

SYMBOL	CPG	beta_case_avg	beta_control_avg	statistic
APEX2	cg00145348	0.304378043	0.525155809	4
APEX2	cg05961595	0.086223841	0.391721523	0
AR	cg21966410	0.165473217	0.442882615	5
ARAF	cg10455133	0.161405482	0.377744027	3
ARMCX2	cg19055639	0.243267762	0.469073221	4
ARMCX4	cg20085077	0.148357351	0.448889984	3
ATP6AP1	cg18742441	0.251936481	0.579558783	4
ATP6AP2	cg06731599	0.234928945	0.440567345	1
BCORL1	cg23269489	0.177700273	0.452990623	1
BEX1	cg21509846	0.248093251	0.456332464	5
BEX1	cg23936476	0.216536417	0.508821366	4
CCDC22	cg26606552	0.169091479	0.391232317	0
CHRDL1	cg05921207	0.159465331	0.378257517	5
CXorf17	cg04944936	0.224055191	0.432080854	0
CXorf34	cg13286902	0.212864925	0.484243372	5
DXS9879E	cg20641280	0.348963779	0.615338396	0
EBP	cg13771629	0.164444754	0.425900556	4
EFNB1	cg04907664	0.263685845	0.480712929	4
EFNB1	cg15977272	0.190310963	0.557484275	4
EFNB1	cg23545272	0.180778395	0.517216093	3
ELF4	cg06428055	0.180094512	0.437961331	4
EMD	cg09229960	0.095908109	0.560263425	1
ESX1	cg04721883	0.271735193	0.491698969	5
FAM11A	cg21030483	0.171941029	0.431038485	4
FAM3A	cg23698956	0.165340271	0.399881743	3
FAM58A	cg01140782	0.12326633	0.387522994	4
FHL1	cg14506668	0.236270414	0.443527637	4
FLJ10178	cg03057808	0.168680352	0.400217251	4
FLJ30058	cg24813163	0.180266345	0.444843904	3
FMR1	cg08434396	0.243858603	0.490003472	0
FTSJ1	cg06489418	0.286942932	0.577463477	4
FUND2	cg21697779	0.185036681	0.425358975	3
G6PD	cg12536534	0.17148449	0.445852352	1
GK	cg15636587	0.111602098	0.417954521	1
GLT28D1	cg19963797	0.136983004	0.40076927	2
GNL3L	cg10318351	0.157282069	0.396195388	2
GPC4	cg08798116	0.097173207	0.411775381	2
GPRASP2	cg23066860	0.196610735	0.407603926	1
GRIA3	cg23424962	0.224118391	0.486331128	3
HMGB3	cg05935584	0.143363298	0.555679439	4
HTATSF1	cg09923855	0.159923557	0.451902157	4
IDH3G	cg27271445	0.1591432	0.434428052	5
LAMP2	cg18307604	0.193233245	0.47666536	4
LDOC1	cg20104776	0.350885507	0.598905037	1
LONRF3	cg06944050	0.178982692	0.410301992	5
LRP5	cg21115990	0.196765586	0.520013937	4
MAOA	cg15014034	0.210766446	0.487646532	5
MAOA	cg19441691	0.138548779	0.344942246	3
MED12	cg21693321	0.237428295	0.502640439	5
MID1IP1	cg21888438	0.178615057	0.383851658	5
MID2	cg19771541	0.153746525	0.384310089	5
MPP1	cg25813820	0.139703872	0.464287783	2
MTCP1	cg24341236	0.151009226	0.453832534	5
MTMR1	cg23947872	0.21833549	0.497888585	4
NAP1L2	cg04297329	0.290915069	0.493751231	3
NHS	cg14345281	0.21174874	0.419606741	1
OCRL	cg21365235	0.19689435	0.488781346	5
OTUD5	cg09928375	0.211600623	0.571535129	1
PDK3	cg18256128	0.260932572	0.490686479	3
PDK3	cg18414950	0.187498946	0.533587446	4
PHKA1	cg11806565	0.21734436	0.431896887	1
PHKA1	cg20816612	0.326796695	0.558035836	4
PHKA2	cg06700462	0.084757912	0.456942204	0
PLXNA3	cg07428182	0.258011478	0.549816068	1
PORCN	cg08785133	0.127244496	0.429593456	1
RAB33A	cg24340926	0.244906898	0.504783677	2

RBMX	cg12517167	0. 17545547	0. 440471369	4
RBMX2	cg26655138	0. 209321879	0. 505485972	4
RP11-311P8.3	cg19011603	0. 242817404	0. 460233588	1
RP13-360B22.2	cg07911663	0. 276739848	0. 519803864	4
RP2	cg24511534	0. 238243269	0. 473737938	5
RPGR	cg25933726	0. 203449146	0. 495773542	4
RPL36A	cg18507125	0. 272709406	0. 521253815	5
RPS6KA3	cg19696622	0. 149529089	0. 351029127	2
SCML2	cg08300622	0. 197497502	0. 419489336	5
SCML2	cg26246138	0. 06003286	0. 431944554	2
SLC35A2	cg14132995	0. 163863558	0. 413026678	1
SLC9A7	cg18799866	0. 144533121	0. 47016249	4
SNX12	cg14892037	0. 159835515	0. 3684968	3
SOX3	cg02847500	0. 230237938	0. 473383018	4
SYN1	cg05254049	0. 402120748	0. 609487246	4
TFE3	cg01241836	0. 192984511	0. 424319917	2
USP11	cg25316166	0. 169342239	0. 378322956	4
USP51	cg25424556	0. 106648838	0. 346664469	1
UXT	cg19206010	0. 25807478	0. 477079958	0
WDR44	cg13674559	0. 160607581	0. 389307809	5
ZDHHC15	cg11272332	0. 217129608	0. 420221629	5
ZMYM3	cg25226891	0. 099358734	0. 413846898	4
ZNF41	cg01887353	0. 124544434	0. 352518963	5
ZNF449	cg19392138	0. 156177403	0. 36951108	5

pvalue	raw_pvalue	beta_change	status
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0.015151515	0.015151515	-0.216338545	hypomethylation
0.025974026	0.025974026	-0.225805459	hypomethylation
0.015151515	0.015151515	-0.300532633	hypomethylation
0.025974026	0.025974026	-0.327622302	hypomethylation
0.004329004	0.004329004	-0.2056384	hypomethylation
0.004329004	0.004329004	-0.27529035	hypomethylation
0.041125541	0.041125541	-0.208239213	hypomethylation
0.025974026	0.025974026	-0.292284949	hypomethylation
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0.041125541	0.041125541	-0.271378447	hypomethylation
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0.015151515	0.015151515	-0.336437698	hypomethylation
0.025974026	0.025974026	-0.257866819	hypomethylation
0.004329004	0.004329004	-0.464355316	hypomethylation
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0.015151515	0.015151515	-0.264577559	hypomethylation
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0.015151515	0.015151515	-0.240322294	hypomethylation
0.004329004	0.004329004	-0.274367862	hypomethylation
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0.008658009	0.008658009	-0.263786266	hypomethylation
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0.004329004	0.004329004	-0.210993191	hypomethylation
0.015151515	0.015151515	-0.262212737	hypomethylation
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0. 041125541	0. 041125541	-0. 227974529	hypomethylation
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SYMBOL	CPG	CHR	MAPINFO	CPG ISLAND	CPG ISLAND LOCATIONS
ZNF124	cg21918500	1	245402094	TRUE	1:245401260-245402151
TTLL7	cg03098721	1	84236672	TRUE	1:84236652-84237966
BCAN	cg21475402	1	154878764	TRUE	1:154878094-154879230
CNIH3	cg00290506	1	222870849	TRUE	1:222870113-222872558
SRD5A2	cg15403517	2	31659779	TRUE	2:31658633-31660643
EN1	cg22231902	2	119321371	TRUE	2:119320039-119321504
TRPC1	cg24794531	3	143926527	TRUE	3:143925285-143926748
EIF5A2	cg26209058	3	172109215	TRUE	3:172108452-172109716
PEX5L	cg21176048	3	181237929	TRUE	3:181236808-181238032
CRMP1	cg03544320	4	5945592	TRUE	4:5944246-5946191
POU4F2	cg13262687	4	147779029	TRUE	4:147778503-147781596
CART	cg23300372	5	71051188	TRUE	5:71050507-71051626
IRF4	cg12741420	6	337131	TRUE	6:336092-339080
SNX9	cg26845300	6	158163821	TRUE	6:158163446-158165173
HIST1H2BI	cg02192855	6	26381178	TRUE	6:26381046-26381970
ZNF96	cg02622316	6	28475389	TRUE	6:28474985-28475928
HIST1H3D	cg08307092	6	26308153	TRUE	6:26307702-26308258
HIST1H4E	cg16706631	6	26312802	TRUE	6:26312577-26313287
ACTL6B	cg08572611	7	100091850	TRUE	7:100091590-100092362
GATA4	cg00090147	8	11599776	TRUE	8:11598711-11600557
NEF3	cg18267374	8	24827178	TRUE	8:24826692-24829288
ADRB3	cg17619823	8	37942632	TRUE	8:37941431-37943204
GATA4	cg08369065	8	11600092	TRUE	8:11598711-11600557
LHX2	cg07109287	9	125813894	TRUE	9:125813052-125815466
HTR7	cg06291867	10	92607142	TRUE	10:92606622-92608182
INA	cg23642747	10	105026635	TRUE	10:105026442-105028852
GAD2	cg04599297	10	26545448	TRUE	10:26543757-26547625
EGR2	cg19355190	10	64245804	TRUE	10:64244521-64245891
PRAP1	cg03743584	10	135010898	FALSE	
FLJ46831	cg19884262	10	129425958	TRUE	10:129424072-129426344
CYP2E1	cg13315147	10	135191518	TRUE	10:135191138-135192648
C10orf125	cg12251804	10	135021073	TRUE	10:135020610-135021994
INA	cg25764191	10	105027205	TRUE	10:105026442-105028852
WT1	cg16092786	11	32412311	TRUE	11:32411271-32413831
FOXB1	cg22777952	15	58083717	TRUE	15:58083184-58086207
FOXB1	cg08583049	15	58084107	TRUE	15:58083184-58086207
HS3ST2	cg19064258	16	22733618	TRUE	16:22732005-22734135
IRF8	cg24826867	16	84490354	TRUE	16:84489299-84490591
MGAT5B	cg00654814	17	72376663	TRUE	17:72375680-72377919
RND2	cg05270634	17	38430971	TRUE	17:38429704-38431262
GAS7	cg22471346	17	10042198	TRUE	17:10041659-10043517
HOXB13	cg21842478	17	44161045	TRUE	17:44160495-44161328
CA4	cg04532952	17	55582527	TRUE	17:55581878-55583315
GALR1	cg04534765	18	73091357	TRUE	18:73090255-73093032
F2RL3	cg19006008	19	16860768	FALSE	
GNA11	cg14917512	19	3045685	TRUE	19:3044235-3046095
EDN3	cg04048259	20	57308741	TRUE	20:57308563-57309693
SYNGR1	cg19713460	22	38075476	TRUE	22:38075299-38076737
S100A9	cg16139316	1	151597382	FALSE	
HK2	cg18638581	2	74913110	FALSE	
GNLY	cg11752275	2	85774547	FALSE	
CPA3	cg13424229	3	150064527	FALSE	
C3orf60	cg07109801	3	49032665	TRUE	3:49032563-49032797
CFB	cg17741572	6	32022284	FALSE	
FURIN	cg26377677	15	89213122	FALSE	
SLC16A3	cg14417329	17	77779562	TRUE	17:77779304-77780821
SDCBP2	cg16173067	20	1257722	FALSE	
BCAP31	cg02205962		152643001	TRUE	X:152642005-152643632

