47755596	176	29	466064	3.0644	0.00109
ENSG00000121152	NCAPH	2	97001525	97039583	59	8	466064	2.3191	0.01019
ENSG00000121388	RP11-408E5.4	13	19756173	19761496	14	5	466064	2.0041	0.02253
ENSG00000121797	CCRL2	3	46448654	46454488	19	5	466064	1.876	0.03033
ENSG00000121807	CCR2	3	46395225	46402419	18	3	466064	2.325	0.01004
ENSG00000121900	TMEM54	1	33360195	33367039	17	5	466064	1.6967	0.04487
ENSG00000122223	CD244	1	1.61E+08	1.61E+08	77	7	466064	1.8228	0.03416
ENSG00000122304	PRM2	16	11369496	11370337	5	2	466064	2.0346	0.02095
ENSG00000122390	NAA60	16	3493611	3536963	96	15	466064	1.7456	0.04044
ENSG00000122420	PTGFR	1	78769568	79005434	924	37	466064	2.1568	0.01551
ENSG00000122435	TRMT13	1	1.01E+08	1.01E+08	54	6	466064	2.1781	0.0147
ENSG00000122565	CBX3	7	26240782	26252976	27	9	466064	1.8961	0.02898
ENSG00000122691	TWIST1	7	19060614	19157295	237	37	466064	1.6811	0.04637
ENSG00000122729	ACO1	9	32384618	32454767	180	29	466064	2.0435	0.0205
ENSG00000123094	RASSF8	12	26111962	26232825	367	30	466064	2.2259	0.01301
ENSG00000123104	ITPR2	12	26490342	26986131	1548	82	466064	1.6607	0.04839
ENSG00000123405	NFE2	12	54685895	54694905	35	8	466064	1.7958	0.03627
ENSG00000123407	HOXC12	12	54348618	54352740	2	1	466064	1.814	0.03484
ENSG00000123444	KBTBD4	11	47593749	47600567	9	6	466064	1.7053	0.04407
ENSG00000124067	SLC12A4	16	67977377	68003504	33	7	466064	2.2326	0.01279
ENSG00000124089	MC3R	20	54823788	54824871	4	2	466064	2.0399	0.02068
ENSG00000124092	CTCF	20	56071035	56100708	49	6	466064	1.9313	0.02672
ENSG00000124157	SEMG2	20	43849941	43853099	3	1	466064	1.6882	0.04569
ENSG00000124253	PCK1	20	56136136	56141513	15	5	466064	1.7491	0.04014
ENSG00000124299	PEPD	19	33877856	34012700	367	43	466064	2.0798	0.01877
ENSG00000124743	KLHL31	6	53512699	53530506	71	11	466064	2.1208	0.01697
ENSG00000124787	RPP40	6	4994966	5004297	48	9	466064	1.9201	0.02742
ENSG00000124788	ATXN1	6	16299343	16761722	1460	157	466064	2.1167	0.01714
ENSG00000124802	EEF1E1	6	8073593	8102811	85	13	466064	1.6557	0.04889
ENSG00000125149	C16orf70	16	67143861	67182442	32	10	466064	1.8853	0.0297
ENSG00000125820	NKX2-2	20	21491648	21494664	9	4	466064	2.9915	0.00139
ENSG00000125912	NCLN	19	3185561	3209573	97	9	466064	1.6731	0.04715
ENSG00000126249	PDCD2L	19	34895289	34917073	45	6	466064	1.7544	0.03968
ENSG00000126261	UBA2	19	34919257	34960853	137	8	466064	2.0142	0.02199
ENSG00000126603	GLIS2	16	4364762	4389598	63	11	466064	2.4223	0.00771
ENSG00000126934	MAP2K2	19	4090319	4124126	89	17	466064	1.7814	0.03742
ENSG00000127334	DYRK2	12	68042118	68059186	51	13	466064	2.0469	0.02034
ENSG00000127418	FGFRL1	4	1003724	1020685	62	14	466064	1.9054	0.02837
ENSG00000127423	AUNIP	1	26158414	26185903	81	12	466064	2.0505	0.02016
ENSG00000127527	EPS15L1	19	16466050	16582896	264	23	466064	2.6992	0.00348
ENSG00000127528	KLF2	19	16435628	16438685	5	3	466064	1.8999	0.02872
ENSG00000127774	EMC6	17	3572109	3572962	8	4	466064	1.842	0.03274
ENSG00000128284	APOL3	22	36536372	36562225	84	17	466064	2.4409	0.00732
ENSG00000128536	CDHR3	7	1.06E+08	1.06E+08	425	49	466064	2.0102	0.02221
ENSG00000128610	FEZF1	7	1.22E+08	1.22E+08	23	6	466064	1.6918	0.04534
ENSG00000128881	TTBK2	15	43030932	43213007	177	25	466064	1.8949	0.02905
ENSG00000129292	PHF20L1	8	1.34E+08	1.34E+08	336	42	466064	1.7578	0.03939
ENSG00000129450	SIGLEC9	19	51628165	51639908	5	2	466064	1.8985	0.02881
ENSG00000129465	RIPK3	14	24805227	24809251	14	5	466064	1.9186	0.02752
ENSG00000129480	DTD2	14	31915242	31926716	50	10	466064	1.7677	0.03855
ENSG00000130508	PXDN	2	1635659	1748624	402	47	466064	1.8151	0.03475
ENSG00000130684	ZNF337	20	25654851	25677477	43	9	466064	2.1125	0.01732
ENSG00000130695	CEP85	1	26560691	26605299	93	17	466064	1.7922	0.03655
ENSG00000131236	CAP1	1	40505905	40538321	106	12	466064	2.1498	0.01579
ENSG00000131238	PPT1	1	40538379	40563375	113	10	466064	1.7048	0.04411
ENSG00000131370	SH3BP5	3	15296360	15382875	252	30	466064	2.5393	0.00555
ENSG00000131504	DIAPH1	5	1.41E+08	1.41E+08	243	17	466064	2.3647	0.00902
ENSG00000131591	C1orf159	1	1017198	1051741	96	11	466064	1.8628	0.03124
ENSG00000132130	LHX1	17	35294084	35301917	24	4	466064	3.0202	0.00126
ENSG00000132321	IQCA1	2	2.37E+08	2.37E+08	509	47	466064	2.4916	0.00636
ENSG00000132846	ZBED3	5	76367897	76383148	43	7	466064	1.7055	0.04405
ENSG00000133226	SRRM1	1	24958207	24999758	147	17	466064	1.7252	0.04224
ENSG00000133488	SEC14L4	22	30884900	30901698	36	8	466064	1.8235	0.03411
ENSG00000133706	LARS	5	1.45E+08	1.46E+08	150	14	466064	1.8485	0.03226
ENSG00000133789	SWAP70	11	9685624	9774538	313	15	466064	2.2995	0.01074
ENSG00000133835	HSD17B4	5	1.19E+08	1.19E+08	398	31	466064	2.5609	0.00522
ENSG00000134278	SPIRE1	18	12446511	12658133	602	32	466064	2.5455	0.00546
ENSG00000134460	IL2RA	10	6052652	6104288	193	35	466064	1.6834	0.04615
ENSG00000135048	TMEM2	9	74298282	74431606	417	42	466064	1.807	0.03538
ENSG00000135063	FAM189A2	9	71939488	72007371	133	27	466064	2.35	0.00939

ENSG00000135144	DTX1	12	1.13E+08	1.14E+08	120	29	466064	1.886	0.02965
ENSG00000135299	ANKRD6	6	90142889	90343553	415	35	466064	1.8519	0.03202
ENSG00000135636	DYSF	2	71680852	71913898	597	57	466064	1.8607	0.0314
ENSG00000135637	CCDC142	2	74699113	74710535	42	2	466064	2.372	0.00885
ENSG00000135722	FBXL8	16	67193834	67198473	8	3	466064	1.9646	0.02473
ENSG00000135740	SLC9A5	16	67271586	67306093	45	10	466064	1.7381	0.0411
ENSG00000135747	ZNF670	1	2.47E+08	2.47E+08	519	33	466064	1.7181	0.04289
ENSG00000135899	SP110	2	2.31E+08	2.31E+08	138	20	466064	1.7323	0.04161
ENSG00000135940	COX5B	2	98262503	98264846	7	3	466064	2.1041	0.01769
ENSG00000135951	TSGA10	2	99613724	99771427	421	25	466064	1.6485	0.04962
ENSG00000135976	ANKRD36	2	97779233	97930258	299	17	466064	1.9187	0.02751
ENSG00000136059	VILL	3	38029550	38048679	54	11	466064	2.4164	0.00784
ENSG00000136141	LRCH1	13	47127303	47327175	563	44	466064	1.7941	0.0364
ENSG00000136279	DBNL	7	44084239	44109055	65	13	466064	1.6583	0.04863
ENSG00000136425	CIB2	15	78396948	78423886	56	14	466064	2.0357	0.02089
ENSG00000136541	ERMN	2	1.58E+08	1.58E+08	18	9	466064	3.5562	0.00019
ENSG00000136542	GALNT5	2	1.58E+08	1.58E+08	174	19	466064	3.8604	5.66E-05
ENSG00000136574	GATA4	8	11534468	11617511	342	25	466064	1.8748	0.03041
ENSG00000136758	YME1L1	10	27399383	27444195	201	20	466064	1.9924	0.02317
ENSG00000136867	SLC31A2	9	1.16E+08	1.16E+08	47	12	466064	1.9528	0.02542
ENSG00000137103	TMEM8B	9	35814448	35854844	70	11	466064	1.8072	0.03536
ENSG00000137124	ALDH1B1	9	38392661	38398658	29	10	466064	2.3024	0.01066
ENSG00000137142	IGFBPL1	9	38408991	38424444	63	13	466064	1.9922	0.02318
ENSG00000137185	ZSCAN9	6	28192664	28201260	25	5	466064	1.8947	0.02907
ENSG00000137310	TCF19	6	31126319	31134936	73	12	466064	1.7291	0.0419
ENSG00000137338	PGBD1	6	28249314	28270326	50	13	466064	1.8691	0.0308
ENSG00000137343	ATAT1	6	30594619	30614600	74	7	466064	2.225	0.01304
ENSG00000137440	FGFBP1	4	15937192	15940363	7	2	466064	1.8532	0.03193
ENSG00000137727	ARHGAP20	11	1.1E+08	1.11E+08	385	24	466064	2.0662	0.0194
ENSG00000137878	GCOM1	5	57884106	58006943	425	26	466064	1.7482	0.04021
ENSG00000138018	EPT1	2	26531415	26618759	248	36	466064	2.3082	0.0105
ENSG00000138166	DUSP5	10	1.12E+08	1.12E+08	43	6	466064	2.0666	0.01939
ENSG00000138172	CALHM2	10	1.05E+08	1.05E+08	19	2	466064	2.8481	0.0022
ENSG00000138185	ENTPD1	10	97471536	97637023	367	37	466064	2.5698	0.00509
ENSG00000138443	ABI2	2	2.04E+08	2.04E+08	366	41	466064	2.5113	0.00601
ENSG00000138696	BMPR1B	4	95679119	96079599	1461	70	466064	3.1214	0.0009
ENSG00000138758	11-Sep	4	77870856	77961537	219	18	466064	2.4541	0.00706
ENSG00000138759	FRAS1	4	78978724	79465423	1119	70	466064	1.8321	0.03347
ENSG00000139190	VAMP1	12	6571403	6580153	14	4	466064	1.7	0.04457
ENSG00000139209	SLC38A4	12	47158546	47226191	219	29	466064	2.1112	0.01738
ENSG00000139233	LLPH	12	66516842	66524548	43	7	466064	2.3144	0.01032
ENSG00000139737	SLAIN1	13	78272023	78338377	146	13	466064	1.6653	0.04792
ENSG00000139826	ABHD13	13	1.09E+08	1.09E+08	43	9	466064	1.9127	0.02789
ENSG00000139874	SSTR1	14	38677204	38682272	33	3	466064	2.6533	0.00399
ENSG00000139988	RDH12	14	68168603	68201169	40	4	466064	1.6589	0.04857
ENSG00000140105	WARS	14	1.01E+08	1.01E+08	193	32	466064	2.208	0.01362
ENSG00000140107	SLC25A47	14	1.01E+08	1.01E+08	10	5	466064	2.4816	0.00654
ENSG00000140443	IGF1R	15	99192200	99507759	1082	67	466064	2.1756	0.01479
ENSG00000140937	CDH11	16	64977656	65160015	578	43	466064	1.9365	0.02641
ENSG00000140939	NOL3	16	67204057	67209643	13	3	466064	1.8162	0.03467
ENSG00000140945	CDH13	16	82660408	83830204	6558	320	466064	2.2868	0.0111
ENSG00000141096	DPEP3	16	68009566	68014732	9	2	466064	1.65	0.04947
ENSG00000141867	BRD4	19	15347647	15443356	142	15	466064	2.5558	0.0053
ENSG00000141977	CIB3	19	16272179	16284336	27	10	466064	2.161	0.01535
ENSG00000141985	SH3GL1	19	4360367	4400544	99	20	466064	1.805	0.03554
ENSG00000142025	DMRTC2	19	42348806	42356401	10	2	466064	2.6107	0.00452
ENSG00000142459	EVI5L	19	7895119	7929862	97	24	466064	2.6562	0.00395
ENSG00000142515	KLK3	19	51358171	51364020	30	4	466064	1.8058	0.03547
ENSG00000142609	C1orf222	1	1853396	1935276	163	17	466064	2.1708	0.01497
ENSG00000142751	GPN2	1	27202624	27216788	24	8	466064	1.8984	0.02882
ENSG00000142789	CELA3A	1	22328149	22339032	25	8	466064	2.6053	0.00459
ENSG00000142798	HSPG2	1	22148738	22263790	523	40	466064	2.4826	0.00652
ENSG00000143079	CTTNBP2NL	1	1.13E+08	1.13E+08	77	13	466064	2.2272	0.01297
ENSG00000143162	CREG1	1	1.67E+08	1.68E+08	80	22	466064	2.0203	0.02168
ENSG00000143199	ADCY10	1	1.68E+08	1.68E+08	391	52	466064	1.7635	0.03891
ENSG00000143340	FAM163A	1	1.8E+08	1.8E+08	289	21	466064	2.2885	0.01105
ENSG00000143365	RORC	1	1.52E+08	1.52E+08	56	6	466064	2.0503	0.02017
ENSG00000143753	DEGS1	1	2.24E+08	2.24E+08	25	4	466064	1.7682	0.03852
ENSG00000143889	HNRNPPLL	2	38789120	38830728	75	6	466064	1.8032	0.03568
ENSG00000143891	GALM	2	38893052	38968379	141	23	466064	1.818	0.03453
ENSG00000143942	CHAC2	2	53994929	54002333	16	4	466064	1.9458	0.02584
ENSG00000144015	TRIM43	2	96257766	96265526	7	4	466064	1.8795	0.03009
ENSG00000144119	C1QL2	2	1.2E+08	1.2E+08	4	2	466064	1.8106	0.0351

