Barbados – postnatal exposure to protein-energy malnutrition – Peter, Biol Psychiatry 2016

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	CHR	MAPINFO	Probe_SNPs	UCSC_RefGe	UCSC_RefGe	UCSC_CpG_I
cg14793544	chr6	30538842	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg05554000	chr7	158905015	rs143711415	VIPR2	Body	chr7:158905
cg18015044	chr6	30538844	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg13444538	chr7	158905317	NA	VIPR2	Body	chr7:158905
cg13835168	chr6	29648756	rs416560			
cg08041448	chr6	29648901	rs2747432			
cg00678158	chr6	30538836	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg19636627	chr6	29649084	rs3131847			
cg16885113	chr6	29648507	NA			
cg26343358	chr6	31275666	rs1619716			chr6:312762
cg00588198	chr6	29648452	rs3129057			
cg13774539	chr2	74612706	rs73948791	LOC1001895	TSS200	
cg11383134	chr6	29648590	rs114184656			
cg20228636	chr6	29648525	rs2747431			
cg07134666	chr6	29648400	rs17184563			
cg03899827	chr7	158905377	rs137924839	VIPR2	Body	chr7:158905
cg20874785	chr2	74612674	rs73948791	LOC1001895	TSS200	
cg24100841	chr6	29649024	rs3129054			
cg25107000	chr6	31275643	rs34196875			chr6:312762
cg18502630	chr9	139871955	NA	PTGDS;PTGD	5'UTR;1stExo	chr9:139872
cg21862126	chr1	1076296	NA			chr1:107236
cg08479516	chr7	158905536	NA	VIPR2	Body	chr7:158905
cg22098660	chr4	6107339	NA	JAKMIP1;JAK	Body;Body	chr4:610713
cg08620751	chr19	1851750	NA			chr19:18515
cg11719157	chr17	1466715	NA	PITPNA	TSS1500	chr17:14651
cg24297727	chr6	30538686	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg13312337	chr2	74612759	NA	LOC1001895	TSS200	
cg22494932	chr6	29648379	rs17184563			
cg00986350	chr16	88540396	rs114362790	ZFPM1	Body	chr16:88539
cg06697425	chr17	72915897	NA	USH1G	Body	chr17:72915
cg21003654	chr4	6107633	NA	JAKMIP1;JAK	Body;Body	chr4:610713
cg17560136	chr8	21915510	NA	EPB49;EPB4	5'UTR;TSS15	chr8:219142
cg07194846	chr22	19930177	rs737864	COMT;TXNR	5'UTR;TSS15	chr22:19929
cg14801238	chr6	31275664	rs1619716			chr6:312762
cg12097325	chr1	1076431	NA			chr1:107236
cg16046667	chr20	35422698	NA	C20orf117;C	Body;Body	chr20:35422
cg25699073	chr6	29648381	rs17184563			
cg11794033	chr6	31275267	rs2853915			chr6:312762
cg20426671	chr17	1466709	NA	PITPNA	TSS1500	chr17:14651
cg16724588	chr4	6107131	NA	JAKMIP1;JAK	Body;Body	chr4:610713
cg02157626	chr6	29648736	NA			

cg27258561	chr6	31275767	rs28600230			chr6:312762
cg02211646	chr7	114055210	NA	FOXP2;FOXP	1stExon;5'UTR;5'UTR;1stE	
cg19544441	chr11	67211701	NA	CORO1B;COR	TSS1500;TSS1500	
cg04026699	chr6	28834513	NA			chr6:288316
cg04585822	chr17	72916509	rs111033465	USH1G	Body	chr17:72915
cg14141448	chr6	30538684	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg27071793	chr6	31275718	rs28600230			chr6:312762
cg05232889	chr7	114055419	NA	FOXP2;FOXP	5'UTR;5'UTR;5'UTR	
cg08158662	chr12	34489995	NA			chr12:34489
cg06231140	chr4	6107320	NA	JAKMIP1;JAK	Body;Body	chr4:610713
cg03077533	chr2	121107326	NA	INHBB	Body	chr2:121106
cg22502625	chr14	103568366	rs113344928	C14orf73	Body	chr14:10356
cg22667835	chr4	6107791	rs10000296	JAKMIP1;JAK	Body;Body	chr4:610713
cg26690742	chr11	2889602	NA			chr11:28903
cg00508131	chr16	333153	rs45519642	PDIA2;PDIA2	5'UTR;1stExo	chr16:33444
cg05308117	chr19	48547362	rs35637404	CABP5	TSS200	
cg25145670	chr17	46655164	NA	HOXB4	Body	chr17:46655
cg24786986	chr7	114055133	NA	FOXP2;FOXP	1stExon;5'UTR;5'UTR;1stE	
cg00743717	chr17	36831977	rs4795309	C17orf96	TSS1500	chr17:36829
cg01638101	chr2	74612812	NA	LOC1001895	TSS200	
cg11073255	chr6	31762455	NA	VARS	Body	chr6:317632
cg23166781	chr4	6107280	NA	JAKMIP1;JAK	Body;Body	chr4:610713
cg22674497	chr17	72916000	NA	USH1G	Body	chr17:72915
cg02446475	chr6	31275807	rs1634760			chr6:312762
cg18994250	chr4	6107021	rs11735262	JAKMIP1;JAK	Body;Body	chr4:610713
cg18420781	chr6	30124240	NA	TRIM10;TRI	Body;Body	
cg20795372	chr6	30419612	rs9295885			chr6:304188
cg13382072	chr19	1851882	NA			chr19:18515
cg21045547	chr20	35422703	rs61732362	C20orf117;C	Body;Body	chr20:35422
cg10605977	chr10	133961265	NA	JAKMIP3	Body	
cg02780849	chr1	235814163	NA	GNG4;GNG4;	TSS1500;TSS	chr1:235814
cg04464062	chr16	88540349	rs114362790	ZFPM1	Body	chr16:88539
cg25981998	chr6	30124248	NA	TRIM10;TRI	Body;Body	
cg17988187	chr2	74612222	NA	LOC1001895	TSS1500	
cg18871253	chr7	114055137	NA	FOXP2;FOXP	1stExon;5'UTR;5'UTR;1stE	
cg07620992	chr6	33421963	NA	ZBTB9	TSS1500	chr6:334220
cg13175159	chr1	79472643	NA	ELTD1	TSS200	chr1:794722
cg06672250	chr8	21914593	NA	EPB49;EPB4	TSS1500;5'U	chr8:219142
cg25978138	chr6	29648161	rs3129058			
cg07678583	chr20	42142224	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg06281297	chr11	2890190	NA	KCNQ1DN	TSS1500	chr11:28903
cg12076350	chr6	31275791	rs3873388			chr6:312762
cg08787968	chr11	32451777	NA	WT1;WT1;W	Body;Body;B	chr11:32452
cg02779948	chr10	70092852	NA	PBLD;HNRNP	TSS200;5'UT	chr10:70091
cg12814335	chr17	1466713	NA	PITPNA	TSS1500	chr17:14651

