

CpG	log(Fold change)	logCPM	PValue	FDR	Gene_Symbol	Chromosome	Genomic_Coordinate
cg04456219	-1.921396164	3.694124125	5.25747E-12	2.05E-06		7	17274337
cg03290131	-1.817890013	3.622232879	2.30857E-09	0.000180062	DUSP5	10	112263831
cg19519319	-1.78791245	3.656103492	1.20327E-09	0.000156419	MOBK2A	19	2085301
cg05101437	-1.779473557	3.58353246	2.79042E-08	0.000978618	CDK6	7	92262970
cg26063719	-1.768250224	3.687959084	4.6361E-10	9.04008E-05	VIM	10	17273187
cg22274117	-1.735679024	3.609927831	1.58453E-08	0.000699314	ATXN1	6	16713613
cg07101841	-1.711917058	3.563860137	1.31443E-07	0.001767622		17	75315527
cg12435551	-1.710605732	3.602068273	3.76872E-08	0.000979832	SPAG17	1	118679290
cg00664697	-1.709190704	3.64782819	1.75629E-08	0.000699314		16	80061290
cg25416067	-1.705930474	3.564214521	1.31443E-07	0.001767622		17	75315667
cg05343811	-1.698253691	3.643171556	1.79318E-08	0.000699314	NEK9	14	75590896
cg04650676	-1.695424102	3.554871288	9.02091E-08	0.001465845		17	75315486
cg01288184	-1.685588007	3.603422175	1.05296E-07	0.001634935	CABLES1	18	20811408
cg14204586	-1.669487537	3.637461736	4.36581E-08	0.000996854	ARHGEF2	1	155931858
cg21876918	-1.661459613	3.632114883	4.44041E-08	0.000996854	MOBK2A	19	2085483
cg07830160	-1.655369224	3.608993116	1.09E-07	0.001634935		1	159880327
cg22806907	-1.636927764	3.567036706	4.74011E-07	0.004621442	PLEKHH3	17	40826212
cg01702055	-1.634497158	3.71985559	1.7646E-09	0.000172042		6	13303065
cg02326386	-1.625461139	3.727977193	3.19849E-09	0.000207894	MOBK2A	19	2085286
cg20003368	-1.617477333	3.574938095	5.5659E-07	0.005047957		6	44026475
cg01889574	-1.614203627	3.579754399	6.17813E-07	0.00523779	CD82	11	44590889
cg08443563	-1.614064566	3.68252701	1.30751E-08	0.000699314		2	112456811
cg03498081	-1.612671667	3.669061877	3.53414E-08	0.000979832		16	80061357
cg07126235	-1.600933106	3.584267487	6.17813E-07	0.00523779	CUL9	6	43192225
cg22793129	-1.583850332	3.672975513	3.26218E-08	0.000978618	MOBK2A	19	2085297
cg07677157	-1.58226636	3.672715415	3.26218E-08	0.000978618		12	66050928
cg06021088	-1.581151976	3.61548566	2.70477E-07	0.003102414	BIN1	2	127822551
cg08995609	-1.578217122	3.602229294	6.74116E-07	0.005257917	RIN1	11	66104115
ch.10.119748	-1.562893618	3.591753005	6.56702E-07	0.005242065		10	119758791
cg16468729	-1.561388195	3.609355066	6.58642E-07	0.005242065	IL8	4	74606465
cg04470054	-1.560216093	3.660989912	8.15082E-08	0.001382045	RPTOR	17	78830472
cg22579075	-1.554517251	3.652896759	2.03985E-07	0.002485978	SGCE	7	94250352
cg20873416	-1.554475616	3.615809018	2.70477E-07	0.003102414		6	30737068
cg23683800	-1.54757334	3.592411756	1.68152E-06	0.009107901		10	115086103
cg02578087	-1.534837687	3.677443437	6.76087E-08	0.001198474	C3orf32	3	8671361
cg03063658	-1.526754084	3.654089967	4.21625E-07	0.004433731	SH3RF3	2	109949132
cg17184704	-1.521968877	3.665471052	1.68712E-07	0.002122429		10	11727286
