

Table S1. Upregulated genes and miRNAs from various datasets in the study.

Common upregulated genes in PBMC and whole blood transcriptome of patients infected with SARS-CoV-2			
Upregulated genes	log 2 FC in GSE171110	log 2 FC in GSE152418	adjpval
PCSK9	8.578707	2.731885	0
IGHJ6	7.7454	1.67217	1.65E-14
OLAH	6.980635	3.519487	0
TIMP4	6.892707	4.057683	8.13E-13
CD177	6.71479	3.594458	0
IGHV1-24	6.673361	5.83253	0
MAOA	6.571074	1.713816	5.86E-14
EPB41L4B	6.311817	2.619303	9.04E-10
ADAMTS2	6.092189	6.378302	0
IGHV7-4-1	5.987105	5.171362	0
CYP19A1	5.886833	5.337905	0
SDC1	5.682183	5.140477	0
IGHV6-1	5.668846	2.653281	0
METTL7B	5.402139	5.630286	0
KRT38	5.274615	3.054243	1.55E-05
FIGN	5.178458	2.505632	3.07E-13
IGLV3-19	5.160836	3.970032	0
RNASE1	5.15969	5.120694	0
NES	5.005117	3.499585	1.59E-15
GLDN	4.965705	1.472982	2.65E-13
IGLV4-69	4.928639	3.668976	0
ITGA7	4.908659	1.856988	0
SHROOM2	4.889883	2.362614	2.18E-09
IGLV3-25	4.87522	4.492515	0
IGHG1	4.854869	5.281748	0
IGLV3-27	4.84187	4.711517	0
IGLV3-10	4.817215	4.495214	0
IGHV1OR21-1	4.816483	2.477612	4.83E-07
ELANE	4.802643	2.875699	2.77E-16
IGHV1-12	4.75111	4.048329	1.59E-15
IGLVI-70	4.693564	2.995391	0
LHX1	4.684294	2.019159	2.51E-06
DPEP1	4.675396	3.092378	2.29E-11
IGHV4-34	4.624937	4.277759	0
MMP8	4.611395	4.424773	0
H2BC13	4.568637	2.079267	5.92E-14
PAX3	4.523048	2.246103	3.03E-07
IGHV4-4	4.519112	3.896216	3.31E-12
CPE	4.515175	3.610427	0
SYNC	4.450049	1.064275	8.02E-08
DAAM2	4.449827	2.588966	2.07E-11
IGHV2-70D	4.42741	3.445865	9.21E-13
IGLV1-36	4.367812	3.000969	0
OTOF	4.338034	2.956001	0
IGLV6-57	4.31615	4.093058	0
IGHV3-20	4.300223	4.848045	0
IGHV1-46	4.276463	3.53815	0
AMPH	4.263454	1.851292	5.53E-16
ARG1	4.257887	1.308008	0

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IGHV1-69D	4.254345	1.690425	7.62E-12
IGHV3-13	4.23721	3.434863	0
RBP4	4.205533	3.87986	1.13E-12
IGHV3-33	4.160438	3.476511	0
BHLHA15	4.158124	3.593444	0
MLNR	4.13576	2.818361	9.23E-09
SCNN1B	4.12805	2.366227	1.74E-09
KLF14	4.118461	2.146575	6.75E-10
IGHV1-18	4.082661	3.67018	0
UHL1	4.062423	5.227373	0
IGHV2-5	4.05017	2.924702	0
PRTN3	4.019345	3.99431	9.26E-12
OLFM4	4.013548	3.712927	5.06E-11
IGHV2-70	4.012758	4.025779	0
IGKV3D-7	4.000024	3.162725	5.80E-06
IGHV3-43	3.990204	3.608144	0
IL1R2	3.983462	1.916733	2.95E-12
KCNT2	3.968085	2.978782	2.18E-08
IGHV1-69-2	3.953469	5.616879	2.89E-12
FAM20A	3.942362	3.338233	0
IGHV1-58	3.941043	2.511119	0
MAOB	3.940823	4.568634	0
IGLV2-8	3.930672	2.437257	0
MMP1	3.919142	3.022395	4.25E-13
IGHV3-11	3.915224	3.103218	0
IGHV3-73	3.898013	2.277176	0
CCNA1	3.882159	2.262262	1.08E-15
IGKV1-39	3.879653	3.270172	9.69E-12
IGLV1-51	3.876022	3.543219	0
KCTD14	3.866705	2.592241	2.34E-12
OXCT2	3.855921	1.635232	6.68E-15
IGKV2-29	3.852542	2.919383	6.58E-12
IGHV1-45	3.819024	4.794385	1.94E-13
SLC1A3	3.813125	2.01535	0
DEFB1	3.787131	1.789337	1.32E-05
IGHV1-14	3.756862	6.562471	0
KCNN3	3.755212	3.980112	0
RETN	3.730365	2.587217	1.34E-15
IGKV1-8	3.724486	2.87467	0
GLDC	3.720782	3.858505	0
IGHV5-51	3.707825	3.04512	0
IGKV1-12	3.703686	3.351417	0
IGHV7-81	3.670393	2.143301	1.13E-09
H2AC13	3.668417	2.497128	0
IGLV1-47	3.650075	3.637901	0
IGHV4-39	3.648769	3.40931	0
MYBL2	3.644937	3.437006	0
IGHV3-30	3.641033	3.101317	0
IGLC3	3.634023	3.636238	0
IGHV3-21	3.633778	3.112664	0
IGHV3-15	3.631006	2.626452	0
CA12	3.60447	1.680612	4.16E-15
UTS2R	3.598741	3.023731	1.91E-08
IFI27	3.58361	8.725838	0
IGLC2	3.582316	3.584884	0
IGKV1-27	3.581907	3.125125	0
STC2	3.574435	3.041338	1.20E-06
VSIG4	3.569251	1.927171	2.91E-11
IGHG3	3.551064	4.208792	0
TNFAIP8L3	3.550598	3.447454	0

AZU1	3.548408	1.025986	9.40E-09
IGHV4-59	3.54683	3.807899	0
IGLV9-49	3.543303	4.320356	0
IGKV2D-30	3.532909	3.908905	0
MPO	3.530728	1.200425	1.68E-10
LCN2	3.52502	2.733335	0
PYCR1	3.511645	3.183262	0
IGKV3D-20	3.505655	4.912167	0
GALNT14	3.50497	3.250831	0
IGHV3-23	3.490267	3.217983	0
OR52W1	3.488991	1.972463	8.66E-08
C11orf87	3.488448	2.922976	4.23E-07
MZB1	3.466963	3.664382	0
IGLV1-40	3.465071	3.085877	0
H2BC14	3.455085	4.079425	4.53E-12
IGLV1-44	3.451539	3.238287	0
ADAMTS9	3.44971	2.515956	1.15E-07
KCNJ4	3.438682	2.491153	1.97E-06
IGKV3-11	3.436277	2.858794	0
IGLV2-14	3.433001	3.298619	0
XIRP2	3.429179	2.60772	0
H2AC17	3.422726	1.971096	2.88E-15
CDC25A	3.414812	3.093842	0
IGLV5-37	3.411777	4.712081	0
IGLC7	3.406801	2.139167	3.34E-10
DEFA4	3.399959	3.796175	9.11E-10
SPSB4	3.397283	3.443765	2.69E-09
ASS1	3.395827	3.762988	0
FAP	3.39467	2.312812	2.18E-09
IGHV2-26	3.394264	2.389594	0
LTF	3.388095	4.479091	1.06E-14
IGLV2-23	3.377741	3.707784	0
IGLV3-9	3.358072	2.931411	0
IGHV3-49	3.344715	3.114023	0
PPARG	3.312884	3.164904	0
PLXNB3	3.309084	3.09569	0
IGHV4-28	3.303669	3.098364	0
TXNDC5	3.300356	2.594258	0
ABCA13	3.291794	1.300115	1.51E-09
IGHV1OR15-9	3.289806	4.95171	1.59E-15
GCKR	3.28268	3.178886	1.38E-10
OR4C6	3.265834	2.435252	2.30E-05
LINGO1	3.265382	3.049217	5.00E-05
IGHJ5	3.264774	1.74885	0
IGLV2-11	3.257122	3.659463	0
IGHV1-69	3.254967	2.897516	5.23E-14
IGLV1-50	3.251919	2.672312	8.08E-10
CAPN13	3.250556	2.264677	1.76E-10
IGKV1D-16	3.250399	3.712929	0
IGKV3D-11	3.245655	2.912929	0
PKMYT1	3.240623	3.213996	0
IGHV3-7	3.23916	2.640945	0
PGLYRP1	3.234549	2.663653	4.12E-11
MMP2	3.232944	3.474082	3.27E-12
DKK1	3.229242	4.066804	1.39E-05
H3C3	3.22785	3.582866	0
TERT	3.223509	2.102134	0
ALDH1L2	3.221236	2.088785	0
IGLV10-54	3.217404	2.543048	1.26E-14
PCOLCE2	3.20451	4.672771	2.16E-13

