Additional file 13: Table S10A. Differential expression analysis of South Africa cohort (2h)

Max group means: For each group in the statistical comparison, the average reads per kilobase of transcript per million reads mapped (RPKM) is calculated. This value is the maximum of the average RPKM's. Log2 fold change: log2 ratio of gene expression of infected/control. P-value: unadjusted p-value. FDR p-value: the false discovery rate corrected p-value.

Name	Chromosome	Region	Identifier	Max group means	Log2 fold change	p-value	FDR p-value
BSCL2	11	complement(62689289..62709845)	ENSG00000168000	3.0236354	1.409865	2.33361E-13	3.49855E-09
AKAP12	6	151239967..151358559	ENSG00000131016	28.93872	0.609386	9.97186E-12	7.47491E-08
gene:ENSG	12	complement(56285916..56316059)	ENSG00000144785	3.9505878	1.306187	5.24856E-10	2.62288E-06
MT2A	16	56608584..56609497	ENSG00000125148	1766.0052	0.493035	1.2972E-08	4.86191E-05
MT1M	16	56632659..56633981	ENSG00000205364	171.46759	0.846304	2.7656E-08	8.29237E-05
gene:ENSG	1	complement(160997957..1610389	ENSG00000270149	5.9072701	-0.76175	1.26872E-07	0.000237759
MT1A	16	56638666..56640087	ENSG00000205362	86.17611	0.875079	1.11854E-07	0.000237759
MT-ATP8	MT	8366..8572	ENSG00000228253	1169.7826	0.465683	1.0496E-07	0.000237759
MT1H	16	56669814..56671129	ENSG00000205358	72.003411	0.740344	1.59183E-07	0.000265164
MT1G	16	complement(56666730..56668065)	ENSG00000125144	1013.97	0.690287	1.85906E-07	0.00027871
PDCD6-AH	5	271670..438291	ENSG00000288622	0.203082	-4.6936	2.17799E-07	0.00029684
gene:ENSG	7	66628958..66811189	ENSG00000284461	0.9824603	0.788657	6.18164E-07	0.000772292
gene:ENSG	12	complement(6556886..6607367)	ENSG00000285238	3.0257621	-1.24602	6.79587E-07	0.000783721
PPAN-P2R	19	10106223..10114780	ENSG00000243207	0.5296556	-2.39044	8.37152E-07	0.00089647
gene:ENSG	11	31812391..32104665	ENSG00000285283	6.2513767	-0.82052	9.64184E-07	0.000903441
MT1X	16	56682470..56684196	ENSG00000187193	367.39634	0.706729	9.19039E-07	0.000903441
MT1E	16	56625475..56627112	ENSG00000169715	227.33367	0.714194	1.02992E-06	0.000908267
MT1B	16	56651886..56653204	ENSG00000169688	6.6287131	1.281833	1.14722E-06	0.000955503
gene:ENSG	14	complement(31334312..31457441)	ENSG00000203546	0.2731843	1.931727	1.23375E-06	0.000973491
ATF3	1	212565334..212620777	ENSG00000162772	92.506719	0.424943	1.47171E-06	0.00106367
CDK3	17	76000906..76005999	ENSG00000250506	1.6133425	-0.95084	1.48993E-06	0.00106367
HYPK	15	43796142..43804427	ENSG00000242028	5.6481665	0.31444	2.62799E-06	0.001790852
IL36RN	2	113058638..113065382	ENSG00000136695	8.2797449	0.45478	4.33687E-06	0.002826888
HBEGF	5	complement(140332843..1403466	ENSG00000113070	154.70374	0.391975	7.00807E-06	0.0042026
SCGB1A1	11	62405103..62423195	ENSG00000149021	18.010758	0.996231	6.73847E-06	0.0042026
OVOL1	11	65787063..65797214	ENSG00000172818	9.6890093	0.418221	1.32878E-05	0.007661934
ERRFI1	1	complement(8004404..8026309)	ENSG00000116285	38.54294	0.387107	1.62089E-05	0.00900013
CCL3L1	17	complement(36194869..36196758)	ENSG00000276085	416.9838	0.669603	1.87667E-05	0.010048207
MT-ND6	MT	complement(14149..14673)	ENSG00000198695	2104.7213	0.356742	3.85742E-05	0.019941538
gene:ENSG	9	complement(32455323..32552603)	ENSG00000288684	0.5295208	2.758007	4.84944E-05	0.024234266
ARC	8	complement(142611049..1426144	ENSG00000198576	2.4933617	0.607713	5.19594E-05	0.02491927
CCL2	17	34255218..34257203	ENSG00000108691	31.411017	0.399838	5.31895E-05	0.02491927
IL1B	2	complement(112829751..1128368	ENSG00000125538	1733.0887	0.492269	6.69445E-05	0.029518598
TM4SF19-	3	complement(196316082..1963383	ENSG00000273331	4.7087128	0.738273	6.60384E-05	0.029518598
ZBTB2	6	complement(151364115..1513915	ENSG00000181472	12.885117	0.369966	7.41016E-05	0.031740884
G0S2	1	209675412..209676390	ENSG00000123689	296.25493	0.362132	8.78441E-05	0.036033448
gene:ENSG	11	complement(62559603..62591531)	ENSG00000255508	3.6613566	-0.43311	9.19594E-05	0.036033448
MT1F	16	56657731..56660698	ENSG00000198417	164.26356	0.488914	9.15802E-05	0.036033448
C17orf107	17	4899418..4902934	ENSG00000205710	2.8851871	0.486338	9.3737E-05	0.036033448
NDUFA13	19	19515736..19529054	ENSG00000186010	69.690161	0.234599	9.70891E-05	0.03638898
SERPINB2	18	63871692..63903888	ENSG00000197632	164.91586	0.559754	0.000114397	0.041830369
RSRP1	1	complement(25242249..25338213)	ENSG00000117616	9.4503162	-0.35648	0.000143332	0.047971839
CXCL8	4	73740541..73743716	ENSG00000169429	3825.5435	0.329735	0.000139458	0.047971839
UPK3BL1	7	complement(102637025..1026427	ENSG00000267368	2.5622095	-1.78825	0.000134854	0.047971839
MT-ND1	MT	3307..4262	ENSG00000198888	2632.251	0.328995	0.000143992	0.047971839

Additional file 13: Table S10B. Differential expression analysis of South Africa cohort (24h)

Name	Chromosome	Region	Identifier	Max group means	Log2 fold change	p-value	FDR p-value
CXCL10	4	complement(76021118..7602349	ENSG00000169245	62.80219	5.639189	3.29538E-36	4.81521E-32
ISG20	15	88635670..88656483	ENSG00000172183	8.883613	2.709466	1.80396E-32	1.31797E-28
GBP4	1	complement(89181144..8919894	ENSG00000162654	13.56487	2.169912	3.93303E-31	1.91565E-27
IFI35	17	43006740..43014456	ENSG00000068079	93.39062	1.310776	1.53147E-27	5.59448E-24
BATF2	11	complement(64987945..6499701	ENSG00000168062	6.600998	1.95962	1.06523E-26	3.11304E-23
EPSTI1	13	complement(42886388..4299227	ENSG00000133106	17.95844	2.05966	7.4863E-26	1.82316E-22
IDO1	8	39902275..39928790	ENSG00000131203	10.39992	2.019104	3.29293E-25	6.87376E-22
CXCL11	4	complement(76033682..7604141	ENSG00000169248	4.64055	4.749733	6.48941E-25	1.18529E-21
PSMB9	6	32844136..32859851	ENSG00000240065	96.83706	1.3142	1.57247E-24	2.553E-21
C1S	12	6988259..7071032	ENSG00000182326	3.08998	1.933262	4.54502E-24	6.64119E-21
STAT1	2	complement(190908460..191020	ENSG00000115415	57.18212	1.435581	2.84572E-22	3.78015E-19
IFIT3	10	89327307..89377473	ENSG00000119917	61.96066	1.917808	4.17532E-22	5.08415E-19
XAF1	17	6755447..6775647	ENSG00000132530	19.46154	1.956629	9.88361E-22	1.11092E-18
IRF7	11	complement(612553..615983)	ENSG00000185507	29.19599	1.471127	5.45526E-21	5.31415E-18
CCL8	17	34319435..34321402	ENSG00000108700	9.032363	3.613346	5.16389E-21	5.31415E-18
HELZ2	20	complement(63558086..6357423	ENSG00000130589	9.516842	2.009613	1.33276E-20	1.21715E-17
TAP1	6	complement(32845209..3285381	ENSG00000168394	107.2633	1.288834	2.03739E-20	1.7512E-17
ETV7	6	complement(36354091..3638780	ENSG00000010030	1.725751	2.405316	2.16005E-20	1.75348E-17
ISG15	1	1001138..1014540	ENSG00000187608	162.3822	1.93527	7.62771E-20	5.86611E-17
IL15RA	10	complement(5943639..5978187)	ENSG00000134470	5.824782	1.277155	9.9536E-20	7.2721E-17
APOL3	22	complement(36140330..3616617	ENSG00000128284	5.749211	1.436725	1.69421E-19	1.17885E-16
FBXO6	1	11664200..11674354	ENSG00000116663	27.16848	1.111714	4.88611E-19	3.24527E-16
DDX60	4	complement(168216291..168318	ENSG00000137628	4.028236	1.337931	4.81216E-18	3.05718E-15
NLRC5	16	56989485..57083531	ENSG00000140853	4.623732	1.229135	1.67957E-17	1.02258E-14
DHX58	17	complement(42101404..4211271	ENSG00000108771	7.59651	1.170161	2.08585E-17	1.21913E-14
NEXN	1	77888513..77943895	ENSG00000162614	4.221094	2.391494	8.43919E-17	4.74283E-14
LAP3	4	17577198..17607972	ENSG00000002549	162.2877	1.134688	1.01139E-16	5.47349E-14
TNFSF10	3	complement(172505508..172523	ENSG00000121858	4.702353	2.87186	7.07722E-16	3.6933E-13
AIM2	1	complement(159062484..159147	ENSG00000163568	6.502568	1.62214	7.80698E-16	3.93364E-13
CXCR4	2	complement(136114349..136118	ENSG00000121966	17.09953	-0.817534	1.1453E-15	5.39843E-13
IFIT2	10	89283694..89309271	ENSG00000119922	53.51509	2.016237	1.11397E-15	5.39843E-13
TRIM22	11	5689697..5737089	ENSG00000132274	30.08608	1.006517	2.0528E-15	9.37358E-13
CD40	20	46118278..46129863	ENSG00000101017	68.95752	0.974583	3.54009E-15	1.56751E-12
GBP1	1	complement(89051882..8906536	ENSG00000117228	101.1965	1.582148	5.38982E-15	2.31635E-12
IL3RA	X	1336616..1382689	ENSG00000185291	18.23311	0.684418	5.76943E-15	2.40865E-12
PARP9	3	complement(122527924..122564	ENSG00000138496	22.25833	1.125007	7.18036E-15	2.91443E-12
SAMD9L	7	complement(93130056..9314838	ENSG00000177409	27.55765	1.227874	1.4943E-14	5.90128E-12
APOL1	22	36253071..36267530	ENSG00000100342	29.65888	0.974585	1.57666E-14	6.06267E-12
STAT2	12	complement(56341597..5636016	ENSG00000170581	36.42297	0.933715	2.69368E-14	1.00923E-11
GIMAP8	7	150450630..150479393	ENSG00000171115	1.817144	1.5525	6.22936E-14	2.27558E-11
IL27	16	complement(28499362..2851205	ENSG00000197272	4.329771	1.933054	6.40814E-14	2.2838E-11
SP110	2	complement(230165186..230225	ENSG00000135899	9.953133	1.019112	6.89046E-14	2.39722E-11
RTP4	3	187368385..187372076	ENSG00000136514	6.374605	1.127444	7.37973E-14	2.50773E-11
SCIMP	17	complement(5208920..5234860)	ENSG00000161929	17.50675	0.976436	1.51564E-13	5.0333E-11
ADAMTS15	11	130448645..130476645	ENSG00000166106	1.37905	-1.3139	1.74338E-13	5.66093E-11
ANKRD22	10	complement(88819896..8885184	ENSG00000152766	1.53304	2.445187	1.81947E-13	5.77959E-11
VAMP5	2	85584431..85593406	ENSG00000168899	22.60279	1.623946	2.02875E-13	6.17584E-11
OAS2	12	112978395..113011723	ENSG00000111335	30.763	1.542735	2.00973E-13	6.17584E-11
CCL2	17	34255218..34257203	ENSG00000108691	105.6951	1.060229	2.19159E-13	6.53542E-11
TNFSF13B	13	108251240..108308484	ENSG00000102524	17.31771	1.150748	2.39894E-13	7.01068E-11
WARS1	14	complement(100333790..100376	ENSG00000140105	175.7687	1.014859	3.95575E-13	1.13336E-10
IFIH1	2	complement(162267074..162318	ENSG00000115267	31.24539	1.169699	4.1003E-13	1.15218E-10
HERC6	4	88378739..88443097	ENSG00000138642	6.002294	1.263057	4.55894E-13	1.2456E-10

