

Table S2

gene_name	log2 of DESeq normalized counts									
	hD1	hD7	hD8	hD9	hD10	iP2	iP3	iP5	iP6	iP7
SPC24	5,78136	6,06609	6,50779	6,14975	6,24793	4,52356	6,00000	4,52356	4,70044	5,20945
TMEM38A	5,58496	7,10852	5,83289	6,30378	6,33985	4,16993	5,32193	4,24793	4,85798	4,75489
TMEM229B	4,58496	5,78136	5,83289	5,70044	6,49185	5,55459	5,39232	3,90689	4,16993	3,70044
SLC39A5	5,04439	5,24793	6,80735	6,42626	6,06609	4,08746	5,32193	3,00000	3,58496	5,12928
PDE4C	4,70044	5,72792	6,91886	5,04439	6,98868	4,39232	3,90689	3,90689	3,16993	5,52356
COLCA2	4,24793	6,89482	6,04439	4,58496	7,05528	3,00000	5,12928	4,08746	4,24793	3,80735
ME1	4,32193	6,04439	4,90689	5,16993	7,12928	4,16993	4,32193	2,80735	4,32193	4,70044
HHAT	5,64386	5,55459	5,45943	4,80735	4,58496	3,90689	5,20945	4,16993	3,00000	4,08746
UAP1L1	5,32193	5,24793	5,39232	4,58496	5,80735	3,45943	4,58496	4,08746	3,00000	4,08746
RAB6B	5,75489	5,42626	5,67243	4,52356	5,42626	4,75489	3,58496	4,08746	3,16993	4,08746
BHLHE41	5,42626	6,06609	5,78136	4,90689	5,93074	4,32193	4,70044	3,58496	4,70044	4,32193
KLHL17	4,75489	5,35755	5,88264	5,08746	5,00000	3,45943	3,80735	4,39232	4,85798	4,08746
NBPF3	6,32193	6,12928	5,78136	3,58496	6,47573	4,00000	4,39232	3,90689	3,58496	4,24793
C2CD4B	4,75489	5,45943	6,56986	3,80735	6,06609	3,00000	4,70044	4,00000	3,58496	4,08746
CTC1	6,18982	5,35755	5,24793	6,52356	5,70044	5,04439	5,32193	4,85798	3,58496	4,80735
C15orf38	5,42626	5,64386	5,45943	5,58496	6,08746	5,32193	5,04439	4,52356	3,00000	4,32193
CDHR5	5,67243	6,20945	6,47573	6,30378	5,97728	4,45943	4,70044	5,72792	2,80735	5,24793
ECM1	4,75489	6,44294	5,32193	5,20945	5,80735	4,08746	4,80735	4,90689	3,58496	4,45943
NBPF14	4,85798	5,12928	5,28540	6,28540	5,32193	3,32193	4,85798	4,75489	3,70044	4,70044
SYT17	5,78136	5,88264	6,40939	5,52356	5,49185	3,00000	5,42626	5,16993	4,52356	4,16993
CHST11	6,16993	5,20945	5,00000	5,67243	5,61471	3,45943	3,90689	3,80735	4,24793	4,52356
DHRS13	5,97728	4,70044	4,80735	6,39232	5,95420	2,32193	3,80735	4,58496	3,70044	5,16993
DIAPH2	6,06609	5,75489	4,08746	5,52356	5,88264	2,58496	5,28540	4,32193	3,45943	4,85798
ZNF488	6,20945	4,08746	6,53916	6,12928	5,78136	2,58496	4,95420	3,70044	2,80735	5,32193
PDZD3	6,06609	7,03342	6,53916	6,53916	6,75489	1,00000	6,28540	3,00000	5,58496	4,95420
MECOM	5,83289	6,71425	5,08746	6,40939	5,61471	1,58496	5,12928	4,39232	5,49185	3,58496
CLRN3	6,20945	5,61471	5,88264	5,88264	7,51570	1,00000	5,39232	4,64386	4,32193	6,59991
CA2	5,16993	6,93074	6,40939	6,26679	7,43463	1,58496	4,52356	3,58496	3,45943	5,00000
SPP1	6,04439	6,04439	5,70044	7,62205	6,40939	4,16993	4,70044	5,78136	6,42626	4,45943
PIGB	6,35755	5,52356	4,64386	8,24793	5,83289	3,00000	5,83289	5,16993	5,83289	4,58496
RP11-159D12.5	6,84549	7,30378	4,80735	6,33985	6,53916	3,45943	5,12928	5,55459	5,35755	5,16993
ELFN2	6,90689	6,83289	7,34873	6,75489	6,91886	5,12928	5,45943	4,70044	5,32193	5,42626
TTC39A	6,75489	6,22882	6,91886	5,70044	6,20945	5,78136	5,45943	5,20945	5,08746	5,00000
PIDD	5,88264	6,74147	7,53138	6,83289	6,00000	5,12928	4,64386	5,93074	5,78136	5,08746
GPRIN2	5,95420	5,58496	7,65105	6,39232	5,58496	5,49185	5,75489	5,20945	4,24793	5,72792
CCDC24	5,39232	5,52356	6,94251	8,01123	5,58496	5,08746	5,49185	5,52356	5,20945	4,80735
SLC6A20	5,45943	7,00000	8,34430	6,18982	7,28540	3,45943	5,88264	6,02237	5,04439	5,70044
DACT2	4,95420	6,97728	7,55459	5,97728	7,03342	5,61471	6,37504	5,88264	4,95420	2,58496
ZBED3	5,88264	6,88264	6,33985	4,24793	6,56986	4,80735	4,90689	5,58496	4,90689	4,08746
EHD2	5,20945	6,96578	5,90689	5,49185	6,02237	4,00000	3,16993	5,61471	3,70044	3,00000
WNK2	5,67243	6,62936	7,27612	5,80735	6,04439	4,64386	4,95420	4,39232	4,70044	2,58496
EVC	5,58496	6,06609	5,28540	5,78136	6,02237	3,58496	5,45943	5,04439	4,90689	2,32193
NAGPA	5,88264	5,61471	6,16993	7,01123	7,14975	5,20945	5,61471	5,67243	4,95420	5,04439
CYP2C18	6,28540	5,70044	6,24793	6,62936	6,88264	5,20945	5,24793	4,85798	4,24793	5,45943