TSPYL2	cg24779040
SLC9A6	cg08695223
PRDX4	cg07581973
PHF16	cg19194595
RPL10	cg18923230
EDA	cg20540913
PGRMC1	cg07876586
ELF4	cg04544154
WDR45	cg17552650
PHF8	cg09920632
MGC39606	cg17231524
RP1-112K5.2	cg20504202
NDUFA1	cg14541939
GPC3	cg07297906
SLC9A7	cg14841098
RP13-360B22.2	cg11839979
ELK1	cg21860846
BCORL1	cg18535534
TMEM29	cg03936963
BEX2	cg12549513
OPHN1	cg04702045
HADH2	cg04241572
WWC3	cg12064213
OTUD5	cg18780401
POLA	cg14520892
HTATSF1	cg19949137
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WDR13	cg25053301
RNF113A	cg23180270
FLJ20298	cg04238548
RBMX	cg14642832
PRAF2	cg14368286
TMSB4X	cg21400640
CXorf26	cg25591670
FSHPRH1	cg14743649
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GPC4	cg14600040
SYTL4	cg12382941
KIF4A	cg17206029
DNASE1L1	cg09202373
PDCD8	cg25317260
CXorf41	cg06350796
BHLHB9	cg15309236
MGC39606	cg09347151
UPF3B	cg15681351
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119268820	TRUE	X:119268363-119269844
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101862253	TRUE	X:101862184-101862707
134383206	TRUE	X:134383127-134384321
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122821750	TRUE	X:122821066-122822021
152699674	TRUE	X:152699478-152699970
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beta case avg	beta control avg	pvalue	delta	Methyl Status
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0.68506169	0.479273022	0.015151515	0.205788668	hypermethylation
0.564209671	0.305028012	0.041125541	0.259181659	hypermethylation
0.53105589	0.172197506	0.041125541	0.358858384	hypermethylation
0.699679624	0.497785226	0.008658009	0.201894398	hypermethylation
0.507442771	0.224199703	0.004329004	0.283243068	hypermethylation
0.435564336	0.192886545	0.015151515	0.242677791	hypermethylation
0.395627982	0.144553221	0.025974026	0.251074761	hypermethylation
0.55622763	0.251478328	0.041125541	0.304749302	hypermethylation
0.79298173	0.581241444	0.041125541	0.211740286	hypermethylation
0.556142609	0.333223641	0.015151515	0.222918968	hypermethylation
0.547032932	0.316040175	0.015151515	0.230992757	hypermethylation
0.350698226	0.142667632	0.002164502	0.208030594	hypermethylation
0.444916887	0.219262716	0.015151515	0.225654171	hypermethylation
0.500983824	0.25514035	0.008658009	0.245843474	hypermethylation
0.494460653	0.235770782	0.025974026	0.258689871	hypermethylation
0.466027644	0.205626076	0.008658009	0.260401568	hypermethylation
0.622133084	0.33299321	0.025974026	0.289139874	hypermethylation
0.707768086	0.418393208	0.015151515	0.289374878	hypermethylation
0.609457492	0.39969596	0.025974026	0.209761532	hypermethylation
0.681369545	0.426758935	0.041125541	0.25461061	hypermethylation
0.609054932	0.353599607	0.015151515	0.255455325	hypermethylation
0.60417398	0.333918079	0.008658009	0.270255901	hypermethylation
0.590469951	0.340885494	0.015151515	0.249584457	hypermethylation
0.525736231	0.324347643	0.041125541	0.201388588	hypermethylation
0.486353798	0.283322214	0.041125541	0.203031584	hypermethylation
0.584754179	0.364560446	0.041125541	0.220193733	hypermethylation
0.482261174	0.261554377	0.041125541	0.220706797	hypermethylation
0.560173454	0.326838199	0.041125541	0.233335255	hypermethylation
0.473486133	0.232480245	0.041125541	0.241005888	hypermethylation
0.660729257	0.415836929	0.041125541	0.244892328	hypermethylation
0.454442721	0.207316709	0.041125541	0.247126012	hypermethylation
0.546815555	0.297104121	0.025974026	0.249711434	hypermethylation
0.526145443	0.319808709	0.025974026	0.206336734	hypermethylation
0.462219356	0.229531318	0.015151515	0.232688038	hypermethylation
0.372530751	0.133115948	0.025974026	0.239414803	hypermethylation
0.557193681	0.335321939	0.015151515	0.221871742	hypermethylation
0.646020156	0.292228927	0.015151515	0.353791229	hypermethylation
0.480014426	0.270977888	0.015151515	0.209036538	hypermethylation
0.503657874	0.261230658	0.002164502	0.242427216	hypermethylation
0.623721737	0.36153968	0.041125541	0.262182057	hypermethylation
0.469443599	0.205120852	0.025974026	0.264322747	hypermethylation
0.573884038	0.276184478	0.025974026	0.29769956	hypermethylation
0.637935002	0.354346004	0.041125541	0.283588998	hypermethylation
0.48791394	0.282605661	0.041125541	0.205308279	hypermethylation
0.534912035	0.281843287	0.015151515	0.253068748	hypermethylation
0.64051804	0.391745434	0.025974026	0.248772606	hypermethylation
0.623878547	0.321025117	0.015151515	0.30285343	hypermethylation
0.546991501	0.756440014	0.015151515	-0.209448513	hypomethylation
0.542835105	0.749444327	0.025974026	-0.206609222	hypomethylation
0.473469316	0.673529817	0.002164502	-0.200060501	hypomethylation
0.522524967	0.729632532	0.002164502	-0.207107565	hypomethylation
0.415598144	0.619103901	0.015151515	-0.203505757	hypomethylation
0.556855828	0.815639421	0.002164502	-0.258783593	hypomethylation
0.553756671	0.793247083	0.002164502	-0.239490412	hypomethylation
0.206515192	0.454316727	0.002164502	-0.247801535	hypomethylation
0.538916934	0.757875733	0.041125541	-0.218958799	hypomethylation
0.158479209	0.57095172	0.041125541	-0.412472511	hypomethylation

