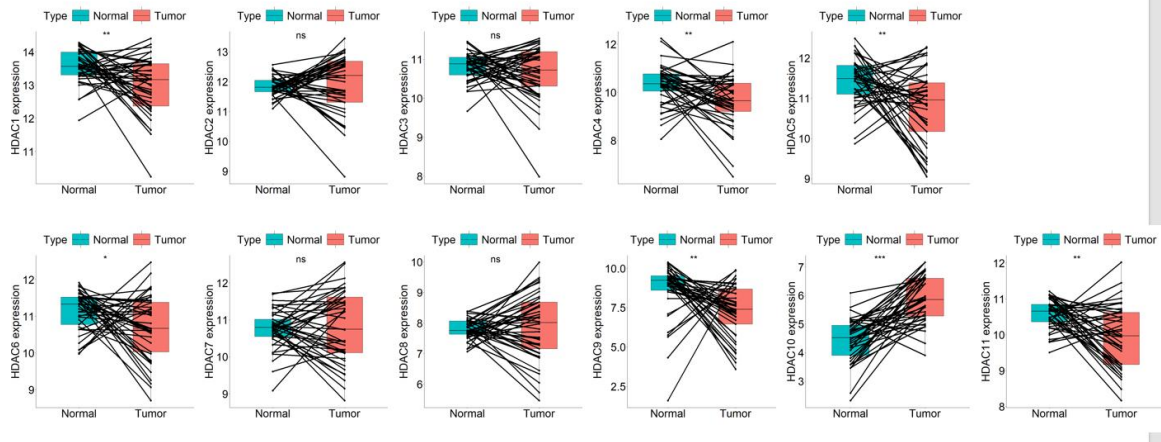
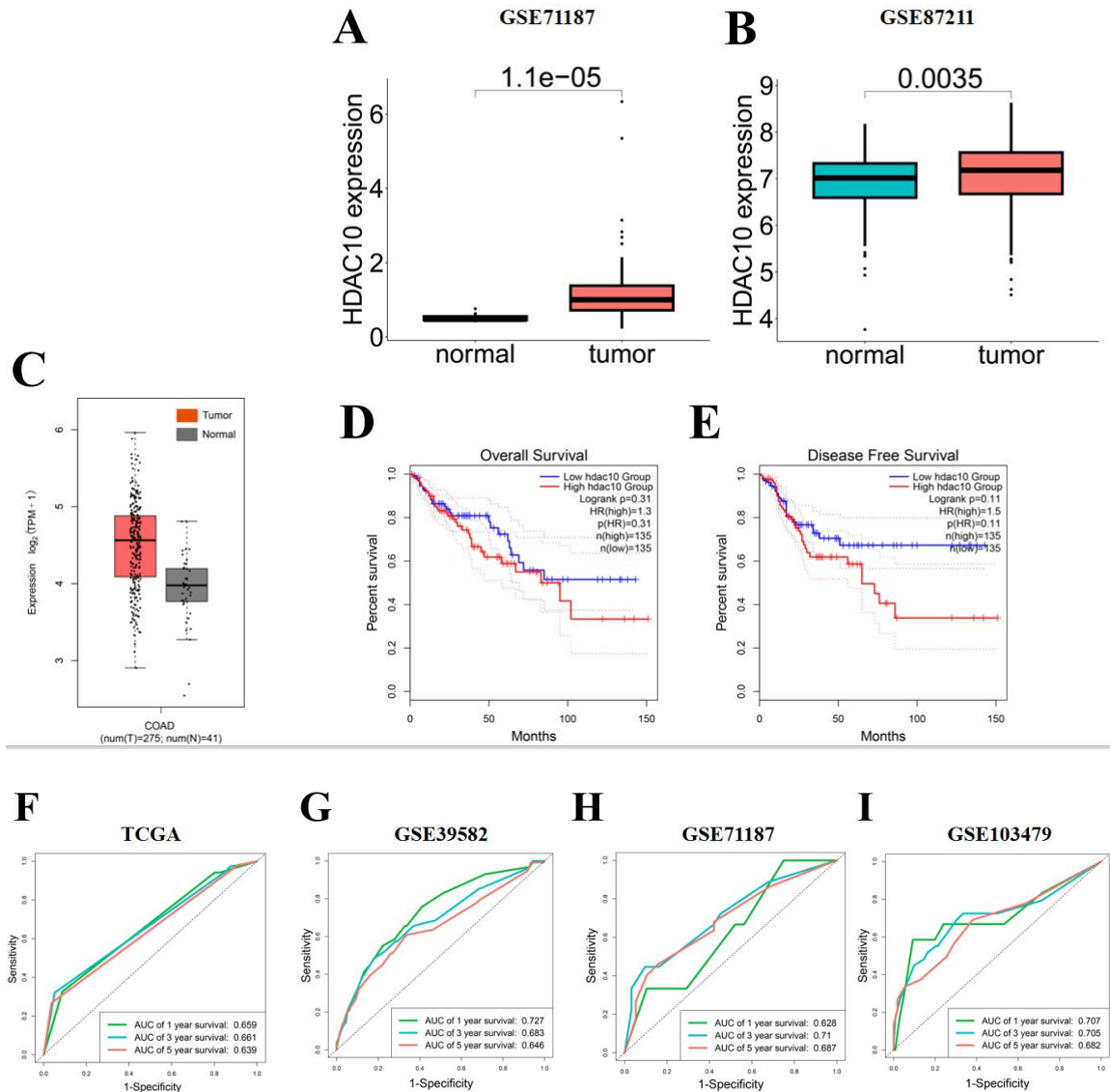
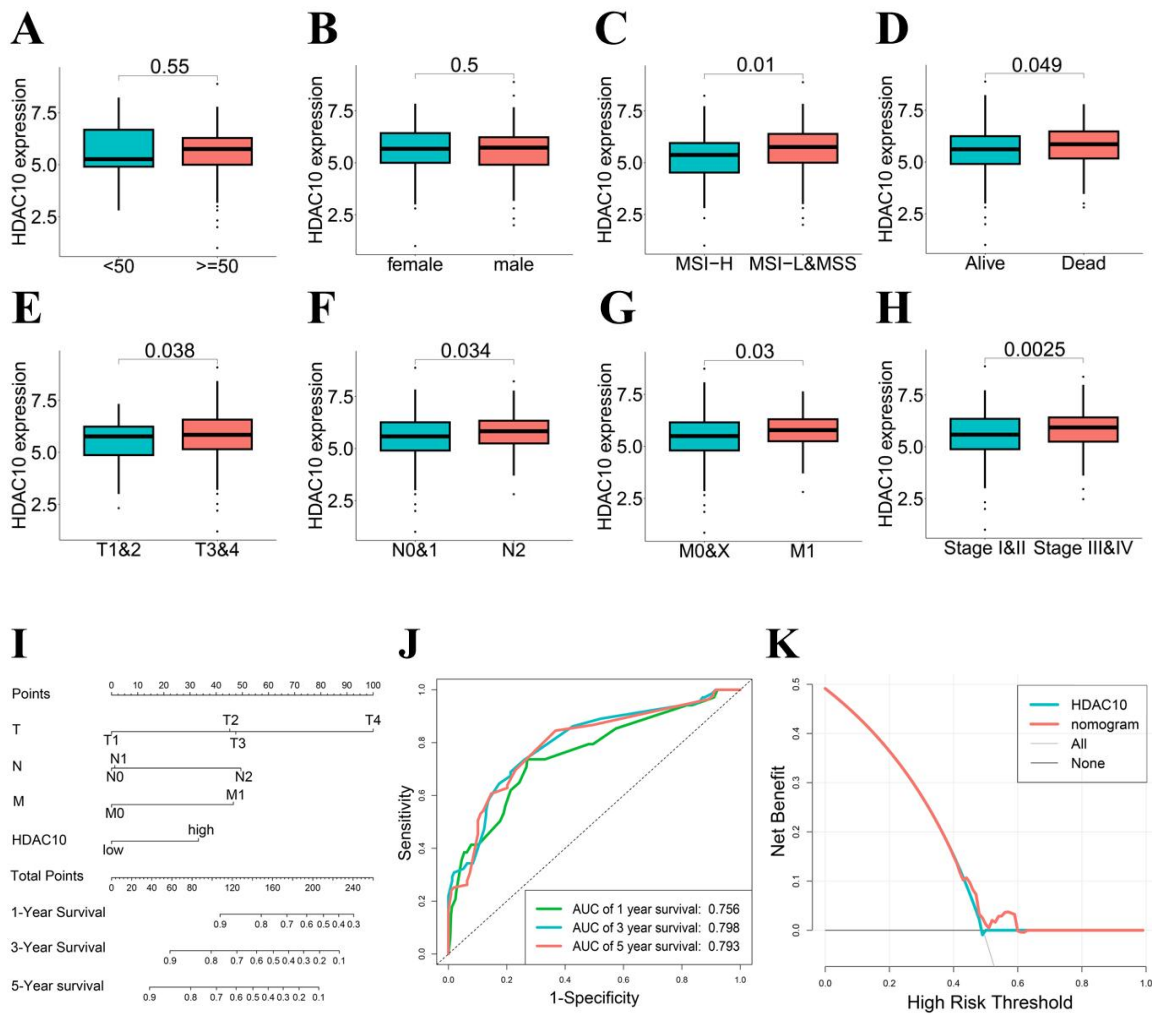




Supplementary Figure 1 The expression of histone deacetylases (HDACs: HDAC1-11) in colorectal cancer (CRC). * P value < 0.05, ** P value < 0.01, *** P value < 0.001, ns: No significance.

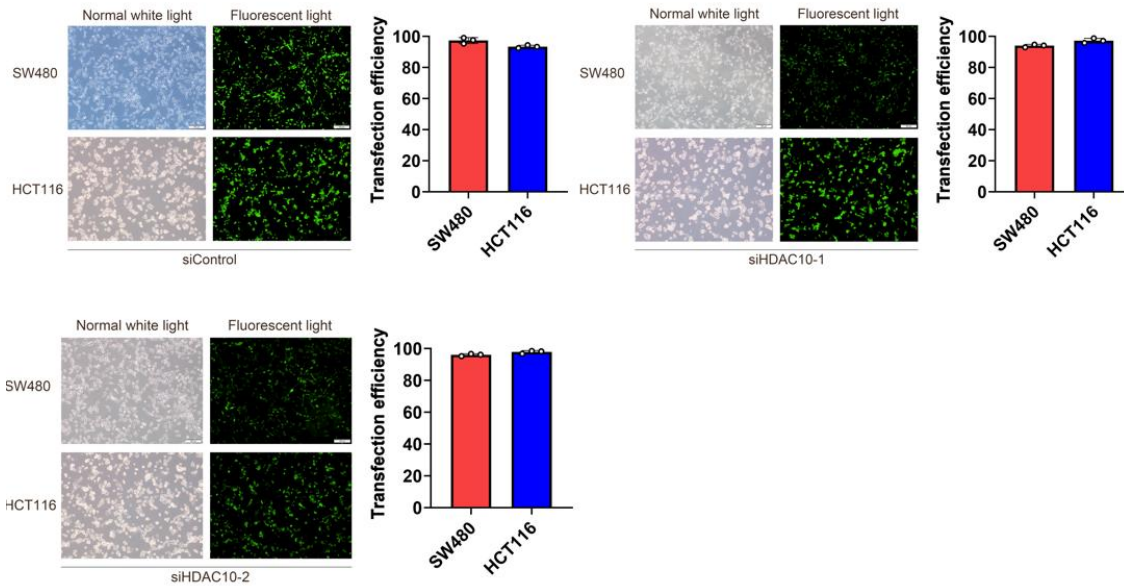


Supplementary Figure 2 The expression of **histone deacetylases 10** (HDAC10) and prognostic prediction in CRC. **A-B**: Differential expression of HDAC10 between normal and tumor samples from GSE71187 and GSE87211; **C**: Higher HDAC10 expression in CRC than normal tissues from GEPIA2; **D-E**: High HDAC10 expression indicated that short **overall survival** (OS), **disease free survival** (DFS); **F-I**: **Receiver operating characteristic** (ROC) curve based on HDAC10 for predicting 1-, 3-, 5-year OS.

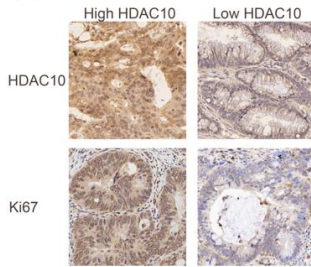


Supplementary Figure 3 HDAC10 expression were associated with clinicopathological characteristics and the prognostic prediction of HDAC10 in CRC based on TCGA cohort. **A**: Differential analysis for HDAC10 expression in patients with different age; **B**: Gender; **C**: TCGA_type; **D**: Status; **E**: T stage; **F**: N stage; **G**: M stage; **H**: Pathologic stage; **I**: Nomogram for predicting the 1-, 3-, and 5-year OS of CRC patients in the TCGA cohort; **J**: ROC curve of the nomograph for predicting 1-, 3-, 5-year OS; **K**: **Decision curve analysis** (DCA) for determining survival.

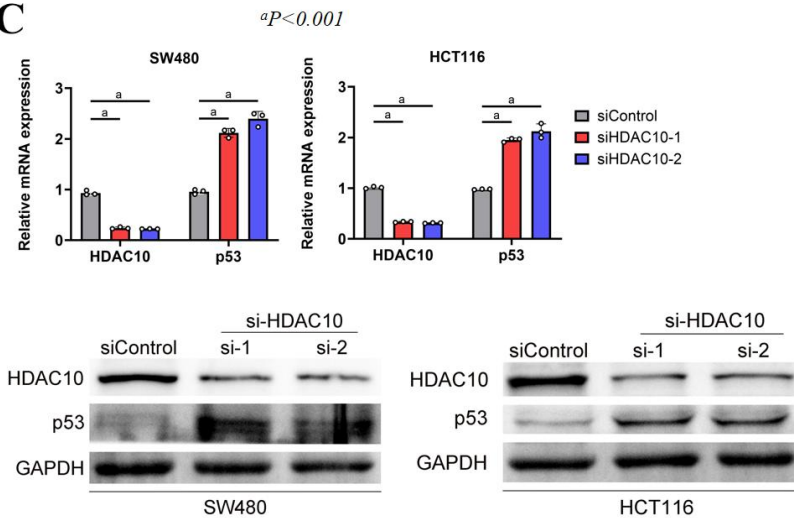
A



B



C



Supplementary Figure 4 HDAC10 depletion decreased Ki67 expression and increased p53 expression. **A:** At 24 h post transfection, fluorescence photographs of CRC cells transfected with siRNA using lipo3000; **B:** HDAC10 expression positively correlated with Ki67; **C:** HDAC10 depletion increased p53 expression at transcriptional and translational levels. Compared with the siControl group, $^aP < 0.01$.

Supplementary Table 1 clinicopathological characteristics of 90 patients

ID	T	N	M	Grad e	CD 8	PDL 1	PD 1	Stage	fusta t	futim e	Gende r	Ag e
D15A625 4	T 3	N 2	M 0	G3& 4	0.0 2	0.01	0.0 1	Stage III	1	2	Femal e	61
D15A625 3	T 4	N 2	M 1	G3& 4	0.0 1	0.01	0.0 1	Stage III	1	4	Male	67
D15A625 2	T 4	N 2	M 0	G3& 4	0.0 1	0.01	0.0 1	Stage III	1	10	Femal e	29
D15A624 9	T 2	N 0	M 0	G1& 2	0.1 5	0.45	0.0 2	Stage II	0	47	Femal e	51
D15A624 8	T 4	N 2	M 0	G3& 4	0.0 7	0.15	0.0 1	Stage II	0	47	Male	81
D15A624 7	T 2	N 0	M 0	G1& 2	0.2 5	0.25	0.0 7	Stage II	0	48	Femal e	83
D15A623 1	T 4	N 0	M 0	G1& 2	0.1 5	0.15	0.0 5	Stage II	0	49	Femal e	55
D15A623 0	T 4	N 0	M 0	G1& 2	0.0 5	0.6	0.0 3	Stage II	0	49	Femal e	65
D15A622 9	T 3	N 2	M 0	G1& 2	0.0 3	0.05	0.0 1	Stage II	0	50	Femal e	76
D15A622 8	T 3	N 2	M 0	G3& 4	0.3 5	0.01	0.0 1	Stage II	0	50	Femal e	75
D15A622 4	T 3	N 2	M 0	G1& 2	0.0 1	0.05	0.0 2	Stage II	1	24	Femal e	86
D15A622 2	T 3	N 0	M 0	G1& 2	0.0 5	0.45	0.0 2	Stage II	0	51	Male	69
D15A622 1	T 3	N 2	M 1	G4	0.0 2	0.3	0.0 2	Stage II	0	51	Male	77

D15A622 0	T 4	N 2	M 1	G3& 4	0	0.01	0.0 1	Stage III	1	13	Male	76
D15A621 9	T 4	N 0	M 0	G1& 2	0.1	1	0.0 5	Stage II	0	51	Femal e	81
D15A621 8	T 3	N 0	M 0	G1& 2	0.0 1	0.25	0.0 1	Stage II	0	51	Male	54
D15A621 7	T 4	N 2	M 1	G4	0.0 1	0.01	0.0 5	Stage II	0	51	Femal e	44
D15A621 4	T 4	N 0	M 0	G1& 2	0.0 5	0.1	0.0 7	Stage II	0	51	Male	80
D15A621 3	T 3	N 0	M 0	G1& 2	0.0 5	0.15	0.1 5	Stage III	0	52	Femal e	71
D15A621 2	T 2	N 0	M 0	G1& 2	0.0 1	0.05	0.0 1	Stage II	0	52	Femal e	57
D15A621 1	T 4	N 2	M 1	G4	0	0.01	0.0 1	Stage III	0	52	Femal e	42
D15A621 0	T 4	N 0	M 0	G1& 2	0.3 5	0.01	0.0 3	Stage II	1	26	Femal e	40
D15A620 9	T 4	N 0	M 0	G1& 2	0.1 5	0.45	0.0 1	Stage II	0	52	Male	61
D15A620 8	T 4	N 0	M 0	G3& 4	0.0 1	0.01	0.0 1	Stage II	0	52	Male	65
D15A620 7	T 2	N 0	M 0	G1& 2	0.0 1	0.01	0.0 3	Stage II	0	52	Femal e	79
D15A620 6	T 3	N 0	M 1	G1& 2	0.2 5	0.01	0.0 3	Stage II	0	53	Male	48
D15A620 5	T 4	N 2	M 0	G1& 2	0.1	0.3	0.1	Stage II	1	8	Femal e	49
D15A620	T	N	M	G3&	0.0	0.01	0.0	Stage	1	17	Femal	56

4	4	2	0	4	3		3	II			e	
D15A620	T	N	M	G1&	0.0	0.01	0.0	Stage	1	29	Femal	68
2	4	0	0	2	5		1	II			e	
D15A620	T	N	M	G4	0.2	0.45	0.0	Stage	1	11	Male	55
1	4	1	0		5		1	II				
D15A620	T	N	M	G3&	0.0	0.03	0.0	Stage	1	14	Femal	60
0	4	2	0	4	5		5	III			e	
D15A619	T	N	M	G3&	0.0	0.01	0.0	Stage	0	53	Male	79
9	3	0	1	4	1		1	III				
D15A619	T	N	M	G1&	0.0	0.2	0.0	Stage	1	10	Male	46
8	4	2	0	2	5		3	II				
D15A619	T	N	M	G3&	0	0.35	0	Stage	0	54	Femal	78
7	4	1	1	4				II			e	
D15A619	T	N	M	G1&	0.0	0.2	0.0	Stage	0	54	Male	68
5	2	0	0	2	7		5	II				
D15A619	T	N	M	G1&	0.1	0.05	0.0	Stage	0	54	Male	67
4	2	0	0	2	5		7	II				
D15A619	T	N	M	G1&	0.0	0.45	0.0	Stage	0	55	Male	62
2	4	0	0	2	2		1	II				
D15A619	T	N	M	G1&	0.3	0.01	0.0	Stage	0	55	Male	58
1	2	0	0	2	5		3	II				
D15A603	T	N	M	G3&	0.0	0.01	0.0	Stage	1	1	Male	63
4	3	2	0	4	1		1	III				
D15A588	T	N	M	G1&	0.0	0.05	0.2	Stage	0	59	Male	51
5	4	0	0	2	1			II				
D15A588	T	N	M	G3&	0.0	0.01	0.0	Stage	0	60	Male	78
4	4	1	1	4	3		1	II				
D15A588	T	N	M	G3&	0.0	0.25	0.0	Stage	0	61	Femal	79
3	4	1	0	4	5		5	II			e	

D15A588 2	T 3	N 0	M 0	G1& 2	0.2	0.05	0.2	Stage III	0	61	Femal e	60
D15A588 0	T 4	N 2	M 0	G3& 4	0	0.1	0.0 1	Stage II	1	10	Male	39
D15A587 9	T 4	N 1	M 0	G3& 4	0.0 2	0.2	0.0 1	Stage II	1	18	Femal e	73
D15A587 8	T 4	N 2	M 1	G1& 2	0.0 1	0.01	0.0 7	Stage II	0	64	Femal e	67
D15A587 7	T 4	N 0	M 0	G1& 2	0.7	0	0.0 1	Stage III	1	9	Male	60
D15A587 6	T 3	N 0	M 0	G1& 2	0.0 3	0.25	0.0 2	Stage II	0	65	Femal e	80
D15A587 5	T 4	N 1	M 0	G3& 4	0.0 1	0.05	0.0 1	Stage III	0	66	Femal e	73
D15A587 4	T 2	N 0	M 0	G1& 2	0.0 5	0.01	0.0 1	Stage II	0	70	Femal e	43
D15A585 2	T 3	N 1	M 0	G3& 4	0.0 2	0	0.0 2	Stage II	1	28	Male	44
D15A585 1	T 4	N 2	M 1	G4	0.0 3	0.05	0.0 3	Stage III	1	9	Male	81
D15A584 8	T 4	N 0	M 1	G1& 2	0.0 1	0.01	0.0 5	Stage II	0	69	Male	48
D15A582 0	T 3	N 0	M 1	G1& 2	0.4 5	0.45	0.0 1	Stage III	1	31	Femal e	60
D15A581 9	T 4	N 2	M 0	G3& 4	0.0 2	0	0.0 3	Stage II	1	40	Femal e	57
D15A581 8	T 3	N 2	M 0	G1& 2	0.0 3	0.01	0.0 2	Stage II	0	59	Femal e	78
D15A581	T	N	M	G1&	0	0.1	0.0	Stage	0	59	Femal	68

7	4	0	1	2			5	II			e	
D15A581	T	N	M	G1&	0.2	0.05	0.0	Stage	0	59	Male	65
6	4	0	0	2	5		3	II				
D15A581	T	N	M	G3&	0	0.25	0.0	Stage	0	59	Femal	49
5	3	1	0	4			1	II			e	
D15A581	T	N	M	G3&	0.0	0.01	0.1	Stage	0	60	Femal	74
4	3	2	0	4	2			II			e	
D15A581	T	N	M	G3&	0.0	0.01	0.0	Stage	0	60	Femal	31
3	3	1	1	4	1		2	II			e	
D15A581	T	N	M	G3&	0.0	0.01	0.0	Stage	0	60	Male	51
2	3	0	0	4	2		2	II				
D15A581	T	N	M	G1&	0.0	0.01	0.0	Stage	0	60	Male	57
1	3	0	0	2	3		2	II				
D15A581	T	N	M	G3&	0	0.1	0	Stage	1	25	Femal	72
0	4	2	0	4				III			e	
D15A580	T	N	M	G1&	0.0	0.01	0.0	Stage	0	61	Femal	62
9	3	0	0	2	1		1	II			e	
D15A580	T	N	M	G1&	0	0.2	0.0	Stage	0	61	Male	57
8	2	0	0	2			1	II				
D15A580	T	N	M	G3&	0.0	0.01	0.0	Stage	0	62	Male	66
6	3	1	0	4	3		3	III				
D15A580	T	N	M	G1&	0.0	0.01	0.0	Stage	0	63	Male	78
5	3	0	0	2	2		3	II				
D15A580	T	N	M	G1&	0.0	0.01	0.0	Stage	1	28	Male	72
4	3	2	1	2	2		2	II				
D15A580	T	N	M	G1&	0.0	0.01	0.0	Stage	0	63	Femal	66
3	4	0	0	2	1		3	II			e	
D15A580	T	N	M	G1&	0.0	0.05	0.0	Stage	0	64	Femal	77
2	3	0	0	2	3		5	II			e	

D15A580 1	T 4	N 0	M 0	G1& 2	0.0 1	0.25	0.0 2	Stage II	0	64	Male	
D15A580 0	T 4	N 0	M 0	G4	0.0 1	0.01	0.0 1	Stage II	0	66	Male	86
D15A579 7	T 4	N 1	M 0	G3& 4	0.0 5	0.15	0.0 5	Stage III	0	68	Male	58
D15A579 6	T 4	N 2	M 1	G3& 4	0.1 5	0.01	0.0 1	Stage III	0	66	Femal e	69
D15A579 5	T 4	N 2	M 0	G1& 2	0.0 5	0.05	0.0 5	Stage II	0	66	Femal e	51
D15A579 4	T 4	N 2	M 0	G1& 2	0.0 1	0.01	0.0 1	Stage III	0	67	Femal e	49
D15A579 3	T 3	N 0	M 0	G3& 4	0.0 1	0.01	0.0 2	Stage II	0	68	Male	64
D15A579 2	T 3	N 1	M 0	G3& 4	0.0 2	0.01	0.0 5	Stage II	0	66	Male	49
D15A579 0	T 4	N 0	M 1	G1& 2	0.0 2	0.01	0.0 1	Stage II	0	68	Male	78
D15A517 3	T 3	N 0	M 0	G1& 2	0.0 1	0.15	0.0 1	Stage II	0	76	Male	69
D15A516 9	T 4	N 2	M 0	G3& 4	0	0.01	0	Stage III	1	51	Femal e	57
D15A515 7	T 4	N 0	M 0	G1& 2	0.2 5	0.01	0.0 1	Stage II	0	75	Male	65
D15A515 2	T 4	N 1	M 0	G3& 4	0.0 1	0.01	0.0 1	Stage II	0	74	Femal e	70
D15A515 1	T 4	N 1	M 0	G3& 4	0.0 1	0.25	0	Stage III	0	74	Femal e	77
D15A515	T	N	M	G3&	0.0	0.05	0.0	Stage	1	19	Femal	70

0	4	1	0	4	1		1	II			e	
D15A514 7	T 4	N 0	M 0	G1& 2	0	0.05	0.0 1	Stage III	1	0.37	Male	75
D15A514 6	T 4	N 1	M 1	G4	0.0 1	0.01	0.0 1	Stage III	1	2	Femal e	57
D15A514 4	T 3	N 0	M 0	G1& 2	0.0 3	0.05	0.0 1	Stage II	0	75	Male	64
D15A514 1	T 3	N 0	M 0	G1& 2	0.0 5	0.35	0.0 1	Stage II	0	76	Male	71

Supplementary Table 2 Differentially expressed genes in TCGA-COAD

id	logFC	AveExpr	t	P.Value	adj.P.Val	B	group
RGS5	-1.2105	7.8273	-4.0363	6.32E-05	0.00045	1.03957	down
CTSE	-1.1802	8.24073	-4.0106	7.02E-05	0.00049	0.94027	down
REG1A	-1.1779	9.6126	-3.2176	0.00138	0.00615	-1.8267	down
CLDN18	-1.1587	4.07583	-3.8022	0.00016	0.001	0.15755	down
MMP13	-1.0845	4.3557	-5.1031	4.82E-07	6.54E-06	5.67159	down
CPS1	-1.0457	5.93808	-4.5388	7.16E-06	6.92E-05	3.0977	down
TCN1	-1.0287	6.80447	-3.722	0.00022	0.00131	-0.1333	down
COL10A1	-0.9902	8.16027	-3.9424	9.26E-05	0.00062	0.68001	down
CPA3	-0.9875	7.02121	-5.3822	1.15E-07	1.85E-06	7.04421	down

REG4	-0.9755	11.1579	-2.8343	0.00479	0.01722	-2.956	down
MARCO	-0.9681	5.4781	-3.9382	9.42E-05	0.00063	0.66393	down
SPP1	-0.9595	10.7404	-4.2697	2.36E-05	0.00019	1.96779	down
PLN	-0.9247	6.74402	-4.7063	3.30E-06	3.52E-05	3.83325	down
CYP1B1	-0.9174	6.22384	-4.5077	8.24E-06	7.80E-05	2.96403	down
IGFL2	-0.9026	4.97687	-4.4239	1.20E-05	0.00011	2.60755	down
CCL18	-0.9008	8.01376	-3.9621	8.55E-05	0.00058	0.75483	down
TLR8	-0.8958	5.37391	-5.0217	7.23E-07	9.32E-06	5.28328	down
SLC16A7	-0.8895	5.86472	-4.9356	1.10E-06	1.36E-05	4.87884	down
MMP8	-0.8847	2.72353	-4.5504	6.79E-06	6.61E-05	3.14789	down
CNTN1	-0.8845	3.88746	-4.5064	8.29E-06	7.85E-05	2.95824	down
OLR1	-0.8794	6.54152	-4.5651	6.35E-06	6.24E-05	3.21164	down
KCND2	-0.8602	3.27832	-4.7905	2.22E-06	2.49E-05	4.21206	down
OLFM4	-0.8599	13.346	-2.6012	0.00958	0.03045	-3.575	down
SERPINB2	-0.856	2.65766	-3.9995	7.35E-05	0.00051	0.89757	down
AQP9	-0.8554	6.27454	-4.1663	3.67E-06	0.00028	1.55043	down

				5			
RAB27B	-0.8553	8.00676	-4.9139	1.23E-06	1.48E-05	4.778	down
SUCNR1	-0.8487	5.08251	-5.1725	3.39E-07	4.85E-06	6.00662	down
FPR2	-0.8453	4.66631	-4.2105	3.04E-05	0.00024	1.72797	down
POSTN	-0.8371	11.592	-4.5043	8.36E-06	7.91E-05	2.94944	down
SFRP2	-0.8361	8.93415	-3.1155	0.00195	0.00821	-2.141	down
MSR1	-0.8302	8.31425	-4.948	1.04E-06	1.28E-05	4.93678	down
REG1B	-0.8267	6.13561	-2.3053	0.02157	0.0589	-4.2861	down
CLEC4E	-0.8179	4.86167	-4.5712	6.17E-06	6.08E-05	3.23832	down
MMRN1	-0.8154	5.40643	-4.0413	6.19E-05	0.00044	1.05916	down
LYZ	-0.8085	12.4241	-4.0511	5.94E-05	0.00043	1.09696	down
CD109	-0.7979	7.94536	-4.3139	1.95E-05	0.00017	2.14916	down
GREM1	-0.7967	10.8979	-4.1447	4.02E-05	0.00031	1.46481	down
ANXA10	-0.796	2.51243	-3.2763	0.00113	0.00517	-1.6419	down
CXCL8	-0.7957	10.5601	-4.1152	4.55E-05	0.00034	1.34777	down
PLA2G3	-0.7947	4.13879	-2.9733	0.00309	0.01199	-2.5624	down
TFF2	-0.7895	5.46834	-3.1318	0.00184	0.00784	-2.0915	down
B4GALNT2	-0.7866	5.49339	-2.6501	0.00831	0.02709	-3.4494	down

SPINK4	-0.7812	9.10649	-2.5543	0.01095	0.03388	-3.6931	down
ASPN	-0.7784	8.1313	-3.8749	0.00012	0.00079	0.42622	down
ANGPTL1	-0.7777	4.16002	-3.6452	0.0003	0.00168	-0.4061	down
MS4A2	-0.7775	4.4224	-4.4915	8.86E-06	8.35E-05	2.8945	down
EPYC	-0.7773	3.42706	-3.2003	0.00146	0.00647	-1.8808	down
FCGR3B	-0.7719	5.44734	-3.729	0.00022	0.00128	-0.1081	down
HMX3	-0.7697	2.72313	-3.7364	0.00021	0.00125	-0.0812	down
ANOS1	-0.7618	7.54454	-4.5614	6.46E-06	6.34E-05	3.19543	down
SDR16C5	-0.7517	7.67869	-3.4498	0.00061	0.00309	-1.0762	down
XKR9	-0.7508	4.78813	-3.6367	0.00031	0.00173	-0.436	down
RGS13	-0.7507	3.17563	-4.2937	2.13E-05	0.00018	2.06608	down
TREM1	-0.7468	6.64343	-4.2072	3.08E-05	0.00024	1.71468	down
SEMG1	-0.7451	2.93707	-3.0654	0.0023	0.00941	-2.2917	down
SLITRK6	-0.7444	5.8513	-2.8652	0.00435	0.01591	-2.87	down
OMD	-0.7433	3.26864	-3.3177	0.00098	0.00456	-1.5094	down
CCL7	-0.743	2.49814	-4.5897	5.67E-06	5.67E-05	3.31866	down
TMEM45A	-0.7414	7.23364	-5.4514	7.99E-08	1.34E-06	7.39458	down
IBSP	-0.7296	3.70794	-3.3776	0.00079	0.00383	-1.315	down
ZIC5	-0.7294	3.88171	-2.4428	0.01493	0.04382	-3.966	down
CLEC5A	-0.7259	5.69563	-4.1683	3.64E-05	0.00028	1.55856	down
BMP3	-0.7222	4.17947	-3.3336	0.00092	0.00436	-1.4582	down
LUM	-0.7217	12.5276	-4.5407	7.09E-0	6.87E-05	3.10617	down

				6			
PLA2G4A	-0.7193	7.35042	-3.7739	0.00018	0.0011	0.05433	down
TNFAIP6	-0.7128	6.41512	-4.1497	3.94E-05	0.0003	1.48469	down
SCN7A	-0.7125	3.29846	-3.23	0.00132	0.00593	-1.7879	down
SERPINB7	-0.7108	2.61091	-3.4296	0.00066	0.00328	-1.1435	down
VGLL3	-0.7101	6.59073	-3.7673	0.00019	0.00113	0.03045	down
PDE10A	-0.7082	6.46902	-4.4238	1.20E-05	0.00011	2.60723	down
BCAT1	-0.7075	7.9922	-4.486	9.09E-06	8.52E-05	2.87092	down
TM4SF4	-0.7016	4.75922	-2.9556	0.00327	0.01259	-2.6134	down
MRC1	-0.7006	8.16445	-4.0996	4.86E-05	0.00036	1.28654	down
CXCL5	-0.699	7.12361	-2.6899	0.0074	0.02469	-3.3455	down
CR1	-0.6962	5.18706	-3.7668	0.00019	0.00113	0.02854	down
KLRD1	-0.695	5.82661	-3.9882	7.69E-05	0.00053	0.85453	down
AVPR1A	-0.6921	4.97875	-4.2901	2.16E-05	0.00018	2.0514	down
GJB5	-0.6896	5.00169	-2.6634	0.00799	0.02623	-3.4147	down
JCHAIN	-0.6884	11.2036	-2.8353	0.00477	0.0172	-2.9532	down
DUSP4	-0.6878	9.68872	-3.9133	0.0001	0.00069	0.56999	down
SPOCK1	-0.686	7.95709	-3.4018	0.00073	0.00357	-1.2355	down
FAP	-0.6851	7.78525	-3.8994	0.00011	0.00073	0.51771	down
PTGS2	-0.6842	7.97969	-3.6863	0.00025	0.00148	-0.2608	down
NEFL	-0.6828	2.87267	-3.5525	0.00042	0.00225	-0.7282	down
SLC25A21	-0.6803	3.11625	-3.7357	0.00021	0.00125	-0.084	down
PDGFRL	-0.6758	5.40003	-4.1409	4.08E-05	0.00031	1.44978	down

				5			
SPON1	-0.6738	9.37396	-3.8897	0.00011	0.00075	0.48139	down
MMP1	-0.6717	10.3692	-3.343	0.00089	0.00425	-1.4276	down
FGF7	-0.6713	6.57086	-3.6579	0.00028	0.00161	-0.3613	down
MMP12	-0.6699	10.1742	-3.7596	0.00019	0.00115	0.00264	down
PNMA2	-0.6686	6.18818	-3.6826	0.00026	0.00149	-0.2738	down
COL11A1	-0.6643	9.30642	-3.3446	0.00089	0.00423	-1.4223	down
CYBB	-0.6622	9.66304	-4.4373	1.13E-0	0.0001	2.66398	down
				5			
CHRM2	-0.6606	2.60356	-2.7007	0.00716	0.02406	-3.3169	down
BCL2A1	-0.6571	6.636	-4.3051	2.02E-0	0.00017	2.11277	down
				5			
FER1L6	-0.6558	5.44977	-2.7184	0.0068	0.02303	-3.27	down
NXPE2	-0.654	5.53194	-3.3336	0.00092	0.00436	-1.458	down
HEPACAM2	-0.6511	7.10353	-2.5678	0.01054	0.03288	-3.6595	down
FGF10	-0.6508	4.6006	-3.8007	0.00016	0.00101	0.15202	down
SULF1	-0.6493	11.9701	-3.8266	0.00015	0.00093	0.24734	down
B3GNT6	-0.6487	6.22869	-2.2118	0.02745	0.07156	-4.4935	down
ALDH1A2	-0.6485	4.44268	-3.0574	0.00236	0.00961	-2.3153	down
GABRP	-0.6458	5.83325	-2.7712	0.0058	0.02017	-3.1286	down
PTGFR	-0.6453	5.2078	-3.9342	9.57E-0	0.00064	0.64899	down
				5			
MEOX2	-0.6452	3.9674	-3.3688	0.00082	0.00393	-1.3436	down
PRRX1	-0.643	8.62214	-3.8306	0.00014	0.00092	0.26215	down
SERPINB5	-0.6423	10.0853	-3.1481	0.00175	0.0075	-2.0417	down
PLPPR1	-0.6408	3.38087	-2.9863	0.00297	0.01159	-2.5245	down
TLR1	-0.6397	6.2585	-4.2858	2.20E-0	0.00018	2.03376	down
				5			
TRIM61	-0.6395	2.95799	-4.8312	1.83E-0	2.11E-05	4.39727	down

				6			
PTPRC	-0.6393	9.28953	-3.9876	7.71E-05	0.00053	0.85207	down
TENM3	-0.6373	5.9704	-3.1322	0.00184	0.00784	-2.0901	down
INHBA	-0.6373	9.73764	-3.9344	9.57E-05	0.00064	0.64948	down
CHL1	-0.636	5.74138	-3.649	0.00029	0.00166	-0.3927	down
FGL2	-0.6356	8.73373	-4.2561	2.50E-05	0.00021	1.9124	down
PHLDB2	-0.6353	7.97026	-4.1272	4.33E-05	0.00033	1.39522	down
PLXDC2	-0.635	9.76362	-4.1012	4.82E-05	0.00036	1.29285	down
LY96	-0.6346	5.69283	-4.4884	8.99E-06	8.45E-05	2.88117	down
GAS1	-0.6315	6.59018	-3.1718	0.00161	0.00703	-1.969	down
CXCL13	-0.6308	6.31142	-2.8367	0.00475	0.01713	-2.9492	down
GPM6A	-0.6299	2.84722	-2.9592	0.00324	0.01248	-2.6031	down
ADAM12	-0.6289	8.63884	-3.4595	0.00059	0.00299	-1.0438	down
GCNT4	-0.6287	5.13829	-4.2692	2.36E-05	0.00019	1.96565	down
PRND	-0.6272	3.08975	-3.4671	0.00057	0.00292	-1.0182	down
OGN	-0.6268	4.53487	-2.5407	0.01138	0.03501	-3.7272	down
SEMA3E	-0.6262	2.3991	-3.1943	0.00149	0.00658	-1.8994	down
CD69	-0.6253	6.28656	-4.0795	5.28E-05	0.00039	1.20792	down
GPC6	-0.6251	7.75277	-4.2958	2.11E-05	0.00018	2.0746	down
KCND3	-0.6249	6.6395	-3.7471	0.0002	0.0012	-0.0428	down
CHRNA3	-0.6244	5.12993	-3.679	0.00026	0.00151	-0.2867	down

MNDA	-0.6233	6.81482	-3.9842	7.82E-05	0.00054	0.83887	down
SRGN	-0.6232	10.1774	-4.5936	5.57E-06	5.58E-05	3.33571	down
TNFSF4	-0.6227	6.75858	-4.2557	2.51E-05	0.00021	1.91082	down
FCGR3A	-0.6214	9.26253	-3.6405	0.0003	0.00171	-0.4226	down
BMPR1B	-0.6212	3.68094	-3.1326	0.00184	0.00783	-2.089	down
PLEK	-0.6211	8.52358	-3.9113	0.0001	0.0007	0.56265	down
SCEL	-0.6204	4.38139	-2.6491	0.00834	0.02716	-3.4518	down
HLA-DQA2	-0.6199	7.048	-2.8053	0.00523	0.01854	-3.0358	down
RSPO3	-0.6183	5.52108	-3.4436	0.00062	0.00314	-1.097	down
SAMSN1	-0.6182	7.09939	-4.2793	2.26E-05	0.00019	2.00715	down
COLGALT2	-0.6182	4.70498	-3.055	0.00238	0.00967	-2.3225	down
GPMB	-0.6164	10.6426	-3.7929	0.00017	0.00104	0.12378	down
EVI2A	-0.6163	5.97041	-4.1975	3.21E-05	0.00025	1.6756	down
SERTAD4	-0.6147	6.41811	-3.8099	0.00016	0.00098	0.18574	down
FPR3	-0.6142	8.34302	-4.0132	6.95E-05	0.00049	0.95022	down
LRRC4C	-0.6141	2.70557	-3.5674	0.0004	0.00215	-0.6771	down
PTGER2	-0.6141	6.94156	-4.2029	3.14E-05	0.00025	1.69729	down
GPR34	-0.6135	6.42974	-4.2891	2.17E-05	0.00018	2.04706	down
SLC4A4	-0.6114	7.17773	-2.8173	0.00504	0.01796	-3.0029	down
GPR183	-0.6102	7.31131	-4.2271	2.83E-05	0.00023	1.79458	down

DCN	-0.6101	11.9004	-4.1056	4.74E-05	0.00035	1.30999	down
FGF5	-0.6048	2.03677	-3.6759	0.00026	0.00152	-0.2977	down
KITLG	-0.6027	9.47092	-4.5943	5.55E-06	5.57E-05	3.33891	down
DAPPI	-0.6027	7.3892	-3.8971	0.00011	0.00073	0.5091	down
MRO	-0.6023	3.39665	-4.1308	4.26E-05	0.00032	1.40955	down
CCL8	-0.6019	4.72298	-3.269	0.00116	0.00527	-1.6649	down
CD86	-0.6006	7.29569	-4.2881	2.18E-05	0.00018	2.04298	down
KCNJ15	-0.5994	4.94662	-3.393	0.00075	0.00366	-1.2645	down
CD300E	-0.5982	5.18183	-3.3806	0.00078	0.0038	-1.3049	down
CTHRC1	-0.5981	9.35849	-3.8742	0.00012	0.00079	0.42359	down
VNN2	-0.5972	5.34469	-3.3834	0.00077	0.00376	-1.2958	down
MFAP5	-0.5961	6.61512	-3.0048	0.0028	0.01104	-2.4707	down
ZFHX4	-0.596	5.13769	-2.9396	0.00344	0.01312	-2.6596	down
TFEC	-0.596	6.04603	-3.546	0.00043	0.0023	-0.7505	down
ANGPT1	-0.5956	5.83093	-4.0895	5.07E-05	0.00037	1.24703	down
COL24A1	-0.5945	5.07765	-3.5061	0.0005	0.0026	-0.8868	down
ARHGAP20	-0.594	4.27088	-3.9057	0.00011	0.00071	0.54153	down
DCLK1	-0.594	5.01337	-3.53	0.00046	0.00242	-0.8055	down
BRINP3	-0.5937	2.40187	-2.7943	0.00541	0.01906	-3.0658	down
AGR3	-0.5935	9.22671	-2.954	0.00329	0.01264	-2.6182	down
MEP1B	-0.5932	3.68838	-3.2763	0.00113	0.00517	-1.6419	down
RGS1	-0.5929	9.44954	-3.6349	0.00031	0.00174	-0.4423	down
DCSTAMP	-0.5922	3.02764	-3.4676	0.00057	0.00292	-1.0165	down
SAMD5	-0.5918	9.46083	-3.1687	0.00163	0.00709	-1.9785	down

