

**Supplemental Table 2. Annotation of most variable CpG probes (n=1515).**

Probe_ID	chr	pos	strand	Unique_Genes_Mapped	Gene_Region_Mapped	Relation_to_Island	Island_Name
cg16691821	chr1	2375627	-	intergenic	none	Island	chr1:2374818-2375814
cg22337407	chr1	11046185	-	intergenic	none	OpenSea	
cg13788258	chr1	13840381	-	intergenic	none	Island	chr1:13839505-13840613
cg05046525	chr1	35395821	+	intergenic	none	Island	chr1:35394747-35396206
cg03257575	chr1	46951318	-	intergenic	none	Island	chr1:46951168-46951792
cg04908380	chr1	47915862	+	intergenic	none	Island	chr1:47915639-47915952
cg13906377	chr1	63792695	-	intergenic	none	N_Shelf	chr1:63795363-63796140
cg22025849	chr1	70032907	-	intergenic	none	N_Shore	chr1:70032967-70034495
cg24525913	chr1	72749880	+	intergenic	none	S_Shore	chr1:72748471-72749736
cg24437625	chr1	72750671	-	intergenic	none	S_Shore	chr1:72748471-72749736
cg07923233	chr1	76080727	+	intergenic	none	Island	chr1:76080454-76080808
cg21081832	chr1	76081379	-	intergenic	none	Island	chr1:76081378-76082365
cg20467168	chr1	76081408	+	intergenic	none	Island	chr1:76081378-76082365
cg27547954	chr1	76081962	+	intergenic	none	Island	chr1:76081378-76082365
cg10101533	chr1	83648176	+	intergenic	none	OpenSea	
cg26611723	chr1	91173030	+	intergenic	none	S_Shore	chr1:91172102-91172771
cg01722423	chr1	111150133	+	intergenic	none	Island	chr1:111148983-111150186
cg08770506	chr1	111150185	+	intergenic	none	Island	chr1:111148983-111150186
cg19356191	chr1	116371337	-	intergenic	none	S_Shore	chr1:116370810-116371303
cg12062819	chr1	156358231	+	intergenic	none	Island	chr1:156358050-156358252
cg26248173	chr1	166853578	-	intergenic	none	Island	chr1:166853253-166853790
cg06623935	chr1	214159131	-	intergenic	none	N_Shore	chr1:214160798-214161034
cg11537367	chr1	218338772	-	intergenic	none	Island	chr1:218337780-218339033
cg14468913	chr1	218338809	-	intergenic	none	Island	chr1:218337780-218339033
cg06146698	chr1	241587099	-	intergenic	none	N_Shore	chr1:241587601-241587883
cg15454726	chr1	241587609	-	intergenic	none	Island	chr1:241587601-241587883
cg16003102	chr1	241587783	+	intergenic	none	Island	chr1:241587601-241587883
cg21452805	chr1	244014465	+	intergenic	none	Island	chr1:244013802-244014592
cg21597595	chr2	5506228	-	intergenic	none	OpenSea	
cg17213402	chr2	5813650	+	intergenic	none	Island	chr2:5813482-5813710
cg24770624	chr2	20068871	+	intergenic	none	Island	chr2:20068428-20068907
cg06168026	chr2	45162196	-	intergenic	none	Island	chr2:45161427-45163058

cg20459525	chr2	45395870	-	intergenic	none	Island	chr2:45395869-45398186
cg09862801	chr2	45396991	-	intergenic	none	Island	chr2:45395869-45398186
cg06131143	chr2	48757612	+	intergenic	none	Island	chr2:48757211-48757785
cg19384241	chr2	55393977	+	intergenic	none	OpenSea	
cg00015058	chr2	66652949	-	intergenic	none	Island	chr2:66652691-66654218
cg10089527	chr2	66653254	+	intergenic	none	Island	chr2:66652691-66654218
cg19656974	chr2	66653415	-	intergenic	none	Island	chr2:66652691-66654218
cg13451280	chr2	68870812	-	intergenic	none	Island	chr2:68870351-68871055
cg01717446	chr2	71503566	-	intergenic	none	Island	chr2:71503547-71504233
cg13686615	chr2	71503742	-	intergenic	none	Island	chr2:71503547-71504233
cg22686854	chr2	79220029	+	intergenic	none	N_Shore	chr2:79220192-79220592
cg25479788	chr2	79220217	+	intergenic	none	Island	chr2:79220192-79220592
cg10156366	chr2	79220381	+	intergenic	none	Island	chr2:79220192-79220592
cg02340018	chr2	105469315	-	intergenic	none	Island	chr2:105468851-105473488
cg11014373	chr2	105479054	-	intergenic	none	Island	chr2:105478600-105479188
cg17456678	chr2	119532314	+	intergenic	none	Island	chr2:119532065-119532315
cg27664844	chr2	119532486	-	intergenic	none	S_Shore	chr2:119532065-119532315
cg20593831	chr2	119532492	-	intergenic	none	S_Shore	chr2:119532065-119532315
cg09385093	chr2	119607885	+	intergenic	none	Island	chr2:119607378-119607910
cg11236727	chr2	119609592	-	intergenic	none	N_Shore	chr2:119611296-119611881
cg18522518	chr2	127534476	+	intergenic	none	N_Shore	chr2:127534732-127535186
cg08535260	chr2	127643971	+	intergenic	none	Island	chr2:127643800-127644104
cg23460843	chr2	127644075	+	intergenic	none	Island	chr2:127643800-127644104
cg22830113	chr2	127783168	+	intergenic	none	Island	chr2:127783081-127783311
cg02139871	chr2	127783370	-	intergenic	none	S_Shore	chr2:127782613-127782829
cg14261272	chr2	127976400	-	intergenic	none	Island	chr2:127976389-127977667
cg11107669	chr2	127976613	+	intergenic	none	Island	chr2:127976389-127977667
cg03738707	chr2	128453335	+	intergenic	none	Island	chr2:128453174-128453446
cg06480249	chr2	130635166	-	intergenic	none	OpenSea	
cg08901662	chr2	131595321	-	intergenic	none	S_Shore	chr2:131594139-131595302
cg12796383	chr2	144694405	-	intergenic	none	N_Shore	chr2:144694666-144695180
cg16263943	chr2	144695179	+	intergenic	none	Island	chr2:144694666-144695180
cg12769138	chr2	168150203	-	intergenic	none	Island	chr2:168149033-168150797
cg23064609	chr2	175208594	-	intergenic	none	Island	chr2:175208415-175209076

cg13501907	chr2	176997504	+	intergenic	none	S_Shore	chr2:176993479-176995557
cg04739123	chr2	177502854	+	intergenic	none	Island	chr2:177502240-177502910
cg22696982	chr2	177502905	-	intergenic	none	Island	chr2:177502240-177502910
cg16650529	chr2	182548750	-	intergenic	none	Island	chr2:182547873-182549177
cg08302913	chr2	182548786	-	intergenic	none	Island	chr2:182547873-182549177
cg20019410	chr2	207939050	-	intergenic	none	OpenSea	
cg16844875	chr2	237476791	+	intergenic	none	Island	chr2:237476311-237477263
cg22991512	chr3	14643854	-	intergenic	none	Island	chr3:14643718-14644830
cg00901264	chr3	14644790	+	intergenic	none	Island	chr3:14643718-14644830
cg07040834	chr3	44063541	-	intergenic	none	Island	chr3:44063314-44063837
cg14484056	chr3	62365084	-	intergenic	none	S_Shore	chr3:62364017-62364316
cg05939970	chr3	127795340	-	intergenic	none	Island	chr3:127794369-127796136
cg13719885	chr3	127795394	-	intergenic	none	Island	chr3:127794369-127796136
cg02020882	chr3	128336728	+	intergenic	none	Island	chr3:128336406-128337113
cg15595044	chr3	128336857	-	intergenic	none	Island	chr3:128336406-128337113
cg12879143	chr3	138679347	-	intergenic	none	Island	chr3:138679244-138679579
cg21624902	chr3	138679358	-	intergenic	none	Island	chr3:138679244-138679579
cg07393736	chr3	172167810	+	intergenic	none	Island	chr3:172167526-172167866
cg13519184	chr3	173114306	+	intergenic	none	N_Shore	chr3:173115404-173115775
cg04599965	chr4	571042	-	intergenic	none	Island	chr4:570950-571768
cg07245225	chr4	571120	-	intergenic	none	Island	chr4:570950-571768
cg08480901	chr4	1515011	-	intergenic	none	Island	chr4:1514858-1515210
cg14964336	chr4	1523275	+	intergenic	none	Island	chr4:1521703-1523281
cg17214502	chr4	4869172	+	intergenic	none	Island	chr4:4868440-4869173
cg10946669	chr4	20253130	-	intergenic	none	N_Shore	chr4:20253276-20256868
cg13755796	chr4	20253514	-	intergenic	none	Island	chr4:20253276-20256868
cg06973595	chr4	55093096	+	intergenic	none	Island	chr4:55092961-55093242
cg21585438	chr4	62067189	-	intergenic	none	Island	chr4:62065883-62068801
cg10870083	chr4	62068185	-	intergenic	none	Island	chr4:62065883-62068801
cg15205733	chr4	113627483	+	intergenic	none	Island	chr4:113626739-113627507
cg22649311	chr4	134067896	+	intergenic	none	N_Shore	chr4:134069162-134070442
cg22366088	chr4	154713789	-	intergenic	none	Island	chr4:154713537-154714240
cg00966099	chr4	184718401	+	intergenic	none	Island	chr4:184718263-184719754
cg05648010	chr5	53545	-	intergenic	none	Island	chr5:53111-54264

cg18738814	chr5	92385	-	intergenic	none	Island	chr5:92007-92438
cg25378916	chr5	1875013	-	intergenic	none	Island	chr5:1874907-1879032
cg14024788	chr5	1875611	+	intergenic	none	Island	chr5:1874907-1879032
cg26195178	chr5	1885716	+	intergenic	none	Island	chr5:1881924-1887743
cg12523526	chr5	2756005	-	intergenic	none	Island	chr5:2748368-2757024
cg05659097	chr5	2757244	-	intergenic	none	S_Shore	chr5:2748368-2757024
cg01939562	chr5	3105012	+	intergenic	none	OpenSea	
cg10427452	chr5	3122030	-	intergenic	none	OpenSea	
cg11857997	chr5	3591992	+	intergenic	none	Island	chr5:3590644-3592000
cg04144394	chr5	3594178	+	intergenic	none	N_Shore	chr5:3594467-3603054
cg27586797	chr5	13664584	-	intergenic	none	OpenSea	
cg22697364	chr5	32709859	+	intergenic	none	N_Shore	chr5:32709910-32714450
cg17045804	chr5	32710009	-	intergenic	none	Island	chr5:32709910-32714450
cg18064852	chr5	36690457	-	intergenic	none	Island	chr5:36690207-36690658
cg00132108	chr5	36690657	+	intergenic	none	Island	chr5:36690207-36690658
cg06843889	chr5	42949542	+	intergenic	none	N_Shore	chr5:42951076-42952410
cg13930261	chr5	42949882	-	intergenic	none	N_Shore	chr5:42951076-42952410
cg10932018	chr5	54516487	+	intergenic	none	Island	chr5:54516267-54516919
cg08350776	chr5	54516538	+	intergenic	none	Island	chr5:54516267-54516919
cg24828151	chr5	54516779	+	intergenic	none	Island	chr5:54516267-54516919
cg18456523	chr5	54516805	+	intergenic	none	Island	chr5:54516267-54516919
cg23378989	chr5	131991993	+	intergenic	none	Island	chr5:131991554-131992304
cg11608150	chr5	135415948	-	intergenic	none	N_Shore	chr5:135416204-135416475
cg24799909	chr5	145724482	+	intergenic	none	Island	chr5:145724294-145724551
cg11601027	chr5	153852690	-	intergenic	none	N_Shore	chr5:153853056-153853551
cg24202381	chr5	153862450	+	intergenic	none	Island	chr5:153862142-153862451
cg02326568	chr5	158533621	-	intergenic	none	Island	chr5:158533557-158534000
cg01088410	chr5	170739179	-	intergenic	none	Island	chr5:170735169-170739863
cg13004182	chr5	172665707	-	intergenic	none	Island	chr5:172665306-172666072
cg05849109	chr5	180531288	+	intergenic	none	S_Shore	chr5:180531008-180531218
cg00631329	chr6	26305371	+	intergenic	none	OpenSea	
cg13736514	chr6	26305472	-	intergenic	none	OpenSea	
cg13974773	chr6	27463217	+	intergenic	none	Island	chr6:27463176-27463379
cg09987651	chr6	27463667	+	intergenic	none	S_Shore	chr6:27463176-27463379

cg27131891	chr6	27513414	+	intergenic	none	OpenSea	
cg05310764	chr6	27513479	-	intergenic	none	OpenSea	
cg27658416	chr6	28603033	+	intergenic	none	Island	chr6:28602853-28603295
cg06466508	chr6	28641622	-	intergenic	none	OpenSea	
cg03442350	chr6	28641629	-	intergenic	none	OpenSea	
cg23691021	chr6	28641651	+	intergenic	none	OpenSea	
cg02841000	chr6	28642062	-	intergenic	none	OpenSea	
cg08957069	chr6	28743700	+	intergenic	none	OpenSea	
cg05404698	chr6	28956247	-	intergenic	none	Island	chr6:28956106-28956578
cg25255293	chr6	28979290	-	intergenic	none	Island	chr6:28979246-28979499
cg21107549	chr6	28979307	-	intergenic	none	Island	chr6:28979246-28979499
cg08789053	chr6	28979437	-	intergenic	none	Island	chr6:28979246-28979499
cg02665416	chr6	28984461	+	intergenic	none	Island	chr6:28984418-28984686
cg26816707	chr6	101842034	-	intergenic	none	S_Shore	chr6:101841425-101841905
cg20295992	chr6	108440280	-	intergenic	none	Island	chr6:108437998-108441208
cg09386619	chr6	125420923	-	intergenic	none	Island	chr6:125420743-125421141
cg06700935	chr7	1704584	-	intergenic	none	Island	chr7:1703861-1710517
cg06134410	chr7	1705349	+	intergenic	none	Island	chr7:1703861-1710517
cg20753954	chr7	1706809	+	intergenic	none	Island	chr7:1703861-1710517
cg11362988	chr7	1706883	+	intergenic	none	Island	chr7:1703861-1710517
cg06367154	chr7	1707338	+	intergenic	none	Island	chr7:1703861-1710517
cg23617583	chr7	20817296	-	intergenic	none	N_Shore	chr7:20817455-20818227
cg08637618	chr7	27279329	-	intergenic	none	Island	chr7:27278945-27279469
cg03704308	chr7	42533414	+	intergenic	none	S_Shore	chr7:42533076-42533283
cg13990351	chr7	64349133	+	intergenic	none	N_Shore	chr7:64349424-64350151
cg19082708	chr7	64349557	-	intergenic	none	Island	chr7:64349424-64350151
cg24002887	chr7	64407743	+	intergenic	none	Island	chr7:64407589-64408299
cg05841659	chr7	64712472	+	intergenic	none	Island	chr7:64712213-64712786
cg12004183	chr7	71217124	-	intergenic	none	OpenSea	
cg01680010	chr7	96647117	-	intergenic	none	S_Shore	chr7:96645786-96646599
cg08832624	chr7	98099917	+	intergenic	none	Island	chr7:98099882-98100289
cg24494316	chr7	113726705	+	intergenic	none	Island	chr7:113724924-113727795
cg03793066	chr7	113726854	-	intergenic	none	Island	chr7:113724924-113727795
cg24490630	chr7	113726873	-	intergenic	none	Island	chr7:113724924-113727795

cg07959771	chr7	121956740	-	intergenic	none	Island	chr7:121956543-121957341
cg00158528	chr7	121956859	-	intergenic	none	Island	chr7:121956543-121957341
cg21005154	chr7	140340155	+	intergenic	none	Island	chr7:140339997-140341136
cg07028821	chr7	140773905	+	intergenic	none	Island	chr7:140772358-140774560
cg20183619	chr7	155241490	-	intergenic	none	Island	chr7:155241323-155243757
cg14521995	chr7	157263638	-	intergenic	none	S_Shore	chr7:157262951-157263458
cg00280177	chr8	24799870	-	intergenic	none	Island	chr8:24799703-24800147
cg08097281	chr8	26724744	+	intergenic	none	S_Shore	chr8:26721642-26724566
cg09516839	chr8	26724782	+	intergenic	none	S_Shore	chr8:26721642-26724566
cg17504341	chr8	26724836	+	intergenic	none	S_Shore	chr8:26721642-26724566
cg11787346	chr8	55367611	+	intergenic	none	Island	chr8:55366180-55367628
cg22682682	chr8	57070217	+	intergenic	none	S_Shore	chr8:57069687-57070047
cg19749660	chr8	65284514	+	intergenic	none	N_Shore	chr8:65286067-65286659
cg16464373	chr8	65293734	+	intergenic	none	S_Shelf	chr8:65290108-65290946
cg00588920	chr8	72917147	-	intergenic	none	N_Shore	chr8:72917305-72917641
cg16814680	chr8	91681699	+	intergenic	none	OpenSea	
cg00563873	chr8	93115461	-	intergenic	none	Island	chr8:93114056-93115979
cg26980111	chr8	132321917	+	intergenic	none	OpenSea	
cg22863209	chr8	142425581	+	intergenic	none	Island	chr8:142425440-142425716
cg06573787	chr8	143070187	-	intergenic	none	OpenSea	
cg16296826	chr8	143530749	+	intergenic	none	Island	chr8:143530645-143530872
cg06166932	chr8	143530800	-	intergenic	none	Island	chr8:143530645-143530872
cg02707869	chr8	143532613	+	intergenic	none	Island	chr8:143531118-143534495
cg04812475	chr9	17906561	+	intergenic	none	Island	chr9:17906419-17907488
cg02649279	chr9	29212689	+	intergenic	none	Island	chr9:29212171-29212819
cg14583869	chr9	34701531	-	intergenic	none	Island	chr9:34701218-34701834
cg02671126	chr9	34701735	+	intergenic	none	Island	chr9:34701218-34701834
cg14172603	chr9	37037526	+	intergenic	none	Island	chr9:37034135-37038341
cg17534202	chr9	96721102	+	intergenic	none	Island	chr9:96720586-96723189
cg18794404	chr1	22542024	+	intergenic	none	Island	chr10:22540707-22542739
cg03319479	chr1	23487758	-	intergenic	none	Island	chr10:23487757-23488543
cg18937827	chr1	27547704	-	intergenic	none	Island	chr10:27547668-27548402
cg07875430	chr1	27547845	-	intergenic	none	Island	chr10:27547668-27548402
cg11986813	chr1	43429144	-	intergenic	none	Island	chr10:43428167-43429460