0.183104399	0.576574543	0.025974026	-0.393470144	hypomethylation
0.17353961	0.543612768	0.025974026	-0.370073158	hypomethylation
0.116534963	0.481134568	0.041125541	-0.364599605	hypomethylation
0.167364166	0.51823232	0.015151515	-0.350868154	hypomethylation
0.158605871	0.509041923	0.025974026	-0.350436052	hypomethylation
0.125485865	0.475613416	0.041125541	-0.350127551	hypomethylation
0.194969411	0.541742985	0.008658009	-0.346773574	hypomethylation
0.540271279	0.86538776	0.002164502	-0.325116481	hypomethylation
0.187979462	0.513058761	0.041125541	-0.325079299	hypomethylation
0.187687835	0.503432589	0.015151515	-0.315744754	hypomethylation
0.24933314	0.556801448	0.008658009	-0.307468308	hypomethylation
0.197958868	0.49486886	0.041125541	-0.296909992	hypomethylation
0.150654673	0.441061229	0.004329004	-0.290406556	hypomethylation
0.184401425	0.466254644	0.015151515	-0.281853219	hypomethylation
0.201153582	0.482775362	0.041125541	-0.28162178	hypomethylation
0.186820074	0.467819076	0.041125541	-0.280999002	hypomethylation
0.210040023	0.487001263	0.015151515	-0.27696124	hypomethylation
0.185885119	0.461386924	0.025974026	-0.275501805	hypomethylation
0.287382104	0.562057254	0.004329004	-0.27467515	hypomethylation
0.123617528	0.396854103	0.025974026	-0.273236575	hypomethylation
0.130973441	0.404075547	0.025974026	-0.273102106	hypomethylation
0.180955461	0.449671376	0.041125541	-0.268715915	hypomethylation
0.14271773	0.409064494	0.041125541	-0.266346764	hypomethylation
0.192345644	0.458550941	0.041125541	-0.266205297	hypomethylation
0.150751066	0.405326319	0.041125541	-0.254575253	hypomethylation
0.109518775	0.363642859	0.015151515	-0.254124084	hypomethylation
0.176361848	0.428920353	0.041125541	-0.252558505	hypomethylation
0.362377339	0.607350159	0.025974026	-0.24497282	hypomethylation
0.438970277	0.683674613	0.004329004	-0.244704336	hypomethylation
0.199344632	0.436685026	0.004329004	-0.237340394	hypomethylation
0.26302819	0.497922832	0.015151515	-0.234894642	hypomethylation
0.225332639	0.45918263	0.015151515	-0.233849991	hypomethylation
0.257073234	0.489770881	0.041125541	-0.232697647	hypomethylation
0.172372737	0.404734092	0.025974026	-0.232361355	hypomethylation
0.301888296	0.533171313	0.025974026	-0.231283017	hypomethylation
0.166637553	0.397180441	0.025974026	-0.230542888	hypomethylation
0.223065921	0.45027951	0.041125541	-0.227213589	hypomethylation
0.146693337	0.372446746	0.041125541	-0.225753409	hypomethylation
0.170840896	0.395430298	0.025974026	-0.224589402	hypomethylation
0.160726484	0.384837009	0.008658009	-0.224110525	hypomethylation
0.288697452	0.512373637	0.025974026	-0.223676185	hypomethylation
0.182685114	0.405135098	0.015151515	-0.222449984	hypomethylation
0.27609342	0.497968916	0.041125541	-0.221875496	hypomethylation
0.196727416	0.41223549	0.008658009	-0.215508074	hypomethylation
0.246615147	0.461855814	0.015151515	-0.215240667	hypomethylation
0.257290357	0.471485836	0.025974026	-0.214195479	hypomethylation
0.199012673	0.413038784	0.025974026	-0.214026111	hypomethylation
0.182171175	0.389476558	0.041125541	-0.207305383	hypomethylation
0.355195213	0.559772149	0.041125541	-0.204576936	hypomethylation
0.204176138	0.408441852	0.025974026	-0.204265714	hypomethylation
0.121894853	0.323211414	0.015151515	-0.201316561	hypomethylation
0.264622269	0.47305734	0.025974026	-0.208435071	hypomethylation

SYMBOL	NAME	CHR	MAPINFO	CPG_ISLAND	CPG_ISLAND_LOCATIONS
ZNF124	cg21918500	1	245402094	TRUE	1:245401260-245402151
TTLL7	cg03098721	1	84236672	TRUE	1:84236652-84237966
S100A9	cg16139316	1	151597382	FALSE	
CNIH3	cg00290506	1	222870849	TRUE	1:222870113-222872558
BCAN	cg21475402	1	154878764	TRUE	1:154878094-154879230
GNLY	cg11752275	2	85774547	FALSE	
EN1	cg22231902	2	119321371	TRUE	2:119320039-119321504
SRD5A2	cg15403517	2	31659779	TRUE	2:31658633-31660643
HK2	cg18638581	2	74913110	FALSE	
CPA3	cg13424229	3	150064527	FALSE	
C3orf60	cg07109801	3	49032665	TRUE	3:49032563-49032797
TRPC1	cg24794531	3	143926527	TRUE	3:143925285-143926748
EIF5A2	cg26209058	3	172109215	TRUE	3:172108452-172109716
PEX5L	cg21176048	3	181237929	TRUE	3:181236808-181238032
POU4F2	cg13262687	4	147779029	TRUE	4:147778503-147781596
CRMP1	cg03544320	4	5945592	TRUE	4:5944246-5946191
CART	cg23300372	5	71051188	TRUE	5:71050507-71051626
IRF4	cg12741420	6	337131	TRUE	6:336092-339080
CFB	cg17741572	6	32022284	FALSE	
HIST1H2BI	cg02192855	6	26381178	TRUE	6:26381046-26381970
HIST1H3D	cg08307092	6	26308153	TRUE	6:26307702-26308258
SNX9	cg26845300	6	158163821	TRUE	6:158163446-158165173
ZNF96	cg02622316	6	28475389	TRUE	6:28474985-28475928
HIST1H4E	cg16706631	6	26312802	TRUE	6:26312577-26313287
ACTL6B	cg08572611	7	100091850	TRUE	7:100091590-100092362
GATA4	cg08369065	8	11600092	TRUE	8:11598711-11600557
ADRB3	cg17619823	8	37942632	TRUE	8:37941431-37943204
GATA4	cg00090147	8	11599776	TRUE	8:11598711-11600557
NEF3	cg18267374	8	24827178	TRUE	8:24826692-24829288
LHX2	cg07109287	9	125813894	TRUE	9:125813052-125815466
INA	cg25764191	10	105027205	TRUE	10:105026442-105028852
PRAP1	cg03743584	10	135010898	FALSE	
GAD2	cg04599297	10	26545448	TRUE	10:26543757-26547625
HTR7	cg06291867	10	92607142	TRUE	10:92606622-92608182
C10orf125	cg12251804	10	135021073	TRUE	10:135020610-135021994
CYP2E1	cg13315147	10	135191518	TRUE	10:135191138-135192648
EGR2	cg19355190	10	64245804	TRUE	10:64244521-64245891
FLJ46831	cg19884262	10	129425958	TRUE	10:129424072-129426344
INA	cg23642747	10	105026635	TRUE	10:105026442-105028852
WT1	cg16092786	11	32412311	TRUE	11:32411271-32413831
FURIN	cg26377677	15	89213122	FALSE	
FOXB1	cg22777952	15	58083717	TRUE	15:58083184-58086207
FOXB1	cg08583049	15	58084107	TRUE	15:58083184-58086207
HS3ST2	cg19064258	16	22733618	TRUE	16:22732005-22734135
IRF8	cg24826867	16	84490354	TRUE	16:84489299-84490591
RND2	cg05270634	17	38430971	TRUE	17:38429704-38431262
SLC16A3	cg14417329	17	77779562	TRUE	17:77779304-77780821
MGAT5B	cg00654814	17	72376663	TRUE	17:72375680-72377919
CA4	cg04532952	17	55582527	TRUE	17:55581878-55583315

HOXB13	cg21842478	17	44161045	TRUE	17:44160495-44161328
GAS7	cg22471346	17	10042198	TRUE	17:10041659-10043517
GALR1	cg04534765	18	73091357	TRUE	18:73090255-73093032
GNA11	cg14917512	19	3045685	TRUE	19:3044235-3046095
F2RL3	cg19006008	19	16860768	FALSE	
EDN3	cg04048259	20	57308741	TRUE	20:57308563-57309693
SDCBP2	cg16173067	20	1257722	FALSE	
SYNGR1	cg19713460	22	38075476	TRUE	22:38075299-38076737
ELF4	cg04544154	X	129073190	TRUE	X:129071186-129073330
HTATSF1	cg09923855	X	135407132	TRUE	X:135406317-135407906
TMEM29	cg03936963	X	53003738	TRUE	X:53003573-53004951
FLJ20298	cg04238548	X	105932481	TRUE	X:105932462-105933253
NDUFA1	cg14541939	X	118889941	TRUE	X:118888580-118890917
DXS9879E	cg20641280	X	153360987	TRUE	X:153359988-153361104
RNF113A	cg23180270	X	118890865	TRUE	X:118888580-118890917
EFNB1	cg04907664	X	67966530	TRUE	X:67965268-67967122
CXorf41	cg06350796	X	106336523	TRUE	X:106335539-106336710
PGRMC1	cg07876586	X	118254384	TRUE	X:118253585-118255522
SYTL4	cg12382941	X	99873203	TRUE	X:99872942-99873874
NHS	cg14345281	X	17303505	TRUE	X:17302835-17305853
MGC39606	cg17231524	X	134384171	TRUE	X:134383127-134384321
RPL36A	cg18507125	X	100532762	TRUE	X:100532246-100532948
MTMR1	cg23947872	X	149613021	TRUE	X:149611916-149613219
HMGB3	cg05935584	X	149902481	TRUE	X:149901718-149904046
GPC3	cg07297906	X	132947244	TRUE	X:132946499-132947763
TSC22D3	cg07473550	X	106905847	TRUE	X:106905712-106906660
DNASE1L1	cg09202373	X	153293868	TRUE	X:153292621-153293883
PHF8	cg09920632	X	54087466	TRUE	X:54086783-54088233
OTUD5	cg09928375	X	48699217	TRUE	X:48699066-48701313
PRAF2	cg14368286	X	48818897	TRUE	X:48817890-48819021
RBMX	cg14642832	X	135790803	TRUE	X:135789863-135790845
BHLHB9	cg15309236	X	101862253	TRUE	X:101862184-101862707
LAMP2	cg18307604	X	119487249	TRUE	X:119486553-119487414
PHF16	cg19194595	X	46656828	TRUE	X:46656361-46658460
MAOA	cg19441691	X	43400293	TRUE	X:43400130-43400730
HTATSF1	cg19949137	X	135407646	TRUE	X:135406317-135407906
ELK1	cg21860846	X	47395451	TRUE	X:47394182-47395634
FLJ10178	cg03057808	X	105741952	TRUE	X:105741531-105742091
OPHN1	cg04702045	X	67570323	TRUE	X:67569334-67570801
MED12	cg05511752	X	70255381	TRUE	X:70254864-70255742
ATP6AP2	cg06731599	X	40325648	TRUE	X:40324583-40325764
SLC9A6	cg08695223	X	134895459	TRUE	X:134895007-134896000
MGC39606	cg09347151	X	134383206	TRUE	X:134383127-134384321
ARAF	cg10455133	X	47305452	TRUE	X:47305171-47306159
BEX2	cg12549513	X	102452607	TRUE	X:102451844-102452762
GPC4	cg14600040	X	132377430	TRUE	X:132375857-132378130
FSHPRH1	cg14743649	X	100240009	TRUE	X:100239491-100240120
UPF3B	cg15681351	X	118871191	TRUE	X:118870555-118871381
KIF4A	cg17206029	X	69426419	TRUE	X:69426172-69427271
BCORL1	cg18535534	X	128943139	TRUE	X:128941358-128946562