CLEC6A	-0.591	1.80134	-4.1988	3.20E-05	0.00025	1.6806	down
NCAM2	-0.5881	4.66731	-3.3722	0.00081	0.00389	-1.3327	down
GALNTL6	-0.588	3.34208	-2.9964	0.00287	0.01129	-2.4952	down
SELE	-0.5877	6.2001	-3.3838	0.00077	0.00376	-1.2947	down
TLL1	-0.5877	3.67152	-3.4551	0.0006	0.00303	-1.0584	down
FCN1	-0.5873	5.64834	-3.3214	0.00096	0.00452	-1.4974	down
CD84	-0.5863	7.54539	-3.6065	0.00034	0.0019	-0.5415	down
PLPP4	-0.5863	5.55071	-3.1216	0.00191	0.00807	-2.1225	down
FCRLA	-0.5862	3.74238	-3.2924	0.00107	0.00493	-1.5903	down
UGT2B15	-0.586	5.66075	-2.9048	0.00384	0.01437	-2.7585	down
IL1RN	-0.5852	8.65872	-3.6657	0.00027	0.00157	-0.3336	down
RAB31	-0.5845	10.2929	-4.1097	4.66E-05	0.00035	1.32616	down
COLEC12	-0.5827	6.88663	-3.5105	0.00049	0.00257	-0.8717	down
C5orf46	-0.5825	3.05764	-3.0937	0.00209	0.00871	-2.2068	down
SCN9A	-0.5822	4.74503	-3.4106	0.0007	0.00348	-1.2064	down
TMEM255A	-0.5822	4.18751	-3.8721	0.00012	0.00079	0.41562	down
CCL13	-0.5819	4.85165	-2.8553	0.00449	0.01634	-2.8976	down
CASQ2	-0.5815	3.56072	-2.5947	0.00975	0.03092	-3.5913	down
RGS18	-0.5806	4.45435	-4.0338	6.38E-05	0.00045	1.02994	down
IL7R	-0.5784	8.79375	-3.8334	0.00014	0.00091	0.27248	down
MITF	-0.5776	7.21804	-4.0122	6.97E-05	0.00049	0.94644	down
INA	-0.5769	2.63666	-3.506	0.0005	0.0026	-0.8869	down
DPT	-0.5768	5.09631	-2.9441	0.0034	0.01297	-2.6465	down
DPYD	-0.5756	7.54672	-3.7722	0.00018	0.00111	0.04823	down
FDCSP	-0.575	3.50184	-2.4611	0.0142	0.04207	-3.9221	down

CACNA2D1	-0.5747	6.49156	-3.598	0.00035	0.00195	-0.5711	down
FRMD6	-0.5742	8.23038	-3.9675	8.37E-05	0.00057	0.77542	down
KCNMA1	-0.5725	7.77211	-3.3996	0.00073	0.00359	-1.2427	down
CDH2	-0.5721	5.323	-3.2347	0.0013	0.00585	-1.7733	down
ROR1	-0.5712	5.81078	-3.5226	0.00047	0.00247	-0.8306	down
CD163	-0.5705	8.70297	-3.3118	0.001	0.00465	-1.5283	down
HOPX	-0.5704	7.90848	-3.789	0.00017	0.00105	0.10928	down
PNPLA3	-0.5701	4.44135	-2.7729	0.00577	0.0201	-3.1239	down
HABP2	-0.5699	3.15917	-2.3342	0.01999	0.05526	-4.2203	down
MEGF10	-0.5689	2.88163	-3.7044	0.00024	0.00139	-0.1963	down
MS4A4A	-0.5684	7.18986	-3.8632	0.00013	0.00082	0.38279	down
NOX4	-0.5682	5.77749	-3.5214	0.00047	0.00248	-0.8346	down
F13A1	-0.567	7.80281	-3.1246	0.00189	0.00801	-2.1134	down
FLRT3	-0.5657	6.8342	-3.3342	0.00092	0.00435	-1.4561	down
ADGRG6	-0.5638	9.14954	-3.5972	0.00035	0.00195	-0.5738	down
CALCRL	-0.5636	8.2551	-3.9885	7.68E-05	0.00053	0.85556	down
NRK	-0.5622	3.55751	-2.7341	0.00649	0.02221	-3.2284	down
PAX9	-0.5616	5.51637	-3.0442	0.00246	0.00995	-2.3546	down
GPR141	-0.5616	3.06641	-3.6804	0.00026	0.0015	-0.2818	down
NXF3	-0.5612	3.60222	-2.3905	0.01721	0.0491	-4.09	down
SGMS2	-0.5609	9.63694	-4.316	1.93E-05	0.00016	2.15765	down
IL1A	-0.5607	5.53383	-3.2009	0.00146	0.00646	-1.8788	down
EVI2B	-0.5597	7.30598	-3.8203	0.00015	0.00095	0.22401	down
MMP7	-0.5591	9.65987	-2.4683	0.01392	0.0414	-3.9047	down
PDCD1LG2	-0.559	5.37101	-3.5231	0.00047	0.00247	-0.829	down
CCDC80	-0.5579	9.65604	-3.2731	0.00114	0.00521	-1.6519	down

GNB4	-0.5569	8.09381	-4.0356	6.33E-05	0.00045	1.03692	down
FABP2	-0.5568	6.48684	-2.5326	0.01164	0.03565	-3.7472	down
SGCD	-0.5555	7.23467	-3.3985	0.00073	0.0036	-1.2464	down
NR1H4	-0.5553	3.60658	-2.5954	0.00974	0.03086	-3.5895	down
CCBE1	-0.5553	3.9099	-2.9964	0.00287	0.01129	-2.4952	down
NRXN1	-0.554	2.25639	-2.9804	0.00302	0.01177	-2.5418	down
FGF2	-0.5538	6.04985	-3.5326	0.00045	0.0024	-0.7965	down
KYNU	-0.5537	6.79441	-3.7293	0.00021	0.00128	-0.107	down
CYBRD1	-0.5524	9.9081	-3.8942	0.00011	0.00074	0.49836	down
FCGR2B	-0.5515	6.08899	-3.4588	0.00059	0.003	-1.046	down
CLIC4	-0.5499	11.4121	-4.1971	3.22E-05	0.00025	1.67408	down
FPR1	-0.5493	6.93453	-3.2897	0.00108	0.00497	-1.5989	down
CTSG	-0.549	3.38239	-2.791	0.00546	0.01922	-3.0747	down
VEPH1	-0.5488	3.88089	-3.6765	0.00026	0.00152	-0.2956	down
TDO2	-0.548	6.73221	-3.5709	0.00039	0.00212	-0.6649	down
PDE4B	-0.5479	8.42376	-4.0937	4.98E-05	0.00037	1.26337	down
SLIT2	-0.5464	6.58134	-2.9293	0.00356	0.01349	-2.6888	down
TLR7	-0.5455	5.41244	-3.5479	0.00043	0.00228	-0.7443	down
FGF1	-0.5444	4.94564	-3.8147	0.00015	0.00097	0.20344	down
ODAM	-0.5443	5.36784	-2.4415	0.01499	0.04394	-3.9692	down
PPBP	-0.5437	4.69688	-2.0055	0.04547	0.10699	-4.9212	down
NEGR1	-0.5431	6.30917	-3.7087	0.00023	0.00137	-0.1809	down
KCTD12	-0.5431	10.2221	-3.6015	0.00035	0.00193	-0.5591	down
IL33	-0.5425	9.51413	-2.8571	0.00446	0.01627	-2.8926	down
SELL	-0.5425	6.95564	-3.4663	0.00057	0.00293	-1.0209	down
CXCL10	-0.5416	8.74872	-2.8817	0.00413	0.01527	-2.8238	down

SEMA3D	-0.5415	3.8041	-2.6948	0.00729	0.02439	-3.3326	down
DDR2	-0.5392	8.85551	-3.2805	0.00111	0.00511	-1.6285	down
PABPC4L	-0.5389	3.58545	-3.8616	0.00013	0.00082	0.37657	down
ADGRF1	-0.5388	5.08293	-2.71	0.00697	0.0235	-3.2924	down
CYP7B1	-0.5378	6.55539	-3.2767	0.00113	0.00516	-1.6406	down
PIK3CG	-0.5363	6.93053	-3.9419	9.28E-05	0.00062	0.67793	down
HTR2B	-0.536	3.11736	-2.8015	0.00529	0.0187	-3.0462	down
ERMN	-0.5359	3.99586	-3.3531	0.00086	0.00412	-1.3949	down
PI15	-0.5353	5.53401	-2.6035	0.00951	0.03029	-3.569	down
SIGLEC6	-0.5352	3.44348	-3.4498	0.00061	0.00309	-1.0761	down
PLP1	-0.5333	2.83133	-2.8339	0.00479	0.01723	-2.9571	down
P2RY14	-0.5332	5.63046	-3.7004	0.00024	0.00141	-0.2104	down
GALNT15	-0.5331	5.66212	-3.2697	0.00115	0.00526	-1.6627	down
TNFSF13B	-0.5327	6.94142	-3.4855	0.00054	0.00276	-0.9563	down
NAP1L3	-0.5316	4.45791	-3.4368	0.00064	0.00321	-1.1195	down
CSRNP3	-0.5316	4.64206	-3.0754	0.00222	0.00916	-2.2617	down
CLEC4D	-0.5313	2.08571	-3.4347	0.00064	0.00323	-1.1264	down
LOX	-0.5301	8.85317	-3.7436	0.0002	0.00122	-0.0552	down
CLC	-0.5297	3.65812	-2.2327	0.02602	0.06858	-4.4478	down
GAP43	-0.5273	3.39572	-2.8795	0.00416	0.01535	-2.83	down
CXCL11	-0.527	7.90905	-2.6067	0.00942	0.03007	-3.5608	down
ARSJ	-0.5261	7.78587	-3.3796	0.00078	0.00381	-1.3084	down
SLC1A3	-0.526	6.4884	-3.1677	0.00163	0.00711	-1.9816	down
CCL21	-0.5253	7.6702	-2.3938	0.01705	0.04877	-4.0821	down
SPATA18	-0.525	7.45179	-3.8743	0.00012	0.00079	0.42401	down
CLMP	-0.5244	7.83092	-3.49	0.00053	0.00273	-0.9412	down
CXCR1	-0.5244	4.26259	-2.8505	0.00455	0.01654	-2.911	down
TWSG1	-0.5237	9.95839	-4.6342	4.62E-05	4.74E-05	3.51375	down

				6			
FCAR	-0.5236	3.19646	-3.0676	0.00228	0.00935	-2.2852	down
EDIL3	-0.5232	9.06057	-3.8266	0.00015	0.00093	0.24724	down
ANXA1	-0.5223	10.9498	-3.9987	7.37E-05	0.00051	0.89473	down
PTAFR	-0.5222	8.38266	-3.9487	9.03E-05	0.00061	0.7037	down
ANTXR1	-0.522	11.1282	-3.2953	0.00106	0.00489	-1.5812	down
RAB3B	-0.5209	6.64712	-3.0399	0.0025	0.01006	-2.3672	down
NEXN	-0.5207	7.45984	-3.0455	0.00245	0.00992	-2.3509	down
RGS2	-0.5203	8.87699	-4.0153	6.88E-05	0.00048	0.9585	down
CTNNA3	-0.5202	2.25767	-3.1618	0.00167	0.00723	-1.9996	down
GLIS3	-0.5185	6.61748	-3.2756	0.00113	0.00517	-1.6439	down
CARD6	-0.518	7.52027	-3.9341	9.58E-05	0.00064	0.64859	down
CLIP4	-0.5173	6.39611	-3.346	0.00088	0.00421	-1.4178	down
VNN1	-0.5168	6.94437	-2.6114	0.0093	0.02973	-3.549	down
CDH19	-0.5164	2.47375	-2.5669	0.01056	0.03294	-3.6616	down
GPR65	-0.5163	5.7674	-3.9086	0.00011	0.0007	0.5523	down
LYVE1	-0.5162	5.65067	-3.2729	0.00114	0.00521	-1.6525	down
HTR3A	-0.5161	2.24556	-3.0844	0.00216	0.00894	-2.2348	down
TNFSF18	-0.5159	3.04165	-3.6639	0.00028	0.00158	-0.34	down
DGKB	-0.5158	2.68623	-2.7759	0.00572	0.01997	-3.1157	down
HOXC6	-0.5148	4.15329	-2.2194	0.02692	0.07048	-4.477	down
PCDH10	-0.5136	1.76257	-3.3834	0.00077	0.00376	-1.2959	down
PYGO1	-0.513	5.37699	-3.1784	0.00158	0.00689	-1.9486	down
HMSD	-0.5129	2.63701	-3.321	0.00097	0.00453	-1.4986	down
RNF180	-0.5126	4.69048	-3.2171	0.00138	0.00616	-1.8283	down

PENK	-0.5123	2.04802	-2.7399	0.00637	0.02189	-3.2128	down
NKX3-1	-0.5117	4.76439	-3.2608	0.00119	0.0054	-1.6908	down
PCDH7	-0.5114	7.55151	-3.3643	0.00083	0.00399	-1.3584	down
CNTN4	-0.5102	5.53563	-3.5329	0.00045	0.00239	-0.7955	down
DACT1	-0.5101	7.83195	-3.5693	0.00039	0.00213	-0.6704	down
MSRB3	-0.5099	8.55904	-3.3541	0.00086	0.00411	-1.3917	down
AKAP12	-0.5098	8.92997	-2.923	0.00363	0.0137	-2.7068	down
BICC1	-0.509	7.91076	-3.5871	0.00037	0.00202	-0.609	down
GCSAML	-0.5089	2.40281	-3.6479	0.00029	0.00167	-0.3967	down
RGS4	-0.5082	5.61142	-3.0349	0.00254	0.0102	-2.3821	down
PRKAR2B	-0.5077	7.20805	-3.5224	0.00047	0.00247	-0.8313	down
EPHA7	-0.5077	4.43069	-2.7725	0.00578	0.02012	-3.1251	down
PDZRN4	-0.5073	3.4991	-2.6196	0.00908	0.02913	-3.528	down
TFF1	-0.5067	10.3596	-2.2071	0.02777	0.07229	-4.5036	down
FMO2	-0.5052	3.51477	-2.6234	0.00898	0.02885	-3.5183	down
STEAP4	-0.5051	6.20263	-3.1216	0.00191	0.00807	-2.1224	down
KIAA1549L	-0.5049	5.86254	-2.4035	0.01661	0.04769	-4.0593	down
ITGAV	-0.5045	11.3992	-4.0491	5.99E-05	0.00043	1.08919	down
CALD1	-0.5045	12.0584	-3.4419	0.00063	0.00316	-1.1025	down
KLK11	-0.5028	6.86851	-2.2157	0.02718	0.07102	-4.485	down
DSE	-0.5025	8.36334	-3.9259	9.90E-05	0.00066	0.61758	down
NMUR2	-0.5022	2.08664	-2.4214	0.01583	0.04593	-4.0172	down
THSD7A	-0.5003	5.2321	-3.1214	0.00191	0.00808	-2.1232	down
FYB1	-0.5002	7.92634	-3.1573	0.00169	0.00732	-2.0135	down
DISP3	0.5000 4	3.24998	3.6633 5	0.00028	0.00159	-0.3421	up
IDH3G	0.5000	11.3449	5.7880	1.28E-0	2.64E-07	9.15504	up

	6		5	8			
MRM1	0.5002	8.73698	5.0952	5.01E-0	6.76E-06	5.63348	up
	8			7			
GDPD4	0.5003	1.79437	4.3460	1.69E-0	0.00015	2.28198	up
	3		6	5			
SHARPIN	0.5004	10.9435	5.0169	7.40E-0	9.52E-06	5.26076	up
	1		2	7			
AXIN2	0.5004	11.6611	3.1924	0.0015	0.00662	-1.9052	up
	3		2				
GYG2	0.5004	8.78054	3.2530	0.00122	0.00554	-1.7155	up
	3		3				
UFSP1	0.5004	6.13653	5.7303	1.77E-0	3.52E-07	8.84672	up
	7		4	8			
CLEC18A	0.5006	1.99561	4.2210	2.91E-0	0.00023	1.77018	up
	1		1	5			
NUPR1	0.5007	7.05191	3.6425	0.0003	0.0017	-0.4153	up
	8		7				
PFN4	0.5008	3.15918	4.1349	4.19E-0	0.00032	1.42615	up
	1		9	5			
FITM2	0.5008	10.0128	4.7787	2.35E-0	2.61E-05	4.15852	up
	6			6			
SPAG4	0.5008	7.5012	4.8278	1.86E-0	2.13E-05	4.38184	up
	7		2	6			
NRTN	0.5008	5.59023	4.9257	1.16E-0	1.41E-05	4.83294	up
	8			6			
RIIAD1	0.5009	3.68991	2.6340	0.00871	0.02811	-3.4908	up
			3				
GPR143	0.5010	6.93338	2.2237	0.02663	0.06984	-4.4675	up
	9		6				

PLCH2	0.50118	6.76485	3.3524 5	0.00086	0.00413	-1.397	up
C9orf16	0.50119	10.8016	4.8319 9	1.82E-0 6	2.10E-05	4.40085	up
SMTNL1	0.5012 3	2.8241	3.5555 8	0.00041	0.00223	-0.7178	up
EEF1D	0.5012 6	11.2737	5.7538 9	1.55E-0 8	3.13E-07	8.97222	up
PLAGL1	0.5016 1	9.4126	3.7475 2	0.0002	0.0012	-0.0412	up
HDAC6	0.5018 5	10.6108	5.6098 6	3.42E-0 8	6.23E-07	8.21165	up
DLX4	0.5019 3	4.39013	3.7190 6	0.00022	0.00132	-0.1437	up
SLC6A9	0.5021 8	8.79856	4.4032 9	1.31E-0 5	0.00012	2.52084	up
TNNI3	0.5022	3.73616	2.6151 4	0.0092	0.02945	-3.5393	up
CDHR2	0.5023 8	9.65694	2.8951 5	0.00396	0.01474	-2.7859	up
NOC4L	0.5027 1	10.0338	5.0526 2	6.20E-0 7	8.11E-06	5.4301	up
GBX2	0.5027 5	2.31478	3.11716	0.00194	0.00817	-2.1359	up
EBLN2	0.5028 8	4.51964	3.4601 8	0.00059	0.00299	-1.0415	up
TSEN54	0.5030 3	10.6585	5.9278 2	5.86E-0 9	1.31E-07	9.91292	up
DGKZ	0.5032	11.5475	5.8287	1.02E-0	2.15E-07	9.37415	up

			6	8			
CSNK1E	0.5032 3	11.0627	6.1154	1.99E-0 9	5.03E-08	10.9544	up
AKAP8L	0.5032 7	9.60607	6.4408 8	2.88E-1 0	8.87E-09	12.8271	up
NT5DC4	0.5033 7	2.8895	3.4295 3	0.00066	0.00328	-1.1437	up
MBD3	0.5035 6	10.4388	5.4360 8	8.67E-0 8	1.44E-06	7.31659	up
F12	0.5036 6	8.60869	4.6955 7	3.47E-0 6	3.68E-05	3.78531	up
CC2D1A	0.5037 8	11.3821	5.1378 9	4.04E-0 7	5.62E-06	5.83898	up
UBE2V1	0.5039 5	6.20328	4.4320 1	1.16E-0 5	0.00011	2.64178	up
L3HYPDH	0.5040 1	7.12049	5.5899 7	3.81E-0 8	6.86E-07	8.10797	up
SZT2	0.5043 1	9.86106	4.8956 2	1.34E-0 6	1.60E-05	4.69344	up
ADAMTS17	0.5044 1	5.83878	3.71131	0.00023	0.00136	-0.1714	up
ADRA2C	0.5044 6	6.1223	2.8219 2	0.00497	0.01774	-2.9901	up
CARD9	0.5046 5	6.33474	4.1449	4.02E-0 5	0.00031	1.46547	up
SLC22A31	0.5047 2	3.29527	2.4594 5	0.01427	0.04225	-3.9261	up
PTGES2	0.5049 7	11.5696	5.9499	5.17E-0 9	1.17E-07	10.0341	up

CDH24	0.5050 6	8.45966	5.4022 9	1.04E-0 7	1.69E-06	7.14545	up
ARHGEF19	0.5050 6	8.91985	4.4325 9	1.15E-0 5	0.00011	2.64425	up
PPM1J	0.5051 4	5.0962	5.5362 8	5.09E-0 8	8.90E-07	7.82965	up
CREB3L3	0.5053 2	4.14608	2.8229 1	0.00496	0.0177	-2.9873	up
CFAP70	0.5053 4	4.87698	3.4778 3	0.00055	0.00283	-0.9822	up
AC003002.2	0.5055 5	1.29203	4.9907 7	8.42E-0 7	1.07E-05	5.13742	up
RBP2	0.5057 1	5.61233	2.1022 9	0.03605	0.08903	-4.7256	up
PRKAR1B	0.5058 2	10.4046	5.1669 8	3.49E-0 7	4.96E-06	5.97981	up
ANO8	0.5059 4	8.4605	5.1012 8	4.86E-0 7	6.58E-06	5.66268	up
TYSND1	0.5064 7	10.2	6.2888 9	7.18E-1 0	2.04E-08	11.9424	up
ODF3B	0.5065 5	7.84864	4.6276 7	4.76E-0 6	4.87E-05	3.48496	up
GPR179	0.5066	2.21764	3.9147 2	0.0001	0.00069	0.57538	up
NELFCD	0.5066 4	12.1224	5.3996 2	1.05E-0 7	1.71E-06	7.13197	up
RALY	0.5073 5	13.1574	5.8499 9	9.09E-0 9	1.94E-07	9.48894	up
ARHGAP27	0.5074	11.5863	6.0267	3.33E-0	8.01E-08	10.4586	up

	7		2	9			
QRICH2	0.5075	6.19897	4.5890	5.69E-0	5.67E-05	3.31595	up
	6		7	6			
HEXIM2	0.5077	5.4249	6.1870	1.31E-0	3.47E-08	11.3598	up
			8	9			
ALOX12	0.5079	4.93088	4.9592	9.82E-0	1.23E-05	4.98957	up
	2		7	7			
PMM1	0.5083	9.31567	5.9656	4.72E-0	1.08E-07	10.1207	up
	8		5	9			
PDE4C	0.5084	1.54646	4.1468	3.98E-0	0.0003	1.47316	up
	2		4	5			
TUBG2	0.5088	7.81066	5.6064	3.48E-0	6.32E-07	8.19367	up
	9		1	8			
DAPK2	0.5090	9.35857	4.3698	1.52E-0	0.00013	2.38109	up
	3		9	5			
TULP1	0.5091	1.77204	4.6566	4.16E-0	4.33E-05	3.61259	up
	2		4	6			
VPS9D1	0.5092	8.35097	6.0910	2.30E-0	5.67E-08	10.8179	up
	8		8	9			
KCNAB3	0.5093	4.70009	4.5331	7.34E-0	7.08E-05	3.07341	up
	9		4	6			
CLEC18B	0.5094	2.11415	3.8072	0.00016	0.00099	0.17607	up
	9		3				
RNF44	0.5097	11.5513	5.6054	3.50E-0	6.35E-07	8.18853	up
	6		3	8			
P4HTM	0.51011	10.5718	6.9397	1.27E-11	5.24E-10	15.8539	up
MAFK	0.5104	10.2286	4.8920	1.36E-0	1.63E-05	4.67697	up
	4		6	6			
FCHO1	0.5105	8.79311	3.9678	8.36E-0	0.00057	0.7767	up

	2		7	5			
PRAF2	0.5107	6.77084	5.5229	5.46E-0	9.52E-07	7.76103	up
	3		7	8			
CPNE6	0.51109	3.2994	2.7802	0.00564	0.01975	-3.1039	up
			7				
ZBTB48	0.51118	8.95976	6.4279	3.12E-1	9.51E-09	12.751	up
			3	0			
CDX2	0.51123	12.616	3.8256	0.00015	0.00093	0.24358	up
NDUFA7	0.51134	3.43675	5.3942	1.08E-0	1.75E-06	7.10472	up
			2	7			
BTBD2	0.5114	11.6278	5.846	9.29E-0	1.98E-07	9.46736	up
				9			
PALD1	0.51171	10.2681	3.9421	9.27E-0	0.00062	0.67885	up
			2	5			
GGT1	0.51196	4.17191	3.3413	0.0009	0.00427	-1.4331	up
			2				
VAV2	0.51199	10.9657	4.0554	5.83E-0	0.00042	1.11396	up
			6	5			
AFP	0.5121	2.25786	3.0869	0.00214	0.00888	-2.2272	up
	2						
NOL3	0.5122	9.35426	6.0408	3.07E-0	7.42E-08	10.5374	up
			9	9			
RBM6	0.5123	10.9103	4.6858	3.63E-0	3.84E-05	3.74202	up
	1		4	6			
EML3	0.5123	10.2064	6.2134	1.12E-0	3.04E-08	11.51	up
	2		7	9			
KCNS1	0.5126	3.0244	3.6760	0.00026	0.00152	-0.297	up
			7				
UAP1L1	0.5127	9.08638	5.0513	6.24E-0	8.15E-06	5.42395	up

	4		3	7			
ADAMTSL2	0.5127	7.77578	3.6122	0.00034	0.00187	-0.5214	up
	4		8				
STMN3	0.5128	9.35257	3.1789	0.00157	0.00688	-1.9469	up
	9		3				
TOGARAM2	0.5131	3.64283	4.4587	1.03E-0	9.50E-05	2.75516	up
	3		8	5			
HSF1	0.5131	11.7643	5.5417	4.94E-0	8.68E-07	7.85769	up
	4		1	8			
DHRS12	0.5133	7.08669	5.5052	6.00E-0	1.04E-06	7.66979	up
	4		3	8			
GNMT	0.5134	2.80638	5.3707	1.22E-0	1.95E-06	6.98644	up
	5		3	7			
BCS1L	0.5135	9.89396	6.6190	9.66E-11	3.30E-09	13.8867	up
			4				
WNT6	0.5135	2.94559	3.0780	0.0022	0.00909	-2.2537	up
	4		8				
PLIN1	0.5135	4.35208	2.9077	0.00381	0.01429	-2.7502	up
	5		4				
NAT8L	0.5135	3.92141	3.0539	0.00238	0.00969	-2.3258	up
	7						
NR2F6	0.5136	10.9521	6.5822	1.21E-1	4.04E-09	13.6657	up
			2	0			
DDX27	0.5136	11.3017	4.7437	2.77E-0	3.00E-05	4.00084	up
	9		4	6			
ZNF577	0.5137	7.16202	3.6845	0.00026	0.00148	-0.2668	up
	4		8				
ITIH2	0.5139	2.53693	3.6375	0.0003	0.00172	-0.433	up
	6		4				

AC114296.1	0.5140 1	2.86676	3.1518	0.00172	0.00743	-2.0304	up
ZNF703	0.5141 7	12.7229	4.7469 1	2.73E-0 6	2.97E-05	4.01509	up
SGSM2	0.5141 9	9.48986	5.7567 8	1.53E-0 8	3.08E-07	8.98765	up
ACBD4	0.5142 9	8.3909	5.7235 3	1.84E-0 8	3.64E-07	8.81048	up
FLYWCH1	0.5143 1	9.8807	6.3129 4	6.22E-1 0	1.80E-08	12.0812	up
PHGDH	0.5144 5	10.243	3.0852 7	0.00215	0.00892	-2.2321	up
CITED4	0.5145 2	7.6019	3.8348 1	0.00014	0.0009	0.27752	up
ASXL1	0.5145 2	11.3879	5.6205 6	3.23E-0 8	5.91E-07	8.26757	up
RAB11B	0.5146 4	11.5	5.9986 1	3.91E-0 9	9.22E-08	10.3027	up
ZNF524	0.5147 3	9.37966	5.2813 9	1.94E-0 7	2.96E-06	6.54079	up
AC068896.1	0.5147 5	1.63704	4.7993 4	2.13E-0 6	2.40E-05	4.2521	up
DCAF15	0.5148 8	10.2259	5.7298 2	1.77E-0 8	3.53E-07	8.84393	up
ACSF3	0.5149 7	10.2312	6.7064 7	5.60E-11	2.00E-09	14.4154	up
ENTPD2	0.5149 8	9.72769	3.8279 2	0.00015	0.00092	0.25212	up
MRPL41	0.5150	10.4383	5.2779	1.98E-0	3.01E-06	6.52383	up

	4		6	7			
FAAP100	0.5150	10.4664	5.8350	9.88E-0	2.08E-07	9.40799	up
	5		2	9			
CXCR3	0.5151	7.31367	4.1357	4.18E-0	0.00032	1.42904	up
	5		2	5			
TMEM80	0.5160	9.04708	5.9430	5.37E-0	1.21E-07	9.9963	up
	3		3	9			
ADGRB1	0.5160	3.99125	3.7589	0.00019	0.00116	6.09E-0	up
	5		4			5	
ZNF837	0.5160	6.12003	4.9581	9.88E-0	1.23E-05	4.98417	up
	7		2	7			
CTXND1	0.5161	2.54528	2.9210	0.00365	0.01377	-2.7125	up
	9		1				
ZNF541	0.5162	3.46724	2.8459	0.00462	0.01673	-2.9236	up
	3		5				
FAM189A1	0.5162	5.34767	2.1572	0.03148	0.08	-4.6105	up
	4		9				
SFXN5	0.5163	8.9692	5.27511	2.01E-0	3.04E-06	6.50972	up
	1			7			
C1orf127	0.5163	3.82802	3.8399	0.00014	0.00089	0.29632	up
	3						
TRAPPC5	0.5164	4.31767	6.8198	2.74E-11	1.05E-09	15.1096	up
	2		4				
ACD	0.5166	9.63095	5.6837	2.28E-0	4.37E-07	8.59994	up
	1		9	8			
FSD1	0.5167	4.20842	4.66116	4.08E-0	4.26E-05	3.63259	up
	6			6			
ZDHHC19	0.5169	1.77392	4.6143	5.06E-0	5.13E-05	3.4266	up
	8		8	6			

PPP1R12C	0.5170 4	10.9283	5.8085 4	1.15E-0 8	2.37E-07	9.26517	up
GUCA1B	0.5170 6	4.59089	4.3128 5	1.96E-0 5	0.00017	2.14473	up
SRM	0.5172 1	11.318	5.6835 8	2.29E-0 8	4.37E-07	8.59884	up
MRPL55	0.5174 5	9.83178	5.9504 7	5.15E-0 9	1.17E-07	10.0372	up
NTHL1	0.5176 9	10.0749	4.8428 1	1.73E-0 6	2.01E-05	4.45036	up
TVP23A	0.5177 2	4.30224	5.3622 9	1.28E-0 7	2.02E-06	6.94404	up
WNK4	0.51811	9.82156	3.6212	0.00032	0.00182	-0.4903	up
MEX3A	0.5181 8	8.59698	3.4426 8	0.00063	0.00315	-1.0999	up
HSD11B2	0.5183 4	11.4618	4.0735 6	5.41E-0 5	0.00039	1.18452	up
TUT1	0.5187 6	8.52396	6.0142 3	3.58E-0 9	8.55E-08	10.3892	up
U2AF1L5	0.5190 5	3.7191	2.6681 6	0.00788	0.02596	-3.4024	up
PRPF6	0.5191 5	12.4905	5.1361 3	4.08E-0 7	5.66E-06	5.83046	up
MPP3	0.5191 9	6.81988	4.6709 2	3.90E-0 6	4.09E-05	3.6758	up
PAFAH1B3	0.5193 4	10.0944	5.5560 9	4.57E-0 8	8.09E-07	7.93207	up
LRRC29	0.5196 6	5.66397	5.6272 7	3.11E-08	5.74E-07	8.30273	up

CEP72	0.5196 8	8.36409	5.2835 7	1.92E-0 7	2.93E-06	6.55161	up
RABEP2	0.5197 2	10.0774	5.6458 4	2.81E-0 8	5.27E-07	8.40006	up
PRPF40B	0.5201 6	7.34515	5.0386 6	6.64E-0 7	8.64E-06	5.36376	up
HS6ST2	0.5202 1	7.85539	2.1891 2	0.02907	0.07506	-4.5425	up
ZNF707	0.5205 1	8.54895	5.1379 9	4.04E-0 7	5.62E-06	5.83946	up
NOL4L	0.5205 5	11.2281	5.2351 3	2.47E-0 7	3.66E-06	6.31266	up
SHISA9	0.5205 5	3.1889	1.9824 8	0.04799	0.11171	-4.9663	up
C1orf194	0.5205 6	2.00811	4.2265 2	2.84E-0 5	0.00023	1.79242	up
SULT2B1	0.5206	8.74218	3.7575 6	0.00019	0.00116	-0.0049	up
TAF4	0.5206 7	10.2728	5.5099 6	5.85E-0 8	1.02E-06	7.69408	up
DLK2	0.5208 6	5.1511	5.0257 4	7.08E-0 7	9.15E-06	5.3025	up
SLC35E4	0.5212 4	9.14119	4.5447 9	6.96E-0 6	6.76E-05	3.12369	up
FBXL19	0.5214 3	9.86221	5.2727 9	2.03E-0 7	3.07E-06	6.49826	up
IL12A	0.5214 9	3.88683	3.6743	0.00027	0.00153	-0.3033	up
CACTIN	0.5217	9.10876	6.11894	1.95E-0	4.95E-08	10.9744	up

	4			9			
ELMO3	0.5218	11.0362	5.3141	1.64E-0	2.54E-06	6.70341	up
	5		4	7			
FAM50A	0.5221	11.063	5.6225	3.19E-0	5.86E-07	8.27793	up
	2		4	8			
PKP3	0.5221	12.4871	5.1820	3.23E-0	4.64E-06	6.05297	up
	3		2	7			
CTSV	0.5222	8.51304	3.5043	0.0005	0.00261	-0.8927	up
	8		4				
AMACR	0.5228	7.40522	4.7760	2.38E-0	2.63E-05	4.14633	up
	6		1	6			
KIF25	0.5228	3.53188	3.1290	0.00186	0.0079	-2.0998	up
	9		6				
SLC19A1	0.5229	10.1956	5.8649	8.35E-0	1.81E-07	9.57014	up
	6		6	9			
LSM7	0.5230	11.2764	5.8910	7.21E-0	1.59E-07	9.71193	up
	8		3	9			
SCRT1	0.5231	1.16965	4.8177	1.95E-0	2.22E-05	4.33604	up
	2		9	6			
SCTR	0.5232	2.2652	3.6924	0.00025	0.00145	-0.2387	up
			8				
ME3	0.5232	9.36849	5.4233	9.27E-0	1.53E-06	7.25192	up
	5		3	8			
DOT1L	0.5232	10.5703	6.1884	1.30E-0	3.45E-08	11.3673	up
	8			9			
ZNF169	0.5232	6.96611	5.4292	8.99E-0	1.49E-06	7.28175	up
	9		2	8			
RABL6	0.5234	12.2314	5.4349	8.72E-0	1.45E-06	7.31078	up
	8		4	8			

DYNLRB1	0.5235 4	8.6856	6.9726 7	1.03E-11	4.30E-10	16.0606	up
SYP	0.5238 2	5.99631	4.3365 2	1.76E-0 5	0.00015	2.24248	up
EPS8L3	0.5240 1	12.2033	4.5361 8	7.24E-0 6	6.99E-05	3.08651	up
RHBDD3	0.5241 3	9.26557	5.6287 7	3.09E-0 8	5.70E-07	8.31056	up
AGAP3	0.5242 5	11.3833	5.9288 1	5.82E-0 9	1.31E-07	9.91833	up
KHK	0.5243 3	8.64119	4.9402 5	1.08E-0 6	1.33E-05	4.90072	up
NISCH	0.5249 5	10.9874	6.1638 3	1.50E-0 9	3.93E-08	11.2279	up
IL34	0.5250 9	6.68422	3.7438 5	0.0002	0.00122	-0.0545	up
DEXI	0.52511	6.98288	4.8347 8	1.80E-0 6	2.08E-05	4.41363	up
RPUSD1	0.52511	10.2841	5.5354 3	5.11E-08	8.94E-07	7.82526	up
TIGD1	0.5251 2	7.37698	4.8309 4	1.83E-0 6	2.11E-05	4.39606	up
MED25	0.5251 7	10.8995	5.8820 3	7.59E-0 9	1.66E-07	9.66291	up
CEBPB	0.5252 5	10.7622	6.6529 6	7.82E-11	2.73E-09	14.0912	up
SLC4A9	0.5255	2.05605	4.3610 5	1.58E-0 5	0.00014	2.34426	up
ZNF74	0.5255	9.17996	6.4521	2.69E-1	8.37E-09	12.8936	up

			8	0			
MTRNR2L12	0.5255 5	5.05947	3.6877 4	0.00025	0.00147	-0.2555	up
CDHR5	0.5256 3	11.3917	3.9310 4	9.70E-0 5	0.00065	0.63691	up
CEBPA	0.5257 5	9.37342	4.7587 3	2.58E-0 6	2.83E-05	4.0683	up
TRAIP	0.5260 1	8.26516	6.2184 6	1.09E-0 9	2.96E-08	11.5385	up
TOP1MT	0.5260 4	10.9747	4.7875 2	2.25E-0 6	2.52E-05	4.19845	up
SSH3	0.5262 6	10.6894	5.6425	2.86E-0 8	5.33E-07	8.38254	up
SLC22A13	0.5263 3	2.02315	5.0356 9	6.74E-0 7	8.74E-06	5.34964	up
SKOR1	0.5264 3	3.62907	4.6783 3	3.76E-0 6	3.96E-05	3.70866	up
AC099489.1	0.5267 2	4.75402	4.2345 4	2.74E-0 5	0.00022	1.82491	up
SPRN	0.5270 3	2.99713	4.4267 8	1.18E-0 5	0.00011	2.61971	up
MAMSTR	0.5273	5.51117	5.3832 9	1.14E-0 7	1.84E-06	7.04959	up
MICAL1	0.5273 3	10.9236	5.99711	3.95E-0 9	9.29E-08	10.2944	up
DDAH2	0.5273 5	11.14	4.4736 5	9.60E-0 6	8.94E-05	2.8184	up
FAAH	0.5275 3	10.5405	5.3573 7	1.31E-0 7	2.07E-06	6.91936	up

GMEB2	0.5276 4	10.0498	6.0044 1	3.78E-0 9	8.98E-08	10.3348	up
TSNAXIP1	0.5277 7	3.77005	4.9282 2	1.14E-0 6	1.40E-05	4.84468	up
ATXN2L	0.5278 8	11.9576	6.11706	1.97E-0 9	4.99E-08	10.9638	up
HIRA	0.5279	9.11094	6.8885 3	1.77E-11	7.06E-10	15.5349	up
TIGD5	0.5281 7	8.85199	5.9592 9	4.90E-0 9	1.12E-07	10.0857	up
GPR83	0.5282 3	2.39976	3.7314 2	0.00021	0.00127	-0.0993	up
MYPOP	0.5283 2	8.05982	7.0971 7	4.58E-1 2	2.04E-10	16.8479	up
CIART	0.5286 1	4.9092	4.1575 6	3.81E-0 5	0.00029	1.5158	up
PNPLA1	0.5286 2	4.01911	3.4450 4	0.00062	0.00313	-1.0921	up
WNT10A	0.5286 3	5.68072	3.3366 4	0.00091	0.00433	-1.4482	up
HDAC5	0.5286 8	10.4958	5.3747 1	1.20E-0 7	1.92E-06	7.00643	up
IRF3	0.5287 3	10.9363	6.12511	1.88E-0 9	4.81E-08	11.0091	up
KCTD13	0.5287 3	9.43316	6.6053 2	1.05E-1 0	3.55E-09	13.8042	up
YPEL3	0.5287 5	9.5974	5.2285 1	2.55E-0 7	3.78E-06	6.28016	up
CRTC1	0.5288	9.09589	6.2779	7.66E-1	2.16E-08	11.8791	up

	4			0			
PPOX	0.5291	8.5571	7.0279	7.20E-1	3.10E-10	16.4088	up
	3		6	2			
STXBP2	0.5292	10.6444	6.8938	1.71E-11	6.84E-10	15.5679	up
	3		3				
SEMA3B	0.5294	10.236	4.2871	2.19E-0	0.00018	2.03912	up
	2		4	5			
PIEZO1	0.5295	12.2263	5.6253	3.14E-0	5.79E-07	8.2924	up
	6			8			
GOLGA7B	0.5296	7.59982	3.6494	0.00029	0.00166	-0.3911	up
	7		6				
AC004805.1	0.5299	0.71583	6.5828	1.21E-1	4.04E-09	13.6694	up
	7		4	0			
NPPA	0.5299	1.66416	5.4541	7.88E-0	1.33E-06	7.40846	up
	7		4	8			
RXFP4	0.5302	5.8496	3.5060	0.0005	0.0026	-0.8868	up
	4		7				
TMEM63A	0.5302	12.5106	5.5589	4.50E-0	7.98E-07	7.94706	up
	8		8	8			
LRRC69	0.5304	4.15228	3.8952	0.00011	0.00073	0.50236	up
	1		7				
GPR17	0.5304	3.30005	3.4769	0.00055	0.00284	-0.9851	up
	4		9				
DGAT1	0.5306	11.8465	5.3301	1.51E-0	2.37E-06	6.78294	up
				7			
TUBB3	0.5307	4.21695	4.4568	1.04E-0	9.56E-05	2.74679	up
	8		1	5			
DENND4B	0.5309	10.4569	6.3303	5.61E-1	1.64E-08	12.1819	up
	5		4	0			

HIC2	0.53112	8.29188	5.4326 6	8.83E-0 8	1.46E-06	7.29921	up
MTG2	0.5312 6	10.4863	5.3946 2	1.08E-0 7	1.75E-06	7.10674	up
EPN1	0.5314 6	12.6517	5.5803	4.01E-0 8	7.21E-07	8.05767	up
PTDSS2	0.5315 8	9.96293	6.3472 5	5.07E-1 0	1.50E-08	12.28	up
NHLH1	0.5317 3	2.21109	5.0398 7	6.60E-0 7	8.61E-06	5.36952	up
DNM1	0.5318 5	8.63449	4.6543 7	4.21E-0 6	4.37E-05	3.6026	up
ZNHIT2	0.5320 5	8.34844	5.0693 6	5.70E-0 7	7.55E-06	5.50987	up
C8orf82	0.5320 9	9.93271	6.2872 1	7.25E-1 0	2.05E-08	11.9327	up
SLC5A10	0.5322 9	2.43645	4.8216 1	1.91E-0 6	2.19E-05	4.35348	up
ZC3H3	0.5323 1	10.1073	5.6077 4	3.46E-0 8	6.29E-07	8.20063	up
PARP6	0.5323 7	9.60431	4.7790 8	2.34E-0 6	2.61E-05	4.16025	up
DUS1L	0.5324 9	12.2181	5.6906 4	2.20E-0 8	4.24E-07	8.63614	up
DDX11	0.5327 5	9.95615	5.2772 2	1.99E-0 7	3.01E-06	6.52013	up
CBY3	0.5328 3	1.07396	5.8133	1.12E-0 8	2.32E-07	9.29079	up
LRRC71	0.5332	1.34702	5.2393	2.41E-0	3.59E-06	6.3336	up