cg10786572	chr1 0	5463232 2	-	intergenic	none	S_Shore	chr10:5463121 1-54631426
cg07451261	chr1 0	1024150 86	+	intergenic	none	Island	chr10:1024144 25-102416315
cg22689833	chr1 0	1024159 91	-	intergenic	none	Island	chr10:1024144 25-102416315
cg24053165	chr1 0	1024692 94	-	intergenic	none	N_Shore	chr10:1024698 06-102470341
cg17453460	chr1 0	1183694 23	+	intergenic	none	Island	chr10:1183685 79-118369424
cg26678605	chr1 0	1189250 11	+	intergenic	none	N_Shore	chr10:1189252 71-118925529
cg19111459	chr1 0	1227087 39	+	intergenic	none	Island	chr10:1227085 10-122708899
cg07998396	chr1 0	1300085 59	-	intergenic	none	Island	chr10:1300085 58-130009620
cg20099104	chr1 0	1303396 69	+	intergenic	none	Island	chr10:1303395 26-130339777
cg25446309	chr1 0	1317702 23	+	intergenic	none	Island	chr10:1317611 69-131771696
cg05825559	chr1 0	1332525 19	+	intergenic	none	OpenSea	
cg15344220	chr1 1	8040551	-	intergenic	none	Island	chr11:8040409- 8041558
cg13569486	chr1 1	8290738	-	intergenic	none	S_Shore	chr11:8289532- 8290322
cg00589305	chr1 1	1936762 1	-	intergenic	none	Island	chr11:1936665 3-19368234
cg06619621	chr1 1	3235474 2	+	intergenic	none	N_Shore	chr11:3235476 0-32355484
cg08214423	chr1 1	3235495 8	-	intergenic	none	Island	chr11:3235476 0-32355484
cg19908556	chr1 1	3235502 2	-	intergenic	none	Island	chr11:3235476 0-32355484
cg24573719	chr1 1	4360003 2	-	intergenic	none	N_Shore	chr11:4360071 2-43601409
cg04067139	chr1 1	5867316 7	-	intergenic	none	Island	chr11:5867285 1-58673288
cg21825879	chr1 1	9195845 8	-	intergenic	none	Island	chr11:9195763 5-91960290
cg17432267	chr1 1	1223114 46	+	intergenic	none	OpenSea	
cg14917395	chr1 1	1233008 49	-	intergenic	none	N_Shore	chr11:1233010 49-123302149
cg13945107	chr1 1	1239472 30	+	intergenic	none	OpenSea	
cg17945233	chr1 1	1247133 94	+	intergenic	none	Island	chr11:1247130 05-124713395
cg23152235	chr1 1	1338372 65	+	intergenic	none	OpenSea	
cg06807966	chr1 2	4274034	+	intergenic	none	Island	chr12:4273819- 4274491
cg25500050	chr1 2	8171633	+	intergenic	none	Island	chr12:8171336- 8171790
cg06598091	chr1 2	1165360 0	+	intergenic	none	Island	chr12:1165323 2-11653775
cg25134647	chr1 2	2545499 0	-	intergenic	none	OpenSea	
cg05131696	chr1 2	3149932 0	-	intergenic	none	OpenSea	
cg13990926	chr1 2	5413344 7	-	intergenic	none	S_Shore	chr12:5413214 8-54132353
cg06858186	chr1 2	5414492 1	+	intergenic	none	Island	chr12:5414456 2-54145470
cg10792302	chr1 2	5437601 9	-	intergenic	none	N_Shelf	chr12:5437869 6-54380102
cg03719428	chr1 2	5437609 4	+	intergenic	none	N_Shelf	chr12:5437869 6-54380102

cg03030717	chr1 2	6521806 9	-	intergenic	none	N_Shore	chr12:6521824 5-65219143
cg04797725	chr1 2	7771932 6	-	intergenic	none	Island	chr12:7771845 3-77719440
cg20893031	chr1 2	1083064 67	-	intergenic	none	OpenSea	
cg14835517	chr1 2	1139174 17	-	intergenic	none	Island	chr12:1139173 94-113918107
cg24675150	chr1 2	1192121 60	-	intergenic	none	Island	chr12:1192121 10-119212393
cg18235050	chr1 2	1266760 48	-	intergenic	none	Island	chr12:1266755 61-126676195
cg15532640	chr1 2	1295545 66	-	intergenic	none	OpenSea	
cg14657728	chr1 2	1304987 01	+	intergenic	none	OpenSea	
cg07546255	chr1 2	1312001 34	+	intergenic	none	Island	chr12:1311998 24-131200157
cg14197169	chr1 2	1312003 94	+	intergenic	none	N_Shore	chr12:1312005 09-131200726
cg15698568	chr1 2	1312007 25	+	intergenic	none	Island	chr12:1312005 09-131200726
cg11453719	chr1 3	2855205 2	-	intergenic	none	Island	chr13:2855151 4-28552973
cg19716887	chr1 3	4678589 7	+	intergenic	none	OpenSea	
cg05359130	chr1 4	2922897 0	+	intergenic	none	OpenSea	
cg25566568	chr1 4	3699500 9	+	intergenic	none	S_Shore	chr14:3699348 8-36994488
cg16539957	chr1 4	3806687 3	-	intergenic	none	N_Shore	chr14:3806744 6-38069207
cg19578835	chr1 4	3806762 2	-	intergenic	none	Island	chr14:3806744 6-38069207
cg21731375	chr1 4	3806774 2	+	intergenic	none	Island	chr14:3806744 6-38069207
cg15425541	chr1 4	6111875 1	-	intergenic	none	S_Shelf	chr14:6111410 2-61116552
cg21495612	chr1 4	9634225 0	+	intergenic	none	Island	chr14:9634220 9-96343570
cg15156226	chr1 4	1020310 29	+	intergenic	none	Island	chr14:1020259 89-102031567
cg18823007	chr1 4	1037454 32	+	intergenic	none	Island	chr14:1037452 32-103746271
cg02979001	chr1 4	1053104 21	+	intergenic	none	Island	chr14:1053096 90-105310500
cg10832239	chr1 4	1061837 70	-	intergenic	none	N_Shore	chr14:1061857 41-106186041
cg13562462	chr1 5	2411474 4	-	intergenic	none	OpenSea	
cg18139256	chr1 5	2632749 6	-	intergenic	none	Island	chr15:2632749 5-26327896
cg16263224	chr1 5	2632789 5	+	intergenic	none	Island	chr15:2632749 5-26327896
cg26134913	chr1 5	2632804 9	+	intergenic	none	S_Shore	chr15:2632749 5-26327896
cg23804921	chr1 5	3086117 2	+	intergenic	none	N_Shelf	chr15:3086478 2-30865586
cg04657205	chr1 5	3480705 0	+	intergenic	none	Island	chr15:3480649 0-34807382
cg24381412	chr1 5	4599678 7	+	intergenic	none	S_Shore	chr15:4599645 3-45996735
cg01663018	chr1 5	5309777 7	-	intergenic	none	Island	chr15:5309756 1-53098476
cg12036633	chr1 5	6375895 8	-	intergenic	none	OpenSea	
cg12002303	chr1 5	6811347 8	-	intergenic	none	Island	chr15:6811324 1-68113520



cg26338453	chr15	82340023	+	intergenic	none	S_Shore	chr15:82335472-82339937
cg27196768	chr15	98971673	-	intergenic	none	Island	chr15:98971490-98971876
cg20065768	chr16	29796685	+	intergenic	none	Island	chr16:29796361-29796757
cg08394412	chr16	50875140	-	intergenic	none	Island	chr16:50875063-50875322
cg08529345	chr16	54971700	+	intergenic	none	Island	chr16:54970301-54972846
cg03426023	chr16	54972078	+	intergenic	none	Island	chr16:54970301-54972846
cg01317772	chr16	55405200	+	intergenic	none	OpenSea	
cg00274640	chr16	88238863	+	intergenic	none	S_Shore	chr16:88237669-88237893
cg08103988	chr17	6558365	-	intergenic	none	Island	chr17:6558221-6558441
cg04264908	chr17	35303330	-	intergenic	none	Island	chr17:35303284-35303572
cg17964505	chr17	36609863	-	intergenic	none	Island	chr17:36609705-36610320
cg08848774	chr17	43047733	+	intergenic	none	Island	chr17:43047547-43047954
cg02622647	chr17	43578911	+	intergenic	none	OpenSea	
cg11361827	chr17	45867446	+	intergenic	none	Island	chr17:45867103-45867744
cg20401567	chr17	46619555	+	intergenic	none	N_Shore	chr17:46620367-46621373
cg01469027	chr17	46714130	+	intergenic	none	Island	chr17:46713926-46714131
cg14689219	chr17	58217357	+	intergenic	none	Island	chr17:58216793-58217515
cg01781617	chr17	60216199	-	intergenic	none	Island	chr17:60214775-60216785
cg20242280	chr17	64826184	-	intergenic	none	OpenSea	
cg21000227	chr17	70216183	+	intergenic	none	OpenSea	
cg17300544	chr17	75369091	+	intergenic	promoter_and_body	Island	chr17:75368688-75370506
cg27591450	chr17	75525004	-	intergenic	none	Island	chr17:75524589-75525152
cg12865552	chr17	77721631	+	intergenic	none	Island	chr17:77721246-77722497
cg02159489	chr17	79459563	-	intergenic	none	S_Shelf	chr17:79454734-79455823
cg03152033	chr18	4453856	+	intergenic	none	N_Shore	chr18:4453969-4455647
cg07897451	chr18	44778083	+	intergenic	none	Island	chr18:44777632-44778084
cg11749010	chr18	47794623	-	intergenic	none	Island	chr18:47794450-47794996
cg07064197	chr19	32715640	-	intergenic	none	Island	chr19:32715384-32715800
cg04319276	chr19	42445244	+	intergenic	none	Island	chr19:42444020-42445255
cg03241649	chr19	44405924	+	intergenic	none	Island	chr19:44405817-44406053
cg26027796	chr19	55962686	-	intergenic	none	Island	chr19:55962482-55964247
cg10925433	chr20	25065524	+	intergenic	none	Island	chr20:25063838-25065525
cg09775533	chr20	32857151	-	intergenic	none	Island	chr20:32856659-32857248
cg16661628	chr20	32857227	+	intergenic	none	Island	chr20:32856659-32857248

cg25508217	chr2 0	4493742 6	+	intergenic	none	S_Shore	chr20:4493593 2-44937310
cg19499754	chr2 0	5491915 5	+	intergenic	none	Island	chr20:5491903 6-54919357
cg11251113	chr2 0	5491923 9	+	intergenic	none	Island	chr20:5491903 6-54919357
cg05059291	chr2 0	6170336 2	+	intergenic	none	N_Shore	chr20:6170352 6-61704022
cg24606762	chr2 0	6180697 2	+	intergenic	none	Island	chr20:6180625 4-61810867
cg09200260	chr2 1	3657753 9	+	intergenic	none	OpenSea	
cg05306070	chr2 1	4577029 8	-	intergenic	none	OpenSea	
cg02184772	chr2 1	4706302 8	+	intergenic	none	Island	chr21:4706177 3-47064308
cg13466481	chr2 2	1784984 8	+	intergenic	none	Island	chr22:1784947 4-17850733
cg00944631	chr2 2	2046494 7	+	intergenic	none	S_Shelf	chr22:2045926 7-20461473
cg02038168	chr2 2	3978448 1	-	intergenic	none	Island	chr22:3978435 4-39785104
cg24399712	chr2 2	3978479 6	-	intergenic	none	Island	chr22:3978435 4-39785104
cg07370646	chr2 2	4231087 4	+	intergenic	none	Island	chr22:4231005 7-42311669
cg27175294	chr2 2	4231103 9	+	intergenic	none	Island	chr22:4231005 7-42311669
cg10214827	chr2 2	5006486 7	+	intergenic	none	Island	chr22:5006465 5-50064984
cg04056343	chr1 6	7137080	-	A2BP1	body	OpenSea	
cg00590139	chr1 6	7354254	+	A2BP1	body	N_Shore	chr16:7354333- 7354608
cg17960051	chr7	8725767 3	-	ABCB1; RUNDC3B	promoter	Island	chr7:87256958- 87258444
cg11981631	chr1 1	1749796 7	-	ABCC8	body	Island	chr11:1749746 3-17498626
cg05280794	chr1 7	1040653	-	ABR	promoter_and_body	OpenSea	
cg16968596	chr1 5	8934662 9	+	ACAN	promoter	Island	chr15:8934604 3-89347203
cg18061904	chr2	1584541 10	+	ACVR1C	promoter_and_body	Island	chr2:15845379 9-158454111
cg21442003	chr2	1584542 43	-	ACVR1C	promoter_and_body	S_Shore	chr2:15845379 9-158454111
cg02725069	chr5	1570028 17	+	ADAM19	promoter	Island	chr5:15700217 4-157003182
cg07781332	chr5	1287966 96	-	ADAMTS19	body	Island	chr5:12879550 3-128797417
cg08232905	chr4	7343403 5	+	ADAMTS3	body	Island	chr4:73433783- 73434289
cg13643796	chr4	7343420 9	-	ADAMTS3	body	Island	chr4:73433783- 73434289
cg15102770	chr4	7343459 1	+	ADAMTS3	promoter	N_Shore	chr4:73434855- 73435321
cg11243196	chr4	7343485 6	-	ADAMTS3	promoter	Island	chr4:73434855- 73435321
cg13684379	chr1 0	1511173	-	ADARB2	body	OpenSea	
cg20759084	chr5	7395875	-	ADCY2	promoter	Island	chr5:7394986- 7397022
cg02978184	chr3	1231677 70	-	ADCY5	promoter	Island	chr3:12316621 8-123168567
cg13483026	chr3	1231679 73	-	ADCY5	promoter	Island	chr3:12316621 8-123168567
cg20165074	chr7	3109181 3	+	ADCYAP1R1	promoter	Island	chr7:31091717- 31093077

cg17617930	chr7	31091825	+	ADCYAP1R1	promoter	Island	chr7:31091717-31093077
cg02263377	chr1	105195816	-	ADSSL1	promoter_and_body	OpenSea	
cg16260421	chr1	50489319	+	AGBL4	body	N_Shore	chr1:50489417-50489846
cg03038003	chr1	49242900	+	AGBL4; BEND5	promoter_and_body	S_Shore	chr1:49242371-49242810
cg07790169	chr1	49242932	+	AGBL4; BEND5	promoter_and_body	S_Shore	chr1:49242371-49242810
cg24730157	chr1	984428	-	AGRN	body	Island	chr1:984206-984429
cg12065138	chr1	4771201	-	AJAP1	body	N_Shore	chr1:4771652-4772545
cg17484154	chr1	77747875	-	AK5	promoter_and_body	Island	chr1:77747314-77748224
cg02099814	chr1	77748190	-	AK5	promoter_and_body	Island	chr1:77747314-77748224
cg21359747	chr1	101420636	-	ALDH1A3	body	Island	chr15:101419261-101421133
cg07034362	chr3	125899552	-	ALDH1L1	promoter	Island	chr3:125898662-125899568
cg14163665	chr2	30144579	+	ALK	promoter	Island	chr2:30142831-30144624
cg11207534	chr8	41686438	+	ANK1	body	Island	chr8:41685748-41686674
cg16129172	chr8	41686467	+	ANK1	body	Island	chr8:41685748-41686674
cg26530758	chr8	41754060	+	ANK1	promoter_and_body	Island	chr8:41753340-41755250
cg21101720	chr1	27940509	-	ANKRD13B	body	Island	chr17:27939298-27940770
cg26828839	chr1	2	6054749	+	ANO2	body	OpenSea
cg22710306	chr1	5	90358103	+	ANPEP	promoter	Island
cg02518161	chr2	0	6924040	+	ANTXR1	promoter_and_body	Island
cg02304863	chr2	9	6924042	+	ANTXR1	promoter_and_body	Island
cg11078738	chr2	3	6924045	+	ANTXR1	promoter_and_body	Island
cg14383422	chr2	62	2014509	+	AOX1	body	Island
cg13334650	chr1	1	6440065	-	APBB1	promoter	Island
cg05475934	chr1	0	26727318	-	APBB1IP	promoter_and_body	Island
cg03306486	chr1	9	1467952	+	APC2	body	Island
cg21406100	chr1	1	110582247	+	ARHGAP20	body	Island
cg15044384	chr1	9	1811866	-	ARRDC2	promoter_and_body	N_Shore
cg00086670	chr1	0	104629122	-	AS3MT	promoter	Island
cg26866482	chr1	2	103351443	-	ASCL1	promoter	N_Shore
cg20034091	chr1	8	31158527	+	ASXL3	promoter	OpenSea
cg12361352	chr1	8	31158540	+	ASXL3	promoter_and_body	OpenSea
cg27109877	chr1	8	31158549	+	ASXL3	promoter_and_body	OpenSea
cg22237200	chr1	7	7555298	+	ATP1B2	body	Island
cg02770054	chr1	9	36049123	-	ATP4A	body	Island

cg047518 11	chr2	7119244 5	+	ATP6V1B1	none	Island	chr2:71192094- 71192495
cg236354 29	chr1 0	1168524 70	+	ATRNL1	promoter	Island	chr10:1168522 61-116854094
cg237643 81	chr1 0	1168526 87	-	ATRNL1	promoter	Island	chr10:1168522 61-116854094
cg185428 42	chr3	6385791 4	+	ATXN7	promoter	OpenSea	
cg170271 95	chr7	6906409 3	-	AUTS2	promoter_and_body	Island	chr7:69062374- 69065037
cg140651 27	chr2 0	3063238	-	AVP	none	Island	chr20:3063005- 3064146
cg230859 12	chr1 2	6354552 3	+	AVPR1A	promoter_and_body	S_Shore	chr12:6354363 6-63544967
cg056007 40	chr1 2	5802601 0	+	B4GALNT1	promoter	Island	chr12:5802566 1-58027056
cg128461 39	chr1 7	7937224 2	-	BAHCC1	promoter	Island	chr17:7936680 6-79374742
cg071393 30	chr8	1435915 96	-	BAI1	body	Island	chr8:14359156 7-143592674
cg140311 78	chr6	6934442 3	+	BAI3	promoter	N_Shore	chr6:69345216- 69345483
cg127903 24	chr6	6994314 0	-	BAI3	body	OpenSea	
cg137325 89	chr9	1354573 39	+	BARHL1	promoter	Island	chr9:13545516 4-135458586
cg141922 91	chr9	1354654 35	-	BARHL1	none	Island	chr9:13546458 6-135466240
cg143064 51	chr5	1721877 8	+	BASP1; LOC285696	promoter	Island	chr5:17217788- 17219021
cg038740 92	chr2	6078041 5	-	BCL11A	promoter_and_body	N_Shore	chr2:60781019- 60782284
cg012256 98	chr1 1	2774235 5	+	BDNF	promoter_and_body	N_Shore	chr11:2774347 2-27744564
cg254579 56	chr1 1	2774366 4	+	BDNF	promoter	Island	chr11:2774347 2-27744564
cg016264 59	chr6	5682077 8	-	BEND6; DST	promoter	S_Shore	chr6:56818873- 56820308
cg004658 41	chr8	6549445 1	+	BHLHE22	body	Island	chr8:65492935- 65494452
cg100737 23	chr7	3394421 3	-	BMPER	promoter	Island	chr7:33943665- 33945509
cg035330 05	chr7	3394435 9	-	BMPER	promoter	Island	chr7:33943665- 33945509
cg139738 13	chr7	3394492 4	+	BMPER	promoter	Island	chr7:33943665- 33945509
cg175614 35	chr7	3394492 7	+	BMPER	promoter	Island	chr7:33943665- 33945509
cg043894 26	chr9	1687110 6	-	BNC2	promoter	Island	chr9:16870123- 16872020
cg105293 87	chr3	1129311 94	+	BOC	promoter	Island	chr3:11293043 7-112931506
cg123232 74	chr1 8	3483460 5	+	BRUNOL4	body	Island	chr18:3483355 4-34834606
cg172271 56	chr1 8	3514600 1	-	BRUNOL4	promoter	Island	chr18:3514490 7-35147628
cg250232 75	chr1 8	3514645 0	-	BRUNOL4	promoter	Island	chr18:3514490 7-35147628
cg232434 63	chr1 8	3514645 4	-	BRUNOL4	promoter	Island	chr18:3514490 7-35147628
cg179731 64	chr1 8	3514659 1	+	BRUNOL4	promoter	Island	chr18:3514490 7-35147628
cg240410 78	chr1 1	1113838 89	+	BTG4; MIR34C	promoter	Island	chr11:1113831 68-111383892
cg105403 64	chr1 0	2178353 9	-	C10orf114	none	Island	chr10:2178319 8-21786420
cg033975 75	chr1 0	2363351 8	+	C10orf67	body	OpenSea	