cg07094298	-1.52048073	3.608994759	1.58709E-06	0.009107901	TNIP2	4	2748026
cg27115863	-1.519954234	3.606694826	1.58709E-06	0.009107901		22	37921640
cg02389317	-1.517352316	3.69695461	4.85664E-08	0.000996854		12	76577488
cg23907053	-1.515748234	3.599403487	1.6508E-06	0.009107901	RAB3IP	12	70215816
cg25954539	-1.512461001	3.638577972	5.11431E-07	0.004864654	HLA-B	6	31323677
cg10502118	-1.511712485	3.612732862	1.49967E-06	0.009107901	RFTN1	3	16553697
cg05876246	-1.511000434	3.61859939	6.31595E-07	0.005240706		8	81831079
cg03272310	-1.51031234	3.645139845	4.66356E-07	0.004621442		17	39704454
cg15832822	-1.507703976	3.673366493	1.51712E-07	0.001972181		15	45018591
cg13942186	-1.499269499	3.633409547	5.5536E-07	0.005047957	EXD3	9	140305942
cg06474225	-1.490815132	3.727364233	5.40886E-08	0.001004467	HTRA1	10	124228770
cg23261919	-1.484911939	3.686475237	1.20435E-07	0.00173955		10	135072960

cg02753187	-1.482681086	3.630445155	1.28491E-06	0.008082202	CALCOCO2	17	46919180
cg10025586	-1.478638868	3.736509456	4.67865E-08	0.000996854	WHAMM	15	83501699
cg13289884	-1.478627635	3.593295175	1.68152E-06	0.009107901	CDKN1B	12	12872686
cg18082788	-1.478036877	3.592945713	1.68152E-06	0.009107901	ZC3H12D	6	149806339
cg04786142	-1.477885127	3.656722941	4.21625E-07	0.004433731		1	234908381
cg07474842	-1.476976298	3.651829877	9.44797E-07	0.006579601	MAP3K5	6	136915088
cg13787850	-1.471486191	3.651394702	9.44797E-07	0.006579601		9	102195951
cg09029902	-1.468241673	3.631154814	1.28491E-06	0.008082202	ZNF217	20	52199594
cg21435684	-1.468235177	3.60052449	1.6508E-06	0.009107901		17	80255457
cg14665413	-1.467200082	3.631430445	1.28491E-06	0.008082202	TLR6	4	38859728
cg13921921	-1.45829373	3.649430987	9.44797E-07	0.006579601	ARHGFE2	1	155931763
cg19239199	-1.426358397	3.655108377	1.84582E-06	0.0097276		7	852714
cg27132471	-1.421274324	3.654288005	1.84582E-06	0.0097276	SLCO3A1	15	92613280
cg11201447	-1.4177971	3.760638379	5.26299E-08	0.001004467	MIR1204;PVT1	8	128808063
cg25874782	-1.411511638	3.689717766	9.14625E-07	0.006579601	NSMAF	8	59508474
cg19163395	-1.408404216	3.702634087	3.73783E-07	0.004164863	HDAC5	17	42164433
cg07093324	-1.406869578	3.681392563	1.06048E-06	0.007130567	ACTR3	2	114652143
cg21708130	-1.40432498	3.694247289	4.3202E-07	0.004433731	LRRFIP1	2	238596537
cg16107628	-1.403112753	3.690634107	9.14625E-07	0.006579601	TAGLN2	1	159894061
cg10777887	-1.401263963	3.696429764	7.86476E-07	0.006014011	RAB8B	15	63484315
cg16709353	-1.394500331	3.682206181	1.06048E-06	0.007130567	TPCN2	11	68856817
cg26680608	-1.363506977	3.733151506	6.12668E-07	0.00523779	MAP3K5	6	136915556
cg18670236	-1.348005628	3.707917467	1.189E-06	0.007859198	CHCHD6	3	126630478
cg07156249	-1.344025251	3.694165315	1.63853E-06	0.009107901	PSMB9;TAP1	6	32822911
cg06228828	-1.270954746	3.765763295	1.6052E-06	0.009107901	DLEU2	13	50653048