	5		9	7			
XAB2	0.5334	10.9361	5.7216	1.86E-0	3.67E-07	8.80053	up
	6		6	8			
CDKL3	0.5335	3.45907	5.4801	6.86E-0	1.17E-06	7.54113	up
			3	8			
FAM3A	0.5335	10.8653	5.5933	3.74E-0	6.76E-07	8.12553	up
	3		4	8			
C11orf42	0.5336	2.95315	4.2057	3.10E-0	0.00025	1.70869	up
	6		6	5			
NEURL3	0.5337	5.41312	3.9768	8.06E-0	0.00056	0.81087	up
	8		3	5			
LTC4S	0.5337	4.65351	5.7078	2.00E-0	3.90E-07	8.72702	up
	9			8			
C7orf61	0.5338	1.9868	5.3417	1.42E-0	2.23E-06	6.8409	up
	8			7			
KCNAB2	0.534	9.79502	4.8231	1.90E-0	2.18E-05	4.36044	up
			4	6			
SH3BP1	0.5340	8.45096	5.5369	5.07E-0	8.88E-07	7.83333	up
	6		9	8			
ARHGAP11B	0.5343	4.10696	3.7848	0.00017	0.00106	0.09417	up
	4		3				
CCDC61	0.5345	8.6902	6.5731	1.28E-1	4.26E-09	13.6115	up
	5		6	0			
DNMT3B	0.5345	7.52438	4.7279	2.98E-0	3.22E-05	3.93007	up
	7		7	6			
ZNF517	0.5347	8.2921	5.9870	4.18E-0	9.78E-08	10.2386	up
			1	9			
ZNF385C	0.5347	5.32369	4.0254	6.60E-0	0.00047	0.99768	up
	7		6	5			

SLC10A4	0.5348 5	2.56464	4.0144 2	6.91E-0 5	0.00049	0.95506	up
ETFB	0.5348 5	9.75181	7.1603 7	3.03E-1 2	1.38E-10	17.2519	up
VAMP1	0.5349 9	7.28285	5.2225 1	2.63E-0 7	3.88E-06	6.25075	up
GPR75	0.5350 8	4.31809	4.5342	7.31E-0 6	7.05E-05	3.07797	up
EIF6	0.5356 3	12.1266	5.9578 8	4.94E-0 9	1.13E-07	10.078	up
RIN1	0.5359 5	9.48073	5.2244	2.61E-0 7	3.85E-06	6.25999	up
PHGR1	0.5361 2	11.6808	3.4833 8	0.00054	0.00278	-0.9635	up
BMP7	0.5361 5	9.038	2.3584 3	0.01875	0.05259	-4.1646	up
MTRNR2L3	0.5364 9	1.94106	4.0126	6.96E-0 5	0.00049	0.94809	up
LAGE3	0.5365	9.49498	5.5628 6	4.41E-0 8	7.85E-07	7.96717	up
CORO7	0.5365 5	8.75439	6.2948 2	6.93E-1 0	1.98E-08	11.9766	up
MTMR11	0.5365 8	11.0652	4.6219 6	4.89E-0 6	4.99E-05	3.45984	up
REXO1	0.5366 5	10.1789	6.2693 1	8.07E-1 0	2.26E-08	11.8297	up
PCBP4	0.5369 1	9.74007	5.7070 7	2.01E-0 8	3.91E-07	8.72311	up
KREMEN2	0.5372	5.47286	4.2633	2.42E-0	0.0002	1.94184	up

	3		3	5			
GABRR2	0.5373 1	4.16381	4.1361 9	4.17E-0 5	0.00032	1.43091	up
FAM183A	0.5373 3	2.64472	3.0778 8	0.0022	0.0091	-2.2543	up
HGFAC	0.5375 4	1.5392	4.5265 9	7.56E-0 6	7.27E-05	3.04518	up
RAB36	0.5376 2	8.26941	4.7439 9	2.77E-0 6	3.00E-05	4.00198	up
MIIP	0.5378	9.72785	5.8361 5	9.82E-0 9	2.07E-07	9.41407	up
PAOX	0.5378 8	3.53548	6.3894 8	3.93E-1 0	1.18E-08	12.5259	up
FANCA	0.5378 9	9.61598	5.9266 6	5.90E-0 9	1.32E-07	9.90657	up
KCNQ1	0.5383 9	11.7539	4.1423 8	4.06E-0 5	0.00031	1.45546	up
MLLT6	0.5384	12.3447	5.4980 1	6.24E-0 8	1.08E-06	7.63274	up
ISYNA1	0.5384 2	8.65945	4.0319 7	6.43E-0 5	0.00046	1.02282	up
NOTCH1	0.5386 5	12.0051	5.3525 1	1.34E-0 7	2.12E-06	6.89502	up
ZBTB12	0.5388 9	7.90258	4.9532 6	1.01E-0 6	1.26E-05	4.96145	up
ADAT2	0.5389 9	9.01781	5.4266 9	9.11E-08	1.51E-06	7.26895	up
SBK1	0.539	7.02997	3.11269	0.00196	0.00827	-2.1495	up
CCHCR1	0.5391	10.0416	5.8543	8.87E-0	1.90E-07	9.51264	up

			6	9			
CLCNKA	0.5391 4	1.58027	4.6646 1	4.01E-0 6	4.20E-05	3.64788	up
RLN2	0.5391 5	3.41993	3.3532 2	0.00086	0.00412	-1.3944	up
IFITM5	0.5391 6	1.2898	4.1889 6	3.33E-0 5	0.00026	1.64123	up
GIT1	0.5393 4	11.6646	5.5532 8	4.64E-0 8	8.20E-07	7.91754	up
CABP7	0.5394 1	2.37781	4.2705 7	2.35E-0 5	0.00019	1.97137	up
GNG3	0.5395 3	2.1517	5.11984	4.43E-0 7	6.09E-06	5.75192	up
BCKDHA	0.5396 4	3.83205	4.3570 4	1.61E-0 5	0.00014	2.32758	up
SP6	0.5397 2	9.27878	3.8559	0.00013	0.00084	0.35559	up
TTC16	0.5397 2	3.24819	3.8627 8	0.00013	0.00082	0.38114	up
RAB17	0.5398 2	9.68775	5.5471 2	4.80E-0 8	8.45E-07	7.88568	up
CFAP73	0.5398 5	2.79198	4.1632	3.72E-0 5	0.00029	1.53825	up
BIN1	0.5401 4	11.0964	5.1546 4	3.72E-0 7	5.21E-06	5.92	up
GPR61	0.5407	2.36039	4.8626 1	1.57E-0 6	1.85E-05	4.54122	up
STK11	0.5408 6	11.2377	6.7918 9	3.27E-11	1.22E-09	14.9376	up

FAM3B	0.5409 9	7.88838	2.1563 8	0.03155	0.08014	-4.6124	up
POLA2	0.54117	7.90464	7.3244 1	1.02E-1 2	4.91E-11	18.3138	up
SLC9A8	0.5415 4	10.1399	5.7365 4	1.71E-0 8	3.41E-07	8.87967	up
FASTK	0.5416 1	11.1313	6.2832 9	7.42E-1 0	2.10E-08	11.9101	up
PICK1	0.5417 5	9.70125	6.6242 2	9.35E-11	3.22E-09	13.9179	up
KMT2B	0.5417 5	11.1406	5.5288	5.29E-0 8	9.25E-07	7.7911	up
GOLGA6L10	0.5419 3	3.73817	4.0374 2	6.29E-0 5	0.00045	1.04395	up
SPATA2	0.5419 5	10.3607	5.8515 1	9.01E-0 9	1.93E-07	9.49717	up
CNPY2	0.5426 6	7.20494	8.7208 8	4.50E-1 7	4.96E-15	28.1	up
RNF166	0.5427 1	8.5062	7.3797 2	7.01E-1 3	3.46E-11	18.6762	up
CORO6	0.5428 2	4.17906	4.7090 4	3.26E-0 6	3.49E-05	3.8454	up
PLEKHH3	0.5428 7	9.14818	5.8570 8	8.73E-0 9	1.88E-07	9.52737	up
AGT	0.5428 9	9.15153	3.8502 7	0.00013	0.00086	0.3347	up
ZAP70	0.5429	6.85017	4.2031 7	3.14E-0 5	0.00025	1.69829	up
SLC45A2	0.5429	2.49705	4.2018	3.16E-0	0.00025	1.69291	up

	4		3	5			
MRI1	0.543	8.5237	7.1832	2.60E-1	1.20E-10	17.3988	up
			5	2			
SCN5A	0.5430	3.82571	3.3572	0.00085	0.00408	-1.3813	up
	8		6				
IQGAP3	0.5435	11.051	5.3698	1.23E-0	1.96E-06	6.98206	up
			6	7			
DDC	0.5438	10.4967	3.2909	0.00107	0.00495	-1.5952	up
	5						
TSC2	0.5438	11.5111	6.4196	3.28E-1	9.98E-09	12.7024	up
	7		4	0			
OGFR	0.5438	11.1331	5.9441	5.34E-0	1.21E-07	10.0024	up
	9		4	9			
LZTS3	0.5443	9.99359	4.3371	1.76E-0	0.00015	2.24502	up
	7		4	5			
CHP2	0.5444	7.80836	2.0290	0.043	0.10255	-4.8744	up
	4		7				
HNF1A	0.5444	9.06307	5.1592	3.63E-0	5.11E-06	5.94226	up
	8		4	7			
ELL3	0.5444	3.71215	6.11273	2.02E-0	5.09E-08	10.9394	up
	9			9			
ARGLU1	0.5449	11.622	4.7494	2.69E-0	2.93E-05	4.02666	up
	2		8	6			
DUS3L	0.5449	9.94545	5.8728	7.99E-0	1.74E-07	9.6132	up
	3		9	9			
SLC7A5	0.5454	12.3407	4.7644	2.51E-0	2.76E-05	4.09399	up
	1		2	6			
MCF2L	0.5455	10.5827	5.1932	3.05E-0	4.42E-06	6.10778	up
	1		7	7			

CLK2	0.5455 9	10.1023	6.8075 5	2.96E-11	1.12E-09	15.0339	up
ACSF2	0.5456 6	9.78577	5.1470 6	3.86E-0 7	5.40E-06	5.88329	up
ACOT8	0.5460 9	9.74103	6.4695 2	2.42E-1 0	7.61E-09	12.9958	up
ZNF513	0.5465 1	8.92858	5.4218 6	9.35E-0 8	1.54E-06	7.24447	up
ABHD17A	0.5465 7	9.97854	6.7831 5	3.46E-11	1.29E-09	14.8839	up
GFER	0.5470 1	8.27558	6.4477 4	2.76E-1 0	8.54E-09	12.8674	up
ADAP1	0.5471 2	10.5052	5.8197 1	1.08E-0 8	2.25E-07	9.32532	up
RUBCNL	0.5474 2	10.879	2.9620 5	0.00321	0.01238	-2.5949	up
LGI4	0.5477 3	6.29646	3.9140 8	0.0001	0.00069	0.57297	up
CD164L2	0.5478 5	3.12091	3.7860 5	0.00017	0.00106	0.0986	up
PHYKPL	0.5480 7	10.0916	6.4839 4	2.22E-1 0	7.04E-09	13.081	up
TTC21A	0.5483 2	6.53437	5.8332 7	9.98E-0 9	2.10E-07	9.3985	up
ZNF444	0.5483 4	9.99198	6.1008 6	2.17E-0 9	5.39E-08	10.8727	up
AC020915.1	0.5484 1	2.9725	4.213	3.01E-0 5	0.00024	1.73785	up
LRRC43	0.5485	4.06412	3.8468	0.00014	0.00087	0.32207	up

	5		6				
PKDCC	0.5487	10.2646	3.8349	0.00014	0.0009	0.27793	up
	5		2				
KRT15	0.5488	7.65669	4.2909	2.15E-0	0.00018	2.05481	up
	2		7	5			
PNMA3	0.5488	2.4252	4.0950	4.95E-0	0.00036	1.26855	up
	6		2	5			
FAM118A	0.5493	9.8674	5.8408	9.57E-0	2.03E-07	9.43933	up
	8		2	9			
FAM186B	0.5494	3.80797	5.0862	5.24E-0	7.02E-06	5.59073	up
	5		7	7			
NAT9	0.5494	10.1357	6.3249	5.79E-1	1.69E-08	12.1505	up
	9		1	0			
SLC25A10	0.5495	9.18191	5.6696	2.47E-0	4.67E-07	8.52514	up
	7		1	8			
SLC22A1	0.5499	3.24841	4.8209	1.92E-0	2.20E-05	4.35029	up
	1		1	6			
HAUS5	0.5499	9.43273	6.3639	4.58E-1	1.36E-08	12.3768	up
	7		1	0			
FCHSD1	0.5499	8.81805	6.2177	1.09E-0	2.97E-08	11.5346	up
	8		8	9			
ZNF296	0.55011	7.55702	5.4938	6.38E-0	1.10E-06	7.61116	up
				8			
HHIPL2	0.5502	2.2729	4.6569	4.16E-0	4.33E-05	3.61375	up
	5			6			
ABCA7	0.5504	9.38264	5.5885	3.84E-0	6.91E-07	8.10054	up
			4	8			
SPDYE3	0.5507	1.79739	4.28511	2.21E-0	0.00018	2.03082	up
	8			5			

PPP1R3E	0.5510 3	7.80865	5.7939 8	1.24E-0 8	2.56E-07	9.18688	up
KCNG1	0.5510 6	4.45422	3.0984 1	0.00206	0.0086	-2.1926	up
PRRT1	0.5512 5	4.80289	4.7140 5	3.18E-0 6	3.41E-05	3.86778	up
MYT1	0.5514 4	3.72228	3.1269 3	0.00187	0.00795	-2.1063	up
GRIN2D	0.5515 5	9.97966	4.0739 8	5.40E-0 5	0.00039	1.18618	up
SPATA2L	0.5516 3	9.19045	5.7665	1.45E-0 8	2.94E-07	9.0396	up
C6orf163	0.5519 4	3.77018	3.9027 3	0.00011	0.00072	0.53032	up
ANKZF1	0.5522 1	10.4654	6.4790 3	2.28E-1 0	7.23E-09	13.052	up
ANKMY1	0.5527 2	8.89127	6.2957 4	6.89E-1 0	1.98E-08	11.9819	up
RUNDC3A	0.5529 5	3.93074	3.5564 9	0.00041	0.00222	-0.7147	up
PTCD1	0.5529 6	6.94149	8.6059 8	1.08E-1 6	1.09E-14	27.2468	up
MAZ	0.5531 5	9.56755	7.3554 6	8.25E-1 3	4.03E-11	18.5169	up
SEC14L4	0.5532 4	2.36709	2.8246 8	0.00493	0.01762	-2.9824	up
CAMSAP3	0.5535 5	10.9426	5.6497 7	2.75E-0 8	5.17E-07	8.42071	up
SLC52A2	0.5536	11.714	4.9252	1.16E-0	1.41E-05	4.83095	up

	2		7	6			
TMUB1	0.5538	10.8287	5.8521	8.98E-0	1.92E-07	9.50064	up
	3		5	9			
TMEM255B	0.5538	7.7837	4.5740	6.09E-0	6.03E-05	3.25066	up
	4		7	6			
EPO	0.5539	1.1061	6.3737	4.32E-1	1.29E-08	12.4344	up
	6		9	0			
SPATA1	0.5540	3.30478	4.9029	1.29E-0	1.55E-05	4.72725	up
	4		3	6			
SBF1	0.5545	11.8111	5.7167	1.91E-0	3.73E-07	8.7744	up
	2		4	8			
SPG7	0.5545	11.4792	7.4282	5.04E-1	2.57E-11	18.9961	up
	6		8	3			
UNC5CL	0.5549	8.62184	4.4690	9.80E-0	9.11E-05	2.7989	up
	3		7	6			
XRCC3	0.5549	9.11118	6.2597	8.54E-1	2.37E-08	11.7747	up
	8		2	0			
STRADA	0.5550	6.24218	5.3569	1.31E-0	2.07E-06	6.9174	up
	3		8	7			
APOH	0.5556	3.17208	3.2700	0.00115	0.00526	-1.6617	up
	7		3				
SUGP2	0.5562	11.1012	5.8800	7.67E-0	1.68E-07	9.65218	up
			6	9			
NEU4	0.5562	7.21704	3.3381	0.00091	0.00431	-1.4432	up
	6		8				
ENTPD6	0.5564	12.5473	5.7867	1.29E-0	2.65E-07	9.14779	up
	1			8			
SDR42E2	0.5564	1.60947	5.3820	1.15E-0	1.85E-06	7.04347	up
	6		7	7			

DAGLA	0.5568 4	9.35547	5.1890 8	3.12E-0 7	4.50E-06	6.08734	up
CACNA1F	0.5568 9	4.08941	4.5289 5	7.48E-0 6	7.21E-05	3.05534	up
WNT8B	0.5570 5	2.59752	4.0724 6	5.44E-0 5	0.0004	1.18021	up
IGSF9	0.5570 8	9.12113	4.7733 5	2.41E-0 6	2.66E-05	4.1343	up
NPIPA2	0.5573 9	1.00206	5.0665 9	5.78E-0 7	7.65E-06	5.49668	up
MTCP1	0.5575 7	4.135	5.7122 1	1.95E-0 8	3.82E-07	8.75037	up
AANAT	0.5575 8	2.54243	4.4920 6	8.84E-0 6	8.33E-05	2.89702	up
C8G	0.5577 2	5.14208	4.0595 8	5.74E-0 5	0.00041	1.13	up
PHKG1	0.5581 5	4.78258	5.1058 6	4.75E-0 7	6.45E-06	5.68466	up
FRS3	0.5582 2	7.39225	6.0071 9	3.72E-0 9	8.86E-08	10.3502	up
ZNF771	0.5583 4	7.24694	9.0722 2	2.97E-1 8	3.90E-16	30.7595	up
SH3GLB2	0.5585 4	11.5867	7.1708 5	2.82E-1 2	1.30E-10	17.3191	up
HSD11B1L	0.5586 1	6.508	5.7653 1	1.46E-0 8	2.96E-07	9.03323	up
NRXN2	0.5586 4	6.49093	3.4294 2	0.00066	0.00328	-1.1441	up
NGEF	0.5587	9.57007	5.1559	3.69E-0	5.19E-06	5.92629	up

	3		4	7			
CNKSRI	0.5588	10.0165	5.9736	4.51E-0	1.05E-07	10.1649	up
	1		7	9			
GRB14	0.5589	4.62906	2.7778	0.00568	0.01987	-3.1104	up
	2		9				
ATXN7L2	0.5590	7.6303	6.3379	5.36E-1	1.58E-08	12.2263	up
	9		9	0			
HAP1	0.5594	3.54923	4.0633	5.65E-0	0.00041	1.14454	up
	4		1	5			
SLC16A5	0.5594	9.21871	5.0825	5.34E-0	7.14E-06	5.57312	up
	5		9	7			
HELZ2	0.5595	11.4537	4.9164	1.21E-0	1.47E-05	4.7901	up
	2		8	6			
LRRC4B	0.5596	4.72977	5.2218	2.64E-0	3.89E-06	6.24755	up
	8		6	7			
C10orf99	0.5598	9.96402	2.1822	0.02958	0.07608	-4.5574	up
	6						
PLAC8L1	0.5598	3.50132	4.9277	1.15E-0	1.40E-05	4.84258	up
	6		7	6			
SOX12	0.5599	9.50075	5.4438	8.32E-0	1.39E-06	7.35582	up
	4			8			
WDR24	0.5601	8.8567	6.2083	1.16E-0	3.10E-08	11.4811	up
	6		9	9			
LAMA5	0.5604	11.236	4.0382	6.26E-0	0.00045	1.04716	up
	6		5	5			
PIGQ	0.5605	9.97295	6.1391	1.74E-0	4.48E-08	11.0883	up
	4		5	9			
ABHD16A	0.56118	5.92277	7.8793	2.21E-1	1.46E-12	22.0464	up
			3	4			

GLS2	0.5613 6	3.40348	5.5928 8	3.75E-0 8	6.77E-07	8.12312	up
LRRC61	0.5614 8	8.88231	5.6233 2	3.18E-0 8	5.84E-07	8.28201	up
AC107871.1	0.5616 1	4.95103	4.7387 5	2.83E-0 6	3.07E-05	3.97842	up
GTPBP3	0.5619 5	9.52649	6.6267 5	9.21E-11	3.18E-09	13.9331	up
TCIRG1	0.562	11.3048	6.1765 8	1.39E-0 9	3.68E-08	11.3002	up
INAFM1	0.5621 8	7.71588	5.9817 5	4.31E-0 9	1.01E-07	10.2095	up
KLKB1	0.5622 3	3.14263	4.1670 6	3.66E-0 5	0.00028	1.55366	up
DPP7	0.5623 6	11.5273	5.4139 5	9.74E-0 8	1.60E-06	7.2044	up
LEAP2	0.5624 6	4.92138	6.1653 8	1.49E-0 9	3.90E-08	11.2366	up
FAM186A	0.5624 7	3.47279	4.6078 3	5.22E-0 6	5.27E-05	3.39793	up
POLN	0.5625 8	3.05918	4.6251 3	4.82E-0 6	4.92E-05	3.47379	up
KRTAP5-10	0.5625 9	1.3417	5.4634	7.50E-0 8	1.27E-06	7.45567	up
SPDYE5	0.5626 7	3.58398	4.3597 1	1.59E-0 5	0.00014	2.33872	up
PRICKLE4	0.5628 7	1.30012	6.5132 9	1.85E-1 0	5.99E-09	13.2549	up
IFI30	0.5629	3.46204	4.7432	2.77E-0	3.01E-05	3.99883	up

	1		9	6			
CARMIL2	0.5629	6.44289	4.3362	1.77E-0	0.00015	2.24149	up
	2		8	5			
SLC15A1	0.5635	5.26236	2.1986	0.02838	0.07358	-4.5219	up
	8		8				
ARPC1B	0.5637	5.78939	8.2742	1.28E-1	1.08E-13	24.8304	up
			9	5			
RSPO4	0.5641	2.05066	3.0284	0.00259	0.01038	-2.4012	up
			5				
SCRN2	0.5642	9.69455	5.8702	8.11E-09	1.76E-07	9.59862	up
	3		1				
ST20	0.5643	4.41571	5.6685	2.48E-0	4.69E-07	8.5195	up
	1		4	8			
WHRN	0.5646	8.01979	4.6483	4.33E-0	4.48E-05	3.57587	up
	2		2	6			
HOGA1	0.5647	3.52864	3.3617	0.00084	0.00402	-1.3668	up
	4		1				
POLRMT	0.5647	10.9444	6.1390	1.74E-0	4.48E-08	11.0879	up
	8		8	9			
PRR5	0.5652	9.16139	6.2716	7.95E-1	2.23E-08	11.8434	up
	1		8	0			
MTA1	0.5652	10.5882	6.8276	2.61E-11	1.01E-09	15.1575	up
	2						
MAP3K10	0.5658	8.76319	6.1200	1.94E-0	4.93E-08	10.9808	up
	3		9	9			
HES6	0.5661	10.8118	4.5558	6.62E-0	6.48E-05	3.17151	up
	4		4	6			
DDX47	0.5663	4.71349	4.8507	1.66E-0	1.95E-05	4.48691	up
	6		8	6			

LINGO3	0.5664 8	3.06959	4.4143 7	1.25E-0 5	0.00011	2.56742	up
ANAPC2	0.5664 8	10.2311	6.9155 9	1.49E-11	5.99E-10	15.7034	up
PNPLA2	0.5666 4	10.9997	6.9258 9	1.39E-11	5.65E-10	15.7676	up
CLCN7	0.5668	10.6513	6.2766 7	7.72E-1 0	2.17E-08	11.8721	up
TEKT5	0.5668 8	2.97316	3.6791 6	0.00026	0.00151	-0.286	up
TRMT61A	0.5671	10.1023	5.3237 1	1.56E-0 7	2.44E-06	6.75108	up
IL17RE	0.5671 2	10.4645	6.0002 4	3.88E-0 9	9.16E-08	10.3117	up
CROCC2	0.5672 4	1.84589	3.9248 3	9.94E-0 5	0.00066	0.61348	up
SYT7	0.5672 9	10.7157	3.81173	0.00016	0.00097	0.19258	up
CAPN13	0.5673 4	7.14338	2.9058 7	0.00383	0.01434	-2.7555	up
ACTA1	0.5675 4	3.30316	5.8259 4	1.04E-0 8	2.18E-07	9.35891	up
GNB1L	0.5678 4	8.13342	6.2342 2	9.93E-1 0	2.71E-08	11.6286	up
AC068580.4	0.5678 6	3.2572	4.5723 1	6.14E-0 6	6.06E-05	3.24299	up
AQP6	0.5679 9	3.34381	3.7135 8	0.00023	0.00135	-0.1633	up
SRMS	0.5684	7.0744	3.4574	0.00059	0.00301	-1.0505	up

	3		9				
SLC5A9	0.5684 6	5.92374	3.2109 3	0.00141	0.00627	-1.8476	up
SYT8	0.5684 6	5.26793	3.7851 2	0.00017	0.00106	0.09523	up
WDR62	0.5684 6	8.97671	5.8952 9	7.04E-0 9	1.55E-07	9.73511	up
BICRA	0.5684 8	9.10212	6.5024 6	1.98E-1 0	6.35E-09	13.1906	up
TMEM191B	0.5685 9	2.75713	4.8330 6	1.81E-0 6	2.09E-05	4.40578	up
EME1	0.5687 8	6.77561	6.1456 2	1.67E-0 9	4.36E-08	11.1248	up
ANKRD9	0.5688 6	10.1842	6.4814 8	2.25E-1 0	7.14E-09	13.0665	up
PRSS51	0.5689 1	3.70335	2.8049 2	0.00524	0.01855	-3.0367	up
RFNG	0.5689 2	9.94103	6.43	3.08E-1 0	9.42E-09	12.7632	up
IZUMO2	0.5693 5	2.36458	2.8268 3	0.0049	0.01752	-2.9765	up
BOLA2B	0.5698 9	4.64602	4.6832 7	3.68E-0 6	3.88E-05	3.73063	up
KRT4	0.5699	1.7736	3.3048 5	0.00102	0.00474	-1.5506	up
BRAT1	0.5705	11.2245	6.0184 6	3.49E-0 9	8.38E-08	10.4127	up
RTN4RL2	0.5705 8	4.70959	4.6668 6	3.97E-0 6	4.16E-05	3.65784	up

TF	0.5705 9	3.55787	3.2503 2	0.00123	0.00558	-1.724	up
MPST	0.5707 9	12.2544	6.8176 7	2.78E-11	1.06E-09	15.0962	up
ZNF628	0.5708 3	8.00493	5.9668 3	4.69E-0 9	1.08E-07	10.1272	up
CABLES2	0.5708 5	9.18697	5.6837 9	2.28E-0 8	4.37E-07	8.59996	up
MS4A15	0.5709	3.03476	3.01189	0.00273	0.01084	-2.4499	up
SPATA33	0.5709 1	8.46661	6.8705	1.98E-11	7.87E-10	15.4229	up
AL353588.1	0.5713 2	1.49727	5.6752 7	2.39E-0 8	4.54E-07	8.55497	up
MRPL12	0.5714 9	8.8183	4.7921 9	2.20E-0 6	2.48E-05	4.21965	up
VIPR1	0.5721 6	9.61667	5.0741	5.57E-0 7	7.41E-06	5.5325	up
ARHGAP45	0.5722 4	10.4551	6.0864 5	2.36E-0 9	5.78E-08	10.7919	up
SLC22A18	0.5722 5	10.76	5.81177	1.13E-0 8	2.33E-07	9.28257	up
LHX4	0.5723 9	4.99747	4.1748 2	3.54E-0 5	0.00027	1.58462	up
KYAT1	0.5725 1	2.18846	6.0015 8	3.85E-0 9	9.10E-08	10.3191	up
POLD1	0.5730 1	10.2476	6.2096 4	1.15E-0 9	3.09E-08	11.4882	up
NSMF	0.57311	11.4553	5.5605	4.46E-0 8	7.93E-07	7.9549	up

AC013394.1	0.5731 3	3.20451	3.6043	0.00035	0.00191	-0.5492	up
MYOM3	0.5731 9	8.79145	3.2065 4	0.00143	0.00635	-1.8613	up
RECQL5	0.5732 9	9.59042	6.1777 6	1.38E-0 9	3.66E-08	11.3069	up
PUS1	0.5733 2	10.4803	6.9499 6	1.19E-11	4.94E-10	15.9182	up
TJP2	0.5733 8	6.56996	4.9027 5	1.29E-0 6	1.56E-05	4.72642	up
RCCD1	0.5737 3	9.40385	7.8375 7	2.97E-1 4	1.91E-12	21.7582	up
FN3K	0.5738 6	9.49047	5.6463 6	2.80E-0 8	5.26E-07	8.40281	up
CYP2B6	0.5740 4	8.83869	2.5392 3	0.01142	0.03514	-3.7308	up
CHCHD10	0.57411	10.4317	5.7795 9	1.35E-0 8	2.75E-07	9.10964	up
P2RY11	0.5741 7	6.6198	5.8627 2	8.46E-0 9	1.83E-07	9.55799	up
ALDOA	0.5744 9	9.38329	5.6210 9	3.22E-0 8	5.90E-07	8.27036	up
MADCAM1	0.5750 1	4.59381	4.1795 1	3.47E-0 5	0.00027	1.60339	up
SRRM2	0.5756 8	14.0684	5.6895 5	2.21E-0 8	4.26E-07	8.63039	up
MFSD3	0.5757 3	9.92048	5.2129 8	2.76E-0 7	4.04E-06	6.20407	up
LRIT3	0.5757	2.80874	4.6282	4.75E-0	4.86E-05	3.48728	up

	4			6			
KCNQ4	0.5759 8	6.36568	3.8397 3	0.00014	0.00089	0.29569	up
PHACTR3	0.5761 9	5.33828	2.6985 6	0.00721	0.02418	-3.3226	up
GALT	0.5762 7	8.7178	8.11354	4.12E-1 5	3.17E-13	23.6848	up
SS18L1	0.5762 9	9.58122	5.9960 8	3.97E-0 9	9.32E-08	10.2887	up
TNFRSF14	0.5767 7	11.1528	6.9491 2	1.20E-11	4.95E-10	15.9129	up
AATK	0.5768	8.06774	4.1280 7	4.31E-0 5	0.00033	1.39877	up
NEUROG2	0.5768 1	1.93885	2.7478 2	0.00622	0.02145	-3.1915	up
GP6	0.5768 7	2.66916	4.4477 7	1.08E-0 5	9.90E-05	2.70844	up
UNC93A	0.5768 8	5.54042	2.4076 2	0.01643	0.04727	-4.0497	up
DVL1	0.5772 3	11.3384	5.8530 4	8.93E-0 9	1.91E-07	9.50549	up
LIPE	0.5772 3	8.1132	5.5956 2	3.69E-0 8	6.69E-07	8.1374	up
NLRP6	0.5776	4.9028	3.4009 8	0.00073	0.00358	-1.2381	up
SLC12A9	0.5777 1	11.1274	6.2001 5	1.21E-0 9	3.25E-08	11.4341	up
RAB40C	0.5777 2	10.4929	6.2354 6	9.86E-1 0	2.70E-08	11.6357	up

LRRC14	0.5779 3	9.64985	7.0250 7	7.34E-1 2	3.14E-10	16.3906	up
CHD1L	0.5782 6	4.00045	5.5616 6	4.44E-0 8	7.89E-07	7.96095	up
DDX51	0.5783 6	9.88677	6.5123 2	1.86E-1 0	6.01E-09	13.2491	up
ZNF598	0.5784 1	10.7459	6.0643 3	2.68E-0 9	6.53E-08	10.6682	up
AXIN1	0.5785 1	11.2682	6.0257 4	3.35E-0 9	8.05E-08	10.4532	up
UBALD1	0.5788 9	9.62984	6.4883 1	2.16E-1 0	6.87E-09	13.1068	up
DCDC2B	0.5791 9	2.39737	4.4090 5	1.28E-0 5	0.00011	2.54502	up
TROAP	0.5792 9	9.5329	6.0888 2	2.33E-0 9	5.72E-08	10.8052	up
ILK	0.5794 5	4.35273	5.6755 4	2.39E-0 8	4.54E-07	8.5564	up
CRYBA2	0.5794 8	2.67073	3.4974 6	0.00051	0.00267	-0.916	up
PROSER2	0.5794 9	7.99017	4.4159 6	1.24E-0 5	0.00011	2.57411	up
MUC6	0.5804 7	4.73265	2.0903 5	0.03711	0.09109	-4.7503	up
WASHC1	0.5806 8	6.84246	4.4306 4	1.16E-0 5	0.00011	2.636	up
DENND6B	0.5817 7	7.26584	6.2001	1.21E-0 9	3.25E-08	11.4338	up
DBF4B	0.5818	8.37323	6.1880	1.30E-0	3.46E-08	11.3652	up

	5		4	9			
PRELID3A	0.5818	6.69848	6.0865	2.36E-0	5.78E-08	10.7925	up
	6		6	9			
ADGRL1	0.5819	10.4078	5.5567	4.55E-0	8.07E-07	7.93559	up
	3		7	8			
JRK	0.5819	9.34758	6.2981	6.80E-1	1.95E-08	11.9957	up
	6		4	0			
ZNF785	0.5821	7.97345	5.7185	1.89E-0	3.71E-07	8.78422	up
	2		9	8			
SLCO4A1	0.5821	10.8408	5.5051	6.01E-0	1.04E-06	7.66931	up
	8		4	8			
AMH	0.5823	5.3662	2.89711	0.00394	0.01466	-2.7803	up
	4						
SLC2A8	0.5824	10.2918	5.4634	7.50E-0	1.27E-06	7.45601	up
	3		7	8			
DUSP8	0.5825	9.85618	5.9220	6.05E-0	1.35E-07	9.88129	up
	8		5	9			
RBM14-RBM4	0.5830	3.39904	5.1264	4.28E-0	5.92E-06	5.78349	up
	9			7			
MIGA2	0.5834	9.81895	6.4531	2.67E-1	8.34E-09	12.8992	up
	7		3	0			
OXLD1	0.5838	9.4537	6.8237	2.67E-11	1.03E-09	15.1335	up
	4						
RASSF10	0.5838	6.96807	2.9430	0.00341	0.013	-2.6495	up
	7		5				
HOXD4	0.5838	4.15677	4.1330	4.22E-0	0.00032	1.41852	up
	9		6	5			
ASIC1	0.5842	8.90177	5.1013	4.86E-0	6.58E-06	5.66294	up
			4	7			

LPO	0.5842 2	2.91903	3.1515 6	0.00173	0.00743	-2.0311	up
PTGDS	0.5843 3	4.2617	4.4290 2	1.17E-0 5	0.00011	2.62916	up
RNF157	0.5846 1	8.61588	4.1348 6	4.19E-0 5	0.00032	1.42566	up
STPG4	0.5846 7	4.3429	3.0875 4	0.00213	0.00887	-2.2253	up
DOHH	0.5848 9	9.10814	5.5070 7	5.95E-0 8	1.03E-06	7.67925	up
SELENBP1	0.5850 2	12.5093	3.8552 2	0.00013	0.00084	0.35306	up
BSN	0.5853	4.58709	4.3901 7	1.39E-0 5	0.00012	2.46585	up
ZFPM1	0.5853	8.72328	6.1744 1	1.41E-0 9	3.72E-08	11.2878	up
ATG4B	0.5859 8	10.9345	7.6926 2	8.20E-1 4	4.92E-12	20.7667	up
PSMG4	0.5861 5	9.36006	7.6400 6	1.18E-1 3	6.79E-12	20.4108	up
CORT	0.5864 4	2.06203	6.1661 4	1.48E-0 9	3.89E-08	11.2409	up
PRAME	0.5865 8	4.66315	2.2754 5	0.02332	0.06267	-4.3533	up
YDJC	0.5867 5	10.2249	6.1979 2	1.23E-0 9	3.29E-08	11.4214	up
ODF3L2	0.5869 8	2.93214	4.4129 2	1.26E-0 5	0.00011	2.5613	up
PARP10	0.5871	11.0182	5.6526	2.71E-0	5.10E-07	8.4357	up

	3		2	8			
KLHDC4	0.5873	10.3738	7.0183	7.66E-1	3.28E-10	16.3481	up
	5		5	2			
MSLNL	0.5875	2.00261	3.3152	0.00098	0.0046	-1.5174	up
	2						
RHBDF1	0.5883	10.5121	6.3226	5.87E-1	1.71E-08	12.1376	up
	6		9	0			
CDT1	0.5892	10.5602	5.7612	1.49E-0	3.02E-07	9.01124	up
	1			8			
ACSS1	0.5897	11.2111	5.2873	1.89E-0	2.89E-06	6.57008	up
	3			7			
SPIN3	0.5898	8.27353	3.4476	0.00062	0.00311	-1.0835	up
	3		3				
PLA2G4E	0.5901	3.99897	4.10011	4.85E-0	0.00036	1.28856	up
	8			5			
RPS6KL1	0.5902	8.32021	5.9786	4.39E-0	1.02E-07	10.1923	up
			3	9			
CDK18	0.5902	10.3208	5.9568	4.97E-0	1.13E-07	10.0724	up
	9		7	9			
VEGFA	0.5903	12.2975	6.2414	9.52E-1	2.61E-08	11.6697	up
	7			0			
UPK3B	0.5905	4.26231	4.0802	5.26E-0	0.00039	1.21084	up
	2		9	5			
AL360181.3	0.59112	3.60695	4.5528	6.71E-0	6.55E-05	3.15862	up
			6	6			
ADRM1	0.5912	11.4052	6.5080	1.91E-1	6.16E-09	13.224	up
	1		9	0			
TAC3	0.5912	4.2565	4.5154	7.96E-0	7.60E-05	2.9971	up
	2		1	6			

TBC1D3L	0.5913 7	4.53939	3.5095 1	0.00049	0.00257	-0.8751	up
RASL10B	0.5915 7	5.55302	3.5022 2	0.0005	0.00263	-0.8999	up
AKAP17A	0.5915 8	10.6793	7.0710 9	5.44E-1 2	2.39E-10	16.682	up
EXD3	0.5919 1	8.9393	6.7760 8	3.62E-11	1.34E-09	14.8405	up
MMP23B	0.5921 3	2.15159	5.6438 7	2.84E-0 8	5.31E-07	8.38974	up
DOCK6	0.5922 9	11.2546	6.6895 1	6.23E-11	2.20E-09	14.3124	up
MCRIP2	0.5925 6	11.031	6.6607 7	7.45E-11	2.61E-09	14.1384	up
CCDC57	0.5925 9	9.64072	7.1802 7	2.65E-1 2	1.22E-10	17.3796	up
ASPSR1	0.5926 7	10.3205	6.5322 3	1.65E-1 0	5.37E-09	13.3674	up
SELENOH	0.5930 1	8.60054	7.6781 8	9.07E-1 4	5.42E-12	20.6688	up
CNFN	0.5930 3	5.59808	5.0384	6.65E-0 7	8.64E-06	5.36251	up
SH2D5	0.5931 6	3.16832	3.9466 3	9.11E-05	0.00062	0.69594	up
LRRC45	0.5936 2	9.83039	5.9289	5.82E-0 9	1.31E-07	9.91885	up
CDH26	0.5936 5	3.7828	3.7012 1	0.00024	0.0014	-0.2075	up
TP53TG5	0.5942	4.47498	5.7612	1.49E-0	3.02E-07	9.0117	up

	2		8	8			
SAPCD2	0.5944	10.5688	5.6827	2.30E-0	4.39E-07	8.59435	up
	6		3	8			
ANKRD61	0.5948	4.14219	4.6093	5.18E-0	5.23E-05	3.4047	up
	6		8	6			
MNX1	0.5948	8.46213	6.62011	9.59E-11	3.29E-09	13.8931	up
	9						
FBXL15	0.5950	8.98217	6.4889	2.15E-1	6.86E-09	13.1105	up
	1		2	0			
GPR35	0.5952	11.2787	6.5030	1.97E-1	6.34E-09	13.1941	up
	7		5	0			
INTS1	0.5952	12.3101	6.0078	3.71E-0	8.84E-08	10.3539	up
	7		6	9			
ZNF580	0.5954	8.99471	8.3670	6.44E-1	5.77E-14	25.499	up
	7		5	6			
ZNF414	0.5958	8.43153	6.8155	2.82E-11	1.07E-09	15.0833	up
	3		7				
TNK2	0.5958	10.698	6.0061	3.75E-0	8.90E-08	10.3445	up
	4		7	9			
PTGER1	0.5964	3.46072	4.5131	8.04E-0	7.66E-05	2.98738	up
	3		5	6			
HES4	0.5964	7.4967	4.7871	2.25E-0	2.52E-05	4.19689	up
	8		7	6			
SLC5A6	0.5973	11.6947	5.6952	2.15E-0	4.14E-07	8.66059	up
	3		6	8			
ZNF503	0.5973	9.33472	5.2192	2.67E-0	3.93E-06	6.23498	up
	5		9	7			
UVSSA	0.5973	9.68101	6.7995	3.12E-11	1.17E-09	14.9847	up
	7		5				

ANKRD24	0.5974 9	4.92775	5.0801	5.40E-0 7	7.21E-06	5.56121	up
MYH3	0.5981	4.90217	4.6533 8	4.23E-0 6	4.39E-05	3.59822	up
PRC1	0.5985 2	4.52444	6.4495 5	2.73E-1 0	8.46E-09	12.8781	up
MACROD1	0.5986 7	10.263	5.9809 1	4.33E-0 9	1.01E-07	10.2048	up
DHRS11	0.5987 1	9.93118	6.0794 2	2.46E-0 9	6.01E-08	10.7525	up
FABP6	0.5987 4	7.42377	2.8006 5	0.0053	0.01874	-3.0484	up
MINDY4	0.5989 2	4.89082	6.5162 9	1.82E-1 0	5.89E-09	13.2727	up
ENKD1	0.5989 8	8.6551	6.3146 5	6.16E-1 0	1.79E-08	12.0911	up
ROMO1	0.5998 9	11.2193	5.7902	1.27E-0 8	2.61E-07	9.16659	up
PAXX	0.5999 3	10.1612	6.1382	1.75E-0 9	4.49E-08	11.0829	up
MAST1	0.5999 3	4.99047	4.9541 6	1.01E-0 6	1.25E-05	4.96568	up
TRMU	0.6000 5	9.92588	7.9076 9	1.81E-1 4	1.21E-12	22.2429	up
FGFRL1	0.6001 7	11.0979	5.7406 7	1.67E-0 8	3.34E-07	8.90169	up
PSMA2	0.6002 6	4.76436	4.4761 6	9.50E-0 6	8.86E-05	2.82913	up
ARHGAP39	0.6005	9.47399	6.4445	2.82E-1	8.69E-09	12.8488	up

	9		7	0			
MYO7A	0.6008	8.24907	5.0029	7.92E-0	1.01E-05	5.19497	up
	3		9	7			
NR1I2	0.60112	9.92462	3.8540	0.00013	0.00084	0.3486	up
			2				
TAC4	0.6017	2.00223	5.3149	1.63E-0	2.54E-06	6.70752	up
	1		7	7			
SMIM1	0.6017	4.18272	4.4361	1.14E-0	0.0001	2.65917	up
	4		2	5			
TEX29	0.6019	2.38063	5.4557	7.81E-0	1.32E-06	7.41648	up
			2	8			
SHD	0.6019	6.7165	4.3735	1.50E-0	0.00013	2.39642	up
	4		6	5			
TMEM252	0.6022	4.30487	2.5746	0.01033	0.03239	-3.6421	up
	3		5				
KCNJ14	0.6024	5.82572	6.4095	3.48E-1	1.06E-08	12.643	up
	6		1	0			
CARD14	0.6025	6.77736	5.11256	4.59E-0	6.28E-06	5.71686	up
	9			7			
MSS51	0.6030	5.0053	5.9697	4.61E-0	1.07E-07	10.1434	up
	5		7	9			
NAPRT	0.6033	10.5804	5.4666	7.37E-0	1.25E-06	7.47214	up
	4		3	8			
C3orf35	0.6034	4.91776	4.7364	2.87E-0	3.10E-05	3.96813	up
	2		6	6			
ZNF736	0.6041	8.03772	3.6276	0.00032	0.00178	-0.4676	up
	5		7				
TRABD	0.6044	10.8084	6.4768	2.31E-1	7.30E-09	13.0392	up
	7		7	0			