PSME2	14	complement(24143362..2414757	ENSG00000100911	118.5654	0.858642	4.60324E-13	1.2456E-10
IFI44	1	78649796..78664078	ENSG00000137965	39.65962	1.727822	5.25806E-13	1.39263E-10
IFITM3	11	complement(319676..329475)	ENSG00000142089	35.1449	1.589219	5.3372E-13	1.39263E-10
MX1	21	41420020..41470071	ENSG00000157601	63.58998	2.245262	5.4657E-13	1.40114E-10
APOL6	22	35648446..35668404	ENSG00000221963	15.62656	0.84619	5.83469E-13	1.46994E-10
CMPK2	2	complement(6840570..6866635)	ENSG00000134326	16.26845	2.018562	8.55502E-13	2.11875E-10
ADCY1	7	45574140..45723116	ENSG00000164742	0.833372	-1.30496	1.09401E-12	2.66428E-10
PLEKHO1	1	150149183..150164720	ENSG00000023902	36.19575	0.668736	1.26509E-12	3.0304E-10
HAPLN3	15	complement(88877294..8889559	ENSG00000140511	1.413739	3.348866	1.40542E-12	3.31227E-10
ADAP1	7	complement(897900..955407)	ENSG00000105963	20.07915	0.580063	2.16604E-12	5.02383E-10
ACOD1	13	76948511..76958638	ENSG00000102794	2.353769	2.469906	4.00375E-12	9.14106E-10
OCSTAMP	20	complement(46540946..4655065	ENSG00000149635	6.671304	0.917208	4.33253E-12	9.73953E-10
CFB	6	31945650..31952084	ENSG00000243649	7.596869	0.981107	4.91097E-12	1.08726E-09
JAML	11	complement(118193725..118225	ENSG00000160593	28.00029	-1.015487	6.44823E-12	1.40629E-09
NMI	2	complement(151270470..151289	ENSG00000123609	34.07928	0.566204	6.73319E-12	1.42588E-09
IL15	4	141636583..141733987	ENSG00000164136	1.152822	1.053341	6.66119E-12	1.42588E-09
SEMA4D	9	complement(89360787..8949813	ENSG00000187764	3.708495	0.926495	7.99677E-12	1.66927E-09
NUB1	7	151341772..151378449	ENSG00000013374	16.07721	0.554147	8.85709E-12	1.82281E-09
C1RL	12	complement(7089587..7109238)	ENSG00000139178	5.657986	0.769359	1.06665E-11	2.16471E-09
SIGLEC1	20	complement(3686970..3712600)	ENSG00000088827	24.88286	1.758126	1.91646E-11	3.83607E-09
gene:ENSG	12	57772660..57797554	ENSG00000257921	0.564247	-3.85741	1.96034E-11	3.87088E-09
APOBEC3A	22	38952741..38992778	ENSG00000128383	2.403681	3.360353	2.33005E-11	4.53956E-09
DYNLT1	6	complement(158636474..158644	ENSG00000146425	143.9426	0.628322	2.37898E-11	4.5739E-09
SECTM1	17	complement(82321024..8233407	ENSG00000141574	10.20428	1.344277	3.60627E-11	6.84347E-09
CCNG2	4	77157207..77433388	ENSG00000138764	3.317427	-0.614155	3.69669E-11	6.92514E-09
PARP14	3	122680839..122730840	ENSG00000173193	25.14059	0.935561	3.83441E-11	7.0922E-09
DDX58	9	complement(32455302..3252620	ENSG00000107201	12.58762	1.49556	5.94081E-11	1.07169E-08
MEGF9	9	complement(120600811..120714	ENSG00000106780	9.632551	-0.537058	5.92831E-11	1.07169E-08
GPA33	1	complement(167052836..167166	ENSG00000143167	7.86592	-0.65055	7.73373E-11	1.37811E-08
GSDMD	8	143553207..143563062	ENSG00000104518	24.23532	0.526161	9.71695E-11	1.71065E-08
IFIT1	10	89392546..89406487	ENSG00000185745	27.13228	2.592121	9.99951E-11	1.73944E-08
MOV10	1	112673141..112700746	ENSG00000155363	8.237789	0.652207	1.10597E-10	1.90122E-08
PDCD6-AHI	5	271670..438291	ENSG00000288622	0.264964	-4.846208	1.65702E-10	2.8154E-08
OAS3	12	112938051..112976460	ENSG00000111331	26.5667	1.502815	1.89257E-10	3.17864E-08
ADAMTS1	21	complement(26835755..2684540	ENSG00000154734	0.933658	-1.408844	2.77409E-10	4.60626E-08
ARNTL2	12	27332854..27425289	ENSG00000029153	2.587399	0.842987	2.88676E-10	4.73947E-08
PLSCR1	3	complement(146515180..146544	ENSG00000188313	66.02875	0.99609	3.04887E-10	4.95001E-08
USP18	22	18150170..18177397	ENSG00000184979	23.90617	1.947487	3.39451E-10	5.45061E-08
GBP2	1	complement(89106132..8915045	ENSG00000162645	29.06386	1.003244	4.31929E-10	6.78639E-08
MERTK	2	111898607..112029561	ENSG00000153208	1.997928	-1.165517	4.30163E-10	6.78639E-08
IRF9	14	24161265..24166565	ENSG00000213928	35.8381	0.604937	4.77789E-10	7.42707E-08
APOL2	22	complement(36226209..3623995	ENSG00000128335	40.01591	0.588881	5.34293E-10	8.21799E-08
GIMAP4	7	150567369..150573953	ENSG00000133574	13.61163	0.54644	5.6212E-10	8.55594E-08
SHFL	19	10086122..10093252	ENSG00000130813	15.47354	0.639247	9.00498E-10	1.3565E-07
AXL	19	41219223..41261766	ENSG00000167601	16.80568	0.581694	9.60713E-10	1.43244E-07
CIITA	16	10866222..10943021	ENSG00000179583	4.571039	1.142108	1.01625E-09	1.49994E-07
GBP7	1	complement(89131742..8917600	ENSG00000213512	0.77157	2.004322	1.10425E-09	1.60876E-07
IQSEC3	12	66767..178455	ENSG00000120645	1.536856	-0.922706	1.12301E-09	1.60876E-07
PML	15	73994673..74047827	ENSG00000140464	7.833458	0.719609	1.12062E-09	1.60876E-07
SLAMF8	1	159826811..159837492	ENSG00000158714	102.0196	0.932413	1.20829E-09	1.71413E-07
RSPO3	6	127118671..127199481	ENSG00000146374	0.980263	1.755358	1.35279E-09	1.90067E-07
RAPGEF3	12	complement(47734363..4777104	ENSG00000079337	1.573389	-0.811045	1.43661E-09	1.99922E-07
RNF213	17	80260866..80398786	ENSG00000173821	19.98588	0.827949	1.53087E-09	2.11029E-07
COLEC12	18	complement(316737..500722)	ENSG00000158270	12.62186	-0.718562	1.6292E-09	2.20425E-07
CSF2RB	22	36913628..36940439	ENSG00000100368	26.16428	0.674718	1.62675E-09	2.20425E-07
RCN1	11	32091074..32105722	ENSG00000049449	22.88085	0.492853	1.67285E-09	2.24253E-07
EIF2AK2	2	complement(37099210..3715752	ENSG00000055332	7.399838	0.861916	1.99266E-09	2.64697E-07
TPD52L1	6	125119049..125264407	ENSG00000111907	2.006309	-0.917182	2.21382E-09	2.91426E-07

SP140	2	230203110..230313215	ENSG00000079263	6.816703	0.683437	2.33566E-09	3.0472E-07
PSMB8	6	complement(32840717..3284467	ENSG00000204264	93.70427	0.644881	3.18211E-09	4.11478E-07
MMP12	11	complement(102862736..102874	ENSG00000262406	42.25821	0.535296	3.39651E-09	4.33547E-07
GCH1	14	complement(54842008..5490282	ENSG00000131979	15.61963	1.589477	3.41212E-09	4.33547E-07
FPR2	19	51752026..51770531	ENSG00000171049	3.825879	1.004933	3.95857E-09	4.98644E-07
PARP10	8	complement(143977153..144012	ENSG00000178685	35.71873	0.740256	4.0638E-09	5.07524E-07
SLAMF7	1	160739057..160754821	ENSG00000026751	49.66667	1.188415	4.16545E-09	5.11475E-07
JADE2	5	134524312..134583230	ENSG00000043143	2.402367	0.641975	4.14915E-09	5.11475E-07
SPHK1	17	76376584..76387860	ENSG00000176170	19.47371	0.480163	4.39507E-09	5.35174E-07
SMAD6	15	66702236..66782849	ENSG00000137834	6.428983	-0.508498	5.48042E-09	6.61818E-07
DDO	6	complement(110391771..110415	ENSG00000203797	13.05483	0.507842	5.86286E-09	6.9867E-07
PIK3IP1	22	complement(31281594..3129253	ENSG00000100100	4.319591	-0.922339	5.88122E-09	6.9867E-07
SLC46A1	17	complement(28394642..2840719	ENSG00000076351	2.900559	-0.747221	6.61926E-09	7.80006E-07
IFI6	1	complement(27666064..2767221	ENSG00000126709	424.8429	0.975285	7.23318E-09	8.45529E-07
TYMP	22	complement(50525752..5053003	ENSG00000025708	354.0185	0.710538	7.7495E-09	8.98695E-07
UBE2L6	11	complement(57551656..5756828	ENSG00000156587	129.4188	0.753757	9.41723E-09	1.0835E-06
GBP5	1	complement(89258950..8927280	ENSG00000154451	9.347391	2.195589	1.04208E-08	1.1896E-06
TRIM69	15	44728988..44767829	ENSG00000185880	3.703507	0.825239	1.10941E-08	1.25664E-06
CCL7	17	34270221..34272242	ENSG00000108688	16.65857	0.923609	1.12764E-08	1.26746E-06
NCOA7	6	125781161..125932034	ENSG00000111912	6.275193	0.654197	1.21228E-08	1.3522E-06
PLEKHA4	19	complement(48837097..4886861	ENSG00000105559	1.864217	1.285935	1.25747E-08	1.39198E-06
RFX5	1	complement(151340640..151347	ENSG00000143390	11.35687	0.659855	1.3369E-08	1.46878E-06
GPR34	X	41688973..41697275	ENSG00000171659	22.09785	-0.615536	1.79877E-08	1.96146E-06
HERC5	4	88457119..88506163	ENSG00000138646	20.28466	1.417981	1.92806E-08	2.08687E-06
CXCL9	4	complement(76001275..7600750	ENSG00000138755	1.942541	2.467701	1.96572E-08	2.11199E-06
gene:ENSG	20	complement(35632340..3567454	ENSG00000272897	1.371621	4.409821	2.07481E-08	2.21293E-06
HMGB2	4	complement(173331376..173334	ENSG00000164104	16.55825	-0.488863	2.12606E-08	2.25116E-06
NT5C3A	7	complement(33014130..3306279	ENSG00000122643	21.9721	1.007838	2.72457E-08	2.86413E-06
CHST3	10	71964395..72013558	ENSG00000122863	2.100852	0.724816	2.77234E-08	2.89353E-06
ZC3HAV1	7	complement(139043515..139132	ENSG00000105939	6.12402	0.460241	2.80918E-08	2.91119E-06
PDK4	7	complement(95583499..9559651	ENSG00000004799	10.32281	-0.550994	2.94183E-08	3.02719E-06
GPR68	14	complement(91232532..9125392	ENSG00000119714	6.087864	0.679679	3.07308E-08	3.11832E-06
TANC2	17	63009556..63427699	ENSG00000170921	6.082463	-0.537575	3.0587E-08	3.11832E-06
SLC27A1	19	17468769..17506168	ENSG00000130304	3.744934	-0.499074	3.13128E-08	3.15547E-06
TRIM5	11	complement(5663195..5938619)	ENSG00000132256	5.746831	0.711032	3.26022E-08	3.2629E-06
SLC48A1	12	47753916..47782751	ENSG00000211584	7.528418	-0.478778	3.58325E-08	3.5618E-06
IFI44L	1	78619902..78646145	ENSG00000137959	9.952573	2.380568	3.99024E-08	3.93956E-06
CHI3L1	1	complement(203178931..203186	ENSG00000133048	19.51801	0.615945	4.16664E-08	4.07048E-06
gene:ENSG	11	93741664..93812378	ENSG00000284057	1.975849	1.17605	4.17857E-08	4.07048E-06
RAB24	5	complement(177301198..177303	ENSG00000169228	18.62013	0.471616	4.22177E-08	4.08533E-06
TOR1B	9	129803157..129811281	ENSG00000136816	27.16976	0.633538	4.26646E-08	4.10141E-06
TAP2	6	complement(32821833..3283877	ENSG00000204267	38.69986	0.681925	4.39606E-08	4.19838E-06
DOCK4	7	complement(111726110..112206	ENSG00000128512	7.598699	0.576378	4.67833E-08	4.43895E-06
IFI27	14	94104836..94116698	ENSG00000165949	36.36334	0.794426	5.2301E-08	4.93047E-06
UBA7	3	complement(49805209..4981395	ENSG00000182179	14.83577	0.630899	6.10295E-08	5.70996E-06
ADD3	10	109996368..110135565	ENSG00000148700	5.082668	-0.570126	6.13512E-08	5.70996E-06
GBP3	1	complement(89006679..8902289	ENSG00000117226	20.22413	0.439857	6.38304E-08	5.86597E-06
ZBP1	20	complement(57603846..5762057	ENSG00000124256	1.03925	1.692746	6.34764E-08	5.86597E-06
GMPR	6	16238587..16295549	ENSG00000137198	17.21284	1.089199	6.45288E-08	5.89309E-06
STON1	2	48529383..48598513	ENSG00000243244	1.447743	1.262361	6.59038E-08	5.94436E-06
STING1	5	complement(139475533..139482	ENSG00000184584	14.10322	0.748009	6.55971E-08	5.94436E-06
GAS2L3	12	100573683..100628288	ENSG00000139354	3.283345	-0.485335	6.97481E-08	6.25251E-06
PARP12	7	complement(140023749..140062	ENSG00000059378	32.52458	0.613788	8.40749E-08	7.49087E-06
MMD	17	complement(55392622..5542192	ENSG00000108960	10.95124	-0.463735	8.51606E-08	7.49619E-06
APOBEC3G	22	39077067..39087743	ENSG00000239713	8.369537	0.76392	8.5047E-08	7.49619E-06
SIK2	11	111602449..111730855	ENSG00000170145	9.411975	-0.429447	8.93772E-08	7.82023E-06
CCL24	7	complement(75810825..7582335	ENSG00000106178	61.8226	0.884267	9.05203E-08	7.87311E-06
SLC16A10	6	111087503..111231194	ENSG00000112394	1.695196	-0.600762	9.18151E-08	7.93847E-06