FER1L4	3.197809	2.743155	0
IGHJ4	3.194511	1.4859	0
CAV1	3.189958	3.326096	0
IGKV4-1	3.189191	3.133459	0
IGKV3-20	3.18675	2.51916	0
KCNG2	3.174687	1.569206	1.15E-09
IGLV3-16	3.172278	3.713645	0
IGKV2-24	3.164928	4.161251	0
THRSP	3.160223	1.9435	0.000229
FBXO39	3.160167	1.139164	5.78E-08
MT1G	3.158861	3.267209	0
IGKV3-15	3.158692	3.306686	0
IGHA1	3.15673	3.30104	0
IGKV6D-21	3.146452	3.135946	6.44E-13
CDC6	3.138952	2.942361	0
UGT3A2	3.138072	2.087224	8.20E-08
IGLV3-21	3.138067	2.937283	0
OR2T8	3.131208	2.098109	9.12E-06
OR2B6	3.131091	3.754445	0
MCEMP1	3.125312	1.322192	0
TARM1	3.124086	3.367318	0
IGHV4-61	3.124071	3.572589	0
COL17A1	3.122619	2.444701	8.61E-10
IGKV1-5	3.11456	3.291896	0
LY6G6C	3.111481	2.028558	8.20E-16
CDC20	3.110237	3.659699	0
SLC26A8	3.108183	1.785814	0
IGHV1-3	3.106858	3.193457	1.13E-12
IGHV1-2	3.103602	3.693044	0
TTC39DP	3.100327	2.542967	1.41E-05
MCM10	3.096327	3.516135	0
SEMA3F	3.095147	2.150601	1.43E-06
CTSG	3.093402	2.667315	4.43E-07
ESPL1	3.09192	2.799341	0
IGHV3-66	3.091196	2.960424	0
CCL25	3.087907	3.001956	2.77E-16
FN1	3.085422	2.854528	1.72E-11
IGHD3-16	3.084431	2.169881	8.92E-05
GRB10	3.080344	1.632107	2.77E-16
IGKV2D-29	3.078182	3.316719	0
H2BC17	3.078085	3.732352	0
INHBB	3.070869	2.696421	4.38E-10
DEPP1	3.067193	2.611986	0
NCAPG	3.066942	3.2259	0
IGHV3-19	3.065187	3.294559	1.02E-12
IGKV1-16	3.065042	2.964937	0
IGF1	3.056309	4.158115	0
IGKV1-17	3.04985	3.008694	0
SKA3	3.048952	3.278201	0
NKAIN1	3.041056	3.325961	4.55E-07
IGKV6-21	3.039833	2.411663	2.77E-16
RRM2	3.038627	3.819201	0
ABCC11	3.036359	1.015083	5.07E-06
IGHV3-64	3.035266	3.591752	2.77E-16
SLC16A8	3.027625	2.008679	1.06E-06
CADPS2	3.026703	1.797289	6.87E-07
IGLC6	3.022716	2.964824	2.77E-16
KIF20A	3.014591	3.498057	0
SHCBP1	3.00748	3.204858	0
KIF4A	3.001435	3.510548	0

SLCO4A1	2.999686	2.746881	0
BUB1	2.995489	3.118832	0
MT1H	2.995477	2.533886	2.17E-05
MGAM2	2.992172	1.477784	2.42E-14
H2BC5	2.986321	2.079064	0
CEACAM6	2.984269	1.499739	2.46E-07
TPST1	2.980725	2.06531	2.25E-14
MTCO1P12	2.98057	2.69397	3.69E-08
IGLV4-60	2.978323	2.900191	1.34E-15
CD163L1	2.972539	1.15659	8.96E-07
EMX1	2.969013	2.35246	3.18E-05
MET	2.968152	2.872482	0
IGHV3-53	2.958155	2.577257	0
IGLL5	2.953796	1.562559	0
IGKV2D-40	2.937962	3.272438	0
SLC8A2	2.936208	3.409187	1.94E-08
BIRC5	2.935818	3.844212	0
TICRR	2.934662	2.561647	0
CEACAM8	2.92708	4.039917	3.39E-10
TCN1	2.926085	1.729596	1.95E-09
PTGFR	2.925516	1.69147	3.54E-12
MKI67	2.925474	3.158545	0
ANKRD2	2.924033	2.384679	1.19E-06
VNN1	2.921978	1.204994	6.44E-15
ASPM	2.912865	2.959337	0
H1-5	2.910064	3.26875	0
H2AC16	2.909723	1.440591	4.66E-09
GPRC5D	2.908025	3.411141	0
VSTM2L	2.90691	2.104822	2.48E-06
IGHV1-17	2.902509	2.350358	4.27E-12
CDC45	2.896583	3.034004	0
CDCA2	2.894011	3.391304	0
CCM2L	2.893763	1.904939	3.86E-09
IGHM	2.889379	1.611472	0
IGLV2-28	2.889332	2.304866	9.72E-12
IGHV4-55	2.879278	2.676229	0
RAD54L	2.878731	2.86785	0
IGHV3-74	2.877683	2.663063	0
RAP1GAP	2.873855	5.741696	3.30E-14
TEAD4	2.866909	2.15344	0.00094
BMX	2.862701	1.920675	2.96E-14
ITGA8	2.854801	2.998014	2.77E-16
TMEM92	2.851352	2.411413	2.14E-12
IGKV1-9	2.848939	2.863185	0
H4C4	2.845727	1.866144	0
IGLV2-18	2.840577	3.225656	1.34E-15
H3C8	2.838576	3.430551	0
HJURP	2.836392	3.232056	0
E2F8	2.833486	2.838017	0
KIF18B	2.832755	2.98763	0
IGHV1-67	2.831358	4.473656	4.81E-14
PSG11	2.827576	2.493204	7.03E-05
MYH7	2.825546	2.776297	1.88E-05
IQGAP3	2.819078	2.837661	0
FAM72C	2.817966	2.602522	9.64E-15
IGKV2-30	2.817943	3.853298	0
PNMT	2.81533	1.517836	2.09E-06
IGKV5-2	2.810264	3.398886	0
IGHV3-35	2.808111	1.529933	1.22E-09
CDCA5	2.805061	2.863512	0