CEP131	0.6048 7	9.01096	5.9572 9	4.95E-0 9	1.13E-07	10.0747	up
GPT	0.6052 5	7.28967	4.0867 3	5.12E-0 5	0.00038	1.23606	up
ARFRP1	0.6057	10.7248	6.5499 6	1.48E-1 0	4.86E-09	13.473	up
DLEC1	0.6058 9	4.84666	4.8002 5	2.12E-0 6	2.40E-05	4.25622	up
EVPL	0.6059 6	11.709	4.8582 2	1.60E-0 6	1.89E-05	4.52106	up
TMEM240	0.6060 4	4.12922	5.8454 8	9.32E-0 9	1.98E-07	9.46455	up
DECR2	0.6061 3	9.64223	6.8051 7	3.01E-11	1.14E-09	15.0193	up
PIWIL1	0.6063 2	5.88501	2.3720 2	0.01808	0.05112	-4.1331	up
KRTAP5-9	0.6063 8	2.02426	5.0724 1	5.62E-0 7	7.46E-06	5.52444	up
EPS8L2	0.6066 8	11.811	6.4289 1	3.10E-1 0	9.47E-09	12.7568	up
PNLIPRP1	0.6067 6	2.36857	4.0917 9	5.02E-0 5	0.00037	1.25589	up
ZSWIM1	0.6068 1	9.37036	7.3822 1	6.89E-1 3	3.41E-11	18.6926	up
ZNF285	0.6068 3	4.22	3.0375	0.00251	0.01013	-2.3745	up
KAT2A	0.6068 7	11.3614	6.6102 8	1.02E-1 0	3.45E-09	13.834	up
PASK	0.6078	9.21537	6.5728	1.29E-1	4.26E-09	13.6094	up

	3			0			
GAL3ST1	0.6080	7.23529	4.6441	4.41E-0	4.55E-05	3.55745	up
	1		4	6			
CCDC116	0.6081	2.49173	5.8477	9.20E-0	1.96E-07	9.47701	up
	3		8	9			
GRB7	0.6082	10.5842	5.7316	1.76E-0	3.50E-07	8.85353	up
	7		2	8			
ZNF865	0.6084	9.28286	6.8097	2.92E-11	1.11E-09	15.0473	up
			3				
CPLX2	0.6085	5.20766	2.7870	0.00553	0.01942	-3.0856	up
	5		2				
SNRNP70	0.6086	12.4436	7.7719	4.71E-1	2.93E-12	21.3072	up
	1			4			
RNF43	0.6087	11.5213	4.5104	8.14E-0	7.74E-05	2.97569	up
			3	6			
VWA3A	0.6088	1.46325	5.615	3.33E-0	6.07E-07	8.23851	up
	1			8			
TTLL9	0.6088	2.9112	5.2336	2.49E-0	3.69E-06	6.30512	up
	9			7			
TRIM52	0.6090	8.04358	5.8676	8.23E-0	1.79E-07	9.58492	up
	2		9	9			
GCNT7	0.6097	2.79821	4.0955	4.94E-0	0.00036	1.27077	up
	2		9	5			
RSPH14	0.6099	3.94047	4.9582	9.87E-0	1.23E-05	4.985	up
	3		9	7			
MPIG6B	0.6101	4.29478	4.2479	2.59E-0	0.00021	1.8791	up
	9		1	5			
TBX10	0.6102	5.39265	2.9598	0.00323	0.01246	-2.6013	up
	2		2				

DPH7	0.6102 7	9.66205	8.4336 9	3.92E-1 6	3.56E-14	25.9828	up
SLC29A2	0.6104 8	9.98292	6.9053 1	1.59E-11	6.37E-10	15.6393	up
TTYH1	0.61114	4.52808	4.6453 4	4.39E-0 6	4.53E-05	3.56274	up
KCNH6	0.61122	3.27011	3.4919 7	0.00052	0.00271	-0.9345	up
MYBL2	0.61129	11.6008	5.3751 6	1.19E-0 7	1.92E-06	7.0087	up
TRMT2A	0.61152	9.76246	7.5363 4	2.41E-1 3	1.33E-11	19.714	up
MAP6D1	0.61195	2.10086	6.7639 5	3.90E-11	1.44E-09	14.7662	up
TPRN	0.61211	11.2515	6.0923 6	2.28E-0 9	5.64E-08	10.825	up
CASTOR1	0.6132 4	2.5394	6.9892	9.26E-1 2	3.91E-10	16.1645	up
CEACAM19	0.6137 2	7.08225	5.0756 4	5.53E-0 7	7.36E-06	5.5399	up
CAPN15	0.614	11.6318	7.4785 7	3.58E-1 3	1.88E-11	19.3292	up
SPATC1L	0.6140 4	7.23866	3.2307 1	0.00132	0.00592	-1.7857	up
PDZD7	0.6142 1	5.54958	5.4768 4	6.98E-0 8	1.19E-06	7.52432	up
PSEN2	0.6142 8	4.96585	6.7543 8	4.15E-11	1.52E-09	14.7077	up
C1orf159	0.6147	9.00504	7.7550	5.30E-1	3.27E-12	21.192	up

	1		6	4			
ZHX1-C8orf76	0.6154	2.56982	6.9915	9.12E-1	3.86E-10	16.179	up
	5		2	2			
GNG5	0.6158	8.35759	7.3225	1.03E-1	4.93E-11	18.3015	up
	7		3	2			
PHKG2	0.6162	9.69379	8.1742	2.65E-1	2.09E-13	24.1157	up
	3		8	5			
KIF18B	0.6163	9.49514	6.2734	7.87E-1	2.21E-08	11.8535	up
	3		5	0			
COL11A2	0.6164	4.58042	4.3127	1.96E-0	0.00017	2.14438	up
	3		7	5			
FMC1	0.6167	4.77081	6.4062	3.55E-1	1.07E-08	12.6237	up
	8			0			
GATD1	0.6168	11.1154	7.0512	6.19E-1	2.68E-10	16.5562	up
	4		6	2			
OGFOD2	0.6168	4.10786	7.4385	4.70E-1	2.42E-11	19.064	up
	8		5	3			
ING5	0.6170	10.1993	7.4785	3.58E-1	1.88E-11	19.3288	up
	6		1	3			
GEMIN7	0.6175	4.18516	8.7052	5.07E-1	5.52E-15	27.9836	up
	6		7	7			
KRT83	0.6176	2.23692	3.7623	0.00019	0.00114	0.01245	up
	7		6				
RASSF7	0.6178	10.9939	6.0089	3.69E-0	8.80E-08	10.3599	up
	5		4	9			
ZNF514	0.6179	9.15964	5.8148	1.11E-08	2.31E-07	9.29913	up
	1		5				
AC069503.2	0.6180	1.00891	7.5943	1.62E-1	9.17E-12	20.1027	up
	8		2	3			

ZMIZ2	0.6181 6	12.2845	6.5421 5	1.55E-1 0	5.07E-09	13.4264	up
TFAP2E	0.6184 4	4.45667	4.8322 6	1.82E-0 6	2.10E-05	4.40211	up
PPFIA4	0.6184 9	5.21748	4.8224 8	1.90E-0 6	2.18E-05	4.35745	up
PKD1	0.6185 8	10.2726	5.7166	1.91E-0 8	3.73E-07	8.77367	up
MTRNR2L8	0.6186 1	3.87243	3.5739 8	0.00039	0.0021	-0.6544	up
ZNF862	0.6186 3	8.3117	6.1934 5	1.26E-0 9	3.36E-08	11.396	up
CLN3	0.6189 4	5.63141	6.3306 1	5.60E-1 0	1.64E-08	12.1835	up
OSBPL7	0.6189 9	9.73106	6.0659 3	2.66E-0 9	6.48E-08	10.6771	up
SLC9A5	0.619	5.36185	6.0181 2	3.50E-0 9	8.38E-08	10.4108	up
ANGPTL8	0.6190 3	2.01676	5.6070 5	3.47E-0 8	6.31E-07	8.197	up
SCRIB	0.6190 5	12.1272	5.8398 1	9.62E-0 9	2.03E-07	9.43385	up
HOOK2	0.6190 8	10.634	7.9937	9.78E-1 5	7.00E-13	22.8419	up
GNRH1	0.6201 9	4.3363	5.0295 7	6.95E-0 7	8.99E-06	5.32062	up
C6orf141	0.6203	7.02416	3.9666 7	8.40E-0 5	0.00057	0.77212	up
NBEAL2	0.6206	12.1533	6.6724	6.93E-11	2.43E-09	14.2092	up

	3		8				
LRFN4	0.6207	9.74279	6.0900	2.31E-0	5.69E-08	10.8123	up
	2		9	9			
ZNF205	0.6209	8.53061	6.3665	4.51E-1	1.34E-08	12.392	up
	6			0			
ARR3	0.6215	2.90813	4.7102	3.24E-0	3.47E-05	3.85065	up
	6		2	6			
CCDC24	0.6217	8.34937	6.8540	2.20E-11	8.64E-10	15.3212	up
	8		9				
CCDC150	0.6220	6.35181	4.8447	1.71E-0	2.00E-05	4.45928	up
	4		5	6			
LMTK3	0.6223	7.76724	5.2477	2.31E-0	3.46E-06	6.37488	up
	7		8	7			
BCAS4	0.6226	7.89569	5.2468	2.32E-0	3.47E-06	6.37044	up
	1		8	7			
OPLAH	0.6226	10.1494	5.5695	4.25E-0	7.60E-07	8.00187	up
	3		6	8			
ZNF335	0.6229	9.92135	7.2087	2.20E-1	1.02E-10	17.5632	up
	4		8	2			
CCDC130	0.6230	9.5052	7.7944	4.02E-1	2.54E-12	21.4617	up
	6		5	4			
PACSIN3	0.6236	8.8081	4.3327	1.79E-0	0.00015	2.22692	up
	7		6	5			
TAX1BP3	0.6238	3.61743	4.3306	1.81E-0	0.00016	2.21826	up
	2		7	5			
ZNF775	0.62411	7.49643	5.9299	5.79E-0	1.30E-07	9.92477	up
			8	9			
SLC34A3	0.6242	3.46659	4.2108	3.04E-0	0.00024	1.72906	up
	8		1	5			

GRID2IP	0.6243 3	5.45362	5.84115	9.55E-0 9	2.03E-07	9.44112	up
MYL5	0.6245 5	7.74348	7.5247 6	2.61E-1 3	1.44E-11	19.6368	up
MEGF11	0.6247 2	4.04808	3.5857 4	0.00037	0.00202	-0.6137	up
RNASEK	0.6254 3	5.12889	8.6681 8	6.73E-1 7	7.13E-15	27.7076	up
C17orf113	0.6255 9	6.66923	6.1118	2.04E-0 9	5.11E-08	10.9342	up
SYN3	0.6258 2	5.68438	3.0977 4	0.00206	0.00862	-2.1946	up
C8orf44	0.6259 6	6.38752	5.6259 7	3.13E-0 8	5.78E-07	8.29588	up
INO80E	0.6262	10.2675	8.3606 6	6.75E-1 6	5.97E-14	25.4528	up
AL136295.5	0.6263 9	2.81807	6.4771 7	2.31E-1 0	7.30E-09	13.041	up
METTL26	0.6264 2	10.8943	7.3124 9	1.10E-1 2	5.25E-11	18.236	up
TNNT2	0.6268 3	3.24943	3.9386 9	9.40E-0 5	0.00063	0.66587	up
FOXD2	0.6268 6	8.00989	4.9302 5	1.13E-0 6	1.39E-05	4.85412	up
HAGHL	0.6269 2	7.98331	4.8425 1	1.73E-0 6	2.02E-05	4.44901	up
TPGS1	0.6271 6	6.87548	6.7487 2	4.30E-11	1.57E-09	14.673	up
TAS2R4	0.6274	4.23493	4.05112	5.94E-0	0.00043	1.0971	up

	9			5			
CRELD1	0.6275	5.98037	7.3185	1.06E-1	5.05E-11	18.2756	up
	5		7	2			
SRPX2	0.6279	9.62565	3.9994	7.35E-0	0.00051	0.89741	up
	8		3	5			
IGSF9B	0.6280	7.25881	3.9565	8.75E-0	0.00059	0.73376	up
	3		9	5			
BTNL9	0.6285	7.67182	4.4306	1.16E-0	0.00011	2.63587	up
	4		1	5			
GLYCTK	0.6286	9.31556	7.0264	7.27E-1	3.12E-10	16.3991	up
	4		2	2			
NDUFS7	0.6289	8.64057	6.6080	1.03E-1	3.50E-09	13.8205	up
	8		3	0			
AL121753.1	0.6292	2.64168	5.2813	1.95E-0	2.96E-06	6.54041	up
	1		1	7			
PLSCR3	0.6298	1.7315	7.06611	5.62E-1	2.44E-10	16.6504	up
	1			2			
C19orf71	0.6300	5.43444	5.6994	2.10E-0	4.06E-07	8.68248	up
	3			8			
SNAPC4	0.6304	9.55713	6.6931	6.09E-11	2.16E-09	14.3344	up
	7		2				
FBRSL1	0.6305	11.3884	7.8745	2.28E-1	1.50E-12	22.0135	up
	1		7	4			
FGFR4	0.6312	11.5364	4.8475	1.69E-0	1.98E-05	4.47193	up
			1	6			
C17orf49	0.6314	3.31775	7.0660	5.62E-1	2.44E-10	16.6502	up
			8	2			
GCHFR	0.6316	4.63727	5.2027	2.91E-0	4.23E-06	6.15423	up
	7		9	7			

MXD3	0.6324 8	8.33526	7.6058 8	1.50E-1 3	8.55E-12	20.1804	up
PRR36	0.6328	7.16122	3.7449 2	0.0002	0.00121	-0.0506	up
STX16	0.6330 1	11.1447	5.9996 6	3.89E-0 9	9.18E-08	10.3085	up
CDK20	0.6332	7.30381	5.7730 7	1.40E-0 8	2.84E-07	9.07475	up
GALNT9	0.6336 2	3.45294	3.3553 4	0.00086	0.0041	-1.3876	up
MASP2	0.6339 6	4.60761	5.3664 6	1.25E-0 7	1.99E-06	6.96496	up
UNKL	0.6339 6	8.39526	7.3345 1	9.50E-1 3	4.62E-11	18.3798	up
SYNGAP1	0.634	8.60961	6.1386 9	1.74E-0 9	4.49E-08	11.0857	up
SLC2A11	0.6342 8	7.55352	7.4803 6	3.54E-1 3	1.88E-11	19.3411	up
RASL10A	0.6345 4	3.67483	6.6167 1	9.80E-11	3.34E-09	13.8727	up
TOP3B	0.6347 7	2.04835	5.8910 6	7.21E-0 9	1.59E-07	9.71206	up
IGFL4	0.6348	5.39303	3.3407 4	0.0009	0.00427	-1.435	up
MIF	0.6348 7	1.70812	3.9199 2	0.0001	0.00067	0.59495	up
ZNF579	0.6349 2	8.55168	6.9372 1	1.29E-11	5.31E-10	15.8384	up
REM2	0.6351	4.88796	6.4516	2.70E-1	8.39E-09	12.8902	up

	2			0			
BOP1	0.63611	11.7948	5.8143 3	1.11E-08	2.31E-07	9.29632	up
SH2B1	0.6365	10.5305	6.8004 8	3.10E-11	1.17E-09	14.9904	up
FAM155B	0.6365 3	4.76954	2.3092 7	0.02135	0.05838	-4.2772	up
AP1G2	0.6365 8	9.96754	7.7990 4	3.89E-1 4	2.47E-12	21.4932	up
SSBP4	0.6366 6	10.5519	6.8662 8	2.04E-11	8.07E-10	15.3968	up
CNTD1	0.6367	5.7428	6.0016 1	3.85E-0 9	9.10E-08	10.3193	up
LZTR1	0.6372 7	8.71904	8.7439 2	3.78E-1 7	4.24E-15	28.2721	up
USP52	0.6374 3	9.69094	6.6399 4	8.48E-11	2.94E-09	14.0125	up
KLK14	0.6374 3	2.92141	4.2764 3	2.29E-0 5	0.00019	1.99529	up
WDR86	0.6383 2	4.68056	6.5277 5	1.70E-1 0	5.51E-09	13.3408	up
BAIAP3	0.6386 1	6.92629	4.5552 7	6.64E-0 6	6.49E-05	3.16906	up
SAC3D1	0.6393 9	8.80975	6.4537 7	2.66E-1 0	8.32E-09	12.903	up
SMIM5	0.6396	5.58842	5.1713 4	3.41E-0 7	4.87E-06	6.00101	up
JAG2	0.6400 6	10.1713	5.5465 7	4.81E-0 8	8.47E-07	7.88283	up

ASPHD1	0.6400 8	7.74592	4.45611	1.04E-0 5	9.59E-05	2.74384	up
OGT	0.6402 1	12.3656	6.11051	2.05E-0 9	5.14E-08	10.927	up
DXO	0.6415 8	8.50532	8.0712 5	5.60E-1 5	4.16E-13	23.3863	up
COL9A3	0.6418 6	8.23224	3.2430 1	0.00126	0.0057	-1.7471	up
XKR6	0.6418 8	4.67169	3.5677 4	0.0004	0.00215	-0.6759	up
CLCN2	0.6420 8	9.4575	5.9103 1	6.47E-0 9	1.43E-07	9.8171	up
C19orf73	0.64211	5.17244	6.4010 4	3.67E-1 0	1.10E-08	12.5935	up
IGFN1	0.6422 5	3.96594	3.3290 1	0.00094	0.00442	-1.4729	up
ZNF789	0.6422 6	8.30167	6.6231 2	9.42E-11	3.23E-09	13.9113	up
CRYBB2	0.6424 9	2.11687	5.6432 9	2.85E-0 8	5.32E-07	8.38669	up
SCT	0.6426 2	3.48402	4.1263 6	4.34E-0 5	0.00033	1.392	up
PTP4A3	0.6428 1	10.4765	4.7446 7	2.76E-0 6	2.99E-05	4.00502	up
SRRM5	0.6430 8	4.14303	5.6837 6	2.29E-0 8	4.37E-07	8.59978	up
CEP250	0.6431 7	10.7082	6.0975 9	2.21E-0 9	5.48E-08	10.8544	up
PLTP	0.6435	11.0277	4.7183	3.12E-0	3.35E-05	3.88709	up

			7	6			
LIN37	0.6436	4.79317	10.532	1.74E-2	5.47E-21	42.5717	up
	6		8	3			
EFCAB8	0.6437	2.32569	4.7725	2.42E-0	2.67E-05	4.13073	up
	1		6	6			
INPP5E	0.6439	9.19712	8.1686	2.76E-1	2.17E-13	24.0755	up
	3		3	5			
LUC7L	0.6440	10.1447	7.9672	1.18E-1	8.32E-13	22.6568	up
	9			4			
SALL4	0.6442	7.05161	4.1748	3.54E-0	0.00027	1.58458	up
	2		1	5			
IGSF22	0.6442	4.42487	5.7215	1.86E-0	3.67E-07	8.80009	up
	9		7	8			
TRMT1	0.6449	10.5688	7.3381	9.27E-1	4.52E-11	18.4035	up
	5		3	3			
PTCH2	0.6462	5.63193	5.4823	6.78E-0	1.16E-06	7.5527	up
	6		9	8			
STX1B	0.6464	4.83849	5.2097	2.81E-0	4.10E-06	6.18834	up
	5		7	7			
TREX2	0.6466	3.94758	5.4421	8.40E-0	1.40E-06	7.34745	up
	6		5	8			
OGDHL	0.6466	4.87433	2.9153	0.00372	0.01398	-2.7286	up
	7		7				
BAIAP2L2	0.6468	10.542	5.8574	8.72E-0	1.88E-07	9.5293	up
	2		3	9			
SH2B2	0.6468	7.15106	6.7814	3.50E-11	1.30E-09	14.8734	up
	7		3				
DUSP9	0.6469	3.40485	3.4561	0.0006	0.00302	-1.055	up
	1		4				

ZNF23	0.6469 3	4.47599	5.7875	1.29E-0 8	2.64E-07	9.15207	up
STRC	0.6472 2	2.26984	5.2467 1	2.32E-0 7	3.47E-06	6.3696	up
SCAND1	0.6473	10.924	5.4333 9	8.79E-0 8	1.46E-06	7.30294	up
ZFP41	0.6474 5	8.32684	6.2560 6	8.73E-1 0	2.42E-08	11.7537	up
CFAP44	0.6477	7.66172	5.1847 8	3.19E-0 7	4.59E-06	6.06639	up
COL27A1	0.6481 5	9.12442	4.3212 2	1.89E-0 5	0.00016	2.17922	up
HSPB6	0.6491 7	5.33874	3.4619 4	0.00058	0.00297	-1.0356	up
PAQR6	0.6495 5	6.24736	5.4988	6.21E-0 8	1.07E-06	7.6368	up
AC004233.2	0.6495 6	6.54074	5.0589 8	6.00E-0 7	7.89E-06	5.46037	up
MSI1	0.6508 5	5.96986	3.2197	0.00137	0.00612	-1.8202	up
AGXT	0.651	4.29214	3.6692 6	0.00027	0.00156	-0.3212	up
HINT2	0.6510 2	3.01786	7.4467 1	4.45E-1 3	2.30E-11	19.118	up
SLFNL1	0.65112	3.46839	5.1361 9	4.08E-0 7	5.66E-06	5.83073	up
SLC39A4	0.6516	11.4153	5.4536 4	7.90E-0 8	1.33E-06	7.40591	up
CROCC	0.6517	9.23186	6.3285	5.67E-1	1.66E-08	12.1718	up

	5		9	0			
C21orf58	0.6519 2	7.68139	6.4499 3	2.73E-1 0	8.46E-09	12.8804	up
TP53I13	0.6519 5	10.121	7.3785	7.06E-1 3	3.47E-11	18.6681	up
PAH	0.6521 7	4.93328	2.4269 1	0.01559	0.04539	-4.004	up
CSTL1	0.6524 1	2.09664	4.5734 5	6.11E-06	6.04E-05	3.24796	up
WNK2	0.6525 7	11.5632	5.5418 6	4.93E-0 8	8.68E-07	7.8585	up
WFDC10B	0.6526 9	2.70419	4.6792 7	3.75E-0 6	3.95E-05	3.71284	up
RPS21	0.6528	14.4432	6.3407 6	5.27E-1 0	1.55E-08	12.2424	up
SLC2A4RG	0.6535 9	10.6163	6.4605 5	2.56E-1 0	8.00E-09	12.9429	up
E4F1	0.6537 5	9.93621	8.0950 6	4.71E-1 5	3.60E-13	23.5542	up
DLX3	0.6542 8	3.55765	2.6517 2	0.00827	0.02698	-3.4451	up
FGFR3	0.6543 5	9.63151	4.7491 5	2.70E-0 6	2.94E-05	4.02517	up
FTCD	0.6544 9	1.7674	4.6295	4.72E-0 6	4.84E-05	3.49297	up
AP5Z1	0.6553 6	10.6267	6.8593 3	2.13E-11	8.39E-10	15.3537	up
NAA10	0.6556 4	9.98779	8.3481	7.41E-1 6	6.51E-14	25.362	up

CPSF1	0.6557 7	12.0469	6.6891 8	6.24E-11	2.20E-09	14.3104	up
ACAD11	0.6558 8	3.22812	7.2087 7	2.20E-1 2	1.02E-10	17.5632	up
FOXO6	0.6561 3	5.04705	5.0912 3	5.11E-07	6.88E-06	5.61448	up
CELF3	0.6561 4	4.75706	3.6268 4	0.00032	0.00178	-0.4705	up
ATOH7	0.6561 9	2.51322	5.1797 8	3.27E-0 7	4.69E-06	6.04203	up
PCSK1N	0.6563 3	4.6023	2.6224 4	0.00901	0.02891	-3.5206	up
ASIC3	0.6564 4	4.65227	5.3769 1	1.18E-0 7	1.90E-06	7.01749	up
BNIP1	0.6564 9	4.25378	5.9695	4.62E-0 9	1.07E-07	10.1419	up
MRPL2	0.6568 6	6.88234	7.7369 3	6.02E-1 4	3.65E-12	21.0683	up
SERPINA6	0.6570 8	4.63075	2.7675 3	0.00587	0.02038	-3.1385	up
GIPR	0.6576 5	5.80627	4.9999 4	8.04E-0 7	1.02E-05	5.18057	up
CFAP74	0.6582 5	3.31598	4.4729 1	9.64E-0 6	8.96E-05	2.81527	up
TTBK1	0.6582 6	5.80278	4.5734 7	6.11E-06	6.04E-05	3.24805	up
ZNF783	0.6585 9	9.18414	6.9622 6	1.10E-11	4.58E-10	15.9952	up
AC108488.2	0.6587	1.40405	7.4554	4.20E-1	2.19E-11	19.1756	up

	9		1	3			
MAN2C1	0.6591	10.2728	7.3895	6.56E-1	3.26E-11	18.7407	up
	5		3	3			
TSSK3	0.6593	2.19496	6.1261	1.87E-0	4.79E-08	11.0149	up
	6		3	9			
ABCA2	0.6594	11.1458	6.1712	1.44E-0	3.78E-08	11.2699	up
	6		4	9			
NME3	0.6595	9.82244	5.9251	5.95E-0	1.33E-07	9.89833	up
	4		6	9			
RHOT2	0.6595	11.3296	7.4063	5.85E-1	2.94E-11	18.8514	up
	5		4	3			
SLC7A4	0.6599	6.12245	3.2790	0.00112	0.00513	-1.6329	up
	7		7				
TELO2	0.6602	10.7544	6.5486	1.49E-1	4.89E-09	13.4652	up
			5	0			
ARTN	0.6602	5.70151	6.0608	2.73E-0	6.64E-08	10.6486	up
	8		4	9			
TMEM259	0.6604	11.6455	7.8698	2.36E-1	1.54E-12	21.9806	up
	6		1	4			
AMN	0.6612	10.0722	5.01108	7.61E-0	9.78E-06	5.23317	up
	3			7			
C1QTNF12	0.6614	6.21153	4.5247	7.62E-0	7.32E-05	3.03743	up
	4		9	6			
NECAB3	0.6617	9.79552	7.3241	1.02E-1	4.91E-11	18.312	up
	1		3	2			
NKPD1	0.6618	4.42396	5.0203	7.27E-0	9.38E-06	5.27716	up
	7		9	7			
CDRT4	0.6621	3.21524	5.1987	2.97E-0	4.31E-06	6.13441	up
	5		3	7			

ADM5	0.6622 5	4.67815	5.4834 3	6.74E-0 8	1.15E-06	7.55804	up
TMEM175	0.6628 4	8.90592	8.2361 6	1.69E-1 5	1.39E-13	24.5571	up
NANOS3	0.6630 9	4.855	3.6395 8	0.0003	0.00171	-0.4258	up
SLC25A29	0.6633 3	9.3941	7.7737 4	4.65E-1 4	2.90E-12	21.3198	up
CYHR1	0.6636 9	10.5908	7.8458 2	2.80E-1 4	1.81E-12	21.815	up
KLRG2	0.6639 4	3.01928	3.0599 9	0.00234	0.00955	-2.3077	up
PRSS33	0.6640 3	5.74236	2.9185 8	0.00368	0.01386	-2.7194	up
PPFIA3	0.6640 5	9.53023	6.3150 7	6.14E-1 0	1.78E-08	12.0935	up
CCDC114	0.6642 1	3.73488	5.4017 5	1.04E-0 7	1.69E-06	7.14269	up
AGBL2	0.6644 9	5.05756	6.028	3.30E-0 9	7.97E-08	10.4657	up
NDOR1	0.6648 5	8.9379	7.0824 6	5.05E-1 2	2.22E-10	16.7543	up
F10	0.6649	6.48722	3.7754 5	0.00018	0.0011	0.06001	up
SHROOM1	0.6650 7	10.2706	6.9938	8.98E-1 2	3.81E-10	16.1934	up
WBP2NL	0.6655 7	4.02546	4.1941 2	3.26E-0 5	0.00026	1.66194	up
ARRDC1	0.6655	11.0852	7.6619	1.01E-1	5.98E-12	20.559	up

	8		8	3			
POU5F1	0.6657	6.20478	5.5037	6.05E-0	1.05E-06	7.66234	up
	8		8	8			
PLCG1	0.6658	11.3565	6.4041	3.60E-1	1.08E-08	12.6119	up
	7		9	0			
CPNE1	0.6666	12.3893	6.25117	8.98E-1	2.47E-08	11.7256	up
	4			0			
STK36	0.6669	9.38291	7.0667	5.59E-1	2.44E-10	16.6542	up
	7			2			
PPDPF	0.6671	13.3574	6.1436	1.69E-0	4.39E-08	11.1138	up
	7		6	9			
FNDC11	0.6672	4.66377	4.8095	2.03E-0	2.30E-05	4.29863	up
	9		8	6			
NFKBID	0.6673	7.25404	8.2744	1.27E-1	1.08E-13	24.8318	up
	6		9	5			
FAM71F2	0.6676	4.75464	5.2395	2.41E-0	3.59E-06	6.33447	up
	2		7	7			
SFI1	0.6677	9.70445	8.1981	2.23E-1	1.79E-13	24.2858	up
	5		7	5			
AC022400.6	0.6685	6.9592	7.1649	2.94E-1	1.35E-10	17.2813	up
	4		6	2			
TXNDC5	0.6688	5.71326	5.7630	1.48E-0	2.99E-07	9.02113	up
	7		5	8			
ID1	0.669	11.5593	4.4348	1.14E-0	0.0001	2.65368	up
			3	5			
TRPV1	0.6694	6.87468	6.7446	4.41E-11	1.61E-09	14.648	up
	6		2				
TSNARE1	0.6695	9.21636	6.4677	2.45E-1	7.67E-09	12.9856	up
	5		8	0			

CARMIL3	0.6702	6.36579	5.2182 2	2.69E-0 7	3.95E-06	6.22971	up
PABPC3	0.6703 4	5.61855	6.6009 7	1.08E-1 0	3.64E-09	13.7781	up
ISM2	0.67118	4.1801	2.9195 7	0.00367	0.01383	-2.7166	up
TRIM66	0.6712 4	8.56276	6.4037 9	3.61E-1 0	1.08E-08	12.6096	up
FITM1	0.6714 6	3.09441	6.8787 8	1.88E-11	7.50E-10	15.4744	up
PLEKHG5	0.6716 6	9.73132	6.8575 2	2.16E-11	8.47E-10	15.3425	up
WDR83	0.6722 6	6.47348	8.2205 8	1.89E-1 5	1.54E-13	24.4457	up
GRPR	0.6724	3.26291	3.4124 4	0.0007	0.00345	-1.2003	up
ROGDI	0.6726 8	7.9717	9.1838 8	1.23E-1 8	1.72E-16	31.6202	up
MESP1	0.6727 5	5.849	4.2464 6	2.61E-0 5	0.00021	1.87321	up
PALM3	0.6732 9	5.73994	3.4155 7	0.00069	0.00342	-1.19	up
CAPN10	0.6734 9	9.59064	8.2013	2.18E-1 5	1.76E-13	24.3081	up
AQP7	0.6739 8	5.92698	4.6042 9	5.30E-0 6	5.35E-05	3.38243	up
ZNF358	0.6745 1	9.67165	6.6876 2	6.30E-11	2.22E-09	14.301	up
GDPD5	0.6748	9.74502	5.11369	4.57E-0	6.25E-06	5.72231	up

	2			7			
ARMC12	0.6752 4	2.2376	6.2657 7	8.24E-1 0	2.30E-08	11.8094	up
ANKRD13D	0.6760 9	9.68395	9.0102 8	4.83E-1 8	6.11E-16	30.2852	up
HOXA2	0.6761 7	5.57763	4.2772 9	2.28E-0 5	0.00019	1.9988	up
SGK2	0.6762 5	8.86437	4.2139 4	3.00E-0 5	0.00024	1.74166	up
NEK8	0.6765 1	7.54752	7.4159 7	5.48E-1 3	2.78E-11	18.9149	up
FBXO41	0.6769 8	9.27614	6.0430 4	3.03E-0 9	7.34E-08	10.5494	up
TMEM63C	0.6773 6	6.92554	3.4569 8	0.00059	0.00302	-1.0522	up
MYADML2	0.6774 2	4.95594	3.5880 7	0.00037	0.00201	-0.6056	up
KCNH4	0.6779 4	4.08952	4.8754 6	1.48E-0 6	1.75E-05	4.60038	up
TMEM82	0.6783 4	4.89811	3.9351 8	9.54E-0 5	0.00064	0.65257	up
RAD9A	0.6785 3	8.98917	8.2047 2	2.12E-1 5	1.72E-13	24.3325	up
HOXA3	0.6785 4	8.19336	5.1612 5	3.59E-0 7	5.08E-06	5.95203	up
NAPSA	0.6788 8	3.84836	5.3980 4	1.06E-0 7	1.72E-06	7.124	up
C1QTNF4	0.6789 7	2.50181	5.9599 3	4.88E-0 9	1.12E-07	10.0892	up

SPDYE2	0.6791 4	2.25367	5.0503 7	6.27E-0 7	8.19E-06	5.41939	up
SLC13A2	0.6809	6.09058	2.56611	0.01059	0.03298	-3.6636	up
FXYD3	0.6811	7.40653	5.7594 1	1.51E-0 8	3.04E-07	9.00167	up
HPX	0.6819 2	4.4147	5.6210 7	3.22E-0 8	5.90E-07	8.27026	up
TEX22	0.6824 8	3.42203	5.7121 8	1.95E-0 8	3.82E-07	8.75022	up
PKMYT1	0.6829 4	9.75745	6.7197	5.16E-11	1.86E-09	14.496	up
DHX34	0.6829 9	10.1965	7.5194 3	2.71E-1 3	1.48E-11	19.6012	up
FAM227A	0.6836 5	6.06585	5.9212 4	6.08E-0 9	1.35E-07	9.87688	up
MROH1	0.6842 2	11.1908	7.9879 8	1.02E-1 4	7.26E-13	22.8019	up
KCNMB3	0.6842 9	5.06011	5.1227 2	4.36E-0 7	6.02E-06	5.76577	up
TAZ	0.6867	9.83301	8.1933	2.31E-1 5	1.85E-13	24.2511	up
PSORS1C2	0.6876 4	2.60545	4.3467 3	1.69E-0 5	0.00015	2.28478	up
COMTD1	0.6877 1	9.79798	6.7430 9	4.45E-11	1.61E-09	14.6387	up
HYPK	0.6878 4	3.85735	6.4057 6	3.56E-1 0	1.08E-08	12.6211	up
SYCE2	0.6879 7	4.22437	7.1030 4	4.41E-1 2	1.97E-10	16.8853	up

NUTM2G	0.6883 5	2.95528	5.82411	1.05E-0 8	2.20E-07	9.34907	up
TEX45	0.6883 8	6.34138	5.4223 1	9.32E-0 8	1.54E-06	7.24671	up
FBXW12	0.6883 9	2.10048	5.7010 5	2.08E-0 8	4.03E-07	8.69123	up
HCAR1	0.6884 3	4.36376	2.9657 1	0.00317	0.01225	-2.5843	up
FBXO44	0.6890 2	8.36174	6.4088 4	3.50E-1 0	1.06E-08	12.6391	up
CYP4F8	0.6890 9	2.58298	4.1373	4.15E-0 5	0.00031	1.43533	up
NPIPB12	0.6893 6	3.28408	5.8957 3	7.02E-0 9	1.55E-07	9.73754	up
SLC26A6	0.6894 3	10.9715	7.9751 7	1.12E-1 4	7.89E-13	22.7124	up
COX20	0.6896 1	5.05472	7.2251 7	1.97E-1 2	9.24E-11	17.669	up
ZNF497	0.6899	5.04339	7.9328 6	1.51E-1 4	1.04E-12	22.4177	up
POLR2I	0.6900 9	7.75391	6.9619	1.10E-11	4.58E-10	15.993	up
TLE2	0.6903 7	10.14	4.7527 8	2.65E-0 6	2.90E-05	4.04152	up
TRIM17	0.6905 8	3.63631	5.2677 8	2.09E-0 7	3.15E-06	6.47349	up
ST3GAL3	0.6905 9	4.87454	6.5662 8	1.34E-1 0	4.42E-09	13.5704	up
AGAP4	0.6909	5.55797	5.5153	5.69E-0	9.90E-07	7.72187	up

	9		6	8			
APBB3	0.6910	8.06648	8.8866	1.26E-1	1.50E-15	29.3457	up
	8		8	7			
ASGR1	0.6914	6.48348	4.7740	2.40E-0	2.65E-05	4.13748	up
	1		5	6			
PMFBP1	0.6915	6.38966	4.4845	9.15E-0	8.56E-05	2.8648	up
	7		3	6			
CRLS1	0.6928	6.83003	6.6312	8.96E-11	3.10E-09	13.9601	up
	5		3				
TONSL	0.6930	10.1539	6.8728	1.96E-11	7.77E-10	15.4374	up
	9		2				
FBXO2	0.6937	6.60161	3.4987	0.00051	0.00266	-0.9117	up
	9		2				
CLDN3	0.6938	13.25	5.3081	1.69E-0	2.61E-06	6.67374	up
	4		8	7			
FNDC10	0.6938	7.85126	4.6430	4.43E-0	4.57E-05	3.55254	up
	5		3	6			
ARFGAP1	0.6944	11.8678	7.4326	4.90E-1	2.51E-11	19.0251	up
	1		7	3			
RBBP8NL	0.6944	8.75009	5.6804	2.33E-0	4.43E-07	8.58206	up
	9			8			
SRPK3	0.6946	6.41837	4.7791	2.34E-0	2.61E-05	4.16047	up
	9		3	6			
AC138969.1	0.69511	1.61256	5.9237	6.00E-0	1.34E-07	9.89032	up
				9			
MT3	0.6951	3.83266	3.3049	0.00102	0.00474	-1.5503	up
	7		4				
PIK3R2	0.6958	1.91117	7.6482	1.12E-1	6.51E-12	20.4661	up
			4	3			

BHLHA9	0.6959 5	1.51281	4.1716 9	3.59E-0 5	0.00028	1.57211	up
CLASRP	0.6965 2	10.0836	8.2643 7	1.37E-1 5	1.15E-13	24.7592	up
SCLY	0.6978 8	6.6757	8.6405	8.30E-1 7	8.64E-15	27.5022	up
TMEM262	0.6984 4	1.67909	8.0663	5.80E-1 5	4.28E-13	23.3514	up
ARVCF	0.6989 5	9.08252	6.9942 4	8.96E-1 2	3.81E-10	16.1962	up
TBX6	0.6992 4	5.69577	6.2556 5	8.75E-1 0	2.42E-08	11.7513	up
RPS10	0.6993 3	6.83819	5.7188 8	1.88E-0 8	3.71E-07	8.78579	up
SLC23A1	0.7005 7	5.52042	5.0772 2	5.48E-0 7	7.31E-06	5.5474	up
TSSK6	0.7006 9	5.78734	6.7166 3	5.26E-11	1.89E-09	14.4773	up
NR6A1	0.7006 9	8.29925	6.8292 8	2.58E-11	9.98E-10	15.1679	up
C19orf18	0.7022	2.82769	4.4230 4	1.20E-0 5	0.00011	2.60391	up
ANKLE1	0.7022 4	3.94008	5.2560 4	2.22E-0 7	3.33E-06	6.41555	up
RAPSN	0.7024 5	2.47444	6.1028 2	2.14E-0 9	5.34E-08	10.8837	up
SUSD3	0.7024 9	7.2165	4.9786 8	8.93E-0 7	1.13E-05	5.08056	up
ZNF276	0.7032	8.81319	8.3292	8.51E-1	7.41E-14	25.2259	up

	6		5	6			
BIRC7	0.7033	3.89905	4.4324	1.15E-0	0.00011	2.64358	up
	1		4	5			
GABBR1	0.7036	8.61909	5.0413	6.55E-0	8.55E-06	5.3765	up
	6		4	7			
MAP1LC3A	0.7041	9.53352	6.7310	4.80E-11	1.73E-09	14.5649	up
	2		1				
MTFP1	0.7042	5.10864	6.9215	1.43E-11	5.80E-10	15.7408	up
	4		8				
TUBA8	0.7043	2.25496	6.8382	2.44E-11	9.44E-10	15.2235	up
	1		8				
PET100	0.7045	6.02546	9.1918	1.16E-1	1.63E-16	31.6823	up
	6		9	8			
IZUMO4	0.7053	5.32895	7.4785	3.58E-1	1.88E-11	19.3289	up
	1		2	3			
GADD45G	0.7060	7.77384	5.5764	4.10E-0	7.35E-07	8.03782	up
	7		8	8			
DRICH1	0.7060	2.46934	5.6142	3.34E-0	6.09E-07	8.23453	up
	9		4	8			
PTF1A	0.70611	1.21294	3.9133	0.0001	0.00069	0.57005	up
ENDOG	0.7076	6.8839	5.8549	8.84E-0	1.90E-07	9.51586	up
			6	9			
KANTR	0.7096	7.96437	5.0356	6.74E-0	8.74E-06	5.34967	up
			9	7			
BBS1	0.7101	4.09712	7.5061	2.97E-1	1.60E-11	19.5127	up
	4		5	3			
C9orf24	0.7105	4.38535	5.1324	4.16E-0	5.76E-06	5.81249	up
	2		1	7			
LCNL1	0.71132	1.72918	5.8040	1.17E-0	2.43E-07	9.2412	up

			9	8			
PRR5-ARHGAP8	0.71179	3.37423	5.6415 5	2.88E-0 8	5.36E-07	8.37754	up
RGS11	0.71196	5.52098	4.9337	1.11E-06	1.37E-05	4.87018	up
HIF3A	0.7120 2	5.25321	4.6297 8	4.71E-0 6	4.83E-05	3.4942	up
IHH	0.7121 2	10.8602	4.4202 5	1.22E-0 5	0.00011	2.59216	up
TOMM5	0.7122 3	6.87533	7.5488 6	2.22E-1 3	1.23E-11	19.7977	up
E2F1	0.7125 2	9.95641	7.2900 1	1.28E-1 2	6.08E-11	18.0895	up
ZGLP1	0.7138 9	3.94667	7.6418 2	1.17E-1 3	6.76E-12	20.4227	up
ZNF316	0.7139 8	10.3711	8.0813 2	5.21E-1 5	3.91E-13	23.4572	up
CAMKV	0.7147 5	3.52434	3.364	0.00083	0.00399	-1.3594	up
ASPDH	0.7149 9	2.8261	5.6367 9	2.95E-0 8	5.49E-07	8.35262	up
FBF1	0.7155 5	6.7139	7.8003 8	3.86E-1 4	2.46E-12	21.5024	up
MROH6	0.7162 2	9.69553	5.6184 6	3.26E-0 8	5.97E-07	8.25661	up
KMT5C	0.7162 7	8.86315	8.0815 4	5.20E-1 5	3.91E-13	23.4588	up
LRRC36	0.7164 3	6.09265	4.1250 7	4.37E-0 5	0.00033	1.38692	up
PCBP1	0.7168	8.34802	6.2224	1.06E-0	2.90E-08	11.561	up