cg11473876	chr1 1	1092928 03	-	C11orf87	promoter	N_Shore	chr11:1092935 19-109294983
cg11649795	chr1 1	1092954 91	+	C11orf87	none	S_Shore	chr11:1092935 19-109294983
cg10606490	chr1 1	1113854 50	-	C11orf88	promoter	Island	chr11:1113853 37-111385712
cg25782847	chr1 1	1113854 61	-	C11orf88	promoter	Island	chr11:1113853 37-111385712
cg00238770	chr1 2	6809215	+	C12orf53	promoter	Island	chr12:6809214- 6809816
cg12376068	chr1 2	6809512	-	C12orf53	promoter	Island	chr12:6809214- 6809816
cg23833588	chr1 3	4696158 3	+	C13orf18	promoter_and_body	Island	chr13:4696068 4-46961670
cg13455704	chr1 3	3687175 4	-	C13orf38	promoter_and_body	Island	chr13:3687166 7-36872059
cg15167956	chr1 3	3687194 8	-	C13orf38	promoter_and_body	Island	chr13:3687166 7-36872059
cg07139509	chr1 4	7003871 7	+	C14orf162	promoter	Island	chr14:7003810 8-70040302
cg02273846	chr1 4	2924282 3	-	C14orf23	body	N_Shore	chr14:2924340 3-29243763
cg13001868	chr1 7	4333922 3	-	C17orf46; LOC100133991	promoter_and_body	Island	chr17:4333912 4-43339832
cg04992638	chr1 7	4333932 8	+	C17orf46; LOC100133991	promoter_and_body	Island	chr17:4333912 4-43339832
cg13958426	chr1 37	1693966 37	+	C1orf114	promoter_and_body	Island	chr1:16939662 1-169396869
cg00002719	chr1 06	1693967 06	+	C1orf114	promoter	Island	chr1:16939662 1-169396869
cg08047907	chr1 58	1693968 58	-	C1orf114	promoter	Island	chr1:16939662 1-169396869
cg17319142	chr2 81	1199165 81	+	C1QL2	promoter	Island	chr2:11991412 6-119916663
cg24124029	chr2 0	9495572	-	C20orf103	body	Island	chr20:9495253- 9495597
cg08582485	chr2 0	2255751 8	-	C20orf56	body	Island	chr20:2255751 7-22559240
cg05840533	chr2 0	3175594 3	+	C20orf70	promoter	OpenSea	
cg03364108	chr2 2	2489079 4	+	C22orf45; UPB1	promoter	Island	chr22:2489041 2-24891453
cg17968795	chr2 6	9955340 6	-	C2orf55	promoter	Island	chr2:99552185- 99553831
cg04787024	chr2 2	9955344 2	-	C2orf55	promoter	Island	chr2:99552185- 99553831
cg05037927	chr2 7	6137211 7	-	C2orf74	promoter	OpenSea	
cg16328106	chr2 8	6137213 8	-	C2orf74	promoter	OpenSea	
cg19790321	chr2 5	6137216 5	+	C2orf74	promoter	OpenSea	
cg24757310	chr2 6	6137222 6	-	C2orf74	promoter	OpenSea	
cg18158151	chr2 6	6137225 6	-	C2orf74	promoter_and_body	OpenSea	
cg10580144	chr2 6	6137231 6	-	C2orf74	promoter_and_body	OpenSea	
cg13888593	chr2 0	7464247 0	-	C2orf81	body	Island	chr2:74641733- 74643350
cg15059608	chr3 3	6230500 3	-	C3orf14	promoter	S_Shore	chr3:62304514- 62304780
cg22751696	chr3 7	6230514 7	-	C3orf14	promoter	S_Shore	chr3:62304514- 62304780
cg08145590	chr3 61	1194221 61	+	C3orf15	body	Island	chr3:11942185 5-119422334
cg16146432	chr3 20	1679672 20	-	C3orf50	promoter	N_Shore	chr3:16796724 6-167968130

cg13304297	chr3	167968368	-	C3orf50	body	S_Shore	chr3:167967246-167968130
cg02509058	chr5	2753746	+	C5orf38	body	Island	chr5:2748368-2757024
cg12539796	chr5	7850203	+	C5orf49	body	Island	chr5:7849945-7850439
cg02064106	chr6	165722858	+	C6orf118	body	OpenSea	
cg23146534	chr7	99149191	+	C7orf38	promoter	N_Shore	chr7:99149508-99149807
cg14913925	chr7	99149239	-	C7orf38	promoter	N_Shore	chr7:99149508-99149807
cg03566418	chr8	13424080	+	C8orf48	promoter	OpenSea	
cg19805005	chr17	50234775	+	CA10	body	N_Shore	chr17:50235175-50236466
cg23010302	chr17	58227265	+	CA4	promoter	Island	chr17:58227241-58227720
cg19104475	chr22	30116328	+	CABP7	promoter	Island	chr22:30116081-30117160
cg18011401	chr19	13617366	+	CACNA1A	promoter	S_Shore	chr19:13616752-13617267
cg27555529	chr19	13617518	+	CACNA1A	promoter	S_Shore	chr19:13616752-13617267
cg16427096	chr16	1202468	-	CACNA1H	promoter	Island	chr16:1202414-1204624
cg01151699	chr22	37099259	-	CACNG2	promoter	N_Shore	chr22:37099471-37099711
cg10355837	chr17	64961440	+	CACNG4	body	Island	chr17:64961007-64962321
cg02229775	chr17	64961442	+	CACNG4	body	Island	chr17:64961007-64962321
cg19786084	chr17	64961747	-	CACNG4	body	Island	chr17:64961007-64962321
cg08164556	chr17	64961914	-	CACNG4	body	Island	chr17:64961007-64962321
cg03910065	chr11	115372874	+	CADM1	body	N_Shore	chr11:115373574-115375881
cg10043753	chr11	115374739	+	CADM1	body	Island	chr11:115373574-115375881
cg22207272	chr11	115375703	-	CADM1	promoter	Island	chr11:115373574-115375881
cg24621982	chr3	85008061	-	CADM2	promoter	N_Shore	chr3:85008284-85008837
cg03951219	chr1	159141440	+	CADM3	promoter_and_body	Island	chr1:159141202-159141718
cg20276156	chr7	93204739	-	CALCR	promoter	S_Shore	chr7:93204085-93204381
cg03098937	chr3	49907095	+	CAMKV	promoter	Island	chr3:49906737-49907482
cg06756211	chr1	223936799	-	CAPN2	body	Island	chr1:223936342-223937044
cg19598416	chr1	223936812	-	CAPN2	body	Island	chr1:223936342-223937044
cg18391209	chr1	223747670	+	CAPN8	body	S_Shelf	chr1:223741965-223744525
cg11008866	chr3	121902442	-	CASR	promoter	N_Shore	chr3:121902742-121903645
cg27537628	chr19	56159288	+	CCDC106	promoter_and_body	Island	chr19:56159257-56159937
cg08496742	chr19	56159485	+	CCDC106	promoter_and_body	Island	chr19:56159257-56159937
cg13480357	chr2	219906406	+	CCDC108	promoter	S_Shore	chr2:219906107-219906328
cg04342821	chr3	42814752	+	CCDC13	promoter	Island	chr3:42814567-42814893
cg01825831	chr3	42814880	+	CCDC13	promoter	Island	chr3:42814567-42814893

cg20647888	chr10	13043954	+	CCDC3	promoter	S_Shore	chr10:13043094-13043781
cg20166714	chr12	113592444	-	CCDC42B	body	Island	chr12:113592203-113592620
cg23947326	chr19	46504128	-	CCDC61	body	Island	chr19:46504108-46504330
cg01923218	chr11	93063888	-	CCDC67	promoter_and_body	Island	chr11:93063598-93064076
cg05991743	chr2	56412380	-	CCDC85A	body	Island	chr2:56410865-56412539
cg04292718	chr1	208084456	+	CD34	promoter_and_body	Island	chr1:208084098-208084513
cg15994026	chr4	15780306	-	CD38	body	Island	chr4:15779998-15780729
cg26624576	chr16	65156605	-	CDH11	promoter	Island	chr16:65154656-65157664
cg13390630	chr20	44803246	-	CDH22	body	Island	chr20:44803064-44803662
cg17771031	chr20	44875334	-	CDH22	body	Island	chr20:44875253-44875454
cg01763575	chr20	44875431	-	CDH22	body	Island	chr20:44875253-44875454
cg14120010	chr18	63418583	-	CDH7	promoter	Island	chr18:63417775-63418640
cg19451845	chr2	219824051	+	CDK5R2	promoter	N_Shore	chr2:219824151-219825864
cg14831838	chr2	219824308	-	CDK5R2	promoter	Island	chr2:219824151-219825864
cg16531271	chr2	219824324	-	CDK5R2	promoter	Island	chr2:219824151-219825864
cg14910495	chr2	219824329	-	CDK5R2	promoter	Island	chr2:219824151-219825864
cg26682866	chr2	219824395	-	CDK5R2	promoter	Island	chr2:219824151-219825864
cg04026675	chr9	21974514	+	CDKN2A	body	N_Shore	chr9:21974578-21975306
cg13601799	chr9	21974704	+	CDKN2A	body	Island	chr9:21974578-21975306
cg23967742	chr10	90966701	-	CH25H	body	N_Shore	chr10:90967555-90967900
cg17984375	chr10	90967612	-	CH25H	promoter	Island	chr10:90967555-90967900
cg12276513	chr1	6208879	-	CHD5	body	Island	chr1:6208716-6209039
cg00282347	chr1	6241040	+	CHD5	promoter	Island	chr1:6241031-6241251
cg21645164	chr12	133464327	+	CHFR	promoter	Island	chr12:133463807-133464858
cg01295518	chr3	238392	-	CHL1	promoter	Island	chr3:238391-240140
cg22348992	chr20	61979563	+	CHRNA4	body	Island	chr20:61979255-61979573
cg05529816	chr17	4802735	-	CHRNE; C17orf107	promoter_and_body	Island	chr17:4802265-4805402
cg09426197	chr11	45687281	+	CHST1	promoter	Island	chr11:45686160-45687495
cg03853987	chr2	101034279	+	CHST10	promoter	Island	chr2:101033606-101034296
cg07399369	chr3	142838082	-	CHST2	promoter	Island	chr3:142837885-142840838
cg00995327	chr3	142838847	-	CHST2	promoter_and_body	Island	chr3:142837885-142840838
cg27275352	chr19	19652066	-	CILP2	body	S_Shore	chr19:19650683-19651274
cg21389743	chr3	170136499	-	CLDN11	promoter	Island	chr3:170136242-170137886
cg23853484	chr19	7795988	+	CLEC4G	body	Island	chr19:7794793-7796410

cg19200589	chr2 1	3604160 5	+	CLIC6	promoter	Island	chr21:3604130 5-36043224
cg25737323	chr2	2933810 0	-	CLIP4	promoter	Island	chr2:29337983- 29338909
cg13257636	chr2	2933810 9	-	CLIP4	promoter	Island	chr2:29337983- 29338909
cg23428985	chr2	2933811 3	-	CLIP4	promoter	Island	chr2:29337983- 29338909
cg23255835	chr2	2933812 1	-	CLIP4	promoter	Island	chr2:29337983- 29338909
cg02774855	chr2	2933863 6	-	CLIP4	promoter	Island	chr2:29337983- 29338909
cg05038216	chr2	2933909 1	+	CLIP4	promoter	S_Shore	chr2:29337983- 29338909
cg22610211	chr3	1396542 64	-	CLSTN2	body	Island	chr3:13965343 0-139655115
cg20129210	chr1 3	1005471 92	-	CLYBL	none	Island	chr13:1005471 72-100547431
cg21781979	chr1 3	1005472 92	+	CLYBL	none	Island	chr13:1005471 72-100547431
cg11195797	chr1 3	1005473 31	-	CLYBL	none	Island	chr13:1005471 72-100547431
cg18958126	chr1 3	1005473 67	-	CLYBL	none	Island	chr13:1005471 72-100547431
cg09233013	chr1 6	6663841 2	-	CMTM3	promoter_and_body	Island	chr16:6663825 4-66639561
cg26560414	chr1 6	6663843 3	-	CMTM3	promoter_and_body	Island	chr16:6663825 4-66639561
cg13518298	chr9	3458971 1	+	CNTFR	promoter_and_body	Island	chr9:34589113- 34591978
cg27229407	chr1	1035726 15	+	COL11A1	body	OpenSea	
cg18473652	chr6	7591412 2	-	COL12A1	promoter	N_Shore	chr6:75914705- 75916387
cg21080140	chr6	7057705 9	-	COL19A1	promoter	Island	chr6:70576974- 70577572
cg17840061	chr6	7057747 8	-	COL19A1	promoter	Island	chr6:70576974- 70577572
cg24909466	chr1 3	1109610 69	+	COL4A2	body	Island	chr13:1109609 24-110961143
cg27507687	chr3	4863248 4	-	COL7A1	body	Island	chr3:48631882- 48632901
cg26011014	chr1	4078300 3	-	COL9A2	promoter	Island	chr1:40782220- 40783145
cg06283976	chr1 8	4993393	+	COLEC12	body	Island	chr18:499315- 500722
cg15424739	chr1 9	1890166 6	+	COMP	body	Island	chr19:1889903 7-18902284
cg08154437	chr1 9	1700865 0	-	CPAMD8	body	Island	chr19:1700710 1-17008857
cg07295964	chr5	1752239 82	+	CPLX2	promoter	Island	chr5:17522360 9-175224679
cg26121591	chr5	1752985 64	-	CPLX2	promoter_and_body	Island	chr5:17529851 5-175300066
cg24729690	chr5	1753002 17	+	CPLX2	promoter	S_Shore	chr5:17529851 5-175300066
cg12855522	chr6	3680820 7	-	CPNE5	promoter	Island	chr6:36807678- 36808808
cg09557387	chr1	2078183 95	+	CR1L	promoter	Island	chr1:20781838 9-207818952
cg13177758	chr1 5	7863257 2	-	CRABP1	promoter	N_Shore	chr15:7863266 9-78633108
cg16703647	chr1 5	7863259 2	-	CRABP1	promoter	N_Shore	chr15:7863266 9-78633108
cg23337754	chr1 5	7863285 9	-	CRABP1	body	Island	chr15:7863266 9-78633108
cg17133183	chr1 5	7863286 1	-	CRABP1	body	Island	chr15:7863266 9-78633108



cg01864564	chr1	152488269	+	CRCT1	none	Island	chr1:152487978-152488270
cg11093548	chr7	28450001	+	CREB5	promoter	Island	chr7:28448716-28450028
cg04856689	chr17	43862032	-	CRHR1	body	Island	chr17:43860684-43862928
cg24353392	chr17	43862247	+	CRHR1	body	Island	chr17:43860684-43862928
cg22350070	chr2	79738639	+	CTNNA2	promoter	N_Shore	chr2:79739696-79740243
cg01546568	chr2	79740322	+	CTNNA2	promoter_and_body	S_Shore	chr2:79739696-79740243
cg16971380	chr15	48483080	+	CTXN2	promoter	OpenSea	
cg06048524	chr10	44880542	-	CXCL12	promoter	Island	chr10:44879714-44882391
cg17267805	chr10	44880545	-	CXCL12	promoter	Island	chr10:44879714-44882391
cg15574312	chr17	74533845	+	CYGB	promoter	Island	chr17:74533281-74534566
cg07781162	chr17	74533951	-	CYGB	promoter	Island	chr17:74533281-74534566
cg19249708	chr17	74533969	-	CYGB	promoter	Island	chr17:74533281-74534566
cg00958884	chr17	74533976	-	CYGB	promoter	Island	chr17:74533281-74534566
cg16332610	chr15	74658547	+	CYP11A1	promoter_and_body	Island	chr15:74658038-74658574
cg11034245	chr2	72375000	-	CYP26B1	promoter	Island	chr2:72371121-72375004
cg01114088	chr4	50211111	-	CYTL1	body	Island	chr4:5021003-5021329
cg14135551	chr6	39760416	-	DAAM2	promoter	Island	chr6:39760066-39760426
cg19717595	chr1	57887655	+	DAB1	promoter	N_Shore	chr1:57887963-57890637
cg05919360	chr1	57889417	+	DAB1	promoter	Island	chr1:57887963-57890637
cg03384825	chr1	57889604	+	DAB1	promoter	Island	chr1:57887963-57890637
cg20272619	chr1	57890317	-	DAB1	promoter	Island	chr1:57887963-57890637
cg07173275	chr1	57890636	+	DAB1	promoter	Island	chr1:57887963-57890637
cg18242712	chr11	20182324	+	DBX1	promoter	Island	chr11:20181200-20182325
cg13186327	chr12	45444895	-	DBX2	promoter	Island	chr12:45444202-45445386
cg27352765	chr3	98620662	+	DCBLD2	promoter	Island	chr3:98620131-98620910
cg02464093	chr3	98620857	+	DCBLD2	promoter	Island	chr3:98620131-98620910
cg16657397	chr3	186079367	+	DGKG	promoter	Island	chr3:186078710-186080111
cg08675193	chr3	186080245	-	DGKG	promoter	S_Shore	chr3:186078710-186080111
cg14254745	chr1	26758306	-	DHDDS	promoter	N_Shore	chr1:26758492-26758856
cg10086212	chr12	49484169	+	DHH	body	Island	chr12:49483601-49484255
cg24804517	chr20	61560953	+	DIDO1	promoter	Island	chr20:61560433-61560954
cg23340935	chr2	218354150	-	DIRC3	body	OpenSea	
cg07700514	chr16	56228467	-	DKFZP434H168; GNAO1	promoter_and_body	S_Shelf	chr16:56224731-56224980
cg02667667	chr16	56228505	-	DKFZP434H168; GNAO1	promoter_and_body	S_Shelf	chr16:56224731-56224980