RPL10	cg18923230	X	153279607	TRUE	X:153277879-153281110
GLT28D1	cg19963797	X	110811123	TRUE	X:110810870-110811991
OCRL	cg21365235	X	128502446	TRUE	X:128501680-128502582
MPP1	cg22858728	X	153687343	TRUE	X:153686380-153687406
TSPYL2	cg24779040	X	53128332	TRUE	X:53127216-53129170
WDR13	cg25053301	X	48341494	TRUE	X:48339681-48341694
CXorf26	cg25591670	X	75309209	TRUE	X:75309058-75309844
IDH3G	cg27271445	X	152713344	TRUE	X:152712310-152713950
BCAP31	cg02205962	X	152643001	TRUE	X:152642005-152643632
ZBTB33	cg02649608	X	119268820	TRUE	X:119268363-119269844
HADH2	cg04241572	X	53477938	TRUE	X:53477634-53478316
CXorf17	cg04944936	X	54226319	TRUE	X:54225446-54226910
PRDX4	cg07581973	X	23595650	TRUE	X:23595198-23596007
BIRC4	cg09950034	X	122821750	TRUE	X:122821066-122822021
ZDHHC15	cg11272332	X	74659535	TRUE	X:74659346-74660218
PHKA1	cg11806565	X	71851420	TRUE	X:71851306-71852273
RP13-360B22.2	cg11839979	X	109133028	TRUE	X:109131973-109133498
WWC3	cg12064213	X	9942520	TRUE	X:9942388-9944707
EBP	cg13771629	X	48264871	TRUE	X:48264674-48265781
POLA	cg14520892	X	24621554	TRUE	X:24621426-24622402
SLC9A7	cg14841098	X	46503912	TRUE	X:46502730-46504082
MAOA	cg15014034	X	43400488	TRUE	X:43400130-43400730
EFNB1	cg15977272	X	67965634	TRUE	X:67965268-67967122
MSN	cg16204757	X	64804464	TRUE	X:64803987-64804606
WDR45	cg17552650	X	48844907	TRUE	X:48844077-48845653
PHF16	cg17843048	X	46656524	TRUE	X:46656361-46658460
PDK3	cg18414950	X	24393817	TRUE	X:24392800-24393964
ATP6AP1	cg18742441	X	153310416	TRUE	X:153309132-153310681
OTUD5	cg18780401	X	48700069	TRUE	X:48699066-48701313
RP1-112K5.2	cg20504202	X	54483777	TRUE	X:54483309-54483784
EDA	cg20540913	X	68752833	TRUE	X:68752319-68753914
TMSB4X	cg21400640	X	12902888	TRUE	X:12902523-12904636
STK23	cg24496423	X	152699674	TRUE	X:152699478-152699970
USP11	cg25316166	X	46977232	TRUE	X:46977105-46978329
PDCD8	cg25317260	X	129127771	TRUE	X:129126775-129128085
USP51	cg25424556	X	55532208	TRUE	X:55531479-55532401
RPGR	cg25933726	X	38071343	TRUE	X:38070900-38072122
SLC16A2	cg06277838		73558095	FALSE	

beta_case_avg	beta_control_avg	pvalue	delta	statistic	TSS_COORDINATE
0.462797538	0.260650317	0.002164502	0.202147221	36	245401941
0.68506169	0.479273022	0.015151515	0.205788667	33	84237403
0.546991501	0.756440014	0.015151515	0.209448513	3	151596954
0.53105589	0.172197506	0.041125541	0.358858385	31	222870802
0.564209671	0.305028012	0.041125541	0.259181658	31	154878364
0.473469316	0.673529817	0.002164502	0.200060501	0	85774925
0.507442771	0.224199703	0.004329004	0.283243068	35	119322229
0.699679624	0.497785226	0.008658009	0.201894398	34	31659544
0.542835105	0.749444327	0.025974026	0.206609222	4	74913290
0.522524967	0.729632532	0.002164502	0.207107565	0	150065774
0.415598144	0.619103901	0.015151515	0.203505757	3	49032912
0.435564336	0.192886545	0.015151515	0.24267779	33	143925956
0.395627982	0.144553221	0.025974026	0.251074761	32	172109120
0.55622763	0.251478328	0.041125541	0.304749302	31	181237211
0.556142609	0.333223641	0.015151515	0.222918968	33	147779538
0.79298173	0.581241444	0.041125541	0.211740287	31	5945686
0.547032932	0.316040175	0.015151515	0.230992758	33	71050750
0.350698226	0.142667632	0.002164502	0.208030593	36	336760
0.556855828	0.815639421	0.002164502	0.258783593	0	32021752
0.500983824	0.25514035	0.008658009	0.245843474	34	26381183
0.466027644	0.205626076	0.008658009	0.260401569	34	26307443
0.444916887	0.219262716	0.015151515	0.225654171	33	158164282
0.494460653	0.235770782	0.025974026	0.258689872	32	28475487
0.622133084	0.33299321	0.025974026	0.289139874	32	26312852
0.707768086	0.418393208	0.015151515	0.289374878	33	100091986
0.60417398	0.333918079	0.008658009	0.270255902	34	
0.609054932	0.353599607	0.015151515	0.255455324	33	37943341
0.609457492	0.39969596	0.025974026	0.209761532	32	
0.681369545	0.426758935	0.041125541	0.25461061	31	24827212
0.590469951	0.340885494	0.015151515	0.249584457	33	125813710
0.546815555	0.297104121	0.025974026	0.249711434	32	105026910
0.560173454	0.326838199	0.041125541	0.233335255	31	135010901
0.584754179	0.364560446	0.041125541	0.220193734	31	26545600
0.525736231	0.324347643	0.041125541	0.201388588	31	92607651
0.454442721	0.207316709	0.041125541	0.247126012	31	135021519
0.660729257	0.415836929	0.041125541	0.244892328	31	135190857
0.482261174	0.261554377	0.041125541	0.220706797	31	64246133
0.473486133	0.232480245	0.041125541	0.241005887	31	129425942
0.486353798	0.283322214	0.041125541	0.203031584	31	105026910
0.526145443	0.319808709	0.025974026	0.206336734	32	
0.553756671	0.793247083	0.002164502	0.239490412	0	89212889
0.462219356	0.229531318	0.015151515	0.232688038	33	58084427
0.372530751	0.133115948	0.025974026	0.239414803	32	58084427
0.557193681	0.335321939	0.015151515	0.221871742	33	22733361
0.646020156	0.292228927	0.015151515	0.353791228	33	84490275
0.503657874	0.261230658	0.002164502	0.242427216	36	38430791
0.206515192	0.454316727	0.002164502	0.247801536	0	77780236
0.480014426	0.270977888	0.015151515	0.209036539	33	72376393
0.573884038	0.276184478	0.025974026	0.29769956	32	55582131

0.469443599	0.205120852	0.025974026	0.264322747	32	44161087
0.623721737	0.36153968	0.041125541	0.262182057	31	10042593
0.637935002	0.354346004	0.041125541	0.283588998	31	73090721
0.534912035	0.281843287	0.015151515	0.253068747	33	3045530
0.48791394	0.282605661	0.041125541	0.205308279	31	16860826
0.64051804	0.391745434	0.025974026	0.248772606	32	57308894
0.538916934	0.757875733	0.041125541	0.2189588	5	1257826
0.623878547	0.321025117	0.015151515	0.30285343	33	38075900
0.540271279	0.86538776	0.002164502	0.325116481	0	129072153
0.132677439	0.430460164	0.002164502	0.297782725	0	135407337
0.287382104	0.562057254	0.004329004	0.27467515	1	53002901
0.199344632	0.436685026	0.004329004	0.237340394	1	105932575
0.150654673	0.441061229	0.004329004	0.290406556	1	118889762
0.222557718	0.570424866	0.004329004	0.347867148	1	153360790
0.438970277	0.683674613	0.004329004	0.244704336	1	118889818
0.240309248	0.449403027	0.008658009	0.209093779	2	
0.196727416	0.41223549	0.008658009	0.215508074	2	106336518
0.194969411	0.541742985	0.008658009	0.346773574	2	118254291
0.160726484	0.384837009	0.008658009	0.224110525	2	99873154
0.190507538	0.417878522	0.008658009	0.227370985	2	17303464
0.24933314	0.556801448	0.008658009	0.307468308	2	134383537
0.240305228	0.517077138	0.008658009	0.27677191	2	100532600
0.199493815	0.484043167	0.008658009	0.284549351	2	149612503
0.140457051	0.562630795	0.015151515	0.422173744	3	149902421
0.184401425	0.466254644	0.015151515	0.281853219	3	132947332
0.121894853	0.323211414	0.015151515	0.201316561	3	106905673
0.182685114	0.405135098	0.015151515	0.222449985	3	153293621
0.187687835	0.503432589	0.015151515	0.315744754	3	54087036
0.223743018	0.572961131	0.015151515	0.349218113	3	48699837
0.225332639	0.45918263	0.015151515	0.233849991	3	48818606
0.26302819	0.497922832	0.015151515	0.234894641	3	135790605
0.246615147	0.461855814	0.015151515	0.215240667	3	101862310
0.19202539	0.480988292	0.015151515	0.288962902	3	119487189
0.167364166	0.51823232	0.015151515	0.350868154	3	46656812
0.135765253	0.347080526	0.015151515	0.211315273	3	43400353
0.109518775	0.363642859	0.015151515	0.254124083	3	135407337
0.210040023	0.487001263	0.015151515	0.27696124	3	47394964
0.171839699	0.416557591	0.025974026	0.244717891	4	105741909
0.130973441	0.404075547	0.025974026	0.273102106	4	67570372
0.204176138	0.408441852	0.025974026	0.204265714	4	70255298
0.221223002	0.459914924	0.025974026	0.238691922	4	40325160
0.17353961	0.543612768	0.025974026	0.370073158	4	134895293
0.257290357	0.471485836	0.025974026	0.214195479	4	134383537
0.162907613	0.363957685	0.025974026	0.201050072	4	47305451
0.123617528	0.396854103	0.025974026	0.273236575	4	102452601
0.170840896	0.395430298	0.025974026	0.224589402	4	132376871
0.301888296	0.533171313	0.025974026	0.231283017	4	100241454
0.199012673	0.413038784	0.025974026	0.214026111	4	118870996
0.288697452	0.512373637	0.025974026	0.223676186	4	69426687
0.185885119	0.461386924	0.025974026	0.275501805	4	128944350