	9			9			
RSRP1	0.7169	10.5417	7.5149	2.80E-1	1.52E-11	19.5712	up
	3		3	3			
DDTL	0.7181	5.47507	7.5804	1.78E-1	1.00E-11	20.0093	up
	6		2	3			
ANKS3	0.7184	8.79886	9.0475	3.61E-1	4.67E-16	30.5707	up
	3		9	8			
RPS17	0.7188	7.62882	9.6155	3.86E-2	6.68E-18	35.0158	up
	4		1	0			
MYO15B	0.7189	11.8261	6.0147	3.57E-0	8.54E-08	10.3918	up
	6			9			
CHST13	0.7205	5.08724	4.2484	2.58E-0	0.00021	1.88131	up
			5	5			
CBARP	0.721	4.90487	5.2036	2.90E-0	4.21E-06	6.15846	up
			5	7			
KRTAP5-5	0.7210	2.54818	4.4571	1.03E-0	9.56E-05	2.74832	up
	8		7	5			
ADGRD2	0.7217	1.60992	5.6443	2.83E-0	5.30E-07	8.39215	up
	1		3	8			
FAM53A	0.7227	5.64163	6.1228	1.91E-0	4.86E-08	10.9963	up
	1		3	9			
TMEM184A	0.7228	10.1279	6.3050	6.52E-1	1.88E-08	12.0359	up
	1		9	0			
CCDC180	0.72311	3.44467	5.3360	1.47E-0	2.30E-06	6.81249	up
			2	7			
TCTE3	0.7231	6.16856	6.11507	2.00E-0	5.04E-08	10.9526	up
	2			9			
SERHL2	0.7231	5.43743	7.8862	2.10E-1	1.39E-12	22.0945	up
	8		8	4			

KCP	0.7237 6	7.04407	6.2670 7	8.17E-1 0	2.28E-08	11.8168	up
STX1A	0.7243 8	8.1218	7.3237 7	1.02E-1 2	4.91E-11	18.3096	up
ARHGAP8	0.7246 7	5.89829	5.9900 7	4.11E-09	9.63E-08	10.2555	up
MICALL2	0.7248 2	10.6394	7.7856 9	4.28E-1 4	2.68E-12	21.4016	up
UBXN11	0.7252 3	9.11204	8.6086 1	1.06E-1 6	1.08E-14	27.2662	up
PLAC4	0.7255 2	5.04911	3.7495 3	0.0002	0.00119	-0.034	up
MOGAT3	0.7256 1	8.91866	4.5570 4	6.58E-0 6	6.45E-05	3.17672	up
ADCK5	0.7256 4	9.48485	7.2050 4	2.25E-1 2	1.05E-10	17.5391	up
SLC19A3	0.7262 1	7.34709	3.6184 7	0.00033	0.00183	-0.4998	up
MATN4	0.7262 8	2.09089	7.4316	4.93E-1 3	2.52E-11	19.018	up
MRPS24	0.7269 7	3.79568	9.0280 9	4.20E-1 8	5.40E-16	30.4213	up
LY6G6E	0.7269 8	2.05261	4.9838 5	8.71E-0 7	1.10E-05	5.10485	up
WFIKK1	0.7274 8	4.8934	5.5921 3	3.76E-0 8	6.79E-07	8.11923	up
SPACA6	0.7275 5	5.38852	6.2931 3	7.00E-1 0	2.00E-08	11.9668	up
TRPM5	0.7284	5.26765	4.3907	1.39E-0	0.00012	2.46806	up

	5			5			
SDR39U1	0.7287 8	6.41399	9.7265 5	1.55E-2 0	2.96E-18	35.9064	up
SLC5A11	0.7293 1	2.54824	5.3537 1	1.34E-0 7	2.11E-06	6.90104	up
ARID3A	0.7294	10.1841	5.4642 7	7.47E-0 8	1.27E-06	7.46008	up
SPAG8	0.7299 3	3.82796	7.0329 1	6.97E-1 2	3.01E-10	16.4401	up
PFDN5	0.7303 1	6.15857	7.7558 2	5.27E-1 4	3.27E-12	21.1972	up
NUDT3	0.7303 5	5.29672	7.1222 8	3.89E-1 2	1.75E-10	17.008	up
SELENOO	0.7304 2	9.48413	8.7935 5	2.58E-1 7	2.96E-15	28.6439	up
GIGYF1	0.7306 1	10.9446	7.3716 4	7.40E-1 3	3.63E-11	18.6231	up
PDCD6	0.7307 2	7.73523	7.1991 9	2.34E-1 2	1.09E-10	17.5014	up
ATAD3C	0.7310 7	5.91374	4.4318 9	1.16E-0 5	0.00011	2.64129	up
CCDC183	0.7316 6	5.60455	6.6957 9	5.99E-11	2.13E-09	14.3506	up
MIB2	0.7323 4	10.1616	8.3633 8	6.61E-1 6	5.88E-14	25.4725	up
GOLGA6L2	0.7323 8	1.374	4.7773 4	2.36E-0 6	2.62E-05	4.15236	up
LRP3	0.7328 8	9.73112	6.1502 7	1.63E-0 9	4.25E-08	11.1512	up

SPDYC	0.7330 6	3.53788	4.4390 9	1.12E-0 5	0.0001	2.67171	up
SERPINA10	0.7334	4.09004	2.9451	0.00338	0.01293	-2.6437	up
ACAP3	0.7336 6	10.2461	8.3853 7	5.62E-1 6	5.07E-14	25.6317	up
DNLZ	0.7337 3	2.08408	7.5096 7	2.90E-1 3	1.57E-11	19.5361	up
SLC13A4	0.7338	4.69456	5.6476 4	2.78E-0 8	5.23E-07	8.40952	up
C20orf144	0.7349 6	3.46005	6.4316 9	3.05E-1 0	9.35E-09	12.7731	up
DNAH17	0.7351 4	5.9764	7.1514	3.21E-1 2	1.46E-10	17.1943	up
MUTYH	0.7356 2	4.79047	8.0815	5.20E-1 5	3.91E-13	23.4585	up
NDUFA13	0.7363 3	6.42265	8.0308 1	7.49E-1 5	5.41E-13	23.1019	up
DNASE1	0.7370 8	9.20107	6.8633 1	2.08E-11	8.20E-10	15.3784	up
MTG1	0.7388 4	7.18217	11.7766	2.61E-2 8	1.58E-25	53.4804	up
MUC12	0.7390 7	10.9223	3.2425 5	0.00127	0.00571	-1.7485	up
CFAP65	0.7400 9	4.46346	5.2772 7	1.99E-0 7	3.01E-06	6.5204	up
CELSR3	0.7421 9	9.21158	5.3129 4	1.65E-0 7	2.56E-06	6.69739	up
PTOV1	0.7427	9.89651	11.8449	1.39E-2 8	8.73E-26	54.0987	up

NKD1	0.7433 6	10.6334	3.6210 7	0.00032	0.00182	-0.4907	up
TMOD4	0.7442	4.01634	7.9470 4	1.36E-1 4	9.50E-13	22.5163	up
CCDC85B	0.7443 6	9.70738	6.1327 9	1.80E-0 9	4.62E-08	11.0524	up
S100A1	0.7452 2	3.73348	6.1635 4	1.50E-0 9	3.93E-08	11.2262	up
TMEM86B	0.7460 6	5.13134	7.4771 6	3.62E-1 3	1.89E-11	19.3199	up
LIN7B	0.7461 9	6.70068	7.8989 1	1.92E-1 4	1.28E-12	22.182	up
VWA5B1	0.7463 6	2.26118	3.3896 2	0.00076	0.0037	-1.2755	up
ARL2BP	0.7464 8	4.41128	5.4744 1	7.08E-0 8	1.21E-06	7.5119	up
PLXNB1	0.7465	11.9513	7.9461 5	1.37E-1 4	9.51E-13	22.5101	up
FTH1	0.7466 4	11.7648	6.7430 2	4.45E-11	1.61E-09	14.6382	up
ABCC6	0.7470 3	7.99061	6.1264 4	1.87E-0 9	4.78E-08	11.0166	up
PLEKHG4	0.7474 9	10.1864	6.6484 4	8.05E-11	2.80E-09	14.0639	up
PPP1R16A	0.7476	10.3668	7.7903 4	4.14E-1 4	2.60E-12	21.4335	up
U2AF1L4	0.7480 8	5.62123	10.9111	6.40E-2 5	2.41E-22	45.8136	up
PCED1A	0.7481	9.52746	7.6759	9.21E-1	5.48E-12	20.6537	up

			6	4			
SPSB3	0.7486 7	2.81919	8.0464 5	6.69E-1 5	4.87E-13	23.2118	up
TEPSIN	0.7486 8	7.96076	10.212 2	2.70E-2 2	6.55E-20	39.881	up
SPTBN5	0.7493 8	7.20441	4.8539 6	1.64E-0 6	1.92E-05	4.50152	up
GCNA	0.7501 3	5.05913	6.8016 8	3.07E-11	1.16E-09	14.9978	up
INPP5J	0.7506	8.6845	6.9648 4	1.08E-11	4.52E-10	16.0114	up
PRR4	0.7513 9	3.15318	5.9521	5.10E-0 9	1.16E-07	10.0461	up
SLC7A10	0.7514 7	1.75774	4.7317 9	2.93E-0 6	3.16E-05	3.94717	up
CYP4F12	0.7519 6	9.08564	5.6319 4	3.03E-0 8	5.62E-07	8.32717	up
TH	0.7537 7	4.21144	4.0295 6	6.49E-0 5	0.00046	1.01352	up
OMP	0.7546 3	3.11318	6.2672 2	8.17E-1 0	2.28E-08	11.8177	up
PLXNA3	0.7550 4	10.8042	7.9430 2	1.40E-1 4	9.69E-13	22.4883	up
NACA2	0.7559 7	3.82577	5.8607 8	8.55E-0 9	1.85E-07	9.54745	up
TMEM198	0.7559 8	6.67173	5.9685 8	4.64E-0 9	1.07E-07	10.1369	up
ECHDC2	0.756	10.1675	8.0650 6	5.85E-1 5	4.30E-13	23.3427	up

GRIN2C	0.7562 7	4.52158	5.5477 8	4.78E-0 8	8.43E-07	7.88909	up
PIF1	0.7565 1	7.83657	8.3449 5	7.58E-1 6	6.63E-14	25.3393	up
TMEM160	0.7566 9	8.07909	6.8515	2.24E-11	8.72E-10	15.3052	up
PRSS41	0.7572 8	2.3834	4.9196 8	1.19E-0 6	1.45E-05	4.805	up
AMY2B	0.7574 2	6.0391	5.4508 1	8.02E-0 8	1.35E-06	7.3915	up
SPACA3	0.7580 6	3.47421	3.6092 9	0.00034	0.00188	-0.5318	up
AMDHD2	0.7584 6	8.17511	8.2884 2	1.15E-1 5	9.86E-14	24.9318	up
CYP4F2	0.7589 2	6.7874	3.3468	0.00088	0.0042	-1.4153	up
SLC5A2	0.7602 9	4.28582	6.6189	9.67E-11	3.30E-09	13.8859	up
ZNF337	0.7607 9	5.85365	6.0399 8	3.08E-0 9	7.45E-08	10.5324	up
ESPN	0.7609	9.36478	5.2265 7	2.58E-0 7	3.81E-06	6.27066	up
FSCN2	0.7609 6	4.04328	7.0894	4.82E-1 2	2.13E-10	16.7984	up
WBP1	0.7609 8	6.84148	10.356 2	7.93E-2 3	2.18E-20	41.0828	up
FAM193B	0.7620 1	9.79712	8.5349 9	1.84E-1 6	1.78E-14	26.7237	up
MC1R	0.7621	5.7592	7.4801	3.54E-1	1.88E-11	19.34	up

	5		9	3			
TSPOAP1	0.7640	8.30034	4.7780	2.35E-0	2.62E-05	4.15561	up
	5		6	6			
UMODL1	0.7646	4.29812	4.1071	4.71E-0	0.00035	1.31623	up
	6		5	5			
CAPN12	0.7648	6.61877	5.7027	2.06E-0	4.00E-07	8.70043	up
	5		9	8			
IL11RA	0.7650	7.20484	8.3664	6.46E-1	5.77E-14	25.495	up
	3		9	6			
NOP2	0.7652	4.41928	9.5388	7.19E-2	1.19E-17	34.405	up
	3		6	0			
ATG9B	0.7655	6.74797	5.7238	1.83E-0	3.63E-07	8.81225	up
	6		6	8			
SRXN1	0.766	2.54721	4.5096	8.17E-0	7.75E-05	2.97214	up
				6			
LRRC56	0.7663	6.91731	6.6503	7.95E-11	2.77E-09	14.0756	up
			8				
AGAP9	0.7665	6.11414	6.9393	1.28E-11	5.24E-10	15.852	up
	5		9				
TMEM178A	0.7670	4.90813	6.4965	2.05E-1	6.57E-09	13.1559	up
	3		9	0			
ATP6V1C2	0.7677	7.24278	5.4226	9.31E-0	1.54E-06	7.24858	up
			7	8			
SLC1A7	0.7677	6.31105	3.6412	0.0003	0.0017	-0.4201	up
	2		1				
CCL14	0.7686	3.26562	6.4904	2.13E-1	6.81E-09	13.1196	up
	5		7	0			
GNB3	0.7687	4.62082	7.2318	1.89E-1	8.89E-11	17.7119	up
	2			2			

AGAP5	0.7699 2	1.54366	8.1221 5	3.87E-1 5	2.99E-13	23.7457	up
ELAVL2	0.7709 3	3.45072	3.5086	0.00049	0.00258	-0.8782	up
LTB4R2	0.7709 8	4.51287	6.2337 4	9.96E-1 0	2.72E-08	11.6258	up
CRACR2B	0.7710 6	10.228	7.67119	9.52E-1 4	5.63E-12	20.6214	up
TGM1	0.7717 5	4.58202	6.9806 9	9.78E-1 2	4.11E-10	16.1109	up
AC009690.1	0.7719 2	1.7296	7.3263 9	1.00E-1 2	4.86E-11	18.3267	up
GGT7	0.7729 9	9.32319	5.3298 2	1.51E-0 7	2.37E-06	6.78157	up
QTRT1	0.7735 3	10.8022	7.8038 2	3.76E-1 4	2.41E-12	21.526	up
POU5F1B	0.7747 7	6.65707	3.7824 1	0.00017	0.00107	0.08534	up
ATAT1	0.7748 8	8.89345	8.6848 1	5.93E-1 7	6.41E-15	27.8313	up
KCTD19	0.7755 7	2.56004	5.8906 5	7.23E-0 9	1.59E-07	9.70984	up
PIDD1	0.7757 5	9.23362	8.2496	1.53E-1 5	1.27E-13	24.6533	up
GPC2	0.7763 9	5.60754	6.5171 5	1.81E-1 0	5.87E-09	13.2777	up
ANKK1	0.7771 2	3.00787	5.5186 5	5.59E-0 8	9.74E-07	7.73882	up
IGSF23	0.7771	3.78368	4.7213	3.08E-0	3.31E-05	3.90041	up

	2		5	6			
C10orf82	0.7773 2	3.61589	3.2954	0.00106	0.00489	-1.5809	up
WIF1	0.7776 5	3.24541	2.6908 9	0.00737	0.02463	-3.3428	up
ATAD3B	0.7776 6	9.86265	8.0623 5	5.97E-1 5	4.37E-13	23.3236	up
CENPT	0.7783 3	9.37714	10.319 9	1.08E-2 2	2.78E-20	40.7791	up
UBAP1L	0.7793 4	5.82723	7.0504 6	6.22E-1 2	2.69E-10	16.5512	up
EXOC3L4	0.7799 6	7.16126	6.9094	1.55E-11	6.22E-10	15.6648	up
DET1	0.7802 4	4.84267	6.3452 4	5.13E-1 0	1.52E-08	12.2684	up
AL365205.1	0.7810 6	4.12156	8.6802 4	6.14E-1 7	6.59E-15	27.7973	up
NDUFA11	0.7811	8.65554	10.639 3	6.91E-2 4	2.21E-21	43.4772	up
OXER1	0.7819 6	6.15919	5.3725 5	1.21E-0 7	1.94E-06	6.99558	up
ABCC2	0.7824 2	6.63417	4.0140 9	6.92E-0 5	0.00049	0.95382	up
YBX2	0.7828 3	8.90243	6.6915 4	6.15E-11	2.18E-09	14.3247	up
ZDHHC8	0.7833 4	10.0949	7.7038 1	7.59E-1 4	4.58E-12	20.8428	up
NPW	0.7836 9	4.48666	4.8576 5	1.61E-0 6	1.89E-05	4.51843	up

MAPK8IP2	0.7849 4	6.10414	4.7542 5	2.63E-0 6	2.88E-05	4.04812	up
LHFPL5	0.7850 2	6.4816	6.0904 2	2.30E-0 9	5.68E-08	10.8141	up
PPP1R35	0.7850 7	8.39172	7.8964 4	1.96E-1 4	1.30E-12	22.1648	up
PPP1R32	0.7853 1	5.33364	8.5989 8	1.14E-1 6	1.15E-14	27.195	up
SAMD10	0.7857 4	8.81555	7.9137	1.73E-1 4	1.17E-12	22.2845	up
PRAC1	0.7857 6	4.01589	2.0728	0.03872	0.09447	-4.7862	up
TMEM52	0.7864 6	7.13502	6.1931 8	1.26E-0 9	3.36E-08	11.3945	up
MSANTD1	0.7873 6	2.92615	7.6723 3	9.44E-1 4	5.60E-12	20.6291	up
GRIN3B	0.7878 6	2.87877	6.5844 4	1.20E-1 0	4.00E-09	13.679	up
RALGDS	0.7879 8	8.23108	10.699 5	4.09E-2 4	1.48E-21	43.9913	up
SLC26A1	0.7882 2	6.79893	7.6035	1.52E-1 3	8.64E-12	20.1644	up
LRRC75B	0.7909 9	8.02008	8.1498 8	3.17E-1 5	2.47E-13	23.9423	up
UCKL1	0.7920 1	10.8193	9.4071 9	2.08E-1 9	3.10E-17	33.3636	up
PDIA2	0.7920 6	4.95074	4.5978 4	5.46E-0 6	5.50E-05	3.35423	up
RPL36A	0.7921	6.6898	7.2837	1.33E-1	6.33E-11	18.0484	up

	2			2			
AC068946.1	0.7926 8	3.18804	6.2123 1	1.13E-0 9	3.05E-08	11.5034	up
SULT1A2	0.7951 4	2.40145	6.3177 6	6.04E-1 0	1.76E-08	12.1091	up
AC012651.1	0.7956 2	1.79859	7.6033 2	1.52E-1 3	8.64E-12	20.1632	up
TMEM91	0.7960 1	5.54147	9.7406 7	1.38E-2 0	2.70E-18	36.0202	up
MRNIP	0.7971 4	8.53548	9.5247 7	8.06E-2 0	1.32E-17	34.2932	up
ENO3	0.7976	6.88355	8.6128 8	1.02E-1 6	1.06E-14	27.2977	up
PPP2R3B	0.7981 4	8.93472	9.6640 7	2.59E-2 0	4.68E-18	35.4044	up
SSTR5	0.7984 1	4.02327	3.6950 8	0.00025	0.00143	-0.2294	up
CRIP3	0.7991 3	3.08137	5.4498 6	8.06E-0 8	1.35E-06	7.38664	up
SH3D21	0.8000 4	8.60642	6.8495 7	2.27E-11	8.81E-10	15.2933	up
EIF4A1	0.8008 2	6.43289	7.2277 8	1.94E-1 2	9.11E-11	17.6859	up
FBXL6	0.8009 8	10.1326	7.5538 3	2.14E-1 3	1.19E-11	19.831	up
GLI4	0.8032 3	7.87473	9.2961 3	5.06E-1 9	7.34E-17	32.493	up
NNAT	0.8037 9	5.29367	5.36	1.29E-0 7	2.04E-06	6.93257	up

CRYGS	0.8046 6	5.61155	8.2576 4	1.44E-1 5	1.21E-13	24.711	up
TAF1C	0.8051 7	9.92253	8.8859 2	1.27E-1 7	1.50E-15	29.34	up
SLC25A41	0.8053 3	2.88644	6.3663 7	4.52E-1 0	1.34E-08	12.3912	up
IRF9	0.8108 6	6.57957	8.4975 5	2.44E-1 6	2.28E-14	26.4491	up
LCAT	0.81109	6.59631	8.9093 1	1.06E-1 7	1.28E-15	29.517	up
CDH4	0.81147	3.97267	5.3599 8	1.29E-0 7	2.04E-06	6.93248	up
DDX39B	0.81153	10.8303	7.9124 3	1.75E-1 4	1.18E-12	22.2757	up
ASNS	0.81164	5.06211	7.0935 7	4.69E-1 2	2.08E-10	16.825	up
NEURL2	0.81179	3.96978	7.7386	5.95E-1 4	3.63E-12	21.0797	up
AC006254.1	0.8129 6	2.72105	7.5138 8	2.82E-1 3	1.53E-11	19.5642	up
CCDC17	0.8133 9	4.78305	7.8216 7	3.32E-1 4	2.13E-12	21.6487	up
NDST2	0.8146 4	2.91068	9.4139 7	1.97E-1 9	2.96E-17	33.417	up
TAS2R5	0.8159 4	3.93048	6.7956 5	3.19E-11	1.20E-09	14.9608	up
RTKL1	0.8180 4	4.61965	8.4604 7	3.21E-1 6	2.96E-14	26.1781	up
SLC13A3	0.8185	6.24256	3.4882	0.00053	0.00274	-0.947	up

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PBX4	0.8194 2	6.74265	8.9318	8.89E-1 8	1.09E-15	29.6876	up
RNF207	0.8204 4	7.73489	7.4101 5	5.70E-1 3	2.88E-11	18.8765	up
SLC38A3	0.8207 8	3.47474	3.9219 3	0.0001	0.00067	0.60253	up
SLC16A8	0.8237 7	3.59669	6.2831 8	7.43E-1 0	2.10E-08	11.9095	up
SCO2	0.8237 9	3.78247	5.9682 7	4.65E-0 9	1.07E-07	10.1351	up
OBP2B	0.8241 7	1.77173	4.4673 5	9.88E-0 6	9.17E-05	2.79161	up
PABPN1	0.8245 9	8.40732	11.5403	2.27E-2 7	1.17E-24	51.3544	up
FOXH1	0.8250 1	3.44784	5.5508 5	4.70E-0 8	8.30E-07	7.90497	up
SLC39A5	0.8265 7	10.5635	4.3336 3	1.79E-0 5	0.00015	2.23051	up
ACCS	0.8270 6	8.00047	7.8728 1	2.31E-1 4	1.52E-12	22.0013	up
RAB4B	0.8273 8	4.23836	8.0825 5	5.16E-1 5	3.91E-13	23.466	up
AMT	0.8274 2	2.73989	8.3163 8	9.36E-1 6	8.06E-14	25.1331	up
CHRNA10	0.8281 8	4.49648	9.4360 5	1.65E-1 9	2.52E-17	33.591	up
SSUH2	0.8284 4	6.12122	4.9436 3	1.06E-0 6	1.31E-05	4.91647	up

TSPEAR	0.8284 8	4.38546	4.2582 7	2.48E-0 5	0.0002	1.92123	up
TTC34	0.8295 7	3.82415	6.7027	5.74E-11	2.04E-09	14.3925	up
XPNPEP2	0.8300 7	7.1639	3.3919 3	0.00075	0.00367	-1.2679	up
IPO4	0.8305 5	4.01898	8.0399 8	7.01E-1 5	5.09E-13	23.1663	up
SPPL2B	0.8306 8	10.9948	9.0050 1	5.03E-1 8	6.28E-16	30.245	up
TIAF1	0.8310 8	6.11182	7.7470 5	5.61E-1 4	3.44E-12	21.1373	up
IDUA	0.8319 1	8.36303	8.91162	1.04E-1 7	1.27E-15	29.5345	up
PIPOX	0.8323 6	6.29305	4.1919	3.29E-0 5	0.00026	1.65303	up
PLA2G6	0.8326 7	8.4643	9.1360 8	1.80E-1 8	2.44E-16	31.2508	up
LARGE2	0.8332 6	9.83007	5.5695 4	4.25E-0 8	7.60E-07	8.0018	up
SPACA4	0.8340 2	5.04536	7.5919 2	1.65E-1 3	9.29E-12	20.0865	up
INO80B	0.8342 1	3.37195	10.345	8.73E-2 3	2.31E-20	40.9891	up
DPEP1	0.8354 7	11.6901	3.4204	0.00068	0.00337	-1.174	up
PRAP1	0.8384 8	4.34953	5.2367 6	2.45E-0 7	3.63E-06	6.32068	up
AGER	0.83911	6.37877	8.6724	6.51E-1	6.95E-15	27.7391	up

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TCAP	0.8405 8	3.12841	6.5769 8	1.25E-1 0	4.17E-09	13.6343	up
TAF10	0.8409 8	6.71723	11.9463	5.43E-2 9	3.68E-26	55.0219	up
FOXE3	0.8414 7	2.43351	5.8580 2	8.69E-0 9	1.88E-07	9.53249	up
LRIT2	0.8419 3	3.74073	4.2520 2	2.55E-0 5	0.00021	1.89581	up
RNF224	0.8432 4	3.23356	6.1078 2	2.08E-0 9	5.21E-08	10.9118	up
ALS2CL	0.8451	10.1807	7.9844 8	1.04E-1 4	7.41E-13	22.7774	up
CCNL2	0.8453 1	11.4279	9.6978 6	1.97E-2 0	3.63E-18	35.6757	up
SLC17A9	0.8455 1	10.2415	5.9225 2	6.04E-0 9	1.35E-07	9.88387	up
TTLL2	0.8464 4	4.45422	5.5603 5	4.47E-0 8	7.93E-07	7.95412	up
NRBP2	0.8471 7	9.16036	9.0051 5	5.02E-1 8	6.28E-16	30.246	up
NAT16	0.8473 4	2.10109	5.9054 7	6.65E-0 9	1.47E-07	9.79067	up
DNHD1	0.8480 6	7.88682	7.7999 7	3.87E-1 4	2.46E-12	21.4996	up
CAPN3	0.8481 6	6.07116	6.6294 7	9.05E-11	3.13E-09	13.9494	up
NOXA1	0.8488 1	9.02821	7.1345 3	3.59E-1 2	1.63E-10	17.0863	up

MIOX	0.8497 1	2.66615	5.4072 9	1.01E-0 7	1.65E-06	7.1707	up
SCNN1D	0.8504 2	5.1588	7.4483 9	4.40E-1 3	2.28E-11	19.1291	up
ASB16	0.8509 5	4.97174	9.7007 8	1.92E-2 0	3.58E-18	35.6991	up
GOLGA8B	0.8512 5	7.51741	5.3642 2	1.26E-0 7	2.01E-06	6.95376	up
CCDC188	0.8514 3	3.55939	6.61119	1.01E-1 0	3.44E-09	13.8395	up
CDK10	0.8518 8	11.0446	10.015 2	1.42E-2 1	3.17E-19	38.2537	up
CDK11A	0.8520 4	5.98373	10.516 8	2.00E-2 3	6.05E-21	42.436	up
SPIRE2	0.8521 3	10.8123	8.5805 3	1.31E-1 6	1.30E-14	27.0589	up
CLDND2	0.8539 7	4.79189	8.4785 8	2.81E-1 6	2.62E-14	26.3103	up
Z84492.1	0.8544	2.21987	9.0808 3	2.78E-1 8	3.71E-16	30.8256	up
BICDL2	0.8559 8	10.3339	9.4455 3	1.53E-1 9	2.36E-17	33.6658	up
ANKRD13B	0.8575 5	8.94356	8.5183 5	2.08E-1 6	1.98E-14	26.6015	up
PRR7	0.8582 9	8.03601	9.0118	4.77E-1 8	6.09E-16	30.2968	up
MEF2B	0.8583 1	2.0055	9.6361 3	3.26E-2 0	5.76E-18	35.1807	up
PPT2-EGFL8	0.8597	2.79822	8.47511	2.88E-1	2.67E-14	26.285	up

	8			6			
AL121845.3	0.8600	1.09387	8.4438	3.64E-1	3.32E-14	26.0565	up
	5		1	6			
NPIP4	0.8601	6.5399	8.9886	5.72E-1	7.08E-16	30.1197	up
	6			8			
FBXL8	0.8615	7.69997	10.679	4.89E-2	1.73E-21	43.8173	up
	3		1	4			
CTU1	0.8615	7.59296	10.307	1.20E-2	3.05E-20	40.6747	up
	9		4	2			
SPNS1	0.8624	4.26067	9.7849	9.61E-2	1.92E-18	36.3779	up
	5		9	1			
AC040162.1	0.8635	5.22878	10.333	9.64E-2	2.52E-20	40.8911	up
	6		3	3			
FAM229A	0.8636	5.7866	11.4606	4.68E-2	2.21E-24	50.6422	up
	9			7			
PLIN5	0.8641	4.45708	6.5914	1.15E-1	3.84E-09	13.7209	up
	6		3	0			
DCST1	0.8648	3.67628	8.0713	5.59E-1	4.16E-13	23.3873	up
	5		9	5			
SRCIN1	0.8649	8.13066	6.3487	5.02E-1	1.49E-08	12.2887	up
	7		4	0			
RBFOX3	0.8664	3.43848	5.3732	1.21E-0	1.93E-06	6.99883	up
	9			7			
ZNF692	0.8672	9.5101	9.6010	4.34E-2	7.36E-18	34.9004	up
			6	0			
GSTM2	0.8675	5.69275	7.6591	1.03E-1	6.06E-12	20.5398	up
	8		3	3			
ADAT3	0.869	6.99576	8.8578	1.57E-1	1.86E-15	29.1281	up
			8	7			

RIPPLY3	0.8693 5	4.28175	4.0975 4	4.90E-0 5	0.00036	1.27845	up
PRR22	0.8716 1	5.95709	7.3969 9	6.23E-1 3	3.12E-11	18.7898	up
WDR27	0.8716 4	8.40045	8.5625 7	1.49E-1 6	1.48E-14	26.9266	up
DNASE1L2	0.8727	4.77134	7.5031 4	3.03E-1 3	1.62E-11	19.4926	up
SLC6A7	0.8729 7	6.17154	6.213	1.13E-0 9	3.04E-08	11.5074	up
AC090004.1	0.8730 3	3.21684	6.8240 3	2.67E-11	1.03E-09	15.1355	up
ACY1	0.8738 2	4.93946	8.8070 1	2.33E-1 7	2.69E-15	28.745	up
C4orf48	0.8742 3	8.17276	6.9167 8	1.48E-11	5.96E-10	15.7108	up
PNPLA7	0.8748 1	7.50351	7.7370 6	6.01E-1 4	3.65E-12	21.0692	up
RAB24	0.8760 4	6.51106	11.5102	2.99E-2 7	1.49E-24	51.0848	up
KIAA0895L	0.8775	8.97864	10.070 6	8.92E-2 2	2.04E-19	38.7089	up
TTLL10	0.8775 4	3.29497	6.407	3.54E-1 0	1.07E-08	12.6284	up
DOC2A	0.8791 2	5.26908	4.8745 2	1.48E-0 6	1.76E-05	4.59603	up
PRRT2	0.8810 8	5.24002	7.0028 1	8.48E-1 2	3.61E-10	16.2501	up
REC8	0.8822	7.58309	8.5355	1.83E-1	1.78E-14	26.7279	up

	9		6	6			
ZDHHC11	0.8828 4	5.41629	5.3004	1.76E-0 7	2.71E-06	6.63507	up
VGF	0.8833 1	5.84967	5.4462 1	8.22E-0 8	1.37E-06	7.36809	up
TUBGCP6	0.8835 6	10.2469	9.9084 7	3.46E-2 1	7.24E-19	37.3803	up
MYH7B	0.8838 4	6.27606	5.65511	2.67E-0 8	5.03E-07	8.4488	up
KLHL31	0.8854 9	5.47921	6.927	1.38E-11	5.62E-10	15.7746	up
EGLN2	0.8862 9	6.77679	8.6659 4	6.84E-1 7	7.21E-15	27.691	up
RELL2	0.8873 4	6.26361	7.0994	4.52E-1 2	2.02E-10	16.8621	up
PAM16	0.8873 6	6.81135	12.136 7	9.21E-3 0	7.45E-27	56.7647	up
HCN3	0.8874	7.94706	9.6236 1	3.61E-2 0	6.32E-18	35.0806	up
CLDN9	0.8874 2	4.84511	4.9487 5	1.03E-0 6	1.28E-05	4.94037	up
BRSK2	0.8874 4	6.42689	4.4358 2	1.14E-0 5	0.0001	2.65787	up
DUSP15	0.8883 5	5.63688	6.1005 9	2.17E-0 9	5.39E-08	10.8712	up
TRIM54	0.8891 6	4.37591	3.5632 6	0.0004	0.00218	-0.6914	up
RNF31	0.8901 9	3.90469	9.9470 1	2.51E-2 1	5.32E-19	37.6948	up

CES4A	0.8918 9	5.93206	6.7764 3	3.61E-11	1.34E-09	14.8427	up
MZF1	0.8949 3	9.20365	11.6711	6.87E-2 8	3.89E-25	52.5278	up
ALKBH6	0.8958 8	5.4337	9.5800 7	5.15E-2 0	8.56E-18	34.733	up
TMPRSS6	0.8959 8	4.56411	6.9313 7	1.34E-11	5.50E-10	15.8019	up
CCDC189	0.8971 3	3.71595	10.372 2	6.91E-2 3	1.96E-20	41.2175	up
TMPRSS9	0.8982 6	3.80227	8.1488 2	3.19E-1 5	2.47E-13	23.9348	up
CALML4	0.8987 4	3.19797	8.4579 6	3.27E-1 6	3.00E-14	26.1597	up
PROCA1	0.8990 5	5.77523	8.2250 2	1.83E-1 5	1.50E-13	24.4775	up
CATSPER2	0.9000 4	6.43288	7.1202 1	3.94E-1 2	1.77E-10	16.9948	up
AC011448.1	0.9000 8	2.46646	7.953	1.31E-1 4	9.17E-13	22.5578	up
UCN	0.9003 6	4.40378	8.2713 4	1.30E-1 5	1.10E-13	24.8092	up
ZGPAT	0.9009 2	7.55183	10.200 6	2.98E-2 2	7.12E-20	39.7842	up
MROH7	0.9015	4.00316	6.3051 3	6.52E-1 0	1.88E-08	12.0361	up
RECQL4	0.9028	10.0643	8.5183 8	2.08E-1 6	1.98E-14	26.6018	up
GDAP1L1	0.9050	2.24001	6.2883	7.20E-1	2.04E-08	11.9395	up

	2		8	0			
GOLGA8A	0.9050 6	8.00538	5.4597	7.65E-0 8	1.29E-06	7.43679	up
PKLR	0.9062 2	4.73582	3.5750 4	0.00039	0.0021	-0.6507	up
SNX15	0.9084	4.53136	9.3609 7	3.02E-1 9	4.45E-17	33.0004	up
CSAD	0.9095 1	8.00588	9.4590 8	1.37E-1 9	2.17E-17	33.7729	up
PLK5	0.9100 8	2.64282	6.1006 7	2.17E-0 9	5.39E-08	10.8717	up
CRYBB3	0.9120 1	3.43006	8.2362 9	1.69E-1 5	1.39E-13	24.5581	up
CKMT2	0.9132 9	6.8272	3.4467 7	0.00062	0.00311	-1.0863	up
CHTF18	0.9141 5	9.83796	9.2174 4	9.47E-1 9	1.36E-16	31.8804	up
LTB4R	0.9191	7.67735	9.1996	1.09E-1 8	1.54E-16	31.742	up
TMEM89	0.9192 9	2.46875	7.2370 2	1.82E-1 2	8.61E-11	17.7456	up
GTF2H4	0.9197 1	2.06629	10.346	8.65E-2 3	2.31E-20	40.9977	up
CCDC88B	0.9214 8	10.2398	6.2546 3	8.80E-1 0	2.43E-08	11.7454	up
WNT11	0.9216 5	7.8416	4.3531	1.64E-0 5	0.00014	2.3112	up
SLC25A27	0.9225 6	7.18432	6.61125	1.01E-1 0	3.44E-09	13.8399	up

SLC23A3	0.9258 9	4.57331	8.562	1.50E-1 6	1.48E-14	26.9224	up
SCART1	0.9276 4	5.33424	7.6106	1.45E-1 3	8.30E-12	20.2122	up
AC244197.3	0.9295 8	3.21088	7.5027 2	3.04E-1 3	1.62E-11	19.4899	up
LAT	0.9306 2	3.11925	8.7209 5	4.50E-1 7	4.96E-15	28.1006	up
TMEM145	0.9307 4	4.14445	7.0701 6	5.47E-1 2	2.40E-10	16.6761	up
KCNIP2	0.9310 9	4.8308	7.5052 8	2.99E-1 3	1.60E-11	19.5069	up
DCST2	0.9318 6	4.52998	8.5200 3	2.06E-1 6	1.97E-14	26.6139	up
RNF208	0.9328 9	7.86414	7.6435 1	1.15E-1 3	6.70E-12	20.4342	up
AGAP6	0.9335 3	3.18613	6.7665 8	3.84E-11	1.42E-09	14.7824	up
GSTM1	0.9335 8	3.9016	3.0394 7	0.0025	0.01007	-2.3686	up
SYCE1L	0.9356 4	5.07505	7.4098	5.72E-1 3	2.88E-11	18.8742	up
NTN5	0.9378 5	2.79055	7.8542 3	2.64E-1 4	1.72E-12	21.873	up
CHAD	0.9378 7	3.96076	7.39115	6.48E-1 3	3.24E-11	18.7514	up
KRTCAP2	0.9391 3	6.78429	12.408 1	7.16E-3 1	7.15E-28	59.2753	up
NEIL1	0.9394	8.23929	9.0716	2.99E-1	3.90E-16	30.7553	up

	2		7	8			
TMEM238	0.9397	8.75402	8.5312	1.89E-1	1.82E-14	26.6963	up
	5		7	6			
DNAH1	0.9406	8.43795	7.6403	1.18E-1	6.79E-12	20.4126	up
	8		2	3			
SLC35D3	0.9415	6.07386	3.8686	0.00012	0.0008	0.40288	up
	9		3				
PDF	0.9424	5.53258	6.9809	9.76E-1	4.11E-10	16.1124	up
	3		2	2			
CLDN15	0.9445	9.34068	6.11262	2.03E-0	5.09E-08	10.9388	up
	2			9			
CCER2	0.9463	2.55614	7.9214	1.64E-1	1.11E-12	22.3381	up
	1		2	4			
ATG16L2	0.9484	8.97348	10.260	1.79E-2	4.47E-20	40.2829	up
	6		5	2			
LRP5L	0.9487	7.61043	10.428	4.26E-2	1.25E-20	41.6931	up
	5		8	3			
CCDC154	0.9489	3.30535	7.1266	3.78E-1	1.71E-10	17.036	up
	2		6	2			
ARHGAP33	0.9496	7.84463	9.0969	2.45E-1	3.30E-16	30.9491	up
	3			8			
HOXA4	0.9497	3.03743	8.9073	1.07E-1	1.29E-15	29.5021	up
	3		3	7			
PDXP	0.9509	3.93139	8.0708	5.61E-1	4.16E-13	23.3836	up
	5		6	5			
SPOUT1	0.9512	2.39884	10.395	5.69E-2	1.64E-20	41.4086	up
	2			3			
LPIN3	0.9513	9.92164	9.4835	1.13E-1	1.82E-17	33.9665	up
	4		7	9			

CACNG4	0.954	4.61648	3.6299 6	0.00031	0.00177	-0.4596	up
FANCG	0.9569 2	5.37155	13.101 4	9.27E-3 4	1.57E-30	65.812	up
C9orf50	0.9572 2	3.6961	6.7594 9	4.01E-11	1.48E-09	14.7389	up
SLC30A2	0.9572 9	4.98202	3.9809 9	7.92E-0 5	0.00055	0.82678	up
CAPS	0.9616 1	7.7423	6.7935 7	3.24E-11	1.21E-09	14.948	up
MST1	0.9624 3	7.01431	8.6087 9	1.05E-1 6	1.08E-14	27.2675	up
AIRE	0.9629 3	2.40144	6.0636 6	2.69E-0 9	6.54E-08	10.6644	up
MAPK8IP3	0.9638 2	10.564	10.177 4	3.62E-2 2	8.54E-20	39.5921	up
CELF5	0.9664 8	4.56921	5.3178 7	1.61E-0 7	2.50E-06	6.72195	up
QPRT	0.9690 9	10.7408	5.0250 1	7.11E-07	9.18E-06	5.29906	up
EME2	0.9696	8.36325	10.450 4	3.54E-2 3	1.05E-20	41.8753	up
EIF4EBP3	0.9715 9	4.77375	8.1794	2.56E-1 5	2.04E-13	24.1521	up
FOXJ1	0.9762 1	5.59778	3.4177 1	0.00069	0.0034	-1.1829	up
WDR90	0.9762 8	10.4263	10.827 3	1.34E-2 4	4.94E-22	45.089	up
NKD2	0.9767	8.82251	5.7514	1.57E-0	3.16E-07	8.95904	up

	5		3	8			
PROZ	0.9777	3.07786	7.6595	1.03E-1 3	6.06E-12	20.5422	up
ANKRD23	0.9781 9	4.13868	9.1555 6	1.54E-1 8	2.11E-16	31.4012	up
D2HGDH	0.9790 1	9.73276	10.523 4	1.89E-2 3	5.82E-21	42.4922	up
KLHL17	0.9791 7	7.81145	10.249 5	1.97E-2 2	4.84E-20	40.191	up
YJEFN3	0.9798	5.59365	8.0155 5	8.36E-1 5	6.01E-13	22.9949	up
CHKB-CPT1B	0.9798 1	2.23835	9.5840 8	4.98E-2 0	8.37E-18	34.765	up
GPS2	0.9799 3	4.07687	12.154 7	7.78E-3 0	6.60E-27	56.9306	up
TTLL3	0.9816 1	8.47147	8.8513 1	1.66E-1 7	1.94E-15	29.0786	up
CDHR1	0.9865	10.2594	3.945	9.17E-0 5	0.00062	0.68975	up
ATP2A1	0.9874 9	5.40644	8.8255 6	2.02E-1 7	2.35E-15	28.8846	up
NOL12	0.9895 5	6.85099	12.426 9	5.99E-3 1	6.36E-28	59.4504	up
FRMD1	0.9913 9	7.87765	4.7928 8	2.19E-0 6	2.47E-05	4.22276	up
FGF17	0.9923 3	2.30285	8.1762 7	2.61E-1 5	2.07E-13	24.1298	up
TMEM249	0.9924 2	2.71733	6.8525 1	2.23E-11	8.70E-10	15.3114	up

CDK3	0.9927 7	2.73341	9.6939	2.03E-2 0	3.71E-18	35.6439	up
NME2	0.9997 6	6.71845	8.3220 7	8.98E-1 6	7.77E-14	25.1741	up
AARSD1	1.0015 3	5.16097	9.7902 7	9.20E-2 1	1.86E-18	36.4206	up
TERT	1.0046 3	5.4013	7.4157	5.49E-1 3	2.78E-11	18.9131	up
EGFL8	1.0050 8	4.39169	8.7282 4	4.26E-1 7	4.75E-15	28.155	up
FLRT1	1.0073 7	4.49295	7.5785 6	1.81E-1 3	1.01E-11	19.9968	up
CPN1	1.0104 1	2.62654	4.6159 9	5.02E-0 6	5.10E-05	3.43365	up
FKBP2	1.0125 2	3.60241	12.1124	1.16E-2 9	8.92E-27	56.5413	up
MRPL38	1.0162 6	5.77722	15.279 6	2.91E-4 3	2.47E-39	87.33	up
TMEM74B	1.0175 6	5.55547	7.1215 3	3.91E-1 2	1.76E-10	17.0032	up
RHBDL1	1.0177 3	6.91681	8.7092 8	4.92E-1 7	5.39E-15	28.0135	up
SUPT4H1	1.0179 4	2.90035	8.1634 3	2.87E-1 5	2.24E-13	24.0386	up
SEC31B	1.0196 3	7.28337	8.5826 1	1.29E-1 6	1.29E-14	27.0742	up
VAR2	1.0219 1	3.59273	9.0801 3	2.79E-1 8	3.71E-16	30.8203	up
C20orf204	1.0227	4.56767	7.6941	8.11E-14	4.88E-12	20.777	up