C1R	12	complement(7080214..7092540)	ENSG00000159403	0.882042	1.617387	9.73027E-08	8.36345E-06
FCGR1B	1	121087345..121097161	ENSG00000198019	4.323869	0.990086	9.93054E-08	8.48568E-06
JAK2	9	4984390..5129948	ENSG00000096968	6.482527	0.651763	9.99822E-08	8.49384E-06
SELENOP	5	complement(42799880..4288739	ENSG00000250722	1.499014	-1.89145	1.0669E-07	9.01131E-06
SLC31A2	9	113150976..113164140	ENSG00000136867	33.06632	0.697756	1.11268E-07	9.34396E-06
ANGPT2	8	complement(6499632..6563409)	ENSG00000091879	3.790844	-0.618641	1.14239E-07	9.53859E-06
gene:ENSG	7	99325879..99394653	ENSG00000284292	1.619933	-3.67752	1.153E-07	9.5725E-06
IKZF2	2	complement(212999691..213152	ENSG00000030419	1.663374	-0.581036	1.20217E-07	9.92436E-06
RSAD2	2	6865557..6898239	ENSG00000134321	34.65868	1.913605	1.22856E-07	1.00853E-05
PTPN22	1	complement(113813811..113871	ENSG00000134242	4.536184	-0.526895	1.24515E-07	1.01643E-05
KLHDC8B	3	49171598..49176486	ENSG00000185909	20.99318	-0.528105	1.26507E-07	1.02696E-05
HSD11B1	1	209686178..209734949	ENSG00000117594	14.33367	0.980576	1.35349E-07	1.09267E-05
IKBKE	1	206470476..206496889	ENSG00000263528	16.71142	0.722294	1.38349E-07	1.11075E-05
MX2	21	41361999..41409393	ENSG00000183486	13.39512	1.762211	1.63615E-07	1.30641E-05
TMEM170	6	11537749..11583524	ENSG00000205269	3.249403	-0.453865	1.87662E-07	1.49028E-05
APOL4	22	complement(36189124..3620484	ENSG00000100336	5.974058	1.155853	1.97152E-07	1.55718E-05
DTX3L	3	122564338..122575203	ENSG00000163840	13.81315	0.593019	2.07844E-07	1.6328E-05
IFIT5	10	89414568..89421605	ENSG00000152778	6.93844	0.654018	2.14133E-07	1.67321E-05
CISH	3	complement(50606489..5061177	ENSG00000114737	11.95203	0.669125	2.66781E-07	2.07352E-05
PNPLA3	22	43923792..43964488	ENSG00000100344	3.383018	-0.805334	2.69454E-07	2.08321E-05
CD47	3	complement(108043091..108091	ENSG00000196776	21.17849	0.464696	2.80439E-07	2.15672E-05
IFI16	1	158999968..159055155	ENSG00000163565	25.65217	0.588741	2.90548E-07	2.22277E-05
CD274	9	5450503..5470566	ENSG00000120217	44.47215	0.824073	3.07439E-07	2.33974E-05
IRF1	5	complement(132440440..132508	ENSG00000125347	32.43316	0.876852	3.14972E-07	2.38465E-05
FUCA1	1	complement(23845077..2386829	ENSG00000179163	103.8166	-0.618658	3.29501E-07	2.48179E-05
ITIH4	3	complement(52812962..5283068	ENSG00000055955	0.963786	1.403986	3.58743E-07	2.68818E-05
GCHFR	15	40764068..40767708	ENSG00000137880	79.8694	-0.612436	3.61399E-07	2.69427E-05
CPT1B	22	complement(50568861..5057846	ENSG00000205560	3.288857	0.791224	3.87114E-07	2.87133E-05
NFE2L3	7	26152198..26187137	ENSG00000050344	2.99983	0.879902	4.21294E-07	3.10906E-05
IL4I1	19	complement(49889654..4992953	ENSG00000104951	15.74521	0.993181	4.26624E-07	3.13258E-05
MEFV	16	complement(3242027..3256633)	ENSG00000103313	1.131043	1.209372	4.36403E-07	3.18836E-05
TMEM37	2	119429901..119438504	ENSG00000171227	0.985329	-1.730297	4.72293E-07	3.43341E-05
PLAU	10	73909177..73917496	ENSG00000122861	12.80791	0.427564	4.80653E-07	3.47688E-05
LSS	21	complement(46188141..4622882	ENSG00000160285	16.80333	0.604544	5.20302E-07	3.74515E-05
SPRED1	15	38252836..38357249	ENSG00000166068	12.01156	0.52577	5.25036E-07	3.7607E-05
CD48	1	complement(160678746..160711	ENSG00000117091	8.298441	0.72873	7.07863E-07	5.04551E-05
SCARF1	17	complement(1633858..1645744)	ENSG00000074660	4.220269	0.75647	7.28186E-07	5.16517E-05
PTGFRN	1	116909916..116990353	ENSG00000134247	2.524888	-0.530437	7.62333E-07	5.38126E-05
RCAN2	6	complement(46220736..4649197	ENSG00000172348	0.921865	1.52781	7.88401E-07	5.53852E-05
PSMB10	16	complement(67934506..6793686	ENSG00000205220	78.07665	0.509374	8.01923E-07	5.60655E-05
ACSF2	17	50426158..50474845	ENSG00000167107	9.53252	-0.434956	9.25451E-07	6.43937E-05
CBX6	22	complement(38861422..3887224	ENSG00000183741	5.267047	0.421985	9.37994E-07	6.49572E-05
MPZL2	11	complement(118253416..118264	ENSG00000149573	2.318974	-0.825372	9.49935E-07	6.54738E-05
TRIM21	11	complement(4384897..4393702)	ENSG00000132109	25.24479	0.565589	9.87935E-07	6.77733E-05
NCF1	7	74773962..74789376	ENSG00000158517	170.5081	1.001534	1.00186E-06	6.8407E-05
C17orf49	17	7014495..7017525	ENSG00000258315	11.59489	0.469696	1.01041E-06	6.86701E-05
MYO7B	2	127535802..127637729	ENSG00000169994	0.94178	0.745777	1.01751E-06	6.88329E-05
SOX4	6	21593751..21598619	ENSG00000124766	4.847022	-0.587153	1.03005E-06	6.90417E-05
SORL1	11	121452314..121633763	ENSG00000137642	1.864159	-0.47411	1.02823E-06	6.90417E-05
STMN1	1	complement(25884181..2590699	ENSG00000117632	8.251388	-0.658018	1.09868E-06	7.31163E-05
SLC41A2	12	complement(104801801..104958	ENSG00000136052	4.724132	0.605439	1.10085E-06	7.31163E-05
AGRN	1	1020120..1056118	ENSG00000188157	8.351724	0.651215	1.12756E-06	7.45515E-05
SLC25A28	10	complement(99610522..9962060	ENSG00000155287	15.28968	0.569432	1.17467E-06	7.73165E-05
ARID5A	2	96536743..96552634	ENSG00000196843	18.64741	0.397618	1.18488E-06	7.76392E-05
MLKL	16	complement(74671855..7470096	ENSG00000168404	21.17735	0.398838	1.22539E-06	7.99348E-05
CCL15	17	complement(35996440..3600155	ENSG00000275718	19.32062	1.468856	1.27401E-06	8.27371E-05
METTL1	12	complement(57768471..5777211	ENSG00000037897	19.87377	0.415798	1.32933E-06	8.59476E-05
MLLT6	17	38705273..38729795	ENSG00000275023	8.523915	0.525696	1.37733E-06	8.86589E-05

CLEC4E	12	complement(8533305..8540905)	ENSG00000166523	17.74522	0.815034	1.42503E-06	9.13269E-05
CD22	19	35319261..35347361	ENSG00000012124	6.784367	-0.438816	1.48078E-06	9.44857E-05
ECSCR	5	complement(139448560..139462	ENSG00000249751	7.405064	1.070521	1.49486E-06	9.49688E-05
HADH	4	107989714..108035241	ENSG00000138796	6.578969	-0.500986	1.50973E-06	9.54983E-05
TRPM2	21	44350163..44443081	ENSG00000142185	1.637018	0.7453	1.63281E-06	0.000102839
TRIM26	6	complement(30184455..3021342	ENSG00000234127	21.13482	0.38706	1.70185E-06	0.000106727
IQGAP3	1	complement(156525405..156572	ENSG00000183856	3.213257	-0.437984	1.72296E-06	0.000107131
FBXO10	9	complement(37510892..3757638	ENSG00000147912	3.345104	-0.436361	1.71697E-06	0.000107131
ATF5	19	49928702..49933935	ENSG00000169136	18.82582	0.464233	1.84354E-06	0.000114143
SSPN	12	26121991..26299290	ENSG00000123096	3.761352	0.649098	1.89123E-06	0.000116602
RETREG1	5	complement(16473038..1661710	ENSG00000154153	21.39794	-0.516855	1.99125E-06	0.000122253
UBE2F-SCL	2	237967014..238099412	ENSG00000258984	0.285905	3.727595	2.10982E-06	0.000128693
RNF31	14	24146683..24160660	ENSG00000092098	8.771209	0.401745	2.11377E-06	0.000128693
PECR	2	complement(215996329..216082	ENSG00000115425	2.993046	-0.768487	2.19109E-06	0.000132847
ATOX1	5	complement(151742316..151772	ENSG00000177556	10.72813	0.389337	2.22031E-06	0.000134062
VDR	12	complement(47841537..4794304	ENSG00000111424	12.93669	0.382976	2.23544E-06	0.000134421
CD302	2	complement(159768628..159798	ENSG00000241399	4.352604	-0.490996	2.27163E-06	0.000136037
IL1RN	2	113107214..113134016	ENSG00000136689	1260.832	0.661796	2.29855E-06	0.00013684
ACKR3	2	236567787..236582354	ENSG00000144476	2.311207	-0.910157	2.30376E-06	0.00013684
CHDH	3	complement(53812335..5384641	ENSG00000016391	1.985078	-0.63336	2.34271E-06	0.00013859
PPA1	10	complement(70202835..7023391	ENSG00000180817	27.04386	0.394735	2.37724E-06	0.000140065
RHBDF2	17	complement(76470891..7650179	ENSG00000129667	16.47747	0.527428	2.49383E-06	0.000146345
COQ8A	1	226940286..226987544	ENSG00000163050	6.306162	-0.51418	2.51996E-06	0.000147287
TLR2	4	153684070..153706260	ENSG00000137462	15.88173	0.647306	2.53201E-06	0.000147401
TMEM229	14	complement(67447084..6753373	ENSG00000198133	0.657621	0.95748	2.55192E-06	0.000147971
STK39	2	complement(167954020..168247	ENSG00000198648	3.996715	-0.466253	2.61067E-06	0.000150185
HESX1	3	complement(57197838..5722760	ENSG00000163666	1.387571	2.116417	2.60866E-06	0.000150185
F3	1	complement(94529173..9454175	ENSG00000117525	19.11249	0.966994	2.65344E-06	0.000151945
P2RY1	3	152835131..152841439	ENSG00000169860	11.34962	-0.380535	2.66205E-06	0.000151945
CNP	17	41966763..41977740	ENSG00000173786	10.9427	0.495634	2.74548E-06	0.000156097
TUT1	11	complement(62575045..6259163	ENSG00000149016	26.63135	0.64545	2.85261E-06	0.000161559
SAMD9	7	complement(93099513..9311802	ENSG00000205413	8.131122	0.767591	2.8671E-06	0.000161753
ZNF589	3	48241100..48299253	ENSG00000164048	11.60772	-0.561559	2.92181E-06	0.000162952
TBC1D4	13	complement(75283503..7548216	ENSG00000136111	3.666814	-0.408772	2.91931E-06	0.000162952
PSTPIP2	18	complement(45983536..4607227	ENSG00000152229	13.11275	1.032695	2.90731E-06	0.000162952
CTNS	17	3636459..3663103	ENSG00000040531	11.50102	0.384061	2.95704E-06	0.00016429
CMTR1	6	37433219..37482827	ENSG00000137200	11.2629	0.448792	3.03169E-06	0.0001678
HCAR2	12	complement(122701293..122703	ENSG00000182782	19.37386	0.676028	3.25197E-06	0.000179312
CSRNP1	3	complement(39141855..3915456	ENSG00000144655	13.27267	0.588972	3.26774E-06	0.000179505
PNPT1	2	complement(55634061..5569386	ENSG00000138035	9.487355	0.701527	3.30037E-06	0.000180618
TRAF2	9	136881912..136926607	ENSG00000127191	6.785635	0.492562	3.32508E-06	0.000181291
SLC25A29	14	complement(100291116..100306	ENSG00000197119	7.788863	-0.388121	3.47874E-06	0.000188964
SIPA1L1	14	71320449..71741229	ENSG00000197555	1.394227	0.540057	3.58005E-06	0.000193747
HTD2	3	58306262..58320193	ENSG00000255154	2.20299	0.688618	3.62887E-06	0.000195665
FNDC5	1	complement(32862268..3287248	ENSG00000160097	0.441879	-1.83791	3.66462E-06	0.000196866
OPTN	10	13099449..13138308	ENSG00000123240	45.05428	0.672277	3.71681E-06	0.000198938
EEPD1	7	36153254..36301538	ENSG00000122547	8.153997	-0.460417	3.84847E-06	0.000205233
SLC29A1	6	44219553..44234142	ENSG00000112759	6.57705	-0.409064	4.52768E-06	0.000240576
SLC39A8	4	complement(102251080..102431	ENSG00000138821	8.40817	0.674847	4.69211E-06	0.00024841
ISY1-RAB4	3	complement(129087575..129161	ENSG00000261796	6.490515	0.537736	4.8023E-06	0.000253326
HIVEP3	1	complement(41506365..4203592	ENSG00000127124	2.289505	0.545886	5.16383E-06	0.000271417
CYP27B1	12	complement(57762334..5776898	ENSG00000111012	3.252821	1.019221	5.30435E-06	0.000277804
SORBS1	10	complement(95311771..9556141	ENSG00000095637	2.48923	0.513756	5.8962E-06	0.000307697
gene:ENSG	11	complement(62559603..6259153	ENSG00000255508	3.370313	0.743299	6.24068E-06	0.000323364
RIN2	20	19757606..20002457	ENSG00000132669	8.095979	0.382441	6.22017E-06	0.000323364
KIAA0040	1	complement(175156986..175192	ENSG00000235750	2.464401	0.534001	6.36955E-06	0.000328876
ST3GAL5	2	complement(85837120..8590519	ENSG00000115525	5.395183	0.424365	6.42118E-06	0.000329215
GIMAP2	7	150685697..150693641	ENSG00000106560	15.22422	0.396372	6.41185E-06	0.000329215