0.158605871	0.509041923	0.025974026	0.350436052	4	153279912
0.125607685	0.43811335	0.025974026	0.312505664	4	110811069
0.173199452	0.509561186	0.025974026	0.336361734	4	128501933
0.166637553	0.397180441	0.025974026	0.230542888	4	153686957
0.183104399	0.576574543	0.025974026	0.393470143	4	53128287
0.362377339	0.607350159	0.025974026	0.24497282	4	48340845
0.172372737	0.404734092	0.025974026	0.232361355	4	75309173
0.156467557	0.482216466	0.025974026	0.325748909	4	152713161
0.158479209	0.57095172	0.041125541	0.412472511	5	152643081
0.176361848	0.428920353	0.041125541	0.252558505	5	119268635
0.180955461	0.449671376	0.041125541	0.268715915	5	53478045
0.221818121	0.443347135	0.041125541	0.221529014	5	54226416
0.116534963	0.481134568	0.041125541	0.364599605	5	23595566
0.182171175	0.389476558	0.041125541	0.207305383	5	122821729
0.23128271	0.437074452	0.041125541	0.205791742	5	74659600
0.214773706	0.419864521	0.041125541	0.205090815	5	71850612
0.186820074	0.467819076	0.041125541	0.280999002	5	109132999
0.14271773	0.409064494	0.041125541	0.266346765	5	9943612
0.156641317	0.426360257	0.041125541	0.26971894	5	48265201
0.150751066	0.405326319	0.041125541	0.254575252	5	24621985
0.201153582	0.482775362	0.041125541	0.28162178	5	46503416
0.21638598	0.481187199	0.041125541	0.264801218	5	43400353
0.198954529	0.563032782	0.041125541	0.364078253	5	67965556
0.146693337	0.372446746	0.041125541	0.225753409	5	64804236
0.187979462	0.513058761	0.041125541	0.325079299	5	48845003
0.223065921	0.45027951	0.041125541	0.227213589	5	46656812
0.194760459	0.5329129	0.041125541	0.338152441	5	24393475
0.235342203	0.55019282	0.041125541	0.314850617	5	153310215
0.192345644	0.458550941	0.041125541	0.266205297	5	48699837
0.197958868	0.49486886	0.041125541	0.296909992	5	54483578
0.125485865	0.475613416	0.041125541	0.350127551	5	68752636
0.257073234	0.489770881	0.041125541	0.232697647	5	12903148
0.355195213	0.559772149	0.041125541	0.204576936	5	152699704
0.185578902	0.386217868	0.041125541	0.200638967	5	46977258
0.27609342	0.497968916	0.041125541	0.221875497	5	129127489
0.116796247	0.368880164	0.041125541	0.252083917	5	55532356
0.190859372	0.503709647	0.041125541	0.312850275	5	38071732
0.264622269	0.47305734	0.025974026	0.208435072	4	73557810

GENE_STRAND	GENE_ID	SYNONYM
-	GenelD:7678	HZF16; MGC117046;
-	GenelD:79739	FLJ23033; FLJ36855; RP5-836J3.2;
+	GenelD:6280	MIF; NIF; P14; CAGB; CFAG; CGLB; L1AG; LIAG; MRP14; 60B8AG;
+	GenelD:149111	FLJ38993;
+	GenelD:63827	BEHAB; CSPG7; MGC13038;
+	GenelD:10578	519; LAG2; NKG5; LAG-2; D2S69E; TLA519; lymphokine;
-	GenelD:2019	
-	GenelD:6716	
+	GenelD:3099	HKII; HXK2; DKFZp686M1669;
+	GenelD:1359	
+	GenelD:25915	2P1; E3-3; MGC10527; DKFZP564J0123;
+	GenelD:7220	TRP1; HTRP-1;
-	GenelD:56648	EIF-5A2; eIF5AII;
-	GenelD:51555	PXR2; PEX5R; PXR2B;
+	GenelD:5458	BRN3B; BRN3.2; Brn-3b;
-	GenelD:1400	DRP1; DRP-1; DPYSL1;
+	GenelD:9607	
+	GenelD:3662	MUM1; LSIRF;
+	GenelD:629	BF; BFD; GBG; CFAB; PBF2; H2-Bf;
+	GenelD:8346	H2B/k; H2BFK;
-	GenelD:8351	H3/b; H3FB;
+	GenelD:51429	SDP1; WISP; MST155; SH3PX1; MSTP155; SH3PXD3A;
-	GenelD:9753	ZFP96; ZNF305; ZNF29K1; ZSCAN12; KIAA0426; dJ29K1.2;
+	GenelD:8367	H4/j; H4FJ;
-	GenelD:51412	ACTL6; BAF53B;
+	GenelD:2626	MGC126629;
-	GenelD:155	BETA3AR;
+	GenelD:2626	MGC126629;
+	GenelD:4741	NFM; NEFM; NF-M;
+	GenelD:9355	LH2; hLhx2;
+	GenelD:9118	NEF5; NF-66; TXBP-1; MGC12702;
+	GenelD:118471	UPA; PRO1195; MGC126792; RP11-122K13.6;
+	GenelD:2572	GAD65;
-	GenelD:3363	5-HT7;
-	GenelD:282969	FLJ26016;
+	GenelD:1571	CPE1; CYP2E; P450-J; P450C2E;
-	GenelD:1959	CMT1D; CMT4E; KROX20; FLJ14547; DKFZp686J1957;
+	GenelD:399823	FOXI2;
+	GenelD:9118	NEF5; NF-66; TXBP-1; MGC12702;
-	GenelD:7490	GUD; WAGR; WT33; WIT-2;
+	GenelD:5045	FUR; PACE; SPC1; PCSK3;
+	GenelD:27023	FKH5; HFKH-5;
+	GenelD:27023	FKH5; HFKH-5;
+	GenelD:9956	3OST2; 3OST2;
+	GenelD:3394	ICSBP; IRF-8; ICSBP1; H-ICSBP;
+	GenelD:8153	ARHN; RHO7; RhoN;
+	GenelD:9123	MCT3; MCT4;
+	GenelD:146664	GnT-IX; GnT-VB; FLJ25132; KIAA2008;
+	GenelD:762	CAIV; RP17;

- GenelD:10481
- GenelD:8522 MGC1348; KIAA0394;
+ GenelD:2587 GALNR; GALNR1;
+ GenelD:2767 GNA-11;
+ GenelD:9002 PAR4;
+ GenelD:1908 ET3; MGC15067; MGC61498;
- GenelD:27111 ST-2; SITAC18;
+ GenelD:9145 MGC:1939;
- GenelD:2000 MEF; ELFR;
+ GenelD:27336 TAT-SF1; dJ196E23.2;
- GenelD:29057 PRO0659; DKFZp686B22211;
+ GenelD:54885
+ GenelD:4694 MWFE; ZNF183; CI-MWFE;
- GenelD:8270 CVG5; ESO3; ITBA2; DXS9951E;
- GenelD:7737 RNF113; ZNF183;
+ GenelD:1947 CFND; CFNS; EFL3; EPLG2; Elk-L; LERK2; MGC8782;
+ GenelD:139212 MGC35261;
+ GenelD:10857 MPR; HPR6.6;
- GenelD:94121 exophilin-2; DKFZp451P0116;
+ GenelD:4810 SCML1; DKFZp781F2016;
+ GenelD:399668
+ GenelD:6173 L44L; MIG6; RPL44; MGC72020;
+ GenelD:8776
+ GenelD:3149 HMG4; HMG2A; MGC90319;
- GenelD:2719 SGB; DGSX; SDYS; SGBS; SGBS1;
- GenelD:1831 DIP; GILZ; hDIP; DSIP1; TSC-22R; DKFZp313A1123;
- GenelD:1774 XIB; DNL1L; DNAS1L1;
- GenelD:23133 ZNF422; KIAA1111; DKFZp686E0868;
- GenelD:55593 MGC104871; DKFZp761A052;
- GenelD:11230 JM4;
- GenelD:27316 RNMX; HNRPG; RBMXP1; RBMXRT;
+ GenelD:80823 p60TRP; KIAA1701;
- GenelD:3920 LAMPB; CD107b;
+ GenelD:9767 JADE3; KIAA0215;
+ GenelD:4128
+ GenelD:27336 TAT-SF1; dJ196E23.2;
- GenelD:2002
+ GenelD:55086 FLJ14191;
- GenelD:4983 OPN1;
+ GenelD:9968 HOPA; OPA1; CAGH45; TNRC11; TRAP230; KIAA0192;
+ GenelD:10159 M8-9; MRXE; XMRE; ATP6IP2; MSTP009; APT6M8-9; ATP6M8-9;
+ GenelD:10479 NHE6; KIAA0267;
+ GenelD:399668
+ GenelD:369 PKS2; A-RAF; ARAF1; RAFA1;
- GenelD:84707 BEX1; DJ79P11.1;
- GenelD:2239 K-glycan;
+ GenelD:2491 CENPI; LRPR1;
- GenelD:65109 UPF3X; HUPF3B; RENT3B;
+ GenelD:24137 KIF4; KIF4-G1; HSA271784;
+ GenelD:63035 FLJ11362; B930011H20Rik;