cg20864389	chr11	84431970	-	DLG2	body	OpenSea	
cg26228266	chr1	35351340	-	DLGAP3	body	Island	chr1:35350878-35351854
cg23493510	chr17	48049275	-	DLX4	promoter_and_body	Island	chr17:48048953-48050616
cg09150117	chr7	96653867	-	DLX5	body	Island	chr7:96653467-96654199
cg05663341	chr7	96634660	-	DLX6AS; DLX6	promoter_and_body	Island	chr7:96634622-96634915
cg23563008	chr7	96635624	+	DLX6AS; DLX6	body	Island	chr7:96635458-96635749
cg07027116	chr1	65731738	-	DNAJC6	body	Island	chr1:65731411-65731849
cg04399751	chr1	171810376	-	DNM3	promoter	N_Shore	chr1:171810467-171811325
cg08862890	chr5	169064451	-	DOCK2	body	Island	chr5:169064270-169064702
cg19991022	chr20	53091920	-	DOK5	promoter	Island	chr20:53091733-53092993
cg16764494	chr11	117667862	+	DSCAML1	body	Island	chr11:117666634-117668141
cg25010118	chr18	65184398	+	DSEL	promoter	S_Shore	chr18:65183237-65184014
cg00119057	chr18	32073462	-	DTNA	promoter_and_body	Island	chr18:32073444-32074292
cg05293775	chr8	33457483	+	DUSP26	promoter	Island	chr8:33456915-33457515
cg04217450	chr5	158526693	+	EBF1	promoter_and_body	N_Shore	chr5:158527374-158527983
cg26525127	chr2	233350365	+	ECEL1	body	Island	chr2:233350278-233352974
cg07446677	chr10	11784190	+	ECHDC3	promoter	N_Shore	chr10:11784407-11784937
cg02806452	chr2	233499070	+	EFHD1	body	Island	chr2:233497826-233499727
cg07852757	chr10	64575442	+	EGR2	body	Island	chr10:64574660-64578778
cg00981472	chr2	31456761	-	EHD3	promoter	Island	chr2:31456740-31457653
cg18444347	chr2	31456775	+	EHD3	promoter	Island	chr2:31456740-31457653
cg25840208	chr2	31457043	-	EHD3	promoter_and_body	Island	chr2:31456740-31457653
cg15947096	chr7	37488835	+	ELMO1	promoter	S_Shore	chr7:37487354-37488672
cg14378848	chr6	53212618	-	ELOVL5	promoter	Island	chr6:53212617-53214043
cg25514947	chr6	53212650	+	ELOVL5	promoter	Island	chr6:53212617-53214043
cg27599958	chr6	53213028	-	ELOVL5	promoter	Island	chr6:53212617-53214043
cg14048874	chr7	101006573	-	EMID2	body	Island	chr7:101005899-101007443
cg16781647	chr2	73151595	-	EMX1	body	Island	chr2:73151200-73152060
cg03339065	chr10	119304583	+	EMX2; EMX2OS	promoter_and_body	Island	chr10:119301321-119305368
cg24188415	chr10	119304586	+	EMX2; EMX2OS	promoter_and_body	Island	chr10:119301321-119305368
cg12894449	chr10	119304104	+	EMX2OS; EMX2	body	Island	chr10:119301321-119305368
cg12418535	chr2	119607192	+	EN1	promoter	N_Shore	chr2:119607378-119607910
cg03677003	chr13	44359996	-	ENOX1	promoter	Island	chr13:44359858-44361696
cg10482596	chr13	44360259	-	ENOX1	promoter	Island	chr13:44359858-44361696

cg17186025	chr13	44360736	-	ENOX1	promoter	Island	chr13:44359858-44361696
cg09320746	chr13	44361019	-	ENOX1	promoter_and_body	Island	chr13:44359858-44361696
cg19025435	chr13	44361624	-	ENOX1	promoter	Island	chr13:44359858-44361696
cg04281219	chr6	46138847	-	ENPP5	promoter	OpenSea	
cg04403917	chr7	37960974	-	EPDR1	body	Island	chr7:37960316-37961046
cg13231700	chr2	222435709	+	EPHA4	body	N_Shore	chr2:222436034-222438941
cg17194182	chr7	100318154	+	EPO	promoter	Island	chr7:100318106-100318684
cg20893717	chr7	100318190	+	EPO	promoter	Island	chr7:100318106-100318684
cg10864074	chr7	100318194	+	EPO	promoter	Island	chr7:100318106-100318684
cg01692340	chr7	100318319	+	EPO	promoter	Island	chr7:100318106-100318684
cg00011346	chr2	213403859	+	ERBB4	promoter	Island	chr2:213402180-213403867
cg23444468	chr3	56502054	+	ERC2	promoter	Island	chr3:56501868-56502345
cg08065241	chr3	56502265	+	ERC2	promoter	Island	chr3:56501868-56502345
cg09059904	chr5	76012757	-	F2R	body	S_Shore	chr5:76011120-76012292
cg07689907	chr11	61582574	-	FADS1	body	Island	chr11:61582573-61584728
cg23760165	chr11	61595485	-	FADS2	promoter	Island	chr11:61594996-61596710
cg25303599	chr11	61595807	-	FADS2	promoter_and_body	Island	chr11:61594996-61596710
cg03514404	chr7	143579665	+	FAM115A	promoter	N_Shelf	chr7:143582125-143582610
cg01244015	chr2	225266843	+	FAM124B	promoter	OpenSea	
cg09682311	chr7	23053758	+	FAM126A	promoter_and_body	Island	chr7:23052971-23054002
cg01587630	chr7	23053820	+	FAM126A	promoter	Island	chr7:23052971-23054002
cg13002945	chr7	23053827	+	FAM126A	promoter	Island	chr7:23052971-23054002
cg05129610	chr7	23053937	-	FAM126A	promoter	Island	chr7:23052971-23054002
cg07956515	chr7	23053981	+	FAM126A	promoter	Island	chr7:23052971-23054002
cg09006985	chr7	23054001	+	FAM126A	promoter	Island	chr7:23052971-23054002
cg03291960	chr7	23054024	-	FAM126A	promoter	S_Shore	chr7:23052971-23054002
cg07800384	chr2	289254	-	FAM150B	promoter	Island	chr2:287353-290099
cg19839798	chr13	108519318	-	FAM155A	promoter_and_body	Island	chr13:108519292-108521063
cg09551776	chr2	75788246	+	FAM176A	promoter	Island	chr2:75787717-75788312
cg27207796	chr4	17783322	-	FAM184B	promoter	Island	chr4:17782642-17783624
cg11545314	chr3	43021348	+	FAM198A	body	Island	chr3:43020702-43021354
cg03186486	chr3	68980947	+	FAM19A4	promoter	Island	chr3:68980783-68982035
cg01697732	chr17	66597500	+	FAM20A	promoter	Island	chr17:66596072-66597578
cg13618967	chr7	212539	-	FAM20C	body	OpenSea	

cg003524 17	chr3	1944089 01	+	FAM43A	body	Island	chr3:19440644 0-194409045
cg121243 86	chr1	1904447 76	+	FAM5C	promoter	OpenSea	
cg030988 14	chr6	2491130 8	-	FAM65B	promoter	S_Shore	chr6:24910626- 24911285
cg110832 76	chr6	2491131 3	-	FAM65B	promoter	S_Shore	chr6:24910626- 24911285
cg066369 71	chr6	2491155 3	-	FAM65B	promoter	S_Shore	chr6:24910626- 24911285
cg218687 74	chr1	1661342 82	-	FAM78B	body	Island	chr1:16613425 8-166136448
cg092796 15	chr1	1661344 10	+	FAM78B	body	Island	chr1:16613425 8-166136448
cg022299 93	chr1	1661346 99	+	FAM78B	body	Island	chr1:16613425 8-166136448
cg051186 38	chr4	1262373 71	+	FAT4	promoter	Island	chr4:12623589 5-126238930
cg107310 73	chr4	1262373 73	+	FAT4	promoter	Island	chr4:12623589 5-126238930
cg274369 95	chr1 6	743998	-	FBXL16	none	Island	chr16:743924- 745943
cg075515 45	chr1 9	3946631 3	-	FBXO17	promoter_and_body	Island	chr19:3946584 6-39466403
cg147300 85	chr1 9	3952254 8	-	FBXO27	body	Island	chr19:3952226 4-39523227
cg142102 87	chr1	1616956 59	-	FCRLB	body	Island	chr1:16169563 7-161697298
cg090352 84	chr2	2198501 23	+	FEV	promoter_and_body	Island	chr2:21984891 9-219850541
cg142147 06	chr1 3	1030529 43	+	FGF14	body	Island	chr13:1030523 61-103052944
cg182107 32	chr1 1	6951854 5	-	FGF19	body	Island	chr11:6951784 0-69519929
cg241991 12	chr1 1	6959032 8	+	FGF4	promoter	Island	chr11:6958882 6-69590546
cg058941 24	chr4	8118679 5	-	FGF5	promoter	N_Shore	chr4:81187494- 81187913
cg103002 29	chr8	3832499 3	+	FGFR1	promoter	N_Shore	chr8:38325091- 38326374
cg044571 96	chr2	1645932 64	+	FIGN	promoter	Island	chr2:16459291 7-164593511
cg025265 22	chr1 1	1285637 16	-	FLI1	promoter	Island	chr11:1285626 71-128565011
cg184128 34	chr2 0	6188529 1	+	FLJ16779; NKAIN4	promoter_and_body	Island	chr20:6188464 4-61886387
cg273977 87	chr1 9	5055390 7	+	FLJ26850	promoter	N_Shore	chr19:5055401 2-50554492
cg225311 83	chr1 9	5055445 1	+	FLJ26850	body	Island	chr19:5055401 2-50554492
cg081743 73	chr1 0	1029892 54	-	FLJ41350; LBX1	promoter	Island	chr10:1029841 82-102990063
cg190466 97	chr5	9291558 1	+	FLJ42709	body	Island	chr5:92914770- 92917337
cg144211 80	chr9	1328045 10	+	FNBP1	body	Island	chr9:13280427 9-132806003
cg251792 91	chr9	1328057 39	-	FNBP1	promoter	Island	chr9:13280427 9-132806003
cg144659 00	chr9	1328057 55	-	FNBP1	promoter	Island	chr9:13280427 9-132806003
cg142473 32	chr9	1328059 79	-	FNBP1	promoter	Island	chr9:13280427 9-132806003
cg266867 32	chr2 0	2256273 7	-	FOXA2	body	Island	chr20:2256273 6-22566104
cg169631 44	chr2 0	2256697 6	-	FOXA2	promoter	Island	chr20:2256682 1-22567055
cg198094 99	chr1	4788226 5	+	FOXE3	body	Island	chr1:47881896- 47883065

cg15457058	chr1	47882322	+	FOXE3	body	Island	chr1:47881896-47883065
cg05555338	chr16	86542864	-	FOXF1	promoter	Island	chr16:86541430-86545228
cg23511613	chr2	88752322	+	FOXI3	promoter	Island	chr2:88751335-88752865
cg09650487	chr10	14215771	+	FRMD4A	body	OpenSea	
cg06830784	chr2	183731824	-	FRZB	promoter	Island	chr2:183731819-183732093
cg13355047	chr19	4304554	-	FSD1	promoter	Island	chr19:4304542-4305122
cg11398523	chr19	50316423	-	FUZ	promoter_and_body	Island	chr19:50316211-50316469
cg10166205	chr19	50316699	+	FUZ	promoter	S_Shore	chr19:50316211-50316469
cg18209212	chr12	130646256	+	FZD10	promoter	Island	chr12:130645327-130648988
cg25145765	chr4	46391392	-	GABRA2	promoter_and_body	N_Shore	chr4:46391903-46392572
cg23160016	chr4	46391929	-	GABRA2	promoter_and_body	Island	chr4:46391903-46392572
cg11281641	chr2	171674855	+	GAD1	promoter	Island	chr2:171672310-171675447
cg06139006	chr12	132682698	+	GALNT9	body	Island	chr12:132682572-132682895
cg25686860	chr3	128206949	+	GATA2	promoter	Island	chr3:128205495-128212274
cg23520930	chr3	128206967	+	GATA2	promoter	Island	chr3:128205495-128212274
cg09024124	chr3	128207255	-	GATA2	promoter_and_body	Island	chr3:128205495-128212274
cg13845982	chr20	61051029	-	GATA5	promoter	Island	chr20:61049361-61051897
cg20265733	chr20	61051032	-	GATA5	promoter	Island	chr20:61049361-61051897
cg02484469	chr20	61051036	-	GATA5	promoter	Island	chr20:61049361-61051897
cg14980983	chr20	61051039	-	GATA5	promoter	Island	chr20:61049361-61051897
cg16714055	chr20	61051341	-	GATA5	promoter	Island	chr20:61049361-61051897
cg11982072	chr20	61051348	-	GATA5	promoter	Island	chr20:61049361-61051897
cg24500900	chr20	61051423	-	GATA5	promoter	Island	chr20:61049361-61051897
cg08568720	chr20	61051432	-	GATA5	promoter	Island	chr20:61049361-61051897
cg23770904	chr20	61051561	-	GATA5	promoter	Island	chr20:61049361-61051897
cg14388488	chr20	61051777	-	GATA5	promoter	Island	chr20:61049361-61051897
cg03777459	chr20	61051802	-	GATA5	promoter	Island	chr20:61049361-61051897
cg14250833	chr6	10882240	-	GCM2	promoter	N_Shore	chr6:10882926-10883149
cg14000361	chr6	10882336	+	GCM2	promoter	N_Shore	chr6:10882926-10883149
cg09994356	chr20	42875779	-	GDAP1L1	promoter	Island	chr20:42875764-42876184
cg01778345	chr1	118427435	-	GDAP2	body	OpenSea	
cg03351460	chr19	19007311	+	GDF1; LASS1	promoter	Island	chr19:19006031-19007546
cg04110601	chr10	48438724	-	GDF10	promoter_and_body	Island	chr10:48438411-48439320
cg07966910	chr2	20866399	-	GDF7	promoter	Island	chr2:20865289-20867589

cg037536 81	chr2	2086650 0	+	GDF7	promoter_and_body	Island	chr2:20865289- 20867589
cg131079 75	chr1	9294948 8	+	GFI1	promoter	Island	chr1:92945907- 92952609
cg139448 38	chr5	1797409 14	-	GFPT2	body	Island	chr5:17974071 0-179741121
cg232484 24	chr5	1797411 04	+	GFPT2	body	Island	chr5:17974071 0-179741121
cg028913 14	chr5	1797411 20	+	GFPT2	body	Island	chr5:17974071 0-179741121
cg003477 57	chr1	2076856 3	-	GJB2	promoter	S_Shore	chr13:2076620 8-20767779
cg170094 33	chr9	6645686	+	GLDC	promoter_and_body	Island	chr9:6645080- 6645975
cg094056 12	chr7	4227587 0	+	GLI3	promoter	N_Shore	chr7:42276003- 42277850
cg175309 77	chr7	4227587 2	+	GLI3	promoter	N_Shore	chr7:42276003- 42277850
cg087128 66	chr4	1579975 26	-	GLRB	promoter	Island	chr4:15799716 6-157997686
cg067285 79	chr1	5622490 6	-	GNAO1; LOC283856	promoter_and_body	Island	chr16:5622473 1-56224980
cg067142 84	chr1	2358128 40	+	GNG4	promoter	Island	chr1:23581184 1-235814066
cg202855 14	chr1	2358134 44	+	GNG4	promoter	Island	chr1:23581184 1-235814066
cg197013 78	chr1	3473007 1	+	GOLGA8A	promoter	S_Shore	chr15:3472878 7-34729495
cg228213 24	chr4	1769234 39	-	GPM6A	promoter_and_body	Island	chr4:17692307 5-176923630
cg175650 78	chr1	2733472 3	-	GPR12	promoter_and_body	Island	chr13:2733422 6-27335205
cg096397 25	chr1	1349012 0	-	GPR123	promoter	Island	chr10:1349011 98-134902619
cg158257 86	chr1	1349012 0	-	GPR123	promoter	Island	chr10:1349011 98-134902619
cg080539 04	chr1	2008589 6	+	GPR139	promoter	S_Shore	chr16:2008470 7-20085305
cg146157 84	chr5	9495575 6	+	GPR150	promoter	Island	chr5:94955630- 94957244
cg128645 97	chr5	9495578 9	-	GPR150	promoter	Island	chr5:94955630- 94957244
cg023204 54	chr5	9495601 7	+	GPR150	body	Island	chr5:94955630- 94957244
cg244934 46	chr1	4021210 5	-	GPR176	body	Island	chr15:4021196 1-40213444
cg017692 32	chr6	1103002 18	-	GPR6	promoter	Island	chr6:11029936 5-110301267
cg067118 31	chr1	1882191 3	-	GREB1L	promoter	Island	chr18:1882138 3-18823349
cg173124 92	chr1	3301169 5	+	GREM1	promoter	Island	chr15:3300953 0-33011696
cg099805 22	chr1	1054818 1	-	GRIA4	body	S_Shore	chr11:1054811 26-105481422
cg030528 69	chr1	8812629 0	+	GRID1	promoter	Island	chr10:8812292 4-88127364
cg119825 83	chr4	9322593 3	-	GRID2	body	N_Shore	chr4:93226348- 93227007
cg211877 69	chr4	9322649 5	-	GRID2	body	Island	chr4:93226348- 93227007
cg203888 23	chr4	9322727 0	-	GRID2	body	S_Shore	chr4:93226348- 93227007
cg055779 02	chr7	6576152	-	GRID2IP	body	Island	chr7:6575923- 6576389
cg269888 95	chr7	6576353	+	GRID2IP	body	Island	chr7:6575923- 6576389
cg076420 43	chr1	1027667 6	+	GRIN2A	promoter	Island	chr16:1027394 3-10277424

cg25067120	chr7	126893287	+	GRM8	promoter	Island	chr7:126891300-126894205
cg17159473	chr7	126893890	-	GRM8	promoter	Island	chr7:126891300-126894205
cg01163842	chr14	95235125	+	GSC	body	Island	chr14:95234612-95236569
cg10042799	chr14	95236123	-	GSC	body	Island	chr14:95234612-95236569
cg24506221	chr1	110230401	-	GSTM1	promoter	Island	chr1:110230238-110230614
cg23472215	chr1	110282815	+	GSTM3	body	Island	chr1:110282351-110283306
cg17163751	chr10	71812596	+	H2AFY2	promoter_and_body	Island	chr10:71812318-71813693
cg26166804	chr10	71812612	+	H2AFY2	promoter_and_body	Island	chr10:71812318-71813693
cg26976732	chr16	216100	-	HBM	body	Island	chr16:214343-216720
cg07523553	chr1	17700661	+	HCCA2; LOC402778	promoter_and_body	Island	chr11:1768979-1770712
cg17394649	chr6	29760164	-	HCG4	body	Island	chr6:29759946-29760903
cg23244913	chr6	29943401	+	HCG9	body	N_Shore	chr6:29944402-29945169
cg06710082	chr6	29943408	+	HCG9	body	N_Shore	chr6:29944402-29945169
cg04623837	chr6	29943414	+	HCG9	body	N_Shore	chr6:29944402-29945169
cg04109898	chr6	29943455	+	HCG9	body	N_Shore	chr6:29944402-29945169
cg17639394	chr6	29943480	+	HCG9	body	N_Shore	chr6:29944402-29945169
cg17326769	chr20	30639705	-	HCK	promoter	N_Shore	chr20:30639908-30640786
cg04787432	chr6	126071294	-	HEY2	body	Island	chr6:126068722-126071320
cg09633973	chr17	1957365	-	HIC1	promoter	Island	chr17:1952919-1962328
cg17739038	chr17	1957496	+	HIC1	promoter	Island	chr17:1952919-1962328
cg14018363	chr6	29911265	-	HLA-A	body	Island	chr6:29910202-29911367
cg13524302	chr6	33084798	-	HLA-DPB2	body	Island	chr6:33084740-33084995
cg04315646	chr6	33084922	-	HLA-DPB2	body	Island	chr6:33084740-33084995
cg05337177	chr6	33084928	-	HLA-DPB2	body	Island	chr6:33084740-33084995
cg21588215	chr6	32632937	+	HLA-DQB1	body	Island	chr6:32632158-32633027
cg23967822	chr6	32632961	+	HLA-DQB1	body	Island	chr6:32632158-32633027
cg03403720	chr6	32632970	+	HLA-DQB1	body	Island	chr6:32632158-32633027
cg24593918	chr6	32633157	-	HLA-DQB1	body	S_Shore	chr6:32632158-32633027
cg23464743	chr6	32633163	-	HLA-DQB1	body	S_Shore	chr6:32632158-32633027
cg12109566	chr6	30227986	+	HLA-L	body	Island	chr6:30227320-30228255
cg18704691	chr1	221052468	-	HLX	promoter	Island	chr1:221051966-221053673
cg12405785	chr1	221053409	+	HLX	body	Island	chr1:221051966-221053673
cg18685408	chr10	124895448	+	HMX3	promoter	Island	chr10:124894075-124897366
cg06417478	chr19	12876846	-	HOKK2	body	N_Shore	chr19:12876889-12877108