ADGRL2	2.797636	2.207252	2.36E-05
AMPD1	2.790743	2.379601	3.47E-08
IGHV3-52	2.785226	3.748151	1.06E-11
KIF14	2.782281	2.618669	0
H2BC7	2.773222	2.368051	0
BUB1B	2.772578	2.782759	0
LRIG3	2.770393	2.008311	2.02E-06
IGLV4-3	2.769153	2.707069	2.50E-13
TK1	2.7626	3.201233	0
JCHAIN	2.760286	3.578456	0
H3C12	2.75714	3.030132	3.61E-13
IGKC	2.755035	3.1458	0
TMEM54	2.754055	2.278051	3.23E-07
ERICH3	2.743732	1.970404	1.24E-06
SIGLEC1	2.741145	2.155835	4.75E-07
IGLV5-45	2.739846	3.933356	0
DIAPH3	2.735887	3.168508	0
DEPDC1	2.733895	3.535928	0
TROAP	2.733614	3.422048	0
PBK	2.73178	4.078021	0
FOXM1	2.722486	3.079316	0
CCL7	2.716739	3.267224	1.10E-06
CMA1	2.715108	2.66019	9.55E-06
TRIP13	2.714556	3.068156	0
TMPRSS2	2.714214	1.912741	5.33E-05
MTCO1P40	2.70783	2.286017	6.42E-05
GTSE1	2.707648	3.115828	0
HPDL	2.705721	1.812965	0
SIGLEC11	2.703477	2.379715	0
PIR	2.70253	2.891428	0
DGKI	2.702273	3.022495	2.48E-12
PLK1	2.700528	3.878898	0
CRISP3	2.698256	3.325397	4.80E-08
NTSR1	2.69216	2.09411	0
IGHV3-72	2.690988	2.418058	5.65E-13
COL10A1	2.686949	2.511736	2.71E-12
POLQ	2.686146	2.182255	0
ANO2	2.676893	2.909447	1.71E-13
IGKV1D-13	2.676549	4.158857	3.85E-09
EXO1	2.674863	2.681693	0
CD163	2.669642	1.42483	2.78E-09
E2F7	2.668731	2.759432	0
ITGA2B	2.667733	3.117353	0
TEDC2	2.666132	2.386694	0
CYP26C1	2.663158	2.078896	0.000696
CDT1	2.662557	2.785978	0
H2BC8	2.658691	2.019559	0
CLSPN	2.651163	2.645521	0
EFS	2.649147	2.561562	0.000745
H3C2	2.647652	2.873293	2.50E-13
ZNF385B	2.644939	3.32187	1.71E-05
KREMEN1	2.637817	1.932505	0
BEX1	2.630511	1.213739	3.40E-07
E2F1	2.6285	2.718415	0
ANLN	2.616102	2.87313	0
FAM71F1	2.614426	2.586019	0.000173
IGHV3-41	2.614263	2.505327	2.92E-09
RNASE3	2.612615	2.773918	1.38E-11
S100A12	2.602935	2.568207	0
MYL9	2.598523	3.758481	0

DLGAP5	2.597523	3.816064	0
IGFBP2	2.592339	2.014151	2.39E-10
ANXA3	2.59151	3.960528	0
PCK1	2.588245	2.017032	0.000245
OIT3	2.58569	1.840601	2.34E-07
MUC6	2.580754	1.301794	4.23E-05
IGLV7-46	2.57118	3.830531	0
CHST8	2.570435	2.741149	3.97E-14
TMEM119	2.565369	2.027561	0
IGLV8-61	2.56471	2.937663	0
DTL	2.555783	3.15929	0
IFITM3	2.545305	2.158951	0
SPDEF	2.544536	3.162007	5.61E-07
SLC6A19	2.540046	2.715397	5.62E-05
ANKRD34B	2.538575	1.820079	2.24E-09
IGHV3-48	2.537314	3.018045	9.17E-15
CSRNP3	2.528154	2.1851	1.75E-05
ERG	2.525238	1.460871	7.46E-09
CENPA	2.524199	3.609761	0
CENPM	2.523897	1.208057	0
BVES	2.523153	2.697451	3.26E-14
CDC25C	2.5153	4.011879	0
PKHD1L1	2.513363	1.845461	0
CCNB2	2.510654	3.427888	0
RD3L	2.507841	2.614955	4.21E-07
TYMS	2.49846	2.974962	0
IGHV3-22	2.492465	2.337434	6.96E-09
HROB	2.49111	1.264058	0
HMMR	2.486093	2.922076	0
LHFPL4	2.484779	1.025685	9.24E-06
NRN1	2.484222	1.801497	2.05E-12
TPX2	2.483873	3.163158	0
COL1A2	2.482954	2.481404	1.06E-06
KRT8P20	2.482878	2.021368	0.001804
GABRR2	2.480753	1.016742	9.49E-13
IGHA2	2.478683	3.420021	0
GALNT18	2.477095	1.456739	1.95E-09
IGKV3D-15	2.475257	2.867443	1.03E-11
GPIHBP1	2.474766	2.580447	0.000911
CAMP	2.472906	1.295033	2.45E-09
TSHR	2.472159	2.40427	0
TRIM55	2.468839	3.087673	1.65E-09
TOP2A	2.46606	3.168653	0
UBE2C	2.465483	3.5667	0
STOX2	2.451783	2.413395	1.81E-09
APOBEC3B	2.451746	2.270199	0
CKAP2L	2.451735	3.200582	0
AURKB	2.450195	3.214961	0
HASPIN	2.446341	1.888641	0
HSPB6	2.436053	2.668239	1.04E-06
KIF15	2.434881	2.420094	0
PHKA1	2.434536	1.572179	1.89E-14
IGHV3OR16-8	2.434285	2.095566	7.19E-06
ASS1P1	2.432778	1.045392	4.18E-13
SPC25	2.431799	3.878909	0
H2AC12	2.431793	2.636207	0
KIF2C	2.427672	2.904917	0
GGH	2.423429	2.411091	0
TNFRSF17	2.414768	3.393909	0
NT5DC2	2.413358	2.192641	0

CEP55	2.41135	3.468904	0
MELK	2.411287	3.117321	0
IGHV3-71	2.410166	2.37253	1.78E-11
ORC1	2.409342	2.575613	0
RSAD2	2.406751	1.335687	1.60E-05
IGKV1-6	2.404607	2.957651	0
MIXL1	2.400975	3.343853	0
FBXO16	2.396712	3.300293	7.44E-15
H4C8	2.396152	2.511271	0
IRX3	2.392552	1.548909	6.63E-05
IGKV1D-17	2.388569	4.042876	9.56E-08
H2AC14	2.388513	3.343047	0
PRR15	2.384942	2.95532	5.48E-08
PLAAT2	2.363157	1.4023	9.61E-10
TIMP3	2.362645	1.528943	3.28E-08
NEK2	2.360256	2.835465	0
USP18	2.353458	2.182589	2.13E-09
KIFC1	2.344872	2.698832	0
PSG6	2.34169	2.061649	7.44E-06
RNASE2	2.328968	2.55398	0
WFDC1	2.31883	4.923468	0
DYSF	2.316637	1.493812	0
B9D1	2.309669	1.624865	0
S100A8	2.300724	1.970369	0
C1QC	2.299391	3.561355	0
ZNF215	2.297088	1.823452	3.21E-12
IFI44L	2.288698	2.475801	6.22E-08
PSMD8P1	2.288188	1.126277	0.000539
GJA4	2.280083	3.00307	8.98E-10
NLGN1	2.27591	2.458151	5.09E-09
CCNA2	2.273615	3.754225	0
BCAR1	2.273011	1.889714	3.16E-06
CHPF	2.272961	1.537737	0
IGHG4	2.272867	2.645514	3.03E-11
PLIN4	2.270155	1.122771	7.15E-12
SLC10A6	2.268516	2.661139	0.000169
IGHV3OR16-9	2.268343	3.26195	7.57E-11
TRIM80P	2.264189	1.154492	0.000302
H1-3	2.261331	1.431017	0
EGF	2.259701	2.826903	0
INAVA	2.256313	2.596349	2.77E-16
DEFA3	2.253052	3.819971	1.43E-05
C1QB	2.250061	2.905413	0
ZWINT	2.249262	2.369225	0
SKA1	2.242321	3.033931	0
CMTM5	2.241081	2.829363	0
IGHV3-38	2.240377	2.566581	1.92E-07
MS4A4A	2.239778	1.801795	0
CDK1	2.239092	2.729368	0
IGHG2	2.237649	2.215152	1.18E-12
SAMD14	2.23617	3.318998	0
HMGB3	2.233596	1.863117	0
SEMA3B	2.232237	1.206589	8.20E-16
IGKV1D-8	2.231358	2.439332	2.77E-16
ACOXL	2.228328	3.959552	0
TCN2	2.228309	1.491131	1.73E-13
SPC24	2.227155	2.93533	0
ACOX2	2.221046	1.345609	2.02E-11
ELL2	2.218532	1.405244	0
CLU	2.21685	3.240749	0

