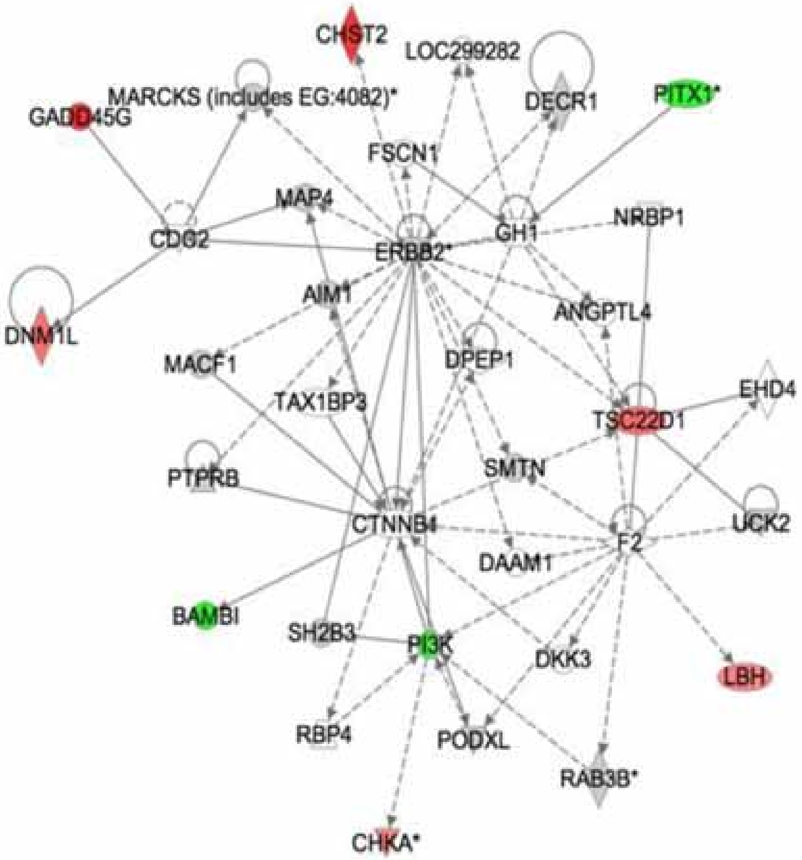
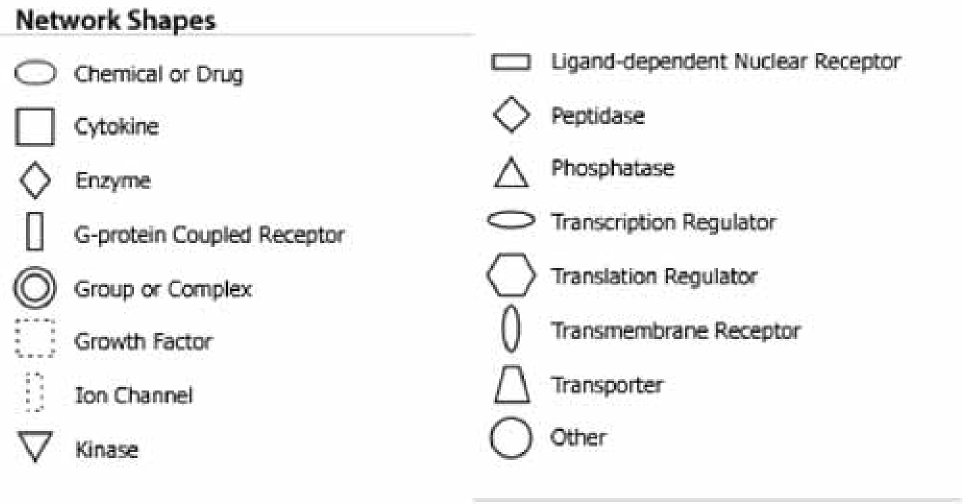
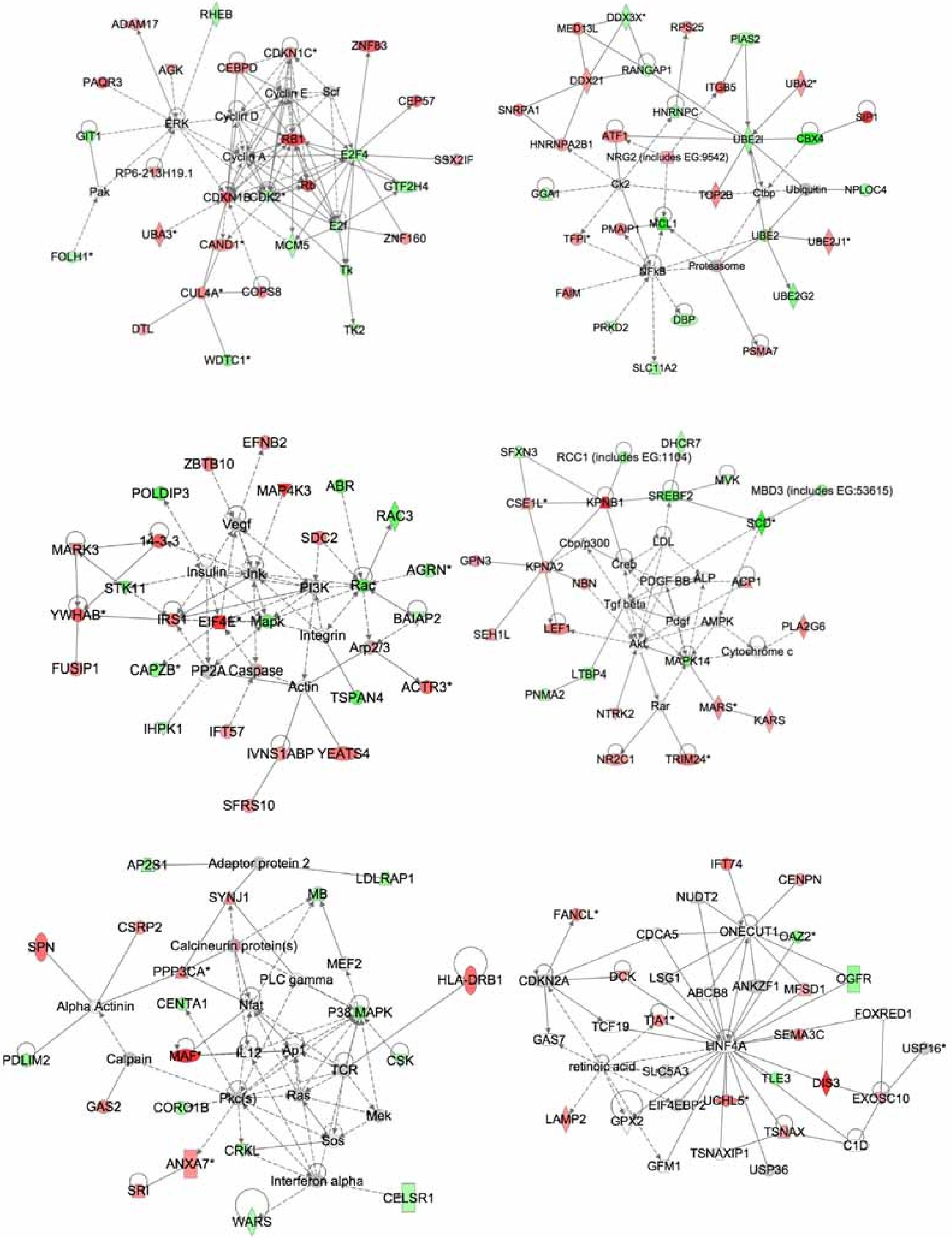


Supplementary Figure 1 Significant biological networks associated with the androgen-responsive genes in R1 cells treated with DHT for 2h. Genes are represented as nodes, and the biological relationship between two nodes is represented as a line (solid line: direct interaction; dashed line: indirect interaction). Genes in green are user input molecules that are downregulated and whose absolute expression values are above the user defined cutoff. Genes in red are user input molecules that are upregulated and whose absolute expression values are above the user defined cutoff. The intensity of the node colour indicates the degree of up- or down-regulation. Genes in gray are user input molecules that are neither up- nor down-regulated, or are below the user defined cutoff. Genes without colour are molecules that are not user specified, but incorporated into the network through relationships with other molecules. Relevant canonical pathways (CP) are overlaid on top of the network.





Supplementary Figure 2 The most significant biological networks associated with androgen-responsive genes in Rv1 cells treated with DHT for 2h.

Supplementary Table 1

Gene Expression differences-R1 vs Rv1 2h 10 nM DHT

higher in R1			higher in Rv1		
Gene	fold cha	P value	**Gene**	fold cha	P value
IGFBP5	58.54	0.03	**TARP /// TR**	99.17	0.05
SNAI2	40.52	0.05	**TARP /// TR**	62.78	0.04
CX3CL1	30.87	0.04	**GPM6A**	59.68	0.05
SHOX2	24.83	0.03	**TARP /// TR**	59.16	0.01
ASS1	24.3	0.03	**STEAP1**	57.92	0.05
NEFL	24.1	0.04	**NEFH**	57.77	0.04
CX3CL1	23.71	0.04	**TARP /// TR**	52.82	0.01
JAG1	17.3	0.01	**GPM6A**	40.33	0.03
THRA	16.58	0.03	**EPHA3**	38.8	0.04
JAG1	15.66	0.00	**NMNAT2**	32.7	0.05
MAPKAPK2	15.54	0.02	**HPGD**	32.22	0.04
ANXA1	14.27	0.01	**HPGD**	30.37	0.03
BCL2	13.94	0.00	**ALB**	29.55	0.02
GALR2	12.5	0.04	**KRT19**	28.66	0.04
MSX2	12.07	0.00	**TOX3**	24.97	0.04
TLE1	12.04	0.02	**TFPI**	24.28	0.03
RHOBTB3	12.03	0.02	**LXN**	22.37	0.05
JAG1	11.95	0.03	**AKR1C3**	21.75	0.01
MET	11.67	0.03	**TNC**	20.32	0.03
LY6E	11.12	0.05	**IGFBP3**	19.78	0.00
MAPKAPK2	11.11	0.00	**NXF2**	19.21	0.03
GALNT12	10.53	0.04	**HPGD**	19.19	0.02
FHL1	10.42	0.04	**SCG3**	19.08	0.01
FER1L3	10.18	0.03	**CA12**	18.85	0.02
MAPKAPK2	9.56	0.02	**NXF2B**	18.75	0.04
TNFRSF12A	9.49	0.00	**HPGD**	17.61	0.05
RMND5A	9.36	0.00	**TACSTD1**	16.34	0.03
SHOX2	9.29	0.02	**BEX1**	16.25	0.03
NDRG1	9.09	0.03	**KBTBD11**	16.07	0.01
IGF2 /// INS	8.89	0.01	**DECR1**	15.65	0.04
HLA-B	8.69	0.04	**CECR1**	15.54	0.02
ANXA2	8.51	0.01	**KLK2**	14.54	0.03
TRIM29	8.5	0.02	**ARMCX6**	14.26	0.02
CBX4	8.39	0.05	**GALNT3**	14.23	0.02

Gene Expression differences R1 vs Rv1 No DHT

higher in R1			higher in Rv1		
Gene	fold cha	P value	**Gene**	fold ch	P value
IGFBP5	66.27	0.05	**TARP /// TR**	89.8	0.05
SNAI2	42.47	0.03	**STEAP1**	53.0	0.02
MSX2	34.64	0.01	**TARP /// TR**	48.3	0.03
SERPINB5	28.21	0.01	**NMNAT2**	44.2	0.03
SHOX2	27.29	0.01	**TARP /// TR**	42.2	0.01
ASS1	23.22	0.02	**TARP /// TR**	40.5	0.01
NEFL	19.96	0.05	**GJA1**	40.0	0.05
CX3CL1	19.81	0.00	**HPGD**	34.6	0.03
CX3CL1	18.73	0.00	**KRT19**	28.2	0.05
ANXA1	17.21	0.04	**HPGD**	22.9	0.03
BCL2	15.62	0.04	**NXF2**	21.9	0.01
MSX2	14.91	0.00	**LXN**	19.5	0.05
JAG1	14.21	0.02	**HPGD**	17.3	0.02
FHL1	11.2	0.02	**CA12**	16.1	0.01
NEFL	11.08	0.03	**TACSTD1**	15.9	0.03
LY6E	10.78	0.00	**BEX1**	15.1	0.03
FHL1	10.08	0.03	**ENO2**	14.8	0.02
JAG1	9.59	0.01	**KBTBD11**	14.8	0.02
ARL4C	9.01	0.04	**HBA1 /// HB**	14.7	0.03
FER1L3	8.75	0.02	**IGFBP3**	14.4	0.01
CADM1	8.7	0.05	**HBA1**	14.0	0.01
ALDH2	7.68	0.00	**TFPI**	14.0	0.05
SDC4	7.58	0.05	**HBA1 /// HB**	13.9	0.02
TRIM29	7.28	0.00	**CECR1**	13.7	0.01
NPTX2	7.06	0.02	**HBA1 /// HB**	13.4	0.02
TLE1	6.96	0.00	**XAGE1 /// X**	13.3	0.00
P4HA2	6.93	0.03	**KLK2**	13.0	0.02
IGF2 /// INS-	6.88	0.01	**B3GALNT1**	12.5	0.00
MET	6.84	0.00	**NLGN1**	12.1	0.04
AKR1B10	6.79	0.00	**CCR10**	11.8	0.03
TNFRSF12A	6.52	0.01	**CLDN3**	11.2	0.02
HLA-A	6.47	0.00	**RAMP1**	10.9	0.02
TIMP3	6.36	0.01	**IGFBP3**	10.6	0.03
ANXA2	6.34	0.00	**ARMCX6**	10.2	0.03

FHL1	8.38	0.00	**HBA1 /// HB**	14.22	0.05	**GALNT12**	6.23	0.05	**TFPI**	9.7	0.02
ECE1	8.36	0.01	**MME**	13.74	0.04	**IFITM1**	6.17	0.01	**AKR1C2**	9.3	0.00
RNF103	8.33	0.01	**HRASLS3**	13.44	0.01	**ASPH**	6.11	0.00	**TOX3**	8.4	0.02
PTBP1	8.3	0.01	**AZGP1**	13.43	0.05	**NDRG1**	6.09	0.02	**UGT2B15 //**	8.3	0.04
SGK1	8.21	0.00	**XAGE1 /// X**	13.35	0.04	**ECE1**	6.04	0.02	**RGS2**	8.3	0.03
RMND5A	8.07	0.04	**CA12**	12.49	0.00	**CRLF1**	5.95	0.02	**HRASLS3**	8.2	0.03
CRLF1	7.95	0.02	**ENO2**	11.95	0.02	**MET**	5.95	0.01	**VPS13A**	8.0	0.03
COL6A2	7.93	0.00	**ARMCX3**	11.72	0.03	**RNF103**	5.95	0.03	**NEFH**	8.0	0.02
SDC4	7.75	0.03	**GAS2**	11.61	0.00	**MAPKAPK2**	5.93	0.01	**AKR1C1**	8.0	0.01
NEFL	7.63	0.04	**CLGN**	11.37	0.02	**TIMP3**	5.83	0.02	**NNT**	7.7	0.05
B4GALT1	7.58	0.02	**B3GALNT1**	11.37	0.00	**COL6A2**	5.77	0.00	**PON1**	7.5	0.03
HLA-F	7.55	0.05	**NMB**	11.33	0.03	**SHOX2**	5.75	0.02	**TMPRSS2**	7.4	0.00
MCL1	7.5	0.01	**SLC27A2**	11.23	0.01	**GADD45A**	5.59	0.01	**SCCPDH**	7.3	0.01
CLPTM1	7.3	0.03	**PRR16**	11.19	0.02	**ANXA2**	5.53	0.00	**tcag7.1314**	7.3	0.01
SDC1	7.26	0.03	**PON1**	11.02	0.01	**GPNMB**	5.39	0.02	**tcag7.1314**	7.1	0.03
SOX11	7.2	0.05	**NEFH**	10.19	0.03	**HLA-A**	5.37	0.01	**PRR16**	7.0	0.01
NKX3-2	7.07	0.03	**TFPI**	10.18	0.00	**HIF1A**	5.24	0.03	**AZGP1**	6.9	0.05
ARL4C	7.02	0.00	**SPINK1**	9.82	0.02	**BMP7**	5.16	0.00	**LPL**	6.9	0.01
HLA-F	7.02	0.04	**MYBPC1**	9.8	0.01	**FXYD6**	5.12	0.01	**TXNIP**	6.9	0.00
ALDH2	7.01	0.01	**HBA1 /// HB**	9.76	0.03	**CRYAB**	5.11	0.02	**CA12**	6.7	0.01
MET	6.78	0.00	**VPS13A**	9.37	0.00	**MAPKAPK2**	5.11	0.05	**DDAH1**	6.7	0.02
HLA-A	6.75	0.01	**TFPI**	9.03	0.04	**PITX1**	5.11	0.01	**RAB17**	6.7	0.01
S100P	6.74	0.00	**GALNT7**	8.95	0.04	**IDH2**	5.08	0.02	**CA12**	6.6	0.02
RMND5A	6.71	0.02	**STK39**	8.82	0.03	**GHR**	5.07	0.02	**STK39**	6.5	0.04
SCGB2A1	6.51	0.01	**ZNF217**	8.78	0.03	**KRT15**	4.93	0.01	**GABRA1**	6.3	0.04
HLA-A	6.36	0.01	**CHGB**	8.69	0.02	**S100P**	4.91	0.00	**HLA-DQB1**	6.3	0.01
NPTX2	6.35	0.04	**TMEPAI**	8.67	0.00	**MPZL2**	4.81	0.00	**DPYSL3**	6.2	0.01
TIMP3	6.33	0.05	**CA12**	8.65	0.02	**FER1L3**	4.79	0.02	**CA12**	6.1	0.04
HLA-B	6.19	0.04	**CCR10**	8.63	0.02	**S100A4**	4.72	0.00	**POU4F2**	6.1	0.01
FER1L3	6.16	0.01	**CGA**	8.55	0.01	**BAMBI**	4.68	0.02	**KLK2**	6.0	0.02
GADD45A	6.1	0.01	**ST6GALNA**	8.46	0.01	**SDC1**	4.63	0.01	**EHF**	6.0	0.04
ANXA2	6.1	0.00	**HIST2H2BE**	8.26	0.02	**NOTCH2**	4.62	0.01	**TRIM36**	6.0	0.04
HLA-B	6.07	0.01	**SMPDL3A**	8.12	0.05	**SOX11**	4.61	0.05	**GMPR**	5.9	0.01
FXYD3	6.04	0.01	**TSPYL4**	8.11	0.01	**CERK**	4.6	0.00	**TXNIP**	5.9	0.00
TMC6	5.99	0.02	**NNT**	8.08	0.03	**HLA-B**	4.54	0.03	**MME**	5.9	0.01
FXYD6	5.96	0.02	**TAOK3**	7.91	0.00	**VIPR1**	4.54	0.00	**VGF**	5.8	0.02
F2R	5.94	0.03	**MME**	7.9	0.02	**DLX5**	4.52	0.02	**CHGB**	5.7	0.02

ASCL2	5.91	0.01	**TXNIP**	7.81	0.04	**DEPDC6**	4.51	0.00	**HLA-DQB1**	5.7	0.02
S100A4	5.9	0.01	**RAMP1**	7.75	0.01	**HLA-B**	4.51	0.00	**CD302**	5.6	0.05
IDH2	5.89	0.00	**GATA2**	7.56	0.01	**EPB41L3**	4.43	0.04	**SLC27A2**	5.4	0.02
MET	5.85	0.02	**RLN2**	7.28	0.02	**BHLHB2**	4.42	0.02	**AKR1C1**	5.4	0.02
ARHGDIA	5.82	0.02	**GABRA1**	6.91	0.03	**JUNB**	4.4	0.03	**CLDN3**	5.3	0.01
PCDHGA10	5.81	0.00	**COLEC12**	6.85	0.00	**DKK1**	4.39	0.03	**CA8**	5.3	0.04
IFITM1	5.66	0.01	**BCOR**	6.82	0.01	**SDC1**	4.39	0.03	**TSPYL4**	5.2	0.03
HLA-G	5.62	0.01	**FAM129A**	6.74	0.03	**HTR2C**	4.31	0.04	**CELSR3**	5.1	0.01
NOTCH2	5.55	0.01	**SCCPDH**	6.73	0.01	**SAT1**	4.27	0.01	**CA12**	5.1	0.01
AKR1B10	5.54	0.04	**SLC27A2**	6.64	0.02	**ANXA2**	4.26	0.02	**SLC43A3**	5.1	0.01
P4HA2	5.51	0.01	**ENPP4**	6.59	0.02	**RMND5A**	4.18	0.05	**KLK3**	5.0	0.02
FLNA	5.48	0.04	**DDAH1**	6.42	0.05	**ACSL1**	4.16	0.01	**TMEPAI**	5.0	0.02
TSPAN4	5.37	0.02	**CA12**	6.41	0.01	**HLA-F**	4.16	0.05	**RHOF**	4.9	0.03
PRPS1	5.36	0.05	**UGT2B15**	6.32	0.05	**TBPL1**	4.14	0.02	**STAT6**	4.9	0.01
CRYAB	5.36	0.01	**GUCY1B3**	6.24	0.03	**FHL1**	4.12	0.02	**SMPDL3A**	4.8	0.03
ATP2B4	5.28	0.02	**SERPINB1**	6.19	0.01	**MPZL2**	4.11	0.05	**SERPINB1**	4.8	0.01
ASPH	5.21	0.02	**DNAJC6**	6.15	0.05	**IFITM1**	4.11	0.01	**IQSEC2**	4.8	0.03
BARX1	5.16	0.02	**PTPRB**	6.09	0.01	**F2R**	4.05	0.02	**VIM**	4.8	0.02
ADAM15	5.14	0.02	**DSC2**	5.94	0.02	**CAPN2**	3.99	0.04	**HOXB13**	4.8	0.01
PDE3A	5.13	0.02	**SCCPDH**	5.92	0.02	**NID1**	3.96	0.01	**DSC2**	4.8	0.04
NID1	5.11	0.05	**CD44**	5.9	0.05	**KLF5**	3.95	0.04	**KLK1**	4.7	0.01
PCDHGA1	5.11	0.01	**PRUNE2**	5.82	0.00	**NID1**	3.91	0.02	**SERPINB6**	4.6	0.04
MAGED4	5.06	0.01	**KLK2**	5.7	0.02	**FXYD3**	3.88	0.02	**HLA-DQB1**	4.6	0.01
SOCS2	4.98	0.02	**HLA-DQB1**	5.64	0.04	**GAS6**	3.88	0.01	**GAS2**	4.6	0.05
TSC22D3	4.97	0.00	**RHOF**	5.64	0.01	**GSN**	3.85	0.01	**INHBB**	4.5	0.02
FLNA	4.96	0.02	**CELSR3**	5.53	0.01	**BTN3A2**	3.8	0.01	**CGA**	4.4	0.03
BMP7	4.96	0.00	**FLJ10038**	5.53	0.02	**SLPI**	3.79	0.03	**MYBPC1**	4.4	0.02
ETS2	4.95	0.01	**RND3**	5.49	0.01	**HLA-B**	3.78	0.00	**PLA2G3**	4.4	0.03
TIMP3	4.92	0.03	**TMEM45A**	5.49	0.05	**BCL3**	3.74	0.02	**C10orf116**	4.3	0.04
AGRN	4.9	0.01	**RGS2**	5.48	0.02	**KLF4**	3.73	0.01	**VIL1**	4.3	0.01
PCDHGA1	4.89	0.01	**HLA-DQB1**	5.44	0.01	**D4S234E**	3.72	0.02	**GULP1**	4.2	0.01
MICA	4.84	0.01	**NOTCH3**	5.4	0.00	**SGK1**	3.66	0.04	**C11orf75**	4.2	0.04
STC2	4.81	0.01	**CLDN3**	5.39	0.01	**MET**	3.63	0.05	**PTPRB**	4.2	0.02
SYMPK	4.79	0.02	**GMPR**	5.39	0.01	**SYPL1**	3.63	0.02	**RLN2**	4.2	0.04
SPDEF	4.73	0.02	**PLA2G3**	5.38	0.01	**HLA-G**	3.57	0.05	**ENSA**	4.1	0.02
D4S234E	4.71	0.05	**GULP1**	5.37	0.05	**ZNF238**	3.57	0.04	**RIMS3**	4.1	0.02
NOTCH2	4.7	0.02	**SERPINB1**	5.21	0.03	**ACSL1**	3.55	0.03	**LPPR4**	4.1	0.01

D4S234E	4.7	0.05	**SDC2**	5.16	0.02	**ATP2B4**	3.53	0.01	**GULP1**	4.1	0.04
GABARAPL	4.68	0.01	**HMGB2**	5.13	0.02	**NAB2**	3.53	0.01	**FOLH1**	4.1	0.05
DAPK3	4.66	0.02	**HGF**	5.13	0.02	**RGS10**	3.48	0.03	**CD44**	4.1	0.04
SYPL1	4.64	0.00	**CA12**	5.12	0.01	**PAM**	3.47	0.02	**ACADL**	4.1	0.05
AMPH	4.62	0.02	**PGAM2**	5.1	0.02	**TMC6**	3.46	0.01	**HOXB6**	4.1	0.02
TMED9	4.62	0.05	**DPYSL3**	5.09	0.03	**ALDOC**	3.45	0.00	**FBXL15**	4.1	0.01
CERK	4.62	0.01	**PPP3CA**	5.07	0.01	**ARSJ**	3.44	0.03	**GLS2**	4.0	0.04
DBN1	4.59	0.01	**RAB17**	5.07	0.01	**C7orf23**	3.44	0.01	**AKTIP**	4.0	0.00
ARHGAP1	4.55	0.02	**SLC43A3**	5.05	0.02	**SLC16A3**	3.44	0.04	**FAM110B**	3.9	0.00
FLNA	4.49	0.01	**KLK3**	5.03	0.02	**SPDEF**	3.39	0.02	**XK**	3.9	0.01
DEPDC6	4.49	0.03	**RB1**	5.02	0.02	**AGR2**	3.38	0.02	**BAG2**	3.9	0.04
BMP1	4.47	0.03	**IRS1**	5	0.01	**D4S234E**	3.37	0.02	**FAM129A**	3.9	0.02
PCDHGA1	4.46	0.01	**RIMS3**	5	0.03	**SEMA3F**	3.37	0.00	**MVP**	3.9	0.01
TP53I11	4.42	0.03	**IQSEC2**	4.98	0.02	**TIMP2**	3.36	0.01	**RND3**	3.9	0.05
KIF1A	4.41	0.02	**GLS2**	4.95	0.01	**HBEGF**	3.35	0.01	**MCCC2**	3.9	0.03
CHST2	4.41	0.05	**CXCR7**	4.9	0.02	**SPDEF**	3.34	0.01	**COLEC12**	3.9	0.03
HIF1A	4.37	0.05	**C11orf75**	4.87	0.02	**SNCA**	3.34	0.02	**FOLH1**	3.9	0.03
B4GALT1	4.36	0.05	**APOLD1**	4.86	0.02	**TLE1**	3.3	0.01	**FLJ10038**	3.8	0.03
FHL1	4.32	0.00	**HNMT**	4.85	0.04	**PAM**	3.29	0.01	**ZNF592**	3.8	0.01
TBPL1	4.31	0.00	**E2F8**	4.85	0.01	**FLNA**	3.26	0.02	**SCNN1A**	3.8	0.01
EPB41	4.31	0.01	**ACADL**	4.72	0.01	**HLA-G**	3.26	0.02	**PPAP2A**	3.8	0.02
DBN1	4.29	0.03	**EIF5B**	4.72	0.05	**SPDEF**	3.26	0.01	**RFPL1S**	3.7	0.02
HOMER3	4.24	0.01	**FAIM**	4.69	0.01	**TIAM1**	3.25	0.04	**GNG4**	3.7	0.03
ABR	4.23	0.01	**IFT57**	4.68	0.03	**IGFBP5**	3.23	0.05	**SLC39A8**	3.7	0.03
ALDOC	4.2	0.01	**MYNN**	4.67	0.02	**IDH2**	3.23	0.01	**GATA2**	3.7	0.01
GAS6	4.2	0.01	**RAPGEF5**	4.65	0.01	**PXDN**	3.22	0.03	**ZNF217**	3.6	0.01
GSN	4.18	0.02	**CDH10**	4.6	0.01	**PAM**	3.21	0.01	**FLJ10038**	3.6	0.02
DDX11	4.18	0.02	**ZNF239**	4.57	0.01	**ARFGEF1**	3.2	0.04	**AMACR**	3.6	0.01
TIAM1	4.18	0.01	**PTCH1**	4.56	0.05	**KLF4**	3.2	0.04	**SLC44A4**	3.5	0.01
PXDN	4.17	0.01	**PPP3CA**	4.55	0.01	**PIK3R3**	3.2	0.00	**FOLH1**	3.5	0.02
SPDEF	4.15	0.03	**BTG1**	4.49	0.03	**PCDHGA1**	3.2	0.01	**AMACR**	3.5	0.02
JUP	4.12	0.00	**EIF4E**	4.42	0.02	**TSPAN6**	3.2	0.03	**ENSA**	3.5	0.03
MPZL2	4.12	0.01	**SMARCA1**	4.41	0.03	**SYPL1**	3.19	0.00	**MYNN**	3.4	0.02
JUND	4.1	0.01	**STAT6**	4.4	0.01	**AMPH**	3.17	0.02	**CD44**	3.4	0.02
POLDIP3	4.1	0.01	**ZBTB10**	4.39	0.01	**ETS2**	3.16	0.01	**ELL2**	3.4	0.02
SYPL1	4.09	0.01	**HBE1**	4.32	0.02	**PCDHGA1**	3.12	0.00	**GDAP1**	3.4	0.01
SLC6A6	4.07	0.05	**MAGEF1**	4.29	0.04	**D4S234E**	3.11	0.05	**C5orf30**	3.4	0.01