	4		4				
PCP2	1.0293 8	2.76925	8.7525 6	3.54E-1 7	4.00E-15	28.3367	up
BGLAP	1.0294	2.35779	9.7337 8	1.46E-2 0	2.82E-18	35.9647	up
DRD4	1.0300 4	4.5229	9.9796 8	1.91E-2 1	4.16E-19	37.962	up
KIF12	1.0314 1	9.59824	7.5259 5	2.59E-1 3	1.43E-11	19.6447	up
LMNTD2	1.0334 4	6.31269	11.2102	4.48E-2 6	1.81E-23	48.425	up
ENGASE	1.0336 9	11.131	8.6442 4	8.06E-1 7	8.45E-15	27.53	up
B4GALNT4	1.0352 2	6.73037	4.2654 8	2.40E-0 5	0.0002	1.95061	up
LY6G6F	1.0372 9	2.17925	6.5431 2	1.54E-1 0	5.05E-09	13.4322	up
ZDHHC11B	1.0385 8	6.33352	5.8181 6	1.09E-0 8	2.27E-07	9.31699	up
RPP21	1.0393 8	4.92482	13.695 8	2.72E-3 6	6.58E-33	71.5476	up
NPEPL1	1.0410 1	8.07458	13.273 8	1.73E-3 4	3.26E-31	67.4637	up
BRICD5	1.04511	5.79485	10.6411	6.80E-2 4	2.21E-21	43.4931	up
PDZD3	1.0498	7.16033	6.6637 7	7.31E-11	2.56E-09	14.1565	up
ATP6V0C	1.0522 7	2.82015	11.3852	9.27E-2 7	3.93E-24	49.9716	up

GET4	1.0522 9	5.69191	12.324 6	1.58E-3 0	1.49E-27	58.5002	up
DRD2	1.0562 1	4.89221	4.3015 8	2.05E-0 5	0.00017	2.09834	up
HAUS7	1.0609 3	4.22894	11.3921	8.71E-2 7	3.79E-24	50.0332	up
ASCL2	1.0619 7	11.0475	5.8777 5	7.77E-0 9	1.70E-07	9.63962	up
PCSK4	1.0623 7	6.36903	8.50611	2.28E-1 6	2.15E-14	26.5118	up
NPIPA1	1.0682 1	6.03455	10.009 2	1.49E-2 1	3.29E-19	38.2043	up
SYNE4	1.0684	6.96074	5.1079 2	4.70E-0 7	6.41E-06	5.69455	up
LY6G6D	1.0685	3.38238	4.4903 5	8.91E-0 6	8.38E-05	2.88969	up
PRSS53	1.0715 4	3.84971	9.6039	4.24E-2 0	7.27E-18	34.9231	up
DBNDD2	1.0728 3	5.88413	12.518 9	2.51E-3 1	3.04E-28	60.3076	up
NPIP3	1.0754 9	5.25442	9.7534	1.25E-2 0	2.46E-18	36.1228	up
ADAMTS13	1.0806 3	6.67714	9.7071 8	1.82E-2 0	3.44E-18	35.7506	up
SLC6A4	1.0839 5	5.38099	4.5257 5	7.59E-0 6	7.29E-05	3.04156	up
GRK1	1.0852 8	2.81372	6.1397 7	1.73E-0 9	4.48E-08	11.0918	up
MAGEB17	1.0876	3.11039	4.2938	2.12E-0	0.00018	2.06674	up

	6		8	5			
MSH5	1.0878 2	6.38008	9.3223 8	4.11E-19	6.01E-17	32.6981	up
GABRE	1.0906 7	9.59214	7.4530 6	4.26E-1 3	2.22E-11	19.16	up
LENG8	1.0913 8	12.0729	11.222	4.03E-2 6	1.67E-23	48.5283	up
JMJD7-PLA2G4B	1.0968 4	5.93719	9.6527 5	2.85E-2 0	5.08E-18	35.3137	up
CEL	1.0998 4	7.74357	3.7747 6	0.00018	0.0011	0.05748	up
ARL6IP4	1.1066 4	3.30212	11.1572	7.19E-2 6	2.84E-23	47.9594	up
SPATA25	1.1081 8	4.89702	7.9250 7	1.60E-1 4	1.09E-12	22.3635	up
CALML6	1.1090 4	2.40488	9.4478 2	1.50E-1 9	2.34E-17	33.6839	up
MLXIPL	1.1101	9.91332	7.9469 7	1.37E-1 4	9.50E-13	22.5158	up
RHPN1	1.11056	9.50506	9.8061 3	8.07E-2 1	1.65E-18	36.5489	up
COQ8A	1.11077	4.46034	12.639 3	7.96E-3 2	1.04E-28	61.4353	up
LY6G5B	1.11168	5.25907	12.019	2.76E-2 9	1.95E-26	55.6858	up
SLC22A11	1.11476	4.84796	4.6432 7	4.43E-0 6	4.57E-05	3.5536	up
PLA2G4B	1.11774	2.85525	10.355 8	7.96E-2 3	2.18E-20	41.0795	up

L3MBTL1	1.11849 6	6.53782	7.9240 6	1.61E-1 4	1.10E-12	22.3565	up
MAMDC4	1.1223 6	8.10105	10.069 4	9.01E-2 2	2.04E-19	38.6992	up
CYP2D6	1.1379 3	5.38059	9.9726 8	2.03E-2 1	4.35E-19	37.9048	up
NPIPB11	1.1418 3	4.95333	10.652 8	6.14E-2 4	2.07E-21	43.593	up
TLX1	1.1430 3	6.08328	6.71193	5.41E-11	1.94E-09	14.4487	up
PLA2G12B	1.1444 7	5.10907	3.95511	8.80E-0 5	0.0006	0.72813	up
SGSM3	1.1508 8	4.83511	14.947 7	8.88E-4 2	5.02E-38	83.9692	up
CCDC78	1.1518 4	6.30956	8.7559 2	3.45E-1 7	3.92E-15	28.3619	up
TEN1-CDK3	1.1623 5	3.80176	11.9107	7.55E-2 9	4.93E-26	54.6974	up
AIFM3	1.1624 7	9.21721	7.0917 3	4.75E-1 2	2.10E-10	16.8132	up
TNNC2	1.1628 6	7.49608	4.8580 4	1.61E-0 6	1.89E-05	4.52021	up
STPG3	1.1743 5	2.57873	9.2139 7	9.73E-1 9	1.39E-16	31.8534	up
NOTUM	1.1826 1	8.23879	4.18511	3.39E-0 5	0.00026	1.62579	up
CHKB	1.1867 3	3.8415	13.6711	3.47E-3 6	7.36E-33	71.307	up
MSH5-SAPCD1	1.1928	3.83143	10.654	6.04E-2	2.07E-21	43.6093	up

	2		8	4			
PGGHG	1.1976	10.6776	9.1706	1.37E-1	1.89E-16	31.5177	up
	2		2	8			
NPIPB13	1.1996	3.35938	9.4277	1.76E-1	2.67E-17	33.5256	up
	4		5	9			
WDR97	1.2074	5.44003	9.4551	1.42E-1	2.22E-17	33.7417	up
	4		4	9			
ABCB6	1.2081	4.88305	13.776	1.22E-3	4.16E-33	72.3307	up
	5		1	6			
TNFRSF25	1.2085	8.84606	13.090	1.03E-3	1.59E-30	65.7072	up
	1		4	3			
SLC9A3	1.2301	8.06872	6.2954	6.90E-1	1.98E-08	11.9802	up
	4		5	0			
SCX	1.2428	5.98636	12.814	1.49E-3	2.10E-29	63.0835	up
	7		2	2			
MAPK15	1.2482	6.9086	8.5559	1.57E-1	1.54E-14	26.8777	up
			4	6			
RTEL1-TNFRSF6B	1.2504	6.21666	11.4425	5.52E-2	2.53E-24	50.481	up
	3			7			
GNG4	1.2548	8.64401	4.6104	5.15E-0	5.21E-05	3.40948	up
	5		7	6			
KCNT1	1.2678	3.6989	7.4525	4.28E-1	2.22E-11	19.1565	up
	2		2	3			
KIFC2	1.271	9.1292	11.5068	3.08E-2	1.49E-24	51.0546	up
				7			
CPT1B	1.2736	3.54811	11.7113	4.75E-2	2.78E-25	52.8902	up
				8			
F7	1.2738	4.14647	5.8753	7.88E-0	1.72E-07	9.62638	up
	7		2	9			

PILRB	1.2779 6	6.81708	9.4636 5	1.32E-1 9	2.12E-17	33.809	up
HSF4	1.2819 7	8.04113	11.4011	8.03E-2 7	3.59E-24	50.1125	up
NPIPB5	1.2827 3	6.42651	11.6171	1.13E-2 7	5.97E-25	52.0428	up
KRTAP5-1	1.2851 3	5.45041	10.153 8	4.43E-2 2	1.03E-19	39.3963	up
ANO9	1.2927	11.7591	10.916 1	6.12E-2 5	2.36E-22	45.8565	up
DHPS	1.3035 5	6.1512	13.723 7	2.06E-3 6	5.82E-33	71.8199	up
STX16-NPEPL1	1.3397 5	3.9931	9.8763 5	4.51E-2 1	9.34E-19	37.1188	up
NPIPB15	1.3703 5	5.50268	5.7508 8	1.58E-0 8	3.17E-07	8.95613	up
CDK5RAP3	1.4054 3	7.83496	14.494 3	9.05E-4 0	3.84E-36	79.4216	up
R3HDML	1.4152 3	4.93743	7.7475 9	5.59E-1 4	3.43E-12	21.141	up
LIME1	1.4250 7	5.83664	12.293	2.12E-3 0	1.90E-27	58.2066	up
SAPCD1	1.4385 1	3.89132	12.479 6	3.64E-3 1	4.11E-28	59.9414	up
PABPC1L	1.5157 7	9.35013	12.020 1	2.73E-2 9	1.95E-26	55.6955	up
CYP2W1	1.5167	8.36515	5.3930 4	1.09E-0 7	1.75E-06	7.09876	up
LCN12	1.5290	6.51724	11.6324	9.80E-2	5.36E-25	52.1794	up

	9			8			
CPNE7	1.5539	9.27671	10.651	6.23E-2	2.07E-21	43.5793	up
	5		2	4			

Supplementary Table 3 Gene set variation analysis of HDAC10-high and low groups in TCGA cohort

id	H D A C 1 0	AN GI OG EN ESI S	A P O P T O SI S	CO MP LE M EN T	H Y P O X I A	IL2_ STA T5_S IGN ALI NG	INFL AMM ATOR Y_RE SPON SE	INTER FERON _GAM MA_RE SPONS E	PI3K_ AKT_ MTOR _SIGN _SIGN ALIN G	TNFA _SIGN ALIN G_VI A_NF KB	WNT_ BETA_ CATEN IN_SIG NALIN G
TCGA-3L-AA 1B-01A -11R-A 37K-07	hi g h	0.4 351 4	-0. 66 64 4	-0. 499 5	0. 0 1 6 9 7	-0.20 1	-0.504 6	0.45922	0.9595	-0.590 4	0.71075 2227
TCGA-4N-A93 T-01A- 11R-A3 7K-07	hi g h	0.5 566 5	-0. 60 21 9	-0. 646 4	-0 .5 5 8 5	-0.29 8	-0.590 9	-0.7723	0.9595	-0.965	-0.1474 58139
TCGA-4T-AA8 H-01A-	hi g h	-0.4 33	-0. 21 43	-0. 560 9	-0 .0 0	-0.14 79	-0.598 1	-0.3629	0.9452 7	-0.287 3	-0.0594 13126

11R-A4			2		7						
1B-07					5						
TCGA-5M-AA	hi	-0.6	-0.	-0.	-0	-0.32	-0.725	-0.827	0.3059	-0.736	-0.2301
T4-01A	g	836	56	592	.4	96	6		7	6	75904
-11R-A	h		43	3	5						
41B-07			2		9						
					5						
TCGA-5M-AA	hi	0.7	-0.	-0.	-0	-0.51	-0.632	-0.6738	0.1866	-0.739	0.31517
T5-01A	g	022	68	630	.6	79	6		4	3	8333
-21R-A	h	4	54	9	1						
41B-07			9		5						
					4						
TCGA-5M-AA	lo	-0.9	0.	0.4	-0	0.530	0.7178	-0.6596	-0.1648	0.4879	-0.2007
T6-01A	w	398	33	883	.1	94	8			5	91691
-11R-A			36	8	6						
41B-07			54		0						
					7						
TCGA-5M-AA	hi	-0.2	-0.	-0.	-0	-0.51	-0.562	-0.4505	0.3760	-0.686	-0.5656
TA-01A	g	786	67	593	.4	08	2		3	2	55664
-31R-A	h		06	2	8						
41B-07			8		9						
					1						
TCGA-5M-AA	hi	-0.0	-0.	-0.	-0	-0.30	-0.522	-0.5928	0.9474	-0.728	0.81751
TE-01A	g	64	74	622	.4	52	9		5	7	0081
-11R-A	h		79	4	1						
41B-07			5		3						
					6						
TCGA-A6-267	hi	0.0	0.	0.3	-0	0.144	-0.340	-0.6913	-0.2874	-0.390	0.07956
	g	837	45	333	.5	47	4			9	8781

1-01A-01R-1410-07	h	4	3637	4	262						
TCGA-A6-2672-01A-01R-0826-07	hi g h	-0.9562	0.273852	0.4164	0.00168	-0.2484	0.52741	0.20525	0.96497	0.88609	-0.713658804
TCGA-A6-2672-01B-03R-2302-07	lo w	-0.7997	0.150137	0.30678	0.054589	0.15774	0.37231	0.10673	0.83142	0.59748	-0.559713381
TCGA-A6-2674-01A-02R-0821-07	hi g h	0.23153	0.447922	0.58983	0.052765	0.3597	0.60657	0.40996	0.68911	0.74042	-0.593850538
TCGA-A6-2674-01A-02R-A278-07	lo w	0.43842	0.489152	0.3856	0.0513	0.32053	0.65528	0.45594	0.36836	0.76423	-0.41195831
TCGA-A6-2674-01B-0	hi g h	0.32129	0.4188	0.5489	0.040	0.46682	0.58201	-0.0126	0.44171	0.71032	-0.469613222

4R-A27 7-07			47		3 5 8						
TCGA-A6-267 5-01A-02R-17 23-07	low	0.0 760 8	0. 52 49 32	0.4 355 6	0. 6 4 5 3 9	0.541 98	0.6101	0.85003	-0.1045	-0.454 4	-0.3901 39796
TCGA-A6-267 6-01A-01R-08 26-07	high	0.1 559 9	-0. 26 91 5	0.4 649 3	0. 3 2 8 7 6	-0.04 17	0.5139 9	0.07389	0.3541 3	0.7683 5	-0.6480 32659
TCGA-A6-267 7-01A-01R-08 21-07	low	0.4 252 9	0. 40 98 41	-0. 180 3	0. 7 8 9 4 7	-0.15 22	-0.464 3	0.0509	-0.6606	-0.873 5	0.16999 186
TCGA-A6-267 7-01A-01R-A2 78-07	low	-0.3 585	0. 59 33 43	0.1 792 8	0. 6 0 3 8 3	-0.27 4	-0.141 1	-0.0936	-0.2852	-0.608 7	0.04676 2972
TCGA-A6-267	high	-0.4 154	0. 19	0.3 408	0. 4	0.439 88	0.4055	0.68363	0.1505 2	-0.451 8	-0.2677 54225

7-01B-0 2R-A27 7-07	h		98 43	9	9 5 7 6						
TCGA-A6-267 8-01A-01R-08 21-07	low	0.8 248 5	0. 19 32 25	0.2 719 4	0. 2 3 0 9 8	0.210 69	0.4668 1	-0.0695	-0.0575	0.1795 2	-0.2079 29725
TCGA-A6-267 9-01A-02R-14 10-07	high	0.3 946 4	0. 39 65 47	-0. 323 7	0. 3 1 9 1	-0.37 64	-0.586 9	-0.8807	-0.2447	-0.085 5	-0.2439 26795
TCGA-A6-268 0-01A-01R-14 10-07	high	-0.3 662	-0. 15 33 4	0.1 559 4	0. 2 2 7 3 9	-0.46 12	-0.519 2	-0.26	-0.1056	-0.667	0.45240 3678
TCGA-A6-268 1-01A-01R-14 10-07	low	0.2 391 9	-0. 58 35 4	0.1 381 2	0. 1 9 9 4 8	-0.02 7	0.0584 9	-0.7723	-0.9475	0.1993 4	-0.0475 28844
TCGA-A6-268	low	0.9 638	0. 10	0.5 515	0. 2	0.337	-0.008 8	0.00055	0.6913	0.8247 5	0.01151 9473

2-01A- 01R-14 10-07		8	95 89	5	9 8 8 2						
TCGA- A6-268 3-01A- 01R-08 21-07	hi g h	-0.4 647	-0. 06 65 9	-0. 590 3	-0 .5 7 8 8	-0.15 23	-0.821 1	-0.9015	0.7909 1	-0.748 6	0.01661 8623
TCGA- A6-268 4-01A- 01R-14 10-07	hi g h	0.5 632 2	0. 65 71 13	0.2 749 7	0. 2 6 8 3 7	0.468 96	-0.034	-0.3191	-0.3355	0.2938 2	0.38553 8698
TCGA- A6-268 4-01A- 01R-A2 78-07	lo w	-0.8 194	0. 58 57 53	0.6 218 6	0. 3 4 1 3 3	0.550 08	0.6574 9	0.82266	-0.0203	0.5943 4	0.19991 266
TCGA- A6-268 4-01C-0 8R-A27 7-07	hi g h	-0.0 848	0. 42 54 6	0.5 945 6	0. 4 3 7 6 4	0.637 31	0.6454 5	0.87411	-0.1177	0.3258 5	-0.1609 70965
TCGA- A6-268	hi g	-0.9 168	0. 52	0.3 110	0. 6	0.345 79	0.4971	0.24247	-0.9869	0.5958 4	0.01738 8778

5-01A-01R-1410-07	h		8219	9	25						
TCGA-A6-2686-01A-01R-A32Z-07	hi g h	-0.1757	-0.25509	0.32778	0.000147	0.17453	0.308	0.73399	0.47455	0.7847	-0.85051149
TCGA-A6-3807-01A-01R-1022-07	hi g h	0.43514	-0.1611	0.03006	-0.1765	-0.0599	0.19141	0.27531	0.81171	0.42735	0.100201196
TCGA-A6-3808-01A-01R-1022-07	lo w	0.41544	0.187407	0.43457	0.05528	0.56024	0.63388	0.82157	-0.2359	0.7207	0.404051106
TCGA-A6-3809-01A-01R-1022-07	lo w	-0.8019	0.815628	0.56073	0.04572	0.24546	0.69047	0.53257	-0.7011	0.87459	-0.578165038
TCGA-A6-3809-01A-	lo w	0.13848	0.7212	0.62348	0.044	0.44294	0.7293	0.86645	-0.1232	0.83242	-0.398772881

01R-A2 78-07			82		2 4 3						
TCGA-A6-380 9-01B-0 4R-A27 7-07	low	-0.2 261	0. 40 81 27	0.6 635 2 1	0. 5 9 1 5 6	0.157 09	0.5975 9	0.64313	0.1308 2	0.6982 5	-0.4215 71979
TCGA-A6-381 0-01A- 01R-10 22-07	low	-0.1 319	0. 28 44 71	0.6 067 5	-0 .0 9 0 6	0.405 74	0.5125 4	0.22058	0.7372 7	0.3969 9	-0.3202 23449
TCGA-A6-381 0-01A- 01R-A2 78-07	low	-0.1 1	0. 59 36 33	0.6 398 3	0. 3 5 2 7 7	0.416 49	0.5757 8	0.37603	-0.029	0.5673 5	-0.3154 98433
TCGA-A6-381 0-01B-0 4R-A27 7-07	low	0.0 782 7	0. 16 93 15	0.4 908 3	0. 7 7 41 1	0.562 22	0.5883 7	0.77449	0.2162	0.0394 3	-0.2656 93176
TCGA-A6-410 5-01A- 02R-17	high	0.9 715 4	0. 30 40 49	0.4 504 5	-0 .0 3 7	0.635 44	0.4953 2	0.54242	0.9824 8	-0.004 4	-0.2342 83029

74-07					3						
TCGA-A6-410	hi	0.6	0.	0.1	-0	0.309	-0.006	0.45047	0.1395	0.2472	-0.1064
7-01A-02R-14	g	015	45	797	.1	92	8		7	2	17992
10-07	h	3	58	7	3						
			9		2						
					6						
TCGA-A6-565	hi	0.0	-0.	-0.	-0	-0.36	-0.725	-0.8818	-0.7022	-0.863	-0.3320
6-01A-21R-18	g	925	55	576	.1	79	1			1	40094
39-07	h		54	1	7						
			7		0						
					7						
TCGA-A6-565	hi	0.1	-0.	-0.	0.	-0.16	-0.271	-0.3541	-0.4012	-0.604	0.13933
6-01A-21R-A2	g	603	30	237	2	76	1			1	0773
78-07	h	7	20	5	9						
			2		6						
					8						
					4						
TCGA-A6-565	lo	0.4	0.	0.5	0.	0.496	0.5682	0.69349	-0.0148	0.0169	-0.3130
6-01B-02R-A27	w	515	24	594	2	36	9			8	27002
7-07		6	14	7	9						
			04		3						
					8						
					6						
TCGA-A6-565	lo	-0.3	-0.	-0.	-0	0.292	-0.372	0.33771	-0.4789	0.0273	0.43813
7-01A-01R-A3	w	125	12	204	.0	6				8	6208
2Z-07			06		7						
			8		5						
					3						
TCGA-	lo	0.5	0.	0.0	-0	0.347	0.0781	0.72414	-0.8435	-0.702	0.56255

A6-565 9-01A- 01R-16 53-07	w	435 1	85 89 94	142 9	.6 7 4 9	06	5			1	0948
TCGA- A6-565 9-01A- 01R-A2 78-07	lo w	0.2 304 3	0. 64 17 31	0.3 481 5	-0 .1 0 6 5	0.214 79	0.5814 6	0.73946	-0.9453	-0.311	0.53857 8583
TCGA- A6-565 9-01B-0 4R-A27 7-07	hi g h	0.3 048 7	0. 15 13 14	0.2 093	0. 7 6 1 8 8	0.539 13	0.3844 9	0.47783	-0.5326	-0.330 8	0.07720 1912
TCGA- A6-566 0-01A- 01R-16 53-07	lo w	0.7 734	0. 84 54 7	0.1 155 9	-0 .8 5 9 3	0.253 86	-0.030 5	0.84346	-0.5249	-0.725 9	0.59641 5889
TCGA- A6-566 1-01A- 01R-16 53-07	lo w	0.5 435 1	0. 48 43 74	0.1 509 2	0. 2 0 2 5 5	-0.23 37	0.6708 1	0.16694	-0.7154	0.7814 9	-0.5372 18793
TCGA- A6-566 1-01B-0	lo w	-0.3 355	0. 06 32	0.5 635	0. 7 5	0.380 84	0.6480 6	0.58511	-0.2348	0.6538 9	-0.4987 78898

5R-230 2-07			23								
TCGA-A6-566 2-01A- 01R-16 53-07	low	0.2 742 2	-0. 27 01 4	-0. 120 8	-0 .7 0 7 3	0.293 89	-0.055 2	0.13957	-0.2863	-0.6117	0.52264 0873
TCGA-A6-566 4-01A- 21R-18 39-07	low	0.8 949 1	0. 26 56 24	0.7 024 5	-0 .1 1 9 6	0.413 54	0.6998 7	0.80405	-0.6869	0.6894 9	0.66877 0455
TCGA-A6-566 5-01A- 01R-16 53-07	low	0.0 125 9	0. 10 09 46	-0. 290 8	-0 .2 7 3 9	-0.28 76	0.2125 5	-0.4713	-0.7395	0.7048 2	-0.7286 1469
TCGA-A6-566 5-01B-0 3R-230 2-07	high	-0.3 64	-0. 38 54 8	0.3 046 4	0. 6 0 21 1	0.335 11	0.5673 2	0.44171	-0.2611	0.5268 3	-0.4120 48394
TCGA-A6-566 6-01A- 01R-16 53-07	low	0.9 660 6	-0. 24 57 1	-0. 197	-0 .6 3 9 6	-0.26 88	-0.136 4	-0.8008	0.5840 2	0.5580 5	0.46011 9384
TCGA-A6-566	low	0.7 307	0. 84	-0. 318	-0 .7	0.163 63	-0.253 9	-0.2994	-0.2414	-0.762 1	-0.1633 69736

7-01A- 21R-17 23-07		1	49 96	8	0 8 1						
TCGA- A6-613 7-01A-1 1R-177 4-07	lo w	-0.8 522	0. 05 45 03	0.0 547 6	-0 .1 5 8 5	-0.03 15	-0.301 1	0.57526	-0.5194	-0.522 5	0.57850 0953
TCGA- A6-613 8-01A-1 1R-177 4-07	lo w	-0.9 715	0. 39 83 95	0.7 345 8	-0 .6 4 7 4	-0.11 18	0.6762 9	0.69787	-0.9442	0.6985 3	0.28636 6478
TCGA- A6-614 0-01A-1 1R-177 4-07	hi g h	-0.3 038	0. 48 27 82	-0. 190 8	-0 .2 8 4 3	-0.03 15	-0.604 8	-0.4647	-0.9891	-0.718 4	0.61492 0461
TCGA- A6-614 1-01A-1 1R-177 4-07	lo w	0.3 628 9	-0. 45 16 8	-0. 196 2	0. 1 5 4 0 4	-0.13 83	-0.183 3	-0.5523	0.9266 6	-0.053 7	0.16630 5828
TCGA- A6-614 2-01A-1 1R-177 4-07	lo w	0.2 862 6	0. 57 36 19	0.4 042 8	-0 .4 8 2 9	0.178 95	0.1990 4	-0.2458	-0.5731	0.6541 2	0.77806 8632

TCGA-A6-664-8-01A-1-1R-177-4-07	hi	0.6 310 9	-0. 61 98 3	-0. 441 1	-0 .3 2 7	-0.25 82	-0.079	0.69787	-0.3793	-0.800 7	0.18435 1399
TCGA-A6-664-9-01A-1-1R-177-4-07	hi	-0.4 724	-0. 70 30 8	-0. 001 3	0. 6 8 9 9 9	-0.01 57	0.1469 6	0.93651	0.5905 9	0.1886 9	-0.5703 8479
TCGA-A6-665-0-01A-1-1R-177-4-07	lo	-0.9 07	-0. 36 56 8	-0. 623 7	-0 .3 4 6	-0.27 54	-0.451	-0.2074	-0.48	-0.895 4	-0.3833 92021
TCGA-A6-665-0-01A-1-1R-A27-8-07	lo	-0.7 701	-0. 47 20 2	-0. 392 6	0. 1 9 2 2 6	-0.57 75	-0.235 9	-0.1067	-0.9475	-0.762 9	-0.4622 93858
TCGA-A6-665-0-01B-0-2R-A27-7-07	lo	-0.6 278	0. 08 76 71	0.2 108 9	0. 5 8 3 6 5	0.102 63	0.2630 2	0.65627	0.4548 4	-0.31	-0.4117 45027
TCGA-	lo	0.2	0.	0.6	0.	0.621	0.6482	0.54242	0.0618	-0.002	0.16467

A6-665 1-01A- 21R-18 39-07	w	950 2	16 46 79	799 8	2 8 3 3 5	66	9		5	2	6652
TCGA- A6-665 2-01A-1 1R-177 4-07	hi g h	-0.3 618	-0. 49 91	-0. 351 8	-0 .6 8 0 3	-0.46 32	-0.477 1	-0.549	0.5446 1	-0.949 6	0.54373 4275
TCGA- A6-665 3-01A-1 1R-177 4-07	lo w	-0.2 567	-0. 61 02 2	0.0 732 1	-0 .0 4 2 9	-0.31 99	0.5363 7	0.09031	0.6956 8	0.8346 1	-0.3082 46444
TCGA- A6-665 4-01A- 21R-18 39-07	lo w	0.0 027 4	-0. 01 89 7	0.5 692 2	0. 4 5 6 1 8	0.609 2	0.8260 8	0.80405	-0.4209	0.7852 7	0.30938 4145
TCGA- A6-678 0-01A-1 1R-183 9-07	hi g h	0.8 325 1	0. 80 98 63	0.3 151 1	0. 4 7 8 6 2	-0.26 91	0.6016 4	-0.3826	0.2183 9	0.4587 8	-0.7886 91554
TCGA- A6-678	hi g	0.7 547	0. 67	0.5 836	0. 6	0.296 06	0.7827 7	0.73071	-0.3826	0.9023 2	-0.4537 28483

0-01A-1 1R-A27 8-07	h	9	72 6	3	1 8 4 1						
TCGA-A6-678 0-01B-0 4R-A27 7-07	lo w	0.1 581 8	0. 53 76 63	0.7 361 6 8 8	0. 6 8 8 6 4	0.440 23	0.7323 8	0.78654	0.0191 6	0.7710 8	-0.4673 61492
TCGA-A6-678 1-01A- 22R-19 28-07	lo w	-0.9 683	-0. 10 37 2	0.6 136 7 5	0. 3 2 5 5 8	0.622 86	0.7491	0.33552	0.1045 4	0.7908	-0.4373 97954
TCGA-A6-678 1-01A- 22R-A2 78-07	lo w	-0.9 267	-0. 10 10 9	0.7 033 5 6	0. 5 1 6 5 5	0.391 93	0.8342 9	0.6289	-0.2501	0.7847 8	-0.5543 21091
TCGA-A6-678 1-01B-0 6R-A27 7-07	lo w	-0.6 201	0. 07 90 06	0.6 624 7 2	0. 5 6 2 5	0.570 53	0.6815	0.64313	0.5249	0.7311 1	-0.5194 71881
TCGA-A6-678	hi g	-0.6 366	0. 45	0.1 139	0. 3	0.535 1	0.2712 8	-0.5884	0.1921 2	-0.769 5	0.41439 0887

2-01A-1 1R-183 9-07	h		05 8	2	1 5 8 4						
TCGA- A6-A56 5-01A- 31R-A2 8H-07	hi g h	-0.9 496	0. 25 11 16	0.1 301 3 4	0. 6 5 4 0 6	0.388 48	0.3711 6	0.80186	-0.1538	0.3582 8	-0.6304 89762
TCGA- A6-A56 6-01A-1 1R-A28 H-07	lo w	0.6 978 7	0. 68 21 92	0.5 601 4	0. 0 2 7 7 6	0.432 73	0.7826 1	0.54461	0.3453 7	0.7765 7	-0.6343 46076
TCGA- A6-A56 7-01A- 31R-A2 8H-07	lo w	0.5 785 4	0. 01 50 84	-0. 07	-0 .0 5 7 4	0.192 06	-0.183 4	-0.0181	0.6190 5	-0.693 1	0.80429 7989
TCGA- A6-A56 B-01A- 31R-A2 8H-07	lo w	-0.6 683	-0. 43 16 2	-0. 582 4	-0 .4 4 6	0.015 81	-0.179	-0.5435	-0.5402	-0.806 7	0.11958 3105
TCGA- A6-A5 ZU-01	lo w	-0.1 33	-0. 07 12	0.3 708 9	-0 .0 7	0.392 95	0.3854 2	-0.4231	0.1275 3	-0.406 1	0.69125 0738

A-11R-A28H-07			3		4						
TCGA-AA-348-9-01A-21R-1839-07	hi g h	-0.8 993	0. 57 81 6	0.6 212 7	0. 2 2 0 7 1	0.360 01	0.5320 7	0.4647	-0.2348	0.1021 7	0.32635 5411
TCGA-AA-349-2-01A-01R-1410-07	lo w	0.6 442 3	0. 42 84 93	0.0 793 3	-0 .1 9 6 2	-0.12 22	0.3087 7	-0.1472	-0.1856	0.6073 1	-0.5516 45152
TCGA-AA-349-4-01A-01R-1410-07	hi g h	0.7 405 6	-0. 26 38 7	-0. 232 4	-0 .4 9 5 2	-0.15 49	-0.438 4	-0.5326	-0.0323	-0.752 8	0.60546 2256
TCGA-AA-349-5-01A-01R-1410-07	hi g h	0.7 088 1	0. 42 13 7	0.5 645 3	0. 7 2 8 1 6	0.055 62	0.1087 1	0.6289	-0.8774	-0.500 9	-0.5125 31187
TCGA-AA-349-6-01A-21R-18	hi g h	-0.5 271	0. 11 31 44	0.1 001	-0 .2 0 1	0.100 6	-0.041 7	0.27531	0.4679 8	-0.654 2	0.68582 0077

39-07					2						
TCGA-AA-350-2-01A-01R-14-10-07	low	0.97154	0.706849	-0.1144	0.5788	0.3487	-0.3986	-0.2184	0.86645	0.70777	-0.330058036
TCGA-AA-350-6-01A-01R-14-10-07	low	0.88506	0.329609	0.2698	0.1181	-0.1588	-0.2551	-0.4483	-0.7219	0.1842	0.077806022
TCGA-AA-350-9-01A-01R-14-10-07	low	-0.0334	-0.04986	0.4787	-0.2008	0.45048	0.31823	0.46907	-0.6223	-0.0739	0.564922224
TCGA-AA-351-0-01A-01R-14-10-07	high	0.87849	0.703014	-0.0734	0.08907	0.03905	0.08524	-0.1418	0.61905	-0.016	0.080432747
TCGA-AA-351-1-01A-21R-18-39-07	low	-0.1286	-0.32812	0.00234	-0.6045	-0.0885	-0.1434	0.75479	0.68801	-0.6156	-0.259351634
TCGA-	high	0.8	0.	-0.1	-0	-0.32	-0.574	-0.7241	0.5763	-0.665	0.37447

AA-351 4-01A- 02R-08 21-07	g h	653 5	12 45 8	13	.4 2 7 5	96	1		5	9	2831
TCGA- AA-351 6-01A- 02R-08 26-07	lo w	-0.2 162	0. 64 44 43	0.0 261	0. 1 2 5 4 2	0.353 02	0.692	0.02244	0.3289 5	0.8242 1	-0.5710 36753
TCGA- AA-351 7-01A- 01R-08 21-07	hi g h	-0.1 812	-0. 38 33 6	-0. 097 6	0. 0 8 5 9 4	-0.38 93	-0.478 4	-0.6355	0.8336 1	-0.763 4	-0.2603 86121
TCGA- AA-351 8-01A- 02R-08 26-07	hi g h	-0.3 848	4. 01 E- 05	-0. 008 6	0. 4 9 0 8 9	-0.02 64	0.2151 7	-0.1626	0.6934 9	0.5777 7	-0.8416 56455
TCGA- AA-351 9-01A- 02R-08 21-07	hi g h	0.7 022 4	0. 00 49 32	0.3 218	0. 2 8 2 2	-0.22 37	-0.128	0.35632	-0.827	-0.094 2	0.03019 2457
TCGA- AA-352	lo w	0.0 257	0. 31	0.2 976	0. 4	0.194 14	0.5054 8	0.83799	-0.5424	0.5229 1	-0.6396 3386

0-01A- 01R-08 21-07		3	26 87	1	5 8 4 6						
TCGA- AA-352 1-01A- 01R-08 21-07	hi g h	-0.7 559	-0. 37 74 4	0.1 57	0. 3 1 9 2 7	-0.00 65	-0.118 3	0.16366	0.9671 6	-0.037 8	0.11690 2499
TCGA- AA-352 2-01A- 01R-08 21-07	lo w	0.2 654 6	0. 70 79 45	0.2 349 5	0. 4 1 7 5 2	0.318 7	0.5435 4	0.62562	-0.7734	0.6161	0.16471 7733
TCGA- AA-352 4-01A- 02R-08 21-07	lo w	-0.2 14	0. 44 72 67	0.6 367 4	0. 1 6 1 7 8	0.105 64	0.1602 9	0.32567	-0.0498	0.5701	-0.3224 76535
TCGA- AA-352 5-01A- 02R-08 26-07	hi g h	0.7 788 7	0. 69 51 51	-0. 217	0. 3 8 3 6 1	-0.10 41	0.3591 3	0.62233	0.7777 8	0.6785 3	-0.6489 74337
TCGA-	hi	0.1	-0.	-0.	-0	-0.06	0.3206	0.83142	0.8128	0.6182	-0.3645

AA-352	g	899	25	063	.4	46	2		1	3	19077
6-01A-	h	3	33	9	6						
02R-A3			7		4						
2Z-07					6						
TCGA-	hi	0.1	0.	0.1	-0	-0.47	-0.415	-0.988	0.7000	-0.452	0.40439
AA-352	g	122	64	436	.2	12	7		5	9	8507
7-01A-	h	1	10		3						
01R-08			07		1						
21-07					9						
TCGA-	lo	0.2	0.	-0.	-0	0.078	-0.384	0.04215	-0.6037	-0.572	-0.0556
AA-352	w	468	38	475	.0	18	8			8	67077
9-01A-		5	39	9	7						
02R-08			47		2						
21-07					2						
TCGA-	hi	-0.1	0.	-0.	0.	0.308	-0.375	0.63437	0.6365	-0.562	-0.4073
AA-353	g	516	57	019	4	27			6	4	18051
0-01A-	h		64	4	5						
01R-10			38		0						
22-07					9						
					2						
TCGA-	hi	-0.2	0.	-0.	-0	-0.33	-0.771	-0.931	0.8084	-0.813	0.21302
AA-353	g	885	01	251	.6	07	6		3	8	3556
1-01A-	h		55	9	5						
01R-08			07		2						
21-07					3						
TCGA-	lo	-0.7	-0.	0.3	0.	0.479	0.4829	0.90038	-0.4034	0.1079	-0.2635
AA-353	w	165	06	159	1	22	1			4	75523
2-01A-			37	8	7						
01R-08			1		91						

21-07					1						
TCGA-AA-353-4-01A-01R-08-21-07	low	0.99015	-0.61628	0.58133	0.00997	-0.05079	-0.0639	0.39573	0.87739	-0.603	0.417092586
TCGA-AA-353-8-01A-01R-08-21-07	low	0.39792	0.18411	0.52063	0.02330	-0.1879	0.21955	0.25123	-0.9781	0.08531	0.501407141
TCGA-AA-354-2-01A-02R-18-73-07	high	0.3607	-0.06971	-0.2586	-0.40419	-0.43	-0.7313	-0.4997	0.40339	-0.845	-0.289268036
TCGA-AA-354-3-01A-01R-08-26-07	high	-0.0104	0.516981	-0.2175	-0.404	-0.282	0.3208	-0.052	-0.1056	0.42935	-0.646261107
TCGA-AA-354-4-01A-01R-18-73-07	high	-0.8643	-0.2153	0.60721	-0.40921	-0.6408	0.17006	0.24028	-0.3103	0.69171	0.619220875
TCGA-	high	0.2	-0.	-0.	-0	0.100	-0.562	-0.3979	0.4515	-0.203	-0.3887

AA-354 8-01A- 01R-18 73-07	g h	446 6	02 23	594 9	.2 7 4 9	72			6	7	72563
TCGA- AA-354 9-01A- 02R-08 21-07	hi g h	0.2 413 8	0. 37 03 65	0.1 837 4	0. 6 2 2 9 1	-0.68 28	-0.382 7	-0.6694	-0.2764	0.1546 4	-0.3822 43456
TCGA- AA-355 2-01A- 01R-08 21-07	hi g h	-0.1 527	0. 78 17 73	-0. 226 6	-0 .0 2 6 8	-0.45 69	-0.355 8	-0.2983	-0.7942	-0.724 5	0.06713 6654
TCGA- AA-355 3-01A- 01R-08 21-07	hi g h	-0.0 805	-0. 12 05 5	0.3 513 6	-0 .0 9 7 6	-0.26 33	-0.155 6	0.31801	0.0224 4	0.297	0.47638 4321
TCGA- AA-355 4-01A- 01R-08 26-07	lo w	-0.7 395	0. 08 80 29	0.3 947 7	0. 7 9 9 5	0.214 48	0.6095 8	0.69787	-0.9496	0.7924 4	-0.2953 15779
TCGA- AA-355 5-01A-	lo w	-0.7 537	0. 07 14	0.4 844 1	0. 0 1	0.475 88	0.5471 8	0.03229	0.5303 8	0.8970 4	-0.1691 41359

01R-08 21-07			31		9 7 6						
TCGA-AA-355 6-01A- 01R-08 21-07	low	0.4 296 7	0. 67 54 25	0.4 436 6	0. 1 9 9 8 1	0.284 52	0.5684 9	0.72195	0.2315 3	0.4578 3	0.55470 0933
TCGA-AA-356 0-01A- 01R-08 21-07	low	0.0 541 9	0. 64 16 44	0.5 648 9	0. 3 7 4 9	0.007 15	0.1260 8	0.22386	-0.3465	0.4435 9	0.10472 9299
TCGA-AA-356 1-01A- 01R-08 21-07	low	0.1 494 3	-0. 29 06 8	0.2 104 2	0. 3 0 6 1 6	0.111 99	-0.109 6	0.65298	0.7515 1	0.4018 3	-0.6820 52716
TCGA-AA-356 2-01A- 02R-08 21-07	high	0.4 012	0. 82 56 22	-0. 340 8	-0 .0 6 9 4	-0.22 18	-0.149	0.38478	-0.7887	-0.785 7	0.24031 6356
TCGA-AA-365 5-01A- 02R-17	low	-0.2 677	-0. 05 99 6	0.3 108 3	-0 .1 7 5	-0.12 66	0.4146 9	-0.5939	-0.341	0.1487 7	-0.5198 05209

23-07					5						
TCGA-AA-366-0-01A-01R-17-23-07	hi g h	-0.1 604	0. 63 20 1	-0. 068 7	-0 .5 7 0 2	-0.00 31	-0.158 3	0.60153	-0.7307	-0.841 7	0.78345 1978
TCGA-AA-366-2-01A-01R-17-23-07	hi g h	-0.3 114	-0. 46 30 1	0.4 559 6	-0 .3 3 5 8	-0.23 27	-0.359 9	0.35523	0.7701 1	-0.052	0.63799 568
TCGA-AA-366-3-01A-01R-17-23-07	lo w	0.9 474 5	0. 17 51 41	0.2 042 1	0. 4 1 0 3 8	-0.06 42	0.4970 5	0.59278	-0.8763	0.8975 9	-0.3449 11445
TCGA-AA-366-4-01A-01R-09-05-07	hi g h	-0.9 65	-0. 00 87 7	0.0 197 9	-0 .3 1 5 3	-0.14 36	0.0766 8	-0.0629	0.3399	0.7367 2	-0.5312 06261
TCGA-AA-366-6-01A-02R-09-05-07	lo w	-0.4 986	0. 39 18 55	0.5 499 6	0. 1 2 7 0 9	-0.47 57	0.4175 1	0.63218	-0.884	0.5854 3	-0.4918 31656
TCGA-	hi	0.1	-0.	-0.	-0	-0.61	-0.748	-0.8971	0.6376	-0.573	0.08612