ERMP1	9	complement(5765076..5833117)	ENSG00000099219	12.53824	-0.364305	6.53912E-06	0.000333988
BST2	19	complement(17402939..1740563	ENSG00000130303	280.476	0.573725	6.55998E-06	0.000333988
MAP3K1	5	56815549..56896152	ENSG00000095015	2.638416	-0.410135	6.67205E-06	0.000338514
gene:ENSG	11	65261928..65326543	ENSG00000285816	0.930991	1.055415	6.80534E-06	0.000344082
ADORA3	1	complement(111499429..111503	ENSG00000282608	1.456768	-1.521317	6.87015E-06	0.000346161
FAM72D	1	145095974..145112696	ENSG00000215784	0.264022	4.206111	7.07343E-06	0.000355179
MS4A6A	11	complement(60172015..6018466	ENSG00000110077	2.084332	-0.958637	7.69807E-06	0.00038522
PPP2R1B	11	complement(111726908..111766	ENSG00000137713	10.08223	-0.364335	7.859E-06	0.000391931
ATP9A	20	complement(51596514..5176839	ENSG00000054793	4.096525	-0.434407	8.32285E-06	0.000413651
FHL1	X	136146702..136211359	ENSG00000022267	13.14913	-0.532292	8.36449E-06	0.000414311
LMNB1	5	126776623..126837020	ENSG00000113368	2.393361	0.622553	8.69309E-06	0.000429044
CBWD6	9	complement(41131306..4119926	ENSG00000215126	1.85265	0.704716	8.72064E-06	0.000429044
GALM	2	38666081..38741237	ENSG00000143891	6.98205	-0.518785	9.2766E-06	0.000453343
BTN3A3	6	26440472..26453415	ENSG00000111801	5.330902	0.410798	9.25055E-06	0.000453343
SP140L	2	230327184..230403732	ENSG00000185404	9.185013	0.36961	1.08999E-05	0.000529943
GPAT3	4	83535914..83605875	ENSG00000138678	32.18164	-0.461402	1.09384E-05	0.000529943
ICAM1	19	10271093..10286615	ENSG00000090339	88.65154	0.948697	1.09528E-05	0.000529943
EIF3CL	16	complement(28379579..2840384	ENSG00000205609	4.914143	-0.581483	1.10305E-05	0.000531938
RNF19B	1	complement(32936445..3296480	ENSG00000116514	27.24603	0.62362	1.16729E-05	0.000561069
JAK3	19	complement(17824780..1784807	ENSG00000105639	0.369384	1.109219	1.17649E-05	0.000563633
ANGPT4	20	complement(869900..916334)	ENSG00000101280	0.866185	-1.364013	1.18613E-05	0.000566399
YPEL2	17	59331655..59401729	ENSG00000175155	1.552135	-0.63484	1.21311E-05	0.000577393
CCL13	17	34356480..34358610	ENSG00000181374	1.566283	2.044993	1.25203E-05	0.000593985
THBS1	15	39581079..39599466	ENSG00000137801	4.510754	-0.65221	1.29618E-05	0.000612939
RELB	19	45001449..45038198	ENSG00000104856	18.37503	0.657592	1.33295E-05	0.000628294
ARL4C	2	complement(234493041..234497	ENSG00000188042	2.138169	-0.609275	1.38897E-05	0.000652592
TMEM176	7	complement(150791285..150801	ENSG00000106565	6.78604	0.480518	1.42102E-05	0.000665513
FAM13A	4	complement(88725955..8911139	ENSG00000138640	1.715727	-0.490932	1.50613E-05	0.000703118
REV3L	6	complement(111299028..111483	ENSG00000009413	1.822175	-0.389155	1.56562E-05	0.000728563
IRS2	13	complement(109752695..109786	ENSG00000185950	4.537434	-0.500015	1.5891E-05	0.000737141
CA12	15	complement(63321378..6338184	ENSG00000074410	3.184646	0.643315	1.63244E-05	0.000754847
PECAM1	17	complement(64319415..6441377	ENSG00000261371	44.76464	-0.53778	1.64654E-05	0.000758966
ODF3B	22	complement(50529710..5053250	ENSG00000177989	4.80422	0.664937	1.66919E-05	0.000766987
FCGR1A	1	149782671..149791675	ENSG00000150337	49.08507	0.622089	1.71961E-05	0.000787678
LYSMD2	15	complement(51723011..5175158	ENSG00000140280	7.69642	0.533292	1.7269E-05	0.000788546
FSCN1	7	5592816..5606655	ENSG00000075618	5.372958	0.632748	1.74013E-05	0.000792111
HES2	1	complement(6412418..6424670)	ENSG00000069812	11.86323	-0.525429	1.76845E-05	0.000795096
BATF3	1	complement(212686417..212699	ENSG00000123685	14.90461	0.578504	1.76516E-05	0.000795096
CYRIA	2	complement(16549459..1666633	ENSG00000197872	4.89832	-0.458228	1.76101E-05	0.000795096
MMP1	11	complement(102789401..102798	ENSG00000196611	39.26134	0.510544	1.75992E-05	0.000795096
MXI1	10	110207605..110287365	ENSG00000119950	2.814366	-0.590316	1.7883E-05	0.000801555
EDN1	6	12290361..12297194	ENSG00000078401	21.46098	0.836389	1.83023E-05	0.00081784
SCG5	15	32641676..32697098	ENSG00000166922	12.36344	0.545783	1.8474E-05	0.000822995
SCD	10	100347233..100364826	ENSG00000099194	199.9672	-0.527754	1.94072E-05	0.000861939
TNS1	2	complement(217799588..218033	ENSG00000079308	5.825498	-0.526589	2.20854E-05	0.000974961
MMP2	16	55389700..55506691	ENSG00000087245	9.431566	-0.41575	2.2078E-05	0.000974961
IFITM1	11	310041..315272	ENSG00000185885	1.131149	1.75556	2.262E-05	0.000995551
UXS1	2	complement(106093308..106194	ENSG00000115652	23.21068	0.412413	2.37645E-05	0.001042783
TMED7-TIC	5	complement(115578642..115626	ENSG00000251201	5.166356	0.427247	2.45988E-05	0.001072949
HS3ST3B1	17	14301081..14349404	ENSG00000125430	1.863629	1.011738	2.45672E-05	0.001072949
UNC5B	10	71212570..71302864	ENSG00000107731	2.53775	-0.452088	2.48352E-05	0.001080037
RAP2B	3	153162226..153170627	ENSG00000181467	7.28722	-0.345951	2.49141E-05	0.001080253
gene:ENSG	7	complement(92131774..9224592	ENSG00000285953	0.434283	-3.959084	2.63092E-05	0.001137367
OR2A4	6	complement(131699644..131701	ENSG00000180658	0.518926	-4.285851	2.70364E-05	0.001165355
CH25H	10	complement(89205629..8920731	ENSG00000138135	1.885933	1.387586	2.82483E-05	0.001210453
PANX1	11	94128841..94181968	ENSG00000110218	6.337599	0.418633	2.82445E-05	0.001210453
MCOLN2	1	complement(84925583..8499711	ENSG00000153898	0.91586	1.166205	3.05201E-05	0.001303978
GAPT	5	58491435..58497090	ENSG00000175857	1.118348	-1.000693	3.08992E-05	0.001316322

ABCC5	3	complement(183919934..184017	ENSG00000114770	2.325092	-0.467702	3.10983E-05	0.001317525
MASTL	10	27154824..27187953	ENSG00000120539	2.624016	0.620574	3.11077E-05	0.001317525
ZBTB4	17	complement(7459366..7484263)	ENSG00000174282	9.503163	-0.340736	3.13864E-05	0.001325484
SLC46A2	9	complement(112878920..112890	ENSG00000119457	2.571382	-0.645637	3.14948E-05	0.001326229
APOBEC3F	22	39040604..39055972	ENSG00000128394	0.447993	0.993717	3.24454E-05	0.001362335
STIMATE	3	complement(52836219..5289754	ENSG00000213533	7.76448	0.421555	3.3765E-05	0.001413681
PRAM1	19	complement(8490056..8502640)	ENSG00000133246	17.93403	-0.350768	3.42933E-05	0.001431697
RBCK1	20	407498..432139	ENSG00000125826	14.33697	0.391632	3.44414E-05	0.001433781
SPTBN1	2	54456317..54671446	ENSG00000115306	0.483286	-0.679829	3.46265E-05	0.001437394
PYGL	14	complement(50857891..5094448	ENSG00000100504	29.54763	-0.384198	3.47425E-05	0.001438124
HES6	2	complement(238238267..238240	ENSG00000144485	4.942333	-0.678873	3.54617E-05	0.001463745
BTN2A2	6	26383096..26394874	ENSG00000124508	10.53403	0.42914	3.59537E-05	0.001479875
LRRC25	19	complement(18391137..1839762	ENSG00000175489	15.09888	-0.467214	3.60956E-05	0.001481542
AQP3	9	complement(33441156..3344759	ENSG00000165272	58.58906	0.560997	3.64603E-05	0.00149232
TIPARP	3	156673235..156706770	ENSG00000163659	12.29623	-0.33732	3.75565E-05	0.001532893
POLR3D	8	22245133..22254601	ENSG00000168495	4.562602	0.359008	3.81535E-05	0.00155292
ZKSCAN8	6	28141883..28159460	ENSG00000198315	3.098235	-0.484947	4.02216E-05	0.001632552
FCMR	1	complement(206903317..206923	ENSG00000162894	10.1367	-0.612479	4.06416E-05	0.001645026
WFIKKN2	17	50834650..50842353	ENSG00000173714	3.741767	-0.509618	4.18952E-05	0.001691085
gene:ENSG	7	complement(1815804..2242215)	ENSG00000286192	0.090166	4.849252	4.26757E-05	0.001717843
FCHO1	19	17747718..17788568	ENSG00000130475	2.066995	-0.553371	4.28708E-05	0.001720957
GTF2B	1	complement(88852633..8889194	ENSG00000137947	20.78915	0.371911	4.34841E-05	0.001740792
SESN1	6	complement(108986437..109094	ENSG00000080546	4.872694	-0.370374	4.37295E-05	0.001745835
OSBPL11	3	complement(125528858..125595	ENSG00000144909	23.00259	-0.325759	4.48853E-05	0.001763264
TDRD7	9	97412096..97496125	ENSG00000196116	11.86886	0.453658	4.48901E-05	0.001763264
CCL23	17	complement(36013056..3601797	ENSG00000274736	31.41274	0.563185	4.46015E-05	0.001763264
KCNN4	19	complement(43766533..4378125	ENSG00000104783	36.61114	0.462607	4.48739E-05	0.001763264
ZNFX1	20	complement(49237946..4927842	ENSG00000124201	19.89827	0.482432	4.47382E-05	0.001763264
KREMEN1	22	29073035..29168333	ENSG00000183762	1.269503	0.841242	4.47287E-05	0.001763264
FCRL6	1	159800511..159816257	ENSG00000181036	0.503157	1.578235	4.62258E-05	0.00181086
PDE4B	1	65792514..66374579	ENSG00000184588	1.850282	0.928933	4.63754E-05	0.001811864
KLHL24	3	183635610..183684519	ENSG00000114796	2.020136	-0.420138	4.70371E-05	0.001823094
CGAS	6	complement(73413515..7345229	ENSG00000164430	5.158125	0.368712	4.70289E-05	0.001823094
MBNL3	X	complement(132369317..132489	ENSG00000076770	1.301302	-0.380452	4.6984E-05	0.001823094
SSH2	17	complement(29625938..2993027	ENSG00000141298	5.788118	-0.331389	4.72999E-05	0.00182843
DDIT4L	4	complement(100185870..100190	ENSG00000145358	2.442209	-0.648048	4.76279E-05	0.001836252
TFPI2	7	complement(93885396..9389075	ENSG00000105825	6.393739	0.69781	4.79887E-05	0.001845292
TRAFD1	12	112125538..112153604	ENSG00000135148	20.01368	0.329064	4.87362E-05	0.001864225
ITGB3	17	47253827..47313743	ENSG00000259207	5.879727	0.346145	4.87336E-05	0.001864225
SLC46A3	13	complement(28700064..2871897	ENSG00000139508	5.787523	-0.370906	5.20784E-05	0.001986865
LY6E	8	143017982..143023832	ENSG00000160932	128.3292	0.542077	5.26301E-05	0.002002684
TNFRSF21	6	complement(47231532..4730990	ENSG00000146072	37.51088	-0.507448	5.42073E-05	0.002052013
CYLD	16	50742050..50801935	ENSG00000083799	7.13961	0.327588	5.41059E-05	0.002052013
EEF1E1-BL	6	complement(8015726..8102530)	ENSG00000265818	0.714704	-3.757234	5.66422E-05	0.002135504
PLCG1	20	41136960..41196801	ENSG00000124181	0.623043	-0.652652	5.67052E-05	0.002135504
SLC2A6	9	complement(133471094..133479	ENSG00000160326	40.57908	0.842887	5.90885E-05	0.002219541
C4A	6	31982057..32002681	ENSG00000244731	0.515752	1.151591	6.30898E-05	0.002363764
PC	11	complement(66848417..6695838	ENSG00000173599	8.804496	-0.393181	6.43932E-05	0.002406427
SLITRK4	X	complement(143622790..143636	ENSG00000179542	1.326013	-0.453414	6.49182E-05	0.002419859
BAK1	6	complement(33572547..3358029	ENSG00000030110	30.72721	0.323781	6.59469E-05	0.002451949
XRN1	3	complement(142306607..142448	ENSG00000114127	4.114745	0.51882	6.66919E-05	0.002473354
UBD	6	complement(29555515..2955973	ENSG00000213886	2.709362	1.323918	6.76284E-05	0.002501738
VLDLR	9	2621182..2660056	ENSG00000147852	0.632252	-0.610522	6.78503E-05	0.002503607
NR1D2	3	23945286..23980617	ENSG00000174738	5.530268	-0.342193	6.85211E-05	0.002521991
PLXNA1	3	126982693..127037389	ENSG00000114554	8.314282	0.321212	6.92993E-05	0.002544225
NEURL3	2	complement(96497646..9650810	ENSG00000163121	0.924296	1.266355	7.02377E-05	0.002572215
CD109	6	73695785..73828316	ENSG00000156535	8.154787	-0.320406	7.2701E-05	0.002655766
TREM2	6	complement(41158506..4116318	ENSG00000095970	109.8331	-0.463308	7.32198E-05	0.002668049