LBH	4.07	0.03	**AKR1C1**	4.28	0.02	**ENC1**	3.1	0.02	**GADD45G**	3.4	0.02
DAPK3	4.04	0.01	**CDK10**	4.27	0.03	**FXYD3**	3.1	0.04	**HBE1**	3.4	0.04
SCD	4.04	0.01	**HLA-DQB1**	4.27	0.03	**BMP7**	3.09	0.01	**LOC441453**	3.4	0.04
HLA-C	4.02	0.01	**DIS3**	4.26	0.04	**LMO1**	3.09	0.03	**SLC39A8**	3.4	0.01
KRT8	4.02	0.03	**EPS8**	4.24	0.02	**FLNA**	3.08	0.00	**FEV**	3.4	0.03
DFNA5	4	0.04	**TMEM47**	4.24	0.01	**MYO1B**	3.08	0.03	**SI**	3.4	0.05
EPN2	3.95	0.01	**C3orf14**	4.23	0.01	**GADD45B**	3.06	0.01	**THBS1**	3.4	0.05
GTF2I	3.95	0.00	**VIL1**	4.19	0.02	**TPD52L1**	3.05	0.01	**C3orf14**	3.3	0.02
FGFR2	3.94	0.01	**EIF4E**	4.17	0.03	**KRT6B**	3.02	0.03	**NASP**	3.3	0.02
TNFRSF10B	3.9	0.01	**UBE2E3**	4.15	0.05	**OPTN**	3.02	0.02	**MT1E**	3.3	0.01
NAB2	3.89	0.01	**ELL2**	4.08	0.04	**PCDHGA1**	3.02	0.01	**CD44**	3.3	0.03
PPFIBP2	3.89	0.03	**P2RX5**	4.02	0.01	**PXDN**	3.01	0.02	**PH-4**	3.3	0.01
TPP1	3.86	0.03	**DEGS1**	4.01	0.04	**SFRP1**	3.01	0.02	**CD44**	3.3	0.01
NOV	3.85	0.01	**VIM**	3.98	0.04	**QKI**	2.98	0.04	**GUCY1B3**	3.3	0.03
RHOBTB3	3.84	0.03	**NASP**	3.98	0.03	**SH3GL3**	2.96	0.02	**P2RX5**	3.3	0.03
RPS6KA1	3.83	0.03	**TRIM2**	3.97	0.02	**SLIT3**	2.95	0.03	**UGT8**	3.3	0.04
FGFR2	3.82	0.03	**MAF**	3.97	0.03	**MBNL2**	2.94	0.02	**C3orf63**	3.3	0.04
SNCA	3.81	0.02	**BCAP29**	3.96	0.02	**RBMS1**	2.94	0.01	**BTG1**	3.2	0.03
NUMA1	3.8	0.03	**SIP1**	3.94	0.03	**GABARAPL**	2.92	0.00	**C11orf71**	3.2	0.05
LAMP1	3.78	0.03	**SEMA3C**	3.93	0.01	**PLOD1**	2.92	0.03	**APOLD1**	3.2	0.04
ACSL1	3.78	0.01	**PDGFRL**	3.93	0.03	**TSC22D3**	2.91	0.01	**MAGEF1**	3.2	0.03
THG1L	3.78	0.01	**SERPINB6**	3.92	0.05	**PCDHGA1**	2.91	0.00	**WTAP**	3.2	0.04
MB	3.77	0.04	**ENSA**	3.92	0.02	**ARL4C**	2.9	0.03	**ASTN2**	3.2	0.02
ARFGEF1	3.77	0.03	**CDC14A**	3.89	0.04	**GSN**	2.89	0.01	**SAP30**	3.2	0.02
N-PAC	3.77	0.03	**FOLH1**	3.89	0.05	**TSPAN6**	2.89	0.01	**PPP3CA**	3.2	0.04
CAPN2	3.76	0.01	**SYNJ1**	3.87	0.03	**VCL**	2.89	0.01	**TMEM45A**	3.2	0.05
PXDN	3.76	0.03	**CPS1**	3.85	0.03	**DPY19L1**	2.87	0.01	**RAP1GAP**	3.2	0.00
SPDEF	3.76	0.02	**MAGOH**	3.84	0.04	**ARL4C**	2.85	0.02	**RNASE4**	3.2	0.05
PTGES	3.74	0.00	**SMARCA1**	3.84	0.02	**EPHX1**	2.84	0.04	**HLA-DQB1**	3.1	0.03
EPB41L3	3.74	0.03	**KPNB1**	3.83	0.01	**LMO4**	2.84	0.01	**MCCC2**	3.1	0.03
LMO1	3.73	0.01	**IFT74**	3.83	0.05	**DDR1**	2.83	0.02	**SMARCA1**	3.1	0.03
SFRP1	3.72	0.01	**AKAP9**	3.82	0.02	**THG1L**	2.83	0.05	**SNAP25**	3.1	0.01
BCL2L1	3.72	0.04	**FABP5 /// FA**	3.81	0.05	**GADD45B**	2.82	0.01	**DDC**	3.1	0.03
NR2F6	3.72	0.04	**ANK3**	3.8	0.01	**STK38L**	2.82	0.05	**KRT19P2**	3.1	0.05
RAB6A	3.71	0.02	**CDKN1B**	3.8	0.03	**VDR**	2.82	0.02	**ATF5**	3.1	0.01
AVPI1	3.66	0.05	**ANP32E**	3.8	0.01	**EFNB3**	2.81	0.01	**CDH10**	3.1	0.04
CASP2	3.65	0.02	**SNAP25**	3.79	0.02	**PDXK**	2.81	0.02	**GPD1L**	3.1	0.02

SEMA3F	3.64	0.02	**CYP1A1**	3.78	0.02
ABHD2	3.64	0.01	**DNMBP**	3.75	0.03
CHKA	3.61	0.05	**MAP1B**	3.73	0.05
ZYX	3.57	0.02	**GARNL1**	3.72	0.01
RAB11B	3.57	0.03	**SLC39A8**	3.7	0.04
OAZ2	3.56	0.01	**ACTR3**	3.7	0.01
FBXW11	3.55	0.03	**LRRC8B**	3.69	0.01
IDH2	3.55	0.03	**PEX7**	3.67	0.02
CSNK1G2	3.54	0.01	**SEC22A**	3.66	0.01
RHOBTB3	3.54	0.01	**CBR4**	3.62	0.03
SDC1	3.52	0.01	**C9orf82**	3.62	0.01
DDIT4	3.51	0.03	**UCHL5**	3.62	0.03
PRKCH	3.51	0.04	**RFPL1S**	3.59	0.04
TNFRSF10B	3.5	0.04	**JARID1D**	3.58	0.01
WDR1	3.5	0.01	**PDS5A**	3.58	0.05
SERPINE2	3.49	0.02	**PSIP1**	3.54	0.02
RHOB	3.46	0.02	**AKTIP**	3.52	0.01
BCL2L1	3.46	0.02	**CNIH4**	3.5	0.01
MAP2K3	3.46	0.02	**DDC**	3.49	0.04
MSN	3.45	0.03	**PBLD**	3.48	0.01
GHR	3.44	0.02	**RGS20**	3.47	0.01
MSX2	3.43	0.05	**PHTF2**	3.44	0.02
CADM1	3.43	0.05	**COL3A1**	3.44	0.05
STK38L	3.43	0.01	**ACOT1 /// A**	3.42	0.02
NCKAP1	3.43	0.02	**DUSP6**	3.42	0.02
SLPI	3.42	0.01	**YWHAB**	3.41	0.04
KLF5	3.41	0.02	**TSNAX**	3.4	0.03
PIK3R1	3.41	0.05	**SERPINI1**	3.39	0.01
MBNL2	3.4	0.03	**SLC12A8**	3.39	0.05
RAB3B	3.4	0.02	**FOLH1**	3.38	0.05
BTBD2	3.39	0.02	**SYP**	3.35	0.03
PAM	3.39	0.02	**ST7**	3.34	0.01
EPS8L2	3.39	0.02	**GNG4**	3.31	0.02
PAM	3.37	0.04	**GCA**	3.3	0.03
G3BP1	3.36	0.01	**RASIP1**	3.3	0.02
CSPG4	3.36	0.04	**FUBP1**	3.28	0.04
AGR2	3.35	0.02	**FAM111A**	3.28	0.03

NFIB	2.8	0.02	**DCPS**	3.0	0.01
ERBB2IP	2.79	0.03	**NRXN1**	3.0	0.01
KRT8	2.79	0.02	**PDE4B**	3.0	0.02
TBX1	2.79	0.05	**EPS8**	3.0	0.01
C5orf13	2.78	0.00	**KCNK12**	3.0	0.02
FLNA	2.78	0.02	**ACOT1 /// A**	3.0	0.02
SOX11	2.77	0.04	**ALDH5A1**	3.0	0.02
IL6R	2.77	0.01	**LIN7A**	2.9	0.04
PRKCH	2.77	0.03	**PPM1E**	2.9	0.03
ARFGEF1	2.75	0.02	**PBLD**	2.9	0.03
CTDSP2	2.75	0.05	**SNAP25**	2.9	0.00
YIPF1	2.74	0.01	**DPY19L2P2**	2.9	0.05
PRSS21	2.74	0.01	**UNC13B**	2.9	0.01
S100A14	2.74	0.03	**DNMBP**	2.9	0.01
DDR1	2.73	0.00	**SOD2**	2.9	0.04
C5orf13	2.72	0.01	**SYP**	2.9	0.04
CSNK2A2	2.71	0.01	**HSD17B8**	2.9	0.04
GM2A	2.71	0.01	**SMARCA1**	2.9	0.04
NUDT11	2.71	0.02	**ECHDC1**	2.8	0.05
BNIP3	2.7	0.01	**LGALS8**	2.8	0.02
DDIT4	2.7	0.02	**NNT**	2.8	0.02
BMP5	2.69	0.04	**MFAP2**	2.8	0.04
DIO1	2.69	0.04	**SLC39A8**	2.8	0.03
PIK3R3	2.69	0.01	**AMIGO2**	2.8	0.03
FZD7	2.68	0.04	**SAP30**	2.8	0.05
IL1R1	2.68	0.01	**CYB5A**	2.7	0.03
HLA-C	2.68	0.04	**LRRC8B**	2.7	0.02
GADD45B	2.67	0.04	**SEC23A**	2.7	0.04
HLA-E	2.67	0.01	**NEDD4L**	2.7	0.01
PPP2R2B	2.67	0.01	**ACADL**	2.7	0.02
NAB2	2.66	0.01	**RASIP1**	2.7	0.02
VPS37B	2.65	0.04	**C1orf218**	2.7	0.05
TIMP3	2.63	0.02	**USP18**	2.7	0.04
SH2B3	2.62	0.04	**ASB9**	2.6	0.02
C16orf5	2.61	0.01	**FAM111A**	2.6	0.04
DDR1	2.61	0.01	**NOS3**	2.6	0.00
DBN1	2.61	0.01	**NIPSNAP3B**	2.6	0.05

D4S234E	3.35	0.02	**SPN**	3.27	0.04	**EPAS1**	2.61	0.03	**SLC12A8**	2.6	0.03
SLC38A2	3.35	0.02	**LGALS8**	3.27	0.04	**HLA-DMA**	2.6	0.03	**ST7**	2.6	0.03
VARS	3.33	0.04	**PICALM**	3.27	0.02	**CFD**	2.59	0.03	**ZSCAN16**	2.6	0.02
HLA-C	3.32	0.01	**GALC**	3.26	0.03	**ACSL4**	2.59	0.05	**GALE**	2.6	0.01
DIO1	3.31	0.00	**CUL4A**	3.25	0.01	**GM2A**	2.59	0.04	**TROVE2**	2.6	0.02
CRIP2	3.31	0.03	**FAM20B**	3.25	0.01	**KCNG1**	2.58	0.01	**PRUNE**	2.6	0.03
HPSE	3.31	0.01	**KIF14**	3.25	0.02	**ETV5**	2.57	0.02	**FAIM**	2.6	0.05
ANXA6	3.29	0.02	**COL5A2**	3.25	0.01	**HOXC13**	2.57	0.00	**SLC35D2**	2.6	0.03
TIMP2	3.29	0.02	**MVP**	3.24	0.04	**ETS2**	2.57	0.02	**PSIP1**	2.6	0.03
TRAF4	3.29	0.05	**UROS**	3.24	0.01	**EPB41**	2.56	0.03	**ASTN2**	2.5	0.05
NAB2	3.27	0.01	**KIAA0240**	3.23	0.01	**ZFYVE21**	2.56	0.03	**CDK10**	2.5	0.00
SLIT3	3.26	0.01	**DAZAP1**	3.22	0.02	**SCGB1D2**	2.56	0.00	**GAL**	2.5	0.02
SLC19A1	3.25	0.00	**FBXL15**	3.22	0.02	**CDKN1C**	2.55	0.04	**ASPHD1**	2.5	0.03
IGFBP5	3.24	0.02	**FLJ10038**	3.21	0.05	**HLA-C**	2.55	0.01	**BBS10**	2.5	0.04
ARL4C	3.23	0.01	**MARCKS**	3.2	0.02	**PRKCH**	2.55	0.02	**HBQ1**	2.5	0.03
SLC38A2	3.23	0.05	**ALDH5A1**	3.2	0.01	**HES2**	2.52	0.04	**LGALS8**	2.5	0.04
DNAJC3	3.22	0.04	**LIMCH1**	3.2	0.01	**MYO1B**	2.52	0.05	**ISG15**	2.5	0.03
COL13A1	3.21	0.02	**CREBL2**	3.19	0.02	**STOM**	2.52	0.05	**RHOBTB1**	2.5	0.05
PRKCH	3.21	0.02	**AZGP1 /// LO**	3.19	0.03	**CDKN1C**	2.51	0.05	**ANGEL2**	2.5	0.03
TES	3.2	0.02	**MRPL24**	3.17	0.02	**HLA-E**	2.51	0.01	**SLC43A3**	2.5	0.03
F2RL1	3.2	0.02	**SNRPN**	3.17	0.02	**MSN**	2.51	0.01	**MRPL24**	2.5	0.02
CASP2	3.19	0.02	**ZBTB11**	3.16	0.02	**CD40**	2.51	0.02	**CEBPD**	2.5	0.05
CASP2	3.19	0.01	**KRIT1**	3.16	0.04	**ARFGEF1**	2.5	0.01	**SBNO2**	2.5	0.02
MAP3K1	3.19	0.03	**HNRPH2**	3.15	0.02	**PDE4A**	2.5	0.04	**TMEM28**	2.5	0.05
WIZ	3.19	0.04	**SSFA2**	3.15	0.04	**PTGES**	2.5	0.03	**CDC2L6**	2.5	0.01
MAF	3.18	0.03	**TMEM5**	3.14	0.01	**COL13A1**	2.49	0.05	**ABCA3**	2.5	0.04
LSS	3.18	0.05	**AMACR**	3.14	0.04	**CDKN1C**	2.49	0.01	**LOC654342**	2.5	0.03
HLA-E	3.17	0.03	**CEP350**	3.14	0.02	**FHL1**	2.49	0.05	**FAM134B**	2.5	0.05
RERE	3.17	0.01	**MAP4K3**	3.13	0.03	**COBLL1**	2.49	0.03	**HIST2H2AA**	2.4	0.00
TSPAN6	3.17	0.02	**FAM134B**	3.13	0.03	**NFIB**	2.49	0.03	**NFASC**	2.4	0.02
IRS2	3.17	0.02	**TPTE**	3.13	0.01	**PCDHGA3**	2.49	0.03	**CDC2L6**	2.4	0.01
AGRN	3.17	0.03	**DKFZP564O**	3.13	0.04	**SACS**	2.48	0.02	**C19orf2**	2.4	0.03
HLA-C	3.16	0.01	**RABIF**	3.12	0.04	**IRS2**	2.47	0.01	**MSL-1**	2.4	0.01
NELF	3.16	0.02	**PSMAL**	3.12	0.01	**SLC6A6**	2.47	0.01	**SNAP91**	2.4	0.01
CBFA2T2	3.14	0.01	**CPT2**	3.11	0.03	**LPIN1**	2.46	0.05	**KIAA1467**	2.4	0.04
MKRN1	3.12	0.01	**CHMP2B**	3.09	0.03	**NCK2**	2.46	0.03	**CAND2**	2.4	0.05
GSN	3.12	0.03	**ACTL6B**	3.09	0.03	**ID4**	2.45	0.04	**CLU**	2.4	0.04

FOXF2	3.11	0.04	**KIAA0776**	3.08	0.05	**RPS6KA2**	2.44	0.05	**ZNF592**	2.4	0.03
PER1	3.1	0.03	**CCDC91**	3.06	0.01	**IRS2**	2.44	0.02	**PRKCD**	2.4	0.01
C5orf13	3.09	0.01	**ZNF83**	3.06	0.01	**RGS3**	2.44	0.01	**NUP210**	2.4	0.01
PYGB	3.09	0.04	**PPP3CA**	3.05	0.02	**PITPNC1**	2.44	0.02	**ATP1B1**	2.4	0.01
EFNB3	3.09	0.01	**C17orf75**	3.05	0.05	**TES**	2.44	0.01	**WTAP**	2.4	0.01
CSNK1A1	3.09	0.01	**KIAA0528**	3.05	0.03	**BMP1**	2.43	0.04	**HIST2H2AA**	2.4	0.01
GADD45B	3.09	0.03	**DZIP3**	3.04	0.04	**LPIN1**	2.43	0.03	**IGFBP2**	2.4	0.02
MAPK14	3.09	0.01	**NHLRC2**	3.04	0.03	**ABAT**	2.43	0.03	**OSBPL1A**	2.4	0.04
CHKA /// LO	3.08	0.01	**IGF2BP3**	3.03	0.01	**CD99**	2.42	0.02	**SIGIRR**	2.4	0.01
FZD1	3.07	0.01	**HYPK**	3.03	0.03	**RHOBTB3**	2.42	0.04	**TIMP1**	2.4	0.03
KRT15	3.07	0.04	**FANCL**	3.02	0.02	**SERPINE2**	2.42	0.01	**ASRGL1**	2.4	0.02
CPSF3L	3.07	0.03	**RP6-213H19**	3.02	0.01	**LBH**	2.41	0.02	**BASP1**	2.4	0.02
PDE4A	3.06	0.03	**ATPIF1**	3.02	0.01	**TP53I11**	2.41	0.04	**TMEM164**	2.4	0.02
COL17A1	3.05	0.04	**TCEAL1**	3	0.01	**DDR1**	2.4	0.04	**C1orf156**	2.4	0.01
ST6GALNA	3.05	0.02	**FLJ12151**	3	0.02	**C20orf19**	2.39	0.02	**FAM20B**	2.4	0.02
FZD2	3.04	0.02	**ASB9**	2.99	0.05	**COL17A1**	2.39	0.02	**LIMCH1**	2.3	0.01
MLXIP	3.04	0.05	**PCMTD2**	2.99	0.01	**AGRN**	2.38	0.01	**PPM1H**	2.3	0.05
ANKH	3.04	0.02	**TROVE2**	2.99	0.05	**ECE1**	2.38	0.03	**PCCB**	2.3	0.02
PTPN21	3.03	0.02	**FKBP3**	2.99	0.05	**CPSF3L**	2.38	0.01	**SLC38A4**	2.3	0.04
SAR1A	3.02	0.04	**ANXA7**	2.98	0.02	**IQGAP1**	2.38	0.01	**HMGCS2**	2.3	0.02
NUDT11	3.02	0.02	**JMJD1B**	2.98	0.04	**ANKH**	2.37	0.04	**AHCTF1**	2.3	0.03
C20orf19	3.02	0.04	**SCN11A**	2.98	0.04	**KCNK1**	2.37	0.02	**HIST1H2AC**	2.3	0.05
SOX11	3.01	0.01	**DCK**	2.97	0.01	**HLA-C**	2.36	0.01	**PRMT5**	2.3	0.01
BTN3A2	3.01	0.03	**C6orf120**	2.97	0.02	**DBN1**	2.36	0.04	**ATP8A1**	2.3	0.02
RGS10	3	0.03	**SLC25A44**	2.97	0.01	**HLA-E**	2.36	0.02	**RABIF**	2.3	0.04
PFKL	3	0.02	**DHRS2**	2.96	0.03	**CADM1**	2.35	0.02	**BAIAP2L2**	2.3	0.02
CLSTN1	2.99	0.01	**RNASE4**	2.95	0.03	**NFIB**	2.34	0.01	**C9orf82**	2.3	0.02
CCBL1	2.99	0.01	**GPD1L**	2.95	0.01	**MYO10**	2.34	0.05	**TRIM14**	2.3	0.03
ST6GALNA	2.99	0.03	**ZNF529**	2.95	0.05	**ANXA6**	2.33	0.03	**USP4**	2.3	0.05
GADD45B	2.98	0.05	**OR2J3**	2.95	0.02	**DST**	2.33	0.03	**TRPC1**	2.3	0.03
FHL1	2.98	0.01	**THOC2**	2.95	0.03	**CCBL1**	2.33	0.03	**MLH3**	2.3	0.05
SLC25A36	2.97	0.02	**HLA-DQB1**	2.94	0.03	**SYT17**	2.32	0.02	**C2orf24**	2.2	0.01
SELENBP1	2.97	0.03	**KIAA0368**	2.94	0.02	**LUM**	2.32	0.03	**SLIT1**	2.2	0.04
PTPRF	2.96	0.03	**HIST1H2AC**	2.94	0.02	**RERE**	2.3	0.02	**C20orf23**	2.2	0.04
M6PRBP1	2.96	0.02	**JTB**	2.92	0.01	**DPYSL4**	2.3	0.04	**CYP1A1**	2.2	0.01
PAFAH1B2	2.96	0.03	**HUS1**	2.92	0.04	**C9orf3**	2.3	0.05	**LOX**	2.2	0.03
MYBL1	2.96	0.03	**PPP1CB**	2.91	0.01	**PGM1**	2.3	0.01	**PFDN2**	2.2	0.01

TIMP3	2.95	0.03	**CUL2**	2.91	0.04	**COTL1**	2.29	0.02	**ATF5**	2.2	0.03
CNN2	2.95	0.03	**PROS1**	2.91	0.03	**TMEM159**	2.29	0.02	**AP3B2**	2.2	0.04
RAC3	2.95	0.02	**PCCB**	2.9	0.02	**KIF1C**	2.29	0.04	**DPEP3**	2.2	0.05
PITX1	2.95	0.03	**YWHAB**	2.9	0.01	**HECA**	2.28	0.01	**SEC22A**	2.2	0.04
C1orf116	2.95	0.03	**ATAD4**	2.9	0.05	**SLC22A18**	2.28	0.01	**MTUS1**	2.2	0.02
PDLIM7	2.94	0.02	**PSIP1**	2.89	0.05	**ZYX**	2.28	0.03	**CENTA2**	2.2	0.02
TPD52L1	2.94	0.01	**LOC341651**	2.89	0.03	**TRAF3IP2**	2.27	0.02	**DEGS1**	2.2	0.04
PDLIM7	2.93	0.01	**DCPS**	2.89	0.01	**EXT2**	2.27	0.01	**FUBP1**	2.2	0.03
RPS6KA2	2.93	0.02	**C19orf2**	2.89	0.02	**HLA-C**	2.27	0.01	**SDC2**	2.2	0.03
KCNK1	2.92	0.02	**NET1**	2.88	0.04	**IGSF3**	2.26	0.04	**CLU**	2.2	0.04
BCL3	2.92	0.02	**PSIP1**	2.87	0.05	**FAM114A1**	2.26	0.03	**TJP2**	2.2	0.03
PGM1	2.91	0.04	**TMEM30B**	2.85	0.04	**PTGES**	2.26	0.03	**PGBD5**	2.2	0.03
BAT2	2.91	0.04	**ELOVL6**	2.84	0.04	**CBX4**	2.25	0.04	**TSNAX**	2.2	0.04
COBLL1	2.9	0.03	**LGALS8**	2.84	0.04	**PRNP**	2.25	0.01	**TM7SF2**	2.2	0.01
TP53	2.9	0.01	**UBQLN4**	2.84	0.04	**GM2A**	2.24	0.02	**ALDH3A2**	2.1	0.01
HLA-G	2.9	0.04	**EIF1AX**	2.83	0.04	**COBL**	2.24	0.01	**XCL2**	2.1	0.04
COTL1	2.9	0.01	**HNRPA3**	2.83	0.01	**PFN1**	2.24	0.01	**RWDD2A**	2.1	0.01
ARL4C	2.89	0.03	**PH-4**	2.83	0.04	**TSC22D1**	2.24	0.03	**RDH14**	2.1	0.03
NCOA2	2.89	0.04	**GBAS**	2.82	0.00	**CSNK1A1**	2.23	0.01	**TCEAL1**	2.1	0.02
TSC22D3	2.89	0.03	**SPAST**	2.82	0.02	**VGLL4**	2.23	0.01	**SLC17A5**	2.1	0.02
NKX3-1	2.89	0.02	**KLK1**	2.81	0.05	**SLC1A4**	2.23	0.01	**TOR3A**	2.1	0.03
PLEC1	2.88	0.04	**IMPACT**	2.81	0.05	**SPOCK1**	2.23	0.03	**MAK10**	2.1	0.03
RSRC1	2.88	0.01	**TOR1AIP1**	2.8	0.05	**JUP**	2.22	0.02	**PSEN2**	2.1	0.02
INSIG1	2.87	0.01	**SLIT1**	2.79	0.02	**MEF2A**	2.22	0.05	**SEPHS1**	2.1	0.02
TP53	2.87	0.04	**TTTY15**	2.79	0.04	**CASP2**	2.21	0.04	**DPM3**	2.1	0.04
CAPZB	2.87	0.03	**SEPHS1**	2.78	0.01	**PNRC1**	2.21	0.01	**ST7**	2.1	0.02
STC2	2.85	0.01	**CYFIP2**	2.78	0.02	**CXADR**	2.2	0.05	**DDB1**	2.1	0.03
CSNK2A2	2.85	0.01	**UNC13B**	2.77	0.03	**GPRC5C**	2.2	0.02	**PLS3**	2.1	0.05
PDLIM2	2.85	0.03	**HIST1H3H**	2.77	0.03	**GSTT1**	2.2	0.02	**PKN1**	2.1	0.03
PIK3R3	2.84	0.04	**GUCY1B3**	2.77	0.05	**ZMIZ1**	2.2	0.04	**WWC1**	2.1	0.05
NCOA2	2.83	0.02	**ANK2**	2.76	0.02	**EHD1**	2.19	0.03	**AMD1**	2.1	0.04
ANKRD57	2.83	0.01	**HNRPA3 ///**	2.76	0.04	**KDELR3**	2.19	0.01	**TNFSF12-TN**	2.1	0.02
RAB3B	2.82	0.03	**PTPLB**	2.76	0.01	**MTFR1**	2.19	0.02	**EFTUD1**	2.1	0.04
MPPE1	2.82	0.03	**CAND2**	2.76	0.04	**KCNK1**	2.19	0.02	**STAT6**	2.1	0.05
UBE2H	2.82	0.01	**AHCTF1**	2.76	0.03	**IFI30**	2.18	0.02	**RBM12**	2.1	0.04
SAT1	2.81	0.02	**UBE2J1**	2.76	0.03	**ABHD2**	2.17	0.01	**PRUNE**	2.1	0.02
RTN2	2.81	0.05	**MBD1**	2.75	0.03	**ST6GALNA**	2.17	0.01	**TOR1A**	2.1	0.05

DDR1	2.8	0.03	**MCCC2**	2.75	0.02	**SEC31A**	2.17	0.01	**TMEM30B**	2.1	0.03
PRSS21	2.78	0.02	**HIST2H2AA**	2.75	0.00	**ZNF277**	2.17	0.02	**PHF15**	2.1	0.03
VPS37B	2.78	0.02	**CHGA**	2.74	0.05	**ITPR3**	2.16	0.01	**DDX50**	2.1	0.03
FKBP8	2.78	0.00	**ITGB5**	2.74	0.03	**STOM**	2.16	0.03	**AUH**	2.1	0.03
TPD52L1	2.77	0.01	**FARSA**	2.74	0.03	**BNIP2**	2.15	0.01	**DIDO1**	2.1	0.03
CD164	2.77	0.01	**CD44**	2.73	0.04	**GGH**	2.15	0.01	**KIF15**	2.1	0.02
HPCAL1	2.77	0.05	**RBM26**	2.73	0.03	**MRPL22**	2.15	0.01	**MAN1A1**	2.1	0.05
DPY19L1	2.77	0.02	**EFTUD1**	2.73	0.02	**BIN1**	2.14	0.03	**TXNRD3**	2.0	0.05
GM2A	2.77	0.02	**TJP2**	2.72	0.01	**TSC22D3**	2.14	0.02	**ARHGAP15**	2.0	0.05
PPP1R10	2.75	0.02	**HNMT**	2.72	0.00	**DEF6**	2.14	0.03	**HIST1H3H**	2.0	0.03
GADD45G	2.75	0.01	**C4orf20**	2.72	0.04	**PDLIM7**	2.14	0.04	**ADAM22**	2.0	0.04
INPP5A	2.74	0.03	**EFNB2**	2.71	0.02	**HOXA1**	2.14	0.03	**RUNDC3A**	2.0	0.02
MAPRE3	2.74	0.01	**BLVRA**	2.71	0.03	**ANKMY2**	2.14	0.02	**ALDH3A2**	2.0	0.01
PRNP	2.74	0.03	**CEP27**	2.71	0.01	**NAGA**	2.14	0.04	**JTB**	2.0	0.04
RFPL3	2.73	0.02	**C1orf107**	2.7	0.02	**SLC1A4**	2.14	0.04	**DNAJC16**	2.0	0.04
PITX1	2.73	0.01	**FAM115A**	2.7	0.02	**SNTA1**	2.14	0.02	**RABIF**	2.0	0.05
C5orf13	2.72	0.02	**EPS15**	2.7	0.04	**B4GALT1**	2.14	0.02	**RPS6KC1**	2.0	0.03
BAT2	2.72	0.02	**LRRC40**	2.7	0.01	**BTN3A2 ///**	2.13	0.03	**BLVRA**	2.0	0.05
EIF4G1	2.72	0.03	**GCNT1**	2.69	0.05	**IQGAP1**	2.12	0.03	**KIAA0133**	2.0	0.01
MXD4	2.72	0.02	**ASB1**	2.69	0.04	**F12**	2.11	0.02	**ULK2**	2.0	0.03
PFN1	2.71	0.02	**RDH14**	2.69	0.02	**FLJ20035**	2.11	0.04	**HOXA10**	2.0	0.04
AP2B1	2.7	0.05	**CASP6**	2.68	0.03	**INPP5A**	2.11	0.01	**EIF2AK1**	2.0	0.03
MAN2A1	2.7	0.01	**YEATS4**	2.68	0.02	**ALDH7A1**	2.1	0.03	**MBD1**	2.0	0.05
CDK2	2.7	0.03	**TRIM8**	2.68	0.04	**ATP2C1**	2.1	0.03	**SIGIRR**	2.0	0.02
GRB14	2.69	0.01	**SBNO2**	2.66	0.03	**ENY2**	2.1	0.01	**OR7E37P**	2.0	0.03
C16orf5	2.69	0.05	**EZR**	2.66	0.02	**ELF3**	2.1	0.02	**C7orf49**	2.0	0.04
ACVR1B	2.68	0.04	**PPAP2A**	2.66	0.02	**EHD1**	2.1	0.05	**RBM16**	2.0	0.05
SLC25A10	2.68	0.03	**CENTB2**	2.66	0.01	**EHD1**	2.1	0.05	**MRS2L**	2.0	0.03
AGPAT2	2.68	0.02	**LOC729799**	2.66	0.03	**DBI**	2.09	0.01	**COL5A2**	2.0	0.04
DISC1	2.67	0.02	**FLJ13611**	2.66	0.03	**AIM1**	2.08	0.03	**PTGER3**	2.0	0.05
HLA-C	2.67	0.05	**BTG1**	2.65	0.03	**AES**	2.08	0.01	**LOC222070**	2.0	0.02
HEY1	2.67	0.05	**RCAN2**	2.65	0.04	**ATP11A**	2.08	0.05	**PITPNA**	2.0	0.02
IQGAP1	2.66	0.05	**CD44**	2.65	0.03	**NFIB**	2.08	0.02	**AP1G2**	2.0	0.05
KIAA1245 //	2.66	0.03	**USP18**	2.65	0.03	**ZNF185**	2.08	0.02	**STX6**	2.0	0.04
ENY2	2.66	0.01	**ATP1B1**	2.64	0.04	**PELI2**	2.07	0.02	**RASA4**	2.0	0.05
BMP5	2.65	0.01	**RAG1AP1**	2.63	0.03	**STC2**	2.07	0.03	**CUTC**	2.0	0.02
NDRG3	2.65	0.04	**PIGA**	2.62	0.04	**SMARCA2**	2.07	0.05	**FAM46A**	2.0	0.03