cg00140112	chr18	3879595	NA	DLGAP1	1stExon	chr18:38792
cg19655952	chr7	114055204	NA	FOXP2;FOXP	1stExon;5'UTR;5'UTR;1stE	
cg13455717	chr1	235814365	NA	GNG4;GNG4;	TSS1500;TSS	chr1:235814
cg04360793	chr1	79472361	NA	ELTD1;ELTD1	5'UTR;1stExo	chr1:794722
cg18534730	chr19	48547448	NA	CABP5	TSS200	
cg06099697	chr16	88539861	NA	ZFPM1	Body	chr16:88539
cg00891025	chr8	21915184	rs62493961	EPB49;EPB4	TSS200;5'UT	chr8:219142
cg22637837	chr5	140730092	NA	PCDHGB1;PC	1stExon;Body	chr5:140731
cg04972348	chr1	1100035	NA			chr1:109804
cg02931604	chr6	74064298	NA	DPPA5	TSS1500	chr6:740635
cg11716608	chr7	65447332	NA	GUSB	TSS200	chr7:654467
cg02589685	chr11	2889629	NA			chr11:28903
cg03198012	chr5	1241099	NA	SLC6A18	Body	chr5:124244
cg02932780	chr6	31762353	rs4713488	VARS	Body	chr6:317632
cg17736443	chr6	27783054	NA	HIST1H2AJ;H	TSS1500;1stE	chr6:277822
cg22100652	chr6	28834404	rs6935576			chr6:288316
cg05497216	chr16	89408076	rs115857356	ANKRD11	5'UTR	chr16:89408
cg16430887	chr4	1497223	rs76137134			chr4:149454
cg15893346	chr7	65447565	NA	GUSB	TSS1500	chr7:654467
cg19301742	chr6	33421180	NA	SYNGAP1;ZB	3'UTR;TSS15	chr6:334220
cg23414861	chr6	74064064	rs185614200	DPPA5	TSS200	chr6:740635
cg08940169	chr16	88540241	NA	ZFPM1	Body	chr16:88539
cg13429614	chr6	31276667	rs115193934			chr6:312762
cg25841114	chr6	31762901	NA	VARS	Body	chr6:317632
cg00270311	chr16	30366760	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg15446391	chr11	32452370	NA	WT1;WT1;W	Body;Body;B	chr11:32452
cg17079325	chr7	130131480	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg20495333	chr2	121107947	NA	INHBB	3'UTR	chr2:121106
cg04344875	chr7	130131484	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg01761710	chr16	333155	NA	PDIA2;PDIA2	5'UTR;1stExo	chr16:33444
cg03555881	chr6	31275551	rs116704042			chr6:312762
cg00286878	chr7	130131633	rs73724326	MEST;MEST;	TSS1500;5'U	chr7:130130
cg23723903	chr1	10856466	rs61645034	CASZ1;CASZ1	5'UTR;5'UTR	chr1:108538
cg22941646	chr1	235814339	NA	GNG4;GNG4;	TSS1500;TSS	chr1:235814
cg13099117	chr6	30538539	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg02767759	chr16	30366751	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg10021428	chr4	53588038	NA			chr4:535881
cg18546840	chr7	114055123	NA	FOXP2;FOXP	1stExon;5'UTR;5'UTR;1stE	
cg01929855	chr4	6107649	NA	JAKMIP1;JAK	Body;Body	chr4:610713
cg06618740	chr1	1100126	NA			chr1:109804
cg08633313	chr20	42142852	rs2072978	L3MBTL;L3M	TSS200;TSS2	chr20:42143
cg10149529	chr19	48547314	rs35637404	CABP5	TSS200	
cg12781568	chr11	32452038	NA	WT1;WT1;W	Body;Body;B	chr11:32452
cg08714996	chr5	140729928	NA	PCDHGB1;PC	1stExon;Body	chr5:140731
cg22380472	chr19	2900542	rs78002149	ZNF57	TSS1500	chr19:29003

cg20684973	chr10	105127632	rs10883857	TAF5	TSS200	chr10:10512
cg24716558	chr17	72915784	NA	USH1G	Body	chr17:72915
cg13311607	chr8	144451523	NA	RHPN1;C8orf	Body;TSS150	chr8:144450
cg14848772	chr6	27099813	NA	HIST1H2AG	TSS1500	chr6:271001
cg26413432	chr4	155702351	NA	RBM46	TSS200	chr4:155702
cg25946459	chr20	35422495	NA	C20orf117;C	Body;Body	chr20:35422
cg23948843	chr2	164204752	NA			chr2:164204
cg24303888	chr6	30852354	rs147143466	DDR1;DDR1;	1stExon;5'UT	chr6:308521
cg04609859	chr17	46655736	NA	HOXB4;HOX	1stExon;5'UT	chr17:46654
cg09260653	chr16	1486064	rs111957036	CCDC154	Body	chr16:14870
cg02992596	chr4	155702220	NA	RBM46	TSS1500	chr4:155702
cg24931658	chr8	21914524	NA	EPB49;EPB4	TSS1500;5'U	chr8:219142
cg09747578	chr1	46769076	NA	LRRC41;UQC	TSS200;TSS1	chr1:467674
cg11491998	chr6	30419493	NA			chr6:304188
cg08149865	chr8	21914600	NA	EPB49;EPB4	TSS1500;5'U	chr8:219142
cg03205258	chr22	19929274	NA	TXNRD2;CO	1stExon;1stE	chr22:19929
cg21240441	chr9	139872871	rs148430937	PTGDS	Body	chr9:139872
cg21475076	chr1	1100493	rs79776491			chr1:109804
cg01306563	chr7	114055074	NA	FOXP2;FOXP	1stExon;5'UTR;5'UTR;1stE	
cg08805748	chr6	30538523	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg01467419	chr19	2900365	rs11084969	ZNF57	TSS1500	chr19:29003
cg18022926	chr10	70093071	NA	PBLD;PBLD;H	TSS1500;TSS	chr10:70091
cg14105566	chr2	121107846	NA	INHBB	3'UTR	chr2:121106
cg25407198	chr7	130131268	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg19187653	chr6	31778919	NA	HSPA1L	Body	chr6:317828
cg17365962	chr6	30538589	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg20188621	chr10	105127192	rs72847518	TAF5	TSS1500	chr10:10512
cg07770370	chr10	133961306	NA	JAKMIP3	Body	
cg24938881	chr2	91937035	NA			chr2:919368
cg09243445	chr2	237123016	NA	ASB18	Body	chr2:237123
cg20412244	chr6	31276664	rs115193934			chr6:312762
cg10433547	chr16	1486536	NA	CCDC154	Body	chr16:14870
cg14824543	chr1	1076166	NA			chr1:107236
cg09796320	chr7	65447328	NA	GUSB	TSS200	chr7:654467
cg05006231	chr19	1852165	NA			chr19:18515
cg01878724	chr6	150346921	NA	RAET1L	TSS1500	
cg10973146	chr14	103568471	NA	C14orf73	Body	chr14:10356
cg01652244	chr6	74063982	NA	DPPA5	TSS200	chr6:740635
cg03228567	chr6	30955421	NA	MUC21	Body	
cg22103164	chr4	155702409	NA	RBM46	TSS200	chr4:155702
cg12637448	chr4	1496981	NA			chr4:149454
cg19439810	chr1	46768592	NA	LRRC41;UQC	Body;TSS150	chr1:467674
cg06805615	chr6	30955716	NA	MUC21	Body	
cg14598950	chr3	37035355	rs4647205	MLH1;MLH1;	1stExon;5'UT	chr3:370342
cg16523380	chr1	10856707	NA	CASZ1;CASZ1	TSS200;TSS2	chr1:108538