TMEM86B	5,88264	5,78136	6,53916	6,12928	7,37504	5,08746	6,04439	5,78136	3,45943	4,95420
DHRS11	6,00000	6,74147	7,05528	7,40939	6,35755	5,20945	6,22882	6,00000	3,16993	6,32193
ZXDC	6,56986	6,52356	5,72792	6,91886	6,47573	5,42626	5,97728	6,35755	3,16993	4,45943
SLC12A8	5,61471	6,39232	6,30378	7,09803	5,72792	4,64386	5,24793	5,39232	5,39232	5,24793
LYPD6	6,16993	5,85798	6,30378	6,67243	5,32193	4,24793	4,70044	5,20945	4,70044	5,39232
RMI2	6,44294	6,37504	5,95420	7,49185	6,47573	5,08746	4,52356	5,28540	5,08746	6,59991
HMHA1	6,79442	6,02237	5,72792	6,82018	4,90689	4,08746	5,49185	4,80735	3,58496	5,95420
KRT13	7,30378	5,70044	8,87036	6,61471	6,84549	4,58496	4,70044	6,22882	3,45943	7,66534
AIFM2	7,53138	6,49185	7,74819	6,37504	6,37504	4,00000	5,24793	6,00000	2,80735	6,72792
AKR1C2	4,70044	7,69349	6,79442	8,20457	8,66534	3,90689	7,45121	7,03342	2,80735	5,95420
SLC16A1	7,40088	8,19476	7,62936	7,33092	8,26209	4,39232	5,42626	5,08746	5,88264	7,04439
NOSTRIN	7,13955	8,30378	6,08746	6,84549	7,24793	3,58496	6,50779	5,39232	6,12928	6,02237
MUC17	8,21917	6,62936	6,20945	6,33985	8,11894	3,45943	6,71425	4,85798	4,45943	6,94251
KIF13A	7,39232	6,37504	6,55459	7,31288	6,39232	4,08746	6,32193	6,08746	4,85798	6,40939
TNNI2	7,19967	7,74147	8,04439	6,28540	5,78136	3,80735	6,70044	3,16993	6,59991	4,45943
CALB2	6,75489	8,14975	6,85798	5,90689	7,33092	4,90689	5,49185	2,32193	4,75489	6,35755

FABP1	10,04712	6,35755	6,28540	9,19229	6,47573	3,45943	5,04439	1,58496	4,90689	6,18982
LYPD6B	5,80735	5,45943	5,67243	5,72792	4,80735	3,00000	4,70044	4,52356	3,70044	2,80735
PASK	4,95420	4,85798	4,75489	5,35755	5,04439	2,58496	4,24793	4,45943	3,00000	3,32193
GLMN	5,85798	4,70044	4,64386	6,22882	4,58496	3,45943	4,52356	3,32193	4,00000	2,32193
BTNL9	5,58496	4,45943	6,84549	6,62936	2,80735	2,32193	5,32193	4,39232	2,32193	2,32193
PF4	5,16993	5,90689	5,67243	7,93664	6,00000	1,58496	5,55459	2,80735	2,80735	2,00000
DKK3	5,97728	6,35755	7,51570	6,18982	3,45943	2,32193	5,12928	3,45943	4,90689	3,70044
SPRR1A	7,70044	2,32193	6,00000	6,26679	4,90689	0,00000	3,90689	5,58496	2,32193	3,45943
GYG2	5,52356	5,52356	5,88264	5,64386	4,58496	0,00000	6,40939	2,58496	0,00000	3,90689
SLC17A9	6,06609	6,10852	5,67243	6,04439	6,78136	3,70044	5,08746	3,90689	0,00000	5,45943
MYZAP	5,12928	5,28540	4,80735	5,45943	5,97728	3,00000	4,00000	4,32193	1,00000	4,95420
MX1	4,70044	4,24793	6,02237	7,12928	5,55459	5,55459	5,12928	4,00000	0,00000	3,00000
APBB1IP	5,64386	4,32193	5,24793	7,32193	4,64386	4,95420	4,85798	3,32193	0,00000	4,80735
PPBP	6,04439	4,85798	5,70044	9,48382	2,00000	4,85798	4,64386	5,85798	0,00000	4,39232
IFI27	5,32193	8,70736	4,24793	8,11894	11,98335	4,39232	3,58496	3,58496	5,24793	2,32193
CLDN18	3,58496	7,99435	5,70044	4,00000	9,51964	5,20945	4,39232	7,39232	5,24793	0,00000
ANKRD50	5,28540	5,24793	4,80735	4,24793	4,16993	6,42626	5,80735	5,04439	6,53916	5,52356
PKIG	4,90689	5,00000	4,70044	3,58496	4,70044	6,45943	5,80735	5,16993	6,14975	5,28540
SH3BP5	4,32193	4,70044	4,75489	4,24793	3,58496	6,24793	5,45943	4,58496	6,26679	5,35755
ACAP1	4,08746	5,12928	5,16993	3,32193	4,52356	6,42626	6,84549	5,58496	4,90689	4,90689
RNF144B	4,08746	4,16993	5,12928	2,00000	5,52356	5,83289	5,24793	5,70044	5,97728	5,72792
ST6GAL2	4,52356	4,08746	4,45943	5,52356	4,64386	5,90689	5,42626	6,83289	6,53916	4,75489
ZNF551	3,70044	4,45943	4,08746	4,75489	4,45943	5,72792	5,24793	5,55459	5,67243	5,04439
ATF3	2,58496	4,90689	3,70044	2,58496	5,42626	4,70044	5,83289	7,58496	6,30378	4,00000
FGA	2,58496	3,80735	5,08746	4,00000	3,00000	4,24793	5,85798	6,71425	5,90689	3,00000
GZF1	4,32193	3,58496	2,58496	4,39232	3,70044	4,39232	4,95420	5,28540	6,49185	4,95420
SESN3	5,35755	4,08746	2,58496	3,45943	2,00000	5,67243	4,32193	4,64386	7,45943	4,08746
EVA1B	4,16993	3,45943	3,32193	3,80735	3,16993	7,11894	3,90689	4,45943	5,83289	5,42626
CD14	2,32193	3,90689	3,80735	4,45943	2,58496	4,70044	4,08746	4,16993	7,20945	4,45943
RAPGEF3	4,08746	3,00000	4,80735	2,58496	3,45943	5,64386	5,39232	5,55459	5,35755	3,45943