EHBP1L1	2.65	0.01	**CHMP4A**	2.62	0.02	**BNIP3L**	2.06	0.04	**ERBB4**	2.0	0.05
IL1R1	2.64	0.04	**DOCK9**	2.61	0.05	**GPC1**	2.06	0.05	**ARMCX5**	2.0	0.03
HPCAL1	2.64	0.03	**RRP15**	2.61	0.04	**ARL6IP5**	2.06	0.01	**BLVRA**	2.0	0.01
DPYSL4	2.64	0.02	**SLC39A8**	2.61	0.01	**DNPEP**	2.05	0.03	**FUBP1**	2.0	0.04
NRXN2	2.64	0.02	**SUCLA2**	2.59	0.03	**EFHA1**	2.05	0.02	**TARS2**	2.0	0.02
SAT1	2.63	0.03	**CREBZF**	2.59	0.01	**SIX2**	2.05	0.03	**GDF15**	2.0	0.02
SREBF2	2.62	0.03	**PAX3**	2.59	0.05	**BIN1**	2.04	0.02	**PSD4**	2.0	0.02
CBX2	2.62	0.03	**LOC644450**	2.59	0.02	**CTSF**	2.04	0.04	**SCAMP3**	2.0	0.03
CLIC4	2.61	0.01	**ACADM**	2.58	0.04	**CHKA**	2.04	0.02	**TAF7L**	2.0	0.05
PDCD4	2.61	0.05	**NUP50**	2.58	0.01	**GPR177**	2.04	0.04	**UCKL1**	2.0	0.03
LOXL2	2.61	0.05	**SIGIRR**	2.58	0.02	**KRT18**	2.04	0.05	**XCL1 /// XC**	2.0	0.05
EEF1D	2.61	0.01	**UBE2D2**	2.57	0.04	**RXRA**	2.04	0.02	**SMCHD1**	2.0	0.02
C20orf11	2.61	0.03	**IMPA1**	2.57	0.03	**CTNNA1**	2.03	0.02	**NEBL**	2.0	0.05
HOXC13	2.61	0.02	**ISG15**	2.57	0.03	**CXorf57**	2.03	0.02	**PARP1**	1.9	0.02
FLJ20323	2.6	0.01	**FUSIP1**	2.57	0.02	**LPCAT1**	2.03	0.04	**C16orf42**	1.9	0.05
DNAJB1	2.59	0.02	**AMACR**	2.57	0.02	**IFI6**	2.03	0.03	**TMEM47**	1.9	0.02
LRPAP1	2.59	0.02	**CCDC109B**	2.57	0.03	**PTEN**	2.03	0.02	**CALM3**	1.9	0.02
EVL	2.59	0.03	**ATMIN**	2.56	0.03	**RFPL3**	2.03	0.02	**HTATIP2**	1.9	0.04
YIPF5	2.59	0.03	**ALDH3A2**	2.55	0.01	**RARG**	2.02	0.05	**LGALS8**	1.9	0.03
USP5	2.58	0.00	**SLC35D2**	2.55	0.02	**RSL1D1**	2.01	0.04	**MARCKS**	1.9	0.05
TSPAN6	2.58	0.02	**PLS3**	2.54	0.02	**ETV5**	2.01	0.01	**RAG1AP1**	1.9	0.05
PDLIM7	2.58	0.03	**MED14**	2.54	0.03	**MTFR1**	2.01	0.03	**RAP1GDS1**	1.9	0.04
N-PAC	2.58	0.04	**NNT**	2.54	0.04	**NCOA2**	2.01	0.03	**MST1**	1.9	0.04
ETS2	2.57	0.05	**CALCB**	2.54	0.02	**TLE2**	2.01	0.02	**GPR126**	1.9	0.03
COL16A1	2.57	0.05	**MEMO1**	2.54	0.03	**EXT1**	2	0.03	**NMU**	1.9	0.02
AP3D1	2.57	0.04	**LGR4**	2.53	0.05	**KRT10**	2	0.03	**NUP98**	1.9	0.05
KIAA0828	2.57	0.01	**OAZ3**	2.53	0.02	**LEPRE1**	2	0.03	**PODXL**	1.9	0.04
S100A14	2.57	0.03	**ZNF764**	2.53	0.04	**FOS**	2	0.04	**UCHL5**	1.9	0.03
CNOT8	2.56	0.04	**SYNCRIP**	2.52	0.04	**SEC31A**	2	0.03	**LPGAT1**	1.9	0.05
TRAF4	2.56	0.02	**KIAA1467**	2.52	0.03	**HSPA4**	1.99	0.01	**LASP1**	1.9	0.02
GAMT	2.56	0.03	**LOC441453**	2.52	0.04	**INSIG1**	1.99	0.02	**CALCB**	1.9	0.03
UBE2G2	2.56	0.03	**PLEKHB2**	2.51	0.04	**KRT10**	1.99	0.01	**CHMP4A**	1.9	0.01
SCARB2	2.55	0.01	**SCNN1A**	2.51	0.05	**PTRF**	1.99	0.05	**AMD1**	1.9	0.03
ZNF185	2.55	0.04	**PAPOLA**	2.51	0.04	**MORC2**	1.98	0.01	**AHI1**	1.9	0.05
MARCKS	2.54	0.01	**TULP4**	2.51	0.02	**LPIN1**	1.98	0.01	**L1CAM**	1.9	0.04
FLJ20323	2.54	0.02	**TBC1D8**	2.5	0.02	**TP53I11**	1.98	0.02	**C6orf120**	1.9	0.02
HLA-DMA	2.54	0.03	**NEDD4L**	2.5	0.02	**PLEC1**	1.98	0.03	**WBSCR22**	1.9	0.02

LGR5	2.53	0.03	**DTL**	2.49	0.01	**TOX**	1.98	0.04	**JTB**	1.9	0.03
PEX5	2.53	0.01	**NMU**	2.48	0.01	**B4GALT1**	1.98	0.01	**KIF13B**	1.9	0.04
GPRC5C	2.53	0.02	**ANXA11**	2.48	0.01	**UCP2**	1.98	0.01	**OCRL**	1.9	0.02
USP36	2.53	0.04	**HOPX**	2.48	0.02	**AMBP**	1.97	0.02	**MTUS1**	1.9	0.03
VCL	2.52	0.03	**DMXL2**	2.48	0.02	**DDX11**	1.97	0.02	**GCH1**	1.9	0.05
EXT1	2.52	0.01	**ARMCX5**	2.48	0.01	**DBI**	1.97	0.03	**TMEM177**	1.9	0.03
DCN	2.52	0.04	**RUFY3**	2.47	0.03	**GAMT**	1.97	0.03	**ITSN2**	1.9	0.05
TLE2	2.51	0.04	**COL9A3**	2.47	0.02	**PITX1**	1.97	0.03	**ICMT**	1.9	0.03
ADA	2.5	0.04	**ETFDH**	2.47	0.01	**PRCP**	1.97	0.02	**SCRN1**	1.9	0.02
ATP2C1	2.5	0.04	**GGCX**	2.47	0.05	**SPATA6**	1.97	0.05	**WWC1**	1.9	0.02
PLOD1	2.49	0.02	**SDHC**	2.47	0.02	**SGPL1**	1.97	0.03	**NEBL**	1.9	0.04
KRT18	2.49	0.02	**CSE1L**	2.46	0.02	**ATP2C1**	1.96	0.03	**PARD6A**	1.9	0.05
EXT2	2.49	0.02	**FAM20B**	2.45	0.03	**BIN1**	1.96	0.03	**CAP2**	1.9	0.04
EPHX1	2.49	0.02	**AKAP11**	2.45	0.05	**CSNK1A1**	1.96	0.00	**HOPX**	1.9	0.02
DDR1	2.49	0.01	**ASTN2**	2.45	0.04	**EPN2**	1.96	0.02	**PPP1R1A**	1.9	0.04
SCAMP1	2.49	0.01	**PPM1H**	2.45	0.02	**YIPF5**	1.96	0.01	**FECH**	1.9	0.03
COBL	2.49	0.01	**SEH1L**	2.45	0.02	**SLC1A4**	1.96	0.02	**CDV3**	1.9	0.01
LTBP4	2.49	0.01	**USP4**	2.44	0.05	**RBM9**	1.96	0.03	**CRELD2**	1.9	0.01
BRCA2	2.49	0.01	**TRIM14**	2.44	0.01	**SSBP2**	1.96	0.05	**MRPS14**	1.9	0.01
PLXNB1	2.49	0.01	**PSMD11**	2.44	0.04	**TRPV6**	1.96	0.04	**NVL**	1.9	0.01
EXOSC4	2.49	0.03	**RWDD2A**	2.44	0.02	**F2RL1**	1.95	0.02	**ACE**	1.8	0.04
PFKFB3	2.48	0.04	**NET1**	2.43	0.04	**EML1**	1.95	0.05	**CSPG5**	1.8	0.03
PDXK	2.48	0.01	**ANG**	2.43	0.01	**IFITM2**	1.95	0.04	**MYO6**	1.8	0.04
IFI6	2.48	0.01	**HNRNPA2B**	2.43	0.01	**LRPAP1**	1.95	0.01	**NELL2**	1.8	0.03
HLA-G	2.48	0.01	**PNPLA4**	2.43	0.04	**MCF2L**	1.95	0.03	**FARSA**	1.8	0.02
SLC1A4	2.48	0.02	**RCBTB1**	2.43	0.02	**NRXN2**	1.95	0.04	**ADAMTS1**	1.8	0.04
PCLO	2.48	0.05	**DNAJC10**	2.43	0.05	**NINJ1**	1.95	0.01	**KIAA0859**	1.8	0.05
NDST1	2.47	0.01	**TOR1A**	2.42	0.03	**G3BP1**	1.95	0.05	**FH**	1.8	0.03
DPYSL4	2.47	0.02	**ITSN2**	2.42	0.05	**USP8**	1.95	0.03	**GOLGA5**	1.8	0.04
VEGFA	2.47	0.01	**CHD9**	2.42	0.05	**ATP1B3**	1.94	0.04	**LRRTM4**	1.8	0.04
MICAL3	2.47	0.02	**PRMT5**	2.42	0.02	**CRIP2**	1.94	0.02	**INTS3**	1.8	0.02
MBOAT2	2.47	0.05	**USP48**	2.42	0.01	**RBM35A**	1.94	0.01	**SARM1**	1.8	0.03
TWF1	2.47	0.05	**PLOD2**	2.41	0.05	**PXN**	1.94	0.01	**TRAF5**	1.8	0.05
RAP2B	2.46	0.03	**HIST1H1C**	2.41	0.05	**CLIC4**	1.93	0.02	**DET1**	1.8	0.02
ENO1	2.46	0.02	**LRCH3**	2.41	0.03	**BEAN**	1.93	0.04	**IVNS1ABP**	1.8	0.04
CORO1B	2.46	0.04	**CENPN**	2.41	0.01	**MB**	1.93	0.02	**SLC29A1**	1.8	0.01
NRGN	2.45	0.02	**ATF5**	2.4	0.03	**SLC16A1**	1.93	0.05	**STX1A**	1.8	0.04

TMEM159	2.45	0.04	**ZNF223**	2.4	0.05	**TYRO3**	1.93	0.04	**TXNRD2**	1.8	0.04
ACSL1	2.44	0.00	**CSHL1**	2.4	0.03	**CD97**	1.92	0.03	**VAV1**	1.8	0.03
SYMPK	2.44	0.01	**TRIM24**	2.4	0.02	**TMC6**	1.92	0.03	**CD2AP**	1.8	0.03
TES	2.44	0.02	**REV1**	2.4	0.03	**RAB15**	1.92	0.01	**C1orf34**	1.8	0.04
KRT36	2.44	0.01	**PRPF4B**	2.39	0.04	**P4HA1**	1.92	0.01	**DUT**	1.8	0.02
ODC1	2.43	0.02	**SMAD2**	2.39	0.05	**STK17A**	1.92	0.02	**ROGDI**	1.8	0.04
ARFGEF1	2.43	0.01	**CENTA2**	2.39	0.03	**CTSC**	1.91	0.03	**C3orf60**	1.8	0.02
SH2B3	2.43	0.02	**ZSCAN16**	2.39	0.03	**HBEGF**	1.91	0.04	**WHSC1**	1.8	0.04
GM2A	2.43	0.01	**ZNF587**	2.39	0.02	**CCNB1IP1**	1.91	0.02	**DECR2**	1.8	0.05
GOLM1	2.43	0.01	**PPP1R1A**	2.38	0.03	**NFIB**	1.91	0.05	**CHD1L**	1.8	0.03
ACCN2	2.42	0.03	**HLA-DRB1**	2.38	0.01	**G3BP1**	1.91	0.01	**KIAA1279**	1.8	0.02
BMP1	2.42	0.01	**PATZ1**	2.37	0.04	**STK38L**	1.91	0.02	**DPAGT1**	1.8	0.03
CBLC	2.42	0.02	**MRPL9**	2.37	0.03	**SLC6A3**	1.91	0.02	**LOC400451**	1.8	0.04
OGFR	2.41	0.03	**PHF15**	2.37	0.03	**DCN**	1.9	0.05	**LUZP2**	1.8	0.03
GLTPD1	2.41	0.03	**SNAPC5**	2.37	0.04	**EFNA1**	1.9	0.03	**DARS2**	1.8	0.02
FXYD1	2.4	0.02	**RNF17**	2.37	0.04	**FXYD5**	1.9	0.04	**WHSC1**	1.8	0.02
C10orf10	2.4	0.02	**SUCLG2**	2.36	0.01	**GTF2E2**	1.9	0.05	**GTF3A**	1.8	0.03
BIN1	2.4	0.05	**PTBP2**	2.36	0.04	**GRHL2**	1.9	0.01	**H2AFX**	1.8	0.02
PIP5K1A	2.4	0.04	**TUSC2**	2.35	0.03	**S100A10**	1.9	0.03	**ATMIN**	1.8	0.03
LPIN1	2.4	0.05	**HES1**	2.35	0.05	**TPM4**	1.9	0.01	**RRM2**	1.8	0.03
OPTN	2.39	0.04	**STX6**	2.35	0.03	**AP3B1**	1.89	0.01	**TIPRL**	1.8	0.03
GSS	2.39	0.02	**ASAH1**	2.35	0.02	**C5orf5**	1.89	0.03	**XPNPEP1**	1.8	0.02
KCND3	2.39	0.01	**ESD**	2.35	0.04	**CD55**	1.89	0.03	**INTS1**	1.8	0.02
LYPLA2	2.39	0.03	**TRIM24**	2.34	0.01	**CAMK2N1**	1.89	0.02	**JTB**	1.8	0.01
VDAC1	2.39	0.03	**HMGCS2**	2.33	0.02	**PGK1**	1.89	0.02	**MAGED1**	1.8	0.03
ABHD2	2.39	0.05	**SRI**	2.33	0.01	**GSTK1**	1.88	0.01	**SEC23A**	1.8	0.03
PGK1	2.38	0.03	**RPS6KC1**	2.33	0.03	**RNF44**	1.88	0.05	**SMUG1**	1.8	0.02
CD99	2.38	0.02	**DECR2**	2.33	0.04	**CLIC4**	1.87	0.02	**XPNPEP1**	1.8	0.03
EPN2	2.38	0.02	**ALK**	2.32	0.04	**HEY1**	1.87	0.03	**C1orf35**	1.8	0.05
SORBS3	2.38	0.03	**C1orf156**	2.32	0.02	**HK2**	1.87	0.02	**GYG1**	1.8	0.04
HECA	2.38	0.02	**C14orf108**	2.32	0.03	**FLJ13236**	1.87	0.02	**ZSCAN18**	1.8	0.05
IFITM2	2.37	0.02	**COMMD8**	2.32	0.04	**ITGA6**	1.87	0.04	**PSME3**	1.8	0.05
MAX	2.37	0.03	**CLMN**	2.32	0.04	**MKNK2**	1.87	0.03	**PPP2R5A**	1.8	0.04
CALU	2.37	0.02	**SCYE1**	2.31	0.04	**QSOX1**	1.87	0.04	**APPL1**	1.8	0.05
ZNHIT4	2.37	0.02	**KIF13B**	2.31	0.05	**SEMA3F**	1.87	0.02	**RFK**	1.8	0.04
SORBS2	2.36	0.05	**GNPAT**	2.3	0.03	**BMP2**	1.86	0.01	**TMEM93**	1.8	0.02
BMP7	2.36	0.02	**KIAA0894**	2.3	0.02	**GOLIM4**	1.86	0.02	**MAOA**	1.8	0.05

EPHB4	2.35	0.05	**RAP1GDS1**	2.3	0.05	**LDLR**	1.86	0.04	**MYO6**	1.8	0.02
PALM	2.35	0.04	**PAXIP1**	2.3	0.02	**SEC14L1**	1.86	0.02	**SSH3**	1.8	0.02
TMED9	2.35	0.04	**CAMK1**	2.29	0.04	**SLC22A18A**	1.86	0.03	**SLC13A3**	1.8	0.05
CCK	2.35	0.05	**CTSZ**	2.29	0.05	**TGIF1**	1.86	0.03	**ACADVL**	1.7	0.02
GTF3C2	2.35	0.01	**SLC5A3**	2.29	0.03	**TRIM29**	1.86	0.05	**EDG7**	1.7	0.05
PIK3CB	2.35	0.01	**ABHD5**	2.29	0.03	**CLSTN1**	1.85	0.03	**C2orf24**	1.7	0.05
TMCO3	2.35	0.04	**PAICS**	2.29	0.03	**KRT36**	1.85	0.03	**DALRD3**	1.7	0.02
SH3BP4	2.35	0.04	**HSDL2**	2.29	0.02	**NAB1**	1.85	0.04	**SMC2**	1.7	0.05
DAP	2.34	0.04	**RABIF**	2.28	0.02	**YAP1**	1.85	0.02	**SNX27**	1.7	0.03
RBMS1	2.34	0.03	**FGF13**	2.28	0.03	**BMP1**	1.84	0.05	**ZNF107**	1.7	0.05
CD40	2.34	0.01	**ELK4**	2.28	0.02	**FRAT1**	1.84	0.02	**CFLAR**	1.7	0.02
TNS1	2.34	0.02	**PAQR3**	2.28	0.05	**GSR**	1.84	0.01	**ME2**	1.7	0.03
CALU	2.33	0.02	**GPATCH2**	2.28	0.04	**SEMA3F**	1.84	0.04	**MAOA**	1.7	0.02
MTFR1	2.33	0.05	**C1GALT1C**	2.28	0.02	**LOC57228**	1.83	0.02	**RGS11**	1.7	0.03
LMO4	2.33	0.04	**PIGV**	2.28	0.04	**OVOL1**	1.83	0.04	**SSH3**	1.7	0.04
MORC2	2.33	0.02	**FDX1**	2.27	0.02	**SIRPA**	1.83	0.05	**GNE**	1.7	0.04
EXOSC4	2.33	0.01	**VPS45**	2.27	0.02	**CTNNA1**	1.82	0.03	**DDX27**	1.7	0.04
SPOCK1	2.32	0.02	**PODXL**	2.26	0.05	**DUSP9**	1.82	0.03	**USP48**	1.7	0.05
HTATSF1	2.32	0.03	**LSM7**	2.26	0.02	**RAN**	1.82	0.03	**LOC644617**	1.7	0.04
TMC6	2.32	0.02	**LIN7A**	2.26	0.02	**ALCAM**	1.81	0.05	**NDUFS2**	1.7	0.03
MCPH1	2.32	0.02	**PRUNE**	2.26	0.04	**RIPK4**	1.81	0.02	**SNUPN**	1.7	0.04
MCF2L	2.32	0.03	**ZMYM1**	2.26	0.04	**CD99**	1.81	0.03	**VRK3**	1.7	0.03
EHBP1L1	2.32	0.03	**C6orf120**	2.26	0.01	**EXT2**	1.81	0.03	**CAMK2B**	1.7	0.04
CRKL	2.31	0.04	**UBA2**	2.25	0.01	**HMOX1**	1.81	0.05	**FH**	1.7	0.01
LHX6	2.31	0.02	**KLHL20**	2.25	0.04	**LRRFIP1**	1.81	0.01	**EIF1AX**	1.7	0.05
CAPZB	2.3	0.03	**PPM1E**	2.25	0.05	**PALM**	1.81	0.03	**NAG18**	1.7	0.03
SIKE	2.3	0.03	**MED13L**	2.25	0.04	**B4GALT1**	1.81	0.02	**PARVB**	1.7	0.03
IRS2	2.3	0.05	**MT1E**	2.25	0.05	**CD24**	1.8	0.01	**USP11**	1.7	0.03
TRAF3IP2	2.3	0.05	**RDH11**	2.25	0.04	**HSF1**	1.8	0.02	**USP21**	1.7	0.02
PTEN	2.3	0.02	**GLT8D1**	2.25	0.02	**HK1**	1.8	0.02	**DDX52**	1.7	0.05
NEDD9	2.29	0.03	**RP3-377H14**	2.25	0.03	**HOXA9**	1.8	0.03	**DEAF1**	1.7	0.01
FGFR1	2.29	0.03	**YY1**	2.24	0.04	**NFIB**	1.8	0.04	**H2AFX**	1.7	0.01
POMGNT1	2.29	0.02	**NEBL**	2.24	0.05	**ITM2B**	1.8	0.02	**HOXA11**	1.7	0.04
SLCO4A1	2.29	0.04	**SAP30**	2.24	0.05	**MAST4**	1.8	0.02	**C5orf23**	1.7	0.05
KLF4	2.29	0.05	**GTF2H5**	2.24	0.04	**LGALS1**	1.8	0.02	**LOC727942**	1.7	0.05
STOM	2.28	0.03	**TWIST1**	2.24	0.03	**MAX**	1.8	0.04	**PDE9A**	1.7	0.05
SKP2	2.28	0.01	**RNF6**	2.23	0.04	**ARHGEF10**	1.8	0.03	**PLS1**	1.7	0.03

EIF4B	2.28	0.02	**GIT2**	2.23	0.03	**FANCE**	1.79	0.04	**STAU2**	1.7	0.03
TPD52	2.27	0.05	**ARHGAP6**	2.23	0.03	**STAT3**	1.79	0.05	**CROT**	1.7	0.04
RXRA	2.27	0.03	**ALB**	2.23	0.05	**FLJ20323**	1.79	0.02	**DEDD**	1.7	0.02
GNS	2.27	0.01	**IVNS1ABP**	2.22	0.01	**ITGA2**	1.79	0.01	**SLC47A1**	1.7	0.05
CANX	2.27	0.01	**TIA1**	2.22	0.03	**SH2D3A**	1.79	0.03	**CCDC92**	1.7	0.05
NFYC	2.27	0.02	**NEBL**	2.22	0.05	**SLC1A5**	1.79	0.03	**SEPHS2**	1.7	0.02
TBC1D9B	2.27	0.05	**KIAA1279**	2.22	0.04	**CTSB**	1.78	0.04	**CDC20**	1.7	0.02
CAMK2N1	2.27	0.01	**C10orf137**	2.22	0.03	**FAM53C**	1.78	0.05	**DPH1 /// OV**	1.7	0.05
ISOC2	2.27	0.02	**IQWD1**	2.22	0.02	**JAM3**	1.78	0.05	**WDR42A**	1.7	0.03
HK1	2.26	0.02	**AGPAT5**	2.22	0.02	**LMNA**	1.78	0.04	**KLHDC2**	1.7	0.04
HLA-E	2.26	0.03	**IER5**	2.22	0.05	**LARS**	1.78	0.03	**MAPK8IP2**	1.7	0.03
SLC20A2	2.26	0.02	**LARS2**	2.22	0.04	**PFKP**	1.78	0.01	**PXMP2**	1.7	0.04
CCDC85B	2.26	0.01	**GALE**	2.21	0.02	**TUBA1A**	1.78	0.05	**PTK2B**	1.7	0.04
ATG4B	2.26	0.01	**PRKCD**	2.21	0.01	**ARL6IP5**	1.78	0.02	**RAP1GDS1**	1.7	0.03
SLC36A1	2.26	0.02	**RBM12**	2.21	0.03	**CTSB**	1.77	0.02	**EZR**	1.7	0.05
WDR6	2.26	0.03	**PPM1B**	2.21	0.03	**GPER**	1.77	0.04	**TOR1AIP1**	1.7	0.03
RBM35A	2.26	0.02	**RPL18A**	2.21	0.03	**MOSC2**	1.77	0.05	**GTF3A**	1.7	0.03
HS2ST1	2.25	0.02	**DPEP3**	2.21	0.04	**TINP1**	1.77	0.01	**MGC5618**	1.7	0.01
ALDH4A1	2.25	0.04	**COPS8**	2.2	0.04	**LDLR**	1.77	0.04	**IARS2**	1.7	0.05
VDR	2.25	0.01	**PEX11B**	2.2	0.03	**TTC33**	1.77	0.03	**ME2**	1.7	0.05
MAX	2.25	0.03	**EID1**	2.2	0.02	**SCMH1**	1.77	0.03	**NPDC1**	1.7	0.03
TAPBP	2.25	0.02	**NOL7**	2.2	0.01	**CSNK1A1**	1.76	0.02	**TXNRD3**	1.7	0.03
ILVBL	2.25	0.03	**HGF**	2.2	0.05	**CTNNA1**	1.76	0.01	**TULP4**	1.7	0.03
C1orf116	2.25	0.03	**CYB5A**	2.19	0.03	**PDLIM7**	1.76	0.04	**TNFSF12-T**	1.7	0.04
C20orf27	2.25	0.02	**HIGD1A**	2.19	0.04	**EPHB3**	1.76	0.01	**ZNF672**	1.7	0.05
ECE1	2.24	0.04	**SNAP25**	2.18	0.02	**SKP2**	1.76	0.01	**METRN**	1.7	0.03
PTPN21	2.24	0.04	**UTX**	2.18	0.05	**POLB**	1.76	0.01	**LIG3**	1.7	0.03
SYT17	2.24	0.04	**HTATIP2**	2.18	0.03	**SCAMP1**	1.76	0.02	**HMHA1**	1.7	0.04
ATP11A	2.24	0.03	**MCCC2**	2.18	0.03	**DDX3Y**	1.75	0.04	**NOVA1**	1.7	0.05
CAMLG	2.23	0.01	**DNAJC9**	2.18	0.05	**GRK6**	1.75	0.04	**UBE2Q1**	1.7	0.01
SCGB1D2	2.23	0.02	**CKAP2**	2.18	0.04	**HPCAL1**	1.75	0.03	**SEC24C**	1.7	0.03
PNRC1	2.23	0.02	**U2AF2**	2.18	0.05	**MXD4**	1.75	0.05	**VCX /// VCX**	1.7	0.05
HLA-G	2.23	0.04	**PPP1R9A**	2.18	0.01	**DNASE2**	1.74	0.01	**R3HDM2**	1.6	0.04
SEC31A	2.23	0.01	**ATF1**	2.18	0.03	**FNBP1**	1.74	0.02	**ECHDC3**	1.6	0.03
DLL3	2.23	0.04	**RFK**	2.17	0.04	**GDI2**	1.74	0.01	**ADCK2**	1.6	0.03
LEPRE1	2.23	0.04	**DENR**	2.17	0.04	**HPCAL1**	1.74	0.01	**MON2**	1.6	0.05
LPCAT1	2.22	0.02	**PPP1R12A**	2.16	0.05	**LRRFIP1**	1.74	0.05	**LBR**	1.6	0.04

SRPX	2.22	0.05
NAB1	2.22	0.05
UBE2I	2.22	0.01
CABIN1	2.22	0.01
IQGAP1	2.21	0.02
HSF1	2.21	0.03
ITGA6	2.21	0.03
PARP12	2.21	0.01
FLJ20035	2.21	0.02
STK11	2.21	0.04
CDH1	2.2	0.05
MAX	2.2	0.03
LPIN1	2.2	0.04
TMEM194	2.2	0.04
MYCL1	2.2	0.02
MYST3	2.2	0.03
GDI2	2.19	0.04
RERE	2.19	0.04
SMARCC1	2.19	0.05
BNIP3	2.19	0.04
NAGA	2.19	0.03
PTPN4	2.19	0.03
CTDSP2	2.19	0.02
IQGAP1	2.19	0.04
GGA2	2.19	0.04
CLIC4	2.19	0.03
RRBP1	2.18	0.02
IFI30	2.18	0.03
PABPN1	2.18	0.03
B4GALT1	2.18	0.04
IGSF3	2.18	0.03
C9orf16	2.18	0.04
HGS	2.18	0.02
EXTL3	2.18	0.03
MYO1B	2.18	0.02
MCF2L	2.18	0.04
APBB2	2.18	0.03
FH	2.16	0.01
CUL5	2.16	0.03
UCHL5	2.16	0.04
ATG5	2.15	0.02
DMXL1	2.15	0.05
DYNLT1	2.14	0.01
TXNL4A	2.14	0.03
NVL	2.14	0.02
C6orf62	2.14	0.04
RNF5	2.14	0.02
CETN3	2.14	0.01
RAB6B	2.14	0.03
HNRPH3	2.13	0.01
CACYBP	2.13	0.04
SLC47A1	2.13	0.04
DET1	2.13	0.05
FLJ22167	2.13	0.02
TLK1	2.12	0.01
WRB	2.12	0.02
LILRA6	2.12	0.03
ISCU	2.12	0.03
FEM1B	2.12	0.02
TRA	2.12	0.05
FLJ32679 //	2.11	0.04
GAL	2.11	0.05
KIF15	2.11	0.03
TMEM118	2.11	0.02
RFC2	2.1	0.03
DHX9	2.1	0.01
NELL2	2.1	0.03
UBA3	2.1	0.03
HERC6	2.1	0.04
CASP3	2.09	0.02
OXCT1	2.09	0.01
EMG1	2.09	0.03
PSEN2	2.09	0.03
WDTC1	2.09	0.04
SH3YL1	1.74	0.04
MCAM	1.74	0.04
NOV	1.74	0.03
RNASET2	1.74	0.05
RNASET2	1.74	0.05
ZFAND5	1.74	0.04
PDXK	1.73	0.05
TBC1D22A	1.73	0.02
MLLT3	1.73	0.05
SPTBN1	1.73	0.05
XRCC3	1.73	0.04
NT5C2	1.72	0.03
EXOC7	1.72	0.02
SCAMP1	1.72	0.01
EHD1	1.71	0.03
EXOSC4	1.71	0.02
CREB3L2	1.71	0.02
DCC1	1.71	0.04
CD24	1.71	0.01
PALLD	1.71	0.03
LMF1	1.7	0.02
SCPEP1	1.7	0.05
ST6GALNA	1.7	0.05
SNCB	1.7	0.03
UBE2B	1.7	0.04
CAMLG	1.69	0.04
CTBP2	1.69	0.03
DNASE2	1.69	0.05
RIBC2	1.69	0.04
GALNS	1.69	0.03
GLA	1.69	0.03
GLG1	1.69	0.03
LMNA	1.69	0.04
LRRFIP1	1.69	0.02
MEF2A	1.69	0.05
NCKAP1	1.69	0.01
NFATC1	1.69	0.04
MRPL9	1.6	0.03
PVRL3	1.6	0.03
PRKACB	1.6	0.04
PTPN18	1.6	0.04
RUVBL1	1.6	0.03
NENF	1.6	0.04
UMPS	1.6	0.02
AK2	1.6	0.04
SETD4	1.6	0.05
EID1	1.6	0.05
FAM63A	1.6	0.05
ICMT	1.6	0.03
MBD5	1.6	0.02
NEDD4L	1.6	0.05
PDHB	1.6	0.04
GBA /// GBA	1.6	0.05
DENND4B	1.6	0.05
ARNT	1.6	0.05
ATP6V1B2	1.6	0.02
CHD1L	1.6	0.03
C14orf94	1.6	0.04
ECHS1	1.6	0.03
DEPDC1	1.6	0.04
MRP63	1.6	0.04
MAPK8IP2	1.6	0.04
NRXN1	1.6	0.03
PARVB	1.6	0.05
JARID1B	1.6	0.04
SLC29A1	1.6	0.03
TRIM32	1.6	0.04
YLPM1	1.6	0.03
ADAR	1.6	0.02
MTX1	1.6	0.04
ASAH1	1.6	0.05
RAD51L3	1.6	0.05
RTN3	1.6	0.04
TXNRD1	1.6	0.05