ENSG00000144290	SLC4A10	2	1.62E+08	1.63E+08	1041	62	466064	2.3467	0.00947
ENSG00000144524	COPSTB	2	2.33E+08	2.33E+08	71	17	466064	1.9138	0.02782
ENSG00000144635	DYNC1LI1	3	32567463	32612366	175	22	466064	1.9654	0.02469
ENSG00000144677	CTDSPL	3	37903451	38025960	300	29	466064	1.7665	0.03866
ENSG00000144736	SHQ1	3	72798428	72911065	186	12	466064	2.9453	0.00161
ENSG00000144962	SPATA16	3	1.73E+08	1.73E+08	678	52	466064	1.6936	0.04517
ENSG00000145198	VWA5B2	3	1.84E+08	1.84E+08	22	6	466064	1.8466	0.0324
ENSG00000145244	CORIN	4	47596015	47840123	597	31	466064	2.2027	0.01381
ENSG00000145703	IQGAP2	5	75699074	76003957	957	45	466064	2.3094	0.01046
ENSG00000145833	DDX46	5	1.34E+08	1.34E+08	191	19	466064	1.8155	0.03473
ENSG00000145979	TBC1D7	6	13266774	13328815	291	15	466064	1.8534	0.03191
ENSG00000146083	RNF44	5	1.76E+08	1.76E+08	2	1	466064	2.5246	0.00579
ENSG00000146112	PPP1R18	6	30644166	30655672	18	7	466064	2.5962	0.00471
ENSG00000146122	DAAM2	6	39760142	39872648	377	46	466064	1.7613	0.0391
ENSG00000146221	TCTE1	6	44246480	44265458	53	16	466064	2.3814	0.00862
ENSG00000146376	ARHGAP18	6	1.3E+08	1.3E+08	350	45	466064	2.2949	0.01087
ENSG00000146535	GNA12	7	2767746	2883958	485	25	466064	1.8008	0.03587
ENSG00000146670	CDCA5	11	64833772	64851636	30	6	466064	1.7769	0.0378
ENSG00000147324	MFHAS1	8	8640864	8751155	630	34	466064	2.1815	0.01457
ENSG00000147548	WHSC1L1	8	38127215	38239790	143	17	466064	1.6855	0.04594
ENSG00000147669	POLR2K	8	1.01E+08	1.01E+08	15	5	466064	1.8044	0.03558
ENSG00000147677	EIF3H	8	1.18E+08	1.18E+08	302	33	466064	1.7848	0.03715
ENSG00000147679	UTP23	8	1.18E+08	1.18E+08	251	28	466064	2.2763	0.01141
ENSG00000148057	IDNK	9	86237964	86259045	36	5	466064	1.7701	0.03836
ENSG00000148110	HIATL1	9	97136833	97223324	221	20	466064	2.2064	0.01368
ENSG00000148154	UGCG	9	1.15E+08	1.15E+08	178	23	466064	1.8257	0.03395
ENSG00000148356	LRSAM1	9	1.3E+08	1.3E+08	155	34	466064	2.1143	0.01725
ENSG00000148671	ADIRF	10	88727949	88743691	89	7	466064	2.3416	0.0096
ENSG00000148798	INA	10	1.05E+08	1.05E+08	24	5	466064	1.8383	0.03301
ENSG00000148834	GSTO1	10	1.06E+08	1.06E+08	97	19	466064	2.3573	0.00921
ENSG00000148835	TAF5	10	1.05E+08	1.05E+08	97	7	466064	1.8505	0.03212
ENSG00000148841	ITPRIP	10	1.06E+08	1.06E+08	47	10	466064	2.8392	0.00226
ENSG00000148843	PDCD11	10	1.05E+08	1.05E+08	142	14	466064	2.3908	0.00841
ENSG00000149043	SYT8	11	1848709	1858751	55	7	466064	2.096	0.01804
ENSG00000149124	GLYAT	11	58407899	58499447	276	13	466064	2.4391	0.00736
ENSG00000149488	TMC2	20	2517253	2622430	363	29	466064	1.7666	0.03865
ENSG00000149735	GPHA2	11	64701943	64703360	3	2	466064	1.727	0.04208
ENSG00000149809	TM7SF2	11	64879317	64883856	5	2	466064	2.0645	0.01948
ENSG00000150076	C10ORF68	10	32832297	33171802	1147	57	466064	1.7241	0.04234
ENSG00000151065	DCP1B	12	2055220	2113701	170	31	466064	1.7477	0.04026
ENSG00000151092	NGLY1	3	25760435	25831530	119	13	466064	1.6611	0.04834
ENSG00000151093	OXSM	3	25824408	25836025	25	4	466064	1.7464	0.04037
ENSG00000151276	MAG11	3	65339200	66024509	2272	152	466064	1.6582	0.04864
ENSG00000151338	MIPOL1	14	37667118	38021566	796	50	466064	1.6681	0.04765
ENSG00000151353	TMEM18	2	667335	677439	24	4	466064	2.3756	0.00876
ENSG00000151474	FRMD4A	10	13685706	14504141	3375	236	466064	3.2302	0.00062
ENSG00000151806	GUF1	4	44680444	44702943	41	5	466064	1.9068	0.02828
ENSG00000152192	POU4F1	13	79172497	79177673	14	3	466064	1.7101	0.04362
ENSG00000152193	RNF219	13	79188426	79233314	168	22	466064	2.2667	0.01117
ENSG00000152213	ARL11	13	50202435	50208008	9	3	466064	2.3256	0.01002
ENSG00000152422	XRCC4	5	82373317	82649606	770	35	466064	1.8066	0.03541
ENSG00000152583	SPARCL1	4	88394487	88452213	57	17	466064	1.8839	0.02979
ENSG00000152749	GPR180	13	95254157	95286899	170	26	466064	1.6651	0.04795
ENSG00000152894	PTPRK	6	1.28E+08	1.29E+08	1394	57	466064	1.9062	0.02831
ENSG00000153147	SMARCA5	4	1.44E+08	1.44E+08	78	12	466064	1.8797	0.03008
ENSG00000153253	SCN3A	2	1.66E+08	1.66E+08	266	17	466064	1.8461	0.03244
ENSG00000153406	NMRAL1	16	4511681	4545764	86	10	466064	3.4026	0.00033
ENSG00000153815	CMIP	16	81478775	81745367	1154	114	466064	1.7302	0.0418
ENSG00000153879	CEBPG	19	33864236	33873592	30	6	466064	1.8557	0.03175
ENSG00000153904	DDAH1	1	85784164	86043933	903	38	466064	2.4432	0.00728
ENSG00000153944	MSI2	17	55333212	55762046	1211	89	466064	3.0012	0.00134
ENSG00000154118	JPH3	16	87635441	87731762	518	48	466064	1.6828	0.04621
ENSG00000154328	NEIL2	8	11627148	11644855	87	20	466064	1.655	0.04896
ENSG00000154511	FAM69A	1	93307724	93427057	263	14	466064	1.6578	0.04868
ENSG00000155052	CNTNAP5	2	1.25E+08	1.26E+08	2368	44	466064	2.3957	0.00829
ENSG00000155363	MOV10	1	1.13E+08	1.13E+08	88	16	466064	2.2151	0.01338
ENSG00000155530	LRGUK	7	1.34E+08	1.34E+08	327	14	466064	1.7071	0.04391
ENSG00000155918	RAET1L	6	1.5E+08	1.5E+08	51	6	466064	1.7426	0.0407
ENSG00000155957	TMBIM4	12	66517709	66563852	186	22	466064	2.2392	0.01257
ENSG00000156136	DCK	4	71858255	71896631	175	15	466064	1.7774	0.03775
ENSG00000156374	PCGF6	10	1.05E+08	1.05E+08	196	20	466064	2.4686	0.00678
ENSG00000156384	SFR1	10	1.06E+08	1.06E+08	12	2	466064	2.6789	0.00369
ENSG00000156413	FUT6	19	5830621	5839742	36	8	466064	2.5818	0.00491

ENSG00000156463	SH3RF2	5	1.45E+08	1.45E+08	281	15	466064	2.5207	0.00586
ENSG00000156466	GDF6	8	97154562	97173020	33	10	466064	4.0661	2.39E-05
ENSG00000156603	MED19	11	57471186	57479693	5	3	466064	1.7658	0.03871
ENSG00000156875	HIAT1	1	1.01E+08	1.01E+08	83	13	466064	1.8643	0.03114
ENSG00000156973	PDE6D	2	2.33E+08	2.33E+08	155	19	466064	2.5888	0.00482
ENSG00000157014	TATDN2	3	10289707	10322902	93	14	466064	1.6715	0.04731
ENSG00000157450	RNF111	15	59157374	59389618	727	65	466064	1.6618	0.04828
ENSG00000157593	SLC35B2	6	44221833	44225291	5	2	466064	2.4092	0.00799
ENSG00000157823	AP3S2	15	90373831	90437574	204	17	466064	2.6304	0.00426
ENSG00000157851	DPYSL5	2	27070615	27173219	163	23	466064	2.1245	0.01682
ENSG00000157978	LDLRAP1	1	25870071	25895377	45	6	466064	1.7093	0.0437
ENSG00000158246	FAM46B	1	27331511	27339327	19	5	466064	2.024	0.02149
ENSG00000158402	CDC25C	5	1.38E+08	1.38E+08	132	14	466064	2.135	0.01638
ENSG00000158417	EIF5B	2	99953816	1E+08	115	11	466064	1.8768	0.03027
ENSG00000158816	VWA5B1	1	20617412	20681387	230	20	466064	1.7936	0.03644
ENSG00000158955	WNT9B	17	44910567	44964096	177	29	466064	2.5935	0.00475
ENSG00000159110	IFNAR2	21	34602206	34637980	99	17	466064	2.0537	0.02
ENSG00000159239	C2orf81	2	74641304	74648718	4	1	466064	2.1943	0.01411
ENSG00000159459	UBR1	15	43235095	43398311	281	13	466064	1.975	0.02414
ENSG00000159479	MED8	1	43849588	43855479	15	3	466064	1.9292	0.02685
ENSG00000159579	RSPRY1	16	57220049	57274387	118	16	466064	1.7068	0.04393
ENSG00000159899	NPR2	9	35792151	35809729	29	4	466064	1.8501	0.03215
ENSG00000160058	BSDC1	1	32830704	32860332	47	10	466064	1.8952	0.02904
ENSG00000160097	FINDC5	1	33327869	33338083	37	8	466064	1.8811	0.02998
ENSG00000160224	AIRE	21	45705721	45718531	23	6	466064	1.6785	0.04663
ENSG00000160256	FAM207A	21	46359925	46396904	143	21	466064	2.0955	0.01806
ENSG00000160401	C9orf117	9	1.3E+08	1.3E+08	19	6	466064	2.6553	0.00396
ENSG00000160404	TOR2A	9	1.3E+08	1.3E+08	6	3	466064	2.1982	0.01397
ENSG00000160460	SPTBN4	19	40972148	41082370	418	31	466064	2.3647	0.00902
ENSG00000160691	SHC1	1	1.55E+08	1.55E+08	35	6	466064	3.0175	0.00127
ENSG00000160712	IL6R	1	1.54E+08	1.54E+08	170	25	466064	1.8684	0.03086
ENSG00000161202	DVL3	3	1.84E+08	1.84E+08	61	8	466064	2.2908	0.01099
ENSG00000161203	AP2M1	3	1.84E+08	1.84E+08	34	8	466064	1.8297	0.03365
ENSG00000161204	ABCF3	3	1.84E+08	1.84E+08	34	8	466064	1.9199	0.02744
ENSG00000161277	THAP8	19	36525887	36545664	69	10	466064	1.649	0.04958
ENSG00000161328	LRRC56	11	537527	554916	110	18	466064	1.8541	0.03186
ENSG00000161509	GRIN2C	17	72838162	72857627	73	7	466064	1.9259	0.02706
ENSG00000161533	ACOX1	17	73937588	73975515	97	20	466064	2.1553	0.01557
ENSG00000161835	GRASP	12	52400724	52409673	33	7	466064	2.0871	0.01844
ENSG00000162078	ZG16B	16	2880170	2888967	34	8	466064	2.8801	0.00199
ENSG00000162144	CYB561A3	11	61116217	61129771	26	6	466064	1.6991	0.04465
ENSG00000162460	TMEM82	1	16068917	16074477	13	4	466064	2.4952	0.00629
ENSG00000162461	SLC25A34	1	16062900	16067891	24	3	466064	1.7319	0.04165
ENSG00000162496	DHRS3	1	12627939	12677737	137	13	466064	1.7519	0.0399
ENSG00000162526	TSSK3	1	32817122	32829913	17	5	466064	1.6757	0.0469
ENSG00000162607	USP1	1	62901968	62917475	20	5	466064	1.7347	0.04139
ENSG00000162618	ELTD1	1	79355449	79472403	404	16	466064	2.3659	0.00899
ENSG00000162851	TFB2M	1	2.47E+08	2.47E+08	129	13	466064	2.1892	0.01429
ENSG00000163064	EN1	2	1.2E+08	1.2E+08	7	2	466064	2.3712	0.00887
ENSG00000163126	ANKRD23	2	97490263	97523671	6	2	466064	2.451	0.00712
ENSG00000163145	C1QTNF7	4	15341442	15447790	296	18	466064	2.2843	0.01118
ENSG00000163281	GNPDA2	4	44684217	44728612	112	9	466064	1.9449	0.02589
ENSG00000163285	GABRG1	4	46037786	46126098	280	16	466064	2.519	0.00588
ENSG00000163344	PMVK	1	1.55E+08	1.55E+08	20	3	466064	3.0457	0.00116
ENSG00000163346	PBXIP1	1	1.55E+08	1.55E+08	17	5	466064	3.0217	0.00126
ENSG00000163586	FABP1	2	88422510	88427635	20	4	466064	1.8089	0.03523
ENSG00000163605	PPP4R2	3	73045936	73118350	191	20	466064	1.6951	0.04503
ENSG00000163754	GYG1	3	1.49E+08	1.49E+08	100	16	466064	2.6486	0.00404
ENSG00000163811	WDR43	2	29117509	29171088	140	18	466064	2.7635	0.00286
ENSG00000163817	SLC6A20	3	45796942	45838027	68	15	466064	2.1702	0.01499
ENSG00000163818	LZTFL1	3	45864808	45957534	235	25	466064	1.7335	0.0415
ENSG00000163820	FYCO1	3	45959396	46037316	244	18	466064	2.5609	0.00522
ENSG00000163823	CCR1	3	46243200	46249887	15	6	466064	2.5128	0.00599
ENSG00000163872	YEATS2	3	1.83E+08	1.84E+08	409	33	466064	1.8979	0.02886
ENSG00000163918	RFC4	3	1.87E+08	1.87E+08	42	13	466064	2.3302	0.0099
ENSG00000163933	RFT1	3	53122499	53164478	89	10	466064	1.7728	0.03813
ENSG00000163961	RNF168	3	1.96E+08	1.96E+08	170	24	466064	1.8133	0.03489
ENSG00000164035	EMCN	4	1.01E+08	1.02E+08	1410	66	466064	2.294	0.0109
ENSG00000164091	WDR82	3	52288437	52322036	51	7	466064	1.8273	0.03383
ENSG00000164134	NAA15	4	1.4E+08	1.4E+08	267	29	466064	1.9277	0.02694
ENSG00000164164	OTUD4	4	1.46E+08	1.46E+08	213	32	466064	1.6978	0.04477
ENSG00000164176	EDIL3	5	83236373	83680611	1035	80	466064	1.9792	0.0239
ENSG00000164241	C5orf63	5	1.26E+08	1.26E+08	64	12	466064	1.929	0.02686

ENSG00000164253	WDR41	5	76721795	76916436	475	36	466064	2.1801	0.01463
ENSG00000164366	CCDC127	5	196986	218330	95	12	466064	2.0734	0.01907
ENSG00000164708	PGAM2	7	44102326	44105186	8	3	466064	1.9834	0.02366
ENSG00000164776	PHKG1	7	56148440	56160689	41	8	466064	1.6613	0.04833
ENSG00000165006	UBAP1	9	34179003	34252521	148	14	466064	1.7055	0.04405
ENSG00000165046	LETM2	8	38243725	38267045	27	6	466064	1.827	0.03385
ENSG00000165071	TMEM71	8	1.34E+08	1.34E+08	272	17	466064	1.8953	0.02903
ENSG00000165185	KIAA1958	9	1.15E+08	1.15E+08	599	41	466064	1.9096	0.02809
ENSG00000165390	ANXA8	10	48255253	48279200	32	6	466064	1.8491	0.03222
ENSG00000165521	EML5	14	89078775	89259096	424	69	466064	1.9729	0.02425
ENSG00000165533	TTC8	14	89290497	89344335	173	20	466064	3.0118	0.0013
ENSG00000165678	GHITM	10	85899196	85913001	36	7	466064	1.8908	0.02933
ENSG00000165730	STOX1	10	70587298	70655188	228	21	466064	1.7589	0.03929
ENSG00000165929	TC2N	14	92246095	92333880	280	42	466064	2.936	0.00166
ENSG00000166165	CKB	14	1.04E+08	1.04E+08	13	5	466064	1.7883	0.03687
ENSG00000166246	C16orf71	16	4784273	4799397	45	8	466064	1.9735	0.02422
ENSG00000166257	SCN3B	11	1.23E+08	1.24E+08	88	17	466064	1.7191	0.0428
ENSG00000166278	C2	6	31865562	31913449	156	30	466064	2.7985	0.00257
ENSG00000166391	MOGAT2	11	75428864	75444003	38	10	466064	2.4997	0.00621
ENSG00000167094	TTC16	9	1.3E+08	1.3E+08	52	10	466064	2.7925	0.00261
ENSG00000167103	PIP5KL1	9	1.31E+08	1.31E+08	31	4	466064	1.7279	0.042
ENSG00000167110	GOLGA2	9	1.31E+08	1.31E+08	59	16	466064	1.8528	0.03196
ENSG00000167210	LOXHD1	18	44056935	44236996	417	27	466064	1.7015	0.04443
ENSG00000167261	DPEP2	16	68021297	68034489	11	3	466064	1.6858	0.04592
ENSG00000167264	DUS2	16	68021649	68113223	133	11	466064	1.7853	0.0371
ENSG00000167363	FN3K	17	80693451	80709073	77	10	466064	1.6686	0.0476
ENSG00000167371	PRRT2	16	29823177	29827201	3	1	466064	2.1262	0.01674
ENSG00000167613	LAIR1	19	54865362	54882165	146	12	466064	2.535	0.00562
ENSG00000167637	ZNF283	19	44331444	44353307	68	9	466064	1.9073	0.02824
ENSG00000167644	C19orf33	19	38794801	38795649	5	1	466064	2.1118	0.01735
ENSG00000167645	YIF1B	19	38795753	38807913	44	9	466064	1.8281	0.03377
ENSG00000167711	SERPINF2	17	1646130	1658562	28	4	466064	1.7233	0.04242
ENSG00000167858	TEKT1	17	6692452	6735080	152	35	466064	1.8035	0.03565
ENSG00000168028	RPSA	3	39448180	39454033	24	3	466064	1.8396	0.03292
ENSG00000168140	VASN	16	4421849	4433529	41	9	466064	2.085	0.01854
ENSG00000168216	LMBRD1	6	70385694	70507003	239	11	466064	1.807	0.03538
ENSG00000168394	TAP1	6	32812986	32821755	76	14	466064	1.8554	0.03177
ENSG00000168421	RHOH	4	40192673	40248587	173	29	466064	1.741	0.04084
ENSG00000168477	TNXB	6	32008931	32083111	124	29	466064	2.9959	0.00137
ENSG00000168564	CDKN2AIP	4	1.84E+08	1.84E+08	16	3	466064	2.3742	0.00879
ENSG00000168566	SNRNP48	6	7590432	7612200	54	8	466064	2.2621	0.01185
ENSG00000168575	LC20A2	8	42273993	42397069	210	18	466064	1.7515	0.03993
ENSG00000168615	ADAM9	8	38854388	38962663	268	42	466064	2.4913	0.00636
ENSG00000168754	FAM178B	2	97541620	97684175	233	10	466064	2.0246	0.02146
ENSG00000168785	TSPAN5	4	99391518	99579780	662	52	466064	1.7549	0.03964
ENSG00000168874	ATOH8	2	85978467	86015189	92	10	466064	2.1972	0.014
ENSG00000168903	BTNL3	5	1.8E+08	1.8E+08	98	15	466064	2.0613	0.01964
ENSG00000169230	PRELID1	5	1.77E+08	1.77E+08	11	7	466064	2.2356	0.01269
ENSG00000169429	IL8	4	74606223	74609433	18	5	466064	2.607	0.00457
ENSG00000169682	SPNS1	16	28985542	28995869	17	5	466064	1.8496	0.03219
ENSG00000170191	NANP	20	25593571	25604811	26	5	466064	1.8448	0.03253
ENSG00000170209	ANKK1	11	1.13E+08	1.13E+08	26	8	466064	2.5366	0.0056
ENSG00000170315	UBB	17	16284112	16286059	4	1	466064	1.8024	0.03574
ENSG00000170322	NFRKB	11	1.3E+08	1.3E+08	123	27	466064	2.1644	0.01522
ENSG00000170348	TMED10	14	75598173	75643334	94	20	466064	1.9262	0.02704
ENSG00000170684	ZNF296	19	45574758	45579846	14	3	466064	1.6485	0.04962
ENSG00000170803	OR2AG1	11	6806248	6807245	3	2	466064	2.4065	0.00805
ENSG00000170871	KIAA0232	4	6783102	6885897	151	24	466064	2.054	0.01999
ENSG00000170889	RPS9	19	54704610	54752862	153	31	466064	1.6641	0.04805
ENSG00000170956	CEACAM3	19	42300369	42315591	10	2	466064	2.1872	0.01437
ENSG00000171017	LRRRC8E	19	7953390	7966901	22	6	466064	2.2446	0.0124
ENSG00000171103	TRMT61B	2	29072687	29093167	40	8	466064	2.6087	0.00454
ENSG00000171119	NRTN	19	5823813	5828335	10	5	466064	1.9857	0.02353
ENSG00000171132	PRKCE	2	45878484	46415129	2012	177	466064	2.4145	0.00788
ENSG00000171303	KCNK3	2	26915619	26956288	81	5	466064	2.7768	0.00274
ENSG00000171345	KRT19	17	39679869	39684560	9	2	466064	2.1426	0.01607
ENSG00000171346	KRT15	17	39669995	39678781	41	2	466064	2.1007	0.01783
ENSG00000171368	TPPP	5	660883	693510	140	20	466064	2.0359	0.02088
ENSG00000171403	KRT9	17	39722096	39728310	4	1	466064	2.7049	0.00342
ENSG00000171475	WIPF2	17	38375556	38440388	179	28	466064	1.9793	0.02389
ENSG00000171481	OR1L3	9	1.25E+08	1.25E+08	2	1	466064	1.6569	0.04877
ENSG00000171763	SPATA5L1	15	45694529	45713617	99	8	466064	1.8659	0.03103
ENSG00000171843	MLLT3	9	20341663	20622542	505	53	466064	2.1087	0.01749