AA-366	g	505	11	018	.1	88	1		6	9	1777
7-01A-	h	2	93	6	2						
01R-09			6		6						
05-07					8						
TCGA-	lo	0.9	0.	0.3	-0	0.003	-0.112	-0.5172	0.6113	0.6095	-0.5270
AA-367	w	846	59	609	.0	03	2		8	3	85686
2-01A-		7	52	7	8						
01R-09			78		4						
05-07					8						
TCGA-	hi	0.9	0.	-0.	-0	-0.31	-0.270	-0.3443	0.7963	-0.551	0.72066
AA-367	g	934	16	220	.2	3	9		9	2	4039
3-01A-	h	3	38	7	5						
01R-09			88		0						
05-07					1						
TCGA-	lo	0.6	-0.	0.2	-0	0.222	0.0490	0.27313	-0.272	0.2431	0.66872
AA-367	w	628	02	870	.3	8	9			5	4171
5-01A-		4	94	5	9						
02R-09			2		6						
05-07					7						
TCGA-	hi	0.1	-0.	0.4	-0	-0.28	-0.590	0.28517	-0.9858	-0.456	0.28126
AA-367	g	242	40	049	.4	19	1			7	3731
8-01A-	h	5	21	7	3						
01R-09			9		3						
05-07					9						
TCGA-	lo	0.7	-0.	0.0	-0	-0.54	-0.299	-0.0148	0.6190	-0.784	0.25913
AA-367	w	635	28	393	.6	79	4		5	7	9909
9-01A-		5	87	1	5						
02R-09			6		5						
05-07					5						

TCGA-AA-368-0-01A-01R-09-05-07	low	0.73618	0.42188	0.33425	0.017	0.03168	-0.0165	0.53147	0.80624	0.18952	0.376961417
TCGA-AA-368-1-01A-01R-09-05-07	low	0.87083	0.604795	0.38013	0.040866	0.20893	0.45827	0.64094	-0.3563	0.62541	0.397632589
TCGA-AA-368-4-01A-02R-09-05-07	high	0.99453	0.348493	0.22118	0.062966	-0.253	-0.3078	-0.4943	0.20744	0.2509	-0.02880896
TCGA-AA-368-5-01A-02R-A3-2Z-07	low	0.17789	0.246575	0.39674	-0.034	0.03326	0.13083	0.89381	-0.5003	0.27318	-0.300212881
TCGA-AA-368-8-01A-01R-09-05-07	high	0.63547	0.660699	-0.0753	0.0148222	-0.4089	-0.5446	0.10783	0.14286	-0.7585	0.655947791

TCGA-AA-369-2-01A-01R-09-05-07	hi g h	0.0 312	0. 66 75 03	0.3 328	0. 0 6 5 4 5	-0.19 88	0.1696 3	0.65298	0.8916 3	0.7614	-0.1995 97023
TCGA-AA-369-3-01A-01R-09-05-07	hi g h	0.6 015 3	0. 27 61 64	0.1 598 6	0. 0 3 3 4 9	-0.09 86	-0.257	0.44828	-0.9573	-0.759 6	0.34253 5377
TCGA-AA-369-5-01A-01R-09-05-07	hi g h	0.9 671 6	0. 14 28 35	-0. 194 7	0. 5 5 3 3 1	-0.10 56	-0.654 8	-0.9179	-0.5961	0.6519 4	-0.4318 94489
TCGA-AA-369-6-01A-01R-09-05-07	lo w	0.9 573 1	0. 36 06 33	0.3 383 9	0. 4 9 3 2 7	-0.15	0.1164 2	-0.0181	0.5807 3	-0.867 6	0.46674 4768
TCGA-AA-369-7-01A-01R-17-23-07	hi g h	0.2 796 9	-0. 32 75 1	0.1 223 3	0. 0 9 0 8	-0.51 55	-0.411 1	0.64094	0.0071 2	-0.699 3	0.19363 6862

					5						
TCGA-AA-371-0-01A-01R-10-22-07	low	0.70334	0.137336	0.43636	0.54721	0.43204	0.63856	0.95074	0.13191	0.8943	-0.759139036
TCGA-AA-371-2-01A-21R-17-23-07	high	-0.7767	-0.15123	-0.1434	-0.1344	-0.3576	0.03249	-0.3268	-0.9551	-0.6643	0.04940687
TCGA-AA-371-3-01A-21R-17-23-07	low	-0.9288	0.269892	-0.10743	0.51418	-0.0467	0.42218	0.73399	-0.214	0.94166	-0.451883222
TCGA-AA-371-5-01A-01R-09-05-07	high	0.43186	0.27221	0.29528	0.614	0.30904	0.17972	-0.5873	0.44499	0.71742	-0.643993644
TCGA-AA-381-1-01A-01R-10-22-07	high	-0.0279	-0.00974	-0.1388	0.5331	-0.0193	0.22676	0.76136	0.22496	0.65944	-0.590801251

					3						
TCGA-AA-381-2-01A-01R-09-05-07	low	0.91571	0.383641	0.31154	0.51658	0.13079	-0.208	-0.4691	0.86207	-0.1073	0.004576413
TCGA-AA-381-4-01A-01R-09-05-07	low	0.28517	0.089315	0.38165	0.63437	0.4712	0.51226	0.80077	0.86316	0.51066	-0.217397621
TCGA-AA-381-5-01A-01R-10-22-07	low	0.3343	0.419381	0.34145	-0.5532	-0.0202	0.5158	-0.0717	-0.0301	0.5931	-0.467910038
TCGA-AA-381-8-01A-01R-09-05-07	high	0.4428	-0.27547	-0.088	-0.1189	-0.055	0.03236	-0.1943	-0.2709	0.12293	0.234397494
TCGA-AA-381-9-01A-01R-09-05-07	high	-0.5446	-0.42702	-0.0621	-0.193	-0.3327	-0.6081	0.48987	0.1133	-0.592	-0.085573231
TCGA-AA-381	high	0.3	-0.	-0.	0.	-0.13	0.5115	-0.0213	0.9124	0.3592	-0.6946

AA-382 1-01A- 01R-10 22-07	g h	650 8	46 8	264 5	4 9 6 2 6	45 9	8 1		2	6	51364
TCGA- AA-383 1-01A- 01R-09 05-07	hi g h	0.1 658 5	0. 65 38 83	-0. 415 5	-0 .1 6 5 1	0.135 42	-0.380 1	0.02463	-0.1297	-0.613 9	-0.1721 55651
TCGA- AA-383 3-01A- 01R-09 05-07	lo w	0.5 270 9	0. 52 94 1	0.3 245 7	0. 5 3 1 6 3	0.192 95	0.5831 5	0.81062	0.3158 2	0.8444 7	-0.4839 9591
TCGA- AA-383 7-01A- 01R-09 05-07	lo w	-0.3 257	0. 79 24 98	0.1 092 5	0. 4 7 0 1 6	-0.12 51	0.1161 5	-0.3191	0.8763	0.0336 8	-0.0786 75578
TCGA- AA-384 1-01A- 01R-09 05-07	hi g h	0.4 668 9	0. 55 51 72	0.2 069 6	-0 .3 8 9	-0.38 11	-0.561 4	-0.7723	-0.2556	-0.498 9	-0.0715 72492
TCGA- AA-384	lo w	-0.6 672	0. 18	0.2 316	-0 .1	-0.10 4	0.4846 4	0.5249	-0.5172	0.6966	-0.5541 48314

2-01A-01R-10 22-07			14 95	5	5 7 3						
TCGA-AA-384 4-01A-01R-10 22-07	hi g h	-0.9 628	0. 72 93 15	-0. 137 1	-0 .0 4 3 5	0.102 7	-0.055 7	0.25233	0.3388 1	0.2475 4	0.22633 6911
TCGA-AA-384 5-01A-01R-10 22-07	lo w	-0.3 158	0. 54 41 19	0.5 699 7	0. 6 7 2 1 5	0.533 54	0.6800 7	0.85441	0.6869 2	0.9058 1	-0.3550 81682
TCGA-AA-384 6-01A-01R-10 22-07	hi g h	-0.7 843	0. 36 38 36	0.2 334 6	0. 1 0 0 4	0.236 11	0.2235 7	0.62999	0.7504 1	0.1645 4	0.58529 5328
TCGA-AA-384 8-01A-01R-09 05-07	hi g h	0.7 186 6	0. 00 76 3	-0. 508 9	0. 2 2 4 2 3	-0.36 4	-0.686 5	-0.9387	-0.1494	-0.906 4	0.11417 6146
TCGA-AA-385 0-01A-	lo w	0.9 025 7	0. 68 61	0.5 041 6	0. 2 91	0.361 46	0.3090 5	0.56103	-0.4603	0.0323 1	0.37072 6399

01R-10 22-07			89		1 5						
TCGA-AA-385 1-01A- 01R-10 22-07	low	0.8 160 9	-0. 23 96	-0. 066	0. 4 5 7 1 2	-0.07 15	0.4754 4	0.72523	-0.0115	-0.097 1	-0.0813 36837
TCGA-AA-385 2-01A- 01R-09 05-07	low	0.0 213 5	-0. 35 10 9	0.4 094	0. 6 6 51 1	0.230 8	0.2422 7	0.40011	0.5030 1	0.6144 6	-0.2298 97314
TCGA-AA-385 4-01A- 01R-09 05-07	low	-0.9 267	0. 30 54 7	-0. 163 6	0. 0 1 6 9 2	-0.16 83	0.2086 9	0.68801	-0.884	0.4996 7	-0.0786 17234
TCGA-AA-385 5-01A- 01R-10 22-07	high	0.8 062 4	0. 30 09 36	0.1 653 9	-0 .1 7 0 2	-0.35 9	-0.669 2	0.74603	0.3694 6	-0.495 6	-0.1127 10849
TCGA-AA-385 6-01A- 01R-09 05-07	high	-0.3 049	0. 26 82 54	0.3 137 7	-0 .4 6 7 2	-0.53 8	-0.534 7	0.57088	-0.145	-0.253 6	0.59548 458

TCGA-AA-385-8-01A-01R-09-05-07	hi g h	-0.0 257	0. 03 72 6	-0. 360 5	-0 .1 7 0 3	-0.17 37	-0.365 3	0.49316	-0.9321	-0.552	0.31077 3121
TCGA-AA-386-0-01A-02R-09-05-07	lo w	0.6 518 9	0. 19 56 16	0.4 475 4	0. 1 4 0 6 6	0.288 85	0.2715 4	0.65517	-0.2611	0.3409 5	-0.5984 82978
TCGA-AA-386-1-01A-01R-10-22-07	lo w	-0.7 417	0. 65 48 24	0.3 665 5	0. 1 5 9 2	-0.06 61	0.1296 9	0.34428	-0.6059	0.7278 2	0.45887 4613
TCGA-AA-386-2-01A-01R-10-22-07	lo w	-0.7 209	0. 44 99 21	0.0 860 7	0. 6 4 0 5 6	-0.05 62	0.5562 5	0.79967	-0.5829	0.7513 7	-0.6317 34164
TCGA-AA-386-4-01A-01R-10-22-07	lo w	0.7 668 3	-0. 03 83 5	0.1 453 7	0. 5 2 2 7 8	0.343 9	0.6154 2	0.69568	0.2085 4	0.7612 3	-0.2460 21078
TCGA-	lo	-0.2	0.	0.7	-0	0.138	0.5694	0.88725	-0.8544	0.6493	0.18920

AA-386 6-01A- 01R-10 22-07	w	414	67 83 56	531 5	.0 4 5 7		6			3	9538
TCGA- AA-386 7-01A- 01R-10 22-07	lo w	-0.0 98	0. 26 24 66	0.2 229 8	0. 2 8 8 1 4	-0.00 5	0.2925 5	0.49644	-0.8358	-0.632 5	0.44326 5243
TCGA- AA-386 9-01A- 01R-10 22-07	lo w	-0.3 924	-0. 35 59 9	0.5 589 2	0. 2 5 9 8 4	-0.06 7	0.3372	0.55665	-0.4953	0.5952 9	0.42913 8523
TCGA- AA-387 0-01A- 01R-10 22-07	lo w	0.0 432 4	-0. 31 40 1	-0. 083 5	0. 0 6 8 6 9	0.168 79	0.4733 3	0.19759	0.2424 7	0.7305 6	-0.3726 6823
TCGA- AA-387 2-01A- 01R-10 22-07	hi g h	-0.3 224	-0. 46 10 3	0.1 375 2	0. 0 3 6 0 2	0.218 64	0.1405 4	-0.0739	-0.6563	0.2124 9	0.47468 3784
TCGA-	hi	-0.1	0.	0.3	0.	0.012	0.0207	0.65846	-0.2293	-0.087	-0.4528

AA-387 5-01A- 01R-09 05-07	g h	341	50 45 27	709 8	0 9 6 4 2	11	9			3	9782
TCGA- AA-387 7-01A- 01R-10 22-07	hi g h	0.9 211 8	-0. 02 03 3	0.3 731 8	0. 5 5 4 6 9	0.211 43	0.5770 9	0.61248	-0.098	0.8242 1	-0.5885 90236
TCGA- AA-393 0-01A- 01R-10 22-07	lo w	-0.8 172	-0. 29 26 7	0.3 295 6	0. 6 1 6 9 4	0.442 14	0.5071 4	0.64313	0.2994	0.7415 3	-0.5217 21253
TCGA- AA-393 9-01A- 01R-10 22-07	lo w	0.8 96	0. 47 97 99	0.2 211 9	0. 5 7 1 7 2	0.528 48	0.6649 2	0.44937	0.5030 1	0.8012	-0.0351 06967
TCGA- AA-394 1-01A- 01R-10 22-07	hi g h	0.6 376 6	0. 36 07 81	-0. 177 6	-0 .1 1 5 5	-0.39 01	-0.328 5	0.62233	-0.364	0.2584 8	0.24449 628
TCGA-	lo	0.3	0.	0.7	0.	0.615	0.7063	0.896	0.1691	0.7661	-0.4909

AA-394 7-01A- 01R-10 22-07	w	891 6	33 32 12	442 2	2 4 1 0 6	42	1		3	6	23085
TCGA- AA-394 9-01A- 01R-10 22-07	lo w	0.5 500 8	0. 32 97 14	0.5 738 7	0. 6 4 9 1 2	0.323 21	0.7352 8	0.8971	-0.1549	0.8537 8	-0.6231 88231
TCGA- AA-395 0-01A- 02R-10 22-07	lo w	0.7 712 1	0. 14 67 5	0.6 911 8	0. 0 1 8 2 3	0.118 26	0.5986 1	0.79967	0.6146 7	0.8132 5	0.23414 313
TCGA- AA-395 2-01A- 01R-10 22-07	hi g h	-0.0 323	0. 64 87 36	0.1 54	0. 3 3 0 0 2	0.103 15	0.0114 3	0.32239	-0.9442	-0.686	-0.7806 27616
TCGA- AA-395 5-01A- 02R-10 22-07	lo w	0.7 931	0. 64 08 43	0.5 463	-0 .0 2 8 2	-0.19 29	-0.234 8	0.80405	-0.6804	-0.857 7	0.29992 7698
TCGA-	lo	-0.9	0.	0.4	0.	0.291	0.1769	0.35961	0.6945	-0.373	0.55112

AA-395 6-01A- 02R-10 22-07	w	321	72 72 3	735 7 9	4 7 9 1 4		1		8	6	777
TCGA- AA-396 6-01A- 01R-11 13-07	lo w	0.9 003 8	0. 14 18 46	0.5 411 3	0. 4 8 0 0 6	0.077 59	0.5396 1	0.55008	-0.3246	0.9583 8	-0.6576 46567
TCGA- AA-396 8-01A- 01R-10 22-07	hi g h	0.9 255 6	-0. 12 98 6	0.5 633 1	-0 .1 0 8 4	0.501 12	0.1802 4	0.83908	0.8412 7	-0.763 4	-0.6264 05495
TCGA- AA-397 0-01A- 01R-10 22-07	lo w	0.9 025 7	0. 13 53 42	0.4 249 2	-0 .1 6 7	0.047 2	0.2835 3	0.73399	0.9803	-0.433 2	-0.2749 55589
TCGA- AA-397 1-01A- 01R-10 22-07	hi g h	0.2 895 5	0. 69 67 44	0.2 850 3	0. 4 6 6 5 9	-0.18 72	-0.285 4	0.88396	0.0432 4	-0.810 6	0.05522 1378
TCGA- AA-397	lo w	-0.9 715	-0. 25	0.5 107	0. 2	-0.09 39	0.0636 2	0.40777	-0.9354	0.4901 4	0.05796 4116

2-01A- 01R-10 22-07			90 8	7	9 8 6 7						
TCGA- AA-397 3-01A- 01R-10 22-07	hi g h	-0.1 319	-0. 59 17 8	0.0 133 4	-0 .6 3 0 4	0.353 34	-0.429 8	-0.9004	-0.6004	-0.796 8	0.13456 8079
TCGA- AA-397 5-01A- 01R-10 22-07	hi g h	-0.8 336	-0. 34 52 9	-0. 225 6	0. 0 0 7 0 1	-0.48 41	-0.579 2	-0.249	-0.8883	-0.783 7	0.45368 9625
TCGA- AA-397 7-01A- 01R-10 22-07	lo w	0.9 956 2	0. 67 83 56	0.5 000 4	0. 4 7 2 8	0.435 04	0.6266 3	0.31801	0.5183 4	0.5772 2	-0.2582 17194
TCGA- AA-397 9-01A- 01R-10 22-07	hi g h	0.7 668 3	0. 13 39 96	-0. 272 7	-0 .2 4 1 2	-0.48	-0.619 6	-0.1549	0.3311 4	-0.869 9	-0.1971 10613
TCGA- AA-398 0-01A- 02R-10	hi g h	0.8 949 1	0. 44 54 79	0.1 541 2	-0 .5 51 1	0.209 86	0.3694 3	0.86097	0.2194 9	0.4173 2	-0.2427 92238

22-07											
TCGA-AA-398-2-01A-02R-10-22-07	low	0.23262	0.0690959	0.50162	0.036891	0.15875	0.17294	0.80405	-0.1396	-0.68	-0.439786928
TCGA-AA-398-4-01A-02R-10-22-07	low	-0.9442	-0.025272	0.31688	0.05674	0.52782	0.53539	0.6092	-0.8905	0.45919	-0.435153242
TCGA-AA-398-6-01A-02R-10-22-07	high	0.86316	0.040548	0.5089	-0.0396	0.32358	-0.1806	0.69896	0.62124	0.05696	0.45067777
TCGA-AA-398-9-01A-01R-10-22-07	high	-0.8095	0.010175	0.11999	0.07568	0.22589	-0.4343	-0.0038	-0.2447	-0.4031	0.445765303
TCGA-AA-399-4-01A-01R-11-13-07	low	0.10454	0.01261	0.06487	0.01602	0.3472	0.35294	0.47017	0.78872	0.73494	0.037725845

					9						
TCGA-AA-A004-01A-01R-A00A-07	hi g h	0.0 038 3	-0. 46 22 6	-0. 18	-0 .3 3 4 8	-0.50 59	-0.703 8	-0.8752	-0.2206	-0.635 7	0.30933 4328
TCGA-AA-A00A-01A-01R-A002-07	hi g h	0.5 205 3	0. 56 85 13	0.1 783 7	0. 1 7 2 1 9	-0.47 67	-0.029 2	-0.7329	0.4865 9	0.2419 9	-0.6122 57461
TCGA-AA-A00D-01A-01R-A002-07	hi g h	-0.9 562	0. 35 54 86	0.1 971 9	-0 .7 4 9 8	-0.42 54	0.3178	0.12644	0.2632 7	0.5284 8	0.44682 5493
TCGA-AA-A00E-01A-01R-A002-07	lo w	0.7 219 5	0. 25 28 65	0.4 865 6	0. 7 4 0 6 8	-0.45 08	0.4952 6	-0.075	-0.1253	0.6708 7	-0.7651 39722
TCGA-AA-A00F-01A-01R-A002-07	hi g h	0.9 157 1	0. 11 43 15	-0. 586 8	0. 6 0 5 5 7	-0.46 46	-0.420 4	-0.5227	-0.8084	-0.680 2	0.20766 7602

TCGA-AA-A0 0J-01A- 02R-A0 02-07	hi g h	0.8 215 7	0. 35 91 27	0.2 708 6	0. 3 1 0 8 6	0.259 97	0.5127 4	-0.3914	1	0.7079 1	-0.4406 6857
TCGA-AA-A0 0K-01A -02R-A 002-07	hi g h	0.6 836 3	0. 20 85 6	-0. 438 5	0. 5 7 6 7 5	-0.22 79	-0.151 5	-0.9004	0.7942	-0.446 6	-0.3232 5857
TCGA-AA-A0 0L-01A -01R-A 002-07	hi g h	0.2 173	0. 15 81 3	-0. 444 2	0. 0 5 2 7 3	-0.53 74	-0.755 8	-0.6355	0.4975 4	-0.982 5	0.27214 7559
TCGA-AA-A0 0N-01A -02R-A 00A-07	lo w	0.7 788 7	0. 40 19 79	0.5 810 9	0. 3 2 9 1	0.545 39	0.5207 4	-0.9496	0.5270 9	0.6051 5	-0.1208 98418
TCGA-AA-A0 0O-01A -02R-A 089-07	hi g h	0.7 372 7	0. 43 70 81	-0. 082 5	-0 .5 4 8 2	0.005 32	-0.264 4	0.39026	0.7777 8	-0.673 1	0.77362 1231
TCGA-	hi	0.1	0.	-0.	-0	-0.11	-0.598	-0.7559	0.2775	-0.031	-0.6026

AA-A0	g	494	14	316	.8	24				8	18586
0Q-01A	h	3	37	4	0						
-01R-A			8		4						
002-07					9						
TCGA-	hi	-0.5	-0.	0.3	-0	0.037	0.5240	-0.306	-0.4001	0.5722	-0.6240
AA-A0	g	632	01	462	.0	95	6			9	56802
0R-01A	h		70	9	5						
-01R-A			5		1						
002-07					3						
TCGA-	hi	0.5	-0.	-0.	-0	-0.67	-0.638	-0.6639	-0.5085	0.1289	0.53750
AA-A0	g	249	58	460	.1	41	8			3	4385
0U-01A	h		60	4	3						
-01R-A			2		4						
002-07					6						
TCGA-	hi	-0.0	-0.	-0.	-0	-0.66	-0.694	-0.8292	0.815	-0.826	0.57116
AA-A0	g	115	10	158	.6	21	4			3	3411
0W-01	h		16	2	8						
A-01R-			2		8						
A002-0					9						
7											
TCGA-	hi	0.8	-0.	-0.	0.	-0.28	-0.711	-0.9168	0.9354	-0.732	-0.0494
AA-A0	g	15	36	566	1	84	6		1	7	14402
0Z-01A	h		78	9	6						
-01R-A			4		8						
002-07					9						
					5						
TCGA-	lo	0.9	0.	-0.	-0	-0.18	-0.171	-0.7077	0.7230	0.2168	0.14889
AA-A0	w	792	55	449	.1	72	6		4	7	2405
10-01A			94	4	1						

-01R-A 089-07			52		6						
TCGA- AA-A0 17-01A -01R-A 00A-07	hi g h	-0.9 912	-0. 05 96 9	-0. 501 5	-0 .4 3 3 5	-0.09 18	-0.773 4	-0.7833	-0.399	-0.653 1	0.03675 2606
TCGA- AA-A0 1C-01A -01R-A 00A-07	lo w	-0.9 256	0. 22 61 97	-0. 447 8	-0 .1 8 0 4	0.027 43	-0.537 8	-0.5982	0.8412 7	-0.691 7	0.04689 9552
TCGA- AA-A0 1F-01A -01R-A 002-07	hi g h	-0.7 767	-0. 05 29 1	-0. 236 1	-0 .2 8 6 9	-0.47 53	-0.579 9	-0.9037	0.3924 5	0.0364	0.10898 3473
TCGA- AA-A0 1G-01A -01R-A 002-07	lo w	0.3 300 5	0. 13 41 15	-0. 443 1	0. 2 3 9 8 2	-0.35 34	-0.551	-0.6037	0.3026 8	-0.956 2	0.68345 3081
TCGA- AA-A0 1I-01A- 02R-A0 89-07	lo w	0.7 350 8	0. 81 16 41	0.0 835 6	0. 6 4 5 3 5	0.356 42	0.2389 9	-0.3749	-0.1932	0.1328 5	0.45162 6237

TCGA-AA-01K-01A-01R-A00A-07	low	0.99453	0.032259	0.33012	-0.6983	0.03267	0.30428	-0.2983	0.29174	0.16865	0.188127038
TCGA-AA-01P-01A-21R-A083-07	high	0.41544	0.0324786	0.13054	-0.77	0.55615	0.45956	0.7734	0.44061	0.91402	-0.293623279
TCGA-AA-01Q-01A-01R-A002-07	high	0.44937	-0.032219	-0.03731	0.08	-0.4393	-0.4489	-0.7537	-0.4559	0.26616	-0.429702634
TCGA-AA-01R-01A-21R-A083-07	high	-0.595	-0.029387	-0.02922	-0.313	-0.0967	-0.5372	-0.8686	0.49316	0.24557	-0.475695248
TCGA-AA-01S-01A-21R-A083-07	high	-0.445	0.0095843	-0.05591	-0.9	-0.5452	-0.7313	-0.9759	0.13519	-0.8702	0.091607241
TCGA-AA-01T-01A-21R-A	high	-0.5632	-0.025585	-0.05625	-0.487	-0.579	-0.784	-0.977	-0.7165	-0.8642	-0.19198953

16W-07					9						
TCGA-AA-A0 1V-01A -23R-A 083-07	hi g h	0.9 529 3	-0. 37 63 8	-0. 562 2	-0 .1 11 1	-0.40 33	-0.689 4	-0.8643	0.5993 4	-0.337 8	0.65396 8921
TCGA-AA-A0 1X-01A -21R-A 083-07	hi g h	0.6 836 3	-0. 50 52 1	-0. 279 2	0. 1 4 5 2 3	-0.15 5	-0.672 5	-0.8095	0.4307 6	-0.755 6	0.76735 6443
TCGA-AA-A0 1Z-01A -11R-A 083-07	lo w	0.9 945 3	-0. 02 86 2	-0. 772 9	-0 .3 1 8 2	-0.58 21	-0.610 4	-0.7044	-0.8303	-0.565 7	0.04935 4777
TCGA-AA-A0 22-01A -21R-A 16W-07	hi g h	-0.7 986	-0. 14 50 6	-0. 326 4	0. 4 6 0 1	0.114 98	-0.452 6	-0.9201	1	0.2166 2	-0.7333 66906
TCGA-AA-A0 24-01A -02R-A 00A-07	lo w	-0.2 961	-0. 16 34 7	-0. 380 8	0. 6 1 2 9 5	-0.38 49	-0.438 1	-0.9945	-0.0739	0.2117 8	0.65613 496
TCGA-	lo	0.8	0.	-0.	0.	-0.70	-0.529	-0.8511	0.7339	0.1451	0.48457

AA-A0	w	850	08	647	5	84	8		9		7543
29-01A		6	82	7	3						
-01R-A			11		1						
00A-07					6						
TCGA-	hi	0.3	0.	-0.	0.	-0.60	-0.543	-0.8588	0.8784	-0.176	0.68371
AA-A0	g	563	05	522	0	97	5		9	8	9548
2E-01A	h	2	00	3	1						
-01R-A			21		5						
00A-07					8						
					5						
TCGA-	hi	-0.5	-0.	-0.	-0	-0.36	-0.564	-0.5446	0.8708	-0.136	0.38366
AA-A0	g	391	56	505	.4	59	8		3	1	2778
2F-01A	h		76	3	1						
-01R-A			7		8						
089-07					5						
TCGA-	hi	0.1	0.	-0.	0.	-0.23	-0.379	-0.6639	0.9989	-0.718	0.33135
AA-A0	g	559	26	131	2	87	1		1		1063
2H-01A	h	9	55	8	2						
-01R-A			87		4						
089-07					4						
					6						
TCGA-	lo	-0.6	-0.	-0.	-0	-0.65	-0.738	-0.8424	-0.4253	-0.754	0.02488
AA-A0	w	716	70	384	.6	57	7			7	6867
2J-01A-			57	3	9						
01R-A0			5		5						
0A-07					6						
TCGA-	hi	0.5	-0.	-0.	-0	-0.41	-0.615	-0.9507	-0.6508	-0.741	-0.1392
AA-A0	g	117	46	692	.5	19				5	18009
2K-01A	h	7	41	3	3						

-03R-A 32Y-07			1		6 1						
TCGA-AA-A0 2O-01A -21R-A 16W-07	hi g h	0.5 938 7	-0. 18 47 7	-0. 584 9	-0 .4 5 6 6	-0.34 19	-0.731	-0.8533	0.9792	-0.735 4	-0.1175 99216
TCGA-AA-A0 2R-01A -01R-A 00A-07	hi g h	-0.3 727	-0. 37 95 9	0.0 511	0. 4 21 11	-0.30 18	0.6078	-0.0509	0.5752 6	0.6741 5	-0.3377 33014
TCGA-AA-A0 2W-01 A-01R- A00A-0 7	hi g h	0.9 474 5	0. 07 11	-0. 412 5	0. 4 3 4 5 8	0.391 8	-0.612	-0.908	-0.2217	-0.704 3	0.59474 9091
TCGA-AA-A0 2Y-01A -43R-A 32Y-07	lo w	-0.7 241	-0. 28 10 7	-0. 525 7	-0 .2 7 2 1	-0.31 35	-0.463	-0.688	-0.8664	0.3205 4	0.26396 0402
TCGA-AA-A0 3F-01A -11R-A 16W-07	hi g h	-0.7 417	-0. 10 17 6	-0. 671 7	-0 .0 1 2 6	-0.52 5	-0.679 9	-0.907	0.6343 7	-0.372 7	0.28875 0882
TCGA-	hi	-0.7	-0.	-0.	-0	-0.50	-0.636	-0.9573	0.4165	-0.673	0.14333

AA-A0	g	154	27	253	.3	39	1		3	1	4029
3J-01A-	h		81	7	1						
21R-A1					3						
6W-07					4						
TCGA-	lo	0.9	-0.	0.4	0.	0.013	0.5292	0.87958	0.1406	0.7026	-0.5449
AD-590	w	047	09	336	0	36	8		7	3	78701
0-01A-1		6	90	1	0						
1R-165			2		81						
3-07					1						
TCGA-	lo	0.9	-0.	0.4	0.	0.180	0.6529	0.71757	-0.9945	0.3634	-0.0113
AD-654	w	124	06	393	1	29	7			8	81858
8-01A-1		2	65	9	9						
1R-183			2		3						
9-07					3						
					5						
TCGA-	hi	0.4	-0.	-0.	-0	-0.52	-0.721	-0.8446	-0.0826	-0.649	0.49241
AD-688	g	745	06	643	.4	3	6				3422
8-01A-1	h	5	94	3	5						
1R-192			5		7						
8-07					7						
TCGA-	hi	0.8	-0.	-0.	-0	0.056	-0.168	-0.5556	0.3442	0.8209	0.12596
AD-688	g	817	15	319	.6	7	1		8	2	7944
9-01A-1	h	7	77	4	11						
1R-192			1		6						
8-07											
TCGA-	hi	0.9	-0.	-0.	-0	-0.28	-0.497	-0.6147	0.5522	-0.779	0.49372
AD-689	g	463	17	452	.1	15	3		7	3	8473
0-01A-1	h	6	76	8	0						
1R-192					9						

8-07					2						
TCGA-AD-689	low	-0.3716	-0.74	-0.492	-0.4	0.31526	0.51489	0.31363	0.27641	0.86489	-0.215150003
5-01A-1			37	2	1						
1R-192			5		4						
8-07					7						
TCGA-AD-689	high	-0.9967	0.79	0.3828	0.5	-0.0001	0.4177	-0.2392	-0.7986	-0.7051	-0.237795765
9-01A-1			39	4	1						
1R-192			97		0						
8-07					59						
TCGA-AD-690	high	0.133	-0.62	-0.116	-0.0	0.15465	0.14982	-0.8818	-0.4034	-0.1928	0.512655748
1-01A-1			27		1						
1R-192			6		2						
8-07					6						
TCGA-AD-696	high	-0.9967	-0.64	-0.506	-0.7	-0.5323	-0.4585	-0.3968	-0.191	-0.0769	-0.177229848
3-01A-1			72	6	0						
1R-192			2		6						
8-07					9						
TCGA-AD-696	low	-0.8292	0.02	0.6700	0.7	0.64506	0.60054	0.40887	0.37165	0.67908	-0.33918759
4-01A-1			99	5	2						
1R-192			48		8						
8-07					91						
TCGA-	low	-0.6	0.	-0.	-0	-0.19	-0.542	-0.0509	-0.7121	-0.8111	0.64371

AD-696	w	606	04	034	.6	81	4				2782
5-01A-1			22	8	4						
1R-192			02		7						
8-07					6						
TCGA-	lo	0.8	-0.	-0.	0.	-0.08	0.4285	-0.7406	-0.7953	0.7853	-0.4427
AD-A5	w	051	51	025	6	96				2	48392
EJ-01A		5	76	3	7						
-11R-A			6		4						
28H-07					5						
					4						
TCGA-	hi	0.7	-0.	-0.	-0	-0.34	-0.542	-0.8073	0.6289	-0.920	0.28373
AD-A5	g	668	42	506	.6	1	8			8	8633
EK-01	h	3	03	8	7						
A-11R-			3		7						
A28H-0					1						
7											
TCGA-	lo	0.9	-0.	-0.	0.	0.275	0.4846	0.92228	-0.919	0.3625	0.46719
AM-58	w	726	46	234	1	94	9			4	4284
20-01A		3	55	1	2						
-01R-16					2						
53-07					8						
					9						
TCGA-	lo	0.1	-0.	0.4	-0	0.432	0.6936	0.52053	0.2413	0.9863	0.15213
AM-58	w	767	24	751	.0	88	8		8	1	1346
21-01A		9	64	8	7						
-01R-16			6		9						
53-07					8						
TCGA-	hi	-0.9	0.	0.3	-0	0.581	-0.059	-0.4111	0.9890	-0.394	-0.5215
AU-377	g	518	14	426	.2	79	1		5		02494

9-01A- 01R-17 23-07	h		10 88	7	0 5 7						
TCGA- AU-600 4-01A-1 1R-172 3-07	hi g h	-0.9 562	0. 06 25 26	0.2 660 3	-0 .4 6 6 5	0.106 32	0.5504 6	-0.1232	0.6015 3	0.6703 2	-0.6538 67252
TCGA- AY-407 0-01A- 01R-11 13-07	hi g h	-0.0 695	-0. 64 69 3	-0. 379 4	-0 .1 5 9 3	-0.50 88	-0.635 4	0.09797	0.3946 4	-0.471 7	-0.4670 27276
TCGA- AY-407 1-01A- 01R-11 13-07	hi g h	-0.6 048	0. 57 16 96	-0. 097 9	-0 .1 2 5 1	-0.11 87	-0.513 6	0.51943	0.5686 9	-0.486 9	-0.5838 55097
TCGA- AY-554 3-01A- 01R-16 53-07	lo w	-0.6 355	-0. 58 84 9	-0. 299 5	-0 .3 3 5 5	-0.50 32	-0.018 5	-0.1626	-0.9726	-0.323 8	0.04572 8245
TCGA- AY-619 6-01A-1 1R-172 3-07	lo w	0.2 030 7	0. 22 82 86	0.6 324 4	0. 1 8 4 6 7	0.631 49	0.6605 6	0.35632	-0.2315	0.4649 5	-0.6278 65127

TCGA- AY-619 7-01A-1 1R-172 3-07	hi g h	-0.6 3	-0. 52 21 2	-0. 296	0. 1 5 2 9 4	-0.49 62	-0.304 6	-0.3399	0.7712 1	0.7344 3	-0.3965 6916
TCGA- AY-638 6-01A- 21R-17 23-07	lo w	0.8 971	0. 44 30 3	-0. 198	-0 .0 4 9	-0.48 45	0.1382 3	-0.1297	-0.6661	0.7771 1	0.57304 8463
TCGA- AY-A54 L-01A- 11R-A2 8H-07	lo w	0.7 569 8	-0. 74 08	-0. 692 7	0. 4 7 6 1	-0.44 41	-0.735 8	-0.699	0.5380 4	-0.056 2	0.78963 6946
TCGA- AY-A69 D-01A- 11R-A3 7K-07	hi g h	0.8 949 1	-0. 11 14 8	-0. 497 1	-0 .0 9 9 1	0.008 94	-0.497 4	-0.4964	-0.0389	-0.592	0.22296 6821
TCGA- AY-A71 X-01A- 12R-A3 7K-07	hi g h	0.9 014 8	-0. 31 49 6	-0. 687 9	-0 .0 5 2 6	-0.38 61	-0.592 1	-0.8435	0.2479 5	-0.760 9	0.48160 2119
TCGA- AY-A8 YK-01	hi g h	-0.7 843	-0. 30 23	-0. 559 1	-0 .4 3	-0.33 71	-0.675 2	-0.4362	-0.3202	-0.898 7	0.58142 9482

A-11R- A41B-0 7			7		2 7						
TCGA- AZ-430 8-01A- 01R-14 10-07	hi g h	-0.5 424	0. 15 54 82	-0. 297 3	-0 .4 0 7 6	-0.16 15	-0.616 8	-0.7811	-0.3651	-0.514 2	-0.2685 35355
TCGA- AZ-431 3-01A- 01R-14 10-07	lo w	-0.0 914	0. 24 08 66	-0. 438	0. 3 4 6 4	-0.11 55	-0.541 8	-0.5665	-0.5129	0.7801	-0.0017 33972
TCGA- AZ-431 5-01A- 01R-14 10-07	lo w	0.7 898 2	0. 69 50 48	-0. 066 1	-0 .2 6 3 9	0.317 13	0.2109 1	-0.8041	0.3968 3	0.3362 5	0.11204 0087
TCGA- AZ-432 3-01A- 21R-18 39-07	hi g h	0.5 905 9	-0. 77 64 8	0.3 502 9	-0 .1 0 9 6	0.312 94	-0.302	0.91024	0.7438 4	0.0082 1	-0.2255 81645
TCGA- AZ-461 4-01A- 01R-14 10-07	hi g h	0.4 033 9	0. 43 78 01	-0. 479 8	-0 .0 6 0 1	-0.76 32	-0.635 5	-0.5074	0.4603 2	-0.07	-0.6418 39938
TCGA-	lo	-0.1	-0.	0.0	0.	0.197	0.6291	0.09141	0.7723	0.8592	-0.4244

AZ-461 5-01A- 01R-14 10-07	w	045	28 30 3	528 3	4 7 9 5 3	4	4	4			6	9883
TCGA- AZ-461 6-01A- 21R-18 39-07	hi g h	0.0 224 4	-0. 11 32 7	-0. 503 5	-0 .7 5 3 4	-0.26 07	-0.445 5	-0.1297	0.6934 9	0.3406 4	0.36881 5339	
TCGA- AZ-468 1-01A- 01R-14 10-07	hi g h	0.6 332 8	0. 12 85 25	-0. 693 6	-0 .1 8 2 1	-0.44 89	-0.703 7	-0.6015	-0.6639	-0.985 2	-0.2710 62991	
TCGA- AZ-540 3-01A- 01R-16 53-07	lo w	0.7 088 1	-0. 07 45 5	0.1 842 5	-0 .1 3 9 9	0.430 17	0.4649 5	0.87521	-0.7077	0.3410 7	-0.3088 31958	
TCGA- AZ-540 7-01A- 01R-17 23-07	lo w	-0.2 972	-0. 15 17 7	-0. 099 9	0. 11 7 9 7	-0.24 18	-0.337 4	0.75588	0.1253 4	0.5862 8	0.05086 7491	
TCGA- AZ-659 8-01A-1 1R-177	lo w	-0.8 84	0. 02 11 71	0.2 151 2	-0 .5 8 2	-0.13 22	0.2464 1	-0.5742	-0.8303	0.7683 5	-0.2141 65057	

4-07					6						
TCGA-AZ-659	hi	-0.5	-0.	-0.	0.	0.169	-0.546	-0.2042	0.6048	0.0186	0.24278
9-01A-1	g	216	02	650	7	25	4		2	5	6876
1R-177	h		45	4	2						
4-07			5		0						
					6						
					3						
TCGA-AZ-660	lo	-0.8	-0.	0.1	-0	-0.17	0.6292	0.87849	-0.7614	-0.0011	-0.3433
0-01A-1	w	051	34	012	.2	73	4				72594
1R-177			81	7	2						
4-07					2						
					5						
TCGA-AZ-660	hi	-0.8	-0.	0.2	-0	-0.17	0.6391	-0.0848	-0.7909	0.7957	-0.6542
1-01A-1	g	183	15	287	.4	2	8			3	98841
1R-177	h		04	8	4						
4-07			1		8						
					2						
TCGA-AZ-660	hi	-0.8	0.	-0.	0.	0.394	-0.347	0.25233	-0.7756	-0.814	0.07764
3-01A-1	g	971	31	501	2	47	6			3	8904
1R-183	h		25	7	5						
9-07			3		6						
					5						
					2						
TCGA-AZ-660	lo	-0.8	0.	0.3	0.	0.628	0.7159	0.90367	-0.8577	-0.137	-0.4657
5-01A-1	w	872	54	953	1	82	2			2	25332
1R-183			00	2	9						
9-07			87		6						
					6						
					9						

TCGA-AZ-660-6-01A-1-1R-183-9-07	hi g h	-0.8 106	-0. 60 71 1	-0. 473	-0 .5 5 1 4	-0.55 4	-0.509 6	-0.6289	0.2621 8	-0.637	0.65990 1262
TCGA-AZ-660-7-01A-1-1R-183-9-07	lo w	-0.4 778	0. 01 30 93	0.4 634 5	0. 6 3 7 6 5	0.469 42	0.6840 6	0.60153	-0.7603 8	0.7962	-0.2431 33485
TCGA-AZ-660-8-01A-1-1R-183-9-07	hi g h	-0.5 84	0. 12 39 33	-0. 628 3	-0 .5 9 1 9	-0.61 69	-0.752 8	-0.8719	-0.7482	-0.789 7	0.49363 682
TCGA-CA-525-4-01A-21R-1839-07	lo w	-0.5 348	-0. 53 16 8	-0. 580 4	0. 3 0 1 8 8	0.246 53	0.1163 5	-0.4297	0.4975 4	0.2614 4	-0.4992 44797
TCGA-CA-525-5-01A-1-1R-183-9-07	lo w	0.9 189 9	-0. 53 58 9	-0. 72	0. 11 5 0 9	-0.22 42	-0.307 8	-0.8489	-0.4559	0.0051	-0.6517 82416
TCGA-CA-525	lo w	0.5 719	0. 45	0.3 736	-0 .1	0.134 35	-0.383 9	0.43842	0.2994	-0.051 7	0.39676 811

6-01A-01R-1410-07		8	42 47	1	7 5 4						
TCGA-CA-5796-01A-01R-1653-07	low	0.2173	0.754961	-0.222	0.14539	0.09276	0.48593	0.10345	-0.5216	0.89103	-0.152715304
TCGA-CA-5797-01A-01R-1653-07	low	0.96825	-0.46226	0.1213	-0.2627	-0.002	0.01761	0.28955	-0.9551	-0.6979	0.40616111
TCGA-CA-6715-01A-21R-1839-07	high	0.66831	-0.7272	-0.0675	-0.2785	-0.3815	-0.6198	-0.4745	-0.3673	-0.6249	0.712699709
TCGA-CA-6716-01A-11R-1839-07	high	0.54899	-0.58489	-0.357	-0.27845	0.43454	-0.4079	0.50192	0.31363	-0.684	0.67765929
TCGA-CA-6717-01A-11R-1839-07	low	-0.8872	-0.32334	0.61292	0.16030	0.57798	0.77602	0.94308	-0.8161	0.67087	0.233059928