cg06857094	chr6	31762442	NA	VARS	Body	chr6:317632
cg10861005	chr6	33266368	NA	RGL2;RGL2	Body;Body	chr6:332663
cg12275723	chr1	10856739	NA	CASZ1;CASZ1	TSS200;TSS2	chr1:108538
cg15606633	chr12	130824403	NA	PIWIL1	5'UTR	chr12:13082
cg19628456	chr6	31779381	NA	HSPA1L	Body	chr6:317828
cg07803420	chr6	30851517	NA	DDR1;DDR1	TSS1500;TSS	chr6:308521
cg04714041	chr19	35068710	NA	LOC643719	TSS200	chr19:35068
cg13377264	chr6	30419135	rs17188876			chr6:304188
cg19132762	chr3	37034739	NA	EPM2AIP1;M	5'UTR;TSS15	chr3:370342
cg23878471	chr6	30419063	rs11753256			chr6:304188
cg22457903	chr20	42142417	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg13581155	chr5	135415781	rs34577747			chr5:135416
cg14476334	chr1	1100557	rs79776491			chr1:109804
cg26708559	chr7	130131730	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg23200020	chr19	35068555	NA	LOC643719	Body	chr19:35068
cg06128195	chr6	166400879	NA	C6orf176;C6	Body;Body;T	chr6:166401
cg08631427	chr6	150346858	rs144356849	RAET1L	TSS200	
cg15084543	chr1	79472408	NA	ELTD1;ELTD1	5'UTR;1stExo	chr1:794722
cg03662049	chr2	164204829	NA			chr2:164204
cg21064451	chr22	38071534	rs929039	LGALS1	TSS200	chr22:38073
cg19673462	chr6	35109353	NA	TCP11;TCP11	TSS200;TSS2	chr6:351088
cg03979582	chr1	46769114	NA	LRRC41;UQC	TSS200;TSS1	chr1:467674
cg12375722	chr5	140729719	NA	PCDHGA2;PC	Body;TSS200	chr5:140731
cg06173536	chr1	235814462	rs10159416	GNG4;GNG4;	TSS1500;TSS	chr1:235814
cg16912957	chr6	30124214	NA	TRIM10;TRI	Body;Body	
cg02169857	chr2	110969641	NA	NCRNA0011	Body	chr2:110969
cg06446163	chr20	42142671	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg02156769	chr9	139872246	NA	PTGDS	Body	chr9:139872
cg01923099	chr11	2889875	NA	KCNQ1DN	TSS1500	chr11:28903
cg17557357	chr5	140729608	NA	PCDHGA2;PC	Body;Body;B	chr5:140731
cg04410181	chr1	46769230	NA	LRRC41;UQC	TSS200;TSS2	chr1:467674
cg12835524	chr6	35109485	NA	TCP11;TCP11	TSS1500;TSS	chr6:351088
cg14551952	chr2	121107444	NA	INHBB	Body	chr2:121106
cg26955996	chr19	48547989	NA	CABP5	TSS1500	
cg19211915	chr11	32452513	rs12575247	WT1;WT1;W	Body;Body;B	chr11:32452
cg11032634	chr22	19929254	NA	TXNRD2;CO	1stExon;TSS2	chr22:19929
cg15388309	chr20	42142559	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg03108330	chr19	2900762	rs12981594	ZNF57	TSS200	chr19:29003
cg01264106	chr22	38071602	NA	LGALS1	TSS200	chr22:38073
cg16587174	chr6	31778842	NA	HSPA1L	Body	chr6:317744
cg24298421	chr1	10856943	NA	CASZ1;CASZ1	TSS1500;TSS	chr1:108538
cg11748904	chr20	35422334	rs35565287	C20orf117;C	Body;Body	chr20:35422
cg16627358	chr16	88540175	rs35471681	ZFPM1	Body	chr16:88539
cg07439128	chr11	2890019	NA	KCNQ1DN	TSS1500	chr11:28903
cg13641903	chr11	32452608	NA	WT1;WT1;W	Body;Body;B	chr11:32452

cg13917504	chr7	130131258	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg21873885	chr6	33267214	NA	RGL2;RGL2	TSS200;TSS2	chr6:332663
cg23657718	chr4	1495933	NA			chr4:149454
cg20818778	chr1	235814145	rs115162768	GNG4;GNG4;	TSS1500;TSS	chr1:235814
cg15225267	chr6	31276187	rs75036475			chr6:312762
cg12886694	chr6	27832992	NA	HIST1H2AL	TSS200	chr6:278331
cg17279912	chr13	111267790	rs74971770	CARKD	TSS1500	chr13:11126
cg02381009	chr5	1241958	rs10043584	SLC6A18	Body	chr5:124244
cg20916175	chr6	27832956	NA	HIST1H2AL	TSS200	chr6:278331
cg17944110	chr1	10856657	NA	CASZ1;CASZ1	1stExon;5'UT	chr1:108538
cg19548470	chr18	3880510	NA	DLGAP1	TSS1500	chr18:38792
cg01579841	chr6	166400494	NA	C6orf176;C6	Body;Body;T	chr6:166401
cg10623826	chr6	31778639	NA	HSPA1L	Body	chr6:317744
cg23762359	chr11	2890082	NA	KCNQ1DN	TSS1500	chr11:28903
cg07438617	chr17	46655289	NA	HOXB4	1stExon	chr17:46655
cg13617204	chr6	27832869	NA	HIST1H2AL	TSS1500	chr6:278331
cg10503232	chr11	2891495	NA	KCNQ1DN	Body	chr11:28903
cg12175949	chr22	19929286	NA	TXNRD2;CO	1stExon;1st	chr22:19929
cg10648573	chr6	29648348	rs2747429			
cg12167167	chr6	166401051	NA	LOC441177;	Body;Body;B	chr6:166401
cg10052908	chr6	74063522	NA	DPPA5	Body	chr6:740635
cg07019740	chr22	19929205	NA	TXNRD2;CO	Body;TSS200	chr22:19929
cg16489689	chr6	30954150	NA	MUC21	Body	
cg20226154	chr6	150346787	rs1544123	RAET1L	TSS200	
cg23483495	chr4	155702533	NA	RBM46;RBM	1stExon;5'UT	chr4:155702
cg25108566	chr6	27775657	rs200485	HIST1H2AI;H	TSS1500;1st	chr6:277753
cg05527785	chr17	46656543	NA	HOXB4	TSS1500	chr17:46655
cg14865393	chr1	10855806	NA	CASZ1;CASZ1	5'UTR;5'UTR	chr1:108538
cg01444206	chr6	33266391	NA	RGL2;RGL2	5'UTR;Body	chr6:332663
cg00787856	chr1	10857110	NA	CASZ1;CASZ1	TSS1500;TSS	chr1:108538
cg06318837	chr4	155702341	NA	RBM46	TSS200	chr4:155702
cg14458834	chr17	46655394	NA	HOXB4	1stExon	chr17:46655
cg06590608	chr3	37035228	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg17750919	chr1	79472917	NA	ELTD1	TSS1500	chr1:794722
cg09234616	chr11	32452592	NA	WT1;WT1;W	Body;Body;B	chr11:32452
cg18934496	chr6	27792502	NA			chr6:277917
cg12949769	chr5	1241224	NA	SLC6A18	Body	chr5:124244
cg16823958	chr7	130131869	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg03939485	chr6	33266076	NA	RGL2;RGL2	Body;Body	chr6:332663
cg00686083	chr6	33421476	NA	ZBTB9	TSS1500	chr6:334220
cg16083838	chr11	2889809	NA	KCNQ1DN	TSS1500	chr11:28903
cg08187750	chr12	130824529	rs4759453	PIWIL1	5'UTR	chr12:13082
cg01693350	chr11	32452187	NA	WT1;WT1;W	Body;Body;B	chr11:32452
cg18911945	chr20	42142784	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg10784143	chr6	30123868	rs115397923	TRIM10;TRI	Body;Body	