ENSG00000171940	ZNF217	20	52183604	52226446	125	18	466064	3.7623	8.42E-05
ENSG00000172081	MOB3A	19	2071037	2096672	64	16	466064	2.1139	0.01726
ENSG00000172175	MALT1	18	56338618	56417371	164	22	466064	1.7225	0.04249
ENSG00000172215	CXCR6	3	45982425	45989845	19	4	466064	1.6574	0.04872
ENSG00000172339	ALG14	1	95439963	95538501	231	30	466064	1.7555	0.03959
ENSG00000172379	ARNT2	15	80696692	80890278	586	65	466064	1.9767	0.02404
ENSG00000172404	DNAJB7	22	41255553	41258130	9	4	466064	2.306	0.01055
ENSG00000172478	C2orf54	2	2.42E+08	2.42E+08	30	7	466064	2.682	0.00366
ENSG00000172482	AGXT	2	2.42E+08	2.42E+08	61	8	466064	2.0887	0.01837
ENSG00000172530	BANP	16	87982850	88110924	487	29	466064	2.0815	0.01869
ENSG00000172673	THEMIS	6	1.28E+08	1.28E+08	395	22	466064	2.5482	0.00541
ENSG00000172775	FAM192A	16	57186378	57220028	69	11	466064	2.1619	0.01531
ENSG00000172824	CES4A	16	67022492	67043661	25	6	466064	1.7608	0.03913
ENSG00000172828	CES3	16	66995140	67009051	16	5	466064	1.7328	0.04157
ENSG00000172890	NADSYN1	11	71164155	71235153	206	35	466064	1.8764	0.0303
ENSG00000172893	DHCR7	11	71139239	71163914	113	11	466064	2.0433	0.02051
ENSG00000172936	MYD88	3	38179969	38184513	5	3	466064	2.1428	0.01607
ENSG00000172939	OXR1	3	38206580	38296979	163	14	466064	2.007	0.02238
ENSG00000172986	GXYLT2	3	72937224	73047289	379	21	466064	1.9604	0.02498
ENSG00000173064	HECTD4	12	1.13E+08	1.13E+08	418	37	466064	2.2091	0.01358
ENSG00000173166	RAPH1	2	2.04E+08	2.04E+08	381	45	466064	2.3315	0.00986
ENSG00000173261	PLAC8L1	5	1.45E+08	1.45E+08	42	6	466064	3.1211	0.0009
ENSG00000173267	SNCG	10	88718375	88723017	15	3	466064	2.3487	0.00942
ENSG00000173269	MMRN2	10	88695297	88729238	132	10	466064	2.3144	0.01032
ENSG00000173366	TLR9	3	52255097	52265206	17	4	466064	1.8368	0.03312
ENSG00000173404	INSM1	20	20348765	20351590	6	1	466064	3.1457	0.00083
ENSG00000173567	GPR113	2	26531041	26569685	113	15	466064	1.822	0.03423
ENSG00000173578	XCR1	3	46058516	46069234	54	8	466064	2.0051	0.02247
ENSG00000173673	HES3	1	6304252	6305638	7	3	466064	2.8304	0.00232
ENSG00000173801	JUP	17	39775692	39943183	402	13	466064	1.9391	0.02625
ENSG00000173848	NET1	10	5454514	5500426	162	21	466064	1.7054	0.04406
ENSG00000173862	RP11-89N17.1	7	33765593	33768068	9	3	466064	2.5051	0.00612
ENSG00000173915	USMG5	10	1.05E+08	1.05E+08	35	3	466064	2.2078	0.01363
ENSG00000173960	UBXN2A	2	24150155	24227779	238	21	466064	2.1088	0.01748
ENSG00000174405	LIG4	13	1.09E+08	1.09E+08	29	7	466064	2.0478	0.02029
ENSG00000174501	ANKRD36C	2	96514587	96657541	161	23	466064	1.976	0.02408
ENSG00000174695	TMEM167A	5	82348665	82373682	40	8	466064	1.6822	0.04626
ENSG00000174697	LEP	7	1.28E+08	1.28E+08	22	9	466064	2.2031	0.01379
ENSG00000174915	PTDSS2	11	448268	491393	128	15	466064	1.7401	0.04093
ENSG00000174945	AMZ1	7	2719156	2815134	437	23	466064	2.1482	0.01585
ENSG00000174990	CA5A	16	87921625	87970135	252	29	466064	1.9007	0.02867
ENSG00000175130	MARCKSL1	1	32799433	32801980	6	3	466064	1.8227	0.03418
ENSG00000175170	FAM182B	20	25744102	25848861	71	15	466064	1.9671	0.02458
ENSG00000175497	DPP10	2	1.15E+08	1.17E+08	3929	92	466064	1.8061	0.03545
ENSG00000175518	UBQLNL	11	5535623	5537935	16	2	466064	2.2046	0.01374
ENSG00000175806	MSRA	8	9911778	10286401	1543	61	466064	2.0067	0.02239
ENSG00000175894	TSPEAR	21	45917775	46131495	856	80	466064	1.9614	0.02492
ENSG00000175931	UBE2O	17	74385532	74449288	176	22	466064	2.2247	0.01305
ENSG00000176102	CSTF3	11	33098734	33183917	216	15	466064	1.7205	0.04267
ENSG00000176299	OR4M1	14	20248401	20249516	5	2	466064	2.1997	0.01392
ENSG00000176381	PRR18	6	1.67E+08	1.67E+08	7	3	466064	1.7506	0.04001
ENSG00000176435	CLEC14A	14	38723308	38725574	2	1	466064	2.6003	0.00466
ENSG00000176635	HORMAD2	22	30476163	30573064	344	22	466064	1.7221	0.04253
ENSG00000176769	TCERG1L	10	1.33E+08	1.33E+08	863	85	466064	2.3063	0.01055
ENSG00000176909	MAMSTR	19	49215999	49222978	17	4	466064	1.7988	0.03602
ENSG00000176912	C18orf56	18	641320	658340	54	10	466064	1.8285	0.03374
ENSG00000176920	FUT2	19	49199228	49209207	24	8	466064	1.9904	0.02327
ENSG00000176925	OR51F2	11	4842551	4843686	4	2	466064	2.011	0.02216
ENSG00000177047	IFNW1	9	21140631	21142144	2	1	466064	2.7626	0.00287
ENSG00000177192	PUS1	12	1.32E+08	1.32E+08	115	19	466064	1.8579	0.03159
ENSG00000177200	CHD9	16	53088945	53363062	709	22	466064	2.5458	0.00545
ENSG00000177294	FBXO39	17	6679542	6700420	77	20	466064	1.7752	0.03794
ENSG00000177455	CD19	16	28943260	28950667	10	4	466064	1.6908	0.04543
ENSG00000177614	PGBD5	1	2.3E+08	2.31E+08	362	43	466064	2.0151	0.02195
ENSG00000177694	NAALADL2	3	1.74E+08	1.76E+08	4641	231	466064	2.1156	0.01719
ENSG00000177706	FAM20C	7	192969	300711	587	65	466064	2.5666	0.00513
ENSG00000177707	PVRL3	3	1.11E+08	1.11E+08	460	25	466064	2.9158	0.00177
ENSG00000177710	SLC35G5	8	11188397	11189717	3	1	466064	2.0616	0.01962
ENSG00000177733	HNRNPA0	5	1.37E+08	1.37E+08	20	4	466064	2.3113	0.01041
ENSG00000177752	YIPF7	4	44624086	44680573	228	16	466064	1.7368	0.04121
ENSG00000177954	RPS27	1	1.54E+08	1.54E+08	1	1	466064	2.1257	0.01676
ENSG00000178233	TMEM151B	6	44238203	44275243	107	24	466064	2.1163	0.01716
ENSG00000178235	SLITRK1	13	84451344	84456528	29	4	466064	2.2737	0.01149

ENSG00000178381	ZFAND2A	7	1191707	1200395	16	6	466064	1.7825	0.03734
ENSG00000178773	CPNE7	16	89642176	89663654	80	14	466064	1.7027	0.04431
ENSG00000178913	TAF7	5	1.41E+08	1.41E+08	1	1	466064	1.7477	0.04026
ENSG00000178999	AURKB	17	8108056	8113918	18	5	466064	1.7045	0.04415
ENSG00000179044	EXOC3L1	16	67218269	67224107	3	1	466064	1.6557	0.04889
ENSG00000179178	TMEM125	1	43735665	43739673	4	2	466064	1.9613	0.02492
ENSG00000179344	HLA-DQB1	6	32627244	32636160	396	18	466064	3.5589	0.00019
ENSG00000179528	LBX2	2	74724644	74730443	8	2	466064	3.139	0.00085
ENSG00000179564	LSMEM2	3	50316458	50325545	9	4	466064	1.7183	0.04287
ENSG00000179580	RNF151	16	2016824	2018976	7	2	466064	2.1452	0.01597
ENSG00000179902	C1orf194	1	1.1E+08	1.1E+08	28	4	466064	1.888	0.02952
ENSG00000180044	C3orf80	3	1.6E+08	1.6E+08	14	5	466064	1.9394	0.02622
ENSG00000180354	MTURN	7	30174426	30202378	68	11	466064	1.8135	0.03488
ENSG00000180592	SKIDA1	10	21802407	21814611	17	7	466064	1.6528	0.04918
ENSG00000180611	MB21D2	3	1.93E+08	1.93E+08	401	55	466064	2.2454	0.01237
ENSG00000180979	LRRC57	15	42834720	42841000	4	2	466064	1.8183	0.03451
ENSG00000181350	FAM211A	17	16344891	16395467	78	13	466064	2.8676	0.00207
ENSG00000181690	PLAG1	8	57073463	57123883	177	18	466064	1.9268	0.027
ENSG00000181885	CLDN7	17	7163222	7167302	2	1	466064	1.8306	0.03358
ENSG00000182095	TNRC18	7	5346421	5465045	420	65	466064	1.8772	0.03025
ENSG00000182168	UNC5C	4	96083655	96470357	822	30	466064	2.0002	0.02274
ENSG00000182230	FAM153B	5	1.75E+08	1.76E+08	226	21	466064	1.7151	0.04317
ENSG00000182319	SGK223	8	8175258	8244008	66	8	466064	2.6001	0.00466
ENSG00000182552	RWDD4	4	1.85E+08	1.85E+08	64	8	466064	1.8509	0.03209
ENSG00000182568	SATB1	3	18386879	18487080	221	38	466064	2.0038	0.02254
ENSG00000182575	NXPH3	17	47653220	47661189	10	3	466064	2.4061	0.00806
ENSG00000182611	HIST1H2AJ	6	27782112	27782607	2	1	466064	2.0876	0.01842
ENSG00000182621	PLCB1	20	8112824	8949003	2653	172	466064	1.8247	0.03403
ENSG00000182768	NGRN	15	90808891	90816463	42	11	466064	2.9556	0.00156
ENSG00000182771	GRID1	10	87359312	88126250	1683	112	466064	1.6816	0.04633
ENSG00000182866	LCK	1	32716840	32751766	72	9	466064	1.8391	0.03295
ENSG00000182909	LENG9	19	54972981	54974894	8	3	466064	1.8607	0.0314
ENSG00000182938	OTOP3	17	72931814	72946087	20	4	466064	1.818	0.03453
ENSG00000183077	AFMID	17	76183398	76203782	43	10	466064	1.9961	0.02296
ENSG00000183090	FREM3	4	1.44E+08	1.45E+08	234	21	466064	1.9761	0.02407
ENSG00000183103	LYPD4	19	42341148	42348760	10	2	466064	2.5592	0.00525
ENSG00000183128	CALHM3	10	1.05E+08	1.05E+08	11	4	466064	2.6511	0.00401
ENSG00000183230	CTNNA3	10	67672276	69455927	5277	152	466064	2.2036	0.01378
ENSG00000183248	CTD-3193O13.9	19	7933605	7939326	30	5	466064	2.5363	0.0056
ENSG00000183255	PTTG1IP	21	46269500	46293752	120	9	466064	1.9799	0.02386
ENSG00000183549	ACSM5	16	20420856	20452658	165	13	466064	2.0232	0.02153
ENSG00000183617	MRPL54	19	3762662	3768573	22	6	466064	1.6831	0.04617
ENSG00000183625	CCR3	3	46205096	46308197	321	17	466064	2.6909	0.00356
ENSG00000183643	C15orf32	15	93014884	93044347	137	37	466064	1.6552	0.04894
ENSG00000183695	MRGPRX2	11	19076002	19082228	21	4	466064	1.71	0.04363
ENSG00000183751	TBL3	16	2022038	2032934	30	6	466064	1.6528	0.04919
ENSG00000183780	SLC35F3	1	2.34E+08	2.34E+08	1442	123	466064	2.5579	0.00527
ENSG00000183889	NPIPA7	16	16411301	16444447	1	1	466064	1.8151	0.03475
ENSG00000184156	KCNQ3	8	1.33E+08	1.33E+08	1336	132	466064	1.7518	0.03991
ENSG00000184345	IQCF2	3	51895645	51897440	4	1	466064	2.2319	0.01281
ENSG00000184348	HIST1H2AK	6	27805658	27806117	4	2	466064	2.1238	0.01684
ENSG00000184575	XPOT	12	64798130	64844907	64	13	466064	1.7097	0.04366
ENSG00000184613	NELL2	12	44902058	45315631	859	39	466064	2.2859	0.01113
ENSG00000184647	PRSS55	8	10383056	10411676	123	15	466064	2.2885	0.01106
ENSG00000184661	CDCA2	8	25316513	25365436	108	15	466064	1.6927	0.04525
ENSG00000184786	TCTE3	6	1.7E+08	1.7E+08	66	8	466064	1.8936	0.02914
ENSG00000184787	UBE2G2	21	46188955	46221934	102	16	466064	2.1037	0.0177
ENSG00000184814	PRR23B	3	1.39E+08	1.39E+08	3	1	466064	1.8113	0.03505
ENSG00000184863	RBM33	7	1.55E+08	1.56E+08	516	87	466064	1.6822	0.04627
ENSG00000184903	IMMP2L	7	1.1E+08	1.11E+08	2163	99	466064	1.812	0.03499
ENSG00000184939	ZFP90	16	68563993	68609975	96	11	466064	1.9268	0.027
ENSG00000185056	C5orf47	5	1.73E+08	1.73E+08	109	15	466064	1.6608	0.04838
ENSG00000185085	INTS5	11	62414320	62420774	23	7	466064	1.6846	0.04603
ENSG00000185100	ADSSL1	14	1.05E+08	1.05E+08	53	7	466064	1.678	0.04667
ENSG00000185215	TNFAIP2	14	1.04E+08	1.04E+08	41	8	466064	1.7552	0.03961
ENSG00000185420	SMYD3	1	2.46E+08	2.47E+08	3255	97	466064	2.2503	0.01222
ENSG00000185453	C19orf68	19	48673949	48700877	65	9	466064	1.9359	0.02644
ENSG00000185627	PSMD13	11	236546	252983	100	14	466064	1.7154	0.04314
ENSG00000185823	NPAP1	15	24920541	24928593	37	15	466064	1.8494	0.0322
ENSG00000185885	IFITM1	11	313506	315272	2	1	466064	1.8549	0.0318
ENSG00000185928	PAGR1	16	29827285	29841948	18	2	466064	1.9737	0.02421
ENSG00000185933	CALHM1	10	1.05E+08	1.05E+08	7	3	466064	2.259	0.01194
ENSG00000186073	C15orf41	15	36871812	37102449	470	78	466064	1.7473	0.0403