FAM205A	2.213635	3.053639	9.28E-05
IGKV3-7	2.212825	2.97332	2.77E-16
ADGRF5	2.210584	2.159423	0.000161
EGFL7	2.21056	2.480562	0
NCAPH	2.205522	2.035177	0
IGLV5-48	2.204176	3.425273	2.75E-12
IFI6	2.199331	2.054823	7.92E-11
HESX1	2.198092	1.678055	8.75E-07
DNAAF3	2.196468	1.647376	0.000184
GINS2	2.194052	2.8075	0
SLCO2A1	2.19124	2.47122	3.37E-08
IGLV7-43	2.189354	2.357579	0
DERL3	2.18808	2.712315	0
TTK	2.187002	2.515091	0
STAB2	2.186784	1.430975	1.28E-08
ARHGAP23	2.185108	1.149025	0
IGKV2D-26	2.18361	2.846153	5.28E-07
IGHJ3P	2.183422	1.627114	0
IGSF21	2.17759	3.204657	0.000126
SUCNR1	2.174167	1.776199	3.53E-13
CLDN18	2.173315	2.139661	1.40E-05
CENPE	2.172506	1.733301	0
KNL1	2.170384	2.04999	0
SPAG5	2.169782	1.715617	0
TNNT1	2.166177	3.063115	2.77E-16
ADM	2.16487	2.295968	0
IGHV3-69-1	2.161852	3.457763	0
GP6	2.161636	2.164859	0
IL10	2.159982	1.130069	0
SELP	2.156814	2.543237	0
COL2A1	2.155503	2.735294	1.87E-05
COL23A1	2.155449	1.799974	6.33E-13
LAMC1	2.150661	1.682492	0
DEPDC1B	2.14884	2.859543	0
E2F2	2.147566	1.806464	0
TNFRSF13B	2.144087	1.583609	0
IGHV3-62	2.137028	2.845386	3.83E-08
ZAR1L	2.135954	1.458234	0.000287
NEIL3	2.133882	2.234236	0
SHROOM4	2.133595	1.271	4.62E-11
CIT	2.131309	1.747417	0
RAPGEF5	2.126568	1.097285	4.39E-10
ANKRD22	2.123775	1.236932	2.01E-09
KIF11	2.118456	2.303965	0
RIPOR3	2.116044	1.553309	0
FABP4	2.115035	3.255558	6.26E-06
IGLV3-6	2.113664	2.578608	1.14E-07
MTDHP3	2.11324	1.549719	1.95E-05
CENPF	2.111329	2.155298	0
FLT3	2.111148	1.327601	1.22E-07
SERPING1	2.108967	1.780288	2.84E-09
CCNB1	2.107358	2.286458	0
SLC16A14	2.104292	2.59187	0
TP73	2.104148	2.212527	0
SH3PXD2B	2.099973	1.157357	4.07E-07
NEXN	2.099868	1.278886	1.10E-12
TRPV5	2.099805	1.598137	8.94E-09
SLPI	2.098892	2.206096	2.25E-10
S100A9	2.097624	1.714788	0
MUC5B	2.091733	1.920593	1.89E-05

GP9	2.090987	2.164394	2.77E-16
COL7A1	2.086139	1.0719	2.19E-13
RLBP1	2.084221	1.349376	0.000692
EDNRB	2.082091	2.956013	4.56E-09
OASL	2.074104	1.39166	1.94E-11
GP1BA	2.07402	1.97388	0
DCC	2.072728	3.816584	0
UHRF1	2.070497	2.799266	0
TSPAN12	2.065797	3.065746	3.30E-05
ACCSL	2.065108	3.060126	6.03E-08
ID1	2.058318	1.172212	1.42E-07
IGKV1-13	2.052866	3.271288	3.50E-09
KCND1	2.052385	1.02783	0
TBX3	2.044833	2.111713	0.000138
OLFML2A	2.044654	1.848894	7.38E-09
KIRREL1	2.042132	2.567824	8.69E-06
PCLAF	2.037228	3.167357	0
ZBTB32	2.027975	1.599382	0
SLC2A5	2.026561	1.831613	0
MND1	2.024271	3.186493	0
MRAP2	2.023767	2.612036	8.96E-06
LHFPL6	2.023762	1.317511	2.47E-07
ESCO2	2.019206	2.616412	0
NMNAT2	2.018058	2.049626	5.95E-11
LSMEM2	2.013369	1.719112	2.19E-06
GSG1L	2.011778	2.351996	8.82E-08
CDCA3	2.011474	2.418435	0
DRC7	2.002791	1.197606	3.08E-07
CRYM	1.998567	2.07116	1.21E-09
GAS2L1	1.998328	1.24443	6.02E-12
RAD51	1.995415	2.528138	0
CMPK2	1.989681	1.52506	6.14E-07
STUM	1.988488	2.249648	4.30E-05
BEND7	1.988413	1.993348	6.79E-13
CLEC2L	1.985268	3.178828	6.24E-13
CENPW	1.983609	1.452934	0
ITGB3	1.975505	2.541259	0
FSTL1	1.966812	2.223291	2.69E-14
SCN1B	1.966339	1.758107	0
COL20A1	1.964871	1.861576	0.000167
SERPINE1	1.964257	1.199244	3.54E-10
ALPK3	1.962479	1.462818	1.49E-10
PTCHD4	1.95762	2.884137	2.47E-05
BCAN	1.956755	1.939864	4.12E-07
MMRN1	1.95512	2.268583	0
FCGR1CP	1.952397	1.562047	4.40E-11
TAF5	1.951593	2.744029	9.52E-05
H1-4	1.949504	1.442665	0
ACSL1	1.94759	1.091093	3.38E-15
CDHR4	1.945216	1.789532	2.62E-05
CREB3L1	1.944848	3.043844	3.94E-12
EYA2	1.942867	1.9634	1.45E-06
DMC1	1.940732	2.597967	0
PEAR1	1.940731	2.195774	0
ASPH	1.940667	1.050802	1.93E-14
SPDYC	1.939494	2.720272	4.29E-05
CRACD	1.939418	2.008667	8.82E-12
MEIS2	1.937786	1.704002	4.50E-08
SAP30	1.93637	1.385022	3.65E-11
AQP10	1.935524	1.934171	1.84E-10