GTPBP1	22	38705742..38738299	ENSG00000100226	7.758719	0.461244	7.68937E-05	0.002794953
CCDC9B	15	complement(40331452..4034096	ENSG00000188549	2.503818	-0.506202	7.95005E-05	0.002882533
SERPINE1	7	101127104..101139247	ENSG00000106366	40.08406	0.578412	8.06467E-05	0.002916855
HPGD	4	complement(174490175..174523	ENSG00000164120	30.7245	-0.492887	8.09694E-05	0.002921295
IFNG	12	complement(68154768..6815974	ENSG00000111537	0.845467	2.448603	8.2126E-05	0.002955726
NFKBIE	6	complement(44258166..4426578	ENSG00000146232	34.01679	0.536395	8.30588E-05	0.002981955
PDCD1LG2	9	5510531..5571282	ENSG00000197646	4.68477	0.502705	8.84934E-05	0.003169279
HLA-F	6	29722775..29738528	ENSG00000204642	64.38438	0.487459	9.09322E-05	0.00324866
TSPAN15	10	69451465..69507666	ENSG00000099282	9.120599	-0.397735	9.20404E-05	0.00328023
IL7R	5	35852695..35879603	ENSG00000168685	102.168	0.80212	9.36565E-05	0.003329707
C15orf48	15	45430579..45448761	ENSG00000166920	229.3933	0.722246	9.86035E-05	0.003497075
MAX	14	complement(65006174..6510269	ENSG00000125952	8.707597	0.320075	9.93153E-05	0.003513789
HRH1	3	11137093..11263557	ENSG00000196639	4.020739	0.434052	0.00010134	0.003576776
IGSF6	16	complement(21639550..2165260	ENSG00000140749	110.2403	0.488606	0.000101996	0.003591255
SH3PXD2A	10	complement(103594027..103855	ENSG00000107957	2.649188	-0.334745	0.000106522	0.003741578
ME1	6	complement(83210402..8343105	ENSG00000065833	9.971414	-0.40289	0.000106822	0.00374314
TAGAP	6	complement(159034468..159045	ENSG00000164691	10.56715	0.573099	0.000108438	0.003790672
CASP4	11	complement(104942866..104969	ENSG00000196954	69.13269	0.346155	0.000109499	0.003818623
CTTN	11	70398404..70436584	ENSG00000085733	8.307177	0.391429	0.000112472	0.003912937
TRIM56	7	101085481..101097967	ENSG00000169871	6.00396	0.313328	0.000114879	0.003987201
TDRD9	14	103928456..104052667	ENSG00000156414	3.742262	-0.543333	0.000115539	0.004000596
VPS9D1	16	complement(89707134..8972089	ENSG00000075399	6.05076	0.514771	0.000115889	0.004003247
CCND1	11	69641156..69654474	ENSG00000110092	1.080473	0.670885	0.000116395	0.00401125
CALHM6	6	116461370..116463771	ENSG00000188820	4.213241	1.625894	0.000116687	0.004011839
FUT4	11	94543921..94549895	ENSG00000196371	4.637037	0.333168	0.000119584	0.004101793
NCAPH2	22	50508224..50524780	ENSG00000025770	8.36784	0.326983	0.000120958	0.004139194
ATP7A	X	77910656..78050395	ENSG00000165240	2.650764	-0.405208	0.000122997	0.004199134
PRPF3	1	150321479..150353233	ENSG00000117360	23.06857	0.314361	0.000126745	0.004317007
RIN3	14	92513781..92688994	ENSG00000100599	15.59675	-0.404078	0.000127134	0.004320193
ITPKB	1	complement(226631690..226739	ENSG00000143772	8.010685	-0.386081	0.000130558	0.004423565
HILPDA	7	128455849..128458418	ENSG00000135245	37.92172	-0.711885	0.000130782	0.004423565
MAPK3	16	complement(30114105..3012350	ENSG00000102882	4.015768	-0.373998	0.000135007	0.00455595
HSPA6	1	161524540..161526894	ENSG00000173110	31.74182	-0.412652	0.000136255	0.004587477
SPSB3	16	complement(1776712..1793700)	ENSG00000162032	7.734937	-0.369016	0.000137156	0.004607183
COL22A1	8	complement(138588235..138914	ENSG00000169436	0.79688	0.82119	0.000138236	0.004632813
gene:ENSG	3	complement(49416777..4942931	ENSG00000283189	0.763214	-1.267592	0.000139179	0.00465374
STIMATE-M	3	complement(52833121..5289756	ENSG00000248592	2.430333	1.360959	0.000140763	0.00469594
MOB3B	9	complement(27325209..2752981	ENSG00000120162	6.181295	0.430785	0.00014363	0.004780697
CCR5	3	46370854..46376206	ENSG00000160791	17.45501	0.312994	0.000148787	0.004941077
C3	19	complement(6677704..6730562)	ENSG00000125730	20.00579	0.679442	0.000150189	0.004976336
gene:ENSG	19	complement(35739252..3574543	ENSG00000267120	0.273628	3.123356	0.000151254	0.005000275
SBNO2	19	complement(1107637..1174268)	ENSG00000064932	18.72481	0.409407	0.000160138	0.005282012
RND3	2	complement(150468195..150539	ENSG00000115963	15.5204	0.407081	0.000164403	0.005410477
GALC	14	complement(87837820..8799366	ENSG00000054983	10.36544	-0.309484	0.000172446	0.005662429
YPEL3	16	complement(30092314..3009691	ENSG00000090238	2.165192	-0.585794	0.000174338	0.005711707
IMPA2	18	11981025..12030877	ENSG00000141401	4.186435	-0.477163	0.000176427	0.005767238
BCL3	19	44747705..44760044	ENSG00000069399	12.74205	0.588496	0.000182207	0.005942865
NIBAN1	1	complement(184790724..184974	ENSG00000135842	17.46062	0.454749	0.00018302	0.0059561
MICALL2	7	complement(1428465..1459470)	ENSG00000164877	3.725194	0.418406	0.000183806	0.005968377
gene:ENSG	19	7629796..7643048	ENSG00000268400	8.577239	-0.754991	0.000186895	0.006055241
STAP1	4	67558727..67607337	ENSG00000035720	1.62136	1.708342	0.000190841	0.006169402
CREM	10	35126791..35212958	ENSG00000095794	3.776073	0.375596	0.000195769	0.006300841
ABHD4	14	22598237..22613215	ENSG00000100439	29.38672	-0.297224	0.000195513	0.006300841
AMIGO3	3	complement(49716829..4971968	ENSG00000176020	0.257526	-2.253107	0.000200708	0.006445592
TNIK	3	complement(171058414..171460	ENSG00000154310	7.029647	0.517466	0.000210425	0.006728084
P2RX7	12	121132819..121188032	ENSG00000089041	18.7706	0.408103	0.000210179	0.006728084
gene:ENSG	19	18153158..18178117	ENSG00000268173	0.127467	-6.903525	0.000213444	0.006809713
RCAN1	21	complement(34513142..3461511	ENSG00000159200	9.932183	0.385726	0.000216296	0.006885655

RUBCN	3	complement(197668867..197749	ENSG00000145016	4.495572	0.384729	0.000222579	0.007070263
NBPF12	1	146938744..146996202	ENSG00000268043	3.225181	-0.325376	0.000225639	0.007138761
SIRPB1	20	complement(1561385..1620061)	ENSG00000101307	7.561586	-0.301086	0.000225712	0.007138761
ALPK1	4	112285509..112442621	ENSG00000073331	4.758158	0.319102	0.000232696	0.007332994
EPOP	17	complement(38671703..3867495	ENSG00000273604	1.487654	0.777663	0.000232857	0.007332994
EXOC3L1	16	complement(67184379..6719018	ENSG00000179044	0.35275	1.421925	0.00023547	0.007399329
CYBB	X	37780059..37813461	ENSG00000165168	336.9395	0.508574	0.000238251	0.007470636
DEF6	6	35297818..35321771	ENSG00000023892	3.198578	-0.61183	0.000240739	0.007500367
IL10RA	11	117986370..118003037	ENSG00000110324	37.75537	0.481835	0.000240154	0.007500367
HS3ST2	16	22814162..22916338	ENSG00000122254	1.360437	-0.813595	0.000240597	0.007500367
DST	6	complement(56457987..5695483	ENSG00000151914	4.788516	-0.436029	0.000244093	0.007573437
GPD1	12	50103982..50111313	ENSG00000167588	112.3401	-0.492917	0.00024412	0.007573437
HCAR3	12	complement(122714756..122716	ENSG00000255398	22.53703	0.614326	0.000244769	0.007577472
PPM1K	4	complement(88257620..8828476	ENSG00000163644	1.644481	0.379274	0.000249266	0.007667949
RASA4	7	complement(102573807..102616	ENSG00000105808	4.269231	0.447811	0.00024899	0.007667949
ZNF503	10	complement(75397830..7540176	ENSG00000165655	1.492165	-0.618247	0.000248466	0.007667949
HCK	20	32052197..32101856	ENSG00000101336	129.9833	0.569479	0.00025481	0.007822016
PDCD4	10	110871795..110900006	ENSG00000150593	20.18838	-0.295757	0.000256102	0.007845194
C1QTNF3-A	5	complement(33987174..3412452	ENSG00000273294	0.148378	3.360253	0.00025818	0.007892306
KCNJ5	11	128891356..128921163	ENSG00000120457	1.209224	-0.698776	0.000261285	0.007970546
ID3	1	complement(23557926..2355950	ENSG00000117318	10.06554	-0.564591	0.00026446	0.008050613
TEX2	17	complement(64147227..6426326	ENSG00000136478	17.64386	-0.321223	0.000265169	0.008055418
MGAT4A	2	complement(98619106..9873113	ENSG00000071073	4.052757	-0.308837	0.000266994	0.008060565
HEBP2	6	138403531..138422197	ENSG00000051620	2.28835	-0.349659	0.000266174	0.008060565
CLEC2D	12	9664969..9699553	ENSG00000069493	1.624735	0.59184	0.00026668	0.008060565
VWA8	13	complement(41566835..4196112	ENSG00000102763	10.05426	0.371108	0.00027131	0.008164063
MMP14	14	22836560..22849041	ENSG00000157227	152.749	0.506957	0.000271539	0.008164063
ARPIN	15	complement(89895006..8991295	ENSG00000242498	1.592317	-0.352212	0.000275765	0.008274082
CORO6	17	complement(29614756..2962291	ENSG00000167549	1.616611	-0.676793	0.00027849	0.008338725
NFIX	19	12995475..13098796	ENSG00000008441	0.872156	0.634546	0.000281392	0.008408395
PPAN-P2RY	19	10106223..10114780	ENSG00000243207	0.503408	-3.163675	0.000284731	0.008490799
ENDOD1	11	95089846..95132645	ENSG00000149218	3.416616	0.385678	0.000286672	0.008523817
GOLGA6D	15	75282835..75295807	ENSG00000140478	0.155743	3.476377	0.000287005	0.008523817
ADPRS	1	36088892..36093932	ENSG00000116863	28.0084	0.391307	0.000291045	0.008626264
UNC93B1	11	complement(67991100..6800498	ENSG00000110057	63.26628	0.435597	0.000294625	0.00871469
URGCP-MR	7	complement(43866558..4390658	ENSG00000270617	0.517544	-4.207844	0.000301729	0.008906788
PLAAT4	11	63536808..63546462	ENSG00000133321	4.321395	0.951572	0.000305779	0.009008147
CLEC7A	12	complement(10116777..1013025	ENSG00000172243	11.59702	0.34727	0.000309684	0.00910484
RASA4B	7	complement(102479976..102517	ENSG00000170667	2.7632	0.605028	0.000315745	0.00926439
NFKB2	10	102394110..102402524	ENSG00000077150	30.8346	0.500891	0.000321149	0.009404071
CD1D	1	158178030..158186427	ENSG00000158473	0.583649	-0.966735	0.000324848	0.009488373
gene:ENSG	7	66087761..66152277	ENSG00000249319	1.912131	-1.429507	0.000325327	0.009488373
VILL	3	37988059..38007188	ENSG00000136059	1.669641	0.660152	0.000327841	0.009542652
LIMK2	22	31212239..31280080	ENSG00000182541	10.29718	0.458366	0.000331491	0.009629704
SASH3	X	129779949..129795201	ENSG00000122122	42.29735	-0.306233	0.000342646	0.009934011
EVI5	1	complement(92508696..9279240	ENSG00000067208	3.009692	-0.377749	0.000346131	0.010015175
ZYG11B	1	52726453..52827336	ENSG00000162378	2.981452	-0.365656	0.000352167	0.01016968
NPL	1	182789293..182830384	ENSG00000135838	35.85177	-0.325026	0.000354197	0.010200482
PCYOX1	2	70257386..70281185	ENSG00000116005	4.164826	-0.367861	0.000354629	0.010200482
TBC1D8	2	complement(101007228..101252	ENSG00000204634	12.53248	-0.294093	0.000356939	0.010246738
CLMN	14	complement(95181940..9531990	ENSG00000165959	2.053417	-0.314377	0.00035926	0.010293144
CD69	12	complement(9752486..9760901)	ENSG00000110848	0.863619	1.130194	0.000364542	0.010424053
MAML3	4	complement(139716753..140154	ENSG00000196782	0.367038	-0.881802	0.000372281	0.010624557
TNIP3	4	complement(121131408..121227	ENSG00000050730	15.16562	0.927491	0.000374021	0.010653396
NECTIN2	19	44846175..44889223	ENSG00000130202	21.09777	0.395597	0.000375703	0.010680479
IMPDH1	7	complement(128392277..128410	ENSG00000106348	30.60343	-0.326738	0.00037732	0.010705641
TLCD4	1	95117355..95197607	ENSG00000152078	0.180969	-1.306822	0.000379964	0.010759767
SOD2	6	complement(159669069..159762	ENSG00000112096	111.9229	0.803627	0.00038492	0.010879007

CLSTN3	12	7129698..7158945	ENSG00000139182	0.710723	0.752815	0.00039662	0.011188054
WDR91	7	complement(135183839..135211	ENSG00000105875	3.772198	-0.367599	0.000403922	0.011372091
GCNT4	5	complement(75025346..7505255	ENSG00000176928	0.479832	0.842445	0.000405383	0.011391261
OAT	10	complement(124397303..124418	ENSG00000065154	12.70423	-0.306062	0.000417665	0.011691417
N4BP1	16	complement(48538726..4862014	ENSG00000102921	8.257987	0.33192	0.000416942	0.011691417
PBXIP1	1	complement(154944076..154956	ENSG00000163346	11.21501	-0.352212	0.000419515	0.011720764
MYO1G	7	complement(44962662..4497908	ENSG00000136286	19.0938	0.416218	0.000420469	0.011724987
MYOF	10	complement(93306429..9348233	ENSG00000138119	76.75592	0.447303	0.000426598	0.011873232
TMEM273	10	complement(49154725..4918858	ENSG00000204161	6.150409	0.372485	0.000429317	0.01192621
JPH4	14	complement(23568035..2357879	ENSG00000092051	0.701959	-0.841989	0.0004304	0.011933588
TRHDE	12	72087266..72670758	ENSG00000072657	1.620537	-0.446558	0.0004422	0.012237562
OAS1	12	112905856..112933219	ENSG00000089127	44.71843	0.486078	0.000443648	0.012254419
APLN	X	complement(129645259..129654	ENSG00000171388	0.531562	-1.347769	0.000446211	0.012301957
SLC47A1	17	19495385..19579034	ENSG00000142494	13.48201	-0.460488	0.00045032	0.012391855
ADAR	1	complement(154581695..154628	ENSG00000160710	32.88446	0.461986	0.000457161	0.012556473
CD101	1	117001750..117036552	ENSG00000134256	10.49891	-0.302811	0.000459479	0.012596451
BMF	15	complement(40087890..4010889	ENSG00000104081	1.862887	-0.501368	0.000469032	0.012834272
DDX60L	4	complement(168356735..168537	ENSG00000181381	24.81859	0.542805	0.000471049	0.012865364
IL17RB	3	53846568..53865794	ENSG00000056736	2.886238	-0.593609	0.000480974	0.013111914
EFNB1	X	68829021..68842160	ENSG00000090776	5.297804	-0.353898	0.000483455	0.013155007
PDGFRL	8	17576433..17644071	ENSG00000104213	0.264214	2.859589	0.000487764	0.013200585
SLC25A22	11	complement(790475..798281)	ENSG00000177542	2.947381	0.439224	0.000486702	0.013200585
CENPN	16	81006552..81033114	ENSG00000166451	2.390106	0.331985	0.00048784	0.013200585
CXCL5	4	complement(73995642..7399867	ENSG00000163735	1497.721	0.582813	0.000490456	0.013246857
FAM214A	15	complement(52581317..5270981	ENSG00000047346	1.557534	-0.370398	0.000494644	0.013310744
AOC3	17	42851184..42858130	ENSG00000131471	22.62057	-0.284806	0.000493812	0.013310744
PRSS23	11	86791059..86952910	ENSG00000150687	1.070456	-0.505391	0.000497283	0.013357169
MYC	8	127735434..127742951	ENSG00000136997	2.649289	0.343211	0.000502986	0.013485569
AIMP2	7	6009255..6023834	ENSG00000106305	7.067287	0.332353	0.000505794	0.013536014
P2RY6	11	73264498..73305103	ENSG00000171631	0.388379	0.709101	0.000519757	0.013877119
TSFM	12	57782761..57808071	ENSG00000123297	7.476726	0.363663	0.000520439	0.013877119
TLE3	15	complement(70047790..7009817	ENSG00000140332	8.307086	-0.330739	0.000525924	0.013997804
PSME1	14	24136163..24138967	ENSG00000092010	107.7307	0.382188	0.000537764	0.014286919
SHMT1	17	complement(18327860..1836356	ENSG00000176974	1.094281	-0.7189	0.000539214	0.014299445
LAMC1	1	183023420..183145592	ENSG00000135862	4.626202	-0.292043	0.000555563	0.014706306
TMIGD3	1	complement(111483348..111563	ENSG00000121933	1.633449	-0.857387	0.000557818	0.014739319
CERK	22	complement(46684410..4673825	ENSG00000100422	6.604007	-0.296691	0.000562112	0.014825957
SOCS3	17	complement(78356778..7836007	ENSG00000184557	18.25027	0.698501	0.000570579	0.015022151
SPIRE1	18	complement(12446512..1265813	ENSG00000134278	9.389555	-0.281826	0.000574105	0.015060729
PROCR	20	35172072..35216240	ENSG00000101000	20.78869	0.293153	0.000573948	0.015060729
ITK	5	157142933..157255185	ENSG00000113263	0.514711	1.042171	0.000582443	0.015252079
SHISA5	3	complement(48467798..4850482	ENSG00000164054	36.51189	0.392007	0.000593061	0.015502342
FOXO1	13	complement(40555667..4066664	ENSG00000150907	1.514945	-0.449539	0.000595728	0.015544234
PLEK	2	68365282..68397453	ENSG00000115956	197.6982	0.446896	0.000597294	0.015557314
ADORA1	1	203090654..203167405	ENSG00000163485	0.666766	-1.041694	0.00059855	0.015562299
AMOTL1	11	94706431..94876748	ENSG00000166025	3.302714	-0.293233	0.000602905	0.015647677
gene:ENSG	6	116399395..116463696	ENSG00000285446	0.590914	-3.108887	0.000609239	0.015784039
ADGRE3	19	complement(14619117..1469002	ENSG00000131355	10.69688	0.449919	0.000617069	0.015958603
SWAP70	11	9664077..9752993	ENSG00000133789	12.72946	-0.276831	0.000634987	0.016392993
gene:ENSG	9	complement(32455323..3255260	ENSG00000288684	0.522711	-2.127487	0.000642999	0.016570559
TMEM171	5	73120569..73131809	ENSG00000157111	1.015402	1.296777	0.000663014	0.017029393
PARP11	12	complement(3791047..3873448)	ENSG00000111224	1.273022	0.475086	0.000663135	0.017029393
SORD	15	45023147..45077185	ENSG00000140263	2.721994	-0.309943	0.000685897	0.017583027
FKBP5	6	complement(35573585..3572858	ENSG00000096060	11.15084	0.423378	0.000688136	0.017609526
MFSD6	2	190408355..190509205	ENSG00000151690	9.479574	-0.279577	0.00069085	0.017648087
AGTRAP	1	11736084..11754802	ENSG00000177674	43.21952	0.336778	0.000700864	0.017872641
SRI	7	complement(88205115..8822699	ENSG00000075142	23.59843	0.273492	0.000712725	0.018115716
LPL	8	19901717..19967259	ENSG00000175445	167.8692	0.459284	0.000712875	0.018115716