BAMBI	2.17	0.01	**MRS2L**	2.09	0.02	**UBE2B**	1.69	0.02	**FDPS**	1.6	0.04
HS1BP3	2.17	0.04	**RBKS**	2.09	0.03	**ABAT**	1.68	0.05	**CHD8**	1.6	0.05
TEAD4	2.17	0.05	**TXNDC13**	2.08	0.02	**DAP**	1.68	0.04	**LRRC61**	1.6	0.04
CD99	2.16	0.03	**CDC7**	2.08	0.04	**DPYSL4**	1.68	0.03	**JAG2**	1.6	0.04
CLPTM1	2.16	0.05	**DOPEY1**	2.08	0.04	**FEM1C**	1.68	0.01	**SLC25A37**	1.6	0.05
GSTT1	2.16	0.01	**GTF3A**	2.05	0.02	**LDHA**	1.68	0.03	**APEH**	1.6	0.05
HK2	2.15	0.01	**TIMP1**	2.05	0.01	**LOH11CR2A**	1.68	0.04	**NAPA**	1.6	0.02
CSNK1A1	2.15	0.02	**MUT**	2.05	0.04	**RBPMS**	1.68	0.02	**NUP133**	1.6	0.02
MRPL35	2.15	0.04	**PLA2G6**	2.05	0.03	**CALM1**	1.67	0.01	**BSCL2 /// H**	1.6	0.03
AKR1A1	2.14	0.01	**PRB1 /// PR**	2.05	0.04	**CSNK1A1**	1.67	0.05	**COX4I1**	1.6	0.05
DDX11	2.14	0.01	**ZNF160**	2.05	0.02	**SHFM1**	1.67	0.05	**RSAD1**	1.6	0.04
REEP5	2.14	0.04	**APPL1**	2.05	0.03	**DYRK3**	1.67	0.02	**RMI1**	1.6	0.04
NCOA1	2.14	0.02	**NCAPG**	2.05	0.03	**EEF1D /// EE**	1.67	0.02	**FCHO1**	1.6	0.04
XRCC3	2.14	0.02	**C17orf42**	2.05	0.02	**KIAA0247**	1.67	0.05	**PNPLA6**	1.6	0.05
IGHM	2.14	0.05	**ACTR3**	2.04	0.03	**PERP**	1.67	0.04	**PATZ1**	1.6	0.04
PTPRF	2.13	0.03	**TIA1**	2.04	0.02	**PSMA6**	1.67	0.02	**POMP**	1.6	0.02
PSAP	2.13	0.03	**PRPS2**	2.04	0.05	**SLC1A4**	1.67	0.03	**MPZL1**	1.6	0.03
CHP	2.13	0.05	**CDKN2C**	2.04	0.04	**LRP12**	1.67	0.04	**KIAA0100**	1.6	0.05
TXNDC1	2.13	0.04	**PMAIP1**	2.04	0.02	**VAMP3**	1.67	0.05	**LARP5**	1.6	0.02
8-Sep	2.13	0.03	**BLVRA**	2.04	0.01	**AKR1A1**	1.66	0.01	**PI4KB**	1.6	0.03
EHD1	2.13	0.02	**FOLH1**	2.04	0.03	**BAK1**	1.66	0.02	**AIFM1**	1.6	0.04
DCTN5	2.13	0.05	**NFYB**	2.04	0.04	**ENO1**	1.66	0.02	**PPP1R14B**	1.6	0.03
SLC1A4	2.13	0.04	**CHMP2A**	2.03	0.02	**RAB15**	1.66	0.01	**REPIN1**	1.6	0.04
FOXO3	2.13	0.03	**CEP57**	2.03	0.05	**JARID2**	1.66	0.02	**RBM8A**	1.6	0.04
LARGE	2.13	0.04	**C1orf25**	2.03	0.04	**PGD**	1.66	0.02	**NEK7**	1.6	0.05
FNDC4	2.13	0.02	**C5orf30**	2.03	0.05	**RB1CC1**	1.66	0.02	**OCRL**	1.6	0.03
ITM2C	2.13	0.05	**NPEPPS**	2.02	0.01	**AHCYL1**	1.66	0.03	**PAXIP1**	1.6	0.04
SLC6A8	2.12	0.02	**SACM1L**	2.02	0.05	**SH3BGRL3**	1.66	0.04	**THOC2**	1.6	0.03
LAD1	2.12	0.02	**SLK**	2.02	0.05	**SDCBP**	1.66	0.03	**WBSCR16**	1.6	0.03
DBI	2.12	0.04	**MTUS1**	2.02	0.04	**ZFP36L2**	1.66	0.01	**ATP6AP2**	1.6	0.05
MXRA7	2.12	0.03	**NDUFA7**	2.01	0.02	**AGPAT2**	1.65	0.05	**PTPN18**	1.6	0.05
KIAA0495	2.12	0.02	**BCAT2**	2.01	0.01	**DNPEP**	1.65	0.01	**RAD23A**	1.6	0.05
FXYD3	2.11	0.01	**ZBTB20**	2.01	0.04	**CALU**	1.65	0.05	**ARIH2**	1.5	0.04
TFAP2C	2.11	0.04	**NENF**	2.01	0.03	**DNAJB9**	1.65	0.04	**C6orf35**	1.5	0.04
ALDH7A1	2.11	0.03	**NAT13**	2.01	0.05	**HES1**	1.65	0.04	**DDX27**	1.5	0.04
ILF3	2.11	0.03	**AGK**	2.01	0.03	**ITPR3**	1.65	0.03	**H2AFZ**	1.5	0.03
SMYD2	2.11	0.04	**CDC73**	2.01	0.03	**INSIG1**	1.65	0.02	**GOLPH3L**	1.5	0.05

PPP1R15A	2.11	0.02
PIK3R3	2.1	0.01
FGFR2	2.1	0.03
CFD	2.1	0.01
P4HA1	2.1	0.02
APLP2	2.1	0.05
SSBP2	2.1	0.03
CTNNA1	2.1	0.05
YIPF1	2.1	0.04
NPLOC4	2.1	0.01
CSK	2.09	0.03
HSPA4	2.09	0.04
UCP2	2.09	0.02
TYRO3	2.09	0.02
MINK1	2.09	0.02
MTMR12	2.09	0.04
TBL1X	2.08	0.02
UNC119	2.08	0.02
MBNL2	2.08	0.03
BCKDHB	2.08	0.05
AHNAK	2.08	0.02
TSC22D1	2.08	0.02
PRRC1	2.08	0.03
CYR61	2.07	0.03
PHGDH	2.07	0.01
JUNB	2.07	0.04
F12	2.07	0.03
GRK6	2.07	0.01
TSC2	2.07	0.05
FAM53C	2.07	0.01
TSPAN12	2.07	0.03
C19orf22	2.07	0.04
NBL1	2.06	0.04
ARFGEF1	2.06	0.05
PTRF	2.06	0.03
LASS6	2.06	0.01
BOP1	2.06	0.04
ABCA11	2.01	0.03
MRPL20	2.01	0.02
H3F3A	2	0.02
SLC30A9	2	0.05
TMEM28	2	0.03
KIAA0368	2	0.03
CDC2L6	2	0.02
MSTP9	2	0.03
TNFRSF21	2	0.02
ZNF14	2	0.02
PDE4C	1.99	0.02
PDE6B	1.99	0.04
POMP	1.99	0.03
ARIH1	1.98	0.03
ZNF268	1.98	0.03
SIAH1	1.97	0.02
C3orf60	1.97	0.01
KLHL9	1.97	0.03
SERHL2	1.97	0.01
C15orf24	1.97	0.02
WDR61	1.97	0.05
GUCY1A3	1.97	0.05
MPO	1.96	0.04
UBR5	1.96	0.03
HSD17B8	1.96	0.04
MLH3	1.96	0.03
ZNF586	1.96	0.04
ETFDH	1.96	0.03
LASP1	1.95	0.04
CHUK	1.95	0.05
HTATIP2	1.95	0.04
RALGPS1	1.95	0.05
NF1	1.95	0.05
HES1	1.94	0.04
FAM136A	1.94	0.04
CECR5	1.94	0.04
ATG3	1.94	0.02
IFNGR1	1.65	0.05
ISG20	1.65	0.03
LANCL2	1.65	0.05
MACF1	1.65	0.02
RAD1	1.65	0.03
TSPAN4	1.65	0.02
AMH	1.64	0.04
TPP1	1.64	0.04
GGCX	1.64	0.03
MPST	1.64	0.02
GNPTAB	1.64	0.02
RASA1	1.64	0.03
ACCN2	1.63	0.05
DST	1.63	0.05
CSNK1A1	1.63	0.01
CD164	1.63	0.01
CD9	1.63	0.03
MNX1	1.63	0.05
EIF2C2	1.63	0.04
MEIS2	1.63	0.05
CALM1	1.62	0.02
GDI2	1.62	0.02
CTDSPL	1.62	0.01
TMEM97	1.62	0.03
PCDHA1	1.62	0.04
SAR1A	1.62	0.01
TEAD4	1.62	0.02
TNFRSF10B	1.62	0.03
WEE1	1.62	0.05
COPS5	1.61	0.04
GM2A	1.61	0.04
CCDC99	1.61	0.03
KLHL21	1.61	0.02
PFDN1	1.61	0.04
PTPLA	1.61	0.05
C11orf67	1.61	0.05
THEM2	1.61	0.03
ZNF586	1.5	0.05
JAG2	1.5	0.02
TMEM24	1.5	0.03
MYO5C	1.5	0.05
RRM2	1.5	0.02
POLR3E	1.5	0.03
SEC11A	1.5	0.05
CCNH	1.5	0.04
SCYL3	1.5	0.04
KLHL22	1.5	0.02
C9orf95	1.5	0.05
MPDU1	1.5	0.05
PSME3	1.5	0.05
VRK3	1.5	0.05
KCTD14	1.5	0.04
IMPDH2	1.5	0.02
INPP1	1.5	0.05
PTN	1.5	0.04
PRSS23	1.5	0.04
PSME3	1.5	0.02
RABAC1	1.5	0.05
ASF1A	1.5	0.04
PTPLAD1	1.5	0.03
CKS1B	1.5	0.04
E4F1	1.5	0.05
GTF3C4	1.5	0.04
GYG1	1.5	0.05
CXorf40A //	1.5	0.05
KIAA0101	1.5	0.04
SERHL	1.5	0.02
BCAT2	1.5	0.04
CKMT1A ///	1.5	0.03
ARPP-19	1.5	0.05
ISG20L2	1.5	0.04
NEK3	1.5	0.05
PSMB4	1.5	0.02
PRC1	1.5	0.04

PITPNC1	2.06	0.03
SLC2A6	2.06	0.05
RIPK4	2.06	0.03
MGAT2	2.05	0.02
GGCX	2.05	0.03
ABAT	2.05	0.02
ACLY	2.05	0.04
NFIB	2.05	0.05
DDAH2	2.05	0.05
MOSC2	2.05	0.02
ACTR1A	2.04	0.02
CHST3	2.04	0.02
CSNK1A1	2.04	0.05
HES2	2.04	0.04
WWC2	2.04	0.02
RAB15	2.04	0.01
DHCR7	2.03	0.03
FEM1C	2.03	0.05
COBLL1	2.03	0.05
TLE2	2.02	0.02
VDAC3	2.02	0.04
AFF4	2.02	0.04
SEMA4C	2.02	0.03
PKM2	2.01	0.05
AIM1	2.01	0.05
APBA3	2.01	0.04
GSTK1	2.01	0.04
HSPC159	2.01	0.03
C9orf16	2.01	0.02
MPST	2	0.01
SAR1A	2	0.04
MCAM	2	0.02
KIR2DS1	2	0.02
ATP13A3	2	0.03
SLC9A3R1	1.99	0.04
DBI	1.99	0.04
TRIM26	1.99	0.02
HSPA5	1.93	0.02
CAMSAP1	1.93	0.03
LOC727942	1.93	0.02
IL15	1.93	0.04
DUS1L	1.93	0.02
NENF	1.93	0.05
PSMG1	1.92	0.03
NUCB2	1.92	0.03
KPNA2	1.92	0.05
Gcom1 /// G	1.92	0.02
GADD45GI	1.92	0.04
FBXL14	1.92	0.05
FBXO5	1.92	0.05
RUVBL1	1.91	0.01
SLC25A13	1.91	0.03
KIF11	1.91	0.03
RAD1	1.91	0.03
JMJD6	1.91	0.03
KIAA0564	1.91	0.01
C1orf107	1.91	0.02
FAM149A	1.91	0.05
CRYL1	1.91	0.03
EIF5B	1.9	0.05
PSMA2	1.9	0.04
FBXO28	1.9	0.05
BLVRA	1.9	0.02
NEB	1.9	0.04
NRG2	1.9	0.02
SMC3	1.89	0.03
C21orf45	1.89	0.04
MAK10	1.89	0.03
TMEM118	1.89	0.02
NDC80	1.88	0.03
POT1	1.88	0.03
FEN1	1.88	0.03
TLOC1	1.88	0.03
LSM14A	1.88	0.02
AGPAT2	1.6	0.04
HMGCR	1.6	0.03
ATF3	1.6	0.01
ERGIC2	1.6	0.03
TBC1D9B	1.6	0.04
TAF7	1.6	0.05
TARS	1.6	0.04
SLC35D1	1.6	0.05
YPEL5	1.6	0.04
FKBP9	1.59	0.02
HS2ST1	1.59	0.05
FAM102A	1.59	0.05
NOSIP	1.59	0.03
PIK3C2B	1.59	0.05
MAFF	1.59	0.04
ADH5	1.58	0.03
CANX	1.58	0.01
GTF2IRD1	1.58	0.02
REEP5	1.58	0.02
MLXIP	1.58	0.05
NFYC	1.58	0.02
NPM1	1.58	0.02
OAZ2	1.58	0.02
SLC7A5	1.58	0.02
SKP2	1.58	0.04
TUBB6	1.58	0.01
LMAN2	1.57	0.04
MCAM	1.57	0.01
ILVBL	1.57	0.05
RAB26	1.57	0.02
RGS14	1.57	0.03
CALML4	1.57	0.03
CHST3	1.56	0.03
GMDS	1.56	0.04
NFYC	1.56	0.01
SIRPA	1.56	0.05
RCN3	1.56	0.04
JARID1B	1.5	0.04
RBM3	1.5	0.05
SEC11A	1.5	0.04
SRM	1.5	0.03
TAF6	1.5	0.04
ASPA	1.5	0.04
SLC37A4	1.5	0.05
MST1R	1.5	0.04
PTGIS	1.5	0.03
NENF	1.5	0.05
CACYBP	1.5	0.02
AP2A2	1.5	0.05
C20orf67	1.5	0.03
C21orf33	1.5	0.03
FADS1	1.5	0.04
H2AFZ	1.5	0.05
BAT3	1.5	0.04
FLJ22167	1.5	0.05
RDH11	1.5	0.04
TERF2IP	1.5	0.05
PATZ1	1.5	0.05
ATP1A1	1.5	0.02
GAL3ST1	1.5	0.04
PIGV	1.5	0.02
TXNDC13	1.5	0.05
CLCC1	1.5	0.05
RFNG	1.5	0.05
GNPAT	1.5	0.05
COMMD4	1.5	0.05
C7orf26	1.5	0.02
KEAP1	1.5	0.05
MMP24	1.5	0.05
PITPNA	1.5	0.05
POLR3K	1.5	0.03
C6orf108	1.5	0.02
WDR61	1.5	0.04
SCAP	1.5	0.05

BRD2	1.99	0.02
ERBB2	1.99	0.03
CDKN1C	1.99	0.04
C14orf1	1.99	0.04
TMBIM1	1.99	0.05
FLJ13236	1.99	0.02
FGF12	1.98	0.05
GLT25D1	1.98	0.03
DERL1	1.98	0.05
EXOSC4	1.98	0.03
DNPEP	1.97	0.02
GTF2F1	1.97	0.02
GPC1	1.97	0.01
TBC1D9B	1.97	0.01
DYRK3	1.97	0.02
FKBP9	1.97	0.02
C14orf32	1.97	0.04
DDX3X	1.97	0.03
CD9	1.96	0.02
TRAM1	1.96	0.02
FAM53B	1.96	0.03
NCK2	1.96	0.01
NUDT4 /// N	1.96	0.04
GM2A	1.96	0.03
CNOT8	1.95	0.03
CABIN1	1.95	0.01
SLC11A2	1.95	0.04
RCC1 /// SN	1.95	0.02
PXN	1.95	0.04
GRINA	1.95	0.02
BOP1 /// LO	1.95	0.04
TMEM132A	1.95	0.04
CDKN1C	1.95	0.03
PRNP	1.94	0.05
PRCP	1.94	0.03
NAGA	1.94	0.04
PI4K2A	1.94	0.04
ZNF26	1.88	0.05
STXBP6	1.88	0.05
BRP44	1.87	0.03
SNRPG	1.87	0.03
TOP2B	1.87	0.05
JMJD6	1.87	0.04
DICER1	1.87	0.04
LOC727942	1.87	0.04
MORC4	1.87	0.04
CHPT1	1.87	0.05
LOC389517	1.87	0.05
CDC20	1.86	0.03
SNAPC3	1.86	0.01
STAU2	1.86	0.04
FBXL5	1.86	0.02
AK2	1.86	0.04
TOR3A	1.86	0.05
SLC4A1AP	1.86	0.05
BOLA1	1.86	0.02
PLA2G2F	1.86	0.02
WASF3	1.85	0.04
FAM115A	1.85	0.05
H2AFX	1.85	0.03
PRKD1	1.85	0.04
ZNF673	1.85	0.04
STX12	1.85	0.03
SUCLG2	1.85	0.03
MED4	1.85	0.04
DARS2	1.85	0.03
ADAT1	1.85	0.04
GDF15	1.85	0.02
VBP1	1.84	0.02
SSX2IP	1.84	0.04
C5	1.84	0.04
MRPL3	1.84	0.03
ITPA	1.84	0.04
ANXA7	1.84	0.04
DDEFL1	1.56	0.05
VAMP3	1.56	0.05
CLTB	1.55	0.05
DGKZ	1.55	0.02
METTL7A	1.55	0.05
TMEM97	1.55	0.03
MAX	1.55	0.05
MRPS30	1.55	0.04
PYGB	1.55	0.04
RABGAP1	1.55	0.04
ABR	1.54	0.02
EIF3E	1.54	0.02
UBXD8	1.54	0.03
KIAA0746	1.54	0.03
LYPLA2	1.54	0.03
NPC2	1.54	0.04
POLE3	1.54	0.03
ATP5SL	1.53	0.02
LASS4	1.53	0.05
GINS4	1.53	0.04
CEP68	1.53	0.05
NDUFA8	1.53	0.04
OSTF1	1.53	0.05
SARS	1.53	0.01
SLC4A3	1.53	0.04
SATB1	1.53	0.05
SDC3	1.53	0.04
TCF3	1.53	0.03
VAMP3	1.53	0.03
ATP6V0E1	1.52	0.03
CDC23	1.52	0.04
C9orf16	1.52	0.05
IL6ST	1.52	0.03
RIOK2	1.52	0.04
GOLSYN	1.52	0.04
LDLR	1.52	0.02
SLC25A32	1.52	0.03
TOP2A	1.5	0.03
XYLB	1.5	0.03
HECTD3	1.5	0.01
EHBP1	1.5	0.05
HLA-DRB4	1.5	0.05
NGFRAP1	1.5	0.04
OSBP	1.5	0.04
PCBP1	1.5	0.02
PLOD3	1.5	0.05
VPS72	1.5	0.04
GTPBP3	1.5	0.01

SLC6A8	1.94	0.02	**C1orf34**	1.84	0.03	**MLLT3**	1.52	0.05
TAGLN2	1.94	0.03	**YLPM1**	1.84	0.05	**RALBP1**	1.52	0.03
GALNS	1.93	0.05	**DNAJC16**	1.84	0.03	**SRD5A1**	1.52	0.02
NKX2-5	1.93	0.04	**SP3**	1.84	0.05	**CTSH**	1.51	0.04
VAMP3	1.93	0.03	**PDE4DIP**	1.84	0.04	**CIDEB**	1.51	0.05
BUB1	1.93	0.05	**OR7E37P**	1.84	0.02	**CDC25C**	1.51	0.05
HNRNPU	1.93	0.03	**WDR5B**	1.84	0.03	**DDB2**	1.51	0.05
C16orf57	1.93	0.01	**ZNF764**	1.84	0.03	**EXOSC4**	1.51	0.01
ANKRD5	1.93	0.05	**EPRS**	1.83	0.05	**GSTA3**	1.51	0.03
ARVCF	1.92	0.05	**SFRS10**	1.83	0.03	**KIAA0323**	1.51	0.03
NR5A2	1.92	0.05	**BNIP1**	1.83	0.04	**MTA1**	1.51	0.03
CANX	1.92	0.01	**PRUNE**	1.83	0.05	**MTA1**	1.51	0.04
TRIM27	1.92	0.04	**C9orf95**	1.83	0.04	**RAB9A**	1.51	0.04
CDK7	1.92	0.04	**RAD23A**	1.82	0.02	**TPBG**	1.51	0.04
ZNF289	1.92	0.03	**ICMT**	1.82	0.03	**CAMK2G**	1.5	0.04
TBC1D9B	1.92	0.03	**CRELD2**	1.82	0.03	**C20orf111**	1.5	0.03
OTUB1	1.91	0.03	**SLC25A15**	1.82	0.05	**DKFZp547E**	1.5	0.05
TBL1X	1.91	0.02	**SCML1**	1.82	0.03	**LCP1**	1.5	0.04
CCT2	1.91	0.04	**IGF2BP2**	1.82	0.04	**PDCD4**	1.5	0.03
FKBP1A	1.91	0.03	**BBS10**	1.82	0.03	**PPP1R13B**	1.5	0.04
DBI	1.91	0.04	**RPS25**	1.81	0.05	**C11orf67**	1.5	0.04
AHNAK	1.91	0.03	**CNIH**	1.81	0.04	**SERPINH1**	1.5	0.05
CPD	1.9	0.04	**CNOT8**	1.81	0.05	**SSX2 /// SS**	1.5	0.02
SLC16A1	1.9	0.03	**RFC2**	1.81	0.04	**TPD52**	1.5	0.03
DDX19A	1.9	0.03	**SNAP91**	1.81	0.04	**ANXA4**	1.49	0.05
NFRKB	1.9	0.03	**PARP1**	1.81	0.01	**BTG2**	1.49	0.03
SORBS3	1.9	0.04	**PTS**	1.81	0.05	**DSTN**	1.49	0.03
NONO	1.9	0.02	**NPY6R**	1.81	0.02	**EPS8L2**	1.49	0.01
SLC6A8	1.9	0.03	**SSX2IP**	1.81	0.02	**GPSN2**	1.49	0.03
CSNK1A1	1.9	0.04	**MINA**	1.81	0.03	**GLT25D1**	1.49	0.02
HARS	1.89	0.02	**TLL2**	1.81	0.04	**RARG**	1.49	0.04
PYCR1	1.89	0.05	**GOLGA5**	1.81	0.05	**SMTN**	1.49	0.03
ZER1	1.89	0.02	**ARID1A**	1.81	0.05	**TRAM1**	1.49	0.04
NPC1	1.89	0.02	**TIPIN**	1.81	0.02	**BLVRB**	1.48	0.05
IL6ST	1.89	0.05	**PRPF18**	1.81	0.04	**CABIN1**	1.48	0.02
AP1B1	1.89	0.05	**FLJ32679 ///**	1.81	0.05	**PDCD4**	1.48	0.05
TBC1D22A	1.89	0.02	**TMEM147**	1.8	0.02	**SLC7A1**	1.48	0.02

PELI2	1.89	0.04	**NTRK2**	1.8	0.05	**MAN1A2**	1.48	0.05
LRP12	1.89	0.05	**NEU1**	1.8	0.03	**TBC1D9B**	1.48	0.04
EHD1	1.89	0.02	**ATP5I**	1.8	0.04	**MAT2A**	1.48	0.02
NUCB1	1.88	0.05	**CLCC1**	1.8	0.03	**PABPC3**	1.48	0.03
PGD	1.88	0.05	**RABL3**	1.8	0.05	**SNCAIP**	1.48	0.04
BTG2	1.88	0.03	**C17orf90**	1.8	0.04	**BCL10**	1.47	0.04
SPTLC2	1.88	0.02	**TOR1AIP1**	1.79	0.03	**DNAJB4**	1.47	0.04
GIT1	1.88	0.02	**VPS52**	1.79	0.05	**EHD4**	1.47	0.04
EDC3	1.88	0.04	**PMS2L2**	1.79	0.04	**LOC653562**	1.47	0.04
APOL3	1.88	0.05	**ATPBD1C**	1.79	0.04	**ETV5**	1.47	0.04
PGRMC1	1.87	0.03	**TSPAN13**	1.78	0.04	**HR**	1.47	0.05
CHD4	1.87	0.04	**COPS4**	1.78	0.04	**TMEM57**	1.47	0.05
ITPR3	1.87	0.05	**MRTO4**	1.78	0.05	**PABPN1**	1.47	0.01
GRSF1	1.87	0.05	**LSG1**	1.78	0.03	**PPP1R15A**	1.47	0.03
FOXK2	1.87	0.04	**DDX27**	1.78	0.05	**OVOL2**	1.47	0.05
LMNA	1.87	0.05	**CKS1B**	1.77	0.02	**ATP6V1C1**	1.46	0.04
GGH	1.87	0.02	**NFYA**	1.77	0.04	**CNOT8**	1.46	0.04
CSNK2A1	1.87	0.04	**SNX4**	1.77	0.03	**CD24**	1.46	0.04
STIP1	1.87	0.03	**DLX2**	1.77	0.03	**HABP4**	1.46	0.04
ERGIC3	1.87	0.03	**CSNK1D**	1.77	0.04	**MAP4K1**	1.46	0.04
APBB2	1.87	0.04	**TMCO1**	1.77	0.02	**PPP2CA**	1.46	0.05
LDLRAP1	1.87	0.03	**WWC1**	1.77	0.03	**CALU**	1.45	0.02
DNM2	1.86	0.03	**PHF11**	1.77	0.03	**MAMLD1**	1.45	0.05
TOMM40	1.86	0.05	**SUOX**	1.76	0.04	**ENO1**	1.45	0.04
RNF44	1.86	0.02	**TTC3**	1.76	0.04	**PABPC1**	1.45	0.04
GTF2H4	1.86	0.02	**JARID1B**	1.76	0.04	**F11R**	1.45	0.03
IFT140	1.86	0.02	**YIPF6**	1.76	0.04	**FOXJ3**	1.45	0.03
IFITM3	1.86	0.03	**MKL1**	1.76	0.04	**FAM62A**	1.45	0.02
HOXA9	1.86	0.05	**GALNT11**	1.76	0.03	**NMT1**	1.45	0.03
SLC6A10P /	1.86	0.04	**PIGZ**	1.76	0.04	**PTTG1**	1.45	0.03
RETSAT	1.86	0.04	**G3BP1**	1.76	0.04	**HIST3H2A**	1.45	0.05
SMEK1	1.86	0.05	**FBP2**	1.75	0.03			
ANKRD13D	1.86	0.04	**PIGK**	1.75	0.03			
RAN	1.85	0.05	**NR4A3**	1.75	0.05			
NCAPD2	1.85	0.04	**YTHDF2**	1.75	0.04			
NFIL3	1.85	0.03	**CHMP4A**	1.75	0.03			
IPO8	1.85	0.04	**TMEM70**	1.75	0.02			