SAPCD2	1.932791	1.677926	0
TULP1	1.927345	2.078119	0.00019
IFI44	1.926248	1.290416	8.82E-08
MS4A3	1.926143	2.269484	2.32E-07
ABCB11	1.92093	2.14653	1.89E-05
SYN2	1.920402	2.615422	1.90E-12
RELN	1.916219	1.907118	4.10E-05
ANKRD9	1.912878	1.589662	1.77E-14
IGKJ5	1.912455	1.718091	9.38E-13
CHEK1	1.909228	1.700168	0
PCP4L1	1.90405	2.392844	4.85E-11
CETP	1.903935	1.88525	0
SLCO2B1	1.90242	2.403627	1.72E-14
CDKN3	1.901008	2.760354	0
MUC21	1.895849	2.961563	1.32E-08
LY6E	1.894864	1.163049	8.98E-10
ERCC6L	1.890355	1.111207	0
NUF2	1.890299	2.125101	0
MEIS3	1.890255	2.08974	1.75E-08
VEGFC	1.889328	2.107727	3.79E-11
SLC6A9	1.888365	3.441152	0
TM4SF18	1.887819	2.427299	0.000989
IGLV1-41	1.886986	2.243138	5.19E-05
MX1	1.880946	1.621157	2.71E-07
RAB13	1.879939	1.440324	2.86E-12
FZD5	1.877909	1.203237	0
WNT11	1.87764	2.282595	1.84E-15
KLHDC8A	1.876251	3.226822	1.29E-07
CALHM3	1.874211	2.246854	5.73E-06
IGKV2D-24	1.872604	3.635148	2.56E-09
CHRNA2	1.869625	1.768104	1.02E-07
H1-2	1.867706	1.839649	0
MCM4	1.865319	1.632901	0
ITGA9	1.864667	1.765565	1.07E-09
TGFB111	1.863895	2.639918	0
PDE2A	1.863887	2.171829	0
AUNIP	1.860798	1.840277	0
ATP9A	1.859066	1.091215	1.72E-11
CT75	1.857124	1.68695	6.86E-08
ESAM	1.856473	2.059086	0
TREML1	1.854232	2.959287	0
LIPH	1.853767	2.78723	1.63E-13
LPO	1.85113	1.545464	9.79E-13
CHRNA2	1.847146	1.302651	3.21E-07
WASF1	1.837804	1.496869	0
DPYS	1.832636	1.703377	0.000274
TRHDE	1.826606	2.098862	1.64E-07
DHCR24	1.825054	1.341536	0
SPATS2L	1.822166	1.517897	2.55E-13
CACNA1E	1.820383	2.061214	7.91E-11
HTRA1	1.818856	1.851927	1.90E-08
MTND5P14	1.816045	1.281022	0.000391
HMGB2	1.813181	1.016307	0
RUNX1T1	1.812561	2.974244	1.95E-09
FA2H	1.811775	1.568403	1.71E-11
H2BC21	1.809013	1.726188	0
H4C11	1.808013	1.322219	1.59E-15
GINS1	1.800812	1.670518	0
CD38	1.799576	1.681593	0
ABLIM3	1.799319	2.820722	0

JSRP1	1.798471	1.792383	2.62E-13
H2AC8	1.796855	2.078934	1.84E-15
PLBD1	1.796804	1.29554	0
DQX1	1.796543	1.973978	2.00E-11
PCYT1B	1.795574	2.529008	2.08E-14
CDC42BPA	1.793293	1.883711	0
TRPM1	1.790745	2.463345	8.72E-07
TMEM132D	1.790054	1.108226	3.36E-09
RHAG	1.78956	5.990704	2.10E-13
SMOX	1.786584	2.374299	0
CALHM5	1.785401	1.962045	7.01E-12
EPHB2	1.782635	1.448362	4.25E-10
LY6G6F	1.782178	2.014348	6.94E-14
XK	1.781288	3.390806	0
POU2AF1	1.779604	1.255566	0
SMIM10	1.779337	1.270077	2.88E-09
IFI27L1	1.776599	1.409438	0
H2BC4	1.772586	2.041166	0
STIL	1.772239	1.793154	0
SCUBE1	1.772062	3.251395	0
SEPTIN4	1.770833	1.402211	5.12E-12
ABCB9	1.769149	1.449658	0
GSTT4	1.767457	2.466405	0.000229
PRDM6	1.76706	1.986253	1.56E-09
COL4A1	1.766991	1.625109	9.30E-07
NALCN	1.764327	2.446577	1.20E-07
CD5L	1.760966	3.503384	4.80E-08
TMEM158	1.758079	2.113601	8.70E-14
LTBP1	1.756685	2.022757	2.61E-14
RECQL4	1.756234	1.587416	0
ASIC4	1.754146	2.248897	2.04E-09
FCGR1A	1.751018	1.575234	4.72E-13
GAS6	1.743565	1.846473	0
COL24A1	1.743507	1.114455	1.08E-15
CBS	1.736356	2.019376	0.000344
ITM2C	1.732175	1.771275	0
SH3TC2	1.729736	2.229034	0
ARHGAP42	1.727034	1.147934	2.18E-11
PHGDH	1.726369	1.441495	0
OGDHL	1.725439	2.546663	1.09E-05
EPAS1	1.723149	1.04389	5.74E-10
GPR26	1.722602	3.06068	1.08E-06
CREB3L3	1.720677	1.987553	1.70E-05
WDR62	1.716706	1.326895	0
H2BC12	1.716	1.295889	0
KIF23	1.715848	1.789887	0
EPSTI1	1.714444	1.149046	8.75E-09
ADGRG3	1.714433	1.13366	5.34E-09
AURKA	1.708745	1.389685	0
CXCL13	1.707698	3.733725	2.80E-09
CDCA8	1.705934	1.868802	0
ETV7	1.705345	1.486637	1.15E-06
CTSD	1.703803	1.239946	0
ESYT3	1.699275	1.397938	2.23E-07
TSPAN9	1.699216	2.269723	1.08E-15
TP53I3	1.696174	1.16868	8.96E-15
EME1	1.693276	1.12847	0
CATSPERD	1.68926	3.220097	8.24E-06
KBTD12	1.688138	2.357178	6.33E-11
SPOCD1	1.687538	2.229993	3.12E-12

PARD3	1.686825	1.785564	1.36E-14
MAP1B	1.686002	1.609389	5.95E-14
BFSP2	1.685558	1.665984	5.83E-12
CAVIN3	1.679575	1.954536	4.59E-07
RHOBTB1	1.679161	2.199661	0
HSD3B7	1.676582	1.075025	2.89E-10
CAV2	1.672914	2.818542	0
CLEC1B	1.672271	1.914511	6.44E-15
OIP5	1.671306	2.228011	0
TLCD4	1.669953	1.959915	1.63E-07
LMNTD1	1.665193	2.468161	4.68E-06
CAPN11	1.663653	1.567128	1.88E-05
PLEKHH3	1.663465	1.183105	0
SLC4A11	1.659015	1.774636	2.65E-10
B4GALT2	1.65623	1.303873	0
PTPRF	1.655441	2.046163	1.00E-10
CCNE1	1.653635	1.130759	8.20E-16
VWFP1	1.650022	2.37908	3.90E-05
CCNE2	1.64569	1.342852	0
SDF2L1	1.637154	1.228772	0
CNKSR1	1.635145	1.363372	1.47E-13
RGN	1.63501	2.416846	2.27E-05
EMP1	1.634953	1.735762	2.33E-09
TMEM198	1.631172	1.358531	3.10E-08
POC1A	1.628549	1.641767	0
PDE3A	1.626965	1.582135	2.97E-09
PIMREG	1.623613	2.585854	0
MROH5	1.621728	1.753229	0.000232
MAP1A	1.621303	1.423968	9.77E-11
FAM111B	1.619662	1.787401	0
H4C9	1.618669	1.203229	0
SSC4D	1.617183	1.439147	2.00E-12
SH3GL3	1.616708	2.581556	1.74E-05
KLF5	1.613665	1.167089	1.48E-09
AOC4P	1.612562	2.613055	6.10E-06
VWF	1.610259	1.730571	1.56E-09
PTTG1	1.609117	1.570295	0
SMTN	1.608578	1.197624	1.34E-15
XKR4	1.606332	3.956576	5.65E-13
GABRD	1.601216	1.841709	0.000112
H1-0	1.599335	1.011183	2.59E-10
ANKRD30BL	1.594195	2.611054	4.60E-07
ARNTL2	1.592885	2.084974	0
MPIG6B	1.591932	2.476005	0
ST8SIA5	1.587773	1.996476	7.80E-10
RHBG	1.587018	1.720704	5.78E-05
GPC5	1.586829	1.194766	0.000243
CEL	1.586394	2.391618	7.35E-09
GPR27	1.582941	1.3197	2.77E-16
XAF1	1.580811	1.058537	9.94E-06
CDKN2A	1.57444	1.198505	8.20E-16
PROS1	1.568183	2.245455	4.99E-11
DNM1	1.564319	1.611042	1.84E-15
ARFGEF3	1.564031	2.992678	6.69E-13
FAM72D	1.560521	1.710299	1.54E-12
PIF1	1.560491	1.665419	0
RNF208	1.557161	1.778955	3.11E-08
REEP1	1.556267	1.837492	9.49E-06
IFITM10	1.554788	2.947535	6.54E-13
SGO1	1.55401	1.766428	0