PTHLH	3,58496	2,32193	4,08746	2,00000	2,32193	5,58496	5,45943	4,64386	4,52356	4,39232
ADAMTS1	3,45943	2,80735	3,90689	4,16993	3,00000	5,49185	6,96578	5,28540	4,70044	3,32193
UGT2B11	4,16993	1,58496	2,58496	6,08746	4,52356	2,58496	6,52356	6,64386	6,87036	6,70044
UGT2B7	3,80735	4,32193	4,45943	5,45943	6,33985	5,95420	5,45943	6,45943	6,52356	6,90689
FRG1B	4,32193	5,16993	3,00000	4,52356	5,64386	6,30378	5,80735	5,64386	6,06609	6,08746
CENPC	4,58496	5,04439	3,00000	5,35755	5,55459	6,47573	4,80735	5,12928	5,52356	8,19476
COPG2	4,16993	5,32193	3,32193	3,32193	5,04439	7,15987	4,52356	4,95420	4,45943	6,58496
BEX5	3,32193	4,24793	3,80735	2,80735	5,39232	7,54689	2,58496	6,75489	5,49185	6,06609
IFT52	4,90689	5,45943	5,58496	5,61471	4,70044	6,64386	5,80735	5,80735	6,75489	6,44294
PEX11G	4,70044	4,70044	5,67243	5,08746	5,49185	6,87036	5,95420	5,42626	6,45943	6,14975
PLEKHG5	5,55459	5,35755	4,90689	5,20945	6,12928	7,66534	6,00000	5,88264	6,06609	7,24793
C4orf48	5,90689	3,90689	5,78136	5,70044	3,80735	8,25739	4,39232	6,28540	7,01123	6,74147
NEDD8-MDP1	6,80735	7,05528	6,28540	6,42626	6,58496	7,78136	7,97154	7,20945	8,88264	6,74147
CASP4	6,79442	6,62936	6,53916	5,83289	6,83289	7,98868	7,67243	7,44294	7,94837	6,82018
GABBR1	6,68650	6,12928	6,26679	6,45943	6,12928	8,59619	7,82018	6,67243	7,78136	6,24793
MDP1	6,20945	6,47573	5,49185	5,80735	5,97728	7,16993	7,37504	6,64386	8,27146	5,93074
PFDN4	6,67243	6,24793	6,18982	6,45943	6,14975	7,98299	6,62936	6,91886	7,83289	7,54689
MED21	6,52356	6,79442	5,24793	6,89482	6,47573	6,20945	7,72792	7,10852	8,23362	7,65105
MAPK11	5,95420	5,85798	6,04439	5,90689	4,58496	8,08746	5,95420	7,26679	7,68650	6,74147
PTK7	4,85798	5,97728	5,83289	5,49185	4,08746	8,40939	6,78136	7,12928	6,40939	6,26679
LRG1	6,10852	6,08746	6,72792	4,70044	4,85798	6,89482	6,90689	6,82018	7,83289	5,72792
PTGES	7,51570	5,85798	6,35755	6,50779	5,20945	9,72451	7,74819	7,26679	7,20945	7,15987
HLA-DMA	6,30378	3,90689	7,12928	2,80735	6,78136	8,40939	7,63662	7,03342	7,48382	4,45943
CST6	5,83289	4,52356	3,80735	5,28540	3,90689	8,55459	6,14975	5,32193	7,53138	4,39232
UBD	5,24793	3,58496	4,90689	4,32193	3,16993	8,40514	7,09803	2,80735	7,12928	4,58496
EFEMP1	6,62936	5,08746	3,32193	3,58496	2,00000	7,12928	6,72792	5,64386	6,30378	6,39232
MFAP5	7,68650	1,00000	1,00000	5,52356	4,90689	9,77643	7,36632	5,35755	6,65821	6,90689
ZNF765	5,16993	4,85798	4,52356	4,52356	4,58496	1,00000	3,80735	4,00000	4,58496	2,80735
CREG2	4,39232	4,32193	3,90689	4,52356	5,04439	1,58496	3,45943	3,80735	3,90689	2,32193
SLC9A4	4,80735	5,12928	4,52356	4,32193	4,85798	0,00000	2,58496	2,80735	4,52356	3,00000
PSAPL1	4,75489	4,75489	5,08746	5,72792	6,49185	0,00000	3,16993	4,08746	3,90689	2,32193
UVSSA	4,58496	5,70044	5,83289	5,04439	4,90689	1,58496	4,58496	5,04439	2,32193	0,00000
TLR6	4,39232	5,00000	3,45943	4,95420	5,85798	0,00000	3,16993	4,00000	2,32193	0,00000

TMEM231	4,52356	4,45943	4,45943	4,52356	4,00000	3,45943	2,58496	2,00000	3,16993	3,00000
GRK4	4,90689	4,64386	4,52356	4,24793	2,00000	4,08746	2,32193	2,58496	2,32193	2,00000
IRAK2	4,39232	4,52356	3,90689	5,35755	4,58496	4,90689	3,16993	3,16993	2,00000	1,58496
BPIFB1	5,00000	4,08746	5,93074	4,52356	3,70044	3,80735	3,32193	3,16993	4,32193	0,00000
SEC16B	4,70044	5,55459	4,45943	2,80735	3,16993	2,32193	4,08746	2,32193	3,00000	1,00000
RUSC2	4,24793	4,08746	3,90689	3,58496	3,90689	2,58496	2,32193	3,00000	1,00000	0,00000
AGAP5	4,00000	4,95420	4,64386	4,90689	3,58496	2,32193	4,08746	3,58496	2,00000	3,00000
AGMO	4,32193	4,32193	4,95420	4,39232	4,85798	0,00000	3,80735	3,32193	1,00000	3,32193
SLC35F3	5,39232	5,39232	4,90689	3,45943	3,32193	1,58496	4,58496	3,58496	0,00000	3,16993
SIMC1	3,80735	4,08746	5,00000	2,58496	4,95420	3,32193	2,58496	2,80735	1,00000	2,80735
CIDEC	3,32193	3,80735	5,08746	4,00000	4,32193	2,32193	2,00000	1,58496	0,00000	2,58496
TNFRSF1B	4,64386	5,49185	5,08746	4,90689	6,49185	3,58496	4,52356	2,32193	1,00000	2,80735
MOGAT3	4,39232	4,75489	4,90689	4,85798	5,20945	2,00000	4,32193	2,32193	0,00000	3,90689