cg04657146	chr19	12876947	+	HOOK2	body	Island	chr19:12876889-12877108
cg11738485	chr19	12877000	+	HOOK2	body	Island	chr19:12876889-12877108
cg23899408	chr19	12877188	-	HOOK2	body	S_Shore	chr19:12876889-12877108
cg05311410	chr7	27225523	+	HOXA11AS; HOXA11	promoter_and_body	Island	chr7:27225050-27225629
cg22943986	chr7	27142700	+	HOXA2	promoter	N_Shore	chr7:27143181-27143479
cg07302069	chr7	27196286	+	HOXA7	promoter_and_body	Island	chr7:27195601-27196567
cg13479204	chr17	46641708	+	HOXB3	promoter	Island	chr17:46641534-46642110
cg08151857	chr17	46691820	-	HOXB8	body	Island	chr17:46691520-46692097
cg25928579	chr17	46692534	-	HOXB8	promoter	S_Shore	chr17:46690390-46691055
cg03107393	chr17	46692553	-	HOXB8	promoter	S_Shore	chr17:46690390-46691055
cg03923561	chr12	54447220	+	HOXC4	promoter	N_Shore	chr12:54447744-54448091
cg07266404	chr12	54447584	-	HOXC4	promoter	N_Shore	chr12:54447744-54448091
cg22747076	chr12	54447873	+	HOXC4	body	Island	chr12:54447744-54448091
cg11746813	chr12	54448090	+	HOXC4	body	Island	chr12:54447744-54448091
cg21726284	chr12	54402909	+	HOXC8	promoter_and_body	Island	chr12:54402682-54403347
cg05022306	chr12	54403254	+	HOXC8	body	Island	chr12:54402682-54403347
cg11418595	chr2	177052486	+	HOXD1	promoter	N_Shore	chr2:177052957-177054350
cg14715697	chr17	77127487	+	HRNBP3	promoter	Island	chr17:77127405-77127606
cg10362542	chr17	77179709	-	HRNBP3	promoter	Island	chr17:77178828-77180229
cg12103626	chr17	14204310	-	HS3ST3B1	promoter	Island	chr17:14204168-14207702
cg12484686	chr17	14204340	-	HS3ST3B1	promoter	Island	chr17:14204168-14207702
cg03739411	chr16	1968124	-	HS3ST6	body	Island	chr16:1967799-1968970
cg23425970	chr2	129076394	+	HS6ST1	promoter	Island	chr2:129075197-129077639
cg24725522	chr19	49339397	+	HSD17B14	body	N_Shore	chr19:49340488-49340774
cg06546677	chr8	145537504	+	HSF1	body	OpenSea	
cg07833420	chr6	87647147	+	HTR1E	promoter_and_body	N_Shore	chr6:87647253-87647707
cg04747634	chr16	71264451	+	HYDIN	promoter	Island	chr16:71264360-71264659
cg08597761	chr16	71264545	+	HYDIN	promoter_and_body	Island	chr16:71264360-71264659
cg09918510	chr16	71264579	+	HYDIN	promoter	Island	chr16:71264360-71264659
cg02293437	chr16	71264678	+	HYDIN	promoter	S_Shore	chr16:71264360-71264659
cg08160350	chr4	996052	+	IDUA	body	Island	chr4:995482-997541
cg13704548	chr15	65714817	+	IGDCC4	body	Island	chr15:65714742-65715571
cg17787134	chr17	47073522	-	IGF2BP1	promoter	Island	chr17:47072820-47076042
cg12314713	chr17	47074576	+	IGF2BP1	promoter	Island	chr17:47072820-47076042



cg02782889	chr17	47074637	-	IGF2BP1	promoter	Island	chr17:47072820-47076042
cg02120774	chr7	45961473	-	IGFBP3	promoter	S_Shore	chr7:45960137-45961347
cg18363918	chr19	51829984	-	IGLON5	body	N_Shore	chr19:51830064-51831145
cg16120742	chr7	50345049	+	IKZF1	promoter	S_Shore	chr7:50342895-50343456
cg20925841	chr2	121104400	+	INHBB	body	Island	chr2:121101800-121104534
cg09062550	chr2	20350481	+	INSM1	body	Island	chr20:20344400-20350605
cg07850604	chr14	36003443	+	INSM2	promoter_and_body	Island	chr14:36002598-36005013
cg19115941	chr12	187284	+	IQSEC3	promoter_and_body	Island	chr12:186863-187610
cg03609666	chr19	49250439	+	IZUMO1	promoter	N_Shelf	chr19:49253688-49254221
cg10596483	chr8	143751796	-	JRK	promoter	S_Shore	chr8:143750759-143751448
cg24634471	chr8	143751801	-	JRK	promoter	S_Shore	chr8:143750759-143751448
cg09588271	chr1	62784651	-	KANK4	promoter	Island	chr1:62784136-62785133
cg14208112	chr1	111149307	+	KCNA2	promoter	Island	chr1:111148983-111150186
cg25281171	chr1	111149507	+	KCNA2	promoter	Island	chr1:111148983-111150186
cg12392473	chr20	48099331	-	KCNB1	promoter	Island	chr20:48098512-48099560
cg00755448	chr8	73448779	+	KCNB2	promoter	Island	chr8:73448659-73449725
cg18555069	chr8	73449519	+	KCNB2	promoter	Island	chr8:73448659-73449725
cg15774465	chr8	73449524	+	KCNB2	promoter	Island	chr8:73448659-73449725
cg27118761	chr11	17756479	+	KCNC1	promoter	Island	chr11:17756056-17758286
cg10203375	chr1	211307178	+	KCNH1	body	Island	chr1:211306667-211307675
cg12989934	chr5	170108187	-	KCNIP1	body	OpenSea	
cg03928539	chr17	21279613	-	KCNJ12	promoter	Island	chr17:21279506-21281574
cg18871020	chr22	38851345	+	KCNJ4	promoter	S_Shore	chr22:38850766-38851285
cg25142308	chr22	38851363	+	KCNJ4	promoter	S_Shore	chr22:38850766-38851285
cg02957576	chr22	38851366	+	KCNJ4	promoter	S_Shore	chr22:38850766-38851285
cg22935149	chr22	38851884	+	KCNJ4	promoter	S_Shore	chr22:38850766-38851285
cg12212555	chr14	90526722	-	KCNK13	promoter	Island	chr14:90526696-90528951
cg21231789	chr14	90528199	+	KCNK13	promoter_and_body	Island	chr14:90526696-90528951
cg19584875	chr14	90528213	+	KCNK13	promoter_and_body	Island	chr14:90526696-90528951
cg22669058	chr14	90528371	-	KCNK13	promoter_and_body	Island	chr14:90526696-90528951
cg01717150	chr8	140716495	+	KCNK9	promoter	Island	chr8:140714585-140718259
cg09405661	chr10	79397455	+	KCNMA1	promoter_and_body	Island	chr10:79396095-79398495
cg13070215	chr8	133493171	+	KCNQ3	promoter	Island	chr8:133492398-133493586
cg22308501	chr8	133493424	+	KCNQ3	promoter	Island	chr8:133492398-133493586

cg06206801	chr1 8	2413137 9	-	KCTD1	promoter	S_Shore	chr18:2412678 0-24131138
cg00989765	chr4	5599186 0	+	KDR	promoter	Island	chr4:55991402- 55992171
cg25467973	chr1	3663705	-	KIAA0495	promoter_and_body	Island	chr1:3662963- 3664085
cg25327452	chr9	1000004 64	-	KIAA1529	promoter	Island	chr9:10000046 3-100000820
cg01950665	chr9	1000007 68	-	KIAA1529	promoter	Island	chr9:10000046 3-100000820
cg19486070	chr7	1626153	+	KIAA1908	body	OpenSea	
cg11752586	chr2	1496325 99	-	KIF5C	promoter	N_Shore	chr2:14963268 2-149633882
cg14986699	chr2	1496327 05	-	KIF5C	promoter	Island	chr2:14963268 2-149633882
cg17245188	chr2	1496327 09	-	KIF5C	promoter	Island	chr2:14963268 2-149633882
cg10457563	chr6	3969315 9	+	KIF6	promoter_and_body	S_Shore	chr6:39692743- 39692966
cg01138981	chr6	3969336 0	-	KIF6	promoter	S_Shore	chr6:39692743- 39692966
cg19495969	chr1 1	1264434 90	+	KIRREL3	body	OpenSea	
cg09803407	chr1 1	1268702 33	+	KIRREL3	body	Island	chr11:1268702 26-126870552
cg06533629	chr7	1304193 70	-	KLF14	promoter	Island	chr7:13041791 2-130419378
cg08478189	chr2	2080306 66	-	KLF7	promoter	N_Shore	chr2:20803085 2-208031477
cg26887632	chr2	2080317 74	-	KLF7	promoter	S_Shore	chr2:20803085 2-208031477
cg16501308	chr1 8	3035022 1	-	KLHL14	body	Island	chr18:3034969 0-30352302
cg10999479	chr2	2360897 5	-	KLHL29	promoter	Island	chr2:23607729- 23610124
cg10909185	chr1 1	7513973 6	+	KLHL35	body	Island	chr11:7513945 4-75139817
cg15506157	chr7	1391684 84	+	KLRG2	promoter	Island	chr7:13916748 0-139168712
cg08131100	chr7	1494116 52	-	KRBA1	promoter	Island	chr7:14941085 8-149412351
cg00060320	chr3	1343699 74	+	KY	promoter	Island	chr3:13436946 4-134370242
cg12307306	chr3	1343699 87	+	KY	promoter	Island	chr3:13436946 4-134370242
cg06037943	chr4	1090880 38	-	LEF1; LOC641518	promoter_and_body	Island	chr4:10908774 7-109090407
cg26679958	chr4	1090885 73	+	LEF1; LOC641518	promoter_and_body	Island	chr4:10908774 7-109090407
cg24761507	chr1 7	3529393 0	+	LHX1	promoter	Island	chr17:3529189 9-35300875
cg04993975	chr1 7	3529447 2	-	LHX1	promoter	Island	chr17:3529189 9-35300875
cg05527869	chr1 7	3529447 6	-	LHX1	promoter	Island	chr17:3529189 9-35300875
cg10043865	chr1 7	3529448 1	-	LHX1	promoter	Island	chr17:3529189 9-35300875
cg10356613	chr1 7	3529449 1	-	LHX1	promoter	Island	chr17:3529189 9-35300875
cg05323725	chr1 7	3529471 3	+	LHX1	promoter_and_body	Island	chr17:3529189 9-35300875
cg13817952	chr9	1249904 56	-	LHX6	body	Island	chr9:12498774 3-124991086
cg19411474	chr1	7560022 4	-	LHX8	body	N_Shore	chr1:75600674- 75601415
cg09131629	chr2	1284333 09	+	LIMS2	promoter	Island	chr2:12843301 0-128433490

cg07262244	chr2	128433489	+	LIMS2	promoter	Island	chr2:128433010-128433490
cg18634211	chr1	26737262	-	LIN28	promoter	Island	chr1:26737246-26738148
cg21842523	chr1	82847461	+	LMO1	body	Island	chr11:8284102-8285032
cg06560887	chr1	33890371	+	LMO2	body	Island	chr11:33890357-33891495
cg27590049	chr1	165205199	-	LMX1A	body	Island	chr1:165204501-165205507
cg23944251	chr1	25464719	+	LOC100128811	body	Island	chr10:25463756-25465639
cg13704680	chr1	77905298	-	LOC100130522	promoter	Island	chr18:77905297-77905566
cg03048083	chr1	43339497	-	LOC100133991; C17orf46	promoter_and_body	Island	chr17:43339124-43339832
cg09392940	chr2	109745828	+	LOC100287216; SH3RF3	promoter_and_body	Island	chr2:109744585-109746833
cg03596016	chr1	246952362	-	LOC149134	promoter	Island	chr1:246952214-246952511
cg12877251	chr8	9760880	+	LOC157627	promoter	Island	chr8:9760750-9761643
cg15248835	chr8	9761171	+	LOC157627; MIR124-1	promoter	Island	chr8:9760750-9761643
cg18440199	chr1	72665282	-	LOC283392; TRHDE	promoter_and_body	N_Shore	chr12:72665683-72667551
cg01030121	chr1	72667236	-	LOC283392; TRHDE	body	Island	chr12:72665683-72667551
cg02954212	chr1	56226350	+	LOC283856; GNAO1	promoter_and_body	Island	chr16:56225255-56226351
cg20062650	chr1	43963907	-	LOC387763	promoter	Island	chr11:43963626-43966048
cg04336379	chr7	5111669	-	LOC389458	promoter	Island	chr7:5111620-5112088
cg11216554	chr1	124638983	+	LOC399815; FAM24B	promoter	Island	chr10:124638743-124639793
cg25923450	chr3	159944518	-	LOC401097	body	S_Shore	chr3:159942916-159944431
cg05085809	chr1	46671083	+	LOC404266; HOXB5	promoter_and_body	Island	chr17:46670522-46671458
cg10153335	chr1	46671293	-	LOC404266; HOXB5	promoter_and_body	Island	chr17:46670522-46671458
cg02293936	chr1	46671298	-	LOC404266; HOXB5	promoter_and_body	Island	chr17:46670522-46671458
cg01774894	chr1	46674395	+	LOC404266; HOXB6	body	N_Shore	chr17:46675044-46675589
cg24527560	chr1	42863508	+	LOC441666	promoter	S_Shore	chr10:42862953-42863216
cg24598948	chr1	42863539	+	LOC441666	promoter	S_Shore	chr10:42862953-42863216
cg03149565	chr4	109092769	-	LOC641518	promoter_and_body	Island	chr4:109092578-109092839
cg12278467	chr5	87971573	-	LOC645323	body	Island	chr5:87969960-87972070
cg24631913	chr5	87971905	+	LOC645323	body	Island	chr5:87969960-87972070
cg07553626	chr1	85359119	+	LPAR3	promoter	Island	chr1:85358359-85359187
cg02996869	chr1	82267171	+	LPHN2	promoter	Island	chr1:82265998-82269048
cg20863963	chr1	82268281	-	LPHN2	promoter	Island	chr1:82265998-82269048
cg04226724	chr1	82268649	-	LPHN2	promoter	Island	chr1:82265998-82269048
cg04118610	chr4	62707027	-	LPHN3	body	OpenSea	
cg00662122	chr8	105601696	-	LRP12	promoter	Island	chr8:105600453-105601704

cg08026618	chr2	142888404	+	LRP1B	promoter_and_body	Island	chr2:142887724-142888553
cg21484213	chr2	142888868	+	LRP1B	promoter_and_body	S_Shore	chr2:142887724-142888553
cg11403874	chr2	170218594	+	LRP2	body	Island	chr2:170218314-170219203
cg13436799	chr2	170218997	+	LRP2	promoter_and_body	Island	chr2:170218314-170219203
cg21645864	chr2	170219019	+	LRP2	promoter_and_body	Island	chr2:170218314-170219203
cg16585827	chr2	170219228	+	LRP2	promoter	N_Shore	chr2:170220772-170221114
cg16691888	chr2	170219230	+	LRP2	promoter	N_Shore	chr2:170220772-170221114
cg02714065	chr2	170219405	+	LRP2	promoter	N_Shore	chr2:170220772-170221114
cg26173847	chr7	127671017	+	LRRC4; SND1	promoter_and_body	N_Shore	chr7:127671158-127672853
cg19849428	chr1	40314978	-	LRRC4C	promoter_and_body	OpenSea	
cg21189727	chr8	67940950	+	LRRC67	promoter	Island	chr8:67940691-67940997
cg10838789	chr8	67940989	+	LRRC67	promoter	Island	chr8:67940691-67940997
cg15674193	chr2	238535910	+	LRRFIP1	promoter	Island	chr2:238535561-238536840
cg09615224	chr3	3842202	-	LRRN1	promoter	Island	chr3:3840513-3842772
cg13826564	chr1	65306731	-	LTBP3	body	Island	chr11:65305935-65308502
cg26559315	chr8	143858636	+	LYNX1	promoter_and_body	Island	chr8:143858279-143859411
cg11364273	chr1	63768032	-	MACROD1	body	Island	chr11:63766058-63768666
cg03103218	chr1	63828672	-	MACROD1	body	OpenSea	
cg09908110	chr1	63828713	-	MACROD1	body	OpenSea	
cg06834240	chr1	79632625	-	MAF	body	Island	chr16:79632619-79635537
cg17865533	chr1	48087087	-	MAPK4	promoter	Island	chr18:48085838-48087589
cg21327887	chr1	43971928	+	MAPT; LOC100128977; LOC100130148	promoter_and_body	Island	chr17:43971410-43975040
cg10780632	chr1	43973522	-	MAPT; LOC100128977; LOC100130148	promoter_and_body	Island	chr17:43971410-43975040
cg00891649	chr1	43972573	-	MAPT; LOC100130148; LOC100128977	promoter_and_body	Island	chr17:43971410-43975040
cg07420190	chr1	220702225	-	MARK1	body	Island	chr1:220701507-220702348
cg06537894	chr1	12978706	+	MAST1	body	Island	chr19:12978359-12978785
cg05068987	chr1	12978714	+	MAST1	body	Island	chr19:12978359-12978785
cg24689196	chr5	65893165	-	MAST4; MAST4	body	Island	chr5:65891877-65893539
cg11256364	chr7	114562847	+	MDFIC	promoter_and_body	Island	chr7:114562170-114563193
cg24255728	chr3	150804063	+	MED12L	promoter	Island	chr3:150802996-150805168
cg02761345	chr5	88179386	+	MEF2C	promoter	N_Shore	chr5:88179866-88180258
cg25611476	chr5	88179989	+	MEF2C	promoter	Island	chr5:88179866-88180258