cg00783905	chr6	31763174	NA	VARS	5'UTR	chr6:317632
cg21161927	chr5	140729653	NA	PCDHGA2;PC	Body;TSS200	chr5:140731
cg13789775	chr17	46655724	NA	HOXB4;HOX	1stExon;5'UT	chr17:46654
cg05656180	chr11	2890258	NA	KCNQ1DN	TSS1500	chr11:28903
cg01877937	chr20	42142847	rs2072978	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg02177317	chr20	42142699	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg06140764	chr6	30539234	NA	ABCF1;ABCF	5'UTR;5'UTR;	chr6:305389
cg08282428	chr4	155702411	NA	RBM46	TSS200	chr4:155702
cg16500454	chr10	105127701	NA	TAF5	TSS200	chr10:10512
cg09174690	chr2	121107018	NA	INHBB	Body	chr2:121106
cg08267489	chr6	166400656	NA	C6orf176;C6	Body;Body;T	chr6:166401
cg25202636	chr3	37035158	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg08570243	chr2	110969853	NA	NCRNA0011	Body	chr2:110969
cg24343973	chr20	42142236	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg13200628	chr6	30852069	NA	DDR1;DDR1	TSS1500;5'U	chr6:308521
cg26577169	chr6	166401612	NA	LOC441177;	Body;TSS200	chr6:166401
cg26138144	chr22	38071188	NA	LGALS1	TSS1500	chr22:38073
cg01785628	chr6	27775888	NA	HIST1H2AI;H	TSS200;TSS2	chr6:277753
cg23081604	chr12	130824224	NA	PIWIL1	5'UTR	chr12:13082
cg27508821	chr14	95786042	NA	CLMN	Body	chr14:95785
cg08313040	chr6	33092243	NA	HLA-DPB2	Body	
cg12495593	chr6	30539072	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg11854860	chr4	6384165	NA	PPP2R2C;PP	Body;TSS150	chr4:638023
cg13014333	chr6	31762776	NA	VARS	Body	chr6:317632
cg09384137	chr19	2900881	rs10420989	ZNF57	TSS200	chr19:29003
cg09541468	chr11	67211245	NA	CORO1B;CO	TSS1500;1stExon;5'UTR	
cg15784913	chr19	2900708	NA	ZNF57	TSS200	chr19:29003
cg13846866	chr3	37035399	NA	MLH1;MLH1;	5'UTR;Body;	chr3:370342
cg16141690	chr14	23563715	NA	C14orf119;A	TSS1500;Bod	chr14:23563
cg07599133	chr19	35068628	NA	LOC643719	TSS200	chr19:35068
cg26097210	chr10	70092729	NA	PBLD;HNRNP	TSS200;5'UT	chr10:70091
cg27151174	chr16	30367227	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg05123447	chr6	30955992	NA	MUC21	3'UTR	
cg11902539	chr5	1241183	NA	SLC6A18	Body	chr5:124244
cg18122606	chr6	31779728	NA	HSPA1L	Body	chr6:317828
cg11930197	chr1	232651427	NA	SIPA1L2	TSS200	
cg09149149	chr6	166401618	NA	LOC441177;	Body;TSS200	chr6:166401
cg02228804	chr6	27775720	rs200485	HIST1H2AI;H	TSS1500;TSS	chr6:277753
cg12686847	chr6	31779716	NA	HSPA1L	Body	chr6:317828
cg15284129	chr12	1928689	NA	LRTM2;LRTM	TSS1500;TSS1500;TSS150	
cg26183708	chr6	30955425	NA	MUC21	Body	
cg26884376	chr6	30539453	rs3132612	ABCF1;ABCF	Body;Body	chr6:305389
cg02989768	chr6	33266413	NA	RGL2;RGL2	5'UTR;Body	chr6:332663
cg20091959	chr20	42142451	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg03374922	chr13	111267935	NA	CARKD	TSS200	chr13:11126

cg04898719	chr1	52456918	NA	RAB3B	TSS1500	chr1:524559
cg21546671	chr17	46655387	NA	HOXB4	1stExon	chr17:46655
cg09777095	chr6	31779308	rs34372373	HSPA1L	Body	chr6:317828
cg12835342	chr11	67211379	NA	CORO1B;CO	TSS200;TSS1500	
cg26346875	chr6	31762719	NA	VARS	Body	chr6:317632
cg12169512	chr17	36831178	rs114805607	C17orf96;C1	5'UTR;1stExo	chr17:36829
cg18366150	chr10	70092816	NA	PBLD;HNRNP	TSS200;5'UT	chr10:70091
cg16448399	chr18	3880076	NA	DLGAP1;DLG	1stExon;5'UT	chr18:38792
cg03020891	chr6	30538179	rs9501023	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg26152485	chr19	19281474	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg03371609	chr8	52322171	NA	PXDNL	Body	chr8:523211
cg15118665	chr8	144451924	NA	RHPN1;C8orf	Body;TSS150	chr8:144450
cg03078400	chr6	31762644	NA	VARS	Body	chr6:317632
cg22230640	chr6	32805807	NA	TAP2;TAP2	Body;Body	chr6:328062
cg26693760	chr6	33267069	NA	RGL2;RGL2;R	5'UTR;Body;	chr6:332663
cg23231670	chr6	150346800	NA	RAET1L	TSS200	
cg16489447	chr11	67211128	NA	CORO1B;CO	TSS200;5'UTR	
cg09068086	chr2	110970204	NA	NCRNA0011	Body	chr2:110969
cg10661629	chr19	2900748	rs12981594	ZNF57	TSS200	chr19:29003
cg06717492	chr7	65447339	NA	GUSB	TSS200	chr7:654467
cg05906740	chr3	37035205	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg23658326	chr3	37034787	NA	EPM2AIP1;M	5'UTR;TSS15	chr3:370342
cg10640731	chr10	70092995	NA	PBLD;PBLD;H	TSS1500;TSS	chr10:70091
cg24305381	chr1	46769030	NA	LRRC41;LRRC	1stExon;5'UT	chr1:467674
cg01449677	chr17	76794888	NA	USP36	Body	chr17:76798
cg25843346	chr6	31762555	NA	VARS	Body	chr6:317632
cg03058556	chr6	33421509	rs2772386	ZBTB9	TSS1500	chr6:334220
cg05802514	chr4	1496822	rs73061861			chr4:149454
cg26422458	chr1	79472452	NA	ELTD1;ELTD1	5'UTR;1stExo	chr1:794722
cg14345497	chr17	46655603	NA	HOXB4	1stExon	chr17:46655
cg14363992	chr6	27776350	NA	HIST1H2AI;H	1stExon;TSS1	chr6:277778
cg02154252	chr1	79472532	rs115510932	ELTD1	TSS200	chr1:794722
cg10360552	chr20	42142766	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg00122254	chr1	46769320	NA	LRRC41;UQC	TSS1500;TSS	chr1:467674
cg02041435	chr13	111268673	rs330550	CARKD	Body	chr13:11126
cg10996201	chr6	33267358	NA	RGL2;RGL2	TSS200;TSS2	chr6:332663
cg21300993	chr2	237123218	NA	ASB18	Body	chr2:237123
cg27223805	chr11	2889616	NA			chr11:28903
cg10253022	chr22	19929467	NA	TXNRD2;CO	TSS200;5'UT	chr22:19929
cg08464208	chr6	27792307	NA			chr6:277917
cg01830271	chr6	31275148	rs74568989			chr6:312762
cg23609811	chr6	27100717	NA	HIST1H2BJ;H	TSS200;TSS2	chr6:271001
cg25140501	chr14	23564641	NA	ACIN1;ACIN1	5'UTR;5'UTR;	chr14:23563
cg04285443	chr6	27774969	NA	HIST1H2AI	TSS1500	chr6:277753
cg07064226	chr3	37034997	NA	MLH1;MLH1;	TSS1500;TSS	chr3:370342