FCGR1B	1.553825	1.0993	1.04E-09
PLOD2	1.546944	2.63972	0
H2BC11	1.543959	2.551012	0
PLA2G4F	1.5437	3.516282	1.68E-09
H1-6	1.543048	3.112793	5.44E-06
KAZALD1	1.537241	1.903556	1.40E-11
FRAS1	1.529302	2.042211	0.000344
SYTL4	1.528661	2.056686	7.99E-12
ORC6	1.527213	1.297368	0
H2BC9	1.526678	2.443584	9.17E-15
MGLL	1.525981	1.330139	1.36E-12
PCSK6	1.52475	2.341373	1.14E-13
PF4V1	1.517894	2.970702	4.31E-12
ASPG	1.516902	2.109666	1.06E-05
POLE2	1.516387	2.061415	0
DENND5B	1.516264	1.097112	2.21E-10
SLC35D3	1.515507	3.130283	3.35E-12
ACSS3	1.514387	1.679475	6.73E-12
LRRC71	1.514221	2.195518	0.000204
RBPMS2	1.51296	1.8713	1.82E-05
ALOX12	1.511425	1.520292	7.75E-13
ITGA1	1.508639	2.107843	0
APOBEC3A	1.508157	1.328241	5.69E-15
RGMA	1.505205	1.49826	3.38E-15
DSCC1	1.501722	2.191904	0
TTLL7	1.49998	2.587402	0
HSP90B1	1.4937	1.057641	0
ZP2	1.492777	3.267275	4.18E-06
SLC7A11	1.49117	1.4718	0
RCVRN	1.487175	1.333	2.72E-05
TMC1	1.484651	1.854301	7.25E-07
CENPU	1.484211	1.948657	0
SLC24A3	1.483483	2.368458	2.66E-12
HTR2A	1.480072	1.728251	1.26E-05
HMCN1	1.478868	2.051021	6.25E-08
PTCRA	1.477409	1.726593	5.43E-12
NFIB	1.477168	1.43938	3.08E-06
IGKV2-26	1.477142	2.28003	1.65E-08
SPARC	1.472229	2.635406	0
CBLN2	1.471423	2.51856	4.18E-06
ITGB5	1.463158	2.14366	1.09E-14
FAM72A	1.463104	1.765886	0
CENPI	1.461108	1.512399	2.77E-16
FAM72B	1.459591	2.202454	0
FAM124A	1.456495	1.850003	3.04E-12
MYDGF	1.454895	1.083191	0
MESP1	1.454463	1.534147	4.43E-10
STMN4	1.45365	2.287982	0.001557
BRCA1	1.448796	1.122637	0
MDK	1.448657	1.61743	0
PROK2	1.446845	1.068661	3.47E-08
CCNF	1.446003	1.040083	0
HTR1F	1.445354	2.213123	7.93E-07
CD300LG	1.444139	2.269433	4.89E-05
SLC12A8	1.439364	1.960737	2.65E-14
JCAD	1.437822	3.244599	4.10E-10
MCM2	1.436163	1.767549	0
ZFH2	1.436066	1.412509	4.81E-09
ARHGAP6	1.434885	2.091639	1.48E-14
TUBG1	1.433683	1.000759	0

CDH7	1.428499	2.17934	2.01E-09
SPATS2	1.427303	1.15738	0
THBS1	1.426822	1.159546	6.62E-05
RHBDL3	1.425626	1.55535	0.000391
CBLIF	1.418072	2.594435	6.35E-05
STAB1	1.411647	1.06109	1.03E-11
SLC34A2	1.408482	2.251359	4.70E-07
FFAR1	1.402329	2.382849	7.32E-10
RAD51AP1	1.399883	1.479088	0
CNTNAP3	1.394965	2.23056	3.00E-05
PITX1	1.394245	2.851726	3.59E-07
SEPTIN5	1.393629	2.302829	2.48E-06
EMILIN1	1.393105	1.113894	8.89E-10
MPL	1.39216	2.262039	2.20E-13
KLHL30	1.387757	2.09874	9.07E-09
ANXA8	1.3875	2.296911	1.15E-06
KRT80	1.387251	1.573317	9.23E-09
KAZN	1.383402	2.186049	7.99E-09
IGF2BP3	1.381548	1.799686	0
PDIA5	1.379392	1.228578	0
PPBP	1.374133	2.29357	5.27E-14
ADRA2A	1.372821	1.973595	3.10E-09
MSRB3	1.371029	1.765153	0
TMEM40	1.370294	2.163614	9.16E-14
FAM151B	1.367873	1.041135	3.15E-14
SLC8A3	1.366848	2.251308	5.79E-11
CACNA1A	1.366829	1.090083	5.98E-12
CLEC4M	1.366117	2.492247	1.59E-05
PLK4	1.36343	1.450649	0
CLGN	1.361041	1.174377	1.25E-05
ACVRL1	1.357862	1.375726	3.68E-11
SCTR	1.35778	2.486043	0.000343
CHRD	1.357153	2.337967	1.13E-05
FRMD1	1.355607	1.945317	1.49E-05
TRPM3	1.35247	2.147284	6.62E-06
FCRL5	1.350129	1.119955	4.62E-09
MTFR2	1.347711	1.848133	0
DYNC1I1	1.345358	1.810452	6.52E-08
NFASC	1.342385	1.37489	2.01E-06
VEPH1	1.341612	1.825814	6.19E-10
RSPH1	1.340372	1.741201	1.20E-06
RHCE	1.339358	2.221731	1.68E-13
CPNE5	1.337742	1.132725	1.43E-14
EPDR1	1.337434	1.254913	4.58E-11
HNF1B	1.333562	1.930391	0.000269
RSPH14	1.332372	1.114166	0.00012
ANKRD33B	1.330329	1.074505	3.42E-14
SRGAP1	1.330038	1.487475	1.39E-08
PKHD1	1.329191	2.535603	9.99E-08
NR5A2	1.32688	1.779704	3.17E-06
GPT2	1.326779	1.10125	1.39E-12
BOC	1.325478	1.367147	0.000966
SPHK1	1.320613	1.286395	1.17E-12
FRMD3	1.320395	1.268713	3.14E-11
ARHGEF17	1.320082	1.036828	1.75E-05
MED12L	1.318019	1.259256	1.57E-10
PHLDA3	1.314612	1.438642	2.15E-12
TRIM7	1.314359	1.561466	0
RHD	1.308814	1.798701	1.21E-05
CABLES1	1.307965	1.635995	1.08E-15