cg13690989	chr5	88180146	+	MEF2C	promoter	Island	chr5:88179866-88180258
cg04280969	chr5	126626092	+	MEGF10	promoter	Island	chr5:126626053-126626901
cg23398076	chr2	66664960	+	MEIS1	body	S_Shelf	chr2:66661118-66661657
cg15978039	chr2	66667065	+	MEIS1	body	OpenSea	
cg17454831	chr2	66667073	+	MEIS1	body	OpenSea	
cg00003994	chr7	15725862	-	MEOX2	body	OpenSea	
cg07499241	chr2	27053934	+	MIAT	body	S_Shore	chr22:27053081-27053629
cg04355791	chr1	43602436	-	MIR129-2	promoter	N_Shore	chr11:43602545-43603215
cg24870774	chr1	61583342	+	MIR1908; FADS1	promoter_and_body	Island	chr11:61582573-61584728
cg10662314	chr1	54384662	-	MIR196A2	promoter	N_Shelf	chr12:54387825-54388732
cg04481923	chr5	135416205	-	MIR886	body	Island	chr5:135416204-135416475
cg20395153	chr1	280313805	-	MKX	body	Island	chr10:28030182-28035211
cg25523538	chr1	280319507	+	MKX	body	Island	chr10:28030182-28035211
cg17222452	chr3	158289160	-	MLF1	promoter_and_body	Island	chr3:158288800-158289271
cg17344755	chr3	154797563	-	MME	promoter	Island	chr3:154797398-154797988
cg20844545	chr1	132312875	+	MMP17	promoter	Island	chr12:132312439-132315739
cg11798909	chr1	1567820	-	MMP23A	promoter_and_body	Island	chr1:1564421-1570006
cg00278028	chr2	28196834	-	MN1	promoter_and_body	Island	chr22:28192793-28198592
cg11213308	chr1	30606612	-	MPPED2	promoter	Island	chr11:30606004-30608128
cg11855526	chr1	30607068	+	MPPED2	promoter	Island	chr11:30606004-30608128
cg24702253	chr1	3240068	+	MRGPRG; C11orf36	promoter_and_body	S_Shore	chr11:3239217-3239988
cg04131969	chr2	33951647	-	MYADML	body	N_Shore	chr2:33952422-33952684
cg22297146	chr1	48470516	-	MYEF2	promoter_and_body	Island	chr15:48470007-48470628
cg14860120	chr1	48470606	-	MYEF2	promoter	Island	chr15:48470007-48470628
cg06011292	chr1	85340137	+	MYH10	promoter_and_body	Island	chr17:8533004-8534933
cg00268185	chr3	123602768	+	MYLK	promoter	Island	chr3:123602588-123603540
cg22344611	chr1	17743610	-	MYOD1	none	Island	chr11:17740789-17743779
cg20686479	chr1	19735701	-	NAV2; LOC100126784	body	S_Shore	chr11:19733936-19735320
cg22681934	chr1	19322563	-	NCAN	promoter	N_Shore	chr19:19322675-19322916
cg08181476	chr1	19322676	-	NCAN	promoter	Island	chr19:19322675-19322916
cg12915892	chr2	134024093	-	NCKAP5	body	Island	chr2:134023947-134024467
cg04474007	chr1	52207269	-	NCRNA00085	body	Island	chr19:52207132-52207731
cg19818998	chr1	52207792	+	NCRNA00085	body	S_Shore	chr19:52206244-52206726
cg02040433	chr1	58497815	+	NDRG4	promoter	Island	chr16:58497033-58498595

cg00984694	chr16	58498151	-	NDRG4	promoter_and_body	Island	chr16:58497033-58498595
cg06650115	chr16	58498585	-	NDRG4	promoter_and_body	Island	chr16:58497033-58498595
cg02070685	chr16	84002370	-	NECAB2	body	Island	chr16:84002269-84002860
cg01583969	chr8	24773148	-	NEFM	promoter_and_body	S_Shore	chr8:24770908-24772547
cg14689623	chr11	20691161	+	NELL1	promoter_and_body	Island	chr11:20690579-20691845
cg04261192	chr11	20691341	-	NELL1	body	Island	chr11:20690579-20691845
cg01563031	chr11	20691429	-	NELL1	body	Island	chr11:20690579-20691845
cg22773093	chr12	45269519	+	NELL2	promoter_and_body	N_Shore	chr12:45269830-45270835
cg10164885	chr12	45269587	+	NELL2	promoter_and_body	N_Shore	chr12:45269830-45270835
cg22932815	chr12	45269604	+	NELL2	promoter_and_body	N_Shore	chr12:45269830-45270835
cg16845486	chr12	45269610	+	NELL2	promoter_and_body	N_Shore	chr12:45269830-45270835
cg14904464	chr12	45269790	-	NELL2	promoter_and_body	N_Shore	chr12:45269830-45270835
cg20459111	chr12	45270374	-	NELL2	promoter_and_body	Island	chr12:45269830-45270835
cg15745385	chr6	31830364	+	NEU1	body	Island	chr6:31830299-31830948
cg25387565	chr6	31830527	+	NEU1	body	Island	chr6:31830299-31830948
cg19036153	chr6	31830561	+	NEU1	promoter_and_body	Island	chr6:31830299-31830948
cg00890041	chr6	31830570	+	NEU1	promoter_and_body	Island	chr6:31830299-31830948
cg02180498	chr6	31830572	+	NEU1	promoter_and_body	Island	chr6:31830299-31830948
cg11401682	chr6	31830616	+	NEU1	promoter_and_body	Island	chr6:31830299-31830948
cg17012202	chr6	31830656	+	NEU1	promoter_and_body	Island	chr6:31830299-31830948
cg14119437	chr6	31830721	+	NEU1	promoter	Island	chr6:31830299-31830948
cg13510327	chr6	31830729	+	NEU1	promoter	Island	chr6:31830299-31830948
cg00255142	chr6	31830812	+	NEU1	promoter	Island	chr6:31830299-31830948
cg27315170	chr6	31830937	+	NEU1	promoter	Island	chr6:31830299-31830948
cg01431993	chr2	182542864	-	NEUROD1	body	OpenSea	
cg21139392	chr17	47573016	-	NGFR	body	Island	chr17:47572345-47575316
cg21309100	chr17	47575150	-	NGFR	body	Island	chr17:47572345-47575316
cg23483765	chr5	156886996	-	NIPAL4	promoter	Island	chr5:156886969-156887440
cg01509237	chr8	63160509	-	NKAIN3	promoter	N_Shore	chr8:63160598-63162064
cg06299833	chr10	126136709	+	NKX1-2	body	Island	chr10:126135809-126138896
cg10155205	chr10	126137517	+	NKX1-2	body	Island	chr10:126135809-126138896
cg02090569	chr14	36989588	+	NKX2-1	promoter	Island	chr14:36986362-36990576
cg10999312	chr14	36989936	-	NKX2-1	promoter	Island	chr14:36986362-36990576
cg08287265	chr10	101292766	-	NKX2-3	promoter_and_body	Island	chr10:101292436-101292851

cg10530851	chr14	37051417	+	NKX2-8	body	Island	chr14:37049333-37051726
cg18894815	chr4	13546292	+	NKX3-2	promoter	Island	chr4:13543562-13546494
cg24845848	chr4	85414873	+	NKX6-1	body	Island	chr4:85413997-85414874
cg09260089	chr10	134599860	+	NKX6-2	promoter	Island	chr10:134597357-134602649
cg21772509	chr8	41503840	+	NKX6-3	none	N_Shore	chr8:41503916-41504266
cg13238990	chr3	173115252	+	NLGN1	promoter	N_Shore	chr3:173115404-173115775
cg26916166	chr1	183387420	-	NMNAT2	promoter_and_body	Island	chr1:183386000-183387664
cg15577010	chr2	232395273	+	NMUR1	promoter	Island	chr2:232394763-232395337
cg16877924	chr2	73429354	+	NOTO	promoter	Island	chr2:73429283-73430647
cg14939652	chr14	33407765	+	NPAS3	promoter	S_Shelf	chr14:33402094-33404079
cg26708548	chr2	232791101	+	NPPC	promoter	Island	chr2:232789995-232791286
cg14311471	chr5	327111095	-	NPR3	promoter	Island	chr5:32709910-32714450
cg24164873	chr5	32711151	-	NPR3	promoter	Island	chr5:32709910-32714450
cg16964348	chr7	24323799	+	NPY	promoter	Island	chr7:24323558-24325080
cg25884711	chr7	24323840	+	NPY	promoter_and_body	Island	chr7:24323558-24325080
cg04407470	chr6	108489977	-	NR2E1	body	Island	chr6:108485671-108490539
cg13776285	chr6	108490264	+	NR2E1	body	Island	chr6:108485671-108490539
cg11504897	chr6	6007412	-	NRN1	promoter_and_body	Island	chr6:6007387-6007797
cg25307691	chr6	6009011	-	NRN1	promoter	Island	chr6:6008857-6009299
cg05495351	chr2	51259693	+	NRXN1	promoter	OpenSea	
cg04324727	chr14	79745579	-	NRXN3	promoter_and_body	Island	chr14:79745153-79746059
cg00297966	chr8	126186709	-	NSMCE2	body	OpenSea	
cg23045719	chr1	40137636	-	NT5C1A	body	Island	chr1:40136988-40138087
cg23415756	chr1	89257527	-	NTN1	body	Island	chr1:8924167-8926920
cg15128200	chr1	107682674	-	NTNG1	promoter_and_body	N_Shore	chr1:107682889-107684463
cg02361557	chr1	107682963	+	NTNG1	promoter	Island	chr1:107682889-107684463
cg07005523	chr1	107683187	-	NTNG1	promoter	Island	chr1:107682889-107684463
cg07155336	chr1	107683775	-	NTNG1	promoter	Island	chr1:107682889-107684463
cg09508770	chr1	107684255	+	NTNG1	promoter	Island	chr1:107682889-107684463
cg06368118	chr1	107684339	+	NTNG1	promoter	Island	chr1:107682889-107684463
cg07470367	chr1	107684425	+	NTNG1	promoter	Island	chr1:107682889-107684463
cg16785690	chr9	135037323	-	NTNG2	promoter	Island	chr9:135036713-135038933
cg01009697	chr9	87283470	+	NTRK2	promoter_and_body	Island	chr9:87283178-87285704
cg14299675	chr9	91149046	-	NXNL2	promoter	N_Shore	chr9:91149945-91150648

cg15167646	chr17	47653306	-	NXPH3	promoter_and_body	Island	chr17:47653211-47654369
cg02527669	chr2	220417030	-	OBSL1	body	Island	chr2:220416863-220417869
cg11531021	chr2	220417249	-	OBSL1	body	Island	chr2:220416863-220417869
cg21323441	chr15	28344349	+	OCA2	promoter	Island	chr15:28344188-28344489
cg22635008	chr10	50970249	-	OGDHL	promoter	Island	chr10:50969658-50970605
cg09647147	chr10	50970575	+	OGDHL	promoter	Island	chr10:50969658-50970605
cg00208967	chr19	10047924	+	OLFM2	promoter	S_Shore	chr19:10046824-10047067
cg15299832	chr21	34398131	+	OLIG2	promoter	Island	chr21:34395128-34400245
cg10835584	chr18	55108852	+	ONECUT2	body	Island	chr18:55103154-55108853
cg02224864	chr11	132934554	-	OPCML	body	S_Shore	chr11:132934059-132934291
cg08366446	chr1	29138936	+	OPRD1	body	Island	chr1:29138501-29139348
cg02164129	chr5	76926550	-	OTP	body	Island	chr5:76925445-76926875
cg13990092	chr13	97646731	+	OXGR1	promoter	Island	chr13:97646394-97646737
cg22996489	chr13	97646736	+	OXGR1	promoter	Island	chr13:97646394-97646737
cg19619174	chr3	8810139	+	OXTR	promoter	Island	chr3:8808961-8811280
cg03987506	chr3	8810549	+	OXTR	promoter	Island	chr3:8808961-8811280
cg06903384	chr3	152553711	+	P2RY1	body	Island	chr3:152552602-152553712
cg25681618	chr2	71454280	+	PAIP2B	promoter	Island	chr2:71453588-71454318
cg04912999	chr3	142682652	+	PAQR9	promoter	Island	chr3:142681137-142683268
cg17627617	chr3	142682682	-	PAQR9	promoter	Island	chr3:142681137-142683268
cg16616521	chr11	31821388	+	PAX6	body	Island	chr11:31820060-31821416
cg21764190	chr11	31835534	-	PAX6	promoter	Island	chr11:31831620-31839038
cg23655970	chr14	37126582	-	PAX9	promoter	N_Shore	chr14:37126786-37128274
cg11591516	chr10	85954316	+	PCDH21	promoter	Island	chr10:85954199-85955303
cg16678602	chr10	85954331	+	PCDH21	promoter	Island	chr10:85954199-85955303
cg03611007	chr10	85954336	+	PCDH21	promoter	Island	chr10:85954199-85955303
cg18117367	chr5	140213783	-	PCDHA	promoter_and_body	N_Shore	chr5:140214068-140214464
cg12629325	chr5	140306458	-	PCDHAC; PCDHA	promoter_and_body	Island	chr5:140305712-140307193
cg06827143	chr5	140430921	-	PCDHB	promoter	OpenSea	
cg09178190	chr5	140529580	-	PCDHB	promoter	N_Shore	chr5:140531157-140532017
cg09066326	chr5	140753415	+	PCDHGA	promoter_and_body	N_Shore	chr5:140753654-140753952
cg02780295	chr5	140855463	-	PCDHGA; PCDHGB; PCDHGC	promoter_and_body	Island	chr5:140855386-140856620
cg13993336	chr5	140855482	-	PCDHGA; PCDHGB; PCDHGC	promoter_and_body	Island	chr5:140855386-140856620
cg00281842	chr5	140855562	+	PCDHGA; PCDHGB; PCDHGC	promoter_and_body	Island	chr5:140855386-140856620



cg10858746	chr5	140855582	-	PCDHGA; PCDHGB; PCDHGC	promoter_and_body	Island	chr5:140855386-140856620
cg06428620	chr5	140864276	-	PCDHGA; PCDHGC; PCDHGB	promoter_and_body	N_Shore	chr5:140864527-140864748
cg17137182	chr7	82792284	+	PCLO	promoter	Island	chr7:82791674-82792412
cg13909585	chr7	82792379	+	PCLO	promoter	Island	chr7:82791674-82792412
cg21878859	chr5	95767724	+	PCSK1	body	N_Shore	chr5:95768874-95769080
cg18840956	chr5	95769005	+	PCSK1	promoter	Island	chr5:95768874-95769080
cg04584301	chr2	17208740	+	PCSK2	body	Island	chr20:17208550-17208756
cg00565070	chr1	10530736	+	PDE4A	promoter	Island	chr19:10529627-10532004
cg12052265	chr1	104034058	-	PDGFD	body	N_Shore	chr11:104034536-104035058
cg07748540	chr1	104034619	-	PDGFD	body	Island	chr11:104034536-104035058
cg04518342	chr5	131593106	-	PDLIM4	promoter	Island	chr5:131593039-131593813
cg11843238	chr5	131593191	-	PDLIM4	promoter	Island	chr5:131593039-131593813
cg18301423	chr5	131593218	-	PDLIM4	promoter	Island	chr5:131593039-131593813
cg11791751	chr1	13910138	-	PDPN	promoter	Island	chr1:13910137-13910868
cg05140069	chr1	13910667	-	PDPN	promoter_and_body	Island	chr1:13910137-13910868
cg05281894	chr1	13910698	-	PDPN	promoter_and_body	Island	chr1:13910137-13910868
cg09804380	chr1	13910700	-	PDPN	promoter_and_body	Island	chr1:13910137-13910868
cg16581884	chr1	100999953	-	PGR	promoter_and_body	Island	chr11:100999946-101000437
cg00758296	chr2	45402995	+	PHF21B	body	N_Shore	chr22:45403036-45406372
cg09021039	chr2	45403893	-	PHF21B	body	Island	chr22:45403036-45406372
cg13103303	chr1	71955113	-	PHOX2A	promoter_and_body	Island	chr11:71954816-71955659
cg07754999	chr1	103991057	-	PITX3	body	Island	chr10:103990213-103991829
cg27649073	chr1	104001259	+	PITX3	promoter	Island	chr10:104000254-104001741
cg26354017	chr1	205819088	+	PM20D1	body	Island	chr1:205818898-205819191
cg14159672	chr1	205819179	+	PM20D1	body	Island	chr1:205818898-205819191
cg11965913	chr1	205819406	-	PM20D1	promoter	S_Shore	chr1:205818898-205819191
cg01394819	chr1	53527665	-	PODN	promoter	Island	chr1:53527572-53528974
cg13764106	chr1	53527693	-	PODN	promoter	Island	chr1:53527572-53528974
cg13357482	chr6	105628017	+	POPDC3	promoter	S_Shore	chr6:105627406-105627830
cg06577045	chr6	105628022	+	POPDC3	promoter	S_Shore	chr6:105627406-105627830
cg24989739	chr6	105628027	+	POPDC3	promoter	S_Shore	chr6:105627406-105627830
cg14422660	chr6	105628044	+	POPDC3	promoter	S_Shore	chr6:105627406-105627830
cg02407659	chr6	105628063	+	POPDC3	promoter	S_Shore	chr6:105627406-105627830
cg05628417	chr6	105628165	+	POPDC3	promoter	S_Shore	chr6:105627406-105627830

cg25488697	chr1	38510383	-	POU3F1	body	Island	chr1:38510102-38513642
cg03636215	chr1	38512601	+	POU3F1	promoter	Island	chr1:38510102-38513642
cg24474130	chr6	99282348	-	POU3F2	promoter	Island	chr6:99279317-99283842
cg02176407	chr6	99282754	+	POU3F2	body	Island	chr6:99279317-99283842
cg16202970	chr6	99283201	+	POU3F2	body	Island	chr6:99279317-99283842
cg22085539	chr6	99284027	-	POU3F2	body	S_Shore	chr6:99279317-99283842
cg21200539	chr4	147562073	-	POU4F2	none	S_Shore	chr4:147559205-147561901
cg08884571	chr19	45901453	+	PPP1R13L	body	Island	chr19:45901452-45901688
cg13645732	chr19	45901649	+	PPP1R13L	promoter	Island	chr19:45901452-45901688
cg08196968	chr19	38746749	+	PPP1R14A	body	Island	chr19:38746638-38747379
cg13564825	chr19	38747201	-	PPP1R14A	promoter	Island	chr19:38746638-38747379
cg22557662	chr19	38747374	-	PPP1R14A	promoter	Island	chr19:38746638-38747379
cg04916107	chr7	94537805	-	PPP1R9A	promoter	S_Shore	chr7:94536849-94537477
cg08073166	chr7	94538182	-	PPP1R9A	promoter	S_Shore	chr7:94536849-94537477
cg17034088	chr7	94538194	-	PPP1R9A	promoter	S_Shore	chr7:94536849-94537477
cg25021259	chr5	146258546	+	PPP2R2B	promoter_and_body	Island	chr5:146257346-146258575
cg05920961	chr14	102248253	+	PPP2R5C	body	Island	chr14:102247660-102248279
cg19391276	chr6	100055785	+	PRDM13	body	Island	chr6:100055641-100055866
cg26762347	chr1	2990031	-	PRDM16	body	Island	chr1:2990030-2990718
cg01961086	chr1	3086487	-	PRDM16	body	OpenSea	
cg10416963	chr4	121844401	-	PRDM5	promoter	S_Shore	chr4:121843148-121844193
cg19157243	chr5	122424706	-	PRDM6	promoter	N_Shore	chr5:122424905-122425958
cg20142271	chr4	81106287	+	PRDM8	promoter	S_Shore	chr4:81104761-81105527
cg26162932	chr4	81106342	+	PRDM8	promoter	S_Shore	chr4:81104761-81105527
cg25591794	chr13	28554842	-	PRHOXNB	body	Island	chr13:28554427-28555065
cg09763175	chr1	57110722	+	PRKAA2	promoter	Island	chr1:57110663-57111337
cg04876835	chr1	57111099	-	PRKAA2	body	Island	chr1:57110663-57111337
cg18601167	chr7	752286	+	PRKAR1B	promoter	S_Shore	chr7:750788-751237
cg13895235	chr7	752292	+	PRKAR1B	promoter	S_Shore	chr7:750788-751237
cg04884011	chr10	52833909	+	PRKG1	promoter_and_body	Island	chr10:52833539-52834752
cg27380599	chr10	52834067	+	PRKG1	promoter_and_body	Island	chr10:52833539-52834752
cg02731293	chr10	52834076	+	PRKG1	promoter_and_body	Island	chr10:52833539-52834752
cg04327529	chr10	52834121	+	PRKG1	promoter_and_body	Island	chr10:52833539-52834752
cg12022294	chr10	52834676	-	PRKG1	body	Island	chr10:52833539-52834752