cg10366439	chr2	110970249	NA	NCRNA0011	Body	chr2:110969
cg19520201	chr4	53588360	NA			chr4:535881
cg23870148	chr6	31763282	NA	VARS	5'UTR	chr6:317632
cg05861708	chr6	166400871	NA	C6orf176;C6	Body;Body;T	chr6:166401
cg08369943	chr20	42142005	rs6017097	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg03632172	chr16	30366690	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg14608180	chr9	139872839	NA	PTGDS	Body	chr9:139872
cg00292662	chr22	38071168	NA	LGALS1	TSS1500	chr22:38073
cg22694153	chr1	46768912	NA	LRRC41;UQC	1stExon;TSS1	chr1:467674
cg07657521	chr6	30539059	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg24213773	chr6	30419201	NA			chr6:304188
cg24687529	chr1	117529954	rs55948695	PTGFRN	3'UTR	
cg26146308	chr6	30851884	rs7757648	DDR1;DDR1;	TSS1500;1st	chr6:308521
cg23626798	chr20	42142494	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg09194159	chr17	46655588	NA	HOXB4	1stExon	chr17:46655
cg24623244	chr6	35109398	NA	TCP11;TCP11	TSS1500;TSS	chr6:351088
cg04199621	chr6	30955712	rs45486491	MUC21	Body	
cg15400532	chr6	27101279	NA	HIST1H2AG;	3'UTR;1stExo	chr6:271001
cg03497419	chr3	37034654	NA	EPM2AIP1;M	5'UTR;TSS15	chr3:370342
cg06893977	chr6	30851928	rs1264326	DDR1;DDR1	TSS1500;5'U	chr6:308521
cg21182196	chr14	95786801	NA	CLMN	TSS1500	chr14:95785
cg25977492	chr6	29365261	NA	OR12D2	1stExon	
cg03500771	chr6	30955950	rs2517416	MUC21	Body	
cg19811425	chr6	31778701	NA	HSPA1L	Body	chr6:317744
cg00349723	chr17	36831276	rs34455076	C17orf96	TSS200	chr17:36829
cg12806763	chr17	46655836	NA	HOXB4	TSS200	chr17:46654
cg02532030	chr6	33092494	rs3130227	HLA-DPB2	Body	
cg00222995	chr6	33421704	rs2274731	ZBTB9	TSS1500	chr6:334220
cg27586588	chr3	37034661	NA	EPM2AIP1;M	5'UTR;TSS15	chr3:370342
cg10046620	chr6	27775042	NA	HIST1H2AI	TSS1500	chr6:277753
cg24750920	chr6	33267354	NA	RGL2;RGL2	TSS200;TSS2	chr6:332663
cg05742354	chr1	10856609	NA	CASZ1;CASZ1	5'UTR;5'UTR	chr1:108538
cg12644888	chr6	29648360	rs365052			
cg05396178	chr6	27833129	NA	HIST1H2AL;H	1stExon;5'UT	chr6:278331
cg14026561	chr6	166401464	NA	LOC441177;	Body;Body;B	chr6:166401
cg05354971	chr2	91936984	NA			chr2:919368
cg03250220	chr2	110970097	NA	NCRNA0011	Body	chr2:110969
cg24899205	chr22	19929184	NA	TXNRD2;CO	Body;TSS200	chr22:19929
cg15038123	chr4	53588397	NA			chr4:535881
cg00245789	chr10	105128183	NA	TAF5	1stExon	chr10:10512
cg02506501	chr1	1228990	NA	ACAP3	Body	chr1:122878
cg02990567	chr6	33266961	NA	RGL2;RGL2;R	5'UTR;Body;	chr6:332663
cg19402991	chr2	164204915	NA			chr2:164204
cg18938469	chr14	23564120	NA	C14orf119;A	TSS1500;Bod	chr14:23563
cg00883712	chr16	30366293	NA	CD2BP2;CD2	5'UTR;TSS20	chr16:30366

cg01712686	chr1	235814419	NA	GNG4;GNG4;	TSS1500;TSS	chr1:235814
cg10706100	chr6	166401536	rs697475	LOC441177;	Body;TSS200	chr6:166401
cg22496683	chr4	155702610	NA	RBM46	5'UTR	chr4:155702
cg01505176	chr6	31763310	NA	VARS	5'UTR	chr6:317632
cg06961071	chr1	46769300	NA	LRRC41;UQC	TSS1500;TSS	chr1:467674
cg21330970	chr6	27100702	NA	HIST1H2BJ;H	TSS200;TSS2	chr6:271001
cg05116896	chr16	30366237	NA	CD2BP2;CD2	5'UTR;Body	chr16:30366
cg19981839	chr16	30366847	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg08628167	chr7	65447138	rs2279903	GUSB	1stExon	chr7:654467
cg03579738	chr19	2900714	NA	ZNF57	TSS200	chr19:29003
cg11418013	chr6	31763277	NA	VARS	5'UTR	chr6:317632
cg06118626	chr6	33267078	rs2282850	RGL2;RGL2;R	5'UTR;Body;	chr6:332663
cg01715949	chr17	36831197	rs189510768	C17orf96	TSS200	chr17:36829
cg03383695	chr1	232651092	NA	SIPA1L2;SIPA	1stExon;5'UTR	
cg27421308	chr10	70092824	NA	PBLD;HNRNP	TSS200;5'UT	chr10:70091
cg25592513	chr5	140729614	NA	PCDHGA2;PC	Body;Body;B	chr5:140731
cg05385119	chr6	30539063	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg01071811	chr20	42143080	NA	L3MBTL;L3M	5'UTR;1stExo	chr20:42143
cg12280168	chr19	2900884	rs10420989	ZNF57	TSS200	chr19:29003
cg11439192	chr6	32806182	NA	TAP2;TAP2	5'UTR;5'UTR	chr6:328062
cg11434705	chr19	1851995	NA			chr19:18515
cg03804148	chr17	1465813	rs142675143	PITPNA	Body	chr17:14651
cg15810744	chr11	67211300	NA	CORO1B;CO	TSS200;TSS1500	
cg04804565	chr6	31778779	NA	HSPA1L	Body	chr6:317744
cg24358465	chr6	27100860	NA	HIST1H2AG;	1stExon;TSS1	chr6:271001
cg23795623	chr13	111268031	NA	CARKD	1stExon	chr13:11126
cg24454695	chr1	235814326	NA	GNG4;GNG4;	TSS1500;TSS	chr1:235814
cg25702652	chr2	164204628	NA			chr2:164204
cg08870433	chr19	2900646	NA	ZNF57	TSS1500	chr19:29003
cg01800816	chr16	30366694	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg21460081	chr17	46656012	NA	HOXB4	TSS1500	chr17:46654
cg23911396	chr17	36831425	NA	C17orf96	TSS1500	chr17:36829
cg02341571	chr15	44968935	NA	PATL2	5'UTR	
cg11224603	chr3	37035282	NA	MLH1;MLH1;	1stExon;5'UT	chr3:370342
cg04264018	chr6	27100671	NA	HIST1H2BJ;H	TSS200;TSS2	chr6:271001
cg01360325	chr10	105127811	NA	TAF5	1stExon	chr10:10512
cg08334962	chr17	36831188	NA	C17orf96	TSS200	chr17:36829
cg26978691	chr10	105128013	NA	TAF5	1stExon	chr10:10512
cg24114154	chr17	46655829	NA	HOXB4	TSS200	chr17:46654
cg12252297	chr6	27833555	NA	HIST1H2AL;H	3'UTR;1stExo	chr6:278351
cg17753711	chr6	30539066	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg11668794	chr6	32805877	NA	TAP2;TAP2	Body;Body	chr6:328062
cg08312215	chr6	33266943	NA	RGL2;RGL2;R	5'UTR;Body;	chr6:332663
cg12851504	chr3	37035222	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg11600697	chr3	37034814	NA	EPM2AIP1;M	TSS200;TSS1	chr3:370342

cg08769356	chr7	65447249	rs2279904	GUSB;GUSB	5'UTR;1stExo	chr7:654467
cg13684918	chr6	33266881	NA	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg23268677	chr22	19929097	NA	TXNRD2;CO	Body;TSS200	chr22:19929
cg14166948	chr1	1099563	NA			chr1:109804
cg16735021	chr14	23564343	NA	C14orf119;A	TSS1500;1st	chr14:23563
cg09422355	chr19	48547158	rs61748769	CABP5	1stExon	
cg21368354	chr13	111267856	NA	CARKD	TSS200	chr13:11126
cg25837710	chr3	37035220	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg04585389	chr16	1486048	NA	CCDC154	Body	chr16:14870
cg06582202	chr11	2889886	NA	KCNQ1DN	TSS1500	chr11:28903
cg04977610	chr16	30366665	NA	CD2BP2;CD2	TSS1500;5'U	chr16:30366
cg23666180	chr6	27100115	rs41269245	HIST1H2AG;	TSS1500;3'U	chr6:271001
cg16792604	chr6	30539044	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg22093805	chr4	53588374	NA			chr4:535881
cg16433211	chr3	37034693	NA	EPM2AIP1;M	5'UTR;TSS15	chr3:370342
cg25588093	chr7	65447242	NA	GUSB;GUSB	5'UTR;1stExo	chr7:654467
cg22562040	chr6	33421819	rs41271245	ZBTB9	TSS1500	chr6:334220
cg09395540	chr6	31778719	NA	HSPA1L	Body	chr6:317744
cg16862791	chr20	42142596	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg03505443	chr6	33267087	rs2282850	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg19435409	chr6	27833121	NA	HIST1H2AL;H	1stExon;5'UT	chr6:278331
cg07101782	chr3	37034495	NA	MLH1;MLH1;	TSS1500;TSS	chr3:370342
cg06797938	chr17	1466136	rs147353202	PITPNA	TSS200	chr17:14651
cg11402700	chr13	111267793	rs74971770	CARKD	TSS1500	chr13:11126
cg26469597	chr16	30366960	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg01761968	chr12	130824831	rs77078301	PIWIL1	5'UTR	chr12:13082
cg01606310	chr6	33266703	NA	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg09867046	chr6	27833050	NA	HIST1H2AL	TSS200	chr6:278331
cg09081266	chr6	29365287	rs2073150	OR12D2	1stExon	
cg02422694	chr17	46655790	rs143310387	HOXB4	TSS200	chr17:46654
cg08474826	chr1	1099630	NA			chr1:109804
cg12119313	chr6	33266931	NA	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg27572120	chr6	30419551	rs9295885			chr6:304188
cg03542248	chr6	33266907	NA	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg13840194	chr1	10856202	NA	CASZ1;CASZ1	5'UTR;5'UTR	chr1:108538
cg21915639	chr1	46769308	NA	LRRC41;UQC	TSS1500;TSS	chr1:467674
cg09601882	chr6	28834502	NA			chr6:288316
cg15156844	chr18	3880020	NA	DLGAP1	1stExon	chr18:38792
cg09301114	chr6	33266964	rs73410003	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg17070338	chr13	111268441	NA	CARKD	Body	chr13:11126
cg08984686	chr6	33267143	NA	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg00002406	chr16	30366435	NA	CD2BP2;CD2	5'UTR;TSS20	chr16:30366
cg11337053	chr1	232651485	NA	SIPA1L2	TSS1500	
cg15565065	chr17	46655476	NA	HOXB4	1stExon	chr17:46655
cg04979706	chr6	33421902	NA	ZBTB9	TSS1500	chr6:334220