FAM222B	17	complement(28755980..2885523	ENSG00000173065	2.812533	-0.314686	0.000717014	0.01818926
HIC1	17	2054154..2063241	ENSG00000177374	0.650354	0.593486	0.000722303	0.018291662
AK4	1	65147549..65232145	ENSG00000162433	2.167173	0.529915	0.000729894	0.018451911
PLEKHG3	14	64704102..64750249	ENSG00000126822	1.447187	0.427046	0.000745113	0.018804132
MOSPD1	X	complement(134887632..134915	ENSG00000101928	15.54449	-0.283783	0.000752552	0.018959129
KLHDC7B	22	50545899..50551023	ENSG00000130487	0.330275	0.925171	0.000759064	0.019090273
TNIP1	5	complement(151029945..151093	ENSG00000145901	84.28743	0.552008	0.000763386	0.019119414
TMEM86A	11	18693122..18704785	ENSG00000151117	4.745363	-0.345543	0.000765457	0.019119414
MMP9	20	46008908..46016561	ENSG00000100985	103.2079	0.50115	0.000765182	0.019119414
RTN4R	22	complement(20241415..2028324	ENSG00000040608	2.411103	-0.581083	0.000762294	0.019119414
PHF11	13	49495610..49528981	ENSG00000136147	14.20771	0.379098	0.000778647	0.0193826
APOC4-APO	19	44942238..44949565	ENSG00000224916	1.020661	-0.999977	0.000778255	0.0193826
MTHFD2	2	74186172..74217565	ENSG00000065911	26.80416	0.453922	0.000795138	0.019759444
FAS	10	88990531..89017059	ENSG00000026103	2.068874	0.485434	0.000805802	0.019990467
CD180	5	complement(67179613..6719679	ENSG00000134061	2.402473	-0.4522	0.000812983	0.020134419
LYRM1	16	20899868..20925006	ENSG00000102897	3.838975	0.321712	0.000817076	0.020201536
UGDH	4	complement(39498755..3952831	ENSG00000109814	4.778788	0.302923	0.000826601	0.020399362
HIRA	22	complement(19330698..1944745	ENSG00000100084	6.420143	0.401891	0.000827869	0.020399362
FOXO3	6	108559835..108684774	ENSG00000118689	4.980713	-0.281349	0.00083082	0.020437608
CYTIP	2	complement(157414619..157488	ENSG00000115165	20.69783	-0.348138	0.000834709	0.020498781
ABHD5	3	43690108..43734371	ENSG00000011198	9.966569	-0.270502	0.000840176	0.020598401
IL18BP	11	71998613..72005715	ENSG00000137496	6.083008	0.477879	0.000853665	0.020894048
ADRB2	5	148826611..148828623	ENSG00000169252	0.785602	-1.002313	0.000862067	0.02106442
ITSN1	21	33642400..33899861	ENSG00000205726	0.834499	-0.398751	0.000869774	0.021217255
DENND3	8	141117278..141195808	ENSG00000105339	1.776392	0.467897	0.000891304	0.021706227
LTV1	6	143843338..143863812	ENSG00000135521	30.10185	0.368732	0.000894998	0.02175992
HAMP	19	35280716..35285143	ENSG00000105697	0.934644	-1.747479	0.00091709	0.022260003
DDIAS	11	82899975..82958277	ENSG00000165490	1.063836	-0.666425	0.000919146	0.022272897
CKAP4	12	complement(106237881..106304	ENSG00000136026	13.81818	0.305806	0.00094554	0.022874561
ICOSLG	21	complement(44217014..4424096	ENSG00000160223	2.326783	0.388052	0.000951344	0.022976913
CCL4L2	17	36210924..36212878	ENSG00000276070	126.6488	1.371092	0.000957481	0.023048955
DOCK11	X	118495815..118686163	ENSG00000147251	26.51048	-0.375709	0.000956509	0.023048955
TCF4	18	complement(55222185..5566478	ENSG00000196628	0.303314	0.589132	0.000970262	0.023318201
NIBAN2	9	complement(127505339..127578	ENSG00000136830	80.34945	0.412625	0.000973185	0.023350043
KYNU	2	142877657..143055833	ENSG00000115919	29.48825	0.543686	0.000978207	0.023369039
DPYSL3	5	complement(147390808..147510	ENSG00000113657	40.33937	0.493141	0.000979155	0.023369039
ASRGL1	11	62337448..62393412	ENSG00000162174	2.362401	-0.509633	0.000979115	0.023369039
ABCA7	19	1039997..1065572	ENSG00000064687	3.635097	-0.391972	0.000980374	0.023369039
BIRC3	11	102317450..102339403	ENSG00000023445	5.293678	0.484599	0.000983142	0.023396863
SLC9A1	1	complement(27098809..2716698	ENSG00000090020	12.45537	-0.267724	0.000997389	0.023658836
NDUFV2	18	9102630..9134345	ENSG00000178127	39.10888	0.284881	0.000997127	0.023658836
SLC37A1	21	42496008..42581440	ENSG00000160190	9.991521	0.356916	0.001001223	0.023711296
TNFRSF6B	20	63696652..63698684	ENSG00000243509	0.315485	3.1939	0.001002997	0.023714865
PRKCH	14	61187559..61550976	ENSG00000027075	10.68083	-0.268984	0.001030208	0.024318902
SLC40A1	2	complement(189560590..189583	ENSG00000138449	0.069149	-2.782256	0.001036677	0.02443214
LCP2	5	complement(170246233..170297	ENSG00000043462	26.02602	0.352997	0.001045122	0.024591492
gene:ENSG	21	5022493..5040666	ENSG00000277117	2.611642	0.566798	0.001059138	0.024881229
gene:ENSG	3	complement(155763043..155854	ENSG00000284952	0.133394	6.464297	0.00106624	0.025007872
DEFB1	8	complement(6870592..6877936)	ENSG00000164825	22.33179	0.44387	0.001071207	0.025084107
SNRPG	2	complement(70281362..7029374	ENSG00000143977	40.47547	0.266391	0.001077096	0.025181634
FAM162A	3	122384176..122412334	ENSG00000114023	8.399694	-0.278815	0.001084817	0.02532163
PLEKHN1	1	966482..975865	ENSG00000187583	0.53779	0.820374	0.001088631	0.025370129
SERF1B	5	70025247..70043113	ENSG00000205572	0.973956	0.999183	0.001095932	0.025499616
MATK	19	complement(3777970..3802129)	ENSG00000007264	27.43386	0.330134	0.001105876	0.025690087
TNFAIP6	2	151357592..151380046	ENSG00000123610	108.6915	1.270939	0.001126392	0.02612515
RPS10-NUD	6	complement(34284887..3442607	ENSG00000270800	6.587681	0.275299	0.001138015	0.026352885
TNFSF13	17	7558292..7561608	ENSG00000161955	36.59494	0.350902	0.001157488	0.026761425
CRTAP	3	33114014..33147773	ENSG00000170275	13.47975	-0.260699	0.001171521	0.027043071

AGRP	16	complement(67482571..6748354	ENSG00000159723	10.63868	-0.774828	0.00120024	0.027662305
STARD4	5	complement(111496033..111512	ENSG00000164211	4.817127	0.324133	0.001203547	0.02769485
CCL17	16	57404767..57416063	ENSG00000102970	2.32087	1.413277	0.001213628	0.027882907
RNF168	3	complement(196468783..196503	ENSG00000163961	4.485978	-0.327424	0.001226932	0.028056237
SH3PXD2B	5	complement(172325000..172454	ENSG00000174705	6.759357	0.438275	0.001225966	0.028056237
CASP7	10	113679162..113730907	ENSG00000165806	19.11854	0.263282	0.001225862	0.028056237
FOSL1	11	complement(65892049..6590057	ENSG00000175592	6.310002	0.376366	0.001231407	0.028114554
CASS4	20	56412112..56460387	ENSG00000087589	0.867618	0.618102	0.00125033	0.028502064
SLC19A2	1	complement(169463909..169485	ENSG00000117479	4.703116	-0.295926	0.001256637	0.028601215
MPHOSPH	16	complement(82147798..8217022	ENSG00000135698	23.97078	0.27017	0.001268651	0.028829754
DNASE2	19	complement(12875209..1288146	ENSG00000105612	75.24249	-0.392882	0.001273611	0.028897532
SNX18	5	54517759..54546586	ENSG00000178996	4.915585	-0.274253	0.001279716	0.02899103
SIGLEC7	19	51142299..51153526	ENSG00000168995	14.55376	-0.284868	0.001288353	0.029141504
LDLRAD3	11	35943981..36232136	ENSG00000179241	1.708717	-0.476797	0.001290559	0.029146297
CDCA7L	7	complement(21900899..2194590	ENSG00000164649	3.568519	-0.31397	0.001292879	0.029153627
CNIH4	1	224356858..224379459	ENSG00000143771	16.22714	0.260572	0.001309492	0.029482742
TAPBP	6	complement(33299694..3331438	ENSG00000231925	41.29662	0.396163	0.001318413	0.029637923
TFCP2L1	2	complement(121216587..121285	ENSG00000115112	1.955239	-0.336726	0.001340458	0.030087202
PER3	1	7784291..7845177	ENSG00000049246	2.248482	-0.370407	0.001353717	0.030338211
SEMA4A	1	156147366..156177752	ENSG00000196189	3.634467	0.558667	0.00138119	0.030859255
MGAT3	22	39457012..39492194	ENSG00000128268	17.44252	0.324205	0.001380843	0.030859255
MFSD2A	1	39955112..39969968	ENSG00000168389	22.82524	0.429691	0.001424129	0.031673323
SAPCD1	6	31762996..31764851	ENSG00000228727	0.252049	4.038613	0.001423801	0.031673323
MSC	8	complement(71841560..7184441	ENSG00000178860	39.33078	0.333129	0.001419858	0.031673323
LRRC32	11	complement(76657524..7667074	ENSG00000137507	0.586555	0.904996	0.001436927	0.031812689
CCL1	17	complement(34360328..3436323	ENSG00000108702	5.162197	1.238961	0.001435937	0.031812689
PDCD5	19	32581190..32587453	ENSG00000105185	19.5411	0.266308	0.001432753	0.031812689
HERC1	15	complement(63608618..6383394	ENSG00000103657	5.151693	-0.255954	0.001456871	0.032205455
RBP7	1	9997206..10016021	ENSG00000162444	4.021857	-0.743423	0.001462463	0.032280226
TXN	9	complement(110243810..110256	ENSG00000136810	1387.004	0.385026	0.001467669	0.032346268
MCTP1	5	complement(94703741..9528457	ENSG00000175471	3.369031	0.418125	0.001477791	0.032520297
INTS9	8	complement(28767661..2889024	ENSG00000104299	5.192398	0.291495	0.001482699	0.032530333
TNFSF14	19	complement(6661253..6670588)	ENSG00000125735	11.61223	0.264463	0.001481493	0.032530333
DPYD	1	complement(97077743..9799500	ENSG00000188641	7.866444	0.358035	0.001514181	0.033171244
GPRIN3	4	complement(89236383..8930780	ENSG00000185477	15.92502	-0.400402	0.001540143	0.033689481
BTG2	1	203305491..203309602	ENSG00000159388	34.04132	0.284739	0.001548969	0.033781388
PVALB	22	complement(36800684..3681947	ENSG00000100362	3.506054	-0.763857	0.001547869	0.033781388
CAT	11	34438934..34472060	ENSG00000121691	60.5272	-0.36221	0.001552594	0.033809997
AACS	12	125065434..125143333	ENSG00000081760	2.096577	0.427452	0.001559148	0.033902188
RIPOR2	6	complement(24804282..2504217	ENSG00000111913	0.260515	0.790459	0.001570531	0.034098967
BLVRB	19	complement(40447765..4046576	ENSG00000090013	66.78657	-0.348418	0.001573413	0.034110842
RTCB	22	complement(32387582..3241224	ENSG00000100220	59.11052	0.368342	0.001588931	0.034396237
NRROS	3	196639694..196662004	ENSG00000174004	34.47052	0.357132	0.00160669	0.034675214
DRAM1	12	101877580..102012130	ENSG00000136048	48.05766	0.371014	0.001608938	0.034675214
TSHZ1	18	75210755..75289950	ENSG00000179981	2.198237	-0.300946	0.001604762	0.034675214
CEACAM3	19	41796587..41811554	ENSG00000170956	0.541425	-1.328058	0.001616114	0.034778584
EIF4EBP1	8	38030534..38060365	ENSG00000187840	31.89234	-0.276218	0.001620389	0.034819295
CCL22	16	57358783..57366189	ENSG00000102962	30.75206	0.530114	0.001666573	0.035759133
SGSH	17	complement(80206716..8022092	ENSG00000181523	10.73697	-0.293997	0.001683252	0.036064034
DDIT4	10	72273919..72276036	ENSG00000168209	18.25204	-0.816471	0.001691063	0.036178349
OLFML2B	1	complement(161983192..162023	ENSG00000162745	4.937931	-0.344389	0.001697194	0.036256441
TOB1	17	complement(50862223..5086797	ENSG00000141232	9.794931	-0.358247	0.001716463	0.036614547
FADS1	11	complement(61799627..6182931	ENSG00000149485	1.891811	-0.286302	0.00172268	0.036693577
CHST14	15	40470984..40473158	ENSG00000169105	2.636815	-0.499582	0.001725604	0.036702364
SMIM30	7	complement(113116718..113118	ENSG00000214194	36.62713	0.261067	0.001770207	0.037596322
DNAAF4	15	complement(55410525..5550823	ENSG00000256061	2.605151	-0.469724	0.001783727	0.037828471
PSMA4	15	78540405..78552417	ENSG00000041357	36.69975	0.358801	0.001800852	0.03813631
OR2I1P	6	29550407..29557721	ENSG00000237988	0.046957	2.568206	0.001820455	0.038495648