ENSG00000186150	UBL4B	1	1.11E+08	1.11E+08	3	1	466064	1.7891	0.0368
ENSG00000186212	SOWAHB	4	77816082	77819002	6	2	466064	1.6944	0.04509
ENSG00000186260	MKL2	16	14165178	14360630	466	38	466064	2.4868	0.00644
ENSG00000186407	CD300E	17	72606026	72619897	43	11	466064	2.9731	0.00147
ENSG00000186431	FCAR	19	55385704	55401838	95	18	466064	2.6246	0.00434
ENSG00000186479	RGS7BP	5	63802084	63908139	165	22	466064	2.813	0.00245
ENSG00000186517	ARHGAP30	1	1.61E+08	1.61E+08	60	14	466064	1.6637	0.04809
ENSG00000186638	KIF24	9	34252379	34329198	156	15	466064	1.8854	0.02969
ENSG00000186654	PRR5	22	45064593	45133561	223	34	466064	2.1447	0.01599
ENSG00000186803	IFNA10	9	21206180	21207142	8	2	466064	1.7561	0.03953
ENSG00000187024	PTRH1	9	1.3E+08	1.3E+08	82	16	466064	2.2707	0.01158
ENSG00000187049	TMEM216	11	61159159	61166335	10	3	466064	1.7153	0.04315
ENSG00000187091	PLCD1	3	38048987	38071253	60	6	466064	2.0501	0.02018
ENSG00000187510	PLEKHG7	12	93115281	93166231	101	20	466064	1.7468	0.04034
ENSG00000187600	TMEM247	2	46656329	46711564	226	26	466064	1.9606	0.02496
ENSG00000187730	GABRD	1	1950780	1962192	42	8	466064	2.3868	0.0085
ENSG00000187766	KRTAP10-8	21	46031996	46032871	1	1	466064	1.883	0.02985
ENSG00000187801	ZFP69B	1	40915774	40929390	71	12	466064	1.668	0.04766
ENSG00000187871	GFRAL	6	55192267	55267291	242	18	466064	1.8501	0.03215
ENSG00000188076	SCGB1C1	11	193080	194573	2	1	466064	1.7182	0.04288
ENSG00000188242	CTD-2228K2.5	5	466239	473213	26	6	466064	2.0001	0.02274
ENSG00000188676	IDO2	8	39792133	39873910	201	18	466064	2.225	0.01304
ENSG00000188687	SLC4A5	2	74443369	74570541	110	14	466064	2.1754	0.0148
ENSG00000188906	LRRK2	12	40590546	40763087	516	41	466064	2.3705	0.00888
ENSG00000188909	BSX	11	1.23E+08	1.23E+08	6	3	466064	2.1166	0.01715
ENSG00000188993	LRRRC66	4	52859868	52883786	74	10	466064	2.6071	0.00457
ENSG00000189253	TRIM64B	11	89602450	89609185	17	2	466064	1.942	0.02607
ENSG00000189350	FAM179A	2	29179477	29284239	351	42	466064	1.6521	0.04925
ENSG00000189366	ALG1L	3	1.26E+08	1.26E+08	26	5	466064	1.7698	0.03838
ENSG00000189433	GJB4	1	35225342	35229325	5	2	466064	2.3706	0.00888
ENSG00000196126	HLA-DRB1	6	32546546	32557625	18	6	466064	2.3566	0.00922
ENSG00000196341	OR8D1	11	1.24E+08	1.24E+08	3	1	466064	1.9768	0.02403
ENSG00000196374	HIST1H2BM	6	27782822	27783267	1	1	466064	2.0887	0.01837
ENSG00000196549	MME	3	1.55E+08	1.55E+08	415	23	466064	1.6559	0.04888
ENSG00000196622	RIMBP3	22	20456003	20461786	9	3	466064	3.2454	0.00059
ENSG00000196693	ZNF33B	10	43084555	43133992	167	22	466064	2.5844	0.00488
ENSG00000196735	HLA-DQA1	6	32595956	32614839	813	15	466064	3.8772	5.28E-05
ENSG00000196843	ARID5A	2	97202480	97218375	31	5	466064	2.2382	0.0126
ENSG00000196866	HIST1H2AD	6	26199079	26199471	3	1	466064	2.2951	0.01086
ENSG00000197125	OR8B8	11	1.24E+08	1.24E+08	4	2	466064	2.0033	0.02257
ENSG00000197157	SND1	7	1.27E+08	1.28E+08	1099	41	466064	2.862	0.0021
ENSG00000197283	SYNGAP1	6	33387847	33421466	78	16	466064	2.2133	0.01344
ENSG00000197381	ADARB1	21	46493768	46646478	687	40	466064	2.5801	0.00494
ENSG00000197472	ZNF695	1	2.47E+08	2.47E+08	215	22	466064	2.3275	0.00997
ENSG00000197555	SIPA1L1	14	71787166	72207946	1527	85	466064	2.06	0.0197
ENSG00000197601	FAR1	11	13690217	13753893	143	28	466064	1.7144	0.04323
ENSG00000197608	ZNF841	19	52567719	52599018	217	27	466064	2.0875	0.01842
ENSG00000197714	ZNF460	19	57791419	57804937	43	9	466064	1.7615	0.03908
ENSG00000197748	WDR96	10	1.06E+08	1.06E+08	316	20	466064	2.5976	0.00469
ENSG00000197846	HIST1H2BF	6	26199748	26200942	7	3	466064	1.6719	0.04727
ENSG00000197914	HIST1H4K	6	27798952	27799305	1	1	466064	2.9936	0.00138
ENSG00000197919	IFNA1	9	21440440	21441315	2	1	466064	1.8367	0.03312
ENSG00000197935	ZNF311	6	28962562	28973093	23	6	466064	2.2762	0.01142
ENSG00000198033	TUBA3C	13	19747910	19755992	20	5	466064	2.0893	0.01834
ENSG00000198035	AGAP9	10	48189612	48237508	97	9	466064	1.6966	0.04489
ENSG00000198053	SIRPA	20	1875154	1920543	208	25	466064	2.4265	0.00762
ENSG00000198185	ZNF334	20	45129701	45142198	25	4	466064	1.8517	0.03204
ENSG00000198203	SULT1C2	2	1.09E+08	1.09E+08	53	8	466064	1.6953	0.04501
ENSG00000198211	TUBB3	16	89985573	90002500	79	15	466064	2.6943	0.00353
ENSG00000198225	FKBP1C	6	63921351	63922929	4	2	466064	2.0412	0.02062
ENSG00000198246	SLC29A3	10	73079015	73123142	83	3	466064	1.7423	0.04073
ENSG00000198276	UCKL1	20	62571186	62587769	122	9	466064	2.1767	0.01475
ENSG00000198502	HLA-DRB5	6	32485120	32498064	16	5	466064	2.9654	0.00151
ENSG00000198518	HIST1H4E	6	26204858	26206266	13	4	466064	1.9313	0.02672
ENSG00000198563	DDX39B	6	31497996	31510225	139	17	466064	3.1062	0.00095
ENSG00000198657	OR8B4	11	1.24E+08	1.24E+08	1	1	466064	2.3009	0.0107
ENSG00000198704	GPX6	6	28471073	28495992	46	12	466064	2.7372	0.0031
ENSG00000198739	LRRTM3	10	68685764	68859588	423	21	466064	2.94	0.00164
ENSG00000198740	ZNF652	17	47366568	47439835	216	15	466064	1.6906	0.04546
ENSG00000198799	LRIG2	1	1.14E+08	1.14E+08	109	14	466064	1.9485	0.02568
ENSG00000198805	PNP	14	20937113	20945253	10	6	466064	2.0496	0.0202
ENSG00000198821	CD247	1	1.67E+08	1.67E+08	281	39	466064	2.0172	0.02184
ENSG00000198830	HMG2	1	26798941	26802463	1	1	466064	2.5459	0.00545

ENSG00000198865	CCDC152	5	42756903	42802462	119	12	466064	2.5231	0.00582
ENSG00000198885	ITPRIPL1	2	96991069	96994091	4	1	466064	2.1212	0.01695
ENSG00000198890	PRMT6	1	1.08E+08	1.08E+08	8	3	466064	1.6914	0.04538
ENSG00000198954	KIAA1279	10	70748487	70776738	159	24	466064	1.8466	0.0324
ENSG00000203710	CR1	1	2.08E+08	2.08E+08	422	28	466064	1.9019	0.02859
ENSG00000203722	RAET1G	6	1.5E+08	1.5E+08	36	7	466064	1.9878	0.02341
ENSG00000203734	ECT2L	6	1.39E+08	1.39E+08	329	19	466064	1.8489	0.03224
ENSG00000203832	NBPF20	1	1.48E+08	1.48E+08	180	22	466064	1.87	0.03075
ENSG00000203907	OOEP	6	74078278	74104856	139	9	466064	1.6943	0.04511
ENSG00000204179	PTPN20A	10	46549955	46641045	27	10	466064	2.6202	0.00439
ENSG00000204209	DAXX	6	33286335	33297046	17	6	466064	3.5916	0.00016
ENSG00000204217	BMPR2	2	2.03E+08	2.03E+08	310	25	466064	1.841	0.03281
ENSG00000204220	PFDN6	6	33257079	33266178	19	5	466064	2.143	0.01606
ENSG00000204227	RING1	6	33176272	33180499	7	3	466064	1.8088	0.03524
ENSG00000204228	HSD17B8	6	33172419	33174608	9	2	466064	1.9939	0.02308
ENSG00000204248	COL11A2	6	33130458	33160276	378	18	466064	2.083	0.01862
ENSG00000204252	HLA-DOA	6	32971955	32977389	23	11	466064	2.8527	0.00217
ENSG00000204283	FLJ45079	17	75875109	75878659	14	3	466064	1.9342	0.02655
ENSG00000204287	HLA-DRA	6	32407619	32412823	55	7	466064	2.51	0.00604
ENSG00000204290	BTNL2	6	32361740	32374905	127	18	466064	4.6892	1.37E-06
ENSG00000204296	C6orf10	6	32256303	32339684	635	19	466064	2.8536	0.00216
ENSG00000204314	PRRT1	6	32116136	32122150	13	6	466064	2.4746	0.00667
ENSG00000204344	STK19	6	31938868	31950598	30	8	466064	2.3118	0.0104
ENSG00000204348	DXO	6	31937587	31940069	7	2	466064	2.1819	0.01456
ENSG00000204351	SKIV2L	6	31926857	31937532	32	10	466064	2.1723	0.01492
ENSG00000204366	ZBTB12	6	31867384	31869769	12	4	466064	2.9578	0.00155
ENSG00000204371	EHMT2	6	31847536	31865464	45	15	466064	2.9221	0.00174
ENSG00000204385	SLC44A4	6	31830969	31846823	50	17	466064	2.7236	0.00323
ENSG00000204387	C6orf48	6	31802385	31807541	11	6	466064	2.03	0.02118
ENSG00000204388	HSPA1B	6	31795512	31798031	6	3	466064	1.6711	0.04735
ENSG00000204389	HSPA1A	6	31783291	31785723	4	2	466064	2.3205	0.01016
ENSG00000204390	HSPA1L	6	31777396	31783437	11	5	466064	2.8861	0.00195
ENSG00000204392	LSM2	6	31765173	31774761	20	8	466064	2.874	0.00203
ENSG00000204394	VARS	6	31745295	31763730	36	10	466064	2.312	0.01039
ENSG00000204396	VWA7	6	31733367	31745108	28	11	466064	2.6597	0.00391
ENSG00000204410	MSH5	6	31707725	31732622	51	13	466064	2.4617	0.00691
ENSG00000204428	LY6G5C	6	31644461	31651817	19	8	466064	2.8719	0.00204
ENSG00000204435	CSNK2B	6	31633013	31638120	24	7	466064	1.6608	0.04837
ENSG00000204444	APOM	6	31620193	31625987	20	6	466064	1.8952	0.02903
ENSG00000204463	BAG6	6	31606805	31620482	43	10	466064	1.863	0.03123
ENSG00000204472	AIF1	6	31582961	31584798	5	2	466064	1.7587	0.03932
ENSG00000204488	PRAMEF16	1	13495254	13498260	18	5	466064	1.7189	0.04281
ENSG00000204495	PRAMEF13	1	13447414	13452656	9	2	466064	2.1842	0.01448
ENSG00000204498	NFKBIL1	6	31514647	31526606	88	12	466064	1.7092	0.0437
ENSG00000204511	MCCD1	6	31496494	31498009	23	3	466064	2.7006	0.00346
ENSG00000204520	MICA	6	31371356	31383092	320	18	466064	3.0669	0.00108
ENSG00000204531	POU5F1	6	31132119	31148508	163	27	466064	2.6134	0.00448
ENSG00000204536	CXCHR1	6	31110216	31126015	129	18	466064	2.3449	0.00952
ENSG00000204560	DHX16	6	30620896	30640814	61	11	466064	1.9109	0.02801
ENSG00000204564	C6orf136	6	30614816	30620987	10	5	466064	2.7521	0.00296
ENSG00000204568	MRPS18B	6	30585486	30594172	19	5	466064	2.786	0.00267
ENSG00000204569	PPP1R10	6	30568177	30586389	41	7	466064	3.721	9.92E-05
ENSG00000204574	ABCF1	6	30539153	30564956	42	10	466064	4.3137	8.03E-06
ENSG00000204576	PRR3	6	30524663	30531500	21	5	466064	3.986	3.36E-05
ENSG00000204577	LILRB3	19	54720147	54746602	72	13	466064	1.7722	0.03818
ENSG00000204590	GNL1	6	30509154	30524951	40	4	466064	4.0316	2.77E-05
ENSG00000204592	HLA-E	6	30457244	30461982	65	7	466064	2.0746	0.01901
ENSG00000204599	TRIM39	6	30294256	30311506	62	12	466064	3.903	4.75E-05
ENSG00000204610	TRIM15	6	30130993	30140473	66	8	466064	5.1765	1.13E-07
ENSG00000204613	TRIM10	6	30119722	30128711	95	6	466064	2.3626	0.00907
ENSG00000204614	TRIM40	6	30103885	30116512	99	19	466064	3.997	3.21E-05
ENSG00000204616	TRIM31	6	30070674	30080883	100	14	466064	2.8429	0.00224
ENSG00000204618	RNF39	6	30038043	30043664	31	8	466064	4.1233	1.87E-05
ENSG00000204619	PPP1R11	6	30034486	30038110	27	5	466064	3.1423	0.00084
ENSG00000204642	HLA-F	6	29690552	29706305	230	19	466064	4.1297	1.82E-05
ENSG00000204644	ZFP57	6	29640169	29648887	41	14	466064	4.843	6.40E-07
ENSG00000204655	MOG	6	29624758	29640149	63	14	466064	3.5432	0.0002
ENSG00000204681	GABBR1	6	29523406	29601753	314	30	466064	3.6367	0.00014
ENSG00000204682	CASC10	10	21781587	21786191	10	3	466064	1.7261	0.04217
ENSG00000204683	C10orf113	10	21414692	21435488	36	9	466064	2.4951	0.0063
ENSG00000204695	OR14J1	6	29274403	29275519	2	1	466064	2.4606	0.00694
ENSG00000204701	OR2J3	6	29079668	29080603	2	1	466064	2.3751	0.00877
ENSG00000204702	OR2J1	6	29068386	29069658	7	3	466064	2.3831	0.00858