cg26585845	chr17	36831195	rs189510768	C17orf96	TSS200	chr17:36829
cg00867446	chr14	23564668	NA	ACIN1;ACIN1	5'UTR;5'UTR;	chr14:23563
cg11247116	chr6	31763377	NA	VARS;VARS	1stExon;5'UT	chr6:317632
cg08410921	chr6	27100831	NA	HIST1H2AG;	1stExon;5'UT	chr6:271001
cg07059148	chr17	36831255	rs34455076	C17orf96	TSS200	chr17:36829
cg06424719	chr10	70093223	NA	PBLD;PBLD;H	TSS1500;TSS	chr10:70091
cg09739036	chr11	67211315	NA	CORO1B;COF	TSS200;TSS1500	
cg14853467	chr6	33422102	NA	ZBTB9	TSS1500	chr6:334220
cg11796507	chr6	27833095	NA	HIST1H2AL	TSS200	chr6:278331
cg01614643	chr6	30124769	NA	TRIM10;TRI	Body;Body	
cg02779707	chr6	32806196	NA	TAP2;TAP2	5'UTR;5'UTR	chr6:328062
cg23657870	chr6	30539005	NA	ABCF1;ABCF1	TSS200;TSS2	chr6:305389
cg21600850	chr6	166401598	NA	LOC441177;	Body;TSS200	chr6:166401
cg16279775	chr7	65447418	NA	GUSB	TSS200	chr7:654467
cg04984575	chr20	42142673	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg24663490	chr6	27832932	NA	HIST1H2AL	TSS200	chr6:278331
cg25803423	chr14	23563820	NA	C14orf119;A	TSS1500;Bod	chr14:23563
cg06414921	chr6	31276504	rs28367688			chr6:312762
cg04958658	chr20	35421865	NA	C20orf117;C	Body;Body	chr20:35422
cg27213157	chr6	33266969	rs73410003	RGL2;RGL2;R	5'UTR;Body;1	chr6:332663
cg17621259	chr3	37035168	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg24836204	chr8	144450966	NA	RHPN1;C8orf	TSS200;TSS2	chr8:144450
cg10156941	chr17	1466296	NA	PITPNA	TSS200	chr17:14651
cg07015911	chr17	46655580	NA	HOXB4	1stExon	chr17:46655
cg23408670	chr17	36831499	NA	C17orf96	TSS1500	chr17:36829
cg18825927	chr11	67211308	NA	CORO1B;COF	TSS200;TSS1500	
cg02205391	chr6	31762409	NA	VARS	Body	chr6:317632
cg08022281	chr6	29648345	rs2747429			
cg07265873	chr6	30851940	rs7757648	DDR1;DDR1	TSS1500;5'U	chr6:308521
cg10592690	chr1	46769564	NA	LRRC41;UQC	TSS1500;Bod	chr1:467674
cg16988810	chr6	31762650	NA	VARS	Body	chr6:317632
cg12090052	chr6	35109435	NA	TCP11;TCP11	TSS1500;TSS	chr6:351088
cg01870456	chr13	111267991	NA	CARKD	TSS200	chr13:11126
cg14671526	chr3	37035200	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg18833958	chr6	33421468	NA	ZBTB9	TSS1500	chr6:334220
cg04876474	chr11	2890091	NA	KCNQ1DN	TSS1500	chr11:28903
cg08089301	chr17	46655561	NA	HOXB4	1stExon	chr17:46655
cg19326232	chr6	33422095	NA	ZBTB9	TSS1500	chr6:334220
cg19081437	chr17	46655796	rs143310387	HOXB4	TSS200	chr17:46654
cg00465975	chr22	19929557	rs3788319	TXNRD2;CON	TSS200;5'UT	chr22:19929
cg02611812	chr6	30955412	NA	MUC21	Body	
cg06108510	chr3	37035063	NA	MLH1;MLH1;	TSS1500;TSS	chr3:370342
cg23001000	chr6	30852307	NA	DDR1;DDR1	TSS200;5'UT	chr6:308521
cg12670305	chr6	31762630	NA	VARS	Body	chr6:317632
cg17184952	chr6	31763373	NA	VARS;VARS	1stExon;5'UT	chr6:317632

cg02465374	chr6	166401700	NA	LOC441177;	Body;TSS200	chr6:166401
cg20185617	chr1	1099651	NA			chr1:109804
cg25713684	chr10	105127687	NA	TAF5	TSS200	chr10:10512
cg08167286	chr6	31779529	NA	HSPA1L	Body	chr6:317828
cg19855366	chr13	111267979	NA	CARKD	TSS200	chr13:11126
cg00550080	chr6	30124792	NA	TRIM10;TRI	Body;Body	
cg10088320	chr6	32805759	NA	TAP2;TAP2	Body;Body	chr6:328062
cg06952307	chr17	47287974	NA	ABI3;GNGT2;	5'UTR;TSS1500;5'UTR;1stE	
cg09502511	chr6	30539237	NA	ABCF1;ABCF	5'UTR;5'UTR;	chr6:305389
cg13792528	chr6	28834507	NA			chr6:288316
cg20050761	chr7	130131923	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg10076931	chr6	27100556	NA	HIST1H2AG;	TSS1500;5'U	chr6:271001
cg23036136	chr6	30955979	NA	MUC21	3'UTR	
cg01787834	chr6	31762723	NA	VARS	Body	chr6:317632
cg13372743	chr8	52322134	NA	PXDNL	Body	chr8:523211
cg18586343	chr10	105127615	rs10883857	TAF5	TSS200	chr10:10512
cg10114372	chr6	31763312	NA	VARS	5'UTR	chr6:317632
cg11394653	chr6	31763370	NA	VARS;VARS	1stExon;5'UT	chr6:317632
cg10470808	chr6	30852092	NA	DDR1;DDR1	TSS1500;5'U	chr6:308521
cg14723918	chr6	31763435	NA	VARS;VARS	1stExon;5'UT	chr6:317632
cg18302582	chr14	95786029	NA	CLMN	Body	chr14:95785
cg02443816	chr2	97220858	NA			
cg11667101	chr10	105127581	NA	TAF5	TSS200	chr10:10512
cg14466680	chr6	33267268	NA	RGL2;RGL2	TSS200;TSS2	chr6:332663
cg22118082	chr6	30124647	rs114536811	TRIM10;TRI	Body;Body	
cg00909847	chr2	133038927	NA			
cg21227785	chr6	30539077	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg23051411	chr2	237123571	NA	ASB18	Body	chr2:237123
cg13057174	chr1	10857091	NA	CASZ1;CASZ1	TSS1500;TSS	chr1:108538
cg25786333	chr6	29364799	rs2073152	OR12D2	1stExon	
cg08835221	chr22	38071607	NA	LGALS1	TSS200	chr22:38073
cg11715943	chr6	33091841	rs9277730	HLA-DPB2	Body	
cg01530101	chr11	2891098	NA	KCNQ1DN	TSS200	chr11:28903
cg12251145	chr6	30124744	rs114536811	TRIM10;TRI	Body;Body	
cg27618777	chr6	32804628	NA	TAP2;TAP2	Body;Body	chr6:328062
cg18312812	chr19	2900898	rs10420989	ZNF57;ZNF5	5'UTR;1stExo	chr19:29003
cg18274559	chr6	31762685	NA	VARS	Body	chr6:317632
cg13973620	chr6	33266652	NA	RGL2;RGL2;R	5'UTR;Body;	chr6:332663
cg16244711	chr1	232651277	NA	SIPA1L2	TSS200	
cg06251929	chr6	30539459	rs3132612	ABCF1;ABCF	Body;Body	chr6:305389
cg21325631	chr6	31778784	NA	HSPA1L	Body	chr6:317744
cg08734637	chr7	130131189	rs3807138	MESTIT1;ME	TSS200;TSS1	chr7:130130
cg14489632	chr12	130824328	NA	PIWIL1	5'UTR	chr12:13082
cg02537149	chr1	46769035	NA	LRRC41;LRRC	1stExon;5'UT	chr1:467674
cg17810098	chr22	19929066	NA	TXNRD2;CO	Body;TSS200	chr22:19929