+	GenelD:6134	QM; NOV; DXS648; DXS648E; FLJ23544;
+	GenelD:55849	ALG13; MDS031;
+	GenelD:4952	LOCR; NPHL2; OCRL1; INPP5F;
-	GenelD:4354	MRG1; PEMP; AAG12; EMP55; DXS552; DXS552E;
+	GenelD:64061	CDA1; CTCL; CINAP; DENTT; SE20-4; HRIHFB2216;
+	GenelD:64743	MG21; FLJ20563;
+	GenelD:51260	MGC874;
-	GenelD:3421	H-IDHG;
-	GenelD:10134	CDM; BAP31; 6C6-AG; DXS1357E;
+	GenelD:10009	ZNF348; ZNF-kaiso;
-	GenelD:3028	ABAD; ERAB; MHBD; HSD17B10; 17b-HSD10;
-	GenelD:54954	ORF34; FLJ20506;
+	GenelD:10549	AOE37-2;
+	GenelD:331	API3; ILP1; MIHA; XIAP;
-	GenelD:158866	MRX91; FLJ31812; MGC119974; MGC119975; MGC119976;
-	GenelD:5255	PHKA;
+	GenelD:84187	FLJ20173; bB360B22.3;
+	GenelD:55841	BM042; KIAA1280;
+	GenelD:10682	CPX; CHO2; CPXD; CDPX2;
+	GenelD:5422	
-	GenelD:84679	NHE7; SLC9A6;
+	GenelD:4128	
+	GenelD:1947	CFND; CFNS; EFL3; EPLG2; Elk-L; LERK2; MGC8782;
+	GenelD:4478	
-	GenelD:11152	JM5; WDRX1; WIPI4; WIPI-4;
+	GenelD:9767	JADE3; KIAA0215;
+	GenelD:5165	
+	GenelD:537	16A; CF2; ORF; Ac45; XAP3; XAP-3; ATP6S1; VATPS1; ATP6IP1; M
-	GenelD:55593	MGC104871; DKFZp761A052;
+	GenelD:90121	MGC20451;
+	GenelD:1896	ED1; HED; EDA1; EDA2; XHED; XLHED; ED1-A1; ED1-A2;
+	GenelD:7114	FX; TB4X; PTMB4; TMSB4;
+	GenelD:26576	MSSK1; SRPK3; MGC102944;
+	GenelD:8237	UHX1;
-	GenelD:9131	AIF; MGC111425;
-	GenelD:158880	
-	GenelD:6103	CRD; RP3; COD1; PCDX; RP15; XLRP3; orf15; CORDX1;
+	GenelD:6567	AHDS; MCT8; XPCT; DXS128; DXS128E;

ACCESSION	GID	ANNOTATION
NM_003431.2	GI:42733607	go_component: nucleus; go_function: DN
NM_024686.3	GI:40255233	novel protein containing a tubulin-tyrosin
NM_002965.2	GI:9845520	S100 calcium-binding protein A9 (calgranul
NM_152495.1	GI:22749038	go_component: membrane; go_componen
NM_198427.1	GI:38372930	isoform 2 is encoded by transcript variant
NM_006433.2	GI:7108343	isoform NKG5 is encoded by transcript vai
NM_001426.2	GI:7710118	go_component: nucleus; go_component:
NM_000348.2	GI:39812446	steroid 5-alpha-reductase 2; go_componen
NM_000189.4	GI:40806188	hexokinase-2; muscle; go_component: me
NM_001870.1	GI:4503000	go_component: secretory granule; go_fur
NM_199069.1	GI:41327780	isoform a is encoded by transcript variant
NM_003304.3	GI:27545448	transient receptor potential channel 1; go
NM_020390.5	GI:33187364	go_function: nucleic acid binding; go_func
NM_016559.1	GI:7706670	Pex5p-related protein; go_component: m
NM_004575.1	GI:4758947	Brn3b POU domain transcription factor; g
NM_001313.3	GI:62422567	isoform 2 is encoded by transcript variant
NM_004291.2	GI:46852394	go_component: extracellular space; go_pi
NM_002460.1	GI:4505286	multiple myeloma oncogene 1; go_compc
NM_001710.4	GI:67782357	C3 proactivator; C3 proaccelerator; glycin
NM_003525.2	GI:21166387	synonyms: H2B/k; H2BFK
NM_003530.3	GI:39812261	go_component: nucleus; go_component:
NM_016224.3	GI:23111056	SH3 and PX domain-containing protein SH
NM_014724.2	GI:44917602	zinc finger protein 305; go_component: n
NM_003545.3	GI:21264600	synonyms: H4/j; H4FJ
NM_016188.3	GI:21536352	hArpN alpha; actin-like 6; actin-related pr
NT_077531.3		GATA-binding protein 4; go_component: r
NM_000025.1	GI:4557266	Beta-3 Adrenergic Receptor; go_componen
NT_077531.3		GATA-binding protein 4; go_component: r
NM_005382.1	GI:4885512	neurofilament 3 (150kD medium); neurofi
NM_004789.3	GI:30795195	LIM HOX gene 2; go_component: nucleus;
NM_032727.2	GI:39725658	neurofilament-66; tax-binding protein; ne
NM_145202.3	GI:48976058	uterine-specific proline-rich acidic protein
NM_000818.1	GI:4503874	Glutamate decarboxylase-2 (pancreas); gl
NM_019859.2	GI:30795198	isoform d is encoded by transcript variant
NM_198472.1	GI:38348261	go_process: carbohydrate transport
NM_000773.3	GI:75709190	microsomal monooxygenase; xenobiotic r
NM_000399.2	GI:9845523	Krox-20 homolog; KROX-20; Drosophila; h
NM_207426.1	GI:46409477	synonym: FOXI2
NM_032727.2	GI:39725658	neurofilament-66; tax-binding protein; ne
NT_009237.17		isoform C is encoded by transcript variant
NM_002569.2	GI:20336193	proprotein convertase subtilisin/kexin typ
NM_012182.1	GI:11386194	go_component: nucleus; go_function: tra
NM_012182.1	GI:11386194	go_component: nucleus; go_function: tra
NM_006043.1	GI:5174462	heparin-glucosamine 3-O-sulfotransferase
NM_002163.2	GI:55953136	interferon consensus sequence binding pr
NM_005440.3	GI:66472870	GTP-binding protein Rho7; ras homolog ge
NM_004207.1	GI:4759111	monocarboxylate transporter 3; go_comp
NM_144677.2	GI:39812180	isoform 1 is encoded by transcript variant
NM_000717.2	GI:9951925	carbonic dehydratase; go_component: me