TLE3	1.85	0.05	**CBWD1 /// C**	1.75	0.03
MFGE8	1.85	0.03	**LEF1**	1.75	0.05
PTBP1	1.85	0.04	**WSB2**	1.74	0.03
CCNE2	1.85	0.04	**TMCO1**	1.74	0.04
TMEM97	1.85	0.04	**PTGDS**	1.74	0.05
ZNF282	1.85	0.05	**RAB22A**	1.74	0.03
RAP2A /// R	1.85	0.05	**RECK**	1.74	0.02
VPS24	1.85	0.02	**EPS15**	1.74	0.02
SIDT2	1.85	0.03	**MFSD1**	1.74	0.03
AHCYL1	1.84	0.05	**MKKS**	1.74	0.04
GAA	1.84	0.04	**FLJ22167**	1.74	0.05
CC2D1A	1.84	0.05	**FIP1L1**	1.74	0.04
RHOBTB2	1.84	0.04	**LAMC1**	1.73	0.03
B3GNT2	1.84	0.04	**FH**	1.73	0.04
FANCE	1.84	0.05	**PFN2**	1.73	0.03
FAM89B	1.84	0.03	**SPA17**	1.73	0.04
B3GAT3	1.84	0.05	**CYP3A4**	1.73	0.05
LDHA	1.83	0.03	**XPNPEP1**	1.73	0.03
AAMP	1.83	0.04	**APPL2**	1.73	0.02
IL13RA1	1.83	0.01	**HSP90B1**	1.72	0.01
C9orf7	1.83	0.05	**AK1**	1.72	0.03
KDELR1	1.82	0.02	**HNRPDL**	1.72	0.05
ACLY	1.82	0.04	**SR140**	1.72	0.03
PACSIN2	1.82	0.01	**NBN**	1.72	0.05
AP3B1	1.82	0.04	**FASTKD3**	1.72	0.04
RBMS1	1.82	0.03	**SNRPE**	1.71	0.01
RCAN1	1.82	0.04	**ALAS1**	1.71	0.03
NAB1	1.82	0.02	**CLCC1**	1.71	0.05
SCAMP1	1.82	0.05	**CLDND1**	1.71	0.03
RHEB	1.82	0.02	**ARPP-21**	1.71	0.04
EZR	1.82	0.05	**UMPS**	1.7	0.05
STEAP3	1.82	0.03	**MSH6**	1.7	0.04
SPSB3	1.82	0.03	**CROT**	1.7	0.03
GCAT	1.82	0.05	**NR2C1**	1.7	0.02
WARS	1.81	0.04	**GALK2**	1.7	0.05
DDAH2	1.81	0.04	**UTF1**	1.7	0.01
RTN2	1.81	0.02	**ZNF614**	1.7	0.03

SLC1A1	1.81	0.03	**C14orf124**	1.7	0.05
SLC6A3	1.81	0.05	**ANAPC5**	1.69	0.03
FSTL1	1.81	0.04	**MTX1**	1.69	0.04
NRXN2	1.81	0.03	**TYMS**	1.69	0.04
CUL4B	1.81	0.03	**LOC222070**	1.69	0.03
RTN4	1.81	0.04	**PSMD4**	1.68	0.05
AP2S1	1.81	0.05	**NFX1**	1.68	0.05
MAP4	1.81	0.03	**IDE**	1.68	0.03
AES	1.81	0.04	**U1SNRNPB**	1.68	0.02
ILF3	1.81	0.04	**DAP3**	1.68	0.03
PDXK	1.81	0.04	**MAN2B1**	1.68	0.05
MRPS30	1.81	0.03	**USP24**	1.68	0.05
KIAA0194	1.81	0.04	**TPSAB1**	1.68	0.05
MGST3	1.8	0.03	**FIS1**	1.68	0.05
HPN	1.8	0.03	**CCDC90B**	1.68	0.04
BIN1	1.8	0.05	**LRRC1**	1.68	0.02
CLIP2	1.8	0.02	**FAM91A2**	1.68	0.04
ALDH4A1	1.8	0.03	**ARHGAP19**	1.68	0.05
ANKMY2	1.8	0.02	**HADH**	1.67	0.03
PIAS2	1.8	0.05	**CSE1L**	1.67	0.03
GOLSYN	1.8	0.04	**ATP5J2**	1.67	0.04
NPM1	1.8	0.02	**CCNT2**	1.67	0.04
CTSB	1.79	0.03	**RNASE2**	1.67	0.04
TACC1	1.79	0.04	**TGDS**	1.67	0.03
DDX3X	1.79	0.04	**ESD**	1.67	0.05
PSCD1	1.79	0.05	**PEG10**	1.67	0.05
KDELR3	1.79	0.02	**NIPA2**	1.67	0.05
MVK	1.79	0.05	**GOLGA4**	1.67	0.05
GANAB	1.79	0.05	**NF2**	1.67	0.03
SLC1A4	1.79	0.03	**RAP1GDS1**	1.67	0.05
DDX11 /// D	1.79	0.05	**LOC283871**	1.67	0.05
LOC89944	1.79	0.01	**IL17RB**	1.67	0.05
RNF130	1.79	0.02	**FLJ12986 ///**	1.67	0.02
RNASET2	1.79	0.04	**CUGBP1**	1.67	0.04
PTPLA	1.79	0.04	**PSME1**	1.66	0.03
SLC3A2	1.78	0.03	**LAMP2**	1.66	0.02
CIB1	1.78	0.01	**CUL4B**	1.66	0.03

SEC14L1	1.78	0.02	**KIFAP3**	1.66	0.01
SCAMP1	1.78	0.04	**TMPO**	1.66	0.04
DGCR6	1.78	0.03	**ADCYAP1**	1.66	0.04
AGPAT2	1.78	0.04	**LOC400506**	1.66	0.04
SAP30L	1.78	0.05	**DDX27**	1.66	0.02
TMEM189-U	1.77	0.03	**LPHN1**	1.66	0.04
EIF5B	1.77	0.05	**CALM3**	1.65	0.02
CTDSPL	1.77	0.03	**FDPS**	1.65	0.03
CLTB	1.77	0.04	**CSTF1**	1.65	0.04
RRAS	1.77	0.04	**MGAT2**	1.65	0.05
JAM3	1.77	0.04	**CDC16**	1.65	0.05
ACOT7	1.77	0.05	**C14orf109**	1.65	0.04
LOC730092	1.77	0.04	**SEC31A**	1.65	0.03
JHDM1D	1.77	0.05	**UBE2Q1**	1.65	0.03
NPM1	1.77	0.03	**RWDD2B**	1.65	0.02
MCM4	1.77	0.02	**USP16**	1.65	0.03
UBE2D2	1.76	0.04	**TOMM70A**	1.64	0.03
IFNGR1	1.76	0.05	**SV2A**	1.64	0.04
PTEN	1.76	0.03	**STBD1**	1.64	0.04
SLC17A7	1.76	0.05	**CCNH**	1.64	0.03
DNASE2	1.76	0.03	**CAMKK2**	1.64	0.03
PACSIN3	1.76	0.02	**LOC92482**	1.64	0.05
EIF4EBP1	1.76	0.01	**TDRD7**	1.64	0.04
CPSF1	1.75	0.04	**DERL2**	1.64	0.05
PLTP	1.75	0.05	**C2orf28**	1.64	0.04
SHROOM2	1.75	0.05	**TMEM80**	1.64	0.05
AHDC1	1.75	0.04	**NRG1**	1.63	0.05
AMH	1.75	0.05	**PARP2**	1.63	0.05
DBP	1.75	0.05	**HTR1F**	1.63	0.02
BTN3A2	1.75	0.03	**ZNF142**	1.63	0.04
ZNF706	1.75	0.03	**KEAP1**	1.62	0.02
MICALL2	1.75	0.04	**LARP5**	1.62	0.02
RIC8B	1.75	0.03	**CYP2B6**	1.62	0.02
ARL6IP5	1.74	0.05	**C7orf49**	1.62	0.05
CTNNA1	1.74	0.02	**TMED2**	1.61	0.02
MCM5	1.74	0.05	**ECHS1**	1.61	0.04
LEPROTL1	1.74	0.04	**CAPZA2**	1.61	0.04

FANCA	1.74	0.05
PDIA5	1.74	0.03
MEGF9	1.74	0.05
NUDT2	1.74	0.04
SDK2	1.74	0.05
FBXO38	1.74	0.05
ATP6V1H	1.74	0.02
RAB15	1.74	0.05
PXN	1.73	0.04
MAP2K4	1.73	0.03
CDK2	1.73	0.05
SH3GLB1	1.73	0.04
SSX3	1.73	0.01
TMEM97	1.73	0.02
TTLL12	1.73	0.04
LPPR2	1.73	0.03
FAM108B1	1.73	0.05
SDC3	1.72	0.05
HBEGF	1.72	0.05
MAN1B1	1.72	0.05
TPP1	1.71	0.03
CKB	1.71	0.03
BIRC2	1.71	0.03
IMPA2	1.71	0.04
APC	1.71	0.05
COL6A1	1.71	0.02
LOC552889	1.71	0.04
KIAA0323	1.71	0.03
CAP1	1.71	0.04
RTN4	1.71	0.04
DR1	1.71	0.03
SFXN3	1.71	0.03
ATP5SL	1.71	0.04
TELO2	1.71	0.04
CYHR1	1.7	0.05
KCMF1	1.7	0.04
WDR55	1.7	0.05
COG2	1.61	0.05
CUL2	1.61	0.02
MYBPC2	1.61	0.04
LSM8	1.61	0.02
ACP1	1.6	0.03
AGL	1.6	0.03
ERCC1	1.6	0.05
FGFBP1	1.6	0.04
AVPR2	1.6	0.04
EI24	1.6	0.03
RRM2	1.6	0.02
PIGL	1.6	0.04
TMF1	1.6	0.04
GLT8D1	1.6	0.05
BCL11A	1.6	0.05
NME7	1.6	0.04
IMPDH2	1.59	0.05
DPAGT1	1.59	0.03
MSL-1	1.59	0.05
ARGLU1	1.59	0.05
APEH	1.58	0.04
PMF1	1.58	0.04
GOLGA1	1.58	0.02
FAM98A	1.58	0.03
YLPM1	1.58	0.05
HRB	1.58	0.05
REPIN1	1.58	0.04
PCID2	1.58	0.02
RPS27A	1.57	0.05
OPRS1	1.57	0.02
PSMB4	1.57	0.04
TIMM8A	1.57	0.04
MED8	1.57	0.04
ARPC2	1.57	0.05
MARS	1.57	0.05
HIST1H3D	1.57	0.05
SCFD1	1.57	0.05

KCTD2	1.7	0.03	**HCG4P6**	1.57	0.04
INTS5	1.7	0.05	**SEC11A**	1.57	0.05
OAZ2	1.69	0.01	**SRBD1**	1.57	0.04
TK2	1.69	0.04	**SH2D4A**	1.57	0.05
TMED3	1.69	0.02	**KARS**	1.56	0.04
RAD17	1.69	0.05	**MED14**	1.56	0.01
RANGAP1	1.69	0.05	**DNAJB9**	1.56	0.02
ZCCHC14	1.69	0.05	**ING3**	1.56	0.05
WEE1	1.69	0.04	**UQCC**	1.56	0.05
GTPBP2	1.69	0.04	**ZBED5**	1.56	0.03
GPR137	1.69	0.03	**CIRBP**	1.55	0.03
LGALS1	1.68	0.04	**ADAR**	1.55	0.03
DDX19A /// D	1.68	0.05	**HTATSF1**	1.55	0.04
TERF2	1.68	0.04	**DKFZp434H**	1.55	0.05
GLRX	1.68	0.05	**HOXB7**	1.55	0.04
APBA2	1.68	0.04	**DIMT1L**	1.55	0.03
RBMX	1.68	0.03	**C12orf47**	1.55	0.01
YKT6	1.68	0.05	**PPM1B**	1.54	0.04
DDEFL1	1.68	0.05	**MINPP1**	1.54	0.05
WDR1	1.67	0.03	**UCK2**	1.54	0.04
HNRNPC	1.67	0.02	**RPL5**	1.54	0.03
CTSB	1.67	0.05	**SFRS2**	1.54	0.05
PJA2	1.67	0.04	**FBXO21**	1.54	0.04
MARS	1.67	0.05	**CSAG3A ///**	1.54	0.04
BLMH	1.67	0.03	**CDCA3**	1.54	0.05
RXRA	1.67	0.04	**KIAA0859**	1.53	0.05
SS18	1.67	0.03	**AURKB**	1.53	0.03
KIAA0746	1.67	0.05	**PA2G4**	1.53	0.03
CCDC99	1.67	0.03	**PSMA7**	1.53	0.05
KIAA0494	1.66	0.03	**ENPEP**	1.52	0.05
GTF2E2	1.66	0.03	**ADAM17**	1.52	0.04
CEBPG	1.66	0.04	**CDH16**	1.52	0.04
ZNF189	1.66	0.03	**DDX21**	1.52	0.04
DLG3	1.66	0.04	**GORASP2**	1.52	0.05
MXD4	1.66	0.03	**DOT1L**	1.51	0.03
MAGEA4	1.66	0.05	**CCDC88C**	1.51	0.05
MACROD1	1.66	0.02	**PNRC2**	1.51	0.05

TINP1	1.65	0.03
KIAA0247	1.65	0.05
E2F4	1.65	0.04
SKP2	1.65	0.03
SMTN	1.65	0.04
MALT1	1.65	0.04
ABI1	1.65	0.04
JMJD2B	1.65	0.05
DLST /// DLS	1.65	0.04
CARHSP1	1.65	0.05
ZCCHC6	1.65	0.02
SCD	1.64	0.05
PTDSS1	1.64	0.05
TCTN3	1.64	0.03
PDXK	1.64	0.02
CLN6	1.64	0.05
SBF1	1.64	0.04
KIAA0494	1.63	0.05
POLS	1.63	0.05
RFX5	1.63	0.05
ACVR2A	1.63	0.04
RNF113A	1.63	0.03
P4HB	1.62	0.03
PPP2CB	1.62	0.02
GRK6	1.62	0.04
PSMA6	1.62	0.04
CLCN7	1.62	0.04
BAIAP2	1.62	0.04
YKT6	1.62	0.03
SDF4	1.62	0.05
NINJ1	1.61	0.05
TGIF1	1.61	0.05
RAD1	1.61	0.03
DYNC1I1	1.61	0.03
TNIP1	1.61	0.04
BAT2	1.61	0.04
EEF1D /// E	1.61	0.03
PPA1	1.51	0.05
C5orf3	1.51	0.05
C14orf138	1.51	0.04
RBM34	1.5	0.04
PMS2	1.5	0.05
DONSON	1.5	0.04
CLDN11	1.49	0.05
POLR3C	1.49	0.04
DAPK1	1.49	0.04
EPHB1	1.49	0.04
BMI1	1.48	0.05
CEBPD	1.48	0.05
CSRP2	1.48	0.02
EXOSC10	1.48	0.05
CLEC11A	1.48	0.04
MAGEA5	1.48	0.03
TCEB2	1.47	0.05
OCA2	1.47	0.04
CDKN2A	1.47	0.04
FAM128A	1.47	0.04
DYSF	1.47	0.05
POLR3K	1.47	0.03
CCT8	1.46	0.04
EZH1	1.46	0.05
SFRS2B	1.46	0.04
ABHD9	1.46	0.03
CCDC28A	1.45	0.05
ZNF552	1.45	0.05

FAS	1.61	0.05
TULP3	1.61	0.03
RANBP2	1.6	0.05
PPP2R5D	1.6	0.04
SGSM3	1.6	0.02
AP3B1	1.6	0.03
NONO	1.6	0.05
ITPK1	1.6	0.03
RAD17	1.6	0.04
POP1	1.6	0.04
WDTC1	1.6	0.05
CYP2W1	1.6	0.04
SND1	1.59	0.02
SLC25A36	1.59	0.04
MORC2	1.59	0.03
NFE2L3	1.59	0.05
CALCOCO2	1.59	0.03
PRELP	1.59	0.04
RAB26	1.59	0.05
TMEM109	1.58	0.04
GART	1.58	0.03
RGS14	1.58	0.02
DCTD	1.57	0.05
ATP6AP1	1.57	0.02
HTATIP	1.57	0.04
PIGO	1.57	0.03
C1orf144	1.57	0.05
SGPL1	1.57	0.02
C1orf160	1.57	0.05
TMEM184B	1.56	0.04
NUP62	1.56	0.05
APLP2	1.56	0.05
TMED7	1.56	0.02
RAB26	1.56	0.02
PRKD2	1.56	0.01
HIP1R	1.56	0.03
RALY	1.55	0.05

CD55	1.55	0.04
FSTL3	1.55	0.05
INPP4A	1.55	0.03
DLG3	1.55	0.05
ERBB2	1.55	0.05
CDCA4	1.55	0.05
PEX14	1.55	0.04
STAB1	1.55	0.01
SLC35E1	1.55	0.02
CCS	1.54	0.03
MPP2	1.54	0.04
FAM62A	1.54	0.03
PNMA2	1.54	0.04
ING1	1.54	0.05
PFKM	1.54	0.02
NUP188	1.54	0.03
GNA11	1.54	0.05
GNA11	1.54	0.05
SCUBE3	1.54	0.04
SIL1	1.54	0.03
ZNF580	1.54	0.04
PILRB	1.54	0.05
CCNL2	1.54	0.04
MBD3	1.54	0.02
NPC2	1.53	0.05
PEPD	1.53	0.04
CTSH	1.53	0.04
TFRC	1.53	0.03
TUBB6	1.53	0.04
RAD1	1.53	0.05
RP11-365K2	1.53	0.02
ANKZF1	1.53	0.02
MRPL22	1.53	0.04
UBE2W	1.53	0.05
TMEM176B	1.53	0.05
HAO2	1.53	0.04
PDHA1	1.52	0.02

SUPT5H	1.52	0.04
SHFM1	1.52	0.05
CBFB	1.52	0.04
CD164	1.52	0.05
EIF3E	1.52	0.05
CSNK1A1	1.52	0.04
IL10RB	1.52	0.04
B9D1	1.52	0.02
EXOC7	1.52	0.05
SLC2A8	1.52	0.03
CENTA1	1.52	0.03
HSPH1	1.51	0.04
GRB10	1.51	0.05
CRADD	1.51	0.04
LRRC23	1.51	0.05
GGA1	1.51	0.04
DSTN	1.5	0.04
GTF2F1	1.5	0.03
TNK2	1.5	0.05
SSX3	1.5	0.02
HMX1	1.5	0.03
OS9	1.5	0.05
GTF2IRD1	1.5	0.04
AKAP1	1.49	0.05
DNAJB2	1.49	0.04
LEPROTL1	1.49	0.04
NCKAP1	1.49	0.05
WBP2	1.49	0.05
SSX2	1.49	0.03
CELSR1	1.49	0.05
GFPT1	1.48	0.03
CLTA	1.48	0.03
BTRC	1.48	0.04
GCAT	1.48	0.04
MACF1	1.48	0.04
RBM38	1.48	0.05
DHFR	1.48	0.05

RCN3	1.48	0.03
AFG3L2	1.47	0.05
E2F6	1.47	0.05
PKMYT1	1.47	0.03
ATP1B3	1.47	0.05
IHPK1	1.47	0.03
GPR137	1.47	0.03
TPP1	1.46	0.03
PFDN1	1.46	0.05
DNM1L	1.46	0.03
EIF1	1.46	0.02
KIAA0692	1.46	0.04
NDRG3	1.46	0.04
LANCL2	1.46	0.03
CALML4	1.46	0.02
PTPN21	1.45	0.03
G3BP1	1.45	0.04
FXR1	1.45	0.05
CD47	1.45	0.04
RPS21	1.45	0.03
NXT1	1.45	0.05
FAM60A	1.45	0.05
TBC1D16	1.45	0.05

Supplementary Table 2 Genes differentially expressed in response to DHT for 2hr in Rv1 cells

Symbol	Entrez Gene Name	Fold Change	P value	Location	Type
EDA	ectodysplasin A	-1.65	0.0503	Extracellular Space	cytokine
FBRS	fibrosin	-1.48	0.0272	Extracellular Space	cytokine
IFNW1	interferon, omega 1	-1.71	0.0139	Extracellular Space	cytokine
ACLY	ATP citrate lyase	-1.48	0.0466	Cytoplasm	enzyme
ADH5 (includes EG:128)	alcohol dehydrogenase 5 (class III), chi polypeptide	1.48	0.0456	Cytoplasm	enzyme
AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	1.67	0.0278	Unknown	enzyme
AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1.69	0.0511	Cytoplasm	enzyme
ALDH1L1	aldehyde dehydrogenase 1 family, member L1	1.67	0.0128	Cytoplasm	enzyme
ALDH4A1	aldehyde dehydrogenase 4 family, member A1	-2	0.0208	Cytoplasm	enzyme
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	1.98	0.0372	Cytoplasm	enzyme
ARF4	ADP-ribosylation factor 4	1.63	0.0413	Cytoplasm	enzyme
ASMTL (includes EG:8623)	acetylserotonin O-methyltransferase-like	-1.79	0.0217	Unknown	enzyme
ASPH	aspartate beta-hydroxylase	1.83	0.0398	Cytoplasm	enzyme
B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	-1.51	0.0279	Cytoplasm	enzyme
B4GALT1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	-2.6	0.0353	Cytoplasm	enzyme
B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	-1.52	0.0498	Cytoplasm	enzyme
BAT3	HLA-B associated transcript 3	-1.54	0.0181	Nucleus	enzyme
CA12	carbonic anhydrase XII	1.61	0.0376	Plasma Membrane	enzyme
CA5B	carbonic anhydrase VB, mitochondrial	-1.49	0.0139	Cytoplasm	enzyme
CASZ1	castor zinc finger 1	-1.82	0.0343	Nucleus	enzyme
CDO1	cysteine dioxygenase, type I	-1.78	0.0438	Cytoplasm	enzyme
CHSY1	chondroitin sulfate synthase 1	1.92	0.0478	Cytoplasm	enzyme
CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase	2.08	0.0309	Nucleus	enzyme
COX11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	1.58	0.0464	Cytoplasm	enzyme
COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	1.54	0.0499	Cytoplasm	enzyme
CRAT	carnitine acetyltransferase	-3.1	0.0155	Cytoplasm	enzyme
CTBP1	C-terminal binding protein 1	-1.52	0.0176	Nucleus	enzyme
CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	-1.86	0.0499	Cytoplasm	enzyme
CYP2A7	cytochrome P450, family 2, subfamily A, polypeptide 7	-1.62	0.0544	Cytoplasm	enzyme
DDAH2	dimethylarginine dimethylaminohydrolase 2	-1.73	0.0235	Unknown	enzyme
DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	1.68	0.0374	Nucleus	enzyme

DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	-2.31	0.0530	Nucleus	enzyme
DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	-1.85	0.0479	Nucleus	enzyme
DHCR24	24-dehydrocholesterol reductase	-1.63	0.0345	Cytoplasm	enzyme
DHCR7	7-dehydrocholesterol reductase	-1.78	0.0322	Cytoplasm	enzyme
DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	1.56	0.0245	Cytoplasm	enzyme
DIS3	DIS3 mitotic control homolog (S. cerevisiae)	3.73	0.0469	Nucleus	enzyme
DNM2	dynamin 2	-1.45	0.0353	Plasma Membrane	enzyme
DOHH	deoxyhypusine hydroxylase/monooxygenase	-1.69	0.0328	Unknown	enzyme
DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	1.55	0.0414	Cytoplasm	enzyme
ETFDH	electron-transferring-flavoprotein dehydrogenase	1.54	0.0432	Cytoplasm	enzyme
FBXL5	F-box and leucine-rich repeat protein 5	1.73	0.0263	Cytoplasm	enzyme
FEN1	flap structure-specific endonuclease 1	-1.48	0.0341	Nucleus	enzyme
FKBP15	FK506 binding protein 15, 133kDa	-2.47	0.0422	Unknown	enzyme
FLJ21865	endo-beta-N-acetylglucosaminidase	-1.96	0.0331	Unknown	enzyme
FTSJ2	FtsJ homolog 2 (E. coli)	1.57	0.0462	Nucleus	enzyme
G3BP2	GTPase activating protein (SH3 domain) binding protein 2	-1.69	0.0356	Nucleus	enzyme
GAA	glucosidase, alpha; acid	-1.7	0.0317	Cytoplasm	enzyme
GALNT11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	1.57	0.0384	Cytoplasm	enzyme
GBP1 (includes EG:2633)	guanylate binding protein 1, interferon-inducible, 67kDa	-2.88	0.0323	Cytoplasm	enzyme
GLT8D1	glycosyltransferase 8 domain containing 1	1.83	0.0372	Unknown	enzyme
GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	1.81	0.0414	Plasma Membrane	enzyme
GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	1.84	0.0387	Nucleus	enzyme
GNPAT	glyceronephosphate O-acyltransferase	1.6	0.0316	Cytoplasm	enzyme
GPLD1	glycosylphosphatidylinositol specific phospholipase D1	-2.56	0.0421	Cytoplasm	enzyme
GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	-2.57	0.0275	Cytoplasm	enzyme
HEXA	hexosaminidase A (alpha polypeptide)	-2.2	0.0533	Cytoplasm	enzyme
HNMT	histamine N-methyltransferase	1.97	0.0496	Cytoplasm	enzyme
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	1.94	0.0533	Cytoplasm	enzyme
HPSE2	heparanase 2	-1.63	0.0451	Unknown	enzyme
IGHMBP2	immunoglobulin mu binding protein 2	-1.53	0.0280	Nucleus	enzyme
IMPAD1	inositol monophosphatase domain containing 1	-1.76	0.0398	Unknown	enzyme
KARS	lysyl-tRNA synthetase	1.5	0.0434	Cytoplasm	enzyme
KAT2A	K(lysine) acetyltransferase 2A	-1.58	0.0463	Cytoplasm	enzyme
LAMP2	lysosomal-associated membrane protein 2	1.89	0.0284	Plasma Membrane	enzyme
LARS2	leucyl-tRNA synthetase 2, mitochondrial	1.59	0.0491	Cytoplasm	enzyme
LYPLA2P1	lysophospholipase II pseudogene 1	-1.74	0.0318	Unknown	enzyme
MAN1B1	mannosidase, alpha, class 1B, member 1	-1.76	0.0459	Cytoplasm	enzyme
MAN2C1	mannosidase, alpha, class 2C, member 1	-1.55	0.0518	Cytoplasm	enzyme

MAPRE3	microtubule-associated protein, RP/EB family, member 3	-2.06	0.0521	Cytoplasm	enzyme
MARS	methionyl-tRNA synthetase	1.85	0.0378	Cytoplasm	enzyme
MAT2A	methionine adenosyltransferase II, alpha	-2.33	0.0352	Cytoplasm	enzyme
MCM5	minichromosome maintenance complex component 5	-1.72	0.0370	Nucleus	enzyme
MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	1.79	0.0457	Cytoplasm	enzyme
MGRN1	mahogunin, ring finger 1	-1.84	0.0498	Cytoplasm	enzyme
MPI	mannose phosphate isomerase	-2.32	0.0132	Cytoplasm	enzyme
MPPE1	metallophosphoesterase 1	-1.72	0.0335	Unknown	enzyme
MVD	mevalonate (diphospho) decarboxylase	-2.89	0.0357	Cytoplasm	enzyme
MYO5A	myosin VA (heavy chain 12, myoxin)	-2.33	0.0271	Cytoplasm	enzyme
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	2.72	0.0124	Cytoplasm	enzyme
NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	-1.69	0.0199	Cytoplasm	enzyme
NCF1	neutrophil cytosolic factor 1	-1.61	0.0333	Cytoplasm	enzyme
NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	1.54	0.0413	Cytoplasm	enzyme
OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-2.44	0.0334	Cytoplasm	enzyme
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	-1.6	0.0479	Cytoplasm	enzyme
PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	2.07	0.0208	Cytoplasm	enzyme
PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	1.68	0.0285	Cytoplasm	enzyme
PDE4DIP	phosphodiesterase 4D interacting protein	1.92	0.0467	Cytoplasm	enzyme
PIGA	phosphatidylinositol glycan anchor biosynthesis, class A	2.17	0.0492	Cytoplasm	enzyme
PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	-1.67	0.0297	Cytoplasm	enzyme
PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	-1.59	0.0282	Cytoplasm	enzyme
PLA2G2F	phospholipase A2, group IIF	1.45	0.0486	Extracellular Space	enzyme
PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	2.05	0.0251	Cytoplasm	enzyme
PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.65	0.0439	Cytoplasm	enzyme
PLSCR3	phospholipid scramblase 3	-2.38	0.0138	Cytoplasm	enzyme
POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	2.06	0.0363	Nucleus	enzyme
POLRMT	polymerase (RNA) mitochondrial (DNA directed)	-1.5	0.0319	Cytoplasm	enzyme
POMGNT1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	-2.74	0.0097	Cytoplasm	enzyme
PPA1	pyrophosphatase (inorganic) 1	1.46	0.0542	Cytoplasm	enzyme
PPIC	peptidylprolyl isomerase C (cyclophilin C)	1.52	0.0295	Cytoplasm	enzyme
PPID	peptidylprolyl isomerase D	1.68	0.0328	Cytoplasm	enzyme
PPME1	protein phosphatase methylesterase 1	-1.61	0.0527	Unknown	enzyme
PRDX2	peroxiredoxin 2	1.6	0.0350	Cytoplasm	enzyme
PRMT1	protein arginine methyltransferase 1	-2.9	0.0508	Nucleus	enzyme