cg02533422	chr6	30419051	rs11753256			chr6:304188
cg08026039	chr16	1486384	rs909974	CCDC154	Body	chr16:14870
cg12846737	chr6	31276088	rs4544954			chr6:312762
cg05729731	chr6	32805962	NA	TAP2;TAP2	Body;Body	chr6:328062
cg04484826	chr6	31779582	NA	HSPA1L	Body	chr6:317828
cg10769891	chr3	37034730	NA	EPM2AIP1;M	5'UTR;TSS15	chr3:370342
cg16317730	chr6	30539486	rs3132612	ABCF1;ABCF	Body;Body	chr6:305389
cg06860277	chr22	19930072	rs737865	COMT;TXNR	5'UTR;TSS15	chr22:19929
cg21073350	chr5	140729813	NA	PCDHGA2;PC	Body;TSS200	chr5:140731
cg17026072	chr1	1229790	NA	ACAP3	Body	chr1:122878
cg18592365	chr1	79472536	rs115510932	ELTD1	TSS200	chr1:794722
cg16537676	chr6	30851624	rs74689782	DDR1;DDR1	TSS1500;TSS	chr6:308521
cg00856580	chr1	52456669	NA	RAB3B	TSS1500	chr1:524559
cg00599401	chr6	30538989	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg22533573	chr11	32452771	NA	WT1;WT1;W	Body;Body;B	chr11:32452
cg14340074	chr6	33266407	NA	RGL2;RGL2	5'UTR;Body	chr6:332663
cg17641046	chr3	37034473	NA	MLH1;MLH1;	TSS1500;TSS	chr3:370342
cg02817123	chr6	27775750	NA	HIST1H2AI;H	TSS1500;TSS	chr6:277753
cg12558012	chr19	19281197	rs1858846	LOC729991-	Body;5'UTR;	chr19:19280
cg26327071	chr17	46655818	NA	HOXB4	TSS200	chr17:46654
cg00142150	chr22	38071001	rs4820294	LGALS1	TSS1500	chr22:38073
cg07355926	chr19	1852127	rs11880925			chr19:18515
cg17664233	chr6	33092513	rs3129277	HLA-DPB2	Body	
cg03343730	chr1	46769302	NA	LRRC41;UQC	TSS1500;TSS	chr1:467674
cg12858693	chr6	150346886	NA	RAET1L	TSS1500	
cg01726393	chr19	19281461	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg04515200	chr5	135415762	NA			chr5:135416
cg14088957	chr7	130131085	NA	MESTIT1;ME	TSS200;TSS1	chr7:130130
cg21771891	chr6	27782126	NA	HIST1H2AJ;H	1stExon;TSS1	chr6:277822
cg04504578	chr17	36831313	NA	C17orf96	TSS200	chr17:36829
cg00940261	chr14	95786011	NA	CLMN	Body	chr14:95785
cg02197677	chr6	30539092	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg25940949	chr6	33267289	NA	RGL2;RGL2	TSS200;TSS2	chr6:332663
cg27331401	chr3	37035207	NA	MLH1;MLH1;	TSS200;Body	chr3:370342
cg20724405	chr6	32805960	NA	TAP2;TAP2	Body;Body	chr6:328062
cg12607514	chr6	33422080	NA	ZBTB9	TSS1500	chr6:334220
cg05936555	chr6	30539508	NA	ABCF1;ABCF	Body;Body	chr6:305389
cg04867406	chr11	67211057	NA	CORO1B;CO	TSS200;5'UTR	
cg16128363	chr18	3880558	NA	DLGAP1	TSS1500	chr18:38792
cg21790626	chr19	58220494	NA	ZNF154;ZNF1	5'UTR;1stExo	chr19:58220
cg08119607	chr6	150347053	rs76959132	RAET1L	TSS1500	
cg09892131	chr6	33422028	NA	ZBTB9	TSS1500	chr6:334220
cg11195444	chr6	33266070	NA	RGL2;RGL2	Body;Body	chr6:332663
cg06874426	chr17	47287526	NA	ABI3;GNGT2;	TSS200;TSS1500;TSS200	
cg03869874	chr13	111267849	NA	CARKD	TSS200	chr13:11126

cg20392088	chr4	6384347	NA	PPP2R2C;PP	Body;TSS150	chr4:638023
cg00893636	chr3	37034840	NA	EPM2AIP1;M	TSS200;TSS1	chr3:370342
cg26465391	chr19	58220773	NA	ZNF154	TSS200	chr19:58220
cg18630363	chr6	30955382	rs2844677	MUC21	Body	
cg10587741	chr22	38071170	NA	LGALS1	TSS1500	chr22:38073
cg27088830	chr6	166401018	NA	C6orf176;C6	Body;Body;T	chr6:166401
cg06241803	chr6	30538984	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg19540702	chr19	19281175	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg20212336	chr13	111268714	NA	CARKD	Body	chr13:11126
cg17165311	chr17	1466280	rs137984928	PITPNA	TSS200	chr17:14651
cg16498314	chr16	30366841	NA	CD2BP2;CD2	TSS1500;TSS	chr16:30366
cg03270204	chr6	30851638	rs73727107	DDR1;DDR1	TSS1500;TSS	chr6:308521
cg03026929	chr6	32806028	NA	TAP2;TAP2	5'UTR;5'UTR	chr6:328062
cg26598649	chr18	3880086	NA	DLGAP1;DLG	1stExon;5'UT	chr18:38792
cg17250082	chr6	31275875	rs1634760			chr6:312762
cg26484464	chr6	30537886	NA	ABCF1;ABCF	TSS1500;TSS	chr6:305389
cg24446071	chr19	19281270	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg10035607	chr16	30366449	NA	CD2BP2;CD2	5'UTR;TSS20	chr16:30366
cg15414745	chr6	74064047	rs185614200	DPPA5	TSS200	chr6:740635
cg21490561	chr3	37034825	NA	EPM2AIP1;M	TSS200;TSS1	chr3:370342
cg16783571	chr6	74064594	NA	DPPA5	TSS1500	chr6:740635
cg26122012	chr8	144450933	NA	RHPN1;C8orf	TSS200;TSS2	chr8:144450
cg03192963	chr3	37034909	NA	EPM2AIP1;M	TSS200;TSS1	chr3:370342
cg11988591	chr8	144451909	NA	RHPN1;C8orf	Body;TSS150	chr8:144450
cg25255679	chr8	144450942	NA	RHPN1;C8orf	TSS200;TSS2	chr8:144450
cg18732587	chr10	105127670	NA	TAF5	TSS200	chr10:10512
cg26404748	chr14	23564693	NA	ACIN1;ACIN1	5'UTR;5'UTR;	chr14:23563
cg12428738	chr6	33267392	NA	RGL2;RGL2	TSS1500;TSS	chr6:332663
cg12422930	chr6	31763285	NA	VARS	5'UTR	chr6:317632
cg18059012	chr15	44969129	NA	PATL2	TSS200	
cg09998591	chr11	2891402	NA	KCNQ1DN	Body	chr11:28903
cg26343883	chr2	164205032	NA			chr2:164204
cg17091610	chr20	42142484	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg24985459	chr3	37035090	NA	MLH1;MLH1;	TSS200;TSS2	chr3:370342
cg01402735	chr1	79472558	NA	ELTD1	TSS200	chr1:794722
cg11978884	chr5	135415819	rs34577747			chr5:135416
cg25478600	chr11	2890605	NA	KCNQ1DN	TSS1500	chr11:28903
cg20297423	chr7	130131138	NA	MESTIT1;ME	TSS200;TSS1	chr7:130130
cg15174905	chr19	19281255	rs759999	LOC729991-	Body;5'UTR;	chr19:19280
cg03239591	chr6	30539540	NA	ABCF1;ABCF	Body;Body	chr6:305389
cg14177328	chr4	53588850	NA			chr4:535881
cg26260794	chr6	32806022	NA	TAP2;TAP2	5'UTR;5'UTR	chr6:328062
cg06771056	chr6	32805223	rs56145201	TAP2;TAP2	Body;Body	chr6:328062
cg03026524	chr6	28834480	NA			chr6:288316
cg22993154	chr6	31276653	rs115456947			chr6:312762