DOT1L	19	2163933..2232578	ENSG00000104885	10.34483	0.249605	0.001825475	0.038546011
STARD5	15	complement(81309053..8132418	ENSG00000172345	2.308316	-0.343531	0.001840185	0.038800549
PLEKHB1	11	73646178..73662819	ENSG00000021300	0.441456	-0.860661	0.001847979	0.038908741
SNRPA	19	40750637..40765389	ENSG00000077312	17.28108	0.269237	0.001853177	0.038962048
AMT	3	complement(49416778..4942268	ENSG00000145020	0.170646	1.820208	0.001872083	0.039302985
GZF1	20	23362182..23373062	ENSG00000125812	2.746933	-0.363281	0.001878267	0.039376242
FES	15	90883695..90895776	ENSG00000182511	5.969065	-0.285052	0.001883311	0.039425423
MAGOHB	12	complement(10604193..1061360	ENSG00000111196	3.546402	0.302626	0.001890878	0.039527204
ATP6V0D2	8	85987323..86154225	ENSG00000147614	41.01259	-0.323327	0.001899432	0.039649278
SMYD2	1	214281102..214337131	ENSG00000143499	10.16976	0.281207	0.001932792	0.04023071
CRIM1	2	36355778..36551135	ENSG00000150938	8.178665	0.462663	0.001932322	0.04023071
C20orf27	20	complement(3753508..3767781)	ENSG00000101220	16.79781	-0.30846	0.001942073	0.040366397
SIK1	21	complement(43414483..4342713	ENSG00000142178	0.21936	2.242013	0.001959553	0.040671856
RPS6KA2	6	complement(166409364..166906	ENSG00000071242	5.861015	-0.372143	0.001969729	0.040825071
GPR183	13	complement(99294539..9930739	ENSG00000169508	11.93095	-0.461386	0.001992012	0.041228448
ABHD15	17	complement(29560547..2956703	ENSG00000168792	6.886084	-0.28919	0.002016855	0.04168358
STAB1	3	52495338..52524495	ENSG00000010327	3.32369	-0.394278	0.002027758	0.041849719
ZNF618	9	113876282..114056591	ENSG00000157657	0.289978	0.734011	0.002039785	0.042038564
CPE	4	165361194..165498547	ENSG00000109472	18.2538	-0.272812	0.002049053	0.042142358
TPK1	7	complement(144451941..144836	ENSG00000196511	4.304725	0.353606	0.00205059	0.042142358
GK	X	30653359..30731462	ENSG00000198814	28.6	0.376832	0.002064543	0.042369532
PFKFB2	1	207034366..207081024	ENSG00000123836	1.309931	-0.349284	0.002069211	0.042405759
CBX7	22	complement(39120167..3915268	ENSG00000100307	2.623675	-0.46244	0.002078592	0.042478859
ARHGEF6	X	complement(136665547..136780	ENSG00000129675	5.236313	-0.267119	0.002076873	0.042478859
EXT1	8	complement(117794490..118111	ENSG00000182197	0.723899	0.470277	0.002083337	0.042516376
SPTBN4	19	40466241..40576464	ENSG00000160460	0.22633	-0.832438	0.002118151	0.043166559
ADORA2B	17	15945130..15975746	ENSG00000170425	40.65199	-0.289942	0.002128292	0.04331282
GZMB	14	complement(24630954..2463426	ENSG00000100453	1.674189	0.824491	0.002136115	0.04341157
EPHB2	1	22710839..22921500	ENSG00000133216	1.199553	0.425396	0.002149411	0.043621104
CD36	7	80369575..80679277	ENSG00000135218	99.73293	-0.365146	0.002164084	0.043797228
TSPYL5	8	complement(97273488..9727792	ENSG00000180543	2.012212	0.423549	0.002161198	0.043797228
PTPA	9	129110950..129148946	ENSG00000119383	17.0187	0.245327	0.002170711	0.043870576
NSMCE4A	10	complement(121957091..121975	ENSG00000107672	7.172746	0.293584	0.002191031	0.044220096
ZNF697	1	complement(119619377..119648	ENSG00000143067	4.707384	0.334346	0.002196019	0.04425962
PAQR8	6	52361421..52407777	ENSG00000170915	2.237662	-0.398672	0.002204627	0.044371907
PPP2R5A	1	212285410..212361853	ENSG00000066027	20.66034	-0.247292	0.002212661	0.044472352
NOP16	5	complement(176383938..176388	ENSG00000048162	10.11128	0.276224	0.002232133	0.044802093
BPGM	7	134646811..134679816	ENSG00000172331	5.406998	0.288151	0.002241397	0.044926326
CXXC5	5	139647299..139683882	ENSG00000171604	18.54452	-0.247676	0.002257903	0.045167847
CABLES1	18	23134564..23260470	ENSG00000134508	3.294013	-0.400829	0.002259629	0.045167847
SPATA12	3	57060664..57075432	ENSG00000186451	0.833727	-0.928362	0.00226744	0.045200322
AMIGO2	12	complement(47075707..4707995	ENSG00000139211	16.37125	-0.248552	0.002266555	0.045200322
MMAA	4	145599042..145660033	ENSG00000151611	2.001577	0.301423	0.002291608	0.04549589
BTN2A1	6	26457904..26476621	ENSG00000112763	17.63508	0.247456	0.002291256	0.04549589
DUSP16	12	complement(12473282..1256286	ENSG00000111266	1.632785	-0.430588	0.002287352	0.04549589
RASSF4	10	44959407..44995891	ENSG00000107551	18.90916	0.361945	0.002297248	0.045545974
MNDA	1	158831351..158849506	ENSG00000163563	56.34384	0.322567	0.002331705	0.046166493
FCER1A	1	159289714..159308224	ENSG00000179639	0.215387	-4.178692	0.002339938	0.046266806
SUB1	5	32531633..32604079	ENSG00000113387	16.20904	0.24538	0.002348638	0.046376074
TP53INP1	8	complement(94925972..9494937	ENSG00000164938	1.270332	-0.469072	0.002352759	0.046394758
TIFAB	5	complement(135444226..135452	ENSG00000255833	0.604527	0.825583	0.002363162	0.046474466
CBSL	21	complement(6444869..6468040)	ENSG00000274276	0.220665	3.584442	0.002361106	0.046474466
PPARD	6	35342558..35428191	ENSG00000112033	21.38555	0.329155	0.00237176	0.046580852
PXN	12	complement(120210439..120265	ENSG00000089159	1.437681	0.433979	0.00238627	0.046802918
TMEM179	11	62787402..62790400	ENSG00000185475	32.82265	0.253969	0.002401127	0.047031194
ELOVL7	5	complement(60751791..6084427	ENSG00000164181	3.540288	0.672469	0.002405345	0.047050739
gene:ENSG	16	complement(71447600..7148931	ENSG00000261611	0.244005	-1.058991	0.0024167	0.047209655
SH2D3C	9	complement(127738317..127778	ENSG00000095370	1.776647	-0.437111	0.002421744	0.04724503

SGPP2	2	222424543..222562621	ENSG00000163082	1.200623	0.682448	0.002435585	0.047388516
HPGDS	4	complement(94298535..9434287	ENSG00000163106	10.23802	-0.284881	0.002434427	0.047388516
MMP10	11	complement(102770502..102780	ENSG00000166670	53.45273	0.31993	0.002454757	0.047698015
GIMAP6	7	complement(150625375..150632	ENSG00000133561	1.506362	0.561981	0.002466566	0.04770129
NFKBIB	19	38899700..38908893	ENSG00000104825	23.96084	0.24776	0.002467553	0.04770129
DOP1B	21	36156782..36294274	ENSG00000142197	6.512558	-0.250909	0.002459452	0.04770129
SLC35E4	22	30635781..30669016	ENSG00000100036	1.410877	-0.474983	0.002467983	0.04770129
ACSL5	10	112374116..112428379	ENSG00000197142	63.64215	0.406788	0.002479698	0.047832282
SCO2	22	complement(50523568..5052646	ENSG00000284194	11.01359	0.446598	0.002481308	0.047832282
FMNL3	12	complement(49636499..4970816	ENSG00000161791	6.727082	0.242802	0.002485253	0.047845211
SMARCC2	12	complement(56162359..5618956	ENSG00000139613	13.73687	-0.244594	0.002506835	0.04813386
HMOX1	22	35380361..35394214	ENSG00000100292	237.0286	-0.377538	0.002505838	0.04813386
SATB1	3	complement(18345377..1844558	ENSG00000182568	0.631225	-0.42954	0.002516545	0.048193654
MSANTD3-	9	100442271..100577636	ENSG00000251349	5.751448	-0.29748	0.00251482	0.048193654
SLFN5	17	35243071..35273655	ENSG00000166750	5.695797	0.414946	0.002526825	0.048327189
HSPE1-MO	2	197500413..197550726	ENSG00000270757	7.50228	0.69812	0.002541831	0.048550624
ME3	11	complement(86441108..8667263	ENSG00000151376	13.70966	-0.328732	0.00255055	0.048653563
MEI1	22	41699503..41799456	ENSG00000167077	1.483418	0.468618	0.002556434	0.048702229
SLC39A13	11	47407132..47416496	ENSG00000165915	7.337154	0.303335	0.00256186	0.048742059
MBNL2	13	97221434..97394120	ENSG00000139793	2.96118	-0.317358	0.002592368	0.049258369
C3AR1	12	complement(8056844..8066359)	ENSG00000171860	18.37685	0.36433	0.002599295	0.049325842
SYS1-DBND	20	45363200..45410610	ENSG00000254806	0.18432	-5.653144	0.002603021	0.04933249
SERPINE2	2	complement(223975045..224039	ENSG00000135919	15.77372	0.601446	0.002607608	0.049355396
MYD88	3	38138478..38143022	ENSG00000172936	107.2344	0.386907	0.002620885	0.049542529

Additional file 13: Table S10C. Differential expression analysis of South Africa cohort (72h)