QTRT1	queuine tRNA-ribosyltransferase 1	-2.43	0.0407	Unknown	enzyme
RAB11B	RAB11B, member RAS oncogene family	-3.99	0.0234	Cytoplasm	enzyme
RAB40C	RAB40C, member RAS oncogene family	-1.69	0.0334	Plasma Membrane	enzyme
RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	-3	0.0196	Cytoplasm	enzyme
RAD1	RAD1 homolog (S. pombe)	2.22	0.0362	Nucleus	enzyme
RANBP2	RAN binding protein 2	2.17	0.0173	Nucleus	enzyme
RECQL5	RecQ protein-like 5	-1.55	0.0143	Nucleus	enzyme
RHEB	Ras homolog enriched in brain	-1.89	0.0148	Plasma Membrane	enzyme
RHOD	ras homolog gene family, member D	-1.79	0.0257	Cytoplasm	enzyme
RHOT2	ras homolog gene family, member T2	-1.6	0.0112	Cytoplasm	enzyme
RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	-1.67	0.0516	Extracellular Space	enzyme
SAR1A	SAR1 homolog A (S. cerevisiae)	-1.78	0.0398	Cytoplasm	enzyme
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-2.02	0.0273	Cytoplasm	enzyme
SEPT9	septin 9	-1.81	0.0379	Cytoplasm	enzyme
SIAH1	seven in absentia homolog 1 (Drosophila)	1.49	0.0472	Nucleus	enzyme
SMOX	spermine oxidase	-1.65	0.0148	Cytoplasm	enzyme
SPAST	spastin	2.51	0.0202	Nucleus	enzyme
SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	2.02	0.0193	Cytoplasm	enzyme
SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	2.15	0.0113	Cytoplasm	enzyme
SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	2.18	0.0445	Nucleus	enzyme
TARS	threonyl-tRNA synthetase	1.64	0.0374	Nucleus	enzyme
TGM4	transglutaminase 4 (prostate)	-1.61	0.0484	Extracellular Space	enzyme
TOP2B	topoisomerase (DNA) II beta 180kDa	2	0.0149	Nucleus	enzyme
TTLL3	tubulin tyrosine ligase-like family, member 3	-1.8	0.0212	Unknown	enzyme
TXNDC13	thioredoxin domain containing 13	1.57	0.0489	Cytoplasm	enzyme
UBA2	ubiquitin-like modifier activating enzyme 2	1.77	0.0134	Cytoplasm	enzyme
UBA3	ubiquitin-like modifier activating enzyme 3	1.99	0.0336	Cytoplasm	enzyme
UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	2.67	0.0104	Cytoplasm	enzyme
UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative)	-1.48	0.0387	Unknown	enzyme
UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	1.97	0.0523	Cytoplasm	enzyme
UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	-2.42	0.0088	Cytoplasm	enzyme
UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	-2.11	0.0303	Nucleus	enzyme
UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	1.87	0.0311	Cytoplasm	enzyme
UBE2S	ubiquitin-conjugating enzyme E2S	-1.81	0.0270	Unknown	enzyme
VARS	valyl-tRNA synthetase	-5.1	0.0232	Cytoplasm	enzyme
WARS	tryptophanyl-tRNA synthetase	-1.64	0.0431	Cytoplasm	enzyme
WWOX	WW domain containing oxidoreductase	-1.56	0.0383	Cytoplasm	enzyme
WWP1	WW domain containing E3 ubiquitin protein ligase 1	2.34	0.0216	Cytoplasm	enzyme
CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	-1.53	0.0405	Plasma Membrane	G-protein coupled receptor
CELSR2	cadherin, EGF LAG seven-pass G-type	-1.48	0.0446	Plasma	G-protein

	receptor 2 (flamingo homolog, Drosophila)			Plasma Membrane	G-protein coupled receptor
GLP1R	glucagon-like peptide 1 receptor	-1.67	0.0217	Plasma Membrane	G-protein coupled receptor
GNRHR	gonadotropin-releasing hormone receptor	-2.39	0.0396	Plasma Membrane	G-protein coupled receptor
GPR27	G protein-coupled receptor 27	-1.8	0.0350	Plasma Membrane	G-protein coupled receptor
GRPR	gastrin-releasing peptide receptor	-1.58	0.0292	Plasma Membrane	G-protein coupled receptor
HRH3	histamine receptor H3	-2.21	0.0496	Plasma Membrane	G-protein coupled receptor
LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	-1.67	0.0364	Plasma Membrane	G-protein coupled receptor
LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	3.93	0.0428	Plasma Membrane	G-protein coupled receptor
OGFR	opioid growth factor receptor	-1.99	0.0304	Plasma Membrane	G-protein coupled receptor
OR7C1	olfactory receptor, family 7, subfamily C, member 1	-2.03	0.0225	Plasma Membrane	G-protein coupled receptor
PTGDR	prostaglandin D2 receptor (DP)	-2.05	0.0419	Plasma Membrane	G-protein coupled receptor
RHO	rhodopsin	-1.73	0.0473	Plasma Membrane	G-protein coupled receptor
TBXA2R	thromboxane A2 receptor	-1.68	0.0270	Plasma Membrane	receptor
AREG	amphiregulin	-3.02	0.0420	Extracellular Space	growth factor
BMP2	bone morphogenetic protein 2	-1.62	0.0365	Extracellular Space	growth factor
FGF6	fibroblast growth factor 6	-1.65	0.0351	Extracellular Space	growth factor
HDGF	hepatoma-derived growth factor (high-mobility group protein 1-like)	-2.41	0.0404	Extracellular Space	growth factor
LTBP4	latent transforming growth factor beta binding protein 4	-2.29	0.0463	Extracellular Space	growth factor
NRG2 (includes EG:9542)	neuregulin 2	1.5	0.0445	Extracellular Space	growth factor
TYMP	thymidine phosphorylase	-1.73	0.0434	Extracellular Space	growth factor
ANXA7	annexin A7	1.87	0.0328	Plasma Membrane	ion channel
CLCN7	chloride channel 7	-1.5	0.0351	Plasma Membrane	ion channel

GPM6A	glycoprotein M6A	2.13	0.0499	Plasma Membrane	ion channel
GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	-1.97	0.0389	Plasma Membrane	ion channel
KCNA4	potassium voltage-gated channel, shaker-related subfamily, member 4	-1.76	0.0226	Plasma Membrane	ion channel
KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	-1.51	0.0337	Plasma Membrane	ion channel
KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	2.54	0.0226	Plasma Membrane	ion channel
KCTD2	potassium channel tetramerisation domain containing 2	-2.04	0.0114	Unknown	ion channel
MCOLN1	mucolipin 1	-1.71	0.0482	Cytoplasm	ion channel
NOX1	NADPH oxidase 1	-1.67	0.0213	Cytoplasm	ion channel
TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	-1.68	0.0358	Cytoplasm	ion channel
TRPM2	transient receptor potential cation channel, subfamily M, member 2	-2.4	0.0283	Plasma Membrane	ion channel
VDAC3	voltage-dependent anion channel 3	-2.01	0.0380	Cytoplasm	ion channel
ADRBK1	adrenergic, beta, receptor kinase 1	-2.1	0.0479	Cytoplasm	kinase
AGK	acylglycerol kinase	1.63	0.0493	Cytoplasm	kinase
AURKB	aurora kinase B	1.48	0.0399	Nucleus	kinase
BAIAP2	BAI1-associated protein 2	-1.68	0.0423	Plasma Membrane	kinase
BRD2	bromodomain containing 2	-1.83	0.0514	Nucleus	kinase
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	-1.81	0.0485	Nucleus	kinase
CAMK2B	calcium/calmodulin-dependent protein kinase II beta	-1.56	0.0239	Cytoplasm	kinase
CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	-1.56	0.0490	Cytoplasm	kinase
CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-2.36	0.0459	Cytoplasm	kinase
CDC2	cell division cycle 2, G1 to S and G2 to M	1.76	0.0514	Nucleus	kinase
CDC2L2	cell division cycle 2-like 2 (PITSLRE proteins)	-1.47	0.0528	Nucleus	kinase
CDK2	cyclin-dependent kinase 2	-1.81	0.0183	Nucleus	kinase
CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-2.25	0.0344	Cytoplasm	kinase
CSK	c-src tyrosine kinase	-1.73	0.0331	Cytoplasm	kinase
DAPK3	death-associated protein kinase 3	-3.41	0.0335	Cytoplasm	kinase
DCK	deoxycytidine kinase	1.85	0.0374	Nucleus	kinase
DMPK	dystrophia myotonica-protein kinase	-1.56	0.0461	Cytoplasm	kinase
EPHA1	EPH receptor A1	-1.63	0.0539	Plasma Membrane	kinase
ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	-1.56	0.0254	Plasma Membrane	kinase
EXOSC10	exosome component 10	1.59	0.0353	Nucleus	kinase
FASTK	Fas-activated serine/threonine kinase	-1.75	0.0483	Cytoplasm	kinase
FRAP1	FK506 binding protein 12-rapamycin associated protein 1	-1.6	0.0250	Nucleus	kinase
GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	-1.71	0.0234	Plasma Membrane	kinase

HK2	hexokinase 2	-1.57	0.0464	Cytoplasm	kinase
IHPK1	inositol hexakisphosphate kinase 1	-1.53	0.0386	Cytoplasm	kinase
IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	-1.63	0.0200	Nucleus	kinase
MAP2K7	mitogen-activated protein kinase kinase 7	-1.56	0.0543	Cytoplasm	kinase
MAP3K3	mitogen-activated protein kinase kinase kinase 3	-1.5	0.0226	Cytoplasm	kinase
MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	3.73	0.0133	Unknown	kinase
MAPK14	mitogen-activated protein kinase 14	-2.59	0.0283	Cytoplasm	kinase
MARK2	MAP/microtubule affinity-regulating kinase 2	-1.56	0.0475	Cytoplasm	kinase
MARK3	MAP/microtubule affinity-regulating kinase 3	1.99	0.0303	Cytoplasm	kinase
MVK	mevalonate kinase	-1.61	0.0096	Cytoplasm	kinase
NRBP1	nuclear receptor binding protein 1	-1.64	0.0467	Nucleus	kinase
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	1.8	0.0377	Plasma Membrane	kinase
PFKL	phosphofructokinase, liver	-2.95	0.0308	Cytoplasm	kinase
PHKB	phosphorylase kinase, beta	1.53	0.0361	Cytoplasm	kinase
PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	1.77	0.0517	Cytoplasm	kinase
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	-1.57	0.0375	Cytoplasm	kinase
PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	-2.11	0.0471	Unknown	kinase
PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	2.03	0.0043	Cytoplasm	kinase
PRKD2	protein kinase D2	-1.7	0.0056	Cytoplasm	kinase
PRKD3	protein kinase D3	1.93	0.0347	Unknown	kinase
PRKDC	protein kinase, DNA-activated, catalytic polypeptide	2.6	0.0263	Nucleus	kinase
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	1.95	0.0510	Nucleus	kinase
PRPS2	phosphoribosyl pyrophosphate synthetase 2	1.96	0.0501	Unknown	kinase
RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	-1.64	0.0519	Cytoplasm	kinase
ROCK1	Rho-associated, coiled-coil containing protein kinase 1	1.77	0.0469	Cytoplasm	kinase
RP6-213H19.1	serine/threonine protein kinase MST4	1.8	0.0271	Nucleus	kinase
RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	-1.6	0.0310	Nucleus	kinase
RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.74	0.0277	Cytoplasm	kinase
SLK	STE20-like kinase (yeast)	2.19	0.0418	Nucleus	kinase
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	-1.5	0.0328	Cytoplasm	kinase
STK11	serine/threonine kinase 11	-2.61	0.0106	Cytoplasm	kinase
TAOK2 (includes EG:9344)	TAO kinase 2	-1.72	0.0420	Cytoplasm	kinase
TGFBR1	transforming growth factor, beta receptor 1	-1.81	0.0543	Plasma Membrane	kinase
TK2	thymidine kinase 2, mitochondrial	-1.76	0.0355	Cytoplasm	kinase
TLK1	tousled-like kinase 1	1.48	0.0237	Cytoplasm	kinase
TMEM134	transmembrane protein 134	-2.53	0.0430	Unknown	kinase
VRK1	vaccinia related kinase 1	1.75	0.0314	Nucleus	kinase

ESRRA	estrogen-related receptor alpha	-2.09	0.0204	Nucleus	ligand-dependent nuclear receptor
NR2F2	nuclear receptor subfamily 2, group F, member 2	2.44	0.0450	Nucleus	ligand-dependent nuclear receptor
NR2F6	nuclear receptor subfamily 2, group F, member 6	-3.15	0.0381	Nucleus	ligand-dependent nuclear receptor
NR6A1	nuclear receptor subfamily 6, group A, member 1	-1.54	0.0381	Nucleus	ligand-dependent nuclear receptor
THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	-2.36	0.0280	Nucleus	ligand-dependent nuclear receptor
THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	-1.52	0.0453	Nucleus	ligand-dependent nuclear receptor
AAMP	angio-associated, migratory cell protein	-2	0.0182	Unknown	other
ABCA11	ATP-binding cassette, sub-family A (ABC1), member 11 (pseudogene)	1.73	0.0476	Unknown	other
ABR	active BCR-related gene	-2.81	0.0491	Unknown	other
ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	2.02	0.0185	Nucleus	other
ACRV1	acrosomal vesicle protein 1	-1.55	0.0398	Cytoplasm	other
ACTG2 (includes EG:72)	actin, gamma 2, smooth muscle, enteric	-1.46	0.0516	Cytoplasm	other
ACTL6A	actin-like 6A	2.68	0.0263	Nucleus	other
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	2.37	0.0313	Plasma Membrane	other
ADAP1	ArfGAP with dual PH domains 1	-2.13	0.0172	Nucleus	other
ADO	2-aminoethanethiol (cysteamine) dioxygenase	1.5	0.0219	Unknown	other
AGRN	agrin	-2.05	0.0423	Plasma Membrane	other
AHDC1	AT hook, DNA binding motif, containing 1	-1.66	0.0130	Unknown	other
ALMS1	Alstrom syndrome 1	1.6	0.0336	Cytoplasm	other
ANK3	ankyrin 3, node of Ranvier (ankyrin G)	2.06	0.0190	Plasma Membrane	other
ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	2.24	0.0163	Nucleus	other
APAF1	apoptotic peptidase activating factor 1	1.75	0.0245	Cytoplasm	other
APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	-1.86	0.0380	Cytoplasm	other
APLP1	amyloid beta (A4) precursor-like protein 1	-1.76	0.0248	Extracellular Space	other
APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	1.46	0.0368	Cytoplasm	other
ARHGAP1	Rho GTPase activating protein 1	-4.68	0.0532	Cytoplasm	other
ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	-1.67	0.0253	Cytoplasm	other

ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	-1.59	0.0520	Cytoplasm	other
ARMC1	armadillo repeat containing 1	2.27	0.0246	Unknown	other
ARVCF	armadillo repeat gene deletes in velocardiofacial syndrome	-1.96	0.0242	Plasma Membrane	other
ASPHD1 (includes EG:253982)	aspartate beta-hydroxylase domain containing 1	-1.92	0.0378	Unknown	other
ATG2A	ATG2 autophagy related 2 homolog A (S. cerevisiae)	-1.78	0.0474	Unknown	other
ATMIN	ATM interactor	1.96	0.0297	Nucleus	other
ATPIF1	ATPase inhibitory factor 1	2.48	0.0087	Cytoplasm	other
BAT2	HLA-B associated transcript 2	-2.76	0.0208	Cytoplasm	other
BBS10	Bardet-Biedl syndrome 10	1.96	0.0227	Unknown	other
BRMS1	breast cancer metastasis suppressor 1	-1.66	0.0343	Unknown	other
BRWD2	bromodomain and WD repeat domain containing 2	3.14	0.0190	Unknown	other
BSG	basigin (Ok blood group)	-2.68	0.0380	Plasma Membrane	other
BTBD2	BTB (POZ) domain containing 2	-3.27	0.0246	Cytoplasm	other
BTG3	BTG family, member 3	1.98	0.0434	Nucleus	other
C10ORF137	chromosome 10 open reading frame 137	1.69	0.0469	Unknown	other
C11ORF24	chromosome 11 open reading frame 24	1.96	0.0195	Extracellular Space	other
C12ORF47	chromosome 12 open reading frame 47	1.57	0.0351	Unknown	other
C12ORF49	chromosome 12 open reading frame 49	-1.97	0.0533	Unknown	other
C14ORF104	chromosome 14 open reading frame 104	2.57	0.0486	Unknown	other
C14ORF108	MU-2/AP1M2 domain containing, death-inducing	1.98	0.0282	Unknown	other
C14ORF118	chromosome 14 open reading frame 118	-1.5	0.0353	Unknown	other
C14ORF65	chromosome 14 open reading frame 65	-1.6	0.0347	Unknown	other
C15ORF24	chromosome 15 open reading frame 24	1.75	0.0223	Extracellular Space	other
C17ORF42	chromosome 17 open reading frame 42	1.5	0.0517	Unknown	other
C19ORF54	chromosome 19 open reading frame 54	-1.62	0.0395	Unknown	other
C1ORF107	chromosome 1 open reading frame 107	1.96	0.0186	Nucleus	other
C1ORF144	chromosome 1 open reading frame 144	-1.79	0.0259	Unknown	other
C20ORF27	chromosome 20 open reading frame 27	-2.3	0.0193	Unknown	other
C21ORF45	chromosome 21 open reading frame 45	1.63	0.0479	Unknown	other
C21ORF66	chromosome 21 open reading frame 66	-1.57	0.0447	Nucleus	other
C5ORF22	chromosome 5 open reading frame 22	1.82	0.0171	Unknown	other
C5ORF4	chromosome 5 open reading frame 4	-1.6	0.0159	Unknown	other
C5ORF44	chromosome 5 open reading frame 44	2.37	0.0405	Unknown	other
C6ORF106	chromosome 6 open reading frame 106	-2.19	0.0393	Unknown	other
C6ORF120	chromosome 6 open reading frame 120	1.79	0.0413	Unknown	other
C7ORF64	chromosome 7 open reading frame 64	3.12	0.0361	Unknown	other
C9ORF7	chromosome 9 open reading frame 7	-1.93	0.0130	Unknown	other
C9ORF82	chromosome 9 open reading frame 82	1.69	0.0244	Unknown	other
CALM3	calmodulin 3 (phosphorylase kinase, delta)	-1.54	0.0284	Plasma Membrane	other
CAPZB	capping protein (actin filament) muscle Z-line, beta	-2.24	0.0199	Cytoplasm	other
CARD9	caspase recruitment domain family, member 9	-1.81	0.0453	Cytoplasm	other
CBX1	chromobox homolog 1 (HP1 beta homolog Drosophila)	1.69	0.0244	Nucleus	other
CCDC101	coiled-coil domain containing 101	-1.64	0.0374	Unknown	other

CCDC21	coiled-coil domain containing 21	-1.86	0.0411	Unknown	other
CCDC59	coiled-coil domain containing 59	1.93	0.0280	Unknown	other
CCDC64	coiled-coil domain containing 64	-1.81	0.0530	Unknown	other
CCDC91	coiled-coil domain containing 91	1.89	0.0367	Unknown	other
CCHCR1	coiled-coil alpha-helical rod protein 1	-1.81	0.0206	Cytoplasm	other
CD48	CD48 molecule	-2.16	0.0397	Plasma Membrane	other
CDC5L	CDC5 cell division cycle 5-like (S. pombe)	-1.55	0.0432	Nucleus	other
CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	2.96	0.0322	Nucleus	other
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	1.56	0.0427	Nucleus	other
CENPM	centromere protein M	-1.57	0.0409	Cytoplasm	other
CENPN	centromere protein N	1.59	0.0389	Unknown	other
CEP27	centrosomal protein 27kDa	2.28	0.0082	Cytoplasm	other
CEP57	centrosomal protein 57kDa	2.52	0.0319	Cytoplasm	other
CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	2.27	0.0088	Nucleus	other
CGGBP1	CGG triplet repeat binding protein 1	-1.53	0.0395	Nucleus	other
CHMP2A	chromatin modifying protein 2A	1.56	0.0399	Cytoplasm	other
CHMP2B	chromatin modifying protein 2B	2.38	0.0091	Cytoplasm	other
CHN1 (includes EG:1123)	chimerin (chimaerin) 1	-1.56	0.0430	Cytoplasm	other
CHODL	chondrolectin	-1.5	0.0101	Plasma Membrane	other
CIDEC	cell death-inducing DFFA-like effector c	-1.47	0.0510	Cytoplasm	other
CISH	cytokine inducible SH2-containing protein	-1.7	0.0463	Cytoplasm	other
CKAP2	cytoskeleton associated protein 2	1.86	0.0403	Cytoplasm	other
CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	-1.67	0.0409	Cytoplasm	other
CLPTM1	cleft lip and palate associated transmembrane protein 1	-7.87	0.0099	Plasma Membrane	other
CNIH	cornichon homolog (Drosophila)	1.98	0.0471	Plasma Membrane	other
CNIH4	cornichon homolog 4 (Drosophila)	3.01	0.0049	Plasma Membrane	other
CNNM3	cyclin M3	-1.85	0.0226	Unknown	other
COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	-1.99	0.0145	Extracellular Space	other
COL5A2	collagen, type V, alpha 2	1.54	0.0383	Extracellular Space	other
COL9A3	collagen, type IX, alpha 3	1.51	0.0359	Extracellular Space	other
COMMD8	COMM domain containing 8	1.67	0.0508	Unknown	other
COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	1.95	0.0403	Cytoplasm	other
CORO1B	coronin, actin binding protein, 1B	-1.9	0.0172	Cytoplasm	other
CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	1.54	0.0523	Nucleus	other
CSDC2	cold shock domain containing C2, RNA binding	-1.89	0.0470	Cytoplasm	other
CSRP2	cysteine and glycine-rich protein 2	1.58	0.0183	Nucleus	other
CST2	cystatin SA	-1.82	0.0424	Extracellular Space	other
CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small	1.84	0.0520	Nucleus	other

	phosphatase-like				
CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	1.73	0.0296	Plasma Membrane	other
CUL4A	cullin 4A	2	0.0164	Nucleus	other
CUL7 (includes EG:9820)	cullin 7	-1.83	0.0215	Cytoplasm	other
DAAM2	dishevelled associated activator of morphogenesis 2	-1.55	0.0084	Unknown	other
DCTN5	dynactin 5 (p25)	-2.12	0.0412	Unknown	other
DEDD	death effector domain containing	-1.45	0.0481	Nucleus	other
DENR (includes EG:8562)	density-regulated protein	2.08	0.0302	Unknown	other
DGCR14	DiGeorge syndrome critical region gene 14	-1.62	0.0526	Nucleus	other
DGCR2	DiGeorge syndrome critical region gene 2	-1.76	0.0277	Plasma Membrane	other
DKFZP434A062	DKFZP434A062 protein	-1.62	0.0408	Unknown	other
DKFZP564C196	DKFZP564C196 protein	-1.73	0.0100	Unknown	other
DLK2	delta-like 2 homolog (Drosophila)	-1.67	0.0352	Extracellular Space	other
DMWD	dystrophia myotonica, WD repeat containing	-1.76	0.0195	Nucleus	other
DMXL1	Dmx-like 1	2.38	0.0422	Unknown	other
DMXL2	Dmx-like 2	1.83	0.0263	Cytoplasm	other
DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	1.76	0.0448	Nucleus	other
DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	2.35	0.0065	Nucleus	other
DSP	desmoplakin	1.47	0.0478	Plasma Membrane	other
DTL	denticleless homolog (Drosophila)	1.51	0.0321	Nucleus	other
DUS2L	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	-1.46	0.0244	Cytoplasm	other
DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	1.79	0.0283	Unknown	other
E2F8	E2F transcription factor 8	2.04	0.0494	Nucleus	other
EFNB2	ephrin-B2	1.9	0.0328	Plasma Membrane	other
EHBP1L1	EH domain binding protein 1-like 1	-1.76	0.0523	Cytoplasm	other
EI24	etoposide induced 2.4 mRNA	1.51	0.0432	Unknown	other
ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	-1.7	0.0279	Nucleus	other
ELN	elastin	-1.98	0.0374	Extracellular Space	other
ENOSF1	enolase superfamily member 1	1.57	0.0286	Unknown	other
ERGIC2	ERGIC and golgi 2	1.73	0.0236	Unknown	other
FAIM	Fas apoptotic inhibitory molecule	2.03	0.0144	Cytoplasm	other
FAIM2	Fas apoptotic inhibitory molecule 2	-1.81	0.0487	Plasma Membrane	other
FAM115A	family with sequence similarity 115, member A	3.23	0.0423	Unknown	other
FAM127A	family with sequence similarity 127, member A	-1.74	0.0400	Plasma Membrane	other
FAM20B	family with sequence similarity 20, member B	1.59	0.0483	Extracellular	other

				Space	
FANCL	Fanconi anemia, complementation group L	2.08	0.0290	Nucleus	other
FASTKD3	FAST kinase domains 3	1.74	0.0351	Unknown	other
FBXO41	F-box protein 41	-1.48	0.0395	Unknown	other
FBXO42	F-box protein 42	-1.94	0.0456	Unknown	other
FBXW12	F-box and WD repeat domain containing 12	2.38	0.0411	Unknown	other
FERMT2	fermitin family homolog 2 (Drosophila)	-1.63	0.0409	Cytoplasm	other
FLJ12151	hypothetical protein FLJ12151	2.59	0.0329	Unknown	other
FLJ22167	hypothetical protein FLJ22167	1.77	0.0327	Unknown	other
FLJ35429	hypothetical protein FLJ35429	2.27	0.0393	Unknown	other
FLOT1	flotillin 1	-1.54	0.0542	Plasma Membrane	other
FNDC3A	fibronectin type III domain containing 3A	1.68	0.0508	Unknown	other
FUSIP1	FUS interacting protein (serine/arginine-rich) 1	2	0.0159	Nucleus	other
GARNL1	GTPase activating Rap/RanGAP domain-like 1	2.35	0.0132	Cytoplasm	other
GAS2	growth arrest-specific 2	2.04	0.0373	Cytoplasm	other
GBAS	glioblastoma amplified sequence	2.18	0.0085	Plasma Membrane	other
GIP	gastric inhibitory polypeptide	-1.5	0.0370	Extracellular Space	other
GIT1	G protein-coupled receptor kinase interacting ArfGAP 1	-2.41	0.0098	Nucleus	other
GLTSCR1	glioma tumor suppressor candidate region gene 1	-1.7	0.0233	Unknown	other
GORASP2	golgi reassembly stacking protein 2, 55kDa	1.49	0.0519	Cytoplasm	other
GPN3	GPN-loop GTPase 3	1.77	0.0475	Unknown	other
GPR137	G protein-coupled receptor 137	-1.85	0.0169	Unknown	other
GRIP2	glutamate receptor interacting protein 2	-1.62	0.0412	Plasma Membrane	other
GRSF1	G-rich RNA sequence binding factor 1	1.75	0.0464	Cytoplasm	other
GTPBP4	GTP binding protein 4	2.03	0.0282	Nucleus	other
H3F3A (includes EG:3020)	H3 histone, family 3A	1.66	0.0336	Nucleus	other
HIP1	huntingtin interacting protein 1	-1.64	0.0470	Cytoplasm	other
HIST1H1D (includes EG:3007)	histone cluster 1, H1d	-1.55	0.0474	Nucleus	other
HIST1H3E	histone cluster 1, H3e	-1.66	0.0411	Unknown	other
HMGN3	high mobility group nucleosomal binding domain 3	1.57	0.0255	Nucleus	other
HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	2.44	0.0244	Nucleus	other
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	1.6	0.0361	Nucleus	other
HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	-1.69	0.0178	Nucleus	other
HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')	2.35	0.0522	Nucleus	other
HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	1.89	0.0204	Nucleus	other
HNRNPL	heterogeneous nuclear ribonucleoprotein L	-1.78	0.0412	Nucleus	other
HOMER3	homer homolog 3 (Drosophila)	-2.36	0.0351	Plasma Membrane	other
HPS1	Hermansky-Pudlak syndrome 1	-1.85	0.0213	Cytoplasm	other
HSPC072	HSPC072 protein	-1.56	0.0510	Unknown	other
IFT57	intraflagellar transport 57 homolog	1.64	0.0257	Cytoplasm	other

	(Chlamydomonas)				
IFT74	intraflagellar transport 74 homolog (Chlamydomonas)	2.47	0.0167	Unknown	other
ING4	inhibitor of growth family, member 4	-1.56	0.0456	Nucleus	other
INTS1	integrator complex subunit 1	-1.57	0.0163	Nucleus	other
IQWD1	IQ motif and WD repeats 1	1.84	0.0523	Nucleus	other
IRS1	insulin receptor substrate 1	2.19	0.0303	Cytoplasm	other
ITGB5	integrin, beta 5	2.6	0.0231	Plasma Membrane	other
ITSN1	intersectin 1 (SH3 domain protein)	-1.85	0.0540	Cytoplasm	other
IVNS1ABP	influenza virus NS1A binding protein	1.68	0.0320	Nucleus	other
JMJD1B	jumonji domain containing 1B	1.56	0.0500	Nucleus	other
KIAA0100	KIAA0100	-1.84	0.0536	Extracellular Space	other
KIAA0240	KIAA0240	2.52	0.0093	Unknown	other
KIAA0284	KIAA0284	-2.34	0.0382	Unknown	other
KIAA0528	KIAA0528	1.96	0.0226	Cytoplasm	other
KIAA0562	KIAA0562	3.29	0.0223	Unknown	other
KIAA0564	KIAA0564	1.51	0.0321	Unknown	other
KIAA0776	KIAA0776	3.72	0.0406	Unknown	other
KIAA1109	KIAA1109	-1.7	0.0527	Unknown	other
KIAA1609	KIAA1609	-1.51	0.0272	Unknown	other
KIF11	kinesin family member 11	1.53	0.0375	Nucleus	other
KIF14	kinesin family member 14	2.45	0.0213	Cytoplasm	other
KLHDC10	kelch domain containing 10	1.77	0.0459	Unknown	other
KRIT1	KRIT1, ankyrin repeat containing	3.28	0.0313	Plasma Membrane	other
KRT10	keratin 10	1.5	0.0407	Cytoplasm	other
LAPTM4B	lysosomal protein transmembrane 4 beta	1.56	0.0447	Unknown	other
LIMCH1	LIM and calponin homology domains 1	1.54	0.0161	Unknown	other
LL22NC03-75B3.6	KIAA1644 protein	-1.56	0.0475	Unknown	other
LOC100129361	hypothetical protein LOC100129361	1.53	0.0535	Unknown	other
LOC652493	similar to Ig kappa chain V-I region HK102 precursor	-1.55	0.0428	Unknown	other
LOC729580	hypothetical LOC729580	-2.07	0.0127	Unknown	other
LOC90379	hypothetical protein BC002926	-1.88	0.0192	Unknown	other
LPPR2	lipid phosphate phosphatase-related protein type 2	-2.08	0.0091	Unknown	other
LRP5	low density lipoprotein receptor-related protein 5	-1.67	0.0354	Plasma Membrane	other
LRRC23	leucine rich repeat containing 23	-1.79	0.0261	Plasma Membrane	other
LRRC40	leucine rich repeat containing 40	2.11	0.0195	Nucleus	other
LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	1.47	0.0377	Cytoplasm	other
LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)	1.74	0.0268	Unknown	other
LSM8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.49	0.0402	Nucleus	other
MAGEA4 (includes EG:4103)	melanoma antigen family A, 4	-1.86	0.0327	Cytoplasm	other
MAP4	microtubule-associated protein 4	-1.95	0.0526	Cytoplasm	other
MAP7	microtubule-associated protein 7	-1.84	0.0450	Cytoplasm	other
MARCKS	myristoylated alanine-rich protein kinase C	1.98	0.0392	Plasma	other