CYP4F2	2,58496	6,10852	5,00000	3,32193	7,33092	3,00000	4,85798	2,80735	0,00000	3,32193
ANK1	3,32193	6,20945	6,74147	4,45943	5,83289	3,45943	5,12928	4,58496	0,00000	0,00000
PDZK1	4,39232	3,80735	3,90689	4,52356	1,58496	0,00000	3,45943	1,58496	0,00000	2,58496
SHANK3	2,80735	3,00000	3,80735	4,85798	2,58496	0,00000	2,58496	2,00000	0,00000	3,00000
TMEM27	4,58496	3,80735	3,00000	4,45943	2,80735	1,00000	3,58496	1,58496	0,00000	1,00000
ADRA2C	2,80735	4,39232	4,90689	4,08746	2,00000	1,00000	3,80735	0,00000	1,00000	2,32193
C2CD4A	3,32193	4,32193	6,24793	4,52356	3,58496	1,00000	2,80735	3,00000	0,00000	2,32193
RNF157	2,00000	4,75489	4,39232	4,45943	3,00000	1,00000	3,45943	2,58496	1,00000	2,00000
SOWAHD	1,58496	2,80735	4,45943	3,00000	4,00000	0,00000	2,58496	1,58496	0,00000	1,58496
KCNH3	2,58496	1,00000	4,90689	4,90689	4,80735	3,00000	3,16993	0,00000	0,00000	2,32193
USPL1	2,80735	3,32193	2,32193	4,90689	6,12928	1,58496	3,16993	3,45943	1,00000	2,58496
EPSTI1	4,16993	3,00000	1,00000	6,26679	4,24793	1,58496	3,32193	1,58496	2,32193	1,00000
PINLYP	3,58496	4,70044	4,64386	2,00000	2,00000	1,00000	2,00000	2,80735	2,32193	0,00000
SLC13A3	3,90689	3,45943	5,39232	2,00000	1,00000	0,00000	2,00000	2,80735	2,32193	0,00000
FOXO2	3,70044	4,39232	4,70044	3,45943	3,32193	0,00000	2,58496	4,00000	2,32193	0,00000
IL1RL1	2,32193	4,64386	4,16993	3,00000	4,58496	0,00000	1,00000	2,00000	3,70044	0,00000
GSTA1	2,00000	2,58496	5,12928	3,45943	4,58496	0,00000	1,00000	2,00000	3,00000	0,00000
METTL21B	2,00000	5,35755	4,08746	3,45943	3,45943	1,00000	2,80735	1,00000	2,00000	0,00000
SLC14A1	0,00000	4,80735	3,45943	3,45943	3,16993	1,58496	1,00000	2,32193	1,00000	0,00000
ODAM	1,00000	5,49185	3,90689	0,00000	3,45943	0,00000	2,32193	1,58496	1,00000	0,00000
DNHD1	4,08746	5,32193	4,70044	2,32193	4,80735	0,00000	4,08746	4,64386	0,00000	0,00000
SULT1B1	2,80735	5,00000	3,16993	1,00000	6,12928	0,00000	3,80735	2,32193	0,00000	1,00000
TMEM213	3,00000	7,79442	4,45943	1,58496	2,00000	0,00000	1,00000	4,45943	0,00000	1,00000
SULT1C2	2,58496	5,24793	0,00000	3,90689	7,32193	0,00000	1,00000	1,00000	0,00000	1,00000
GKN1	2,00000	6,90689	0,00000	0,00000	6,71425	0,00000	0,00000	1,00000	0,00000	0,00000
CCNB3	4,00000	4,52356	0,00000	1,58496	4,90689	2,00000	2,00000	0,00000	0,00000	0,00000
PGC	6,37504	5,16993	3,00000	0,00000	7,38370	4,70044	2,58496	0,00000	0,00000	3,45943
RGN	2,58496	1,58496	3,32193	2,00000	1,58496	1,00000	1,00000	1,00000	0,00000	0,00000
TUBA8	2,80735	2,00000	2,32193	2,32193	1,58496	0,00000	1,00000	1,00000	0,00000	0,00000
CYP3A4	2,58496	2,00000	3,32193	1,58496	2,32193	0,00000	1,00000	1,00000	1,00000	1,00000
C7orf31	3,45943	2,58496	2,32193	1,58496	2,32193	1,58496	0,00000	1,58496	0,00000	0,00000
CTD-3193O13.9	3,00000	1,58496	3,16993	1,58496	2,00000	1,00000	0,00000	0,00000	0,00000	0,00000
CA14	3,45943	3,70044	3,32193	2,00000	2,58496	0,00000	0,00000	1,58496	0,00000	0,00000
ACRC	2,80735	3,70044	2,58496	2,80735	1,00000	0,00000	0,00000	1,00000	0,00000	0,00000
NR1H4	2,32193	1,00000	2,58496	2,80735	2,58496	0,00000	0,00000	0,00000	0,00000	1,00000
USP18	2,32193	0,00000	2,58496	3,58496	2,58496	1,00000	0,00000	0,00000	0,00000	0,00000
VWCE	1,00000	1,00000	4,08746	1,58496	3,32193	1,00000	0,00000	0,00000	0,00000	0,00000
C12orf60	2,58496	2,58496	0,00000	3,00000	3,90689	0,00000	0,00000	1,00000	0,00000	0,00000
DNAH12	1,58496	3,00000	0,00000	2,58496	3,45943	0,00000	0,00000	0,00000	0,00000	0,00000
ZNF239	1,58496	2,80735	1,00000	2,00000	4,08746	0,00000	1,00000	0,00000	1,00000	0,00000
CYP2C19	2,58496	1,00000	0,00000	2,32193	4,16993	0,00000	0,00000	1,00000	0,00000	0,00000
FHAD1	1,00000	1,00000	0,00000	2,80735	4,00000	0,00000	0,00000	1,00000	0,00000	0,00000
TIMP4	2,00000	2,32193	1,00000	2,58496	4,39232	0,00000	0,00000	1,58496	0,00000	1,00000
C11orf86	2,80735	2,32193	0,00000	0,00000	3,45943	0,00000	0,00000	0,00000	0,00000	0,00000
RAET1G	2,58496	2,00000	0,00000	0,00000	3,58496	0,00000	0,00000	0,00000	0,00000	0,00000