ENSG00000204703	OR2B3	6	29053985	29055090	5	2	466064	3.5619	0.00018
ENSG00000204704	OR2W1	6	29011990	29013017	3	2	466064	1.9658	0.02466
ENSG00000204713	TRIM27	6	28870779	28891766	101	19	466064	2.0289	0.02123
ENSG00000204790	CBWD6	9	69204538	69269662	275	43	466064	1.6587	0.04859
ENSG00000204822	MRPL53	2	74699085	74700449	3	1	466064	2.1653	0.01518
ENSG00000204843	DCTN1	2	74588281	74619214	22	7	466064	1.9006	0.02867
ENSG00000204956	PCDHGA1	5	1.41E+08	1.41E+08	353	14	466064	1.802	0.03577
ENSG00000205047	FLJ00104	16	87731749	87739290	41	5	466064	1.946	0.02583
ENSG00000205138	SDHAF1	19	36486090	36487220	2	1	466064	2.3183	0.01022
ENSG00000205336	GPR56	16	57644564	57698944	180	38	466064	1.8015	0.03582
ENSG00000205359	SLCO6A1	5	1.02E+08	1.02E+08	453	31	466064	1.733	0.04155
ENSG00000205441	KRTAP10-7	21	46020497	46022091	4	1	466064	2.2326	0.01279
ENSG00000206260	PRR23A	3	1.39E+08	1.39E+08	4	1	466064	1.7698	0.03838
ENSG00000206344	HCG27	6	31165537	31171745	64	13	466064	2.8217	0.00239
ENSG00000212643	ZRSR1	5	1.12E+08	1.12E+08	1	1	466064	1.8561	0.03172
ENSG00000212900	KRTAP3-2	17	39155447	39156138	2	1	466064	1.7295	0.04186
ENSG00000213079	SCAF8	6	1.55E+08	1.55E+08	361	36	466064	3.0787	0.00104
ENSG00000213171	LINGO4	1	1.52E+08	1.52E+08	18	2	466064	2.0467	0.02034
ENSG00000213337	ANKRD39	2	97502348	97523832	6	2	466064	2.451	0.00712
ENSG00000213347	MXD3	5	1.77E+08	1.77E+08	30	13	466064	1.8312	0.03353
ENSG00000213619	NDUFS3	11	47586888	47606114	29	12	466064	1.7093	0.0437
ENSG00000213654	GPSM3	6	32158543	32163300	14	8	466064	2.3253	0.01003
ENSG00000213676	ATF6B	6	32065953	32096030	56	17	466064	2.0587	0.01976
ENSG00000213699	SLC35F6	2	26987152	27004099	18	3	466064	2.6666	0.00383
ENSG00000213719	CLIC1	6	31698358	31707540	22	9	466064	1.7076	0.04386
ENSG00000213799	ZNF845	19	53837002	53858122	56	23	466064	1.9454	0.02586
ENSG00000213977	TAX1BP3	17	3566196	3571976	18	5	466064	1.7921	0.03656
ENSG00000214050	FBXO16	8	28205804	28347835	467	43	466064	2.022	0.02159
ENSG00000214109	AC008686.1	19	13890884	13900972	21	3	466064	1.8229	0.03416
ENSG00000214248	AC010336.1	19	7963689	7968427	6	3	466064	1.8924	0.02922
ENSG00000214681	IQCF5	3	51907737	51909600	5	2	466064	2.4254	0.00765
ENSG00000214841	AC005493.1	7	34685709	34699772	41	8	466064	2.7542	0.00294
ENSG00000215020	AL591684.1	10	48255279	48279199	32	6	466064	1.8491	0.03222
ENSG00000215183	MSMP	9	35752987	35756610	4	2	466064	2.5405	0.00554
ENSG00000215203	GRXCR1	4	42895284	43032675	424	32	466064	2.0791	0.01881
ENSG00000215271	HOMEZ	14	23741666	23768656	128	17	466064	1.8438	0.0326
ENSG00000215346	AF131215.5	8	10983980	10987745	11	3	466064	2.4114	0.00795
ENSG00000215428	AL354898.1	9	1.33E+08	1.33E+08	42	9	466064	1.9483	0.02569
ENSG00000215455	KRTAP10-1	21	45958864	45960078	8	2	466064	2.1695	0.01502
ENSG00000215717	TMEM167B	1	1.1E+08	1.1E+08	18	6	466064	2.5537	0.00533
ENSG00000215784	FAM72D	1	1.44E+08	1.44E+08	3	2	466064	3.224	0.00063
ENSG00000217825	AC099552.4	7	1.55E+08	1.55E+08	4	2	466064	1.7913	0.03662
ENSG00000217930	PAM16	16	4381550	4405608	59	13	466064	1.9274	0.02697
ENSG00000219073	CELA3B	1	22303514	22325135	54	18	466064	2.2927	0.01093
ENSG00000220201	ZGLP1	19	10415479	10420556	8	4	466064	1.923	0.02724
ENSG00000221914	PPP2R2A	8	26149007	26230196	348	32	466064	1.8668	0.03097
ENSG00000221926	TRIM16	17	15531274	15587625	97	12	466064	2.5047	0.00613
ENSG00000221931	OR6X1	11	1.24E+08	1.24E+08	5	2	466064	2.9796	0.00144
ENSG00000221963	APOL6	22	36044442	36064456	57	11	466064	2.2765	0.01141
ENSG00000221970	OR2A1	7	1.44E+08	1.44E+08	3	1	466064	1.6904	0.04547
ENSG00000221988	PPT2	6	32121218	32134011	27	12	466064	1.9388	0.02626
ENSG00000223501	VPS52	6	33218049	33239824	63	19	466064	2.007	0.02237
ENSG00000223865	HLA-DPB1	6	33043703	33054978	111	10	466064	2.4691	0.00677
ENSG00000225556	C2CD4D	1	1.52E+08	1.52E+08	8	3	466064	2.3285	0.00994
ENSG00000226979	LTA	6	31539831	31542101	15	6	466064	2.4016	0.00816
ENSG00000227057	WDR46	6	33246885	33257304	27	7	466064	2.5113	0.00601
ENSG00000228144	TMBIM4	12	66517697	66563765	185	22	466064	2.2429	0.01245
ENSG00000228278	ORM2	9	1.17E+08	1.17E+08	9	4	466064	1.9906	0.02326
ENSG00000229314	ORM1	9	1.17E+08	1.17E+08	12	6	466064	1.6918	0.04534
ENSG00000230510	PPP5D1	19	46984053	47104457	277	46	466064	1.9545	0.02532
ENSG00000231360	AL592284.1	1	1.44E+08	1.45E+08	83	18	466064	3.4063	0.00033
ENSG00000231500	RPS18	6	33239787	33244287	7	3	466064	2.2662	0.01172
ENSG00000231925	TAPBP	6	33267471	33282164	40	7	466064	1.8003	0.03591
ENSG00000232040	SCAND3	6	28539407	28583989	95	18	466064	2.25	0.01222
ENSG00000232056	AC092687.4	2	10987703	10995081	29	10	466064	2.2845	0.01117
ENSG00000232810	TNF	6	31543344	31546113	12	6	466064	2.2558	0.01204
ENSG00000233280	CRYBG3	3	97540884	97594132	76	6	466064	2.1901	0.01426
ENSG00000234127	TRIM26	6	30152232	30181204	158	15	466064	3.4307	0.0003
ENSG00000234438	KBTBD13	15	65369154	65372276	8	4	466064	1.6649	0.04797
ENSG00000234829	IFNA17	9	21227242	21228221	5	1	466064	2.1884	0.01432
ENSG00000235863	B3GALT4	6	33244917	33252609	20	7	466064	2.6164	0.00444
ENSG00000236104	ZBTB22	6	33282183	33285719	11	5	466064	3.0542	0.00113
ENSG00000236637	IFNA4	9	21186617	21187598	3	1	466064	1.7093	0.0437

ENSG00000237330	RNF223	1	1006346	1009687	6	2	466064	1.8446	0.03255
ENSG00000237441	RGL2	6	33259431	33267101	16	5	466064	2.2658	0.01173
ENSG00000237515	SHISA9	16	12995477	13334272	1326	108	466064	1.8272	0.03384
ENSG00000237541	HLA-DQA2	6	32709119	32714992	166	10	466064	2.1361	0.01634
ENSG00000237649	KIFC1	6	33359313	33377701	40	9	466064	2.7242	0.00322
ENSG00000239305	RNF103	2	86830516	86850989	58	9	466064	2.7343	0.00313
ENSG00000239665	RP11-295P9.3	10	13652047	13710299	258	37	466064	2.8216	0.00239
ENSG00000239732	TLR9	3	52255096	52273183	31	8	466064	1.7365	0.04123
ENSG00000239779	WBP1	2	74685456	74688018	6	1	466064	2.4969	0.00627
ENSG00000240053	LY6G5B	6	31637944	31641553	14	7	466064	2.1986	0.01395
ENSG00000240065	PSMB9	6	32811913	32827362	140	16	466064	1.8095	0.03519
ENSG00000240184	PCDHGC3	5	1.41E+08	1.41E+08	54	11	466064	2.3757	0.00876
ENSG00000240764	PCDHGC5	5	1.41E+08	1.41E+08	33	9	466064	2.5642	0.00517
ENSG00000241186	TDGF1	3	46616045	46668033	177	19	466064	2.3187	0.01021
ENSG00000241322	CDRT1	17	15468798	15522826	182	21	466064	1.689	0.04561
ENSG00000241370	RPP21	6	30312908	30314661	9	3	466064	2.7985	0.00257
ENSG00000241553	ARPC4	3	9834179	9849410	33	10	466064	2.1606	0.01536
ENSG00000241837	ATP5O	21	35275757	35288284	44	8	466064	1.6956	0.04498
ENSG00000242419	PCDHGC4	5	1.41E+08	1.41E+08	39	10	466064	2.5062	0.0061
ENSG00000242498	C15orf38	15	90443159	90456188	33	6	466064	2.056	0.01989
ENSG00000243649	CFB	6	31895475	31919861	61	19	466064	2.152	0.0157
ENSG00000243729	OR5V1	6	29323007	29399744	334	27	466064	2.6776	0.00371
ENSG00000243749	ZMYM6NB	1	35447136	35450954	4	2	466064	1.9848	0.02358
ENSG00000244255	CFB	6	31895475	31919825	61	19	466064	2.152	0.0157
ENSG00000244482	LILRA6	19	54720737	54746649	72	13	466064	1.7722	0.03818
ENSG00000244731	C4A	6	31949801	31970458	64	19	466064	2.2961	0.01084
ENSG00000248167	TRIM39-RPP21	6	30297359	30314631	61	12	466064	3.904	4.73E-05
ENSG00000249624	AP000295.9	21	34619079	34655517	111	19	466064	1.8997	0.02874
ENSG00000249693	THEGL	4	57396775	57469673	272	20	466064	1.7104	0.0436
ENSG00000249852	AC145676.2	7	227554	229557	15	4	466064	2.2523	0.01215
ENSG00000249915	PDCD6	5	271736	353971	256	16	466064	1.7228	0.04246
ENSG00000250021	C15orf38-AP3S2	15	90377540	90456114	238	18	466064	2.5469	0.00543
ENSG00000250151	ARPC4-TTLL3	3	9834766	9877085	110	25	466064	2.0425	0.02055
ENSG00000250506	CDK3	17	73996987	74002080	20	8	466064	1.8535	0.03191
ENSG00000251380	C5orf20	5	1.35E+08	1.35E+08	3	2	466064	1.7414	0.04081
ENSG00000251537	RP11-385D13.1	17	15474805	15554967	216	18	466064	2.1	0.01787
ENSG00000253159	PCDHGA12	5	1.41E+08	1.41E+08	107	16	466064	2.1109	0.01739
ENSG00000253305	PCDHGB6	5	1.41E+08	1.41E+08	167	15	466064	1.8876	0.02954
ENSG00000253426	RP11-10A14.4	8	9009252	9025646	59	9	466064	2.3839	0.00856
ENSG00000253485	PCDHGA5	5	1.41E+08	1.41E+08	284	15	466064	1.8004	0.0359
ENSG00000253537	PCDHGA7	5	1.41E+08	1.41E+08	212	14	466064	1.8273	0.03383
ENSG00000253731	PCDHGA6	5	1.41E+08	1.41E+08	248	14	466064	1.7824	0.03734
ENSG00000253767	PCDHGA8	5	1.41E+08	1.41E+08	195	14	466064	1.8195	0.03442
ENSG00000253846	PCDHGA10	5	1.41E+08	1.41E+08	152	16	466064	1.925	0.02712
ENSG00000253873	PCDHGA11	5	1.41E+08	1.41E+08	142	15	466064	1.9542	0.02534
ENSG00000253910	PCDHGB2	5	1.41E+08	1.41E+08	298	16	466064	1.8208	0.03432
ENSG00000253953	PCDHGB4	5	1.41E+08	1.41E+08	198	14	466064	1.8227	0.03418
ENSG00000254019	RP11-10J21.3	8	1.42E+08	1.42E+08	13	4	466064	2.3415	0.0096
ENSG00000254122	PCDHGB7	5	1.41E+08	1.41E+08	145	16	466064	1.9493	0.02563
ENSG00000254221	PCDHGB1	5	1.41E+08	1.41E+08	329	15	466064	1.7818	0.03739
ENSG00000254245	PCDHGA3	5	1.41E+08	1.41E+08	340	15	466064	1.7946	0.03636
ENSG00000254415	SIGLEC14	19	52145806	52150054	6	3	466064	2.5504	0.00538
ENSG00000254656	RTL1	14	1.01E+08	1.01E+08	8	3	466064	2.9414	0.00163
ENSG00000254870	ATP6V1G2-DDX3	6	31497996	31514385	176	21	466064	2.9713	0.00148
ENSG00000255152	MSH5-SAPCD1	6	31707797	31732628	51	13	466064	2.4617	0.00691
ENSG00000255423	EBLN2	3	73110810	73112488	4	2	466064	2.2615	0.01187
ENSG00000255529	POLR2M	15	57884231	58074960	625	26	466064	1.8263	0.0339
ENSG00000255833	TIFAB	5	1.35E+08	1.35E+08	3	2	466064	1.7414	0.04081
ENSG00000255940	REXO1L10P	8	86756718	86758745	4	2	466064	2.1496	0.01579
ENSG00000256043	CTSO	4	1.57E+08	1.57E+08	59	11	466064	2.075	0.019
ENSG00000257327	RP11-650K20.3	12	1.04E+08	1.04E+08	14	6	466064	1.7575	0.03942
ENSG00000257726	RP11-116D17.1	12	1.16E+08	1.16E+08	20	4	466064	1.6971	0.04484
ENSG00000257949	TEN1	17	73975301	73996667	90	25	466064	2.8954	0.00189
ENSG00000258839	MC1R	16	89978527	89987385	44	11	466064	2.5835	0.00489
ENSG00000258947	TUBB3	16	89987800	90005169	64	13	466064	2.5945	0.00474
ENSG00000260001	TGFBR3L	19	7981030	7983982	10	5	466064	3.023	0.00125
ENSG00000261147	RP11-697E2.6	15	90792788	90815440	140	11	466064	1.742	0.04075
ENSG00000261934	PCDHGA9	5	1.41E+08	1.41E+08	177	14	466064	1.8622	0.03129
ENSG00000262039	RP11-81K2.1	17	47448102	47554350	266	16	466064	2.5517	0.00536
ENSG00000262209	PCDHGB3	5	1.41E+08	1.41E+08	265	16	466064	1.8254	0.03397
ENSG00000262246	CORO7	16	4404543	4475706	185	16	466064	3.0682	0.00108
ENSG00000262576	PCDHGA4	5	1.41E+08	1.41E+08	318	15	466064	1.781	0.03746
ENSG00000263020	CSNK2B-LY6G5E	6	31633879	31641323	30	11	466064	2.2814	0.01126

ENSG00000263136	PAGR1	16	29827832	29831438	6	1	466064	1.9813	0.02378
ENSG00000263155	MYZAP	15	57884139	57977562	330	21	466064	1.7514	0.03994
ENSG00000264324	RP11-287D1.3	2	74438731	74590504	129	16	466064	2.2061	0.01369
ENSG00000265690	RP11-5A19.5	16	67197288	67199718	5	2	466064	2.4818	0.00654
ENSG00000266953	RP11-618P17.4	19	34887220	34900269	35	4	466064	1.8189	0.03446
ENSG00000267748	CTB-102L5.4	19	38779791	38795550	61	8	466064	1.9306	0.02677
ENSG00000267857	PRED58	21	46520728	46534873	39	11	466064	2.602	0.00463
ENSG00000267918	AL117190.2	14	1.01E+08	1.01E+08	4	2	466064	3.0314	0.00122
ENSG00000268154	AL591806.1	1	1.61E+08	1.61E+08	1	1	466064	1.7536	0.03975
ENSG00000268461	AC007204.1	19	20047769	20048639	2	1	466064	1.9908	0.02325
ENSG00000268805	PRED57	21	46511596	46515493	21	4	466064	1.8554	0.03177
ENSG00000268818	AL049747.1	22	36023040	36031181	15	5	466064	1.8739	0.03047
ENSG00000268821	AC068039.1	2	1.73E+08	1.73E+08	13	5	466064	2.6001	0.00466
ENSG00000268885	AC026740.1	5	667759	668839	4	2	466064	2.4068	0.00805
ENSG00000269094	AC006449.1	17	36884086	36884451	4	2	466064	2.3676	0.00895
ENSG00000269308	AL645608.2	1	818043	819983	9	2	466064	2.365	0.00901
ENSG00000269554	AL590822.2	1	2121237	2123179	1	1	466064	1.768	0.03853
ENSG00000269781	FLJ20306	7	6522922	6524873	4	2	466064	1.8691	0.0308
ENSG00000270617	URGCP-MRPS24	7	43906157	43946188	121	16	466064	2.3316	0.00986
ENSG00000270898	ASB3	2	53897430	54087297	521	24	466064	1.6737	0.04709
ENSG00000272410	RP11-438J1.1	3	10291056	10327480	102	14	466064	1.645	0.04999
ENSG00000273079	GRIN2B	12	13693165	14133053	1388	89	466064	2.0661	0.01941
ENSG00000273266	HOXC4	12	54447661	54449814	1	1	466064	1.8351	0.03324