(includes EG:4082)	substrate			Membrane	
MBD3 (includes EG:53615)	methyl-CpG binding domain protein 3	-1.8	0.0388	Nucleus	other
MBD3 (includes EG:53615)	methyl-CpG binding domain protein 3	-1.77	0.0263	Nucleus	other
MBOAT7	membrane bound O-acyltransferase domain containing 7	-1.67	0.0422	Plasma Membrane	other
MCF2L	MCF.2 cell line derived transforming sequence-like	-1.6	0.0229	Cytoplasm	other
MCM3AP	minichromosome maintenance complex component 3 associated protein	-2.1	0.0464	Nucleus	other
MED13L	mediator complex subunit 13-like	2.15	0.0416	Nucleus	other
MEMO1 (includes EG:51072)	mediator of cell motility 1	2.06	0.0322	Unknown	other
METRN	meteorin, glial cell differentiation regulator	-2.48	0.0158	Extracellular Space	other
METTL7A	methyltransferase like 7A	2.1	0.0442	Unknown	other
MEX3D	mex-3 homolog D (C. elegans)	-3.14	0.0214	Unknown	other
MGC5457	chromosome 1 open reading frame 217	1.46	0.0468	Unknown	other
MID2	midline 2	-1.71	0.0509	Cytoplasm	other
MIER2	mesoderm induction early response 1, family member 2	-1.58	0.0328	Unknown	other
MINA	MYC induced nuclear antigen	1.87	0.0333	Nucleus	other
MLANA	melan-A	-1.54	0.0498	Plasma Membrane	other
MLF2	myeloid leukemia factor 2	-1.55	0.0401	Nucleus	other
MPZL1	myelin protein zero-like 1	-1.56	0.0505	Plasma Membrane	other
MRCL3	myosin regulatory light chain MRCL3	1.82	0.0322	Unknown	other
MTDH	metadherin	1.74	0.0318	Cytoplasm	other
MYBPC1	myosin binding protein C, slow type	1.64	0.0337	Cytoplasm	other
MYH14	myosin, heavy chain 14	-1.68	0.0450	Extracellular Space	other
MYO1C	myosin IC	-2.04	0.0493	Cytoplasm	other
N-PAC	cytokine-like nuclear factor n-pac	-2.83	0.0425	Unknown	other
NBN	nibrin	1.58	0.0476	Nucleus	other
NCAPG (includes EG:64151)	non-SMC condensin I complex, subunit G	2.51	0.0148	Nucleus	other
NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	1.84	0.0267	Nucleus	other
NELF	nasal embryonic LHRH factor	-2.83	0.0316	Extracellular Space	other
NOL7	nucleolar protein 7, 27kDa	1.89	0.0210	Nucleus	other
NPLOC4	nuclear protein localization 4 homolog (S. cerevisiae)	-1.9	0.0395	Nucleus	other
NRGN	neurogranin (protein kinase C substrate, RC3)	-1.88	0.0239	Cytoplasm	other
NUCB2	nucleobindin 2	1.7	0.0163	Nucleus	other
NUP205	nucleoporin 205kDa	1.55	0.0455	Nucleus	other
OAZ2 (includes EG:4947)	ornithine decarboxylase antizyme 2	-2.31	0.0344	Cytoplasm	other
OBSL1	obscurin-like 1	1.79	0.0296	Unknown	other

OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	-1.49	0.0186	Unknown	other
ORAI2	ORAI calcium release-activated calcium modulator 2	-1.58	0.0191	Unknown	other
OTUB1	OTU domain, ubiquitin aldehyde binding 1	-1.68	0.0451	Unknown	other
PAK1IP1	PAK1 interacting protein 1	1.81	0.0358	Nucleus	other
PAQR3	progestin and adipoQ receptor family member III	2.39	0.0413	Cytoplasm	other
PARC	p53-associated parkin-like cytoplasmic protein	-1.59	0.0439	Cytoplasm	other
PCDHAC2	protocadherin alpha subfamily C, 2	1.99	0.0511	Plasma Membrane	other
PCDHGA3	protocadherin gamma subfamily A, 3	-1.73	0.0316	Unknown	other
PDLIM2	PDZ and LIM domain 2 (mystique)	-1.92	0.0345	Cytoplasm	other
PELI1	pellino homolog 1 (Drosophila)	2.15	0.0514	Cytoplasm	other
PEX14	peroxisomal biogenesis factor 14	-1.88	0.0116	Cytoplasm	other
PEX16	peroxisomal biogenesis factor 16	-1.79	0.0480	Cytoplasm	other
PHTF2	putative homeodomain transcription factor 2	2.17	0.0128	Cytoplasm	other
PIBF1	progesterone immunomodulatory binding factor 1	2.55	0.0529	Nucleus	other
PICALM	phosphatidylinositol binding clathrin assembly protein	-1.58	0.0168	Cytoplasm	other
PKP3	plakophilin 3	-5.85	0.0200	Plasma Membrane	other
PLEKHA5	pleckstrin homology domain containing, family A member 5	1.93	0.0166	Unknown	other
PLEKHF2 (includes EG:79666)	pleckstrin homology domain containing, family F (with FYVE domain) member 2	2.72	0.0254	Unknown	other
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	2.03	0.0296	Cytoplasm	other
PMEPA1	prostate transmembrane protein, androgen induced 1	1.91	0.0153	Plasma Membrane	other
PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	-1.53	0.0519	Unknown	other
PMS2L11	postmeiotic segregation increased 2-like 11 pseudogene	-1.53	0.0137	Unknown	other
PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene	1.54	0.0304	Unknown	other
POLDIP3	polymerase (DNA-directed), delta interacting protein 3	-3.43	0.0402	Nucleus	other
PPP1R15A (includes EG:23645)	protein phosphatase 1, regulatory (inhibitor) subunit 15A	-1.54	0.0466	Cytoplasm	other
PRDM5	PR domain containing 5	-1.49	0.0507	Nucleus	other
PROCR	protein C receptor, endothelial (EPCR)	1.95	0.0539	Plasma Membrane	other
PRPF39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	2.14	0.0389	Unknown	other
PRR14	proline rich 14	-1.57	0.0433	Unknown	other
PSIP1	PC4 and SFRS1 interacting protein 1	1.68	0.0298	Nucleus	other
PSMG1	proteasome (prosome, macropain) assembly chaperone 1	1.73	0.0452	Plasma Membrane	other
PTH	parathyroid hormone	1.46	0.0540	Extracellular Space	other
RABGAP1	RAB GTPase activating protein 1	1.46	0.0264	Cytoplasm	other
RAD21	RAD21 homolog (S. pombe)	2.37	0.0537	Nucleus	other

RANGAP1	Ran GTPase activating protein 1	-1.59	0.0361	Cytoplasm	other
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	2.11	0.0229	Nucleus	other
RASSF4	Ras association (RalGDS/AF-6) domain family member 4	-1.55	0.0449	Unknown	other
RASSF7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	-1.46	0.0230	Unknown	other
RB1CC1	RB1-inducible coiled-coil 1	1.49	0.0417	Nucleus	other
RBM26	RNA binding motif protein 26	2.18	0.0461	Unknown	other
RCC1 (includes EG:1104)	regulator of chromosome condensation 1	-1.96	0.0381	Nucleus	other
RFPL1	ret finger protein-like 1	-1.68	0.0337	Unknown	other
RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	-1.89	0.0406	Unknown	other
RNF114	ring finger protein 114	-1.75	0.0405	Unknown	other
RNF17	ring finger protein 17	1.93	0.0454	Cytoplasm	other
RNF187	ring finger protein 187	-1.7	0.0468	Unknown	other
RNF220	ring finger protein 220	-1.74	0.0461	Unknown	other
RNF5 (includes EG:6048)	ring finger protein 5	1.48	0.0487	Cytoplasm	other
RNPS1	RNA binding protein S1, serine-rich domain	-2.19	0.0318	Nucleus	other
RNPS1	RNA binding protein S1, serine-rich domain	-1.89	0.0239	Nucleus	other
RP5-1000E10.4	suppressor of IKK epsilon	-2.53	0.0468	Unknown	other
RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	-1.51	0.0349	Cytoplasm	other
RPL13A	ribosomal protein L13a	-1.55	0.0283	Cytoplasm	other
RPL37	ribosomal protein L37	1.81	0.0253	Cytoplasm	other
RPL5 (includes EG:6125)	ribosomal protein L5	1.46	0.0425	Cytoplasm	other
RPS25	ribosomal protein S25	1.9	0.0494	Cytoplasm	other
RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	-1.84	0.0163	Cytoplasm	other
RTN2	reticulon 2	-2.25	0.0179	Cytoplasm	other
RUSC2	RUN and SH3 domain containing 2	-1.73	0.0536	Unknown	other
RWDD3	RWD domain containing 3	1.74	0.0533	Unknown	other
SBNO2	strawberry notch homolog 2 (Drosophila)	-4.15	0.0473	Unknown	other
SCG3	secretogranin III	1.86	0.0541	Extracellular Space	other
SDC2	syndecan 2	2.23	0.0314	Plasma Membrane	other
SDK2	sidekick homolog 2 (chicken)	-1.94	0.0311	Unknown	other
SEC31A	SEC31 homolog A (S. cerevisiae)	1.85	0.0388	Cytoplasm	other
SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	2.06	0.0233	Extracellular Space	other
SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	-1.99	0.0185	Plasma Membrane	other
SEPT11	septin 11	-1.78	0.0429	Nucleus	other
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	-1.46	0.0517	Extracellular Space	other
SEZ6L	seizure related 6 homolog (mouse)-like	-1.52	0.0482	Plasma Membrane	other
SEZ6L2	seizure related 6 homolog (mouse)-like 2	-1.57	0.0544	Unknown	other

SF3A2	splicing factor 3a, subunit 2, 66kDa	-1.8	0.0425	Nucleus	other
SFI1	Sfi1 homolog, spindle assembly associated (yeast)	-1.77	0.0077	Cytoplasm	other
SFRS1	splicing factor, arginine/serine-rich 1	-1.69	0.0403	Nucleus	other
SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	1.62	0.0350	Nucleus	other
SFRS15	splicing factor, arginine/serine-rich 15	-1.67	0.0329	Nucleus	other
SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	-1.59	0.0354	Cytoplasm	other
SIDT2	SID1 transmembrane family, member 2	-1.75	0.0386	Unknown	other
SIP1	survival of motor neuron protein interacting protein 1	3.33	0.0389	Nucleus	other
SKP2	S-phase kinase-associated protein 2 (p45)	-1.56	0.0515	Nucleus	other
SLITRK5	SLIT and NTRK-like family, member 5	1.75	0.0380	Unknown	other
SMA4	glucuronidase, beta pseudogene	2.18	0.0377	Unknown	other
SMG5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.6	0.0507	Nucleus	other
SNRPA1	small nuclear ribonucleoprotein polypeptide A'	1.97	0.0360	Nucleus	other
SNRPG	small nuclear ribonucleoprotein polypeptide G	1.72	0.0227	Nucleus	other
SOCS1	suppressor of cytokine signaling 1	-2.06	0.0470	Cytoplasm	other
SPAG11A	sperm associated antigen 11A	-2.03	0.0289	Unknown	other
SPG11 (includes EG:80208)	spastic paraplegia 11 (autosomal recessive)	1.61	0.0408	Unknown	other
SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	-2.23	0.0287	Unknown	other
SPTBN1	spectrin, beta, non-erythrocytic 1	-1.61	0.0495	Plasma Membrane	other
SSR1	signal sequence receptor, alpha	1.49	0.0254	Cytoplasm	other
SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	1.51	0.0480	Plasma Membrane	other
STAG2	stromal antigen 2	2.55	0.0254	Nucleus	other
STAG3L4	stromal antigen 3-like 4	-1.64	0.0543	Unknown	other
SV2C	synaptic vesicle glycoprotein 2C	-1.77	0.0222	Plasma Membrane	other
SYMPK	symplekin	-2.18	0.0415	Cytoplasm	other
SYTL2	synaptotagmin-like 2	-2.25	0.0303	Cytoplasm	other
TAGLN2	transgelin 2	-2.11	0.0224	Cytoplasm	other
TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	1.93	0.0313	Plasma Membrane	other
TCL1A	T-cell leukemia/lymphoma 1A	-1.46	0.0520	Nucleus	other
TELO2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	-1.57	0.0423	Unknown	other
TEX13B	testis expressed 13B	-1.72	0.0440	Unknown	other
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	1.68	0.0352	Extracellular Space	other
THOC2	THO complex 2	2.08	0.0376	Nucleus	other
THUMPD1	THUMP domain containing 1	1.71	0.0368	Unknown	other
TIA1	TIA1 cytotoxic granule-associated RNA binding protein	1.91	0.0348	Nucleus	other
TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	-2.11	0.0283	Nucleus	other
TMBIM6	transmembrane BAX inhibitor motif containing 6	-1.82	0.0465	Nucleus	other
TMEM135	transmembrane protein 135	1.93	0.0356	Unknown	other

TMEM184C	transmembrane protein 184C	1.52	0.0543	Unknown	other
TMEM5	transmembrane protein 5	2	0.0196	Plasma Membrane	other
TMEM70	transmembrane protein 70	1.76	0.0463	Unknown	other
TNFAIP2	tumor necrosis factor, alpha-induced protein 2	-1.5	0.0390	Extracellular Space	other
TOB2	transducer of ERBB2, 2	2.18	0.0262	Nucleus	other
TOLLIP	toll interacting protein	-1.61	0.0501	Cytoplasm	other
TPRKB	TP53RK binding protein	1.84	0.0459	Unknown	other
TRA@	T cell receptor alpha locus	-1.54	0.0456	Cytoplasm	other
TRAF3	TNF receptor-associated factor 3	1.46	0.0542	Cytoplasm	other
TRAPPC9	trafficking protein particle complex 9	-1.84	0.0202	Plasma Membrane	other
TRD@	T cell receptor delta locus	-1.56	0.0228	Cytoplasm	other
TSPAN13	tetraspanin 13	1.78	0.0460	Plasma Membrane	other
TSPAN4	tetraspanin 4	-3.21	0.0209	Plasma Membrane	other
TSPYL4	TSPY-like 4	1.7	0.0128	Nucleus	other
TUBA1A	tubulin, alpha 1a	1.83	0.0519	Cytoplasm	other
TUBGCP3	tubulin, gamma complex associated protein 3	2.09	0.0352	Cytoplasm	other
UBE2Z	ubiquitin-conjugating enzyme E2Z	-1.64	0.0237	Unknown	other
UBIAD1	UbiA prenyltransferase domain containing 1	-1.75	0.0450	Nucleus	other
UBQLN2	ubiquilin 2	1.93	0.0126	Nucleus	other
UBQLN4	ubiquilin 4	2.32	0.0481	Cytoplasm	other
VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	-1.7	0.0477	Unknown	other
WAPAL	wings apart-like homolog (Drosophila)	2.03	0.0180	Nucleus	other
WBP1	WW domain binding protein 1	-2.12	0.0534	Cytoplasm	other
WBP2	WW domain binding protein 2	-2.17	0.0104	Cytoplasm	other
WDR1	WD repeat domain 1	-2.43	0.0498	Extracellular Space	other
WDR23	WD repeat domain 23	-1.67	0.0199	Unknown	other
WDR42A	WD repeat domain 42A	-1.58	0.0267	Unknown	other
WDR6 (includes EG:11180)	WD repeat domain 6	-1.91	0.0505	Unknown	other
WDTC1	WD and tetratricopeptide repeats 1	-2.37	0.0122	Unknown	other
WIZ	widely interspaced zinc finger motifs	-2.83	0.0536	Nucleus	other
WRB	tryptophan rich basic protein	1.72	0.0289	Extracellular Space	other
YIPF2	Yip1 domain family, member 2	-2.23	0.0127	Unknown	other
YTHDF2	YTH domain family, member 2	1.67	0.0217	Unknown	other
YTHDF3	YTH domain family, member 3	1.52	0.0380	Cytoplasm	other
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	2.6	0.0202	Cytoplasm	other
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	2.77	0.0221	Cytoplasm	other
ZBTB10	zinc finger and BTB domain containing 10	2.17	0.0175	Nucleus	other
ZBTB11	zinc finger and BTB domain containing 11	2.12	0.0306	Nucleus	other
ZC3H15	zinc finger CCCH-type containing 15	2.03	0.0437	Nucleus	other
ZER1	zer-1 homolog (C. elegans)	-1.76	0.0355	Unknown	other
ZFR	zinc finger RNA binding protein	-1.9	0.0325	Nucleus	other
ZNF160	zinc finger protein 160	1.81	0.0251	Nucleus	other
ZNF580	zinc finger protein 580	-1.67	0.0226	Nucleus	other

ZNF710	zinc finger protein 710	-1.5	0.0430	Nucleus	other
ZNF768	zinc finger protein 768	-2.1	0.0436	Unknown	other
ZNF783	zinc finger family member 783	-1.53	0.0479	Unknown	other
ZNF834	zinc finger protein 834	-1.85	0.0447	Unknown	other
ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	-1.52	0.0254	Nucleus	other
ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	-2.29	0.0256	Unknown	other
ADAM15	ADAM metallopeptidase domain 15	-4.29	0.0279	Plasma Membrane	peptidase
ADAM17	ADAM metallopeptidase domain 17	1.58	0.0352	Plasma Membrane	peptidase
ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	2.39	0.0188	Plasma Membrane	peptidase
ATG4B	ATG4 autophagy related 4 homolog B (S. cerevisiae)	-2.02	0.0266	Cytoplasm	peptidase
CAPNS1	calpain, small subunit 1	-1.5	0.0481	Cytoplasm	peptidase
CASP6	caspase 6, apoptosis-related cysteine peptidase	2.22	0.0334	Cytoplasm	peptidase
CLGN	calmegin	2.69	0.0252	Cytoplasm	peptidase
CPN1	carboxypeptidase N, polypeptide 1	-1.87	0.0538	Extracellular Space	peptidase
CTRL	chymotrypsin-like	-1.91	0.0448	Extracellular Space	peptidase
ELA2A	elastase 2A	-1.67	0.0374	Extracellular Space	peptidase
FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	-1.59	0.0249	Plasma Membrane	peptidase
KIAA1967	KIAA1967	-2.49	0.0270	Cytoplasm	peptidase
MBTPS2	membrane-bound transcription factor peptidase, site 2	-1.5	0.0314	Cytoplasm	peptidase
MMP11	matrix metallopeptidase 11 (stromelysin 3)	-1.48	0.0356	Extracellular Space	peptidase
MMP19	matrix metallopeptidase 19	-1.52	0.0465	Extracellular Space	peptidase
PGCP	plasma glutamate carboxypeptidase	-1.58	0.0346	Extracellular Space	peptidase
PREPL	prolyl endopeptidase-like	-1.53	0.0512	Unknown	peptidase
PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	1.55	0.0182	Cytoplasm	peptidase
UCHL5	ubiquitin carboxyl-terminal hydrolase L5	2.21	0.0290	Cytoplasm	peptidase
USP1	ubiquitin specific peptidase 1	1.76	0.0063	Cytoplasm	peptidase
USP21 (includes EG:27005)	ubiquitin specific peptidase 21	-1.58	0.0270	Cytoplasm	peptidase
USP5	ubiquitin specific peptidase 5 (isopeptidase T)	-3.85	0.0156	Cytoplasm	peptidase
ACP1	acid phosphatase 1, soluble	1.63	0.0266	Cytoplasm	phosphatase
ACP2	acid phosphatase 2, lysosomal	-1.82	0.0213	Cytoplasm	phosphatase
CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	3.09	0.0438	Nucleus	phosphatase
CDC25C	cell division cycle 25 homolog C (S. pombe)	-2.12	0.0346	Nucleus	phosphatase

ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	1.87	0.0526	Cytoplasm	phosphatase
INPP5J	inositol polyphosphate-5-phosphatase J	-1.53	0.0329	Cytoplasm	phosphatase
NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	-1.71	0.0215	Cytoplasm	phosphatase
PPFIA3 (includes EG:8541)	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	-1.63	0.0371	Plasma Membrane	phosphatase
PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	4.15	0.0311	Cytoplasm	phosphatase
PPP2R3A (includes EG:5523)	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	-1.52	0.0495	Nucleus	phosphatase
PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	-1.68	0.0307	Cytoplasm	phosphatase
PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	2.27	0.0110	Cytoplasm	phosphatase
PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	-1.95	0.0367	Cytoplasm	phosphatase
SYNJ1	synaptojanin 1	2.11	0.0073	Cytoplasm	phosphatase
SYNJ2	synaptojanin 2	-1.47	0.0425	Cytoplasm	phosphatase
TPTE	transmembrane phosphatase with tensin homology	1.73	0.0419	Plasma Membrane	phosphatase
ARNT	aryl hydrocarbon receptor nuclear translocator	-1.96	0.0283	Nucleus	transcription regulator
ASB1	ankyrin repeat and SOCS box-containing 1	-1.61	0.0263	Nucleus	transcription regulator
ATF1	activating transcription factor 1	2	0.0266	Nucleus	transcription regulator
BTF3	basic transcription factor 3	2.24	0.0077	Nucleus	transcription regulator
BTG2	BTG family, member 2	-1.88	0.0334	Nucleus	transcription regulator
C19ORF2	chromosome 19 open reading frame 2	1.66	0.0536	Nucleus	transcription regulator
CALCOCO1	calcium binding and coiled-coil domain 1	-1.67	0.0524	Nucleus	transcription regulator

CALR	calreticulin	-2.08	0.0482	Cytoplasm	transcription regulator
CAND1	cullin-associated and neddylation-dissociated 1	1.89	0.0295	Cytoplasm	transcription regulator
CBX4	chromobox homolog 4 (Pc class homolog, Drosophila)	-3.93	0.0487	Nucleus	transcription regulator
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	1.83	0.0268	Nucleus	transcription regulator
CNOT8	CCR4-NOT transcription complex, subunit 8	2.55	0.0277	Nucleus	transcription regulator
COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	1.65	0.0359	Nucleus	transcription regulator
CREBZF	CREB/ATF bZIP transcription factor	1.56	0.0356	Nucleus	transcription regulator
CXXC1	CXXC finger 1 (PHD domain)	-1.7	0.0471	Nucleus	transcription regulator
DBP	D site of albumin promoter (albumin D-box) binding protein	-1.67	0.0479	Nucleus	transcription regulator
DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	2.03	0.0294	Nucleus	transcription regulator
E2F4	E2F transcription factor 4, p107/p130-binding	-1.82	0.0406	Nucleus	transcription regulator
ETV4	ets variant 4	-1.72	0.0304	Nucleus	transcription regulator
FEM1B	fem-1 homolog b (C. elegans)	2.14	0.0209	Nucleus	transcription regulator
FUS	fusion (involved in t(12;16) in malignant liposarcoma)	-2.26	0.0279	Nucleus	transcription regulator
GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	-1.88	0.0487	Nucleus	transcription regulator
HES1	hairy and enhancer of split 1, (Drosophila)	1.76	0.0340	Nucleus	transcription regulator
HMGA1	high mobility group AT-hook 1	-1.81	0.0399	Nucleus	transcription regulator
HMX1	H6 family homeobox 1	-1.67	0.0139	Nucleus	transcription regulator
HOXB13	homeobox B13	-2.2	0.0090	Nucleus	transcription regulator

HTATSF1	HIV-1 Tat specific factor 1	1.79	0.0286	Nucleus	transcription regulator
KAT5	K(lysine) acetyltransferase 5	-1.58	0.0232	Nucleus	transcription regulator
KLF10	Kruppel-like factor 10	1.7	0.0438	Nucleus	transcription regulator
LASS6	LAG1 homolog, ceramide synthase 6	1.56	0.0427	Nucleus	transcription regulator
LEF1	lymphoid enhancer-binding factor 1	2.01	0.0175	Nucleus	transcription regulator
LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	-1.75	0.0230	Cytoplasm	transcription regulator
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	3.58	0.0063	Nucleus	transcription regulator
MED16	mediator complex subunit 16	-1.69	0.0444	Nucleus	transcription regulator
MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	-1.87	0.0467	Nucleus	transcription regulator
MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	-1.77	0.0383	Nucleus	transcription regulator
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	-1.6	0.0394	Nucleus	transcription regulator
MZF1	myeloid zinc finger 1	-1.7	0.0405	Nucleus	transcription regulator
NFRKB	nuclear factor related to kappaB binding protein	-1.7	0.0475	Nucleus	transcription regulator
NFYA	nuclear transcription factor Y, alpha	-1.83	0.0176	Nucleus	transcription regulator
NKX2-1	NK2 homeobox 1	-1.59	0.0412	Nucleus	transcription regulator
NR2C1	nuclear receptor subfamily 2, group C, member 1	1.61	0.0262	Nucleus	transcription regulator
PA2G4	proliferation-associated 2G4, 38kDa	1.48	0.0319	Nucleus	transcription regulator
PAX8	paired box 8	-1.49	0.0408	Nucleus	transcription regulator
PDX1 (includes EG:3651)	pancreatic and duodenal homeobox 1	-2.31	0.0441	Nucleus	transcription regulator

PIAS2	protein inhibitor of activated STAT, 2	-1.73	0.0440	Nucleus	transcription regulator
PIR	pirin (iron-binding nuclear protein)	1.71	0.0116	Nucleus	transcription regulator
PTGES2	prostaglandin E synthase 2	-1.86	0.0367	Cytoplasm	transcription regulator
RB1	retinoblastoma 1	3.08	0.0191	Nucleus	transcription regulator
REST	RE1-silencing transcription factor	2.54	0.0188	Nucleus	transcription regulator
RFX5	regulatory factor X, 5 (influences HLA class II expression)	-1.46	0.0414	Nucleus	transcription regulator
RNF14	ring finger protein 14	2.47	0.0534	Nucleus	transcription regulator
RNF6	ring finger protein (C3H2C3 type) 6	2.34	0.0420	Nucleus	transcription regulator
SAP30	Sin3A-associated protein, 30kDa	-2.47	0.0396	Nucleus	transcription regulator
SIN3B (includes EG:23309)	SIN3 homolog B, transcription regulator (yeast)	-2.03	0.0215	Nucleus	transcription regulator
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	1.86	0.0278	Nucleus	transcription regulator
SOX4	SRY (sex determining region Y)-box 4	1.62	0.0254	Nucleus	transcription regulator
SREBF2	sterol regulatory element binding transcription factor 2	-2.93	0.0271	Nucleus	transcription regulator
SSBP2	single-stranded DNA binding protein 2	2.11	0.0378	Nucleus	transcription regulator
SUB1	SUB1 homolog (S. cerevisiae)	1.47	0.0445	Nucleus	transcription regulator
SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	-1.99	0.0351	Nucleus	transcription regulator
SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	-1.51	0.0517	Nucleus	transcription regulator
TAF1C	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	-1.64	0.0514	Nucleus	transcription regulator
TAF2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	2.16	0.0255	Nucleus	transcription regulator

TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	1.57	0.0283	Nucleus	transcription regulator
TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	-1.98	0.0531	Nucleus	transcription regulator
TCERG1	transcription elongation regulator 1	1.6	0.0425	Nucleus	transcription regulator
TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	1.55	0.0489	Nucleus	transcription regulator
TGIF2	TGFB-induced factor homeobox 2	-1.47	0.0250	Nucleus	transcription regulator
TLX2 (includes EG:3196)	T-cell leukemia homeobox 2	-1.81	0.0528	Nucleus	transcription regulator
TMF1	TATA element modulatory factor 1	1.52	0.0460	Cytoplasm	transcription regulator
TRIM24	tripartite motif-containing 24	2.09	0.0236	Nucleus	transcription regulator
TRIM33	tripartite motif-containing 33	1.49	0.0522	Nucleus	transcription regulator
TSC22D1	TSC22 domain family, member 1	1.93	0.0502	Nucleus	transcription regulator
YEATS4	YEATS domain containing 4	2.29	0.0194	Nucleus	transcription regulator
ZBTB16	zinc finger and BTB domain containing 16	3.17	0.0461	Nucleus	transcription regulator
ZBTB32	zinc finger and BTB domain containing 32	-1.5	0.0519	Nucleus	transcription regulator
ZMIZ2	zinc finger, MIZ-type containing 2	-2.65	0.0188	Nucleus	transcription regulator
ZNF268	zinc finger protein 268	2.17	0.0196	Nucleus	transcription regulator
ZNF323	zinc finger protein 323	-1.7	0.0236	Nucleus	transcription regulator
ZNF444	zinc finger protein 444	-1.8	0.0339	Nucleus	transcription regulator
ZNF83	zinc finger protein 83	2.58	0.0145	Nucleus	transcription regulator
EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	1.57	0.0540	Cytoplasm	translation regulator
EIF3A	eukaryotic translation initiation factor 3,	2.06	0.0435	Cytoplasm	translation

	subunit A				regulator
EIF3J	eukaryotic translation initiation factor 3, subunit J	2.89	0.0398	Cytoplasm	translation regulator
EIF4E	eukaryotic translation initiation factor 4E	3.42	0.0079	Cytoplasm	translation regulator
PAIP1	poly(A) binding protein interacting protein 1	2.43	0.0206	Cytoplasm	translation regulator
CHRNA2	cholinergic receptor, nicotinic, alpha 2 (neuronal)	-1.55	0.0379	Plasma Membrane	transmembrane receptor
CLDN4	claudin 4	-2.34	0.0448	Plasma Membrane	transmembrane receptor
HLA-DRB1	major histocompatibility complex, class II, DR beta 1	2.46	0.0306	Plasma Membrane	transmembrane receptor
IL22RA1	interleukin 22 receptor, alpha 1	-1.57	0.0355	Plasma Membrane	transmembrane receptor
IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	-1.54	0.0369	Plasma Membrane	transmembrane receptor
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	4.66	0.0435	Plasma Membrane	transmembrane receptor
PVR	poliovirus receptor	-1.47	0.0361	Plasma Membrane	transmembrane receptor
RARRES2	retinoic acid receptor responder (tazarotene induced) 2	-1.49	0.0507	Plasma Membrane	transmembrane receptor
SPN	sialophorin	2.41	0.0449	Plasma Membrane	transmembrane receptor
TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-1.7	0.0531	Plasma Membrane	transmembrane receptor
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	-2.12	0.0490	Plasma Membrane	transporter
ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4	-1.49	0.0520	Plasma Membrane	transporter
AP1M2	adaptor-related protein complex 1, mu 2 subunit	-1.78	0.0438	Cytoplasm	transporter
AP2S1	adaptor-related protein complex 2, sigma 1 subunit	-1.95	0.0227	Cytoplasm	transporter
APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	-1.74	0.0466	Cytoplasm	transporter

APOM	apolipoprotein M	-1.49	0.0509	Plasma Membrane	transporter
AQP3	aquaporin 3 (Gill blood group)	-1.94	0.0126	Plasma Membrane	transporter
ARF5	ADP-ribosylation factor 5	-1.66	0.0353	Cytoplasm	transporter
ATP13A3 (includes EG:79572)	ATPase type 13A3	-2.22	0.0152	Unknown	transporter
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	2.07	0.0453	Plasma Membrane	transporter
ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-1.47	0.0273	Cytoplasm	transporter
ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	-1.49	0.0286	Cytoplasm	transporter
ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	-2.68	0.0227	Cytoplasm	transporter
ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	-1.48	0.0186	Cytoplasm	transporter
CHP	calcium binding protein P22	-1.72	0.0519	Cytoplasm	transporter
COPB1	coatomer protein complex, subunit beta 1	1.5	0.0430	Cytoplasm	transporter
CSE1L	CSE1 chromosome segregation 1-like (yeast)	1.7	0.0269	Nucleus	transporter
ENSA	endosulfine alpha	-1.68	0.0411	Unknown	transporter
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	1.52	0.0444	Unknown	transporter
EXOC7	exocyst complex component 7	-1.62	0.0528	Plasma Membrane	transporter
FABP7	fatty acid binding protein 7, brain	-1.94	0.0338	Cytoplasm	transporter
FDX1	ferredoxin 1	1.49	0.0458	Cytoplasm	transporter
GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	-2.23	0.0134	Cytoplasm	transporter
KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	1.54	0.0113	Nucleus	transporter
KPNB1	karyopherin (importin) beta 1	3.96	0.0172	Nucleus	transporter
LDLR	low density lipoprotein receptor	-1.78	0.0293	Plasma Membrane	transporter
LDLRAP1	low density lipoprotein receptor adaptor protein 1	-1.9	0.0213	Cytoplasm	transporter
MB	myoglobin	-1.99	0.0441	Cytoplasm	transporter
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	-5.14	0.0438	Cytoplasm	transporter
MFSD1	major facilitator superfamily domain containing 1	1.51	0.0491	Unknown	transporter
NUP50	nucleoporin 50kDa	-1.84	0.0422	Nucleus	transporter
PEX7	peroxisomal biogenesis factor 7	1.97	0.0421	Cytoplasm	transporter
PNMA2	paraneoplastic antigen MA2	-1.57	0.0408	Nucleus	transporter