cg24453580	chr1 2	4969106 4	-	PRPH	body	Island	chr12:4968887 3-49691360
cg16621691	chr5	1198006 87	-	PRR16	promoter	N_Shore	chr5:11980097 1-119801194
cg04480903	chr2 2	4506447 1	+	PRR5	promoter	Island	chr22:4506415 9-45065092
cg13713739	chr9	1324833 77	-	PRRX2	body	S_Shore	chr9:13248147 2-132481745
cg12092561	chr1	1153884 0	-	PTCHD2	promoter	Island	chr1:11538669- 11540342
cg24126187	chr3	4692354 6	+	PTH1R	promoter	Island	chr3:46923265- 46925182
cg13607709	chr3	4694015 3	+	PTH1R	body	Island	chr3:46940054- 46940394
cg11334818	chr1 1	1881319 1	-	PTPN5	promoter_and_body	Island	chr11:1881257 2-18814079
cg24485954	chr1 9	5293011	-	PTPRS	promoter	Island	chr19:5293010- 5294211
cg16733654	chr1 9	5293083	-	PTPRS	promoter	Island	chr19:5293010- 5294211
cg05381423	chr1 9	5340713	-	PTPRS	promoter_and_body	Island	chr19:5339640- 5341061
cg25902187	chr1 5	5588104 4	-	PYGO1	body	Island	chr15:5587979 2-55881228
cg06157277	chr1 2	2159048 0	-	PYROXD1	promoter	Island	chr12:2159046 9-21590785
cg25830696	chr1 7	4203047 9	-	PYY	body	Island	chr17:4203017 3-42030941
cg21816330	chr1 7	2704462 9	+	RAB34	promoter_and_body	Island	chr17:2704416 8-27045049
cg04842146	chr8	8509705 6	-	RALYL	promoter	Island	chr8:85096759- 85097247
cg20668644	chr1 7	3834760 3	-	RAPGEFL1	body	Island	chr17:3834753 3-38347765
cg02636041	chr1 0	4369800 8	+	RASGEF1A	body	Island	chr10:4369777 7-43698177
cg12451631	chr1 0	4369814 1	+	RASGEF1A	body	Island	chr10:4369777 7-43698177
cg00888521	chr5	8025697 1	+	RASGRF2	body	Island	chr5:80255904- 80257006
cg07994622	chr2 0	4804052	-	RASSF2	promoter	Island	chr20:4803013- 4804146
cg06328855	chr1 0	1124043 46	+	RBM20	body	S_Shore	chr10:1124029 53-112404328
cg02685016	chr6	1728233 3	-	RBM24	promoter_and_body	Island	chr6:17280739- 17282334
cg07346310	chr6	1728235 4	-	RBM24	promoter_and_body	S_Shore	chr6:17280739- 17282334
cg20532370	chr3	1392587 30	+	RBP1	promoter	Island	chr3:13925815 2-139258731
cg15229124	chr3	1392589 12	+	RBP1	promoter	S_Shore	chr3:13925771 2-139257949
cg23363832	chr3	1392589 39	+	RBP1	promoter	S_Shore	chr3:13925771 2-139257949
cg21941030	chr1 9	5003101 7	-	RCN3	promoter_and_body	Island	chr19:5003098 1-50031300
cg19403104	chr1 9	5003124 6	-	RCN3	promoter_and_body	Island	chr19:5003098 1-50031300
cg15963326	chr1 9	5003708 5	-	RCN3	body	Island	chr19:5003707 8-50037670
cg13412498	chr9	3603734 0	-	RECK	body	Island	chr9:36036798- 36037564
cg10599900	chr2 0	3006303 6	-	REM1	promoter	Island	chr20:3006296 9-30063281
cg12912737	chr2 0	3006303 8	-	REM1	promoter	Island	chr20:3006296 9-30063281
cg05621401	chr1 0	4357206 5	+	RET	promoter	Island	chr10:4357193 9-43573434

cg00540891	chr10	43572244	+	RET	promoter	Island	chr10:43571939-43573434
cg25566352	chr12	106977562	-	RFX4	body	Island	chr12:106977388-106977713
cg00450784	chr12	106979062	-	RFX4	body	N_Shore	chr12:106979429-106981086
cg02816003	chr6	117198183	-	RFX6	promoter	Island	chr6:117198089-117198705
cg09930033	chr6	117198704	+	RFX6	body	Island	chr6:117198089-117198705
cg09263118	chr19	11531294	-	RGL3; CCDC151	promoter	Island	chr19:11531278-11531590
cg04761198	chr8	54793733	-	RGS20	body	Island	chr8:54791845-54795141
cg02779564	chr8	54794348	+	RGS20	body	Island	chr8:54791845-54795141
cg11679177	chr1	241519652	+	RGS7	promoter	N_Shore	chr1:241520103-241520790
cg04794832	chr17	30593000	-	RHBDL3	promoter	N_Shore	chr17:30593198-30594033
cg16342059	chr12	8849781	+	RIMKLB	promoter	N_Shore	chr12:8849963-8851403
cg22038579	chr12	8849964	-	RIMKLB	promoter	Island	chr12:8849963-8851403
cg08962682	chr12	8850939	-	RIMKLB	promoter	Island	chr12:8849963-8851403
cg03231163	chr19	39360465	+	RINL	body	Island	chr19:39359916-39361160
cg02486253	chr17	55122828	-	RNF126P1	promoter	Island	chr17:55122795-55124018
cg15576900	chr1	44883697	+	RNF220	body	Island	chr1:44883136-44884272
cg13880950	chr1	44884096	-	RNF220	body	Island	chr1:44883136-44884272
cg12548634	chr1	44884109	-	RNF220	body	Island	chr1:44883136-44884272
cg08574592	chr15	61520873	-	RORA	body	Island	chr15:61520423-61521716
cg18136062	chr15	61520931	+	RORA	body	Island	chr15:61520423-61521716
cg07441272	chr3	186857475	+	RPL39L	promoter	Island	chr3:186856927-186857659
cg23358625	chr19	23945641	-	RPSAP58	promoter	N_Shore	chr19:23945713-23946128
cg05605052	chr19	23945659	-	RPSAP58	promoter	N_Shore	chr19:23945713-23946128
cg06427838	chr19	23945722	-	RPSAP58	promoter	Island	chr19:23945713-23946128
cg20342628	chr6	90122369	+	RRAGD	promoter	Island	chr6:90120874-90122370
cg01141940	chr14	60097247	-	RTN1	promoter_and_body	Island	chr14:60097208-60097553
cg19556814	chr14	60337477	+	RTN1	promoter_and_body	S_Shore	chr14:60336951-60337461
cg14769786	chr17	1881333	+	RTN4RL1	body	S_Shore	chr17:1880789-1881116
cg26772766	chr17	1928182	+	RTN4RL1	promoter	Island	chr17:1927051-1929408
cg15414833	chr7	87257767	-	RUNDC3B; ABCB1	promoter_and_body	Island	chr7:87256958-87258444
cg08477332	chr1	153590243	-	S100A14	promoter	OpenSea	
cg18323466	chr1	101702602	-	S1PR1	promoter_and_body	Island	chr1:101702445-101702745
cg00898147	chr1	21994785	-	SALL2	body	OpenSea	
cg06685464	chr22	20790837	+	SCARF2	body	Island	chr22:20790638-20792665

cg20401551	chr2 2	2079098 5	+	SCARF2	body	Island	chr22:2079063 8-20792665
cg15243570	chr2 2	2079221 7	+	SCARF2	promoter	Island	chr22:2079063 8-20792665
cg03952331	chr2 2	2079222 2	+	SCARF2	promoter	Island	chr22:2079063 8-20792665
cg09290614	chr3 1	3869137 1	+	SCN5A	promoter	Island	chr3:38690409- 38691513
cg25116191	chr3 6	3869150 6	+	SCN5A	promoter	Island	chr3:38690409- 38691513
cg16549389	chr1 6	2331348 0	-	SCNN1B	promoter	Island	chr16:2331323 9-23313946
cg26424556	chr1 6	2331350 8	-	SCNN1B	promoter	Island	chr16:2331323 9-23313946
cg20366601	chr4 81	1412946 81	-	SCOC	promoter_and_body	Island	chr4:14129466 6-141295274
cg18592561	chr2 0	644081 0	-	SCRT2	none	Island	chr20:643975- 645233
cg25664438	chr8 3	9750559 3	-	SDC2	promoter	N_Shore	chr8:97505747- 97507607
cg23858558	chr8 0	9750560 0	-	SDC2	promoter	N_Shore	chr8:97505747- 97507607
cg04261408	chr8 5	9750667 5	-	SDC2	body	Island	chr8:97505747- 97507607
cg10292139	chr8 1	9750756 1	-	SDC2	body	Island	chr8:97505747- 97507607
cg26472636	chr5 1594282	1594282 1594282	+	SDHAP3	body	Island	chr5:1594238- 1595027
cg26758486	chr1 7	7153328 6	-	SDK2	body	OpenSea	
cg26307359	chr1 7	2733264 6	-	SEZ6	body	Island	chr17:2733226 8-27333188
cg22831607	chr1 0	9953179 7	+	SFRP5	promoter	Island	chr10:9953102 5-99531968
cg00673557	chr6 5	8982791 5	-	SFRS13B	promoter	Island	chr6:89827134- 89828122
cg03209103	chr7 6	9428439 6	-	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg26464535	chr7 3	9428440 3	-	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg04010684	chr7 1	9428441 1	-	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg08607907	chr7 8	9428442 8	-	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg19734015	chr7 2	9428443 2	-	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg25485192	chr7 9	9428443 9	-	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg23498273	chr7 6	9428452 6	+	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg22090863	chr7 3	9428462 3	+	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg21027820	chr7 9	9428462 9	+	SGCE; PEG10	promoter_and_body	N_Shore	chr7:94284858- 94286527
cg26912242	chr7 2	9428535 2	+	SGCE; PEG10	promoter_and_body	Island	chr7:94284858- 94286527
cg04366249	chr7 1	9428550 1	+	SGCE; PEG10	promoter_and_body	Island	chr7:94284858- 94286527
cg14388858	chr7 0	9428552 0	+	SGCE; PEG10	promoter_and_body	Island	chr7:94284858- 94286527
cg17338501	chr3 54	1538399 54	+	SGEF	body	Island	chr3:15383878 7-153840380
cg05476568	chr3 09	1538401 09	+	SGEF	body	Island	chr3:15383878 7-153840380
cg18290075	chr3 77	1538404 77	+	SGEF	body	S_Shore	chr3:15383878 7-153840380
cg09210519	chr1 0	1054523 52	+	SH3PXD2A	body	Island	chr10:1054523 38-105453230

cg08447324	chr1 9	5117081 6	-	SHANK1	body	Island	chr19:5116965 9-51172023
cg24033558	chr1 5	4547975 5	-	SHF	body	Island	chr15:4547950 9-45480498
cg14866200	chr4	4239984 3	+	SHISA3	promoter	Island	chr4:42399152- 42400802
cg01565320	chr4	4239985 1	+	SHISA3	promoter	Island	chr4:42399152- 42400802
cg02997982	chr1 9	4108229 1	-	SHKBP1; SPTBN4	promoter	N_Shore	chr19:4108261 5-41083355
cg16851417	chr2 1	3807704 2	-	SIM2	body	Island	chr21:3807676 2-38077685
cg07615087	chr2 1	3807734 7	-	SIM2	body	Island	chr21:3807676 2-38077685
cg10456990	chr2 1	3807759 7	+	SIM2	body	Island	chr21:3807676 2-38077685
cg26720125	chr2 1	3807767 3	-	SIM2	body	Island	chr21:3807676 2-38077685
cg14626259	chr2 1	3807901 9	-	SIM2	body	N_Shore	chr21:3807994 1-38081833
cg00937982	chr2 1	3808027 4	-	SIM2	body	Island	chr21:3807994 1-38081833
cg00698204	chr2 1	3808069 4	-	SIM2	body	Island	chr21:3807994 1-38081833
cg01090834	chr2 1	3808119 3	-	SIM2	body	Island	chr21:3807994 1-38081833
cg19193931	chr2 1	3808197 6	-	SIM2	body	S_Shore	chr21:3807994 1-38081833
cg24080247	chr2 1	3808261 3	+	SIM2	body	S_Shore	chr21:3807994 1-38081833
cg04648480	chr2 1	3808309 9	-	SIM2	body	S_Shore	chr21:3807994 1-38081833
cg25446076	chr2 1	3808314 9	-	SIM2	body	S_Shore	chr21:3807994 1-38081833
cg02711647	chr2	4523768 9	-	SIX2	promoter	Island	chr2:45235511- 45237792
cg04954559	chr1 1	2236542 8	-	SLC17A6	body	S_Shelf	chr11:2236286 2-22363377
cg26985666	chr1 1	3544108 8	+	SLC1A2	promoter_and_body	Island	chr11:3544037 5-35441882
cg07724977	chr1 1	3544119 8	+	SLC1A2	promoter	Island	chr11:3544037 5-35441882
cg11755796	chr2 0	1919261 6	+	SLC24A3	promoter	Island	chr20:1919245 9-19193902
cg24766334	chr1 4	9279007 2	+	SLC24A4	promoter	Island	chr14:9278949 4-92790712
cg08718398	chr7	1073022 55	-	SLC26A4; LOC286002	promoter_and_body	Island	chr7:10730120 5-107302416
cg20103758	chr5	1283006 96	-	SLC27A6	promoter	N_Shore	chr5:12830080 0-128301329
cg15490840	chr2 0	3735208 5	+	SLC32A1	promoter	N_Shore	chr20:3735213 0-37357372
cg16782807	chr2 0	3735425 4	+	SLC32A1	body	Island	chr20:3735213 0-37357372
cg13915754	chr2 0	3735596 5	+	SLC32A1	body	Island	chr20:3735213 0-37357372
cg09699039	chr6	1182415 68	+	SLC35F1	body	Island	chr6:11824134 7-118241569
cg00662647	chr1	2343500 51	-	SLC35F3	body	Island	chr1:23434988 4-234350471
cg26490054	chr1 2	1016040 56	-	SLC5A8	promoter	S_Shore	chr12:1016033 87-101603933
cg16164276	chr3	1103434 5	-	SLC6A1	promoter	N_Shore	chr3:11034446- 11035384
cg04210284	chr5	1445561	+	SLC6A3	promoter	Island	chr5:1444678- 1446648
cg27037018	chr5	1445567	+	SLC6A3	promoter	Island	chr5:1444678- 1446648

cg04140862	chr14	70654639	+	SLC8A3	promoter	N_Shore	chr14:70655095-70656077
cg20267521	chr14	70655056	+	SLC8A3	promoter	N_Shore	chr14:70655095-70656077
cg20409590	chr14	70655382	-	SLC8A3	promoter_and_body	Island	chr14:70655095-70656077
cg05203877	chr14	70655686	+	SLC8A3	promoter_and_body	Island	chr14:70655095-70656077
cg08265644	chr14	70655871	+	SLC8A3	promoter	Island	chr14:70655095-70656077
cg07136998	chr5	168728081	-	SLIT3	promoter_and_body	Island	chr5:168727429-168728275
cg06143522	chr13	88330200	+	SLITRK5	body	S_Shore	chr13:88329394-88329885
cg00109076	chr13	88330463	+	SLITRK5	body	S_Shore	chr13:88329394-88329885
cg15447479	chr7	128828765	-	SMO	promoter_and_body	Island	chr7:128828333-128829366
cg18420512	chr7	128828982	-	SMO	promoter_and_body	Island	chr7:128828333-128829366
cg02540477	chr6	168842035	+	SMOC2	promoter_and_body	Island	chr6:168841818-168843100
cg04798314	chr1	246668601	+	SMYD3	body	N_Shore	chr1:246670148-246670768
cg25307902	chr20	101992100	+	SNAP25	promoter	N_Shore	chr20:10200088-10200384
cg20003494	chr4	90757398	+	SNCA	promoter	N_Shore	chr4:90758008-90758870
cg05241924	chr4	90759115	+	SNCA	promoter	S_Shore	chr4:90758008-90758870
cg04062510	chr5	121648346	-	SNCAIP	promoter	Island	chr5:121648312-121648549
cg12544974	chr5	121648479	+	SNCAIP	promoter	Island	chr5:121648312-121648549
cg08253651	chr12	96252105	-	SNRPF	promoter	Island	chr12:96252020-96252246
cg09551147	chr10	106399957	-	SORCS3	promoter	Island	chr10:106399567-106402812
cg06613095	chr3	137483617	+	SOX14	promoter_and_body	Island	chr3:137482964-137484454
cg18184251	chr3	181420086	+	SOX2OT	body	OpenSea	
cg05513806	chr3	181438216	-	SOX2OT	body	S_Shore	chr3:181437184-181437478
cg13294849	chr3	181441571	+	SOX2OT	body	N_Shelf	chr3:181444409-181445000
cg03783410	chr3	181443800	-	SOX2OT	body	N_Shore	chr3:181444409-181445000
cg22256631	chr3	181443971	-	SOX2OT	body	N_Shore	chr3:181444409-181445000
cg07747133	chr3	181428307	+	SOX2OT; SOX2	promoter_and_body	N_Shore	chr3:181430141-181431076
cg04948892	chr3	181428462	+	SOX2OT; SOX2	promoter_and_body	N_Shore	chr3:181430141-181431076
cg17023776	chr12	24714652	-	SOX5	promoter	N_Shore	chr12:24714956-24716243
cg08972130	chr12	24715478	+	SOX5	promoter	Island	chr12:24714956-24716243
cg03625010	chr12	24715484	+	SOX5	promoter	Island	chr12:24714956-24716243
cg17853504	chr12	24715538	+	SOX5	promoter	Island	chr12:24714956-24716243
cg10158080	chr12	24715864	-	SOX5	promoter	Island	chr12:24714956-24716243
cg07813142	chr2	171573223	+	SP5	body	Island	chr2:171569877-171573904
cg27515369	chr3	140770599	+	SPSB4	promoter	Island	chr3:140769886-140771080