ENSG00000183625	3	COCR3	46256646 rs138860	3	46276878 A	T	0.33698	-0.20255	0.08211	1.38E-02	0.59902	0.00775	#####	-0.33813	0.13715	1.37E-02	6.76E-03	4.74E-02	20
ENSG00000184068	3	RNF123	49742947 rs485888	3	49715354 G	A	0.166	0.246242	0.11505	3.27E-02	0.1053	0.01075	1.23E-22	2.3384	1.11833	3.65E-02	3.65E-02	4.38E-02	20
ENSG00000184042	3	CANX2D2	50479954 rs622608	3	50474624 A	G	0.10835	0.45544	0.12604	3.72E-04	0.14247	0.0128	9.98E-29	-3.19759	19.9435	7.01E-04	7.01E-04	8.53E-01	20
ENSG00000114735	3	HEMK	50614474 rs223224	3	50606807 G	G	0.12425	0.348696	0.11207	1.52E-03	-0.21539	0.01238	7.80E-68	-1.61893	5.2033	8.69E-03	1.87E-01	8.53E-02	20
ENSG0000041880	3	PARR3	51979622 rs622603	3	51163444 G	T	0.166	0.222777	0.09847	2.37E-02	0.07132	0.01247	1.06E-08	3.12364	1.48468	3.54E-02	3.54E-02	9.50E-01	6
ENSG00000162244	3	RPL29	52028787 rs116538	3	51907243 C	A	0.01193	1.32137	0.58184	2.31E-02	-0.71998	0.011	1.01E-12	-1.83528	0.84815	3.05E-02	1.52E-01	2.22E-01	18
ENSG00000164807	3	POCIA1	52148987 rs352150	3	52029995 G	A	0.09443	-0.20353	0.10378	4.77E-02	0.32554	0.01528	#####	-0.63137	0.32018	4.78E-02	4.08E-01	9.99E-01	20
ENSG00000114841	3	PCNA	52317052 rs622608	3	52317052 G	G	0.1437	0.31043	0.1437	0.00000	0.00000	0.00000	#####	0.00000	0.00000	0.00000	0.00000	0.00000	20
ENSG00000168297	3	PXK	58365177 rs763555	3	58402336 C	C	0.27734	0.193941	0.01737	6.85E-03	0.31048	0.00928	#####	0.624645	0.23064	6.76E-02	3.00E-01	5.56E-01	20
ENSG00000144744	3	UBA3	69116720 rs676689	3	69120074 C	T	0.39861	-0.1786	0.07344	1.46E-02	0.1149	0.01198	8.81E-22	-1.55442	0.65683	1.80E-02	6.27E-02	1.21E-01	17
ENSG00000144736	3	SHQ1	72854746 rs622616	3	72811827 T	C	0.2326	-0.19554	0.07717	1.18E-02	0.09213	0.00961	5.13E-24	-2.0131	0.62207	1.43E-02	3.24E-02	1.53E-01	20
ENSG00000163320	3	CGGBP1	88150064 rs126295	3	88117228 C	C	0.12227	-0.28942	0.10078	4.48E-03	0.56512	0.0116	#####	-0.50683	0.17863	4.55E-03	1.07E-02	2.51E-01	17
ENSG00000184220	3	PCNA	92542419 rs622608	3	92542419 G	T	0.1437	0.15423	0.1437	0.00000	0.00000	0.00000	#####	0.00000	0.00000	0.00000	0.00000	0.00000	20
ENSG00000360504	3	TBC1D23	100011968 rs492106	3	100034849 A	T	0.44036	0.145767	0.01762	4.18E-02	0.09668	0.0117	1.93E-15	-1.0575	0.76477	4.87E-02	4.87E-02	3.28E-01	20
ENSG00000114439	3	BBX	10738597 rs169768	3	107262113 A	G	0.10437	-0.21784	0.10406	3.63E-02	-0.27184	0.01271	#####	0.801363	0.38464	3.72E-02	2.02E-01	3.88E-01	20
ENSG00000196776	3	CD47	107786008 rs326361	3	107819041 A	G	0.4493	-0.15169	0.07284	3.73E-02	0.31123	0.00778	#####	-0.38783	0.1864	3.75E-02	7.52E-01	3.26E-01	20
ENSG00000121570	3	PDP4A	10950703 rs118365	3	109446621 A	G	0.0696	-0.39294	0.19037	3.90E-02	0.37195	0.01494	#####	-1.05643	0.51358	3.97E-02	1.19E-01	2.00E-01	20
ENSG00000163617	3	CDC191	14272892 rs370793	3	11276860 T	G	0.34118	0.25577	0.06255	5.47E-03	0.40852	0.00929	1.30E-22	-1.18957	0.47865	6.00E-03	6.00E-02	6.00E-01	20
ENSG00000181722	3	ZBTB20	114461529 rs798285	3	114448655 G	C	0.02286	0.58204	0.20626	1.16E-02	-0.38671	0.04698	1.80E-16	-1.50511	0.62381	1.58E-02	1.05E-02	5.32E-02	12
ENSG00000144847	3	IGSF11	118742159 rs678420	3	118931389 C	T	0.0338	0.503689	0.21589	1.98E-02	0.46941	0.01973	#####	1.07303	0.46213	2.02E-02	9.53E-02	5.67E-01	20
ENSG000001176142	3	TMEM39A	119168012 rs117143	3	119129803 C	G	0.36581	-0.15423	0.07167	3.14E-02	-0.09589	0.00838	2.52E-30	1.60837	0.76048	3.04E-02	5.44E-02	8.50E-01	20
ENSG00000082701	3	GSK3B	11967871 rs1697648	3	119827508 T	A	0.22167	-0.18743	0.09484	4.87E-02	0.30276	0.00891	#####	-0.55302	0.27853	4.71E-02	1.61E-01	8.11E-01	20
ENSG00000249864	3	LINC02021	120633971 rs407121	3	120629623 A	G	0.47424	-0.24865	0.09698	3.97E-02	-0.62261	0.01202	#####	0.226419	1.01515	4.01E-02	8.09E-02	6.94E-01	20
ENSG00000196353	3	CPNE4	131628326 rs130777	3	131563648 T	A	0.26243	-0.16234	0.09542	4.12E-02	-0.07567	0.00879	1.74E-18	2.14534	1.0995	4.70E-02	1.38E-01	4.04E-01	20
ENSG00000240890	3	GZE3P1	142106627 rs677693	3	132102933 C	G	0.45726	-0.19352	0.07319	1.89E-03	0.09958	0.01007	4.60E-23	-1.94332	0.7608	1.06E-02	6.40E-02	1.39E-01	18
ENSG00000163755	3	CPA3	148599013 rs176480	3	148619410 T	T	0.38966	0.181146	0.07319	1.33E-02	0.15680	0.00813	3.92E-46	1.56345	0.64111	1.47E-02	9.03E-02	1.25E-01	20
ENSG00000163755	3	HPS3	148989445 rs342914	3	148818651 T	C	0.02485	0.482063	0.2278	3.43E-02	0.53335	0.02231	#####	0.903837	0.42876	3.50E-02	7.01E-01	2.26E-01	20
ENSG00000163681	3	CPNE4	15384973 rs130777	3	15384973 G	T	0.2733	0.24201	0.09255	5.47E-03	0.40852	0.01192	#####	0.634567	0.15824	4.44E-02	1.58E-02	1.98E-01	20
ENSG00000117121	3	KN3MB3	178971160 rs617964	3	178930079 A	C	0.19483	0.245554	0.06621	1.03E-02	0.11347	0.01142	2.99E-23	2.16403	0.87461	1.34E-02	4.08E-02	3.37E-01	20
ENSG000001175193	3	PARL	183574947 rs764474	3	183596184 T	C	0.45129	0.188315	0.07097	7.97E-03	-0.16292	0.00801	5.74E-92	-1.15588	0.43929	8.51E-02	3.42E-01	2.94E-02	20
ENSG00000213139	3	CRYGS	186260360 rs109372	3	186260740 G	A	0.44732	0.163897	0.02172	2.31E-02	0.13546	0.00797	8.70E-65	1.20991	0.53713	2.53E-03	9.24E-02	2.65E-01	20
ENSG00000173890	3	XXYL1T	194980452 rs62270	3	194992240 G	A	0.2167	0.217562	0.06875	8.45E-03	-0.19502	0.01038	9.54E-79	-1.11559	0.43394	1.01E-02	3.98E-01	4.28E-01	20
ENSG000001954805	3	XXYL1	194980452 rs62270	3	194992240 G	A	0.2167	0.217562	0.06875	8.45E-03	-0.19502	0.01038	9.54E-79	-1.11559	0.43394	1.01E-02	3.98E-01	4.28E-01	20
ENSG00000072840	3	EVC	5771848 rs229115	3	5721021 G	C	0.09543	-0.39044	0.16283	1.65E-02	0.1287	0.01461	1.24E-18	-0.3338	3.1099	2.07E-02	4.60E-02	1.42E-01	20
ENSG00000013288	3	MAN2B2	6006995 rs117307	3	6145945 A	T	0.16899	-0.19829	0.09747	4.19E-02	-0.61024	0.0114	#####	0.324929	0.15984	4.21E-02	2.74E-01	1.13E-01	20
ENSG00000109743	3	BST1	15722254 rs345599	3	15730146 G	T	0.43738	0.151751	0.07235	3.98E-02	0.48273	0.00752	#####	0.314358	0.14995	3.60E-02	3.01E-01	7.63E-01	20
ENSG00000153012	3	LGJ2	25016485 rs168785	3	25000060 G	A	0.1332	-0.22736	0.09675	1.78E-02	-0.16928	0.0113	1.00E-50	1.34309	0.57267	1.90E-02	3.77E-02	4.43E-01	16
ENSG0000025117020	3	LINC02506	32033971 rs407121	3	32033971 G	T	0.29125	-0.18103	0.07658	1.81E-02	-0.12098	0.00836	2.21E-98	1.75915	0.73853	2.05E-02	0.9500	1.98E-01	20
ENSG00000109790	3	KLHL5	39087588 rs306073	3	38953128 C	T	0.40159	-0.15141	0.07316	3.85E-02	-0.44089	0.00776	#####	0.343425	0.16603	3.86E-02	3.37E-01	8.87E-01	20
ENSG00000163694	3	RBM47	40529082 rs131401	3	40735334 A	G	0.36779	-0.15169	0.07391	4.01E-02	0.20728	0.00893	#####	-0.7318	0.35797	4.09E-02	3.20E-01	5.65E-01	20
ENSG00000179299	3	NSUN7	40781958 rs352426	3	40734812 G	C	0.36978	-0.15169	0.07391	4.01E-02	0.20728	0.00893	#####	-0.7318	0.35797	4.09E-02	3.20E-01	5.65E-01	20
ENSG00000204870	3	ARL4A2	40788427 rs257318	3	40735769 T	C	0.37873	-0.1479	0.07392	3.54E-02	0.29582	0.02083	9.11E-46	-0.49995	0.25235	4.76E-02	5.00E-02	7.42E-01	20
ENSG00000164042	3	LINC114	413630726 rs622608	3	413630726 G	T	0.39653	0.15895	0.07392	3.25E-02	-0.11299	0.00925	2.43E-47	1.05426	0.6384	4.33E-02	1.95E-02	4.85E-01	20
ENSG00000151806	3	GUF1	44691693 rs345471	3	44678287 T	C	0.53877	0.160855	0.07952	4.24E-02	0.33619	0.00893	#####	0.478466	0.22411	3.28E-02	9.07E-02	7.19E-01	20
ENSG00000163281	3	GNDPA2	44716248 rs117243	3	44725334 C	G	0.24453	0.2034	0.0936	2.98E-02	0.16907	0.00946	1.98E-71	1.20268	0.5577	3.10E-02	9.97E-02	6.44E-02	20
ENSG00000109189	3	USP46	53492921 rs999454	3	53578213 C	G	0.13121	-0.24235	0.10986	2.74E-02	0.14024	0.01225	2.49E-30	-1.72805	0.79779	3.03E-02	1.48E-01	1.30E-02	20
ENSG00000226950	3	DANCR	53582557 rs732486	3	53570498 A	C	0.13121	-0.24235	0.10986	2.74E-02	0.14024	0.01225	#####	-0.35167	0.15785	2.59E-02	1.01E-01	1.95E-02	20
ENSG00000181381	3	LINC114	54422119 rs622608	3	54422119 G	T	0.21869	-0.23073	0.10915	2.17E-02	0.48832	0.01599	#####	0.763348	0.33398	2.23E-02	3.16E-01	5.59E-01	20