GCK	2,80735	1,58496	0,00000	0,00000	3,00000	0,00000	0,00000	0,00000	0,00000	0,00000
RASSF9	2,58496	2,32193	1,00000	1,00000	2,00000	0,00000	0,00000	1,00000	0,00000	0,00000
PGF	1,58496	2,32193	3,16993	1,00000	1,58496	0,00000	0,00000	1,00000	0,00000	0,00000
SYNC	1,00000	2,00000	3,00000	1,00000	2,00000	0,00000	0,00000	1,00000	0,00000	0,00000
KCNQ4	1,58496	2,80735	3,00000	0,00000	1,58496	0,00000	0,00000	1,00000	0,00000	0,00000

C1orf177	1,58496	2,32193	2,58496	0,00000	3,00000	0,00000	0,00000	0,00000	0,00000	0,00000
RP56KA6	2,80735	3,32193	3,32193	0,00000	2,00000	0,00000	0,00000	1,58496	0,00000	0,00000
TCTE1	1,58496	2,80735	3,32193	2,58496	3,00000	0,00000	0,00000	2,58496	0,00000	0,00000
LNP1	1,00000	3,00000	3,00000	2,32193	3,45943	0,00000	0,00000	2,00000	0,00000	0,00000
KCNH8	1,00000	3,32193	4,80735	0,00000	4,16993	0,00000	0,00000	1,58496	0,00000	0,00000
PRSS21	0,00000	0,00000	6,44294	1,00000	2,32193	0,00000	0,00000	1,00000	0,00000	0,00000
SALL1	3,90689	2,32193	3,16993	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000
GRIN3B	2,32193	3,00000	3,16993	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000
KCNN1	2,32193	1,00000	3,32193	0,00000	1,00000	0,00000	0,00000	0,00000	0,00000	0,00000
KCNS1	1,58496	0,00000	3,90689	1,58496	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000
GATA5	3,32193	3,70044	4,90689	3,70044	2,00000	3,70044	0,00000	1,00000	1,00000	2,00000
CDHR3	2,80735	2,80735	3,70044	3,00000	2,00000	2,32193	0,00000	1,58496	1,00000	1,00000
SLC11A1	2,58496	4,08746	3,90689	3,00000	3,58496	3,45943	2,32193	0,00000	0,00000	1,00000
HHIP	2,58496	4,32193	4,16993	1,00000	3,45943	3,32193	0,00000	0,00000	0,00000	0,00000
CNTN1	4,70044	3,45943	4,52356	3,00000	2,80735	0,00000	2,00000	0,00000	1,00000	2,32193
CNTNAP2	2,80735	3,16993	3,80735	3,32193	3,32193	0,00000	0,00000	0,00000	0,00000	2,58496
COL4A1	5,42626	4,08746	3,32193	5,12928	2,80735	2,32193	0,00000	0,00000	0,00000	1,58496
SLC6A12	4,70044	3,45943	5,24793	3,00000	1,58496	1,00000	1,00000	1,00000	4,24793	0,00000
PTGER2	3,16993	3,80735	3,70044	3,45943	0,00000	0,00000	0,00000	0,00000	2,80735	1,00000
NEURL2	2,32193	3,80735	2,32193	2,58496	2,58496	2,32193	1,00000	0,00000	0,00000	0,00000
BRSK2	2,58496	3,00000	2,00000	2,00000	2,32193	1,00000	2,00000	0,00000	0,00000	0,00000
FBLL1	2,00000	4,52356	0,00000	1,58496	2,00000	0,00000	1,00000	1,00000	0,00000	0,00000
DIO1	2,00000	5,16993	2,32193	2,00000	0,00000	0,00000	1,00000	0,00000	0,00000	0,00000
KLHL14	1,00000	2,58496	2,32193	2,00000	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000
SULT4A1	4,70044	1,58496	0,00000	4,24793	0,00000	0,00000	0,00000	0,00000	1,00000	0,00000
LUM	5,49185	2,32193	0,00000	2,32193	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000
UCHL1	3,16993	1,00000	1,00000	3,45943	1,00000	0,00000	0,00000	0,00000	0,00000	1,00000
PALMD	2,32193	2,32193	1,00000	3,90689	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000
CES4A	3,16993	3,80735	2,00000	3,32193	3,00000	1,00000	0,00000	1,00000	0,00000	1,00000
AC022498.1	2,32193	3,32193	1,00000	3,80735	2,58496	0,00000	0,00000	1,58496	0,00000	1,00000
CELSR3	3,70044	3,45943	2,32193	2,80735	3,16993	0,00000	0,00000	3,58496	0,00000	1,58496
SCUBE2	2,58496	3,58496	4,16993	4,70044	0,00000	1,00000	0,00000	3,32193	0,00000	0,00000
CCDC74A	4,24793	4,24793	4,75489	4,08746	5,00000	0,00000	2,00000	2,32193	0,00000	3,58496
HPDL	4,39232	3,90689	4,70044	3,70044	4,08746	0,00000	1,00000	2,00000	0,00000	3,00000
TM6SF2	3,32193	4,24793	4,52356	2,58496	4,70044	0,00000	2,58496	3,00000	0,00000	3,45943
CYP1A1	3,16993	3,80735	5,88264	2,00000	4,24793	0,00000	1,00000	0,00000	0,00000	5,16993
TMEM253	3,00000	3,45943	5,32193	3,70044	4,90689	0,00000	2,32193	1,58496	3,45943	4,08746
PAH	1,58496	5,00000	5,95420	3,32193	6,53916	2,00000	1,00000	4,08746	3,00000	2,58496
GKN2	3,90689	7,11894	3,16993	1,58496	7,52356	1,58496	1,00000	3,32193	0,00000	3,32193
HEPH	7,56986	6,53916	8,65821	4,80735	6,28540	0,00000	2,80735	2,58496	1,00000	6,39232