					7						
TCGA- CA-671 8-01A-1 1R-183 9-07	lo w	-0.4 57	0. 27 86 18	0.0 113 7	-0 .1 1 4 6	0.489 61	0.5933 5	0.16913	0.7635 5	0.7913 5	0.10744 1052
TCGA- CA-671 9-01A-1 1R-183 9-07	lo w	-0.2 709	-0. 05 22	0.3 484 1	-0 .2 1 0 6	0.486 68	0.4743 6	-0.0859	-0.8982	-0.589 3	0.52057 5038
TCGA- CK-494 7-01B-1 1R-165 3-07	lo w	0.1 713 2	0. 17 43 24	0.5 609 1	-0 .1 3 6 5	0.012 97	0.6539 2	0.94964	-0.561	0.5509 3	0.22883 3023
TCGA- CK-494 8-01B-1 1R-165 3-07	hi g h	-0.6 442	-0. 44 25	-0. 387 3	-0 .6 7 0 1	-0.09 79	-0.079 3	-0.4647	-0.8785	0.2011 5	0.68511 2036
TCGA- CK-495 0-01A- 01R-17 23-07	lo w	0.9 660 6	0. 60 91 79	0.0 183 3	0. 0 5 8 5 6	-0.01 65	0.5399 7	0.93432	-0.5862	0.4704 3	0.10532 09
TCGA- CK-495	lo w	-0.9 321	0. 04	0.6 580	0. 3	0.358 25	0.7038 3	0.07827	0.6748 8	0.6741 5	-0.6393 34621

1-01A-01R-1410-07			6185	7	3573						
TCGA-CK-4952-01A-01R-1723-07	low	0.40011	0.036164	-0.142	0.45998	-0.1849	0.30473	0.10345	-0.7373	0.931	-0.166175742
TCGA-CK-5912-01A-11R-1653-07	low	0.7723	0.550888	-0.0394	-0.5917	-0.3945	-0.0735	0.02791	-0.8796	-0.5383	0.717433368
TCGA-CK-5913-01A-11R-1653-07	low	-0.4943	-0.438	0.1357	-0.775	-0.0146	0.68913	0.63656	-0.7165	0.908	-0.646170021
TCGA-CK-5914-01A-11R-1653-07	high	-0.8292	-0.33448	-0.1154	-0.535	-0.3573	-0.2663	-0.6114	0.04981	-0.4469	-0.018790838
TCGA-CK-5915-01A-11R-165	low	0.75151	0.397259	0.00906	-0.2771	-0.2777	-0.4525	0.07389	-0.8697	-0.718	0.312579158

3-07					5						
TCGA-CK-591	lo w	0.0 738	0. 26	0.6 216	-0 .6	0.301 41	0.7440 8	0.93432	-0.8172	0.9255 2	-0.2455 84621
6-01A-1		9	66	5	4						
1R-165			37		2						
3-07					4						
TCGA-CK-674	lo w	-0.8 927	0. 23	0.2 468	-0 .3	0.179 88	0.3991 7	0.12534	0.8773 9	0.8960 2	-0.6751 20769
6-01A-1			45		7						
1R-183			21		3						
9-07					9						
TCGA-CK-674	lo w	0.6 157	0. 90	-0. 073	0. 3	0.038 66	0.1236 6	-0.0148	-0.5972	0.0481 9	0.15658 9072
7-01A-1		6	93	1	0						
1R-183			86		2						
9-07					2						
					5						
TCGA-CK-674	lo w	-0.4 537	0. 50	0.3 107	-0 .2	0.441 74	0.5621 4	0.36727	-0.5096	0.6977	0.51926 1632
8-01A-1			90	7	1						
1R-183			41		0						
9-07					6						
TCGA-CK-675	lo w	-0.5 643	0. 70	-0. 045	0. 2	0.282 13	0.5023 6	0.26546	-0.3257	0.4457 8	0.10069 2119
1-01A-1			26	5	5						
1R-183			89		2						
9-07					4						
					8						
TCGA-	hi	0.2	-0.	-0.	-0	0.026	0.1022	0.98248	0.8642	0.7223	-0.5264

CM-47 43-01A -01R-17 23-07	g h	829 8	15 79 4	586 6	.4 6 8 2	25	6		6	4	18511
TCGA- CM-47 44-01A -01R-A 32Z-07	lo w	0.0 596 6	-0. 15 34 2	-0. 421 2	-0 .6 6 7 3	-0.27 41	-0.326 8	0.18993	-0.9496	0.647	0.60239 4658
TCGA- CM-47 46-01A -01R-14 10-07	hi g h	-0.2 261	0. 70 82 97	-0. 305 3	0. 4 4 3 0 3	-0.30 22	-0.442 7	-0.7843	-0.0564	0.8217 8	0.16675 8091
TCGA- CM-47 47-01A -01R-14 10-07	lo w	-0.5 074	-0. 10 96 5	-0. 448 2	-0 .4 7 0 1	-0.53 44	-0.599 3	-0.9551	0.0322 9	0.1119	0.41579 8135
TCGA- CM-47 48-01A -01R-14 10-07	lo w	0.1 899 3	0. 03 28 77	0.2 846 5	0. 4 0 7 4 4	-0.05 61	0.0687 9	0.25342	0.9310 3	-0.184 6	-0.0647 70476
TCGA- CM-47 51-01A	hi g h	-0.6 125	0. 56 14	-0. 447 9	0. 5 2	-0.05 54	0.3564 5	0.87192	-0.8752	-0.308 3	-0.0215 18334

-02R-18 39-07			01		0 7 8						
TCGA- CM-47 52-01A -01R-14 10-07	hi g h	-0.9 737	0. 45 64 02	-0. 430 5	0. 4 4 0 2	0.357 38	-0.128 5	0.05309	-0.1987	-0.558 3	-0.5634 45304
TCGA- CM-53 41-01A -01R-14 10-07	lo w	0.6 486	0. 57 55 71	0.4 885 2	0. 4 1 2 5 8	0.571 6	0.5296 7	0.86864	0.4449 9	0.9277 4	-0.4519 41245
TCGA- CM-53 44-01A -21R-17 23-07	hi g h	0.1 570 9	-0. 12 29 2	-0. 441	-0 .0 7 0 2	0.344 03	0.0711 5	0.64751	0.5183 4	-0.733 8	-0.1687 148
TCGA- CM-53 48-01A -21R-17 23-07	lo w	-0.8 851	-0. 26 54 2	0.2 243 9	-0 .0 9 9 8	0.440 37	0.6320 8	0.47564	-0.6519	0.3872	-0.6548 41551
TCGA- CM-53 49-01A -21R-17 23-07	lo w	0.4 811 2	0. 44 57 6	0.6 948 6	-0 .3 3 6 9	0.347 89	0.5981 7	0.79639	0.8051 5	0.3030 3	0.32997 8093

TCGA- CM-58 60-01A -01R-16 53-07	lo w	-0.2 14	-0. 12 77 2	0.3 268 2	0. 1 0 2 2	0.343 96	0.6921 9	0.57745	-0.5402	0.4134 7	0.14755 8969
TCGA- CM-58 61-01A -01R-16 53-07	lo w	0.2 118 2	0. 33 72 71	0.2 165 3	-0 .1 9 0 2	-0.25 13	0.6092 7	0.45265	0.2928 3	0.9357	-0.2307 58757
TCGA- CM-58 62-01A -01R-16 53-07	lo w	-0.2 414	-0. 48 57	0.4 717 7	0. 1 0 8 5 5	0.419 06	-0.040 6	0.83908	-0.5577	-0.326 6	0.61481 0396
TCGA- CM-58 63-01A -21R-18 39-07	lo w	-0.4 33	0. 32 38 65	0.2 050 7	0. 4 4 3 0 7	0.285 36	0.6303 4	0.95183	-0.6464	0.7272 7	-0.1562 97339
TCGA- CM-58 64-01A -01R-16 53-07	lo w	0.8 566	-0. 24 21 9	0.1 668	-0 .5 3 8 7	-0.47 9	-0.166 1	-0.3782	0.8544 1	0.5446 8	0.76390 5204
TCGA- CM-58	hi g	-0.6 092	-0. 03	-0. 346	-0 .5	0.062 75	-0.547	-0.4319	-0.2326	-0.743 2	0.28631 7084

68-01A -01R-16 53-07	h		62 5	8	9 9 1						
TCGA- CM-61 61-01A -11R-16 53-07	lo w	0.1 943 1	-0. 49 65 4	0.3 496 2	-0 .0 4 3 9	0.405 34	0.2105 6	0.47893	0.3628 9	0.3169 4	0.57521 197
TCGA- CM-61 62-01A -11R-16 53-07	lo w	-0.3 541	0. 11 03 06	0.5 039 1	0. 5 2 6 1 7	0.634 22	0.8294 7	0.90695	-0.6344	0.7957 3	-0.0729 56665
TCGA- CM-61 63-01A -11R-16 53-07	hi g h	0.2 096 3	0. 32 22 45	0.3 280 9	-0 .5 1 4 8	0.627 33	0.3145 2	0.84455	0.7646 4	-0.789 9	-0.4976 66631
TCGA- CM-61 64-01A -11R-16 53-07	hi g h	-0.0 936	-0. 46 77 9	-0. 540 1	-0 .6 6 4 6	-0.02 97	-0.608 4	-0.098	0.8872 5	-0.567 1	0.40725 3569
TCGA- CM-61 65-01A -11R-16 53-07	lo w	-0.4 888	0. 43 17 69	0.6 078 7	0. 2 0 6 1	0.464 4	0.6153 4	0.97592	0.0322 9	-0.362 4	0.12232 5837

TCGA- CM-61 66-01A -11R-16 53-07	low	0.9 879 6	0. 31 32 45	-0. 339 5	-0 .5 3 1 3	0.295 3	-0.448 9	0.14724	0.7963 9	-0.841 7	0.63483 8175
TCGA- CM-61 67-01A -11R-16 53-07	low	-0.9 956	0. 36 89 23	0.3 089 7	0. 7 5 9 3 2	0.653 18	0.5816 8	0.98905	-0.6486	-0.0011	-0.1464 61876
TCGA- CM-61 68-01A -11R-16 53-07	low	-0.5 151	0. 52 27 4	0.4 853 9	0. 6 6 5 0 8	0.716 17	0.7775 3	0.92337	0.1516 1	0.6681 3	-0.6406 4421
TCGA- CM-61 69-01A -11R-16 53-07	low	0.0 859 3	0. 76 28 66	0.6 803 7	-0 .0 2 2	0.421 76	0.7801 4	0.97263	-0.7657	0.6369 1	0.65750 4196
TCGA- CM-61 70-01A -11R-16 53-07	high	-0.9 956	0. 57 88 33	0.1 787 8	0. 0 4 3 2 1	0.106 16	-0.193	0.41544	0.2786	-0.676 1	-0.1428 07968
TCGA-	high	1	-0.	0.2	-0	-0.04	0.3996	0.23919	0.7985	0.7678	-0.4035

CM-61 71-01A -11R-16 53-07	g h		38 74 5	565	.1 2 0 4	3	8		8		53721
TCGA- CM-61 72-01A -11R-16 53-07	lo w	-0.7 351	0. 59 93 1	0.5 291 1	-0 .0 1 9 4	0.161 03	0.4458 8	0.87083	0.3366 2	-0.654 4	-0.2035 33929
TCGA- CM-66 74-01A -11R-18 39-07	lo w	0.3 946 4	0. 09 56 13	0.4 584 6	0. 1 4 6 4 3	0.353 1	0.7494 8	0.70115	-0.5315 2	0.8220	0.23152 2758
TCGA- CM-66 75-01A -11R-18 39-07	hi g h	0.2 337 2	0. 47 42 01	-0. 498 7	-0 .5 7 3	-0.05 09	-0.01	-0.5402	-0.6059	-0.392 1	-0.5070 17886
TCGA- CM-66 76-01A -11R-18 39-07	hi g h	0.3 070 6	-0. 29 11 4	-0. 424 4	-0 .4 5 2 2	-0.11 52	-0.599 8	-0.4658	0.6343 7	-0.880 1	0.66189 3734
TCGA- CM-66 77-01A -11R-18	lo w	-0.4 22	0. 77 42 48	-0. 449 4	0. 3 2 5	0.480 37	0.0592 6	0.60482	-0.5194	-0.279 3	-0.3551 88765

39-07					1 2						
TCGA- CM-66 78-01A -11R-18 39-07	lo w	0.9 595	-0. 40	-0.1 122	-0 .5 4 1 4	0.336 9	-0.310 5	-0.1834	0.8773 9	-0.075 2	0.75701 8451
TCGA- CM-66 79-01A -11R-18 39-07	hi g h	-0.1 812	0. 70	-0. 477	-0 .6 9 9 8	0.386 45	-0.065 1	-0.0279	-0.6683	-0.787 1	0.18742 928
TCGA- CM-66 80-01A -11R-18 39-07	hi g h	-0.8 664	0. 12	0.0 801	0. 3 3 9 4	0.348 18	0.5052 7	0.25014	0.4920 6	0.5783 8	0.75009 8449
TCGA- D5-553 7-01A- 21R-19 28-07	lo w	0.3 804 1	-0. 39	-0. 374	-0 .5 3 0 6	0.106	-0.339 6	-0.8281	0.3048 7	-0.727 4	0.51472 6138
TCGA- D5-553 8-01A- 01R-16 53-07	lo w	0.2 304 3	0. 81	0.6 434	0. 2 6 9 2 8	0.377 26	0.6246 4	0.35413	-0.815	0.5799 2	-0.1678 55184
TCGA-	lo	-0.6	0.	0.4	0.	0.362	0.7377	0.83908	-0.9704	0.7469	0.02404

D5-553 9-01A- 01R-16 53-07	w	76	28 38 55	232 9	3 8 7 4 9	73	1			9	2215
TCGA- D5-554 0-01A- 01R-16 53-07	lo w	0.7 931	-0. 48 41 5	0.4 497 5	-0 .0 0 3 3	0.366 08	-0.105 6	0.14176	0.4975 4	0.0754 9	0.18528 4867
TCGA- D5-554 1-01A- 01R-16 53-07	hi g h	0.8 478 4	0. 12 37 14	0.3 807 2	-0 .5 8 8 9	0.181 75	0.3304 9	-0.5337	-0.098	-0.186 4	-0.4170 99077
TCGA- D5-652 9-01A-1 1R-177 4-07	lo w	-0.0 421	-0. 43 21	0.2 968 9	-0 .1 2 4 6	0.507 8	0.5150 6	0.35413	0.8773 9	0.7342 5	-0.3773 54996
TCGA- D5-653 0-01A-1 1R-172 3-07	lo w	-0.9 869	0. 93 90 8	0.3 806 8	0. 2 2 1 4 1	-0.06 32	0.5126 4	-0.1188	0.9704 4	0.6763 4	0.00109 7093
TCGA- D5-653 1-01A-1	lo w	0.0 881 2	-0. 03 54	0.0 235	-0 .6 9	0.170 61	0.3728	0.30268	0.0246 3	0.4748 1	0.72065 8448

1R-172 3-07			6		8						
					2						
TCGA- D5-653 2-01A-1 1R-172 3-07	lo w	-0.4 932	0. 60 34 61	-0. 156 4 8	-0 .7 4 8 3	-0.47 78	-0.478	-0.7077	0.6475 1	-0.831 9	0.09706 9941
TCGA- D5-653 3-01A-1 1R-172 3-07	lo w	0.0 093	-0. 60 02 1	0.1 438 6 8	-0 .4 7 8 6	-0.35 62	-0.372 5	-0.4516	-0.2151	-0.538 3	0.52571 4767
TCGA- D5-653 4-01A- 21R-19 28-07	lo w	-0.8 533	0. 14 85 77	0.6 032 5 91 1	0. 5 5 91 1	0.612 1	0.7439 7	0.80296	-0.249	0.6122 7	-0.4994 75028
TCGA- D5-653 5-01A-1 1R-172 3-07	lo w	-0.9 387	0. 23 35 95	0.1 984 2 8	-0 .6 7 8 9	-0.34 02	0.2149 9	-0.514	-0.7581	0.0498 4	-0.0243 57889
TCGA- D5-653 6-01A-1 1R-172 3-07	lo w	0.8 489 3	-0. 69 11 7	0.3 599 6 9 9 6	-0 .0 9 9 6	0.032 39	0.4545 2	-0.5884	0.8533 1	0.6089 8	0.20698 5987
TCGA- D5-653	lo w	0.7 175	-0. 53	-0. 168	-0 .6	0.006 09	-0.446	-0.8424	0.9365 1	0.5535 5	0.56217 8919

7-01A-1 1R-172 3-07		7	09 6	1	2 4 5						
TCGA- D5-653 8-01A-1 1R-172 3-07	hi g h	0.5 730 7	-0. 67 68 2	-0. 180 3	-0 .3 7 8 1	-0.00 57	-0.616 8	-0.4713	0.8664 5	-0.438 3	0.65331 8705
TCGA- D5-653 9-01A-1 1R-172 3-07	lo w	-0.8 851	-0. 06 60 5	0.1 291	0. 2 8 4 8	-0.11 16	0.1208 4	0.92666	-0.9737	0.0701	-0.1732 46508
TCGA- D5-654 0-01A-1 1R-172 3-07	hi g h	0.1 789 8	-0. 29 32 5	-0. 252 4	-0 .1 5 1 4	-0.19 7	0.3798 2	-0.2852	0.9277 5	0.9315 4	-0.5425 34491
TCGA- D5-654 1-01A-1 1R-172 3-07	lo w	0.4 077 7	-0. 02 48 4	0.1 158 9	-0 .2 8 9 7	0.550 18	0.5952 7	0.26875	-0.9803	-0.055 8	0.61894 0038
TCGA- D5-689 8-01A-1 1R-192 8-07	hi g h	0.7 296 1	-0. 06 61 4	0.2 757 1	0. 7 0 9 8 3	0.048 14	0.1957 1	0.36508	0.0640 4	-0.315 7	-0.4831 5267

TCGA-D5-692-0-01A-1-1R-192-8-07	hi g h	0.5 741 7	-0. 02 05 5	0.2 950 4	-0 .1 11 3	-0.05 75	0.0489 8	0.76026	-0.9431	0.1519 8	0.10972 7349
TCGA-D5-692-2-01A-1-1R-192-8-07	hi g h	-0.2 512	-0. 24 93 2	-0. 412 4	0. 0 2 1 7	0.476 23	-0.432 4	-0.4067	-0.9234	-0.750 8	-0.1578 31245
TCGA-D5-692-3-01A-1-1R-A32-Z-07	hi g h	-0.9 168	-0. 33 09 6	0.2 291 4	-0 .3 9 3 8	-0.12 28	-0.393 1	-0.2644	-0.6946	-0.549	-0.3779 55356
TCGA-D5-692-4-01A-1-1R-192-8-07	hi g h	0.1 669 4	0. 43 39 07	0.6 835 8	-0 .4 4 5 9	0.392 71	0.5023 2	0.10454	0.6464 1	-0.059 1	0.44260 7424
TCGA-D5-692-6-01A-1-1R-192-8-07	hi g h	-0.9 814	-0. 52 89	0.2 857 3	-0 .0 2 0 2	0.170 74	-0.127 8	-0.7493	-0.4866	-0.032 9	0.02646 7664
TCGA-D5-692-7-01A-21R-19	hi g h	0.1 997 8	-0. 23 97 5	0.5 693	-0 .4 11 6	0.300 4	0.7729 5	0.36398	-0.4308	0.9462 2	-0.4991 7718

28-07											
TCGA-D5-692 8-01A-1 1R-192 8-07	hi g h	0.5 555 6	-0. 01 43 2	0.1 129 8	0. 5 2 6 3 2	0.407 41	0.5893 3	0.88068	0.1899 3	0.6752 5	-0.4366 54797
TCGA-D5-692 9-01A- 31R-19 28-07	lo w	0.0 202 5	-0. 64 87 5	-0.1 186	-0 .0 81 1	0.299 7	-0.260 2	-0.7876	0.5117 7	-0.807 7	-0.1042 59059
TCGA-D5-693 0-01A-1 1R-192 8-07	lo w	-0.4 089	-0. 46 30 5	0.2 777 7	0. 1 7 5 7 6	0.522 05	0.6477 6	-0.2895	-0.3366	0.7973 7	-0.6300 63967
TCGA-D5-693 1-01A-1 1R-192 8-07	hi g h	0.8 204 7	-0. 10 33 1	-0. 036 3	0. 5 2 2 0 7	0.228 96	0.4518 3	0.83032	-0.9245	0.7231 6	0.29664 5518
TCGA-D5-693 2-01A-1 1R-192 8-07	lo w	-0.9 803	-0. 62 27 4	0.1 844	-0 .5 3 5 9	-0.32 29	-0.380 8	-0.4953	0.4800 2	-0.703 9	0.20980 4077

TCGA-D5-700 0-01A-1 1R-A32 Z-07	hi g h	-0.9 693	0. 18 50 86	-0. 272 9	0. 5 1 9 7 2	0.070 76	0.1860 2	0.3399	-0.4592	0.7075 6	-0.5515 38917
TCGA-DM-A0 X9-01A -11R-A 155-07	hi g h	0.5 391 4	-0. 79 72 6	-0. 612	-0 .5 2 7 2	-0.00 79	-0.491 6	-0.4067	-0.607	-0.639 6	-0.0993 84286
TCGA-DM-A0 XD-01 A-12R- A155-0 7	hi g h	0.1 187 7	-0. 66 57 5	-0. 692 4	-0 .6 5 3 7	-0.17 25	-0.489 3	-0.6661	-0.0629	-0.446 9	0.24270 0877
TCGA-DM-A0 XF-01A -11R-A 155-07	hi g h	-0.1 002	-0. 67 12 3	-0. 248 1	-0 .7 7 7 5	-0.46 34	-0.665	-0.9124	-0.6585	-0.773 8	-0.4452 28448
TCGA-DM-A1 D0-01A -11R-A 155-07	hi g h	-0.4 877	-0. 83 90 2	-0. 541 8	-0 .4 6 6 6	-0.43 88	-0.699 3	-0.7449	0.1133	-0.794 1	0.64572 8294
TCGA-DM-A1	hi g	-0.4 176	-0. 31	-0. 602	-0 .6	-0.41 56	-0.499	-0.7077	-0.3202	-0.618 3	0.20425 8039

D4-01A -21R-A 155-07	h		61 4	9	5 2 3						
TCGA- DM-A1 D6-01A -21R-A 155-07	hi g h	-0.4 461	-0. 11 83 6	-0. 745 6	-0 .1 7 6 4	-0.31 81	-0.541 7	-0.792	-0.098	-0.334 5	0.17771 8678
TCGA- DM-A1 D7-01A -11R-A 155-07	hi g h	0.3 169 1	-0. 76 47 4	-0. 523 8	-0 .5 1 5 4	-0.48 34	-0.573 1	-0.7209	-0.4735	-0.695	-0.2483 30606
TCGA- DM-A1 D8-01A -11R-A 155-07	hi g h	0.0 388 6	-0. 57 71 9	-0. 739	-0 .5 8 5 4	-0.35 04	-0.681 2	-0.7417	0.3497 5	-0.818	0.01743 6265
TCGA- DM-A1 D9-01A -11R-A 155-07	hi g h	-0.0 093	-0. 78 19 3	-0. 672 5	-0 .6 0 7 2	-0.30 58	-0.420 5	-0.5304	-0.5271	-0.501 2	0.50399 3171
TCGA- DM-A1 DA-01 A-11R- A155-0 7	hi g h	-0.2 315	-0. 64 98 6	-0. 524 3	-0 .6 3 4 5	-0.58 06	-0.461 3	-0.7263	0.9168	-0.088 2	0.12561 7115

TCGA-DM-A1DB-01A-11R-A155-07	hi g h	0.8 270 4	-0. 17 60 3	-0. 540 6	-0 .7 9 0 9	-0.19 75	-0.524 7	-0.5884	0.0355 8	-0.795 2	-0.3225 77411
TCGA-DM-A1HA-01A-11R-A155-07	hi g h	0.6 562 7	-0. 59 83 6	-0. 684 5	-0 .6 2 8 6	-0.27 41	-0.673 3	-0.861	0.5172 4	-0.672 1	0.65420 4118
TCGA-DM-A1HB-01A-21R-A180-07	lo w	0.8 160 9	-0. 72 47 3	-0. 446 6	-0 .0 3 8 4	-0.40 92	0.3503 5	-0.8796	-0.526	0.7124 9	-0.3026 68585
TCGA-DM-A280-01A-12R-A16W-07	lo w	-0.1 648	0. 17 32 28	-0. 216 2	0. 0 3 7 3 8	-0.06 68	0.2904 7	-0.1505	-0.8478	0.7869 7	0.40851 5203
TCGA-DM-A282-01A-12R-A16W-07	hi g h	0.2 720 3	-0. 79 55	-0. 499 1	-0 .4 7 7	0.084 61	-0.675 9	-0.5577	-0.1637	-0.703 2	0.41779 5022

TCGA-DM-A2-85-01A-11R-A-16W-07	hi g h	-0.8 161	-0. 78 03 4	-0. 723 4	0. 4 9 7 2 7	-0.09 22	-0.281 2	0.17241	-0.78	-0.554 2	-0.1526 36399
TCGA-DM-A2-88-01A-11R-A-16W-07	lo w	-0.7 745	-0. 40 76 7	-0. 538	0. 1 3 1 0 4	-0.45 56	-0.315 7	-0.5851	0.7734	0.2105 6	0.14381 8623
TCGA-DM-A2-8A-01A-21R-A-32Y-07	hi g h	0.1 767 9	-0. 47 77 9	-0. 540 3	-0 .5 3 5 8	-0.39 57	-0.53	-0.746	0.0738 9	-0.697 2	-0.1278 113
TCGA-DM-A2-8C-01A-11R-A-32Y-07	lo w	0.2 402 8	-0. 16 30 6	-0. 640 4	-0 .5 9 2 7	-0.02 81	-0.592 4	-0.8325	0.4800 2	-0.859 2	0.74876 5771
TCGA-DM-A2-8E-01A-11R-A-32Y-07	hi g h	-0.6 727	-0. 00 25 6	-0. 600 4	-0 .6 3 3	-0.47 41	-0.780 9	-0.4395	0.5533 7	-0.768 3	0.34359 8885
TCGA-DM-A2	hi g	-0.9 343	-0. 71	-0. 721	-0 .5	-0.49 86	-0.717	-0.6377	-0.3213	-0.937	-0.0001 06933

8F-01A -11R-A 32Y-07	h		12 7	8	0 6 8						
TCGA- DM-A2 8G-01A -11R-A 16W-07	hi g h	0.2 424 7	-0. 01 37 5	-0. 630 5	-0 .4 6 9 6	-0.27 5	-0.682 8	-0.8916	0.4548 4	-0.791 3	0.86688 3718
TCGA- DM-A2 8H-01A -11R-A 16W-07	hi g h	0.9 912 4	0. 25 83 42	-0. 525 6	-0 .1 1 4 7	-0.33 6	-0.635 2	-0.5052	0.2424 7	-0.823 1	-0.5515 57584
TCGA- DM-A2 8K-01A -21R-A 32Y-07	lo w	-0.3 355	-0. 75 04	-0. 624 6	0. 5 7 4 0 2	-0.08 74	-0.057 3	-0.8883	0.4690 7	0.4602 3	-0.2735 40554
TCGA- DM-A2 8M-01 A-12R- A16W- 07	lo w	0.0 443 3	-0. 51 24 2	-0. 709	0. 0 9 9 3 3	-0.47 25	-0.371 9	-0.272	0.1822 7	0.0531 3	0.63661 4153
TCGA- F4-645 9-01A-1 1R-177	lo w	0.7 241 4	-0. 12 81 8	0.5 897 5	0. 4 6 1	0.509 99	0.3998 8	0.28407	-0.7417	-0.348 8	-0.2503 42977

4-07					7 3						
TCGA-F4-646 0-01A-1 1R-177 4-07	hi g h	-0.6 322	-0. 69 83 7	0.3 405 2	-0 .0 0 8 5	0.239 81	-0.447	0.36946	0.3377 1	-0.768 3	0.35418 9549
TCGA-F4-646 1-01A-1 1R-177 4-07	lo w	-0.7 614	0. 50 39 43	0.0 110 1	-0 .0 3 9	0.404 58	0.4874 1	0.78872	-0.5632	0.8218	0.51625 9413
TCGA-F4-646 3-01A-1 1R-172 3-07	lo w	0.9 781 1	-0. 44 03 4	0.2 132 3	-0 .3 1 6 9	0.699 84	0.4846 6	0.75917	0.2709 4	-0.311	0.73643 2295
TCGA-F4-656 9-01A-1 1R-177 4-07	lo w	0.3 037 8	0. 30 77 62	0.6 274 5	0. 3 2	0.280 35	0.6929 9	0.38259	-0.9354	0.6719 6	0.50027 4273
TCGA-F4-657 0-01A-1 1R-177 4-07	hi g h	0.3 585 1	0. 15 20 47	0.2 907 9	-0 .3 7 3 4	0.284 28	0.5928 6	0.39464	-0.7964	0.8411 8	-0.5783 23049
TCGA-F4-670	hi g	0.6 726	0. 12	0.6 279	0. 2	0.535 71	0.7690 4	0.64751	-0.2195	0.7639 6	-0.1426 22052

3-01A-1 1R-183 9-07	h	9	79 07	1	4 5 9						
TCGA- F4-670 4-01A-1 1R-183 9-07	hi g h	-0.7 154	-0. 46 80 8	0.0 752 7	0. 2 9 5 1 2	0.279 07	0.4646 6	0.91024	-0.8084	-0.608 3	-0.2576 62542
TCGA- F4-680 5-01A-1 1R-183 9-07	lo w	-0.2 501	0. 55 88 24	0.6 887 5	0. 2 4 4 4 1	0.622 57	0.8023 5	0.92885	-0.3454	0.6703 2	0.10069 1202
TCGA- F4-680 6-01A-1 1R-183 9-07	lo w	0.9 967 2	-0. 14 91 4	-0. 098 1	-0 .0 4 7 6	0.200 83	0.2460 3	-0.2906	0.4855	0.569	0.71091 6072
TCGA- F4-680 7-01A-1 1R-183 9-07	lo w	-0.5 993	-0. 22 40 5	0.5 258 6	0. 5 3 2 9	0.616 82	0.6362 4	0.84455	0.1932 1	0.6637 5	0.23806 9117
TCGA- F4-680 8-01A-1 1R-183	lo w	0.7 361 8	-0. 56 82 2	-0. 535 4	-0 .1 7 2	-0.31 83	-0.652 1	-0.3684	-0.4472	-0.535 3	0.27235 7448

9-07					1						
TCGA- F4-680 9-01A-1 1R-183 9-07	hi g h	-0.1 691	-0. 24 40 6	-0. 153	-0 .2 4 3 5	-0.04 16	-0.151 5	-0.5172	-0.8894	-0.596 9	0.21556 338
TCGA- F4-685 4-01A-1 1R-192 8-07	hi g h	-0.3 946	-0. 76 47	0.0 082 9	-0 .2 8 1 9	-0.17 2	-0.391	-0.0958	-0.3848	-0.767 3	0.02358 7493
TCGA- F4-685 5-01A-1 1R-192 8-07	lo w	-0.3 618	0. 33 88 74	0.3 071 9	0. 4 7 9 4	0.666 5	0.6017 5	0.29174	-0.1133	0.4871 5	0.14097 6413
TCGA- F4-685 6-01A-1 1R-192 8-07	lo w	0.6 967 7	-0. 08 54	0.2 019 2	0. 5 7 8 7 8	0.196 76	0.5060 7	0.24685	-0.4592	0.7627 3	-0.3412 15345
TCGA- G4-629 3-01A-1 1R-172 3-07	lo w	-0.2 447	-0. 20 37 9	0.1 406 3	-0 .3 4 9 9	-0.20 11	-0.529 6	0.41981	-0.4778	-0.030 7	0.91349 8742
TCGA- G4-629	hi g	-0.3 322	-0. 36	-0. 186	-0 .3	-0.12 02	-0.644 5	-0.723	-0.0115	-0.724 5	0.03743 6495

4-01A-1 1R-177 4-07	h		97 4	5	9 7						
TCGA- G4-629 5-01A-1 1R-172 3-07	lo w	-0.8 369	-0. 17 94 2	0.1 169 1	-0 .5 7 0 5	-0.47 29	0.1198 5	0.48221	-0.2217	0.0810 5	0.27741 4538
TCGA- G4-629 7-01A-1 1R-172 3-07	lo w	-0.8 982	-0. 47 42 2	0.4 012 8	0. 2 6 8 2 8	0.499 79	0.5016 9	0.87521	0.0125 9	0.5284 8	-0.3464 51856
TCGA- G4-629 8-01A-1 1R-172 3-07	hi g h	-0.6 782	-0. 70 65 2	-0. 463 2	-0 .4 2 8 9	-0.43 32	-0.606 1	-0.5369	0.4471 8	-0.477	0.80463 9062
TCGA- G4-629 9-01A-1 1R-177 4-07	hi g h	-0.6 377	-0. 65 12	0.1 242 6	-0 .7 4 9	0.070 55	0.2568	-0.7187	0.2381	-0.051 5	-0.5604 23731
TCGA- G4-630 2-01A-1 1R-172 3-07	lo w	0.1 505 2	0. 17 42 9	0.6 000 5	0. 2 7 0 0	0.730 22	0.7147 6	0.88287	0.2348 1	0.5569 6	-0.0041 5336

					3						
TCGA- G4-630 3-01A-1 1R-177 4-07	lo w	-0.3 782	-0. 57 53 6	0.3 414 3	-0 .3 8 0 7	-0.06 9	-0.213 4	0.08703	-0.7734	-0.507 7	0.02907 2957
TCGA- G4-630 4-01A-1 1R-192 8-07	hi g h	-0.3 487	-0. 32 09 9	-0. 649 8	-0 .4 1 4 8	-0.09 59	-0.51	-0.9573	0.9945 3	0.2764 8	0.85562 9297
TCGA- G4-630 6-01A-1 1R-177 4-07	lo w	-0.7 121	-0. 60 54 8	-0. 287 9	-0 .5 9 5 9	-0.55 17	-0.618	-0.8478	0.1067 3	-0.647 9	0.29470 9567
TCGA- G4-630 7-01A-1 1R-172 3-07	hi g h	0.6 891 1	-0. 18 41 8	-0. 610 8	-0 .5 9 2 2	-0.47 46	-0.897 6	-0.8106	-0.0181	-0.938 7	0.35062 6651
TCGA- G4-630 9-01A- 21R-18 39-07	lo w	0.9 113 3	-0. 57 74 4	-0. 042 6	0. 4 6 2 1 3	-0.52 19	0.0292	-0.6606	0.0114 9	0.136	-0.0996 05058
TCGA- G4-631	lo w	0.8 051	-0. 25	-0. 470	-0 .1	0.174 97	-0.323 5	0.99781	0.3607	-0.868	0.41639 0612

0-01A-1 1R-172 3-07		5	73 4	6	6 9 9						
TCGA- G4-631 1-01A-1 1R-172 3-07	low	-0.9 956	-0. 62 89 7	0.3 953 3	0. 0 0 2 4 1	0.226 72	0.61	0.36508	-0.3476	-0.132 5	0.31308 4524
TCGA- G4-631 4-01A-1 1R-172 3-07	high	-0.8 785	-0. 69 38 9	0.0 591 8	-0 .0 1 7 3	0.571 88	0.1663 4	0.94527	-0.4527	-0.544 9	0.73752 4201
TCGA- G4-631 5-01A-1 1R-172 3-07	low	0.5 172 4	-0. 31 36 1	-0. 364 5	-0 .2 4 8 2	-0.49 41	-0.524 6	-0.3826	-0.1407	-0.849 4	0.65014 7047
TCGA- G4-631 7-01A-1 1R-172 3-07	high	0.5 960 6	-0. 23 57 3	-0. 625	-0 .6 3 7 1	-0.59 87	-0.789 6	-0.642	-0.1078	-0.972 1	0.26795 5745
TCGA- G4-631 7-02A-1 1R-206 6-07	high	-0.1 034	0. 18 82 64	-0. 618	-0 .5 71 1	-0.50 32	-0.560 6	-0.8402	0.1351 9	-0.910 2	0.58012 9044

TCGA-G4-632 0-01A-1 1R-172 3-07	hi g h	-0.4 406	-0. 70 60 6	-0. 569 7 0	-0 .4 7 0 9	-0.60 19	-0.582 7	-0.6804	0.8697 3	0.0103 6	-0.4969 32009
TCGA-G4-632 1-01A-1 1R-172 3-07	lo w	-0.4 866	-0. 23 60 9	0.2 178 5 0	0. 3 0 4 2 3	-0.21 76	0.1465 7	0.41215	-0.2895	0.8883 2	-0.5048 84027
TCGA-G4-632 2-01A-1 1R-172 3-07	hi g h	-0.4 056	0. 00 80 59	-0. 484 7 0	0. 0 6 4 6 3	-0.16 51	-0.281 7	-0.4953	0.8292 3	-0.394 4	-0.2055 34613
TCGA-G4-632 3-01A-1 1R-172 3-07	lo w	0.4 657 9	0. 64 73 63	-0. 193 1 0	-0 .3 5 9 6	0.153 81	-0.498 3	0.26327	-0.5764	0.3477 5	0.45600 2929
TCGA-G4-658 6-01A-1 1R-177 4-07	hi g h	-0.5 917	-0. 62 30 1	-0. 492 2 0	-0 .7 5 1 7	-0.68 59	-0.367 1	-0.7625	0.3147 2	0.0925 5	-0.7487 95377
TCGA-G4-658	lo w	-0.9 704	-0. 12	-0. 057	-0 .0	-0.09 85	0.5316 9	-0.3279	-0.5183	0.8981 4	-0.5482 70991

8-01A-1 1R-177 4-07			72 4	8	2 2 2						
TCGA- G4-662 5-01A- 21R-17 74-07	hi g h	0.4 570 3	0. 27 61 36	0.3 161 7	-0 .4 1 4 9	0.022 07	0.5544	0.74603	-0.6858	0.0452 8	-0.4714 83065
TCGA- G4-662 6-01A-1 1R-177 4-07	hi g h	-0.4 439	-0. 54 01	-0. 626 1	-0 .6 2 3 9	-0.60 23	-0.628 9	-0.6957	-0.5205	-0.707 6	-0.5328 73722
TCGA- G4-662 7-01A-1 1R-177 4-07	lo w	0.1 122 1	-0. 01 72 9	0.5 594 8	0. 8 3 9 3 6	0.477 26	0.6970 4	1	-0.0597	0.6818 2	0.21423 9791
TCGA- G4-662 8-01A-1 1R-183 9-07	lo w	-0.6 541	0. 28 78 62	0.0 256 1	-0 .0 3 2 9	0.303 25	0.7111 6	0.73508	0.7493 2	0.8411 8	-0.3277 48089
TCGA- NH-A5 0T-01A -11R-A 28H-07	hi g h	-0.1 253	-0. 11 41	-0. 487 4	-0 .6 1 8 1	-0.24 55	-0.706 3	-0.3782	0.8675 4	-0.674	0.33200 6946

TCGA-NH-A50U-01A-33R-A37K-07	hi g h	-0.5 862	-0. 52 51 8	-0. 669 9 01	0. 0 3 01 1	-0.23 92	-0.636 1	-0.7964	0.2019 7	-0.730 6	-0.0285 2441
TCGA-NH-A50V-01A-11R-A28H-07	hi g h	-0.9 901	-0. 14 63	-0. 298 4	-0 .1 3 6 8	0.026 64	-0.132 3	-0.4165	-0.827	-0.435 4	-0.0822 81953
TCGA-NH-A5I V-01A-42R-A37K-07	hi g h	-0.9 792	0. 06 35 62	-0. 341 2	0. 2 9 3 4 1	-0.07 2	0.0346 9	-0.6946	0.5041 1	-0.368 2	-0.3183 84796
TCGA-NH-A6GA-01A-11R-A37K-07	hi g h	-0.2 184	-0. 48 06 7	-0. 348 2	-0 .2 5 6	-0.47 21	-0.576 2	-0.2994	0.0498 1	-0.7119	-0.0565 00274
TCGA-NH-A6GB-01A-11R-A37K-07	hi g h	-0.4 198	-0. 32 57 6	-0. 182 5	-0 .2 6 7 8	-0.61 15	-0.476 3	-0.6508	-0.1363	-0.204 2	0.55787 164
TCGA-	hi	-0.7	-0.	-0.	-0	-0.09	-0.425	-0.8938	-0.3082	-0.643	0.40983

NH-A6	g	176	59	517	.5	63	8			6	3827
GC-01	h		53	7	3						
A-12R-			8		5						
A41B-0					8						
7											
TCGA-	hi	-0.5	-0.	-0.	-0	-0.27	-0.660	-0.8763	0.9540	-0.836	0.63573
NH-A8	g	884	49	522	.7	48	4		2	3	9152
F7-01A	h		59	3	3						
-11R-A			9		8						
41B-07					1						
TCGA-	hi	-0.4	0.	-0.	-0	-0.35	-0.791	-0.8183	0.0925	-0.978	0.22909
NH-A8	g	253	02	625	.5	17				1	8071
F7-06A	h		73	5	0						
-31R-A			79		4						
41B-07					4						
TCGA-	hi	-0.9	-0.	-0.	-0	-0.14	-0.573	-0.5993	0.0060	-0.686	0.06042
NH-A8	g	748	32	407	.0	4	4		2	2	8583
F8-01A	h		14	4	8						
-72R-A			2		8						
41B-07					8						
TCGA-	hi	-0.0	-0.	-0.	-0	-0.42	-0.720	-0.5709	0.1986	-0.657	0.49750
QG-A5	g	794	51	288	.5	69	3		9	2	8867
YV-01	h		10	9	9						
A-11R-			7		2						
A28H-0					8						
7											
TCGA-	lo	-0.6	-0.	-0.	0.	0.247	-0.199	-0.1319	0.9518	-0.634	-0.4637
QG-A5	w	037	32	230	2	94	1		3	2	1685
YW-01			65	9	5						

A-11R- A28H-0 7			3		8 5						
TCGA- QG-A5 YX-01 A-11R- A28H-0 7	lo w	0.4 154 4	0. 01 53 34	-0. 662 9	0. 5 0 3 8 5	-0.45 24	-0.522 7	-0.7132	0.9047 6	-0.701	-0.5357 61482
TCGA- QG-A5 Z2-01A -11R-A 28H-07	hi g h	-0.9 135	-0. 35 68 6	-0. 396 7	0. 3 6 4 2 5	0.002 73	-0.531 7	-0.6683	0.6967 7	-0.358 5	-0.3071 08134
TCGA- QL-A9 7D-01A -12R-A 41B-07	lo w	-0.7 044	-0. 05 20 5	-0. 124 4	-0 .6 3 1 2	-0.54 2	-0.460 6	-0.0936	0.0147 8	-0.464 4	-0.3390 60591
TCGA- RU-A8 FL-01A -11R-A 37K-07	hi g h	-0.2 578	-0. 01 49 9	-0. 434 7	-0 .5 6	-0.53 16	-0.725 6	-0.6935	-0.6464	-0.859 3	0.38938 2039
TCGA- SS-A7 HO-01 A-21R-	hi g h	0.5 052	-0. 57 56 3	-0. 318 9	-0 .5 9 6	-0.46 58	-0.641	-0.6431	0.9507 4	-0.742 6	0.62095 4471

A37K-07					1						
TCGA-T9-A92-H-01A-11R-A3-7K-07	hi g h	-0.7 635	0. 04 76 19	-0. 632 2	-0 .5 1 3 1	-0.11 92	-0.633 9	-0.9825	0.5161 5	-0.842 8	0.34320 2817
TCGA-WS-AB-45-01A-11R-A-41B-07	lo w	-0.9 091	-0. 22 81 3	0.6 799 4	0. 5 7 9 4	0.653 46	0.7928 6	0.89819	0.4800 2	0.6790 8	-0.3379 9289