NM_006361.4	GI:70167332	homeobox protein HOX-B13; go_component: homeobox protein HOX-B13; go_component: isoform a is encoded by transcript variant
NM_003644.2	GI:41406075	go_component: plasma membrane; go_component: isoform a is encoded by transcript variant
NM_001480.2	GI:6031165	guanine nucleotide-binding protein; Gq cl; go_component: plasma membrane; go_component: isoform a is encoded by transcript variant
NM_002067.1	GI:4504036	guanine nucleotide-binding protein; Gq cl; go_component: plasma membrane; go_component: isoform a is encoded by transcript variant
NM_003950.1	GI:4503638	protease-activated receptor-4; go_component: protease-activated receptor-4; go_component: isoform 1 preprotein is encoded by transcript variant
NM_000114.2	GI:46370058	isoform 1 preprotein is encoded by transcript variant
NM_015685.3	GI:38016915	isoform b is encoded by transcript variant
NM_145738.1	GI:22035699	isoform 1c is encoded by transcript variant
NM_001421.1	GI:4503554	go_component: nucleus; go_component: nucleoplasm; go_component: isoform 1c is encoded by transcript variant
NM_014500.3	GI:34147671	cofactor required for Tat activation of HIV
NM_014138.3	GI:50355985	synonyms: PRO0659; DKFZp686B22211
NM_017752.2	GI:38570100	isoform a is encoded by transcript variant
NM_004541.2	GI:13699820	ubiquinone oxidoreductase complex I protein 1; go_component: cellular_component unknown; go_component: isoform a is encoded by transcript variant
NM_006014.2	GI:24430136	zinc finger protein 183 (RING finger; C3HC4 domain); go_component: cellular_component unknown
NM_006978.1	GI:5902157	zinc finger protein 183 (RING finger; C3HC4 domain); ligand of eph-related kinase 2; eph-related kinase 2 ligand
NT_011669.16		ligand of eph-related kinase 2; eph-related kinase 2 ligand
NM_173494.1	GI:33859792	synonym: MGC35261
NM_006667.2	GI:6857798	progesterone binding protein; go_component: steroid binding; go_component: isoform 1 is encoded by transcript variant
NM_080737.1	GI:18152766	granophilin-a; go_component: membrane protein; go_component: membrane
NM_198270.2	GI:40549455	go_component: nucleus
NM_203306.1	GI:42558267	
NM_021029.3	GI:38683866	ribosomal protein L44; 60S ribosomal protein L44; go_component: ribosome; go_component: isoform 1 is encoded by transcript variant
NM_003828.1	GI:28872760	high-mobility group (nonhistone chromosomal protein HMG-14); go_component: isoform 1 is encoded by transcript variant
NM_005342.2	GI:71143136	high-mobility group (nonhistone chromosomal protein HMG-14); go_component: isoform 1 is encoded by transcript variant
NM_004484.2	GI:5360213	glypican-3 splice variant B; glypican-3 splice variant A; go_component: isoform 1 is encoded by transcript variant
NM_004089.3	GI:62865622	isoform 2 is encoded by transcript variant
NM_006730.2	GI:58430940	DNase I; lysosomal-like; DNase I-like; muscle-specific endopeptidase; go_function: nucleic acid binding; go_function: protein binding; go_function: nucleic acid binding
NM_015107.1	GI:32698699	go_function: protein binding; go_function: nucleic acid binding
NM_017602.2	GI:40353201	synonyms: MGC104871; DKFZp761A052
NM_007213.1	GI:6005793	PRA1 domain family 2; Jena-Muenchen 4; go_function: protein binding; go_function: nucleic acid binding
NM_002139.2	GI:56699408	RNA binding motif protein; X chromosome-linked protein; go_function: protein binding; go_function: nucleic acid binding
NM_030639.1	GI:39930462	p60-like protein; go_function: binding
NM_002294.1	GI:4504956	Lysosome-associated membrane protein-2; go_function: protein binding; go_function: nucleic acid binding
NM_014735.2	GI:23110985	go_function: protein binding; go_function: nucleic acid binding
NM_000240.2	GI:33469954	go_component: membrane; go_component: isoform 1 is encoded by transcript variant
NM_014500.3	GI:34147671	cofactor required for Tat activation of HIV
NM_005229.2	GI:11496880	go_component: nucleus; go_function: sequence-specific DNA binding
NM_018015.3	GI:46195791	RP11-647M7.1; go_function: DNA binding
NM_002547.1	GI:4505506	oligophrenin-1; Rho-GTPase activating protein 1; go_function: protein binding; go_function: nucleic acid binding
NM_005120.1	GI:4827041	thyroid hormone receptor-associated protein 1; go_function: protein binding; go_function: nucleic acid binding
NM_005765.2	GI:15011917	ATPase; H+ transporting; lysosomal (vacuolar) proton pump; go_function: protein binding; go_function: nucleic acid binding
NM_006359.1	GI:5454069	go_component: microsome; go_component: isoform 1 is encoded by transcript variant
NM_203306.1	GI:42558267	
NM_001654.1	GI:4502192	Oncogene ARAF1; v-raf murine sarcoma 3
NM_032621.2	GI:50658085	X-linked protein
NM_001448.2	GI:21614524	dj900E8.1 (glypican 4); go_component: membrane protein; go_component: isoform 1 is encoded by transcript variant
NM_006733.2	GI:41352696	FSH primary response (LRPR1; rat) homolog; go_component: membrane protein; go_component: isoform 1 is encoded by transcript variant
NM_023010.2	GI:18375526	isoform 2 is encoded by transcript variant
NM_012310.2	GI:7305204	chromokinesin; go_component: nucleus; go_component: isoform 1 is encoded by transcript variant
NM_021946.2	GI:33286441	synonyms: FLJ11362; B930011H20Rik

NM_006013.2	GI:15718685	QM gene; 60S ribosomal protein L10; tum
NM_018466.2	GI:20070304	asparagine-linked glycosylation 13 homolog
NM_001587.3	GI:21396492	oculocerebrorenal syndrome of Lowe protein
NM_002436.2	GI:6006024	membrane protein; palmitoylated 1 (55kDa)
NM_022117.1	GI:11545834	cell division autoantigen 1; cutaneous T-cell lymphoma
NM_017883.3	GI:20544181	located at OATL1; go_component: nucleus
NM_016500.3	GI:32306538	2610029G23Rik
NM_004135.2	GI:28178836	isoform a precursor is encoded by transcript variant
NM_005745.6	GI:49472837	accessory protein BAP31; go_component: cytoskeleton
NM_006777.3	GI:41152068	WUGSC:H_DJ525N14.1; kaiso transcription factor
NM_004493.1	GI:4758503	isoform 1 is encoded by transcript variant
NM_017848.3	GI:38348730	BJ-HCC-21 tumor antigen
NM_006406.1	GI:5453548	thioredoxin peroxidase (antioxidant enzyme)
NM_001167.2	GI:32528298	X-linked inhibitor of apoptosis; apoptosis regulator
NM_144969.1	GI:21450652	go_component: membrane; go_componer: membrane
NM_002637.1	GI:4505778	Phosphorylase kinase; muscle; alpha polypeptide
NM_032227.1	GI:14149929	synonyms: FLJ20173; bB360B22.3
NM_015691.2	GI:38570148	synonyms: BM042; KIAA1280
NM_006579.1	GI:5729809	3-beta-hydroxysteroid-delta-8;delta-7-isomerase
NM_016937.1	GI:8393994	polymerase (DNA-directed); alpha (70kD);
NM_032591.1	GI:14211918	nonselective sodium potassium/proton exchanger
NM_000240.2	GI:33469954	go_component: membrane; go_componer: membrane
NM_004429.3	GI:31317225	ligand of eph-related kinase 2; eph-related kinase
NM_002444.2	GI:53729335	go_component: cytoplasm; go_componer: cytoplasm
NM_007075.3	GI:71483644	isoform 1 is encoded by transcript variant
NM_014735.2	GI:23110985	go_function: protein binding; go_function: binding
NM_005391.1	GI:4885544	go_component: mitochondrion; go_function: electron transport
NM_001183.3	GI:37577154	H-ATPase subunit; ATPase; H+ transpotin
NM_017602.2	GI:40353201	synonyms: MGC104871; DKFZp761A052
NM_058163.1	GI:24308387	synonym: MGC20451
NM_001399.4	GI:54112099	isoform EDA-A1 is encoded by transcript variant
NM_021109.2	GI:34328943	thymosin; beta 4; X chromosome; prothymosin
NM_014370.2	GI:63025195	go_component: cellular component unknown
NM_004651.3	GI:75992939	ubiquitin carboxyl-terminal hydrolase; X-linked
NM_004208.2	GI:22202627	isoform 1 is encoded by transcript variant
NM_201286.2	GI:69885216	ubiquitin carboxyl-terminal hydrolase 51; UCH-L1
NM_000328.2	GI:66932995	isoform A is encoded by transcript variant
NM_006517.2	GI:62821799	solute carrier family 16 (monocarboxylic acid transporter)

PRODUCT

zinc finger protein 124
tubulin tyrosine ligase-like family; member 7
S100 calcium-binding protein A9
cornichon homolog 3
brevican isoform 2
granulysin isoform NKG5
engrailed homolog 1
3-oxo-5 alpha-steroid 4-dehydrogenase 2
hexokinase 2
mast cell carboxypeptidase A3 precursor
chromosome 3 open reading frame 60 isoform a
transient receptor potential cation channel; subfamily C; member 1
eIF-5A2 protein
PXR2b protein
POU domain; class 4; transcription factor 2
collapsin response mediator protein 1 isoform 2
cocaine- and amphetamine-regulated transcript
interferon regulatory factor 4
complement factor B preproprotein
H2B histone family; member K
H3 histone family; member B
sorting nexin 9
zinc finger protein 96
H4 histone family; member J
actin-like 6B
GATA binding protein 4
adrenergic; beta-3-; receptor
GATA binding protein 4
neurofilament 3 (150kDa medium)
LIM homeobox protein 2
internexin neuronal intermediate filament protein; alpha
proline-rich acidic protein 1
glutamate decarboxylase 2
5-hydroxytryptamine receptor 7 isoform d
hypothetical protein LOC282969
cytochrome P450; family 2; subfamily E; polypeptide 1
early growth response 2 protein
forkhead box I2
internexin neuronal intermediate filament protein; alpha
Wilms tumor 1 isoform C
furin preproprotein
forkhead box B1
forkhead box B1
heparan sulfate D-glucosaminyl 3-O-sulfotransferase 2
interferon regulatory factor 8
Rho family GTPase 2
solute carrier family 16; member 3
beta(1;6)-N-acetylglucosaminyltransferase V isoform 1
carbonic anhydrase IV precursor

homeo box B13
growth arrest-specific 7 isoform a
galanin receptor 1
guanine nucleotide binding protein (G protein); alpha 11 (Gq class)
coagulation factor II (thrombin) receptor-like 3
endothelin 3 isoform 1 preproprotein
syndecan binding protein 2 isoform b
synaptogyrin 1 isoform 1c
E74-like factor 4 (ets domain transcription factor)
HIV TAT specific factor 1
hypothetical protein LOC29057
hypothetical protein LOC54885 isoform a
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 1
ESO3 protein
ring finger protein 113A
ephrin-B1 precursor
hypothetical protein LOC139212
progesterone receptor membrane component 1
synaptotagmin-like 4 (granophilin-a)
Nance-Horan syndrome protein
hypothetical protein LOC399668
ribosomal protein L36a
myotubularin-related protein 1 isoform 1
high-mobility group box 3
glypican 3
TSC22 domain family; member 3 isoform 2
deoxyribonuclease I-like 1 precursor
PHD finger protein 8
hypothetical protein LOC55593
JM4 protein
RNA binding motif protein; X-linked
basic helix-loop-helix domain containing; class B; 9
lysosomal-associated membrane protein 2 precursor
PHD finger protein 16
monoamine oxidase A
HIV TAT specific factor 1
ELK1 protein
hypothetical protein LOC55086
oligophrenin 1
mediator of RNA polymerase II transcription; subunit 12 homolog
ATPase; H⁺ transporting; lysosomal accessory protein 2
solute carrier family 9 (sodium/hydrogen exchanger); isoform 6
hypothetical protein LOC399668
v-raf murine sarcoma 3611 viral oncogene homolog
brain expressed X-linked 2
glypican 4
follicle-stimulating hormone primary response protein 1
UPF3 regulator of nonsense transcripts homolog B isoform 2
kinesin family member 4
BCL6 co-repressor-like 1