ENSG00000114005	11	PIK3C22A	17164403 rs511119	11	17215117	A	G	0.49702	0.152259	0.07162	3.32E-02	0.48758	0.00891	#####	0.31283	0.14699	3.33E-02	7.95E-02	1.95E-01	20	
ENSG00000170081	11	NUCB2	17300610 rs214081	11	17299564	A	T	0.42842	0.158553	0.02711	2.79E-02	0.41385	0.01151	#####	0.383115	0.17455	2.82E-02	2.28E-02	6.97E-01	20	
ENSG00000179102	11	CSTF3	33141323 rs103360	11	33198260	A	G	0.2333	0.22662	0.07949	3.07E-03	0.1664	0.20679	#####	8.93E-00	-1.24166	4.803E-03	9.74E-03	9.22E-02	1.12E-01	20
ENSG00000166352	11	ITFAP	36655437 rs375887	11	36655089	G	A	0.3236	-0.27698	0.12731	3.01E-02	0.14941	0.01221	1.23E-02	#####	8.5382	0.8865	2.82E-02	1.03E-01	4.52E-01	20
ENSG00000109919	11	MTCH2	47651521 rs143001	11	47722571	A	G	0.06362	0.46068	0.1827	1.17E-02	-0.23929	0.01974	7.9E-34	-1.92519	0.77986	1.36E-02	1.04E-01	2.72E-01	20	
ENSG00000134780	11	DAGLA	61481189 rs169212	11	61417472	G	A	0.54672	-0.17082	0.07275	1.89E-02	-0.12002	0.00797	3.31E-51	1.42322	0.61344	2.03E-02	1.38E-01	7.65E-01	20	
ENSG00000089897	11	GANAB	62403201 rs118903	11	62413673	T	G	0.16103	-0.2996	0.1068	5.03E-03	-0.28793	0.01789	2.73E-58	1.04052	0.3765	5.72E-03	4.44E-03	8.60E-01	20	
ENSG00000165688	11	TRAF3	62519233 rs193669	11	62519233	G	A	0.35587	0.19179	0.07629	3.07E-03	0.1664	0.20679	#####	8.93E-00	-1.24166	4.803E-03	9.74E-03	9.22E-02	1.12E-01	20
ENSG00000185475	11	TIEM17B9	62565382 rs14034	11	62565382	G	A	0.36481	0.17708	0.07321	1.55E-02	-0.11392	0.00823	1.48E-43	1.55549	0.65234	1.71E-02	1.00E-01	1.71E-01	20	
ENSG00000162231	11	NXF1	62566864 rs4693	11	62564009	T	C	0.37674	0.176458	0.07686	1.54E-02	0.20261	0.00809	#####	0.870916	0.36126	1.59E-02	1.12E-01	2.74E-01	20	
ENSG00000168070	11	MAJIN	64722273 rs161030	11	64712696	A	G	0.24752	-0.18715	0.08685	3.12E-02	-0.06519	0.01112	4.63E-09	2.87086	1.41944	4.31E-02	4.31E-02	2.43E-01	12	
ENSG00000149806	11	FAU	64889022 rs769440	11	64889414	G	A	0.51093	0.183477	0.06949	8.29E-03	-0.09061	0.01182	1.76E-14	-2.02485	0.81113	1.25E-02	1.25E-02	8.32E-01	17	
ENSG00000198121	11	GNPFL21	66839520 rs163043	11	66839520	G	A	0.3002	0.1507	0.06506	3.07E-03	0.1664	0.20679	#####	8.93E-00	-1.24166	4.803E-03	9.74E-03	9.22E-02	1.12E-01	20
ENSG00000132740	11	IIGHMP22	66879860 rs496616	11	66872800	C	G	0.29521	-0.15083	0.07419	4.21E-02	0.05534	0.00762	#####	0.23045	1.1324	2.41E-02	8.34E-01	9.74E-01	20	
ENSG00000256518	11	FOLR1P1	71870385 rs301830	11	71852122	G	A	0.46521	-0.14481	0.07181	4.37E-02	-0.41927	0.02095	5.52E-89	0.345376	0.17244	1.48E-02	3.18E-01	9.54E-01	20	
ENSG00000149243	11	LKLH35	75137556 rs301810	11	75141762	T	C	0.42346	0.17669	0.06994	1.81E-02	-0.36211	0.0078	#####	-0.48651	0.19344	1.19E-02	3.97E-02	6.79E-01	20	
ENSG00000151366	11	NDJUF2C	77783037 rs657727	11	77774736	T	C	0.168	0.24932	0.09672	1.16E-02	-0.3501	0.01104	#####	-0.71215	0.28287	1.18E-02	8.35E-02	7.94E-01	20	
ENSG00000198997	11	KCTD21	77891081 rs510318	11	77808818	C	T	0.17296	0.264367	0.07983	4.73E-03	-0.26987	0.01273	1.52E-99	-0.98032	0.36939	9.96E-03	3.54E-01	6.70E-01	20	
ENSG00000151376	11	ME3	86267914 rs170371	11	86383876	A	C	0.12724	-0.20664	0.10415	4.75E-02	0.64985	0.01121	#####	-0.31799	0.16037	1.47E-02	1.68E-01	1.44E-01	20	
ENSG00000137714	11	FDX1	110318106 rs108911	11	110331848	G	C	0.28032	-0.20304	0.07314	1.05E-02	0.3205	0.00884	#####	-0.6335	0.24816	1.70E-02	9.66E-02	5.58E-01	20	
ENSG00000137371	11	FXVD2	11768529 rs112165	11	11769397	T	C	0.44831	0.144098	0.07128	4.59E-02	-0.10799	0.0081	1.41E-40	-1.33437	0.67588	4.84E-02	4.62E-01	1.40E-02	20	
ENSG00000254528	11	RYDB-AS1	11770345 rs127903	11	11770345	T	C	0.14016	0.28927	0.17496	4.59E-02	0.55433	0.01063	#####	0.238691	0.23496	1.52941	4.39E-02	3.82E-01	7.95E-01	20
ENSG00000064309	11	CDON	125879460 rs46725	11	125917325	A	G	0.14414	-0.35828	0.12513	8.02E-03	0.11665	0.0112	2.20E-25	-3.07155	1.9545	1.02E-02	2.70E-02	2.27E-01	20	
ENSG00000134954	11	ETS1	128393046 rs58369	11	128186631	A	C	0.19185	0.178837	0.08303	3.25E-02	-0.07898	0.00944	5.74E-17	-2.26443	1.08552	3.70E-02	2.30E-01	4.65E-01	16	
ENSG00000134909	11	ARGHAP32	128992807 rs112216	11	129207859	A	C	0.23758	-0.22989	0.10703	1.22E-02	0.24128	0.00976	#####	-0.95278	0.41926	2.31E-02	1.81E-01	6.83E-01	20	
ENSG00000080854	11	IGSF8B	133806302 rs329673	11	133798999	C	T	0.20179	0.248744	0.08802	4.71E-02	-0.2257	0.01377	1.14E-87	-1.10217	0.39391	5.14E-03	5.31E-02	6.19E-01	20	
ENSG00000109586	11	ALLEC	13413169 rs793768	11	134211367	A	C	0.12127	0.229401	0.10310	3.72E-02	0.72161	0.00276	#####	0.27757	3.76E-03	2.29E-02	1.37E-01	3.91E-01	20	
ENSG00000255545	11	BGSAT1-DT	134340961 rs877605	11	134281313	G	C	0.12127	0.229401	0.10310	3.72E-02	-0.72161	0.00276	#####	-1.02611	0.15493	7.95E-02	4.83E-01	6.65E-01	20	
ENSG00000102645	11	IQSEC3	231778 rs573719	11	238901	C	G	0.33897	0.170687	0.07831	2.08E-02	0.5802	0.01436	#####	0.284186	0.12742	2.10E-02	9.73E-02	8.69E-01	20	
ENSG00000177406	11	NIJN2-AS1	756464 rs558009	11	752360	A	G	0.13022	0.24604	0.0731	1.01E-02	0.94098	0.01272	#####	0.238691	0.09283	1.01E-02	9.91E-01	9.52E-01	20	
ENSG00000047621	11	C12orf4	4622284 rs108490	11	4597481	C	A	0.1839	-0.25309	0.09867	1.03E-02	-0.20071	0.01095	5.34E-75	1.26998	0.4964	1.11E-02	5.10E-01	2.01E-01	20	
ENSG00000159076	11	CHD1	7851324 rs504587	11	7851324	A	C	0.14016	0.28927	0.17496	4.59E-02	0.55433	0.01063	#####	0.238691	0.23496	1.52941	4.39E-02	3.82E-01	7.95E-01	20
ENSG00000116642	11	CHD4	6697945 rs796917	11	6719280	A	G	0.1342	0.22413	0.09624	2.04E-02	-0.14847	0.01094	6.25E-42	-1.50984	0.6064	2.23E-02	1.28E-01	9.10E-01	20	
ENSG00000164574	11	LPAR5	6736807 rs729441	11	6689866	T	A	0.1332	0.222726	0.09663	1.22E-02	-0.38806	0.01209	#####	-0.57395	0.24964	1.85E-02	2.71E-01	6.36E-01	20	
ENSG00000066115	11	TM7SF3	27146747 rs487578	11	27115395	C	T	0.15805	0.247651	0.10643	1.73E-02	-0.25875	0.01199	#####	-0.95799	0.40485	1.80E-02	4.91E-01	1.83E-01	20	
ENSG00000067542	11	TUBA1A	49580483 rs111868	11	49515130	T	C	0.02783	-0.64116	0.3817	3.97E-02	0.4493	0.04688	1.07E-26	-1.28413	0.63571	3.44E-02	1.26E-01	2.31E-01	19	
ENSG00000198876	11	RAN	54194844 rs19484	11	54194844	G	T	0.20775	-0.2317	0.07985	8.67E-03	0.26705	0.01106	8.98E-78	1.26939	0.48303	9.35E-03	4.17E-02	6.80E-01	20	
ENSG00000063636	11	EIF4B	53417967 rs795744	11	53408580	A	G	0.16799	-0.17598	0.08247	3.29E-02	0.4451	0.01728	#####	-0.38753	0.18221	3.34E-02	1.34E-01	4.22E-01	20	
ENSG00000167778	11	SPRYD3	53465796 rs730263	11	53471929	C	T	0.17594	0.171526	0.06642	4.72E-02	0.18961	0.01024	1.32E-76	0.904648	0.45839	4.84E-02	1.43E-01	2.96E-02	20	
ENSG00000135414	11	GDF11	56143987 rs730220	11	56449435	A	C	0.32704	0.186879	0.07855	1.73E-02	-0.06746	0.00682	4.93E-15	-2.77021	1.21692	2.28E-02	4.55E-02	9.91E-01	19	
ENSG00000139531	11	SUXO	56395694 rs187391	11	56379042	G	C	0.39065	0.172038	0.07397	2.90E-02	-0.33661	0.00787	#####	-0.93109	0.22008	2.02E-02	1.40E-01	9.58E-01	20	
ENSG00000197728	11	RFX5	56438459 rs151319	11	56438459	G	T	0.40855	0.18089	0.07923	2.90E-02	0.34927	0.00854	#####	0.20883	0.519691	2.02E-02	7.67E-01	7.95E-01	20	
ENSG00000065545	11	ERBB3	56484635 rs111717	11	56470625	C	G	0.41451	0.157359	0.07249	2.09E-02	-0.16793	0.01015	2.05E-94	-0.93707	0.43398	3.08E-02	4.72E-02	8.66E-01	20	
ENSG00000111537	11	IFNG	68551037 rs287096	11	68426626	T	C	0.28827	-0.15421	0.07576	4.18E-02	-0.09155	0.00851	2.9E-27	1.68433	0.84217	4.55E-02	2.21E-02	9.47E-01	20	
ENSG00000179941	11	BBS10	76740238 rs344921	11	76804493	C	T	0.23459	-0.17165	0.08634	4.68E-02	-0.24131	0.00898	#####	0.71132	0.38976	4.74E-02	2.83E-01	3.47E-02	20	
ENSG00000179104	11	TMTC2	83304664 rs111197	11	83523857	A	C	0.333	-0.16394	0.13712	2.50E-02	-0.10466	0.00824	4.9E-37	1.56847	0.70948	2.72E-02	1.75E-01	2.74E-01	20	
ENSG00000198107	11	RAN	8503933 rs58369	11	85089320	C	T	0.14016	0.28927	0.17496	4.59E-02	0.55433	0.01063	#####	0.238691	0.23496	1.52941	4.39E-02	3.82E-01	7.95E-01	20
ENSG00000193324	11	TMTC3	88564868 rs111054	11	88490111	T	C	0.01292	-0.23288	0.23529	4.02E-02	0.46462	0.04275	1.65E-27	-1.13722	0.5176	2.80E-02	2.80E-02	5.74E-01	20	
ENSG00000257345	11	LINC02413	93403295 rs476050	11	93349509	T	A	0.11133	0.228142	0.09885	2.06E-02	0.28559	0.02964	5.66E-22	0.798858	0.3549	2.24E-02	1.21E-01	1.72E-01	20	
ENSG00000173598	11	NUDT4	93784341 rs322880	11	93796613	A	C	0.14215	0.217963	0.09867	2.72E-02	-0.14369	0.01137	1.24E-36	-1.19619	0.69712	2.96E-02	1.31E-01	1.85E-01	20	
ENSG00000111142	11	METAP2	95888455 rs301037	11	95877531	C	C	0.08847	0.241394	0.10624	2.31E-02	0.26054	0.01247	5.90E-97	0.926517	0.41015	2.39E-02	1.83E-01	9.49E-01	20	
ENSG00000117145	11	TRAF3	9617996 rs47																		

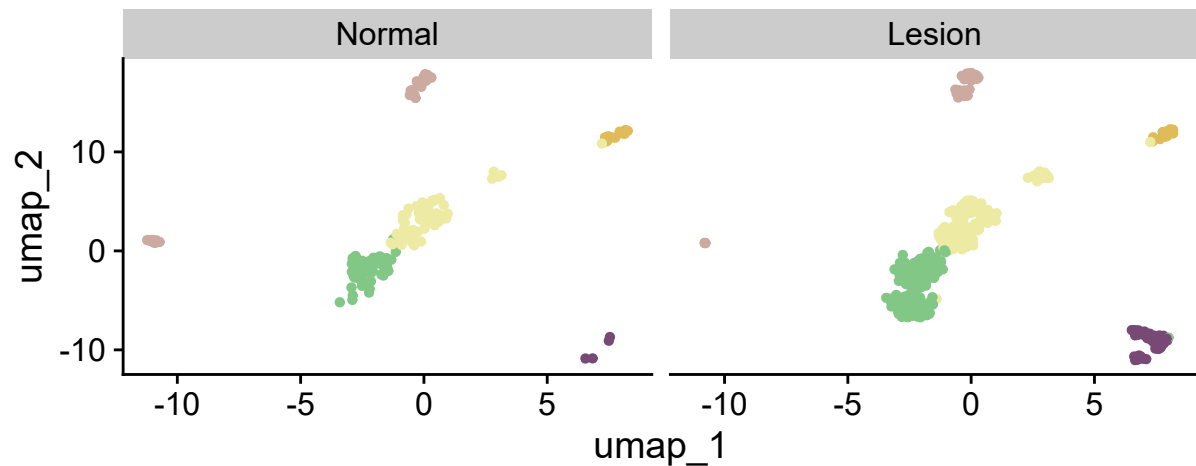
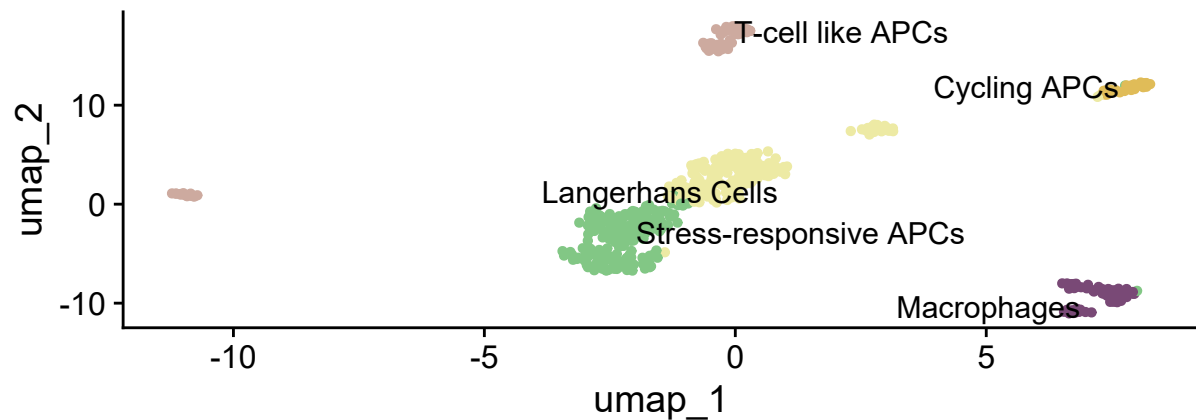
ENSG00000132600	16	PRMT7	68368671	rs795430	16	68387341	T	C	0.11332	0.215577	0.10124	3.32E-02	0.42025	0.01308	#####	0.512972	0.24143	3.36E-02	2.73E-02	3.58E-01	20
ENSG00000184939	16	ZFP90	68588884	rs805831	16	68584151	G	A	0.20875	-0.24184	0.09449	1.05E-02	-0.8445	0.00824	#####	0.266371	0.11193	1.05E-02	7.16E-02	7.66E-02	20
ENSG00000157423	16	HYDIN	7102593	rs764605	16	71037121	G	A	0.0169	0.50024	0.29222	2.91E-02	0.0293	0.2459	#####	0.9655	-1.30174	0.80227	3.37E-02	2.98E-01	24
ENSG00000103196	16	CRISPLD2	84839882	rs805743	16	84839854	C	A	0.27435	0.167226	0.07875	3.32E-02	-0.56417	0.00817	#####	-0.2393	0.13963	3.93E-02	4.07E-01	1.58E-01	17
ENSG00000225614	16	ZNF469	86500522	rs726314	16	86002342	C	G	0.19384	0.2053	0.08306	1.34E-02	-0.0827	0.01165	1.26E-12	-2.48237	1.06344	1.96E-02	6.06E-02	1.97E-01	20
ENSG00000167515	16	TRAPPC2L	88205861	rs382606	16	88927221	T	G	0.34493	-0.23275	0.06785	2.46E-03	-0.27369	0.00956	#####	0.850406	0.28236	2.60E-03	4.82E-02	3.65E-01	20
ENSG00000167523	16	SPATA33	89730945	rs164749	16	89776824	C	G	0.48509	0.150493	0.07127	3.88E-02	0.12599	0.00892	2.29E-47	1.19449	0.58348	4.06E-02	5.60E-03	6.26E-01	20
ENSG00000167530	16	SOX2	9052364	rs707772	17	9052364	G	T	0.22664	0.19491	0.05773	4.02E-02	0.03429	0.00824	#####	0.7665	2.23E-02	0.38227	3.07E-02	2.99E-01	24
ENSG00000066320	17	NTN1	9036088	rs721919	17	91493922	C	G	0.26504	-0.18275	0.08278	2.46E-02	-0.11096	0.00901	4.33E-29	1.64896	0.74716	2.75E-02	2.57E-02	1.26E-01	20
ENSG00000006744	17	ARHGAP44	12793908	rs2523	17	12895815	C	T	0.39364	-0.14658	0.07348	4.61E-02	0.16198	0.00896	5.39E-73	-0.90493	0.4564	4.74E-02	1.78E-01	6.49E-01	20
ENSG00000239704	17	CDRT4	15373127	rs238815	17	15468444	A	C	0.32604	-0.22801	0.07369	1.97E-03	-0.27925	0.00873	#####	0.816942	0.2651	2.07E-03	1.70E-02	6.12E-01	20
ENSG00000223878	17	PPIAIP5	15410424	rs293817	17	15452008	C	G	0.32704	-0.22324	0.07369	1.97E-03	-0.27925	0.00873	#####	0.816942	0.2651	2.07E-03	1.70E-02	6.12E-01	20
ENSG00000187607	17	ZNF286A	15621882	rs124535	17	15613384	G	C	0.37078	-0.15864	0.07476	3.99E-02	-0.7025	0.01616	#####	0.225816	1.0655	3.41E-02	6.40E-03	3.23E-01	20
ENSG00000141027	17	NCOR1	16028108	rs108528	17	16174506	C	C	0.4831	0.155919	0.07182	2.99E-02	-0.31537	0.00779	#####	-0.4944	0.22806	3.02E-02	1.04E-02	7.73E-01	20
ENSG00000108474	17	PIGL	16186319	rs116519	17	16234462	G	A	0.50698	-0.15388	0.07182	3.97E-02	0.20276	0.00798	#####	-0.79302	0.35586	3.43E-02	1.95E-02	7.66E-01	20
ENSG00000169376	17	LRRF5	16370179	rs129387	17	16344100	C	T	0.45527	0.14411	0.07626	4.30E-02	0.40775	0.00638	#####	-0.35349	0.17651	4.44E-02	1.49E-02	7.40E-01	20
ENSG00000181350	17	LRRF75A	16370179	rs129387	17	16344100	C	T	0.45527	0.14411	0.07626	4.30E-02	0.40775	0.00638	#####	-0.35349	0.17651	4.44E-02	1.49E-02	7.40E-01	20
ENSG00000128438	17	TBC1D27P	16832191	rs602654	17	16837274	A	G	0.167	0.26483	0.09847	7.28E-03	0.11572	0.01236	7.55E-21	2.28373	0.88513	1.88E-03	8.35E-02	6.22E-01	20
ENSG00000240505	17	TNFRSF13B	16854140	rs557701	17	16841424	A	C	0.18688	0.225941	0.08016	6.72E-03	-0.06101	0.01013	1.69E-09	-3.7031	0.95179	1.83E-02	1.83E-02	4.66E-01	20
ENSG00000008711	17	PIGS	26889645	rs633274	17	26882994	T	A	0.17893	-0.24949	0.09738	1.04E-02	-0.11565	0.01089	2.39E-26	2.1572	0.86614	1.28E-02	6.28E-02	6.25E-01	20
ENSG00000109147	17	LINCOC	26922607	rs221979	17	27004305	C	A	0.2033	-0.16869	0.07626	2.71E-02	-0.26757	0.00697	#####	0.636841	0.28393	2.75E-02	4.17E-01	1.83E-01	20
ENSG00000161395	17	PGAP3	37840122	rs292155	17	37832735	T	C	0.31809	0.190414	0.07740	4.02E-02	0.35466	0.00823	#####	0.536442	0.21861	1.41E-02	2.67E-01	4.82E-01	20
ENSG00000141736	17	ERBB2	37865423	rs903506	17	37879762	G	A	0.32803	0.22144	0.07241	2.23E-03	0.06866	0.00843	3.68E-16	3.22495	1.2624	4.20E-03	2.57E-02	6.54E-01	20
ENSG00000161405	17	IKZF3	37907819	rs907901	17	37921742	C	G	0.48907	0.166469	0.07255	2.18E-02	-0.3593	0.00771	#####	-0.46331	0.20215	2.19E-02	4.46E-01	6.21E-01	20
ENSG00000173605	17	GSDMB	38068477	rs129362	17	38029120	C	G	0.48509	0.150493	0.07231	2.89E-02	0.83389	0.00643	#####	1.1895	0.08672	2.89E-02	2.03E-01	2.25E-01	20
ENSG00000172057	17	SRFBP2	4391381	rs123636	17	4391381	G	C	0.48509	0.150493	0.07231	2.89E-02	0.83389	0.00643	#####	1.1895	0.08672	2.89E-02	2.03E-01	2.25E-01	20
ENSG00000131095	17	GFAP	42988340	rs991649	17	42987524	C	G	0.26243	-0.15854	0.07421	4.06E-02	-0.06202	0.00803	3.96E-18	1.97426	0.99102	6.64E-02	9.75E-02	7.24E-01	20
ENSG00000228782	17	MRPL45P2	45484896	rs585129	17	45523858	C	T	0.4831	0.21111	0.06961	2.42E-03	-0.43373	0.01682	#####	-0.48674	0.1616	2.62E-03	8.98E-03	3.34E-01	20
ENSG00000141279	17	NPEPPS	45650474	rs104320	17	45624934	C	A	0.47515	-0.18985	0.07604	6.72E-03	-0.22098	0.00846	#####	0.85912	0.31868	7.02E-03	1.99E-02	3.82E-01	20
ENSG00000263766	17	KPNB1-DT	45740006	rs390896	17	45750596	G	A	0.46223	-0.17398	0.07013	1.04E-02	-0.11187	0.01907	4.47E-09	1.6072	0.68412	1.88E-02	1.48E-02	4.27E-01	20
ENSG00000198632	17	SPRY2	4712466	rs112882	17	4712466	C	A	0.42346	0.24991	0.07626	4.30E-02	0.35049	0.01154	#####	0.24584	0.24587	4.98E-02	8.41E-02	7.68E-01	20
ENSG00000173888	17	PHOSPHO1	47304428	rs116509	17	47345552	C	C	0.24354	0.175476	0.08043	3.68E-02	0.18384	0.0092	3.98E-89	0.95453	0.45959	7.98E-02	1.79E-01	5.17E-01	20
ENSG00000108821	17	COL1A1	48268291	rs989818	17	48278507	C	T	0.20676	-0.20224	0.09849	4.00E-02	0.08405	0.01046	1.8E-16	-2.40631	1.20945	4.66E-02	4.66E-02	2.03E-01	20
ENSG00000136449	17	MYCBPAP	48597303	rs650466	17	48580257	C	T	0.43738	-0.14324	0.07129	4.72E-02	-0.29367	0.00792	#####	0.487749	0.24619	4.76E-02	2.58E-01	8.87E-01	20
ENSG00000183691	17	NOG	54672005	rs287776	17	54712328	G	A	0.07058	-0.41508	0.16123	1.00E-02	-0.26928	0.01728	1.00E-54	1.54145	0.60867	1.11E-02	1.44E-02	2.22E-02	20
ENSG00000175156	17	ITP2	5812466	rs105392	17	5806393	T	G	0.44233	0.19777	0.07626	4.30E-02	0.11058	0.01552	2.02E-13	1.36879	0.7688	3.94E-02	3.15E-02	5.98E-01	20
ENSG00000108950	17	FAM20A	66563492	rs118548	17	66575174	G	A	0.18329	-0.22101	0.09304	1.70E-02	-0.15325	0.01013	9.99E-52	-1.44925	0.61461	1.84E-02	5.38E-02	3.24E-01	20
ENSG00000109066	17	TMEM104	72804270	rs349861	17	72773115	A	C	0.44036	0.183631	0.0695	8.24E-03	-0.0619	0.00795	6.98E-15	-2.96637	1.18651	1.24E-02	1.47E-02	4.57E-01	14
ENSG00000108479	17	GALK1	73754733	rs110634	17	73818872	A	G	0.19483	0.241121	0.09811	4.0E-02	-0.26016	0.01041	#####	-0.92682	0.37893	1.44E-02	2.81E-02	5.06E-01	20
ENSG00000220506	17	CDK3	73996533	rs116522	17	73969667	C	T	0.17992	-0.20931	0.10474	5.78E-03	-0.07917	0.01133	2.74E-12	3.65164	1.42241	1.03E-02	3.03E-02	3.09E-02	20
ENSG00000161547	17	SRFBP2	74173196	rs123636	17	74173196	C	T	0.48509	0.150493	0.07231	2.89E-02	0.83389	0.00643	#####	1.1895	0.08672	2.89E-02	2.03E-01	2.25E-01	20
ENSG00000141582	17	CBX4	77810091	rs128525	17	77869802	C	T	0.39662	-0.29467	0.08095	1.15E-02	-0.14916	0.00929	4.98E-137	1.91701	0.54935	1.25E-02	2.19E-02	7.24E-01	20
ENSG00000173821	17	RNF213	78303625	rs807902	17	78274186	T	A	0.31412	0.170407	0.07608	2.51E-02	0.05661	0.00929	1.09E-09	3.10123	1.43179	3.55E-02	7.79E-02	5.44E-01	20
ENSG00000171246	17	NPTX1	78446295	rs341779	17	78669798	T	G	0.18092	-0.22134	0.10699	3.88E-02	-0.34104	0.0102	#####	0.849021	0.31432	3.89E-02	6.72E-02	4.22E-01	20
ENSG00000141954	17	RPTOR	78729395	rs406217	17	78676905	C	T	0.18092	-0.22134	0.10699	3.88E-02	-0.34104	0.0102	#####	0.849021	0.31432	3.89E-02	6.72E-02	4.22E-01	20
ENSG00000207736	17	MIR1250	79121035	rs496940	17	79121035	C	T	0.48933	0.18767	0.06944	6.72E-03	-0.13058	0.01552	2.02E-13	1.36879	0.7688	3.94E-02	3.15E-02	5.98E-01	20
ENSG00000181409	17	AATK	79115486	rs496940	17	79123135	T	C	0.39364	0.182821	0.06998	8.89E-03	-0.05213	0.00998	#####	-0.34036	1.3025	8.97E-03	5.06E-02	2.53E-01	20
ENSG00000186765	17	FSCN2	79499789	rs563242	17	79463324	A	G	0.36183	0.217318	0.07179	2.47E-03	0.06378	0.00937	2.76E-11	-3.48364	1.26419	8.86E-03	5.86E-03	1.96E-01	20
ENSG00000178927	17	CYBC1	80044585	rs375191	17	80406552	C	G	0.12624	0.206231	0.09417	3.20E-02	-0.45289	0.01136	#####	-0.45537	0.21265	3.22E-02	7.98E-01	8.23E-02	20
ENSG00000142458	17	FNBP3	80053381	rs224655	17	80060393	T	A	0.40054	-0.15393	0.07626	4.30E-02	-0.80463	0.00679	2.99E-02	1.00857	0.98857	3.14E-02	3.32E-02	1.11E-01	20
ENSG00000141556	17	TBCD	80085332	rs807258	17	80083822	A	G													