IL1R2	5,42626	4,32193	6,56986	5,61471	5,42626	4,00000	2,80735	3,90689	2,80735	4,39232
GPA33	4,39232	5,24793	6,26679	6,00000	6,18982	2,58496	2,32193	3,58496	2,80735	4,80735
CAPN9	5,12928	3,45943	5,67243	5,04439	6,88264	2,80735	3,32193	5,61471	4,16993	2,32193
PRODH	4,85798	2,58496	6,80735	6,83289	7,58496	5,16993	1,00000	5,49185	3,70044	4,32193
FAM211A	5,00000	3,90689	6,28540	4,90689	4,08746	3,70044	0,00000	0,00000	4,52356	3,80735
MMP24	4,70044	3,45943	4,95420	6,65821	2,00000	2,00000	1,00000	3,58496	4,16993	3,45943
IRF8	2,00000	6,79442	6,04439	4,24793	0,00000	3,00000	2,58496	0,00000	0,00000	1,58496
SLC6A19	0,00000	4,08746	7,52356	5,61471	2,00000	1,00000	2,00000	0,00000	0,00000	0,00000
MUC6	0,00000	7,42626	8,71768	4,95420	0,00000	4,32193	0,00000	2,32193	2,00000	0,00000
SYNE1	3,16993	1,00000	3,00000	1,00000	0,00000	5,20945	3,16993	3,00000	3,58496	2,80735
ZIK1	2,00000	1,58496	2,00000	0,00000	0,00000	4,08746	2,58496	2,80735	5,35755	3,16993
IL2RG	1,00000	2,58496	3,32193	0,00000	1,58496	5,20945	3,58496	3,16993	2,80735	2,58496
IFITM1	2,32193	1,58496	0,00000	0,00000	0,00000	5,49185	2,32193	3,00000	4,95420	1,00000
GNA15	1,00000	2,32193	0,00000	0,00000	1,00000	4,00000	2,00000	4,39232	3,45943	2,32193
CCNA1	0,00000	0,00000	1,00000	1,00000	0,00000	6,08746	3,32193	4,24793	3,45943	1,58496
ICAM1	2,00000	1,00000	0,00000	0,00000	3,80735	5,97728	4,08746	3,16993	3,16993	3,32193
C21orf67	2,00000	0,00000	0,00000	0,00000	1,58496	4,85798	2,00000	3,32193	0,00000	3,16993
C6orf100	2,58496	1,00000	0,00000	1,58496	1,00000	4,08746	4,52356	1,58496	3,00000	1,58496
CDH5	0,00000	0,00000	0,00000	0,00000	0,00000	5,49185	3,90689	0,00000	3,16993	2,32193
SLC16A14	1,58496	0,00000	0,00000	0,00000	1,58496	4,90689	2,00000	3,00000	3,00000	0,00000
NKAPL	1,00000	0,00000	0,00000	0,00000	2,00000	3,90689	1,00000	3,32193	3,00000	1,58496
RP11-297N6.4	0,00000	1,00000	0,00000	0,00000	0,00000	3,70044	0,00000	1,58496	3,90689	1,00000
AKT3	0,00000	0,00000	0,00000	0,00000	0,00000	3,00000	0,00000	1,00000	4,16993	0,00000

CALCB	0,00000	0,00000	0,00000	0,00000	0,00000	4,32193	1,00000	0,00000	2,80735	1,00000
S100A9	0,00000	0,00000	0,00000	0,00000	0,00000	5,00000	2,32193	1,00000	1,00000	0,00000
GATA2	0,00000	0,00000	0,00000	0,00000	0,00000	2,58496	2,00000	1,58496	1,00000	0,00000
SYT5	1,00000	1,00000	0,00000	1,00000	0,00000	2,80735	2,00000	2,58496	2,00000	2,32193
LRRC48	1,00000	0,00000	0,00000	0,00000	0,00000	1,00000	2,00000	1,58496	3,16993	2,00000
HLA-DRA	0,00000	2,00000	0,00000	0,00000	0,00000	4,16993	0,00000	2,80735	5,49185	0,00000
CDKL1	1,58496	2,32193	1,00000	2,32193	1,00000	3,80735	3,32193	2,00000	3,58496	4,08746
MT1G	0,00000	3,00000	0,00000	2,32193	1,58496	3,45943	2,58496	2,32193	4,58496	4,16993
SOX8	1,58496	3,45943	0,00000	1,00000	1,58496	2,00000	2,80735	5,00000	5,35755	3,80735
GABRB3	2,00000	3,45943	1,00000	0,00000	3,90689	3,32193	5,32193	1,00000	4,95420	6,06609
DHRS2	1,00000	1,58496	2,00000	0,00000	3,70044	0,00000	4,24793	3,58496	5,12928	6,40939
ST8SIA6	0,00000	0,00000	0,00000	1,58496	1,00000	0,00000	4,39232	3,80735	4,45943	3,00000
ZFP57	0,00000	0,00000	0,00000	0,00000	0,00000	0,00000	4,95420	3,45943	5,83289	2,32193
SERPINB2	2,32193	1,00000	0,00000	2,58496	4,00000	5,72792	3,32193	1,00000	0,00000	7,39232
CORO1A	2,58496	0,00000	0,00000	3,90689	2,58496	8,31288	4,85798	4,95420	5,24793	5,52356
TMEM173	4,08746	0,00000	0,00000	1,58496	2,00000	6,45943	5,45943	5,16993	5,12928	4,16993
MLF1	3,45943	1,00000	2,00000	3,32193	2,00000	5,83289	3,32193	5,45943	5,67243	5,55459
FLI1	0,00000	1,58496	0,00000	4,16993	3,45943	4,80735	5,85798	4,32193	4,32193	4,95420
DUSP10	4,08746	1,58496	0,00000	2,00000	1,58496	5,20945	4,39232	4,08746	2,32193	4,08746
ADAMTS14	3,32193	1,00000	0,00000	2,58496	1,00000	5,42626	3,90689	4,08746	4,00000	3,70044
CPE	3,80735	0,00000	0,00000	1,00000	0,00000	3,80735	3,80735	4,90689	2,00000	3,45943
IQCG	3,00000	1,00000	0,00000	3,00000	2,00000	2,58496	3,58496	4,64386	3,90689	4,32193
TCF15	2,58496	1,00000	3,32193	2,00000	2,58496	4,90689	4,39232	4,58496	2,00000	6,14975