ribosomal protein L10
glycosyltransferase 28 domain containing 1
phosphatidylinositol polyphosphate 5-phosphatase isoform b
palmitoylated membrane protein 1
TSPY-like 2
WD repeat domain 13 protein
hypothetical protein LOC51260
isocitrate dehydrogenase 3 (NAD+) gamma isoform a precursor
B-cell receptor-associated protein 31
kaiso
hydroxyacyl-Coenzyme A dehydrogenase; type II isoform 1
hypothetical protein LOC54954
thioredoxin peroxidase
baculoviral IAP repeat-containing protein 4
zinc finger; DHHC domain containing 15
phosphorylase kinase; alpha 1 (muscle)
hypothetical protein LOC84187
hypothetical protein LOC55841
emopamil binding protein (sterol isomerase)
polymerase (DNA-directed); alpha
solute carrier family 9; member 7
monoamine oxidase A
ephrin-B1 precursor
moesin
WD repeat domain 45 isoform 1
PHD finger protein 16
pyruvate dehydrogenase kinase; isoenzyme 3
ATPase; H⁺ transporting; lysosomal accessory protein 1 precursor
hypothetical protein LOC55593
hypothetical protein LOC90121
ectodysplasin A isoform EDA-A1
thymosin; beta 4
serine/threonine kinase 23
ubiquitin specific protease 11
programmed cell death 8 isoform 1
ubiquitin specific protease 51
retinitis pigmentosa GTPase regulator isoform A
solute carrier family 16; member 2

DISTANCE_TO_TSS	CPG_ISLAND	CPG_ISLAND_LOCATIONS	MIR_CPG_ISLAND	MIR_NAMES
153	TRUE	1:245401260-245402151		
731	TRUE	1:84236652-84237966		
428	FALSE			cg16139316
47	TRUE	1:222870113-222872558		
400	TRUE	1:154878094-154879230		
378	FALSE			cg11752275
858	TRUE	2:119320039-119321504		
235	TRUE	2:31658633-31660643		
180	FALSE			cg18638581
1247	FALSE			cg13424229
247	TRUE	3:49032563-49032797		
571	TRUE	3:143925285-143926748		
95	TRUE	3:172108452-172109716		
718	TRUE	3:181236808-181238032		
509	TRUE	4:147778503-147781596		
94	TRUE	4:5944246-5946191		
438	TRUE	5:71050507-71051626		
371	TRUE	6:336092-339080		
532	FALSE			cg17741572
5	TRUE	6:26381046-26381970		
710	TRUE	6:26307702-26308258		
461	TRUE	6:158163446-158165173		
98	TRUE	6:28474985-28475928		
50	TRUE	6:26312577-26313287		
136	TRUE	7:100091590-100092362		
	TRUE	8:11598711-11600557		
709	TRUE	8:37941431-37943204		
	TRUE	8:11598711-11600557		
34	TRUE	8:24826692-24829288		
184	TRUE	9:125813052-125815466		
295	TRUE	10:105026442-105028852		
3	FALSE			cg03743584
152	TRUE	10:26543757-26547625		
509	TRUE	10:92606622-92608182		
446	TRUE	10:135020610-135021994		
661	TRUE	10:135191138-135192648		
329	TRUE	10:64244521-64245891		
16	TRUE	10:129424072-129426344		
275	TRUE	10:105026442-105028852		
	TRUE	11:32411271-32413831		
233	FALSE			cg26377677
710	TRUE	15:58083184-58086207		
320	TRUE	15:58083184-58086207		
257	TRUE	16:22732005-22734135		
79	TRUE	16:84489299-84490591		
180	TRUE	17:38429704-38431262		
674	TRUE	17:77779304-77780821		
270	TRUE	17:72375680-72377919		
396	TRUE	17:55581878-55583315		

42	TRUE	17:44160495-44161328
395	TRUE	17:10041659-10043517
636	TRUE	18:73090255-73093032
155	TRUE	19:3044235-3046095
58	FALSE	
153	TRUE	20:57308563-57309693
104	FALSE	
424	TRUE	22:38075299-38076737
1037	TRUE	X:129071186-129073330
205	TRUE	X:135406317-135407906
837	TRUE	X:53003573-53004951
94	TRUE	X:105932462-105933253
179	TRUE	X:118888580-118890917
197	TRUE	X:153359988-153361104
1047	TRUE	X:118888580-118890917
	TRUE	X:67965268-67967122
5	TRUE	X:106335539-106336710
93	TRUE	X:118253585-118255522
49	TRUE	X:99872942-99873874
41	TRUE	X:17302835-17305853
634	TRUE	X:134383127-134384321
162	TRUE	X:100532246-100532948
518	TRUE	X:149611916-149613219
60	TRUE	X:149901718-149904046
88	TRUE	X:132946499-132947763
174	TRUE	X:106905712-106906660
247	TRUE	X:153292621-153293883
430	TRUE	X:54086783-54088233
620	TRUE	X:48699066-48701313
291	TRUE	X:48817890-48819021
198	TRUE	X:135789863-135790845
57	TRUE	X:101862184-101862707
60	TRUE	X:119486553-119487414
16	TRUE	X:46656361-46658460
60	TRUE	X:43400130-43400730
309	TRUE	X:135406317-135407906
487	TRUE	X:47394182-47395634
43	TRUE	X:105741531-105742091
49	TRUE	X:67569334-67570801
83	TRUE	X:70254864-70255742
488	TRUE	X:40324583-40325764
166	TRUE	X:134895007-134896000
331	TRUE	X:134383127-134384321
1	TRUE	X:47305171-47306159
6	TRUE	X:102451844-102452762
559	TRUE	X:132375857-132378130
1445	TRUE	X:100239491-100240120
195	TRUE	X:118870555-118871381
268	TRUE	X:69426172-69427271
1211	TRUE	X:128941358-128946562

305	TRUE	X:153277879-153281110
54	TRUE	X:110810870-110811991
513	TRUE	X:128501680-128502582
386	TRUE	X:153686380-153687406
45	TRUE	X:53127216-53129170
649	TRUE	X:48339681-48341694
36	TRUE	X:75309058-75309844
183	TRUE	X:152712310-152713950
80	TRUE	X:152642005-152643632
185	TRUE	X:119268363-119269844
107	TRUE	X:53477634-53478316
97	TRUE	X:54225446-54226910
84	TRUE	X:23595198-23596007
21	TRUE	X:122821066-122822021
65	TRUE	X:74659346-74660218
808	TRUE	X:71851306-71852273
29	TRUE	X:109131973-109133498
1092	TRUE	X:9942388-9944707
330	TRUE	X:48264674-48265781
431	TRUE	X:24621426-24622402
496	TRUE	X:46502730-46504082
135	TRUE	X:43400130-43400730
78	TRUE	X:67965268-67967122
228	TRUE	X:64803987-64804606
96	TRUE	X:48844077-48845653
288	TRUE	X:46656361-46658460
342	TRUE	X:24392800-24393964
201	TRUE	X:153309132-153310681
232	TRUE	X:48699066-48701313
199	TRUE	X:54483309-54483784
197	TRUE	X:68752319-68753914
260	TRUE	X:12902523-12904636
30	TRUE	X:152699478-152699970
26	TRUE	X:46977105-46978329
282	TRUE	X:129126775-129128085
148	TRUE	X:55531479-55532401
389	TRUE	X:38070900-38072122
285	FALSE	

cg06277838

Patient	Age	Sex	Smoke	Stage	grade
No.1	70	M	Y	T2aN0M0, Ib	Adenocarcinoma, Acinar predominant, poorly-moderately differentiated
No.2	59	F	Y	T3N0M0, IIb	Adenocarcinoma, Papillary predominant with mucin production, well-differentiated
No.3	49	F	Y	T3N2M0, IIIa	Adenocarcinoma, Solid predominant and Acinar predominant , poorly-moderately differentiated
No.4	59	M	Y	T2N1M0, IIb	Adenocarcinoma, Acinar predominant and Solid predominant with mucin production, poorly-moderately differentiated
No.5	74	F	Y	T3N2M0, IIIa	Adenocarcinoma, Acinar predominant, Papillary predominant and Solid predominant mixed subtype , poorly-moderately differentiated
No.6	79	M	Y	T2N0M0, Ib	Adenocarcinoma, Acinar predominant and Solid predominant mixed subtype, poorly differentiated
No.7	69	F	N	T1N0M,Ib	Adenocarcinoma, Acinar predominant and BAC mixed subtype , poorly-moderately differentiated
No.8	70	M	N	T3N0M0, IIb	Adenocarcinoma, Acinar predominant and Papillary predominant mixed subtype , poorly-moderately differentiated,Intrapulmonary metastases in the same lobe
No.9	72	F	N	T1N1M0, IIa	Adenocarcinoma, Acinar predominant and Solid predominant mixed subtype, poorly-moderately

					differentiated, cancer embolus in lymphangion
No.10	56	M	N	T2N0M0, Ib	Adenocarcinoma, Acinar predominant, Invading the visceral pleura
No.11	51	F	N	T3N2M0, IIIa	Adenocarcinoma, Solid predominant with mucin production and Acinar predominant mixed subtype, Invading the visceral pleura, Invading the other lobe
No.12	52 F	F	N	T1N2M0, IIIa	Adenocarcinoma, Acinar predominant and Papillary predominant mixed subtype Invading the visceral pleura, poorly-moderately differentiated