cg02884884	chr7	75831418	-	SRRM3	promoter	Island	chr7:75831068-75831542
cg04573550	chr14	38680313	+	SSTR1	none	Island	chr14:38678245-38680937
cg27066284	chr17	71161258	-	SSTR2	promoter_and_body	Island	chr17:71160922-71162350
cg01234063	chr11	12622607	-	ST3GAL4	promoter	Island	chr11:12622535-126226073
cg12726960	chr3	36421703	-	STAC	promoter	Island	chr3:36421702-36422210
cg19055231	chr3	36422397	-	STAC	body	S_Shore	chr3:36421702-36422210
cg07280482	chr17	37382173	+	STAC2	promoter	Island	chr17:37380953-37382363
cg06609197	chr8	80524611	+	STMN2	body	Island	chr8:80523975-80525765
cg03524572	chr20	62284488	+	STMN3	body	Island	chr20:62283516-62284835
cg10957242	chr4	184826299	-	STOX2	promoter	Island	chr4:184826253-184828177
cg11354594	chr4	184826704	-	STOX2	promoter_and_body	Island	chr4:184826253-184828177
cg02500300	chr4	184827754	-	STOX2	promoter_and_body	Island	chr4:184826253-184828177
cg02043600	chr16	31021933	-	STX1B	promoter	OpenSea	
cg05293820	chr3	120627406	-	STXBP5L	promoter	Island	chr3:120626880-120627579
cg25742540	chr15	91643000	-	SV2B	promoter	Island	chr15:91642908-91643702
cg08326075	chr15	91643003	-	SV2B	promoter	Island	chr15:91642908-91643702
cg18144285	chr15	91643026	-	SV2B	promoter	Island	chr15:91642908-91643702
cg18750433	chr15	91643036	-	SV2B	promoter	Island	chr15:91642908-91643702
cg06705526	chr5	75379336	-	SV2C; SV2C	promoter_and_body	Island	chr5:75378974-75380796
cg09546168	chr16	77246495	-	SYCE1L	body	Island	chr16:77245944-77247013
cg01504555	chr16	77246968	-	SYCE1L	none	Island	chr16:77245944-77247013
cg05470389	chr22	33197618	-	SYN3; TIMP3	promoter_and_body	Island	chr22:33197380-33198267
cg26620959	chr6	152958489	+	SYNE1	promoter_and_body	S_Shore	chr6:152957810-152958472
cg09948076	chr15	99645088	+	SYNM	promoter	Island	chr15:99645030-99646444
cg10637512	chr15	99645096	+	SYNM	promoter	Island	chr15:99645030-99646444
cg03863616	chr1	79257853	+	SYT1	promoter_and_body	OpenSea	
cg10377414	chr17	80832836	-	TBCD	body	S_Shelf	chr17:80829533-80829871
cg06747745	chr11	120894801	-	TBCEL	promoter	Island	chr11:120894689-120895082
cg22794704	chr2	162273437	+	TBR1	body	Island	chr2:162273294-162273725
cg01697719	chr22	19754125	+	TBX1	body	Island	chr22:19753312-19755013
cg01765249	chr17	59476334	-	TBX2	promoter	Island	chr17:59473060-59483266
cg11031701	chr17	59478068	+	TBX2	body	Island	chr17:59473060-59483266
cg26281453	chr17	45810610	-	TBX21	promoter_and_body	Island	chr17:45810589-45811388
cg19597776	chr18	53254863	+	TCF4	promoter	N_Shelf	chr18:53257018-53257309



cg23482397	chr18	53257226	-	TCF4	promoter	Island	chr18:53257018-53257309
cg21624739	chr2	85359957	-	TCF7L1	promoter	Island	chr2:85359956-85362593
cg20663042	chr1	67349407	+	TEKT1	promoter	OpenSea	
cg04462627	chr1	58019123	-	TEPP	body	Island	chr16:58018400-58019471
cg13848707	chr1	70321243	-	TET1	promoter	S_Shore	chr10:70320130-70320822
cg12630147	chr1	70321574	+	TET1	promoter	S_Shore	chr10:70320130-70320822
cg02774862	chr1	70321580	+	TET1	promoter	S_Shore	chr10:70320130-70320822
cg17608103	chr6	169653612	+	THBS2	promoter	OpenSea	
cg18490616	chr2	88469792	+	THNSL2	promoter	Island	chr2:88469691-88470386
cg02455397	chr1	119293385	+	THY1	promoter	Island	chr11:119293320-119293943
cg13486354	chr2	32931082	-	TIAM1	promoter	Island	chr21:32929927-32932017
cg16867777	chr2	32932073	+	TIAM1	promoter	S_Shore	chr21:32929927-32932017
cg00498604	chr4	166793789	+	TLL1	promoter	N_Shore	chr4:166794545-166795341
cg08908184	chr1	102890974	+	TLX1	promoter	N_Shore	chr10:102891010-102891794
cg03020810	chr1	102890984	+	TLX1; TLX1NB	promoter	N_Shore	chr10:102891010-102891794
cg21492832	chr1	105993308	-	TMEM121	promoter	Island	chr14:105992499-105996414
cg08774452	chr1	128850550	-	TMEM132C	body	Island	chr12:128850549-128850755
cg18505401	chr7	19812570	-	TMEM196	promoter	Island	chr7:19812569-19813005
cg27341472	chr7	19812592	-	TMEM196	promoter	Island	chr7:19812569-19813005
cg15042080	chr8	109799756	+	TMEM74	promoter_and_body	Island	chr8:109799429-109799847
cg10061361	chr4	122078167	-	TNIP3; TNIP3	body	OpenSea	
cg26745222	chr2	42543878	+	TOX2	promoter_and_body	Island	chr20:42543097-42545137
cg07665260	chr2	42544086	+	TOX2	promoter_and_body	Island	chr20:42543097-42545137
cg23540518	chr1	228604566	-	TRIM17	promoter_and_body	Island	chr1:228603706-228604567
cg15497761	chr1	155147397	-	TRIM46	body	Island	chr1:155147185-155147444
cg19275632	chr1	38443950	-	TRPC4	promoter	Island	chr13:38443682-38444228
cg24994173	chr5	110408997	-	TSLP	promoter_and_body	Island	chr5:110408704-110409039
cg15558982	chr1	115632262	-	TSPAN2	promoter	Island	chr1:115631850-115632584
cg06043114	chr1	115632455	-	TSPAN2	promoter	Island	chr1:115631850-115632584
cg27363327	chr6	43211208	-	TTBK1	promoter	Island	chr6:43211114-43211345
cg16620382	chr6	43211213	-	TTBK1	promoter	Island	chr6:43211114-43211345
cg15241920	chr1	54926514	+	TTYH1	promoter	N_Shore	chr19:54927902-54928225
cg04043591	chr7	19155806	+	TWIST1	none	N_Shore	chr7:19156050-19158042
cg14859874	chr1	154238265	+	UBAP2L	body	OpenSea	

cg24917673	chr1 9	1779875 5	+	UNC13A	body	Island	chr19:1779867 9-17799329
cg12903638	chr2	2106363 50	-	UNC80	promoter	Island	chr2:21063634 4-210636935
cg24915947	chr2	2106367 83	-	UNC80	promoter_and_body	Island	chr2:21063634 4-210636935
cg24588482	chr1	1603702 53	-	VANGL2	promoter	Island	chr1:16037011 2-160370658
cg07821427	chr1 6	7782241 9	-	VAT1L	promoter	Island	chr16:7782237 5-77823134
cg25602490	chr1	1085070 78	+	VAV3	body	N_Shore	chr1:10850725 1-108507841
cg23885415	chr2	7112725 5	+	VAX2	promoter	Island	chr2:71126720- 71129209
cg20518889	chr2	7112752 9	-	VAX2	promoter	Island	chr2:71126720- 71129209
cg03595100	chr2	7112753 8	-	VAX2	promoter	Island	chr2:71126720- 71129209
cg00567749	chr5	8276790 8	+	VCAN	promoter	N_Shore	chr5:82768387- 82769268
cg07478641	chr5	8276848 8	-	VCAN	promoter	Island	chr5:82768387- 82769268
cg01018701	chr3	1571559 98	+	VEPH1; PTX3	body	S_Shore	chr3:15715526 7-157155826
cg16566171	chr7	1008095 07	-	VGF	promoter	S_Shore	chr7:10080627 9-100809064
cg12615137	chr3	8704028 6	+	VGLL3	promoter	Island	chr3:87039610- 87040516
cg07558275	chr3	8704073 9	+	VGLL3	promoter	S_Shore	chr3:87039610- 87040516
cg11973177	chr1 0	1727100 6	+	VIM	promoter	Island	chr10:1727043 0-17272617
cg26983469	chr1 0	1727105 1	+	VIM	promoter	Island	chr10:1727043 0-17272617
cg22388634	chr2 0	2505842 9	+	VSX1	body	Island	chr20:2505828 8-25058726
cg00063174	chr2	2287362 53	+	WDR69	promoter	Island	chr2:22873623 0-228736544
cg20647610	chr2	2287362 58	+	WDR69	promoter	Island	chr2:22873623 0-228736544
cg23807890	chr2	2287363 57	+	WDR69	promoter_and_body	Island	chr2:22873623 0-228736544
cg26831241	chr2	1755469 16	-	WIPF1	promoter	Island	chr2:17554686 2-175547880
cg25537217	chr2	1755471 23	-	WIPF1	promoter	Island	chr2:17554686 2-175547880
cg13563298	chr9	9594805 9	-	WNK2	body	S_Shore	chr9:95946147- 95947835
cg12379948	chr1 7	4489642 4	-	WNT3	promoter	Island	chr17:4489580 0-44897025
cg01051310	chr1	2281944 43	+	WNT3A	promoter	Island	chr1:22819409 6-228196512
cg05802452	chr1	2281944 76	+	WNT3A	promoter	Island	chr1:22819409 6-228196512
cg26841013	chr1	2282480 13	-	WNT3A	none	S_Shore	chr1:22824663 1-228247197
cg00828602	chr3	5552083 4	-	WNT5A	body	Island	chr3:55520226- 55522344
cg02708401	chr3	5552152 9	+	WNT5A	promoter	Island	chr3:55520226- 55522344
cg07657743	chr3	1392068 9	-	WNT7A	body	Island	chr3:13919939- 13922335
cg01755467	chr8	3089061 7	+	WRN; PURG	promoter_and_body	OpenSea	
cg18324126	chr8	3089062 0	+	WRN; PURG	promoter_and_body	OpenSea	
cg22773661	chr4	4849222 5	-	ZAR1	promoter	Island	chr4:48492117- 48493589

cg14906390	chr11	113930251	-	ZBTB16	promoter	Island	chr11:113929633-113932190
cg09768093	chr1	32930511	+	ZBTB8B	promoter	Island	chr1:32930500-32931061
cg12758636	chr10	31609882	+	ZEB1	promoter_and_body	Island	chr10:31607227-31610094
cg18465286	chr10	31609896	+	ZEB1	promoter_and_body	Island	chr10:31607227-31610094
cg23712359	chr10	31609905	-	ZEB1	promoter_and_body	Island	chr10:31607227-31610094
cg06944257	chr17	49815987	-	ZFP3	promoter	Island	chr17:4981357-4981979
cg12019773	chr19	38146906	-	ZFP30	promoter	Island	chr19:38145826-38147219
cg25480336	chr20	50720908	-	ZFP64	body	N_Shore	chr20:50721310-50721912
cg14032025	chr20	50721129	+	ZFP64	body	N_Shore	chr20:50721310-50721912
cg23468878	chr3	147126425	+	ZIC1	promoter	N_Shore	chr3:147126988-147128999
cg24714905	chr13	100637241	+	ZIC2	body	Island	chr13:100637112-100637472
cg07406191	chr3	147105190	+	ZIC4	body	N_Shelf	chr3:147108511-147111703
cg17655978	chr19	58125659	-	ZNF134	promoter	Island	chr19:58125530-58125902
cg02835214	chr19	58125672	-	ZNF134	promoter	Island	chr19:58125530-58125902
cg07697981	chr19	58125678	-	ZNF134	promoter	Island	chr19:58125530-58125902
cg17334978	chr4	331502	-	ZNF141	promoter	Island	chr4:330162-332068
cg05533953	chr4	331685	-	ZNF141	promoter_and_body	Island	chr4:330162-332068
cg02970696	chr3	125076372	+	ZNF148	promoter	Island	chr3:125075915-125076481
cg08228914	chr19	53606538	-	ZNF160	promoter_and_body	Island	chr19:53606059-53606784
cg12586262	chr19	53606654	-	ZNF160	promoter_and_body	Island	chr19:53606059-53606784
cg18708075	chr19	52074312	-	ZNF175	promoter	Island	chr19:52074311-52074536
cg25824543	chr19	52074410	-	ZNF175	promoter	Island	chr19:52074311-52074536
cg26870460	chr1	69477591	-	ZNF215	promoter_and_body	Island	chr11:6947520-6948212
cg08390760	chr6	28973318	+	ZNF311	promoter	OpenSea	
cg15171221	chr6	28973328	+	ZNF311	promoter	OpenSea	
cg09435617	chr6	28973353	+	ZNF311	promoter	OpenSea	
cg21310336	chr6	28973446	-	ZNF311	promoter	OpenSea	
cg26883712	chr6	28973466	-	ZNF311	promoter	OpenSea	
cg24884572	chr19	58661833	-	ZNF329	promoter	Island	chr19:58661737-58662287
cg12792011	chr19	58661915	+	ZNF329	promoter	Island	chr19:58661737-58662287
cg11332363	chr19	54023999	-	ZNF331	promoter	Island	chr19:54023868-54024560
cg07952047	chr19	54024110	-	ZNF331	promoter	Island	chr19:54023868-54024560
cg25809635	chr19	37341103	+	ZNF345	promoter	Island	chr19:37340918-37341262
cg03100040	chr19	37341870	-	ZNF345	promoter	Island	chr19:37341731-37342000

cg24708545	chr1 9	5366272 3	+	ZNF347	promoter	S_Shore	chr19:5366143 0-53661848
cg25835225	chr1 9	5249019 9	-	ZNF350	promoter	OpenSea	
cg16580934	chr1 9	5249031 0	+	ZNF350	promoter	OpenSea	
cg06695611	chr2	1807263 28	+	ZNF385B; MIR1258	promoter	Island	chr2:18072571 7-180726465
cg26335602	chr6	2812961 6	-	ZNF389	promoter	OpenSea	
cg00843623	chr1 9	1214616 3	-	ZNF433	body	Island	chr19:1214603 0-12146649
cg15079762	chr1 9	1214640 4	+	ZNF433	promoter_and_body	Island	chr19:1214603 0-12146649
cg12868305	chr1 9	1214643 9	-	ZNF433	promoter_and_body	Island	chr19:1214603 0-12146649
cg14665716	chr1 9	1214650 9	+	ZNF433	promoter_and_body	Island	chr19:1214603 0-12146649
cg15787284	chr1 9	1214662 9	+	ZNF433	promoter	Island	chr19:1214603 0-12146649
cg03293697	chr1 9	1214663 9	+	ZNF433	promoter	Island	chr19:1214603 0-12146649
cg16306498	chr1 9	1214669 6	-	ZNF433	promoter	S_Shore	chr19:1214603 0-12146649
cg01404518	chr1 9	1214701 0	-	ZNF433	promoter	S_Shore	chr19:1214603 0-12146649
cg09669356	chr1 9	3715756 5	+	ZNF461	promoter	N_Shore	chr19:3715763 2-37158119
cg26613140	chr1 9	3715777 6	-	ZNF461	promoter	Island	chr19:3715763 2-37158119
cg00498155	chr1 9	3715787 9	-	ZNF461	promoter	Island	chr19:3715763 2-37158119
cg27545919	chr1 9	3715799 5	-	ZNF461	promoter	Island	chr19:3715763 2-37158119
cg01485075	chr1 9	2281737 1	+	ZNF492	promoter	Island	chr19:2281727 4-22817546
cg02073558	chr3	4477097 3	-	ZNF501	promoter	Island	chr3:44770936- 44771137
cg12476763	chr1 9	5811164 7	-	ZNF530	body	Island	chr19:5811122 9-58111770
cg06458239	chr1 9	5803857 3	-	ZNF549	promoter	Island	chr19:5803857 2-58039208
cg10729426	chr1 9	5803858 5	-	ZNF549	promoter	Island	chr19:5803857 2-58039208
cg19060970	chr1 9	5803858 8	-	ZNF549	promoter	Island	chr19:5803857 2-58039208
cg11497957	chr8	1259858 46	+	ZNF572	promoter	OpenSea	
cg12738197	chr8	1259858 83	+	ZNF572	promoter	OpenSea	
cg11287850	chr1 9	3526415 8	+	ZNF599	promoter	Island	chr19:3526364 8-35264275
cg03293882	chr1 9	5253143 8	+	ZNF614	promoter	Island	chr19:5253132 3-52531724
cg05165378	chr7	9915573 9	+	ZNF655	promoter	N_Shore	chr7:99155871- 99156969
cg21950525	chr7	9915576 7	+	ZNF655	promoter	N_Shore	chr7:99155871- 99156969
cg12457529	chr7	9915589 2	-	ZNF655	promoter	Island	chr7:99155871- 99156969
cg22758700	chr7	9915612 6	-	ZNF655	promoter_and_body	Island	chr7:99155871- 99156969
cg05312305	chr7	9915638 7	-	ZNF655	promoter_and_body	Island	chr7:99155871- 99156969
cg17693420	chr7	9915705 9	-	ZNF655	promoter	S_Shore	chr7:99155871- 99156969
cg24384244	chr3	4294769 0	-	ZNF662	promoter_and_body	Island	chr3:42947480- 42948170

cg19361542	chr1 9	2386998 5	+	ZNF675	promoter_and_body	OpenSea	
cg24114314	chr1 9	5375823 3	-	ZNF677	promoter	S_Shore	chr19:5375781 9-53758148
cg27517351	chr1 9	2394187 1	-	ZNF681	promoter	S_Shore	chr19:2394124 0-23941538
cg10598034	chr1 9	5307330 9	-	ZNF701	promoter	Island	chr19:5307330 8-53074039
cg16040993	chr1 9	5349644 0	-	ZNF702P	body	N_Shore	chr19:5349673 2-53497028
cg19429281	chr1 9	5349673 8	+	ZNF702P	body	Island	chr19:5349673 2-53497028
cg10734240	chr1 9	3732909 0	+	ZNF790	promoter	Island	chr19:3732889 6-37329518
cg18876786	chr1 9	3732938 1	+	ZNF790	promoter	Island	chr19:3732889 6-37329518
cg09567473	chr1 9	3732940 3	+	ZNF790	promoter	Island	chr19:3732889 6-37329518
cg07482795	chr1 9	3799773 0	-	ZNF793	promoter	N_Shore	chr19:3799779 0-37998125
cg22510337	chr1 9	5839996 7	+	ZNF814	body	Island	chr19:5839994 5-58400276
cg15746696	chr1 9	5840049 4	+	ZNF814	promoter	S_Shore	chr19:5839994 5-58400276
cg21540810	chr1 9	5314137 2	+	ZNF83	promoter_and_body	Island	chr19:5314117 5-53141813
cg08351203	chr1 9	5314179 3	-	ZNF83	promoter_and_body	Island	chr19:5314117 5-53141813
cg06476192	chr1 6	3145394 8	+	ZNF843	promoter	Island	chr16:3145394 3-31454561
cg12561338	chr1 9	1217550 5	+	ZNF844	promoter	Island	chr19:1217546 0-12176057
cg05015306	chr1 9	1216312 7	-	ZNF878	body	N_Shore	chr19:1216332 6-12163560
cg19022827	chr1 9	1216353 3	-	ZNF878	body	Island	chr19:1216332 6-12163560
cg26626525	chr1 9	1216358 2	+	ZNF878	body	S_Shore	chr19:1216332 6-12163560
cg18235573	chr1 9	1216398 4	+	ZNF878	body	S_Shore	chr19:1216332 6-12163560
cg00432059	chr1 9	2001248 9	+	ZNF93	body	S_Shore	chr19:2001191 0-20012238
cg02622316	chr6	2836741 0	+	ZSCAN12	promoter_and_body	Island	chr6:28367124- 28367651
cg14145801	chr2	1877137 11	-	ZSWIM2	body	N_Shore	chr2:18771384 6-187714069