MYBPC1	1.304267	2.332259	4.55E-07
LANCL3	1.301564	1.732482	7.75E-13
LEP	1.299412	2.104243	1.98E-06
FGF13	1.29724	1.40909	2.12E-09
PGLYRP4	1.295894	2.726422	0.000206
LYVE1	1.293948	1.82929	2.75E-07
VIL1	1.293812	1.63677	2.16E-08
MT2A	1.293415	1.401389	8.26E-13
PSAT1	1.290839	1.522177	0
LRRC55	1.287979	2.693636	1.03E-05
EXOC3L4	1.286074	1.532549	7.83E-05
TRIML2	1.283335	2.783081	8.38E-10
FMN1	1.282722	1.446701	9.95E-08
CX3CL1	1.280389	2.042656	0.000209
SCD	1.276236	1.151145	5.09E-11
FCRL4	1.27436	3.134229	7.58E-08
IGKV1D-43	1.272453	3.464147	2.82E-07
GRIK5	1.271555	1.840947	4.06E-07
LGALS3BP	1.271188	1.077583	1.12E-05
PANX2	1.270273	1.013517	7.33E-07
GMNN	1.270115	1.170444	0
FEN1	1.268243	1.184594	0
FOLR3	1.268058	1.556075	0.000184
VSIG10L	1.267999	1.105142	3.37E-10
CTTN	1.263269	1.881336	7.50E-13
MAB21L3	1.260884	1.631914	1.68E-08
SHROOM3	1.260662	1.663015	2.63E-05
H4C14	1.256979	2.049563	1.40E-08
PDIA4	1.255979	1.04346	0
TGM2	1.254658	1.214992	6.71E-08
DOCK1	1.25167	1.361243	5.29E-12
FAM20C	1.249751	1.109039	1.24E-08
PDE6H	1.248737	1.265771	1.39E-06
SHOX	1.247791	3.242818	3.98E-09
TMCC2	1.247085	2.092982	2.60E-11
FKBP9P1	1.24369	3.123311	6.08E-09
LSMEM1	1.243653	1.223357	7.09E-07
TMEM108	1.241765	1.270473	2.46E-06
TM4SF20	1.239724	1.777453	0.000198
NWD1	1.237638	1.58132	3.44E-07
CTSA	1.236414	1.177645	0
MOXD1	1.233143	1.769241	1.34E-15
PARPBP	1.232351	1.305065	0
CHAC2	1.230896	1.441258	1.08E-15
AQP9	1.223258	1.135708	9.04E-10
AMER3	1.222893	3.188636	3.05E-07
EHD2	1.221676	2.119932	4.63E-12
SEC11C	1.221246	1.390895	0
GRTP1	1.220415	1.302606	1.65E-06
LGALSL	1.219918	1.181169	5.36E-10
MANF	1.219751	1.181963	0
CCDC150	1.216641	1.52995	0
CYP4F2	1.21522	3.097113	2.36E-07
FADS6	1.214464	2.559918	2.11E-05
RAB3IL1	1.213521	2.968414	1.34E-10
TRIM58	1.212339	2.919441	0
TOM1L1	1.209975	2.062821	2.69E-08
OSBPL6	1.209102	1.079111	3.10E-07
HLX	1.20645	1.52245	3.95E-12
INKA1	1.205597	1.168565	8.25E-07

DHFR	1.205074	1.755466	0
DIPK1B	1.204925	1.440902	7.89E-07
CTNNAL1	1.204884	2.17994	0
PALMD	1.203645	3.588169	7.84E-08
CDH5	1.202944	1.517017	7.65E-06
MYLK	1.201539	2.140531	7.91E-14
ECM1	1.200116	2.071995	2.10E-12
FANCI	1.199728	1.088784	0
IGHV3-65	1.199709	2.854593	2.51E-08
CPXM2	1.198444	3.408647	3.28E-08
TUBA8	1.198243	1.288673	5.72E-07
ASGR2	1.197946	1.126571	6.83E-09
MMP25	1.194519	1.002003	2.98E-06
NRGN	1.186499	1.885336	1.16E-12
PTGR1	1.185086	2.754499	0
FFAR2	1.183274	1.373371	1.03E-10
CALD1	1.183049	2.192443	3.84E-13
IGKV2-18	1.177929	1.594633	0.00073
TLN2	1.177032	1.055058	0.000128
PTGS1	1.175622	1.467359	1.75E-10
ELOVL7	1.173605	2.245456	9.64E-15
NDUFA4L2	1.172945	1.277857	0.000105
MACC1	1.171273	1.308164	9.27E-12
GUCY1B1	1.167462	1.280647	6.08E-09
EBI3	1.167127	1.302334	5.74E-09
MGST1	1.163039	1.160574	4.53E-12
CDKN2C	1.16215	1.198528	0
ADGRF2	1.160972	2.702017	0.000745
SEC14L5	1.154546	2.067446	2.71E-08
C15orf65	1.154013	1.05394	2.17E-06
TCEAL9	1.14943	1.25124	1.23E-09
CENPN	1.148205	1.082056	0
PRR27	1.144965	2.802474	2.30E-05
GCOM1	1.144133	1.496066	8.42E-05
PLCH1	1.143294	1.394704	0.000111
NME1	1.140611	1.200468	0
H3C10	1.140551	2.361636	9.73E-14
CTDSPL	1.136854	1.50413	2.99E-09
PTPRVP	1.134439	1.289988	3.34E-07
H2AJ	1.133379	1.112648	0
FABP5	1.131671	1.292734	0
FBXO43	1.131111	2.683039	0
H2AC11	1.130335	1.675173	0
CDH6	1.129508	1.902956	3.64E-07
NDC80	1.129462	1.606833	0
UNC13C	1.128517	2.080793	2.45E-05
ASB18	1.12698	3.165754	3.95E-08
ABCC3	1.126808	1.021497	1.08E-06
C8orf86	1.125628	3.342797	3.50E-09
DMBT1L1	1.123105	2.358006	3.88E-05
C1orf167	1.122754	1.821355	6.44E-08
MYL6B	1.121674	1.420935	0
SLCO5A1	1.121435	1.45191	2.72E-11
CD63	1.121175	1.301449	0
LURAP1L	1.120724	1.847353	1.24E-05
CPNE4	1.119409	1.798159	3.90E-05
KIF3C	1.118936	1.097453	3.55E-09
DPF1	1.11658	1.408489	1.56E-08
OSMR	1.114136	1.049404	1.85E-05
MLXIPL	1.113635	2.350299	7.78E-07

RADIL	1.112946	2.880614	1.31E-10
NPAS3	1.111787	2.381242	0.000326
MFSD2B	1.110621	2.666413	1.02E-13
CYB5R2	1.10858	1.129459	7.72E-07
SLC6A17	1.107648	2.396015	2.94E-06
LPAR4	1.103204	2.522471	0.000721
XRCC2	1.10269	1.340289	5.18E-15
MAPK10	1.101761	1.649639	9.60E-09
OXTR	1.101362	2.097583	3.34E-10
STRIP2	1.099155	1.837893	2.77E-16
SRCIN1	1.098987	2.580559	2.34E-06
KDEL3	1.098084	1.166626	6.12E-06
TTC7B	1.097345	1.927016	1.59E-15
FGD5	1.095465	1.997376	5.27E-08
COL6A3	1.092511	1.168619	2.16E-05
ANG	1.091387	1.424609	3.33E-10
CDR2L	1.090826	2.182764	3.24E-07
BHLHE41	1.089164	1.343715	5.14E-10
ITIH3	1.087523	1.68168	1.57E-06
LILRB4	1.087158	1.07022	1.94E-13
CHMP4C	1.084346	1.731139	5.62E-05
CNN1	1.082328	2.907993	3.54E-07
PTGIS	1.08225	2.463067	2.92E-07
BMP6	1.081635	1.869003	3.14E-15
CAVIN1	1.075958	1.871287	4.93E-11
FAT3	1.073029	1.962263	1.34E-05
KCNA2	1.07214	1.254971	1.77E-11
TMEM145	1.07177	2.552564	6.19E-07
AKR1B10	1.068702	3.001784	0.000117
PARM1	1.067778	1.060577	7.13E-09
C3orf70	1.06659	1.914257	2.65E-07
NOSTRIN	1.062224	1.990512	2.18E-06
ZNF969P	1.0609	3.325657	7.47E-09
KANK2	1.060554	1.123467	2.12E-05
SLC27A2	1.058665	1.556265	1.77E-09
TMEM255B	1.057472	1.639121	2.14E-13
MT1E	1.055615	2.045911	0
H2AC6	1.054106	1.973386	0
ARHGAP28	1.054026	3.071127	1.11E-09
CCDC71L	1.051336	1.036472	2.77E-16
TOX2	1.047102	1.278459	9.54E-12
FHL2	1.045706	2.013639	2.74E-11
CNTNAP5	1.044811	3.197783	1.28E-05
SMIM5	1.044107	2.242208	3.52E-12
PIEZO2	1.041937	2.813869	1.20E-09
AOX2P	1.041762	2.241231	8.03E-06
FKBP11	1.039472	1.043462	0
ATP2A1	1.03862	1.234787	1.37E-08
PRDX4	1.035057	1.141121	0
EFCC1	1.033523	1.105467	3.23E-05
FAM135B	1.032751	2.965159	2.57E-08
SLC22A16	1.032608	1.455174	4.68E-06
CLEC18B	1.02956	1.505004	7.48E-05
UPK1A	1.026919	1.904466	5.48E-05
LGALS1	1.026429	1.269058	8.20E-16
DCLK1	1.024358	3.054371	1.69E-05
RYR2	1.021698	1.841587	4.01E-07
IZUMO1	1.020196	1.881869	0.000422
FAXDC2	1.020055	2.05506	4.22E-11
MIPOL1	1.019711	1.49981	1.67E-09