ENSG00000211658	22 IGLV3-27	23011017 rs287706	22 23013171 C	T	0.05964	-0.30242	0.14382	3.55E-02	0.72368	0.04631	4.74E-55	-0.41789	0.20053	3.72E-02	7.57E-03	8.82E-01	20
ENSG00000253234	22 IGLV2-5	23199075 rs390407	22 23258231 C	T	0.24354	0.155208	0.07448	3.72E-02	-0.34048	0.0215	1.72E-56	-0.45586	0.22063	3.88E-02	5.36E-02	7.93E-01	20
ENSG00000211672	22 IGLV4-3	23213950 rs455941	22 23256260 G	T	0.24752	0.149271	0.07457	4.53E-02	-0.26249	0.02165	8.14E-34	-0.56868	0.28795	4.83E-02	4.83E-02	8.70E-01	20
ENSG00000211678	22 IGLJ3	23247117 rs285409	22 23249040 T	C	0.4841	0.158123	0.07442	3.36E-02	0.2992	0.02233	6.26E-41	0.528494	0.25185	3.59E-02	1.88E-01	8.43E-01	20
ENSG00000099974	22 DDTL	24311905 rs573897	22 24312629 G	C	0.10437	0.272789	0.11518	1.79E-02	0.59283	0.06357	1.10E-20	0.460146	0.20045	2.17E-02	9.43E-02	6.65E-01	20
ENSG00000180957	22 PITPNB	28281889 rs575266	22 28339350 T	C	0.05666	0.381561	0.17284	2.73E-02	0.38978	0.02555	1.51E-52	0.978912	0.44804	2.89E-02	1.24E-02	1.89E-01	20
ENSG00000100220	22 RTCB	32795905 rs12530	22 32783904 C	T	0.14811	-0.2144	0.08941	1.65E-02	-0.16488	0.01101	1.12E-50	1.30033	0.54917	1.79E-02	2.73E-02	9.45E-01	20
ENSG00000100336	22 APOL4	36593029 rs132735	22 36597891 T	G	0.27038	0.256808	0.07198	3.60E-04	0.13569	0.00874	2.19E-54	1.89267	0.54432	5.07E-04	4.23E-03	2.17E-01	20
ENSG00000100201	22 DDX17	38891555 rs226739	22 38889657 T	C	0.30418	0.191242	0.07544	1.12E-02	0.23051	0.00846	#####	0.82965	0.32869	1.16E-02	5.08E-02	9.69E-01	20
ENSG00000100216	22 TOMM22	39079385 rs575719	22 39038790 C	A	0.29523	0.163325	0.0763	3.23E-02	-0.11556	0.009	9.34E-38	-1.41335	0.66938	3.47E-02	2.38E-01	2.72E-01	20
ENSG00000100221	22 JOSD1	39089554 rs575066	22 39080638 A	T	0.29324	0.156356	0.07637	4.06E-02	-0.2491	0.00891	#####	-0.62769	0.30739	4.12E-02	4.37E-02	6.48E-01	20
ENSG00000183741	22 CBX6	39262887 rs729207	22 39266451 A	C	0.17197	0.196992	0.09888	2.84E-02	-0.4063	0.00968	#####	-0.48485	0.22151	2.86E-02	3.12E-01	3.66E-01	20
ENSG00000100401	22 RANGAP1	41661935 rs565585	22 41700361 G	A	0.43339	-0.14928	0.07192	3.79E-02	0.10472	0.00796	1.52E-39	-1.42551	0.69527	4.03E-02	6.69E-02	3.89E-02	20
ENSG00000093000	22 NUP50	45571807 rs729082	22 45527815 T	C	0.27932	0.197705	0.08099	1.46E-02	-0.26679	0.0088	#####	-0.74106	0.30456	1.50E-02	7.12E-03	9.17E-02	20
ENSG00000196576	22 PLXNB2	50729732 rs622412	22 50747507 A	G	0.43042	-0.1847	0.0725	1.08E-02	-0.28094	0.01021	#####	0.657445	0.25917	1.12E-02	6.38E-01	6.48E-01	20
ENSG00000205593	22 DENND6B	50757940 rs622412	22 50753973 C	T	0.34493	-0.15431	0.0745	3.83E-02	-0.30089	0.01001	#####	0.512863	0.2482	3.88E-02	1.32E-01	8.81E-01	20

Supplementary Table S4 Primer sequences used for quantitative real-time PCR (qPCR)

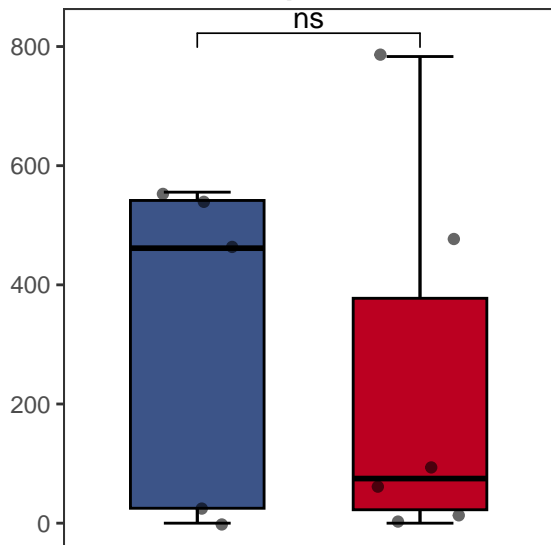
Primer Name	Primer Sequence (5' to 3')
Human TAPBP forward	CCTGGAGGTAGCAGGTCTTTC
Human TAPBP reverse	ATCCTTGCAGGTGGACAGGTA □
Human HLA class I forward	AAAAGGAGGGAGTTACACTCAGG
Human HLA class I reverse	GCTGTGAGGGACACATCAGAG
Human ACTB forward	CATGTACGTTGCTATCCAGGC □
Human ACTB reverse	CTCCTTAATGTCACGCACGAT □

APC Subgroups

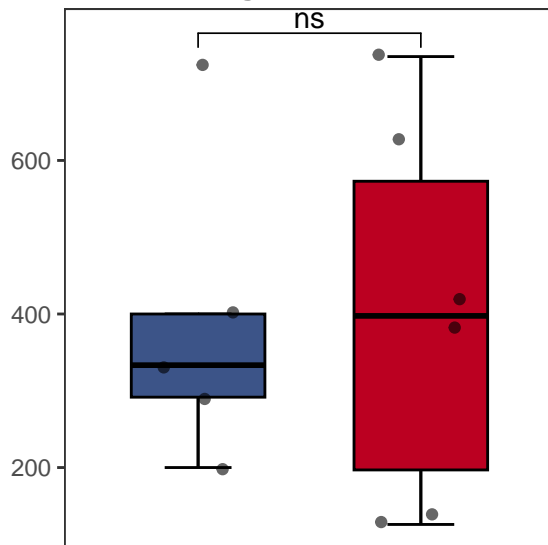


APC Subgroup Infiltration

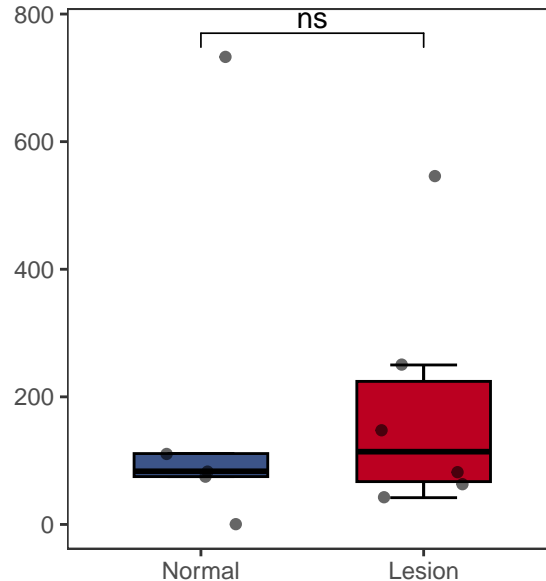
Stress-responsive APCs



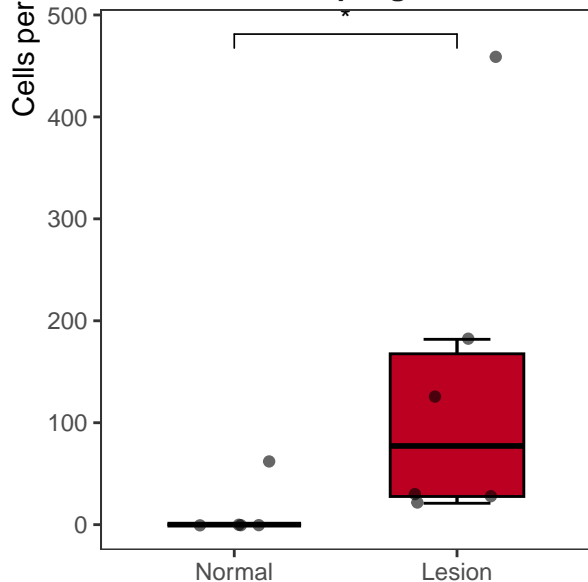
Langerhans Cells



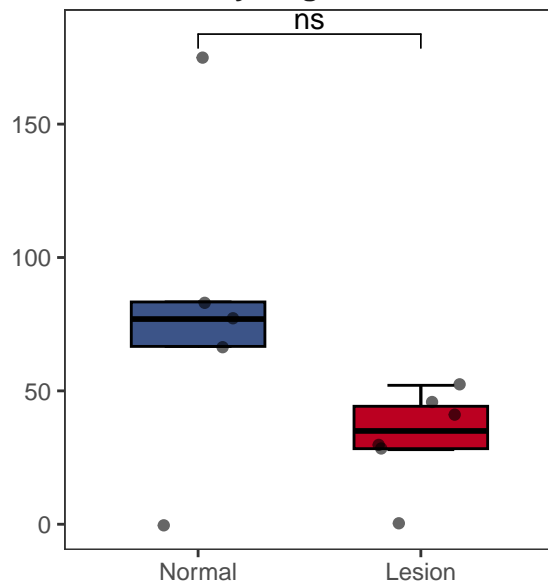
T-cell like APCs



Macrophages



Cycling APCs



group