RACGAP1	Rac GTPase activating protein 1	1.45	0.0139	Cytoplasm	transporter
RBP4	retinol binding protein 4, plasma	-1.52	0.0451	Extracellular Space	transporter
SCAMP1	secretory carrier membrane protein 1	-2.07	0.0313	Cytoplasm	transporter
SCAMP2	secretory carrier membrane protein 2	-1.54	0.0336	Cytoplasm	transporter
SEC22A	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	1.71	0.0229	Cytoplasm	transporter
SEC62	SEC62 homolog (S. cerevisiae)	1.55	0.0233	Cytoplasm	transporter
SEH1L	SEH1-like (S. cerevisiae)	1.75	0.0312	Cytoplasm	transporter
SFXN3	sideroflexin 3	-1.63	0.0370	Cytoplasm	transporter
SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	-1.92	0.0255	Plasma Membrane	transporter
SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	-2.13	0.0464	Plasma Membrane	transporter
SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	2.41	0.0150	Plasma Membrane	transporter
SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	-3.56	0.0294	Plasma Membrane	transporter
SLC19A1	solute carrier family 19 (folate transporter), member 1	-1.63	0.0525	Plasma Membrane	transporter
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	1.98	0.0513	Plasma Membrane	transporter
SLC22A4 (includes EG:6583)	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	-1.64	0.0401	Plasma Membrane	transporter
SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	-1.83	0.0498	Plasma Membrane	transporter
SLC25A10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	-2.14	0.0384	Cytoplasm	transporter
SLC25A13	solute carrier family 25, member 13 (citrin)	1.71	0.0135	Cytoplasm	transporter
SLC25A22	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	-2.08	0.0517	Cytoplasm	transporter
SLC25A44	solute carrier family 25, member 44	1.65	0.0418	Cytoplasm	transporter
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	2.26	0.0518	Cytoplasm	transporter
SLC39A9	solute carrier family 39 (zinc transporter), member 9	-1.78	0.0415	Unknown	transporter
SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	-1.58	0.0488	Plasma Membrane	transporter
SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	1.51	0.0516	Plasma Membrane	transporter
SNAP23	synaptosomal-associated protein, 23kDa	1.83	0.0461	Plasma Membrane	transporter
SNX13	sorting nexin 13	-1.58	0.0361	Cytoplasm	transporter
SRI	sorcin	1.93	0.0153	Cytoplasm	transporter
SYT2	synaptotagmin II	-2.28	0.0512	Cytoplasm	transporter

TCOF1	Treacher Collins-Franceschetti syndrome 1	1.69	0.0345	Nucleus	transporter
TMED1	transmembrane emp24 protein transport domain containing 1	-1.91	0.0443	Extracellular Space	transporter
TSNAX	translin-associated factor X	1.64	0.0226	Nucleus	transporter
USO1	USO1 homolog, vesicle docking protein (yeast)	-1.7	0.0266	Cytoplasm	transporter
VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	2.57	0.0098	Cytoplasm	transporter
ZFYVE16	zinc finger, FYVE domain containing 16	2.13	0.0216	Nucleus	transporter

Genes differentially expressed in response to DHT for 2h in R1 cells

Symbol	Entrez Gene Name	Fold Change	p-value	Location	Type
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	2.92	0.0038	Cytoplasm	enzyme
DNM1L	dynamin 1-like	1.7	0.0234	Cytoplasm	enzyme
FKBP5	FK506 binding protein 5	4.45	0.0370	Nucleus	enzyme
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	3.18	0.0107	Cytoplasm	enzyme
ODC1	ornithine decarboxylase 1	1.72	0.0101	Cytoplasm	enzyme
PDE9A	phosphodiesterase 9A	1.77	0.0392	Cytoplasm	enzyme
POP1	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)	1.54	0.0404	Nucleus	enzyme
F2R	coagulation factor II (thrombin) receptor	1.57	0.0206	Plasma Membrane	G-protein coupled receptor
FZD1	frizzled homolog 1 (Drosophila)	1.83	0.0443	Plasma Membrane	G-protein coupled receptor
FZD5	frizzled homolog 5 (Drosophila)	2.04	0.0269	Plasma Membrane	G-protein coupled receptor
JAG1	jagged 1 (Alagille syndrome)	1.93	0.0090	Extracellular Space	growth factor
KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	2.27	0.0271	Plasma Membrane	ion channel
BBS10	Bardet-Biedl syndrome 10	2.7	0.0282	Unknown	other
C1ORF107	chromosome 1 open reading frame 107	1.75	0.0351	Nucleus	other
C1ORF116	chromosome 1 open reading frame 116	3.11	0.0359	Unknown	other
CCNE2	cyclin E2	1.96	0.0284	Nucleus	other
GADD45G	growth arrest and DNA-damage-inducible, gamma	11.03	0.0105	Nucleus	other
HSPC159	galectin-related protein	1.67	0.0207	Unknown	other
MBOAT2	membrane bound O-acyltransferase domain containing 2	1.77	0.0413	Unknown	other
MRFAP1L1	Morf4 family associated protein 1-like 1	1.45	0.0524	Unknown	other
NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	1.91	0.0529	Nucleus	other
ORC5L	origin recognition complex, subunit 5-like (yeast)	1.67	0.0456	Nucleus	other
PER1	period homolog 1 (Drosophila)	2.49	0.0135	Nucleus	other
PHF20L1	PHD finger protein 20-like 1	1.53	0.0424	Unknown	other
SOCS2	suppressor of cytokine signaling 2	6	0.0089	Cytoplasm	other
SPHAR	S-phase response (cyclin-related)	2.21	0.0117	Unknown	other
TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	3.28	0.0118	Unknown	other
TNFAIP8	tumor necrosis factor, alpha-induced protein 8	2.38	0.0479	Cytoplasm	other
ZNF22	zinc finger protein 22 (KOX 15)	1.64	0.0201	Nucleus	other
ACTG2	actin, gamma 2, smooth muscle, enteric	-1.49	0.026604	Cytoplasm	other
CLEC2B	C-type lectin domain family 2, member B	-1.47	0.050511	Plasma Membrane	other
GON4L	gon-4-like	-1.55	0.035377	Unknown	other
LMO4	LIM domain only 4	-1.47	0.038536	Nucleus	other
LOC4951 /// OCM	oncomodulin 2	-2.05	0.022975	Unknown	other

PHF7	PHD finger protein 7	-1.6	0.021672	Nucleus	other
PLEKHM1	pleckstrin homology domain containing, family M (with RUN domain) member 1	-2.1	0.045489	Cytoplasm	other
S100A7	S100 calcium binding protein A7	-1.96	0.050181	Cytoplasm	other
TREM1	triggering receptor expressed on myeloid cells 1	-1.71	0.030421	Plasma Membrane	other
MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	1.55	0.0289	Cytoplasm	peptidase
ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	1.64	0.0513	Plasma Membrane	transporter
HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	-1.45	0.044667	Cytoplasm	enzyme
HRH3	histamine receptor H3	-1.46	0.024069	Plasma Membrane	G-protein coupled receptor
BMP2	bone morphogenetic protein 2	-2.2	0.011801	Extracellular	growth factor
DKK1	dickkopf homolog 1	-2.49	0.013399	Extracellular	growth factor
HBEGF	heparin-binding EGF-like growth factor	-1.97	0.017622	Extracellular	growth factor
CHKA	choline kinase alpha	1.5	0.0265	Cytoplasm	kinase
NDRG1	N-myc downstream regulated 1	1.66	0.0103	Nucleus	kinase
PDK4	pyruvate dehydrogenase kinase, isozyme 4	3.9	0.0220	Cytoplasm	kinase
SGK1	serum/glucocorticoid regulated kinase 1	6.92	0.0051	Cytoplasm	kinase
ACVR2B	activin A receptor, type IIB	-1.49	0.042086	Plasma Membrane	kinase
EPHB3	EPH receptor B3	-2.13	0.017336	Plasma Membrane	kinase
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	-1.67	0.030496	Cytoplasm	kinase
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	3.07	0.0279	Nucleus	transcription regulator
FOXA1	forkhead box A1	1.46	0.0444	Nucleus	transcription regulator
HEY1	hairy/enhancer-of-split related with YRPW motif 1	2.04	0.0182	Nucleus	transcription regulator
LBH	limb bud and heart development homolog (mouse)	1.51	0.0492	Nucleus	transcription regulator
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	2.14	0.0249	Nucleus	transcription regulator
NKX3-1	NK3 homeobox 1	1.91	0.0277	Nucleus	transcription regulator
PIAS1	protein inhibitor of activated STAT, 1	1.55	0.0404	Nucleus	transcription regulator
TSC22D1	TSC22 domain family, member 1	1.8	0.0143	Nucleus	transcription regulator
ZBTB16	zinc finger and BTB domain containing 16	4.63	0.0327	Nucleus	transcription regulator
ELF3	E74-like factor 3	-2.15	0.01564	Nucleus	transcription regulator
HES1	hairy and enhancer of split 1	-1.83	0.043713	Nucleus	transcription regulator
ID2	nhibitor of DNA binding 2, dominant negative helix-loop-helix protein	-1.87	0.02263	Nucleus	transcription regulator
ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	-1.47	0.028394	Nucleus	transcription regulator
ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	-2.34	0.020332	Nucleus	transcription regulator
JUNB	jun B proto-oncogene	-1.98	0.038572	Nucleus	transcription

					regulator
MSX2	msh homeobox 2	-3.56	0.008277	Nucleus	transcription regulator
PITX1	paired-like homeodomain 1	-1.56	0.029816	Nucleus	transcription regulator
TOB1	transducer of ERBB2, 1	-1.6	0.024468	Nucleus	transcription regulator
ZFP36L2	zinc finger protein 36, C3H type-like 2	-1.86	0.010737	Nucleus	transcription regulator
CLDN4	claudin 4	-1.75	0.024505	Plasma Membrane	transmembrane receptor
---		-2.32	0.030849		
---		-1.71	0.040187		
---		-1.61	0.045368		
---		-1.61	0.035459		
BAMBI		-3.42	0.012109		

Supplementary Table 3 Direct AR target genes by coupling analysis of gene expression profile and ChIP-on-chip in Rv1 cells

Rv1								R1				
Closest gene	**Gene annotation**	**chromosome**	**start**	**end**	**distance_to_TSS**	**distance_to_TES**	**location**	**start**	**end**	**distance_to_TSS**	**distance_to_TES**	**location**
Transcriptional Regulation												
BTF3	basic transcription factor 3	chr5	72829283	72829611	-558	-7756	TSS_upstream					
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	chr8	48810874	48811546	2112	818	TES_downstream	48810874	48811512	2129	835	TES_downstream
NR2F2	nuclear receptor subfamily 2, group F, member 2	chr15	94670166	94670345	-4694	-12789	TSS_upstream					
NR6A1	nuclear receptor subfamily 6, group A, member 1	chr9	126571126	126571291	2188	-246685	intron					
POLDIP3	polymerase (DNA-directed), delta interacting protein 3	chr22	41341510	41341922	-811	-32045	TSS_upstream					
			41346902	41347342	-6217	-37451	TSS_upstream					
SSBP2	single-stranded DNA binding protein 2	chr5	81086222	81087276	-3922	-335321	TSS_upstream	81084102	81084428	-1438	-332837	TSS_upstream
			81087631	81088127	-5052	-336451	TSS_upstream	81084870	81087848	-3532	-334931	TSS_upstream
TLE3	transducin-like enhancer of split 3	chr15	68173921	68174283	2109	-44630	intron	68174070	68174212	2070	-44669	intron
			68177489	68177899	-1483	-48222	TSS_upstream	68177412	68177899	-1444	-48183	TSS_upstream
			68179274	68179399	-3125	-49864	TSS_upstream	68179168	68179525	-3135	-49874	TSS_upstream
YEATS4	YEATS domain containing 4	chr12	68040290	68040575	634	-30409	intron					

ZBTB10	zinc finger and BTB domain containing 10	chr8	81560014	81560388	-801	-35120	TSS_upstream					
			81626217	81627334	65773	31454	TES_downstream					
ZNF444	zinc finger protein 444	chr19	61344893	61345356	757	-18948	5'UTR					
ZNF710	zinc finger protein 710	chr15	88343227	88343474	-2405	-81678	TSS_upstream					
Cell Cycle												
CDC14A	CDC14 cell division cycle 14 homolog A	chr1	100593181	100593441	2677	-144290	intron					
CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	chr12	12758279	12758544	-3164	-8157	TSS_upstream					
			12758865	12759247	-2519	-7512	TSS_upstream					
			12760267	12760982	-951	-5944	TSS_upstream	12760478	12760620	-1026	-6019	TSS_upstream
			12762024	12764574	1724	-3269	3'UTR	12762024	12762322	598	-4395	exon
			12765035	12765219	3552	-1441	3'UTR					
			12765950	12767701	5250	257	TES_downstream	12767356	12767812	6009	1016	TES_downstream
			12769732	12770929	8755	3762	TES_downstream	12769363	12769913	8063	3070	TES_downstream
PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	chr2	28822967	28823757	-4755	-55946	TSS_upstream	28822859	28823670	-4853	-56044	TSS_upstream
			28829333	28829574	1324	-49855	intron	28829106	28829914	1381	-49798	intron
PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	chr4	102485656	102485786	1654	-322112	intron					
			102489257	102490309	-2408	-326174	TSS_upstream					
RB1CC1	RB1-	chr8	53794702	53795411	-5512	-97485	TSS_upstream					

	inducible coiled-coil 1											
Metabolic Process												
METTL7A	methyltransferase like 7A	chr12	49603391	49603847	-1181	-8946	TSS_upstream					
			49604479	49605762	320	-7445	exon	49604479	49605762	320	-7445	exon
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	chr8	18110919	18111701	-584	-13788	TSS_upstream	18110919	18111665	-602	-13806	TSS_upstream
			18112903	18113032	1073	-12131	5'UTR					
PLA2G6	phospholipase A2, group VI	chr22	36905769	36906048	1798	-68460	5'UTR					
			36906395	36906609	1204	-69054	5'UTR					
Apoptosis												
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	chr1	148816234	148816449	1522	-3577	intron					
			148817093	148817381	2418	-2681	3'UTR					
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	chr18	55781534	55781886	63494	59194	TES_downstream					
			55783811	55784198	65788	61488	TES_downstream					
			55789717	55790039	71662	67362	TES_downstream					
Ion Transport												
CHRNA2	cholinergic receptor, nicotinic, alpha 2 (neuronal)	chr8	27390315	27393415	809	-17683	5'UTR	27391084	27393378	443	-18049	5'UTR
1A2	solute carrier family 11 (proton-coupled divalent	chr12	49704740	49705712	1182	-39183	5'UTR	49704816	49705098	1451	-38914	5'UTR

	metal ion transporters), member 2											
Small GTPase Mediated Signal Transduction												
LOC150786	RAB6C-like	chr2	131835345	131836168	2444	-1221	3'UTR					
RAB11B	RAB11B, member RAS oncogene family	chr19	8359105	8359247	-2119	-15302	TSS_upstream					
			8360200	8360381	-1005	-14188	TSS_upstream					
Transport												
G3BP2	GTPase activating protein (SH3 domain) binding protein 2	chr4	76816497	76816804	691	-29660	5'UTR	76815748	76816767	1084	-29267	5'UTR
LAPTM4B	lysosomal protein transmembrane 4 beta	chr8	98859358	98859629	2509	-74511	intron					
Translational Initiation												
DENR	density-regulated protein	chr12	121799802	121800199	-3323	-21904	TSS_upstream					
EIF4E	eukaryotic translation initiation factor 4E	chr4	100048660	100049607	21005	-28898	intron	100048843	100049571	20931	-28972	intron
			100073606	100073867	-3598	-53501	TSS_upstream					
Cytokinesis												
AURKB	aurora kinase B	chr17	8055406	8055578	-885	-6718	TSS_upstream					
Actin Cytoskeleton Organization												
CAPZB	capping protein (actin filament) muscle Z-line, beta	chr1	19619827	19620733	64298	-82421	intron	19619827	19620434	64448	-82271	intron
								19623835	19625401	59960	-86759	intron
								19625964	19626286	58453	-88266	intron

Kinase Activity												
CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	chr12	120124968 120222395	120125607 120222773	93600 -2091	34592 -62705	TES_downstream TSS_upstream	120222395	120222738	-2073	-62687	TSS_upstream
Cell-Cell Adhesion												
CLDN4	claudin 4	chr7	72879660	72880083	-3257	-5078	TSS_upstream	72795422	72796055	-87390	-89211	TSS_upstream
Nuclear Translocation												
CEP57	centrosomal protein 57kDa	chr11	95168576	95168799	5398	-36814	intron					
DNA Repair												
USP1	ubiquitin specific peptidase 1	chr1	62676337	62676553	1475	-13615	5'UTR					
Lipopolysaccharide Biosynthetic Process												
CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase	chr12	22088113	22088748	-1995	-21437	TSS_upstream					
Collagen Fibril Organization												
COL5A2	collagen, type V, alpha 2	chr2	189632866	189633366	119733	-28230	intron	189632866	189633366	119733	-28230	intron
Cholesterol Biosynthetic Process												
DHCR24	24-dehydrocholesterol reductase	chr1	55126716	55126901	-1300	-38921	TSS_upstream					
Proteolysis												
FOLH1	folate hydrolase (prostate-specific membrane	chr11	49412231	49412567	-225602	-287636	TSS_upstream	49412277	49412531	-225607	-287641	TSS_upstream

	antigen) 1											
Microtubule Cytoskeleton Organization												
MAP7	microtubule-associated protein 7	chr6	136913993	136915278	-1151	-209070	TSS_upstream	136914220	136915412	-1332	-209251	TSS_upstream
			136915641	136915786	-2229	-210148	TSS_upstream					
S-adenosylmethionine Biosynthetic Process												
MAT2A	methionine adenosyltransferase II, alpha	chr2	85618173	85618757	-1333	-7446	TSS_upstream					
Visual Perception, Response to Stimulus												
RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	chr14	20857801	20858272	32061	-31261	exon					
Fatty Acid Biosynthetic Process												
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	chr10	102120550	102121010	24019	6204	TES_downstream					
Transmembran Receptor Protein Tyrosine Kinase Signaling Pathway												
SEMA3C	sema domain, immunoglobulin domain (Ig)	chr7	80387118	80387383	-648	-177460	TSS_upstream	80387118	80387383	-648	-177460	TSS_upstream
			80388257	80388983	-2018	-178830	TSS_upstream	80388325	80389019	-2070	-178882	TSS_upstream
			80389522	80389775	-3046	-179858	TSS_upstream					
			80391365	80391798	-4979	-181791	TSS_upstream					
Regulation of Chromatin Assembly or Disassembly												
TLK1	tousled-like kinase 1	chr2	171732348	171732786	-7362	-175752	TSS_upstream					
Regulation of ARF GTPase Activity												
CENTB2	ArfGAP with coiled-coil, ankyrin repeat and PH domains	chr3	196476225	196477723	168066	-207	3'UTR					

	2											
Unknown												
ANP{32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	chr1	148473061	148473603	1751	-15854	intron					
C6orf106		chr6	34671460	34671749	100998	-8555	intron	34671392	34672010	100901	-8652	intron
KIAA0265	kelch domain containing 10	chr7	129497062	129497337	-385	-63629	TSS_upstream					
MTDH	metadherin	chr8	98727134	98727280	1625	-80503	intron					
PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	chr8	96208607	96209050	-6385	-29258	TSS_upstream	96208867	96209050	-6255	-29128	TSS_upstream
SMA4	glucuronidase, beta pseudogene	chr5	69010165	69010943	287	-39509	intron					
			69011881	69014078	2157	-2516	5'UTR	69013760	69013937	-3007	-42803	TSS_upstream
			69041207	69041566	-30545	-70341	TSS_upstream	69041207	69041566	-30545	-70341	TSS_upstream
			69042725	69043062	-32052	-71848	TSS_upstream	69042725	69043062	-32052	-71848	TSS_upstream
			69043534	69044102	-32977	-72773	TSS_upstream	69043534	69044533	-33192	-72988	TSS_upstream
WDR42A	WD repeat domain 42A	chr1	158497235	158498168	901	-45573	5'UTR					

Green: significantly down-regulated

red: significantly up-regulated

🟦 common binding in Rv1 and R1 and significantly changed in the expression array in both Rv1 and R1

Direct AR target genes by coupling analysis of gene expression profile and ChIP-on-chip in R1 cells

		R1						Rv1				
Closest gene	**gene annotation**	**chromosome**	**start**	**end**	**distance_to_TSS**	**distance_to_TES**	**location**	**start**	**end**	**distance_to_TSS**	**distance_to_TES**	**location**
					Transcriptional regulation							
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	chr8	48810874	48811512	2129	835	TES_downstream	48810874	48811546	2112	818	TES_downstream
HES1	hairy and enhancer of split 1	chr3	194752948	194755504	-582401	-584865	TSS_upstream					
HEY1	hairy/enhancer-of-split related with YRPW motif 1	chr8	81153124	81156474	-312147	-315999	TSS_upstream	81153124	81153824	-310822	-314674	TSS_upstream
			81156980	81157390	-314533	-318385	TSS_upstream	81154226	81156273	-312597	-316449	TSS_upstream
			81157654	81158003	-315176	-319028	TSS_upstream					
			81158544	81158889	-316064	-319916	TSS_upstream					
			81159480	81160276	-317226	-321078	TSS_upstream					
			81246929	81247568	-404596	-408448	TSS_upstream					
			81248268	81248624	-405794	-409646	TSS_upstream	81248379	81248624	-405849	-409701	TSS_upstream
			81372903	81373382	-530490	-534342	TSS_upstream	81373158	81373382	-530618	-534470	TSS_upstream
ID2	inhibitor of DNA binding 2	chr2	8735091	8735500	-4268	-6736	TSS_upstream	8734980	8735464	-4341	-6809	TSS_upstream
			8735789	8736101	-3618	-6086	TSS_upstream					
			8737175	8737977	-1987	-4455	TSS_upstream	8737401	8737872	-1927	-4395	TSS_upstream
			8740610	8740986	1235	-1233	3'UTR	8740201	8741285	1180	-1288	3'UTR
			9059142	9060487	320251	317783	TES_downstream	9059142	9060452	320234	317766	TES_downstream
MSX2	msh homeobox 2	chr5	173243782	173244367	-840106	-846432	TSS_upstream					
NKX3-1	NK3 homeobox 1	chr8	23593953	23594537	2149	-2073	3'UTR	23593953	23594645	2095	-2127	3'UTR
								23595043	23595418	1164	-3058	intron
PER1	period	chr17	7964234	7964559	32030	20118	TES_dow	7964198	7964522	32066	20154	TES_do

	homolog 1						nstream					wnstream
			7996673	7997182	-501	-12413	TSS_upstream					
			7997443	7998109	-1350	-13262	TSS_upstream	7997509	7998169	-1413	-13325	TSS_upstream
			7998810	7999799	-2878	-14790	TSS_upstream	7998599	7999944	-2845	-14757	TSS_upstream
PIAS1	protein inhibitor of activated STAT, 1	chr15	65601473	65601685	-532046	-665876	TSS_upstream	65601507	65601949	-531897	-665727	TSS_upstream
ZNF22	zinc finger protein 22	chr10	44817001	44818205	1676	-3175	5'UTR	44817032	44817866	1522	-3329	5'UTR
Metabolic process												
ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	chr1	116718550	116718930	1382	-30176	intron					
			116719418	116719823	2262	-29296	intron					
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	chr8	18110919	18111665	-602	-13806	TSS_upstream	18110919	18111701	-584	-13788	TSS_upstream
			18287836	18288299	176173	162969	TES_downstream	18112903	18113032	1073	-12131	5'UTR
			18619490	18619644	507673	494469	TES_downstream					
			18913030	18913999	801620	788416	TES_downstream	18913030	18913719	801480	788276	TES_downstream
			18914268	18914983	802731	789527	TES_downstream					
ODC1	ornithine decarboxylase 1	chr2	10509469	10509731	-3697	-11642	TSS_upstream					
			10510574	10510788	-4778	-12723	TSS_upstream					
PDK4	pyruvate dehydrogenase kinase, isozyme 4	chr7	95064004	95064989	-636	-13748	TSS_upstream	95064286	95064688	-627	-13739	TSS_upstream
			95065386	95065609	-1637	-14749	TSS_upstream					
			95066348	95067006	-2817	-15929	TSS_upstr					

			95236812 95794769	95237135 95795094	-173113 -731071	-186225 -744183	eam TSS_upstream TSS_upstream	95236812	95237407	-173249	-186361	TSS_upstream
Cell-cell adhesion												
CLDN4	claudin 4	chr7	72795422 73075006	72796055 73075902	-87390 192326	-89211 190505	TSS_upstream TES_downstream	72879660	72880083	-3257	-5078	TSS_upstream
Mitochondrial membrane organization												
DNM1L	dynamin 1-like	chr12	32724068	32725482	1285	-63034	intron	32724068	32725451	1269	-63049	intron
Multicellular organismal development												
DKK1	dickkopf homolog 1	chr10	53130157	53130342	-613797	-617172	TSS_upstream	52313813	52315451	-1429414	-1432789	TSS_upstream
Cell-cell signaling												
FZD1	frizzled homolog 1	chr7	90172702 90730088	90174838 90731487	-557948 -931	-562296 -5279	TSS_upstream TSS_upstream	90172607 90730125	90174765 90731390	-558032 -961	-562380 -5309	TSS_upstream TSS_upstream
Protein folding												
FKBP5	FK506 binding protein 5	chr6	35801888 35804112 35804898 35807932 35809573	35803468 35804602 35805771 35808621 35809895	-37987 -39666 -40643 -43585 -45043	-153333 -155012 -155989 -158931 -160389	TSS_upstream TSS_upstream TSS_upstream TSS_upstream TSS_upstream	35762853 35801888 35805243 35808293 35809573	35763773 35803408 35805510 35808621 35809895	1378 -37957 -40685 -43766 -45043	-113968 -153303 -156031 -159112 -160389	5'UTR TSS_upstream TSS_upstream TSS_upstream TSS_upstream
DNA repair, regulation of cell cycle												
GADD45G	growth arrest and DNA-damage-inducible, gamma	chr9	91245556	91245815	-164062	-165601	TSS_upstream					
Signal transduction												
HRH3	histamine receptor H3	chr20	60246354	60246635	-17788	-23073	TSS_upstream					
Proteolysis												
MALT1	mucosa	chr18	54487870	54488635	-1345	-80097	TSS_upstr	54488870	54489100	-612	-79364	TSS_up

	associated lymphoid tissue lymphoma translocation gene 1						eam					stream
Response to metal ion												
NDRG1	N-myc downstream regulated 1	chr8	134401832	134402376	-23425	-83509	TSS_upstream					
			134403184	134404468	-25147	-85231	TSS_upstream	134403738	134404468	-25424	-85508	TSS_upstream
			134407388	134408683	-29356	-89440	TSS_upstream	134407780	134408683	-29552	-89636	TSS_upstream
			134409159	134409765	-30783	-90867	TSS_upstream					
tRNA catabolic process												
POP1	processing of precursor 1, ribonuclease P/MRP subunit	chr8	99199178	99199711	201	-40368	5'UTR	99199178	99199676	184	-40385	5'UTR
		chr8	99378899	99379519	179966	139397	TES_downstream					
DNA replication												
SPHAR	S-phase response (cyclin-related)	chr1	226930302	226930964	-576270	-577237	TSS_upstream	226929901	226930999	-576453	-577420	TSS_upstream
		chr1	227474815	227475761	-31615	-32582	TSS_upstream	227474815	227475802	-31595	-32562	TSS_upstream
		chr1	227476136	227476381	-30645	-31612	TSS_upstream	227476136	227476381	-30645	-31612	TSS_upstream
		chr1	227476737	227476988	-30041	-31008	TSS_upstream	227476737	227477204	-29933	-30900	TSS_upstream
Protein amino acid ADP-ribosylation												
TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	chr3	157874243	157874772	-565	-32715	TSS_upstream	157876804	157877112	1886	-30264	5'UTR
		chr3	158017653	158018473	142991	110841	TES_downstream	158017653	158018331	142920	110770	TES_downstream
Apoptosis												

TNFAIP8	tumor necrosis factor, alpha-induced protein 8	chr5	115938808	115939295	-2693265	-2819140	TSS_upstream	115938763	115939295	-2693287	-2819162	TSS_upstream
		chr5	118633912	118634812	2046	-123829	intron	118634154	118634812	2167	-123708	intron
		chr5	118816698	118816979	184522	58647	TES_downstream	118816626	118816979	184486	58611	TES_downstream
Unknown												
C1orf107		chr1	208025278	208026194	-42219	-71794	TSS_upstream	208025133	208026232	-42273	-71848	TSS_upstream
C1orf116		chr1	205270288	205272441	1350	-12873	5'UTR	205270288	205272381	1380	-12843	5'UTR
								205272983	205273374	-464	-14687	TSS_upstream
								205278225	205278413	-5605	-19828	TSS_upstream
HSPC159	galectin-related protein	chr2	64186543	64186779	-348504	-352634	TSS_upstream	64062483	64062705	-472571	-476701	TSS_upstream
		chr2	64528363	64529986	-5991	-10121	TSS_upstream	64597496	64597828	62497	58367	TES_downstream
MBOAT2	membrane bound O-acyltransferase domain containing 2 elevated in prostate cancer	chr2	8735091	8735500	326031	178856	TES_downstream	8734980	8735464	326104	178929	TES_downstream
		chr2	8735789	8736101	325381	178206	TES_downstream					
		chr2	8737175	8737977	323750	176575	TES_downstream	8737401	8737872	323690	176515	TES_downstream
		chr2	8740610	8740986	320528	173353	TES_downstream	8740201	8741285	320583	173408	TES_downstream
		chr2	9059142	9060487	1512	-145663	intron	9059142	9060452	1529	-145646	intron
MRFAP1L1	Morf4 family associated protein 1-like 1	chr4	6685829	6686388	76346	74227	TES_downstream	6685829	6686388	76346	74227	TES_downstream
		chr4	6746019	6746297	16296	14177	TES_downstream	6748931	6749281	13348	11229	TES_downstream
PHF20L1	PHD finger protein 20-like 1	chr8	133568262	133569209	-288050	-325883	TSS_upstream	133565088	133565307	-291588	-329421	TSS_upstream

Red color: significantly up-regulated in response to DHT for 2h

Green color: significantly down-regulated in response to DHT for 2h

🟦 significantly changed in both R1 and Rv1 cells in response to DHT for 2h