Name	Chromosome	Region	Identifier	Max group means	Log2 fold change	p-value	FDR p-value
IFI44L	1	78619902..78646145	ENSG00000137959	13.99063	4.689464	3.42266E-37	4.99948E-33
RSAD2	2	6865557..6898239	ENSG00000134321	16.00564	4.003576	2.60012E-16	1.899E-12
IFIT1	10	89392546..89406487	ENSG00000185745	30.12772	2.936679	2.58611E-15	9.44382E-12
SIGLEC1	20	complement(3686970..3712600)	ENSG00000088827	45.8506	3.795357	2.29864E-15	9.44382E-12
USP18	22	18150170..18177397	ENSG00000184979	16.17522	3.007769	6.88705E-15	2.01198E-11
IFITM3	11	complement(319676..329475)	ENSG00000142089	55.49363	3.159885	1.29028E-13	3.1412E-10
TNFSF10	3	complement(172505508..172523475	ENSG00000121858	5.610958	3.194075	4.84808E-13	1.01166E-09
CMPK2	2	complement(6840570..6866635)	ENSG00000134326	10.85801	2.823145	6.99344E-13	1.27692E-09
CXCL11	4	complement(76033682..76041415)	ENSG00000169248	3.931194	4.642152	6.61637E-12	1.07384E-08
APOBEC3A	22	38952741..38992778	ENSG00000128383	2.391491	7.151215	3.13851E-11	4.58442E-08
ISG20	15	88635670..88656483	ENSG00000172183	11.67377	3.574123	3.97264E-11	5.2753E-08
MX2	21	41361999..41409393	ENSG00000183486	15.68062	2.636156	7.68441E-11	9.35385E-08
MX1	21	41420020..41470071	ENSG00000157601	58.92567	3.21008	9.5765E-11	1.07603E-07
HELZ2	20	complement(63558086..63574239)	ENSG00000130589	7.908044	2.773628	1.61366E-10	1.68363E-07
C1S	12	6988259..7071032	ENSG00000182326	5.425181	2.646515	7.34289E-10	7.15051E-07
OAS3	12	112938051..112976460	ENSG00000111331	20.02884	2.41625	2.04098E-09	1.86329E-06
IFI6	1	complement(27666064..27672212)	ENSG00000126709	1441.857	2.922421	2.71741E-09	2.20518E-06
IL4I1	19	complement(49889654..49929539)	ENSG00000104951	39.63912	2.666248	2.70566E-09	2.20518E-06
NEXN	1	77888513..77943895	ENSG00000162614	1.974158	2.876259	3.37774E-09	2.59677E-06
IFI27	14	94104836..94116698	ENSG00000165949	51.56795	2.194661	4.325E-09	3.15877E-06
IDO1	8	39902275..39928790	ENSG00000131203	7.792875	3.142542	6.6545E-09	4.62868E-06
gene:ENSG	21	5022493..5040666	ENSG00000277117	2.308514	4.310688	7.40565E-09	4.91702E-06
GCH1	14	complement(54842008..54902826)	ENSG00000131979	16.09649	2.846347	8.70337E-09	5.52739E-06
CXCL10	4	complement(76021118..76023497)	ENSG00000169245	15.4367	3.4947	1.57237E-08	9.56985E-06
GPR35	2	240605430..240631259	ENSG00000178623	4.172565	2.594906	2.04188E-08	1.19303E-05
ISG15	1	1001138..1014540	ENSG00000187608	190.1057	2.403584	2.85477E-08	1.54443E-05
LRG1	19	complement(4536402..4540036)	ENSG00000171236	2.193014	2.656598	2.84489E-08	1.54443E-05
IRF7	11	complement(612553..615983)	ENSG00000185507	33.30131	2.055776	2.96632E-08	1.54747E-05
GRM3	7	86643909..86864879	ENSG00000198822	0.676374	3.747179	3.54422E-08	1.78519E-05
BATF2	11	complement(64987945..64997018)	ENSG00000168062	3.741642	2.524138	4.46515E-08	2.17408E-05
HAPLN3	15	complement(88877294..88895597)	ENSG00000140511	1.199424	3.491274	1.35981E-07	6.40735E-05
EBI3	19	4229523..4237528	ENSG00000105246	17.66902	3.460078	2.5184E-07	0.000114957
GBP4	1	complement(89181144..89198942)	ENSG00000162654	8.91822	2.019059	2.86134E-07	0.000126653
SELENOP	5	complement(42799880..42887392)	ENSG00000250722	3.719648	-2.24411	2.9722E-07	0.000127691
SLC2A6	9	complement(133471094..133479127	ENSG00000160326	40.68079	2.482864	4.43355E-07	0.000185031
CFB	6	31945650..31952084	ENSG00000243649	29.96105	2.419185	5.51429E-07	0.000223742
CCL15	17	complement(35996440..36001553)	ENSG00000275718	11.31566	3.585261	6.44732E-07	0.00025453
HERC5	4	88457119..88506163	ENSG00000138646	19.08678	1.880817	6.99758E-07	0.000268983
NCF1	7	74773962..74789376	ENSG00000158517	263.897	2.60679	7.34343E-07	0.00027504
IGFBP4	17	40443450..40457725	ENSG00000141753	2.299959	2.74315	8.14242E-07	0.000297341
TOP2A	17	complement(40388525..40417896)	ENSG00000131747	1.397676	-2.07104	9.98764E-07	0.000355828
UBE2F-SCL	2	237967014..238099412	ENSG00000258984	0.588012	5.162514	1.0368E-06	0.000360584
OAS2	12	112978395..113011723	ENSG00000111335	30.45014	1.807967	1.22518E-06	0.00040673
KRT23	17	complement(40922700..40937646)	ENSG00000108244	2.464647	3.361681	1.21917E-06	0.00040673
HESX1	3	complement(57197838..57227606)	ENSG00000163666	1.388203	2.922873	1.73433E-06	0.000539008
DDIAS	11	82899975..82958277	ENSG00000165490	1.589055	-2.05275	1.66752E-06	0.000539008
PTGIR	19	complement(46620468..46625089)	ENSG00000160013	3.345894	3.173305	1.70235E-06	0.000539008
APOL3	22	complement(36140330..36166177)	ENSG00000128284	8.843511	1.98105	1.88211E-06	0.000572751
C1R	12	complement(7080214..7092540)	ENSG00000159403	2.666205	2.136543	2.35967E-06	0.000689354
CCL8	17	34319435..34321402	ENSG00000108700	2.076141	3.208953	2.3494E-06	0.000689354
EPSTI1	13	complement(42886388..42992271)	ENSG00000133106	21.14567	1.713873	2.6041E-06	0.000745844
C4B	6	32014795..32035418	ENSG00000224389	0.32239	3.045643	2.9624E-06	0.00083215
IFITM1	11	310041..315272	ENSG00000185885	3.075528	3.033759	3.1694E-06	0.000873499
XAF1	17	6755447..6775647	ENSG00000132530	18.22453	1.728062	3.3482E-06	0.000905689
DLGAP5	14	complement(55148112..55191608)	ENSG00000126787	0.662436	-2.38435	3.61546E-06	0.000960201

gene:ENSG	17	complement(7312661..7319174)	ENSG00000261915	0.479037	4.556632	4.21223E-06	0.001098716
IL15RA	10	complement(5943639..5978187)	ENSG00000134470	20.14319	2.035722	4.36771E-06	0.001119283
ZBP1	20	complement(57603846..57620576)	ENSG00000124256	1.368426	2.468501	4.46198E-06	0.001123726
PLEKHG6	12	6310436..6328506	ENSG00000008323	3.047757	2.588141	4.64367E-06	0.001149663
GPR84	12	complement(54362445..54364487)	ENSG00000139572	10.87589	2.238031	5.15397E-06	0.001254733
HMMR	5	163460203..163491941	ENSG00000072571	0.845608	-2.11743	8.35109E-06	0.001999743
SEMA4A	1	156147366..156177752	ENSG00000196189	7.197557	1.818326	9.63452E-06	0.002269862
CD38	4	15778275..15853232	ENSG00000004468	0.940311	2.113976	9.86867E-06	0.002288121
CA12	15	complement(63321378..63381846)	ENSG00000074410	16.01199	2.045512	1.03612E-05	0.002364774
ICAM1	19	10271093..10286615	ENSG00000090339	67.21367	1.936791	1.10786E-05	0.002489613
RTEL1-TNF	20	63659300..63698684	ENSG00000026036	0.259379	4.418371	1.17019E-05	0.002589843
MINAR2	5	129748094..129766732	ENSG00000186367	0.835207	3.304794	1.28652E-05	0.002804812
IFI44	1	78649796..78664078	ENSG00000137965	43.06461	1.603923	2.29765E-05	0.004935548
LRRC32	11	complement(76657524..76670747)	ENSG00000137507	1.279411	2.345062	2.37124E-05	0.00501982
OTOF	2	complement(26457203..26558756)	ENSG00000115155	0.111658	4.997258	2.65727E-05	0.005481071
FAM111B	11	59107185..59127412	ENSG00000189057	0.803077	-2.04785	2.66417E-05	0.005481071
gene:ENSG	11	66509079..66533613	ENSG00000256349	1.189676	2.024694	2.85423E-05	0.00579052
ANLN	7	36389821..36453791	ENSG00000011426	0.832835	-2.02178	3.05237E-05	0.005944805
gene:ENSG	7	99325879..99394653	ENSG00000284292	0.317736	-5.25214	3.02232E-05	0.005944805
IFIT3	10	89327307..89377473	ENSG00000119917	53.01457	1.631672	3.0197E-05	0.005944805
CMKLR1	12	complement(108288044..108339317	ENSG00000174600	5.343464	1.794346	3.19445E-05	0.00604495
ALOX15B	17	8039034..8049134	ENSG00000179593	15.24938	1.588561	3.22795E-05	0.00604495
JUP	17	complement(41754604..41786931)	ENSG00000173801	6.337923	1.83551	3.16163E-05	0.00604495
N4BP3	5	178113532..178126081	ENSG00000145911	0.796671	3.163791	3.59212E-05	0.006558759
CEP55	10	93496612..93529092	ENSG00000138180	1.077028	-1.90104	3.55193E-05	0.006558759
TIFAB	5	complement(135444226..135452351	ENSG00000255833	2.069445	1.74426	4.2648E-05	0.007690861
ADAM8	10	complement(133262420..133276868	ENSG00000151651	23.92759	1.610914	4.36693E-05	0.00777899
TNIP3	4	complement(121131408..121227466	ENSG00000050730	5.650665	2.133899	4.51625E-05	0.007831335
DHX58	17	complement(42101404..42112714)	ENSG00000108771	9.466933	1.640078	4.45366E-05	0.007831335
CFP	X	complement(47623172..47630305)	ENSG00000126759	8.322526	1.850711	4.55715E-05	0.007831335
NEURL3	2	complement(96497646..96508109)	ENSG00000163121	2.639953	2.673818	4.6526E-05	0.007871069
IFIT2	10	89283694..89309271	ENSG00000119922	45.8107	1.597596	4.68805E-05	0.007871069
IFI35	17	43006740..43014456	ENSG00000068079	89.14779	1.685072	4.81437E-05	0.007991302
LY6E	8	143017982..143023832	ENSG00000160932	300.6909	1.87038	5.30601E-05	0.00865397
EPOP	17	complement(38671703..38674957)	ENSG00000273604	3.520957	1.74188	5.33208E-05	0.00865397
PCLAF	15	complement(64364304..64387687)	ENSG00000166803	0.737131	-2.14229	6.24781E-05	0.010028764
SOCS1	16	complement(11254417..11256204)	ENSG00000185338	2.736046	2.392327	6.61502E-05	0.010502775
CDK1	10	60778331..60794852	ENSG00000170312	1.66461	-1.90197	7.85385E-05	0.012335609
TRPM2	21	44350163..44443081	ENSG00000142185	4.670006	1.676526	8.16556E-05	0.012688766
GP1BA	17	4932277..4935023	ENSG00000185245	2.774553	2.217965	8.39967E-05	0.012915156
SPATC1	8	144012280..144047114	ENSG00000186583	1.079085	2.139369	9.58116E-05	0.01457834
IFIH1	2	complement(162267074..162318684	ENSG00000115267	28.62744	1.45508	9.76317E-05	0.014702129
PDGFB	22	complement(39223359..39244982)	ENSG00000100311	8.195521	1.479881	0.000111101	0.016559672
RGPD6	2	complement(110513802..110577222	ENSG00000183054	0.963212	-1.62316	0.000118243	0.017446157
GMPR	6	16238587..16295549	ENSG00000137198	14.99579	1.695895	0.000122165	0.017844626
SCARF1	17	complement(1633858..1645744)	ENSG00000074660	6.891631	1.530218	0.000126308	0.018267072
TMEM176	7	150800403..150805118	ENSG00000002933	9.775382	1.769887	0.00012882	0.018447805
HSH2D	19	16134028..16158575	ENSG00000196684	0.377961	2.77065	0.000138374	0.01962358
CXCL9	4	complement(76001275..76007509)	ENSG00000138755	2.21858	1.963654	0.000149121	0.020924019
PDE6G	17	complement(81650459..81663112)	ENSG00000185527	8.57294	1.51406	0.000150409	0.020924019
CCL4	17	36103827..36105621	ENSG00000275302	182.0497	2.331444	0.000156285	0.021536415
ETV7	6	complement(36354091..36387800)	ENSG00000010030	0.827362	2.170386	0.000167957	0.022716191
IL27	16	complement(28499362..28512051)	ENSG00000197272	8.299176	1.635397	0.000167929	0.022716191
KITLG	12	complement(88492793..88580851)	ENSG00000049130	0.309701	-1.77711	0.000174387	0.023369514
BUB1B	15	40161023..40221123	ENSG00000156970	0.52425	-2.02206	0.000176956	0.023498165
BCL3	19	44747705..44760044	ENSG00000069399	13.04759	1.626333	0.000178876	0.023539141
LAG3	12	6772512..6778455	ENSG00000089692	0.857053	2.499802	0.000186777	0.02435935
PPAN-P2RY	19	10106223..10114780	ENSG00000243207	0.260006	4.825021	0.000195266	0.025241162
AIM2	1	complement(159062484..159147096	ENSG00000163568	8.953319	1.713803	0.00021611	0.027213123
MT1H	16	56669814..56671129	ENSG00000205358	41.71205	2.308783	0.00021448	0.027213123

RELB	19	45001449..45038198	ENSG00000104856	14.10966	1.487069	0.000215788	0.027213123
WNT5A	3	complement(55465715..55490539)	ENSG00000114251	0.86885	2.024822	0.000236232	0.029492598
STAT1	2	complement(190908460..191020960	ENSG00000115415	56.43578	1.515577	0.000247829	0.030586584
IL32	16	3065297..3082192	ENSG00000008517	3.478458	1.668301	0.000249182	0.030586584
FCAR	19	54874235..54891420	ENSG00000186431	0.804449	1.891905	0.000253885	0.030904165
TNFAIP6	2	151357592..151380046	ENSG00000123610	799.2822	2.646047	0.000258804	0.031242603
CLU	8	complement(27596917..27614700)	ENSG00000120885	0.770083	1.483051	0.000262917	0.03147889
CCL5	17	complement(35871491..35880793)	ENSG00000271503	18.62323	1.872057	0.00027564	0.032733942
SPTLC3	20	13008972..13169103	ENSG00000172296	0.286882	-2.62838	0.000295397	0.034797289
TMEM176B	7	complement(150791285..150801360	ENSG00000106565	18.17965	1.553965	0.000315577	0.036877036
FCER1A	1	159289714..159308224	ENSG00000179639	0.587088	-3.94262	0.000329279	0.03817285
UBD	6	complement(29555515..29559732)	ENSG00000213886	1.737051	2.385073	0.000346993	0.039597848
PSTPIP2	18	complement(45983536..46072272)	ENSG00000152229	15.66556	1.388633	0.000345142	0.039597848
DDIT4	10	72273919..72276036	ENSG00000168209	73.00737	1.553868	0.000352851	0.039646888
CELF4	18	complement(37243040..37565827)	ENSG00000101489	0.337066	2.295556	0.000351669	0.039646888
ZSWIM4	19	13795460..13832230	ENSG00000132003	3.702802	1.489519	0.000355704	0.039662335
OASL	12	complement(121017763..121039242	ENSG00000135114	26.94545	1.361185	0.00037484	0.041479492
ZC3H12A	1	37474580..37484377	ENSG00000163874	36.82314	1.484111	0.000380598	0.041799995
TRAF1	9	complement(120902393..120929173	ENSG00000056558	27.28013	1.684391	0.000405242	0.043847218
SOCS3	17	complement(78356778..78360077)	ENSG00000184557	23.48187	1.765662	0.000405074	0.043847218
ANGPTL4	19	8363289..8374370	ENSG00000167772	11.9998	1.650705	0.000423859	0.045195254
POU2F2	19	complement(42086110..42196585)	ENSG00000028277	1.010457	1.466706	0.000423889	0.045195254
CAVIN1	17	complement(42402449..42423256)	ENSG00000177469	3.734707	1.539715	0.00042823	0.04532719
NFKB2	10	102394110..102402524	ENSG00000077150	40.67971	1.514006	0.000437472	0.045901484
RPS4Y1	Y	2841602..2932000	ENSG00000129824	53.11353	-2.44606	0.00043994	0.045901484
GPX3	5	151020438..151028992	ENSG00000211445	75.51416	1.592401	0.000446473	0.046252662
ATF5	19	49928702..49933935	ENSG00000169136	25.60583	1.399031	0.000454335	0.046735722
AGRN	1	1020120..1056118	ENSG00000188157	22.53067	1.64405	0.000467129	0.047715762
PLEKHG3	14	64704102..64750249	ENSG00000126822	1.799427	1.494591	0.000478762	0.048230463
SIPA1L1	14	71320449..71741229	ENSG00000197555	2.783985	1.391314	0.000478772	0.048230463
CRISPLD2	16	84819985..84920768	ENSG00000103196	0.196627	2.162078	0.000488916	0.048915072
C1QTNF1	17	79022814..79049788	ENSG00000173918	0.738731	2.785381	0.000496733	0.049358994
CH25H	10	complement(89205629..89207317)	ENSG00000138135	1.20667	2.41993	0.000500687	0.04941575