PLCB4	1.018734	1.277769	8.05E-05
TRPM6	1.017353	2.603692	8.46E-10
NT5M	1.014982	2.120625	8.86E-13
DAB2	1.014799	1.000196	3.12E-09
ADCY6	1.013786	1.22419	5.85E-05
STON2	1.013581	1.740857	1.35E-09
VSX1	1.00979	3.000385	3.67E-06
C1QA	1.007556	1.711292	1.28E-09
GALR1	1.005996	2.69812	5.91E-09
SPAG6	1.001726	1.46243	1.18E-05
PF4	1.001687	2.091025	2.26E-12
HSPA4L	1.000889	1.562096	6.02E-07

Upregulated DE miRNAs in regularly exercising individuals

miRNA	log ² FC	Wald test p value
hsa-miR-486-5p	2.281786	0.009494
hsa-miR-215-5p	2.861558	0.022054
hsa-miR-941	2.554967	0.042998

Table S2. GO Biological Process of the mRNAs regulated by hsa-miR-486-5 p and hsa-miR-941.

GO Biological Process of the mRNAs regulated by hsa-miR-486-5p				
ID	Description	p.adjust	geneID	Count
GO:0002576	platelet degranulation	0.04053	CD63/SPARC/CLU/ITGB3/PROS1/IGF1	6
GO:0002523	leukocyte migration involved in inflammatory response	0.04053	TRIM55/CX3CL1/FFAR2	3
GO:0098884	postsynaptic neurotransmitter receptor internalization	0.04053	DNM1/GSG1L/ITGB3	3
GO:0140239	postsynaptic endocytosis	0.04053	DNM1/GSG1L/ITGB3	3
GO Biological Process of the mRNAs regulated by hsa-miR-941				
ID	Description	p.adjust	geneID	Count
GO:0072401	signal transduction involved in DNA integrity checkpoint	0.017789283	CCNB1/AURKA/E2F1/BRCA1/CDK1	5
GO:0072422	signal transduction involved in DNA damage checkpoint	0.017789283	CCNB1/AURKA/E2F1/BRCA1/CDK1	5
GO:0072395	signal transduction involved in cell cycle checkpoint	0.017789283	CCNB1/AURKA/E2F1/BRCA1/CDK1	5
GO:0007098	centrosome cycle	0.017789283	STIL/AURKA/BRCA1/CDK1/SGO1/NEK2	6
GO:0071158	positive regulation of cell cycle arrest	0.017799894	CCNB1/AURKA/E2F1/BRCA1/CDK1	5
GO:0031023	microtubule organizing center organization	0.018334756	STIL/AURKA/BRCA1/CDK1/SGO1/NEK2	6
GO:0000077	DNA damage checkpoint	0.018334756	CCNB1/AURKA/CLSPN/E2F1/BRCA1/CDK1	6
GO:0031570	DNA integrity checkpoint	0.018334756	CCNB1/AURKA/CLSPN/E2F1/BRCA1/CDK1	6
GO:0007093	mitotic cell cycle checkpoint	0.018334756	CCNB1/AURKA/CLSPN/E2F1/BRCA1/CDK1	6
GO:0006939	smooth muscle contraction	0.018334756	CNN1/MYLK/CD38/CHRN2/EDNRB	5
GO:0044773	mitotic DNA damage checkpoint	0.018334756	CCNB1/AURKA/CLSPN/E2F1/CDK1	5
GO:0006977	DNA damage response signal transduction by p53 class mediator resulting in cell cycle arrest	0.018334756	CCNB1/AURKA/E2F1/CDK1	4
GO:0030330	DNA damage response signal transduction by p53 class mediator	0.018334756	CCNB1/AURKA/E2F1/BRCA1/CDK1	5
GO:0044774	mitotic DNA integrity checkpoint	0.018334756	CCNB1/AURKA/CLSPN/E2F1/CDK1	5
GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	0.018334756	CCNB1/AURKA/E2F1/CDK1	4
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	0.018334756	CCNB1/AURKA/E2F1/CDK1	4
GO:0071156	regulation of cell cycle arrest	0.018334756	CCNB1/AURKA/E2F1/BRCA1/CDK1	5
GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	0.018334756	CCNB1/AURKA/E2F1/CDK1	4
GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	0.018334756	CCNB1/AURKA/E2F1/CDK1	4
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	0.019530657	CCNB1/AURKA/E2F1/CDK1	4
GO:0031571	mitotic G1 DNA damage checkpoint	0.019530657	CCNB1/AURKA/E2F1/CDK1	4
GO:0044783	G1 DNA damage checkpoint	0.019530657	CCNB1/AURKA/E2F1/CDK1	4
GO:0044819	mitotic G1/S transition checkpoint	0.019530657	CCNB1/AURKA/E2F1/CDK1	4
GO:0007052	mitotic spindle organization	0.02071892	STIL/CCNB1/AURKA/SPC25/NEK2	5

GO:0000082	G1/S transition of mitotic cell cycle	0.028043583	DHFR/CCNB1/AURKA/E2F1/ORC6/CDKN3/CDK1	7
GO:0042770	signal transduction in response to DNA damage	0.030955025	CCNB1/AURKA/E2F1/BRCA1/CDK1	5
GO:0010389	regulation of G2/M transition of mitotic cell cycle	0.031339932	CCNB1/AURKA/CLSPN/BRCA1/CDK1/NEK2	6
GO:0000075	cell cycle checkpoint	0.035239112	CCNB1/AURKA/CLSPN/E2F1/BRCA1/CDK1	6
GO:0044843	cell cycle G1/S phase transition	0.038336716	DHFR/CCNB1/AURKA/E2F1/ORC6/CDKN3/CDK1	7
GO:0008608	attachment of spindle microtubules to kinetochore	0.038336716	CCNB1/SGO1/NEK2	3
GO:1902850	microtubule cytoskeleton organization involved in mitosis	0.038336716	STIL/CCNB1/AURKA/SPC25/NEK2	5
GO:1902749	regulation of cell cycle G2/M phase transition	0.038336716	CCNB1/AURKA/CLSPN/BRCA1/CDK1/NEK2	6
GO:0031572	G2 DNA damage checkpoint	0.038336716	CLSPN/BRCA1/CDK1	3
GO:0044818	mitotic G2/M transition checkpoint	0.040349945	CLSPN/BRCA1/CDK1	3
GO:0016572	histone phosphorylation	0.045779688	CCNB1/AURKA/CDK1	3
GO:0007050	cell cycle arrest	0.048167895	CCNB1/AURKA/E2F1/BRCA1/CDKN3/CDK1	6
GO:0014820	tonic smooth muscle contraction	0.048167895	MYLK/CD38	2
GO:0099149	regulation of postsynaptic neurotransmitter receptor internalization	0.048167895	GSG1L/ITGB3	2

Table S3: Upregulated genes and miRNAs from various datasets in the study.