DCLK1	1,58496	3,00000	1,00000	3,32193	2,32193	7,22882	4,08746	3,70044	2,80735	3,32193
CELF2	0,00000	3,16993	0,00000	1,58496	2,00000	7,15987	3,58496	4,95420	2,80735	1,58496
IGFL1	2,80735	2,58496	2,32193	2,80735	0,00000	6,52356	3,90689	3,90689	4,90689	0,00000
FOSB	2,80735	3,80735	0,00000	1,00000	1,58496	5,67243	6,89482	8,98584	0,00000	0,00000
HLA-DQB1	5,12928	1,00000	0,00000	0,00000	5,88264	0,00000	0,00000	8,83920	7,97728	6,33985
AC174470.1	7,37504	6,71425	7,73471	7,45121	6,83289	10,18239	7,69349	7,84549	9,09011	9,18735
FAM195B	7,37504	6,68650	7,65821	7,39232	6,83289	10,17866	7,57743	7,83920	9,07146	9,17243
CDKN2A	7,29462	6,87036	8,43045	8,05528	8,11374	10,38802	7,54689	7,27612	9,28309	9,33539
HYAL2	8,33985	8,11894	8,88570	7,90689	8,11374	10,97011	7,95420	8,64746	8,93958	9,30150
KRT16	8,18488	8,17493	7,78790	8,63300	8,29921	10,24436	7,15987	9,21432	8,97441	9,46964
SH3BP5L	7,47573	7,42626	7,19967	6,98868	9,52552	10,10460	7,30378	9,04439	7,78790	10,08082
PRMT1	7,60733	7,35755	7,83289	6,75489	8,60363	10,01262	7,33092	7,98868	8,33092	9,16491
CTD-3214H19.16	7,65105	7,71425	8,36194	7,52356	7,45943	9,23840	8,34873	8,14466	9,58120	8,74819
TRAPPC5	7,65105	7,71425	8,36194	7,52356	7,45943	9,23840	8,34873	8,14466	9,58120	8,74819
DPCD	7,96578	7,92481	7,83289	7,89482	7,55459	8,83920	8,31288	8,31741	10,79279	7,96000
C8orf59	7,01123	7,47573	7,10852	7,82018	8,07682	8,72451	7,95420	7,40939	10,04166	8,25267
APLP1	8,08746	7,04439	8,56986	6,79442	7,78790	9,15987	8,35755	9,41574	9,31288	7,80735
MT2A	6,47573	6,52356	7,62205	7,01123	5,70044	9,94251	8,72110	9,06609	9,98014	8,22882
SERTAD1	7,34873	6,91886	6,91886	6,75489	7,09803	8,12928	8,00562	7,97728	8,23840	8,37069
MGMT	6,33985	6,87036	6,26679	7,07682	7,17991	8,68650	7,29462	7,53138	8,58871	7,55459
GALK1	5,52356	7,33985	7,15987	6,68650	7,53138	8,29462	8,09803	8,16491	8,13955	8,14466
ZG16B	6,37504	7,45121	7,49185	6,37504	6,26679	9,00843	8,03342	7,26679	8,78790	6,61471
OAZ2	6,93074	6,33985	6,55459	6,71425	7,79442	9,36194	7,00000	7,03342	7,15987	8,68650
CCDC124	6,32193	6,16993	6,61471	5,93074	7,40939	9,09803	6,00000	7,06609	7,13955	8,38802
TSSC4	6,78136	6,45943	7,54689	6,79442	7,84549	9,36194	6,47573	6,94251	8,51570	8,93074
STMN2	7,01123	5,58496	3,80735	6,82018	5,08746	9,25974	8,54303	10,04029	9,98014	9,76155
APOL1	8,75154	8,31741	8,92778	9,01123	9,85175	9,78627	10,42417	10,88417	10,36960	9,86882
JUN	8,22882	8,99435	8,98584	9,07682	8,89482	9,73640	9,44915	11,39714	8,69697	9,02514
IFITM2	9,21432	7,53138	10,24079	7,80090	8,35315	10,87958	9,87652	10,55075	10,34983	8,56605
TSPAN13	8,45533	9,03342	8,35755	8,83289	9,28771	9,29002	9,95565	8,53916	11,88874	9,02514
RNASET2	8,82018	8,17493	8,39232	7,80090	8,53138	9,82337	10,35094	9,62022	9,75822	7,36632
EGR1	8,54303	8,27612	7,87036	8,55459	8,01681	7,94251	10,10591	10,91214	8,84235	7,45943
SDF2L1	8,31741	7,85175	8,40939	8,87958	9,58496	10,49685	8,14975	8,69349	9,02237	11,64746
U2AF2	7,77479	8,03342	8,54689	7,83920	10,20823	11,29175	7,83289	8,85487	8,54303	11,13443
HNRNPA0	9,13699	9,08746	9,37504	8,87652	9,70044	9,80574	8,96000	9,26444	8,98299	13,91308
SLC7A7	9,16491	8,70736	9,33985	9,22641	8,92778	5,70044	7,79442	8,52748	6,33985	8,64746
B3GALT5	9,72281	8,60363	8,83605	8,65105	9,11634	5,55459	8,33539	7,53916	6,78136	8,81057
LOXL4	9,80896	8,62571	9,45943	9,94105	7,67243	7,67948	8,58120	8,30834	8,33539	8,29462
FKBP11	9,31515	9,43671	9,12928	8,48784	8,23362	7,92481	7,39232	7,72110	7,96000	7,53138
ANO1	8,85487	9,21432	9,14720	8,82337	8,63662	7,63662	7,34873	7,82018	7,55459	7,88874

S100A4	9,21432	9,23601	9,17742	7,62205	8,70736	8,36632	6,79442	7,12928	7,40939	8,13955
CAPN8	8,52356	9,73132	8,94544	8,88264	8,92481	6,44294	8,73132	7,72110	7,59991	6,89482
IMPA2	7,75489	8,54689	8,98868	8,29462	8,77808	6,10852	7,79442	7,20945	7,51570	7,44294
CA12	7,67243	9,33762	8,92481	7,75489	7,69349	7,37504	7,27612	7,70044	7,98299	6,37504
SLC43A1	6,44294	8,45533	8,51964	9,03342	8,92481	6,40939	7,61471	8,25739	6,93074	6,74147
ACSS1	7,98868	8,75489	8,24793	7,82018	8,51570	6,04439	7,78136	6,16993	6,83289	6,02237
C2orf72	8,81378	7,83289	8,67243	7,89482	6,75489	5,32193	7,71425	7,06609	6,70044	6,58496
SYT8	8,16993	9,43045	9,98014	7,20945	8,82972	7,33092	6,40939	5,08746	9,15482	7,08746
MYEOV	9,54689	7,79442	9,43879	8,93664	7,93664	7,03342	7,30378	3,80735	6,78136	8,68299
TSKU	7,28540	7,60733	7,52356	7,22882	8,16491	6,37504	6,35755	7,14975	5,95420	6,75489
AUTS2	6,93074	7,97154	7,59246	7,56224	8,13955	5,90689	6,26679	7,00000	6,47573	6,45943
AC073610.5	7,69349	7,73471	7,68650	6,95420	6,79442	6,40939	5,80735	6,47573	6,62936	6,02237
ETV4	6,32193	6,87036	8,63662	7,02237	7,37504	6,88264	6,82018	6,18982	5,80735	6,04439
FAM198B	7,33092	5,78136	6,47573	6,44294	7,93664	6,12928	6,32193	5,45943	6,04439	5,67243
WSCD1	6,82018	7,30378	7,71425	8,47168	7,27612	5,58496	6,52356	5,97728	6,62936	6,94251
SIRPA	7,87652	6,39232	7,00000	9,03892	6,40939	5,42626	6,65821	5,42626	6,62936	6,32193
MYLK	8,68299	6,94251	7,08746	8,44294	5,97728	6,85798	6,06609	7,08746	6,06609	6,37504
TM4SF5	8,52748	7,85175	8,51570	8,84235	8,56605	6,16993	7,01123	7,39232	5,39232	7,43463
SLCO2B1	8,65105	7,85798	8,78136	7,65821	8,09803	5,75489	7,37504	5,75489	3,90689	7,94837
AMN	7,09803	8,08746	7,49185	7,84549	8,09803	4,95420	7,06609	7,11894	5,20945	5,85798
KLF2	7,28540	7,57743	6,89482	7,04439	8,61839	5,24793	6,40939	7,62205	3,58496	7,17991
LGALS1	7,20945	9,47371	8,28540	8,71425	7,29462	7,07682	8,82655	7,44294	5,72792	2,80735
NDRG4	10,90162	5,24793	7,67948	8,62936	5,24793	5,67243	8,05528	6,74147	6,47573	6,68650
CNOT1	8,78463	9,04166	9,24793	13,58942	9,53722	8,04439	9,09540	9,31967	8,43045	9,25974
AKR1B10	7,85175	9,53528	9,76818	10,40195	11,10525	7,00000	8,22882	7,61471	7,26679	9,30150
GSTM4	9,92333	11,18177	10,62205	10,30720	9,55075	8,18488	9,67772	9,01681	7,37504	7,67948
CEACAM5	10,28656	10,47573	11,27146	8,59991	11,19106	4,80735	7,63662	8,96000	6,82018	9,28771
UGT1A1	10,89785	10,59898	8,30834	9,60733	9,67243	4,32193	8,15987	6,16993	6,52356	8,95710
ALDH3A1	7,09803	12,01959	10,66000	7,47573	12,86438	7,97728	7,28540	7,10852	8,25267	9,68124
PCK1	7,75489	11,52209	10,22521	7,65105	11,08547	7,29462	10,24793	7,70044	7,12928	6,30378
DPCR1	8,47168	10,89026	7,12928	7,97154	11,01890	6,78136	4,52356	7,00000	4,24793	8,93074
PSCA	9,43879	11,98335	6,80735	7,27612	6,79442	4,39232	6,56986	10,24079	6,18982	6,61471
RPS5	10,67507	10,84392	11,60548	10,66000	11,39767	13,20105	11,49085	11,42522	12,70304	12,51274
RPL18A	9,94398	10,48884	11,18549	10,35975	10,75405	11,56415	10,82416	12,29290	11,86225	11,17617
ADAM15	9,52943	9,62022	10,14720	9,16491	11,51274	12,87094	10,13057	11,44139	10,36741	11,56367
KLK10	12,14179	10,93884	9,13443	8,96578	11,55794	13,34207	9,82337	12,63095	12,43593	11,03136
RPL6	9,83920	9,69870	9,69349	9,85953	9,79116	10,17742	10,29232	12,35590	10,22762	10,39124
SPINK1	9,51964	9,40088	8,20457	9,30606	11,12412	9,27845	11,47523	12,27088	11,25267	10,34319
SLC2A3	10,45635	8,80413	9,72622	10,22038	8,27146	11,66800	11,31232	10,97370	10,28077	11,05053
TIMP2	12,11927	9,80252	11,01193	10,80977	9,21432	10,03617	10,15861	9,91139	9,51570	9,97871
SPINK4	11,21614	11,16554	12,14530	10,47675	10,10591	8,58120	7,92481	9,84078	10,42206	10,34096
MUC5AC	10,90989	11,66133	12,89936	12,18239	12,83881	10,79523	8,22882	11,12606	9,99718	9,51175
MMP1	12,31430	14,04226	13,28179	13,26766	12,95529	9,40514	11,87114	11,45584	13,47649	12,52674
REG4	12,86728	12,55746	14,61442	13,81328	13,55315	10,21675	10,57270	10,93295	11,28829	13,51138
AQP3	11,84667	13,97719	13,62970	11,16993	11,15987	11,07548	11,19353	10,09408	12,59898	11,31515
TFF2	10,88188	12,86225	12,33260	11,27903	12,83249	10,51274	10,82893	10,09144	11,45892	11,88798
CYSTM1	13,31288	13,33497	13,99789	13,29247	13,24377	11,71596	12,99894	12,51274	12,49685	11,97298
TFF1	11,79360	13,98789	13,21796	13,47485	14,92152	11,68475	13,01924	13,00440	12,10263	12,88760
RPS9	11,80574	11,69957	12,42495	11,30435	12,54352	14,43313	11,90651	12,48003	12,79726	13,09358