cg09003373	chr7	130130995	NA	MESTIT1;ME	Body;TSS150	chr7:130130
cg20252111	chr20	42143211	NA	L3MBTL;L3M	1stExon;1stE	chr20:42143
cg05984845	chr6	30124942	NA	TRIM10;TRI	Body;Body	
cg09080913	chr7	130131887	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg08668790	chr19	58220662	NA	ZNF154	TSS200	chr19:58220
cg04117396	chr17	76795028	NA	USP36	Body	chr17:76798
cg09706029	chr6	33266089	NA	RGL2;RGL2	Body;Body	chr6:332663
cg19208331	chr3	37035345	NA	MLH1;MLH1;	1stExon;5'UT	chr3:370342
cg12254291	chr6	166400936	NA	C6orf176;C6	Body;Body;T	chr6:166401
cg08090385	chr1	1099583	NA			chr1:109804
cg07546106	chr6	32806236	NA	TAP2;TAP2	5'UTR;5'UTR	chr6:328062
cg07579404	chr6	150346721	rs1544123	RAET1L	TSS200	
cg20898522	chr6	32806156	rs2071544	TAP2;TAP2	5'UTR;5'UTR	chr6:328062
cg11955762	chr13	111268705	NA	CARKD	Body	chr13:11126
cg16574737	chr5	140730469	NA	PCDHGB1;PC	1stExon;Body	chr5:140731
cg01921382	chr5	1241848	NA	SLC6A18	Body	chr5:124244
cg23560159	chr6	32805748	NA	TAP2;TAP2	Body;Body	chr6:328062
cg03947814	chr11	2890419	NA	KCNQ1DN	TSS1500	chr11:28903
cg12790037	chr3	37035117	NA	MLH1;MLH1;	TSS200;TSS2	chr3:370342
cg05661282	chr19	58220370	NA	ZNF154;ZNF1	5'UTR;1stExo	chr19:58220
cg25299750	chr6	35109124	rs78614904	TCP11;TCP11	5'UTR;1stExo	chr6:351088
cg12078775	chr6	30419543	rs9295885			chr6:304188
cg17910470	chr17	76795278	rs74001255	USP36	Body	chr17:76798
cg18512930	chr4	1496880	rs62286822			chr4:149454
cg18370200	chr6	33267248	NA	RGL2;RGL2	TSS200;TSS2	chr6:332663
cg25762195	chr8	144450925	NA	RHPN1;C8orf	TSS200;TSS2	chr8:144450
cg04714201	chr6	30538986	NA	ABCF1;ABCF	TSS200;TSS2	chr6:305389
cg27057652	chr8	52322137	NA	PXDNL	Body	chr8:523211
cg21351768	chr6	33421913	NA	ZBTB9	TSS1500	chr6:334220
cg19093782	chr2	242904793	rs114993155			
cg09027493	chr6	35109548	NA	TCP11;TCP11	TSS1500;TSS	chr6:351088
cg22675922	chr11	2889840	NA	KCNQ1DN	TSS1500	chr11:28903
cg13159388	chr8	144451643	NA	RHPN1;C8orf	Body;TSS150	chr8:144450
cg18052665	chr6	74064140	rs62440583	DPPA5	TSS200	chr6:740635
cg26601317	chr11	2890575	NA	KCNQ1DN	TSS1500	chr11:28903
cg05369791	chr7	130131146	NA	MESTIT1;ME	TSS200;TSS1	chr7:130130
cg10397774	chr8	144451413	rs62524011	RHPN1;C8orf	Body;TSS150	chr8:144450
cg22660147	chr17	46656093	NA	HOXB4	TSS1500	chr17:46654
cg19221044	chr6	32806167	rs2071544	TAP2;TAP2	5'UTR;5'UTR	chr6:328062
cg08207377	chr19	19281140	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg09514717	chr6	31763318	NA	VARS	5'UTR	chr6:317632
cg17880703	chr19	2900938	NA	ZNF57;ZNF57	5'UTR;1stExo	chr19:29003
cg25266281	chr2	242904768	rs114993155			
cg12378817	chr10	133961235	NA	JAKMIP3	Body	
cg06100421	chr7	130131136	NA	MESTIT1;ME	TSS200;TSS1	chr7:130130

cg27590105	chr6	150346816	NA	RAET1L	TSS200	
cg14099468	chr1	235814814	NA	GNG4;GNG4	TSS1500;TSS	chr1:235811
cg27049766	chr19	58220516	NA	ZNF154;ZNF1	5'UTR;1stExo	chr19:58220
cg27338480	chr7	130131885	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg16289417	chr6	166400665	NA	C6orf176;C6	Body;Body;T	chr6:166401
cg00269553	chr8	52321814	NA	PXDNL	Body	chr8:523211
cg05763097	chr14	103569340	rs76657117	C14orf73	Body	chr14:10356
cg06791151	chr3	37034956	NA	EPM2AIP1;M	TSS200;TSS1	chr3:370342
cg07007778	chr13	111268017	NA	CARKD;CARK	5'UTR;1stExo	chr13:11126
cg13900773	chr12	130824015	NA	PIWIL1	5'UTR	chr12:13082
cg20743065	chr4	53588673	NA			chr4:535881
cg03877020	chr6	31762680	NA	VARS	Body	chr6:317632
cg01879039	chr1	52456656	NA	RAB3B	TSS1500	chr1:524559
cg11546621	chr9	139872161	NA	PTGDS	Body	chr9:139872
cg01937247	chr1	1229534	NA	ACAP3	Body	chr1:122878
cg21396998	chr6	32806006	NA	TAP2;TAP2	Body;Body	chr6:328062
cg25855592	chr4	1496293	NA			chr4:149454
cg20529070	chr20	42142751	NA	L3MBTL;L3M	TSS1500;TSS	chr20:42143
cg08771706	chr11	2890394	NA	KCNQ1DN	TSS1500	chr11:28903
cg27075939	chr13	111268702	NA	CARKD	Body	chr13:11126
cg00137234	chr4	155703138	NA	RBM46	5'UTR	chr4:155702
cg05716556	chr17	47287410	NA	ABI3;GNGT2;	TSS200;TSS1500;TSS200	
cg20692059	chr14	23563979	NA	C14orf119;A	TSS1500;Bod	chr14:23563
cg21646955	chr6	35108921	NA	TCP11;TCP11	Body;5'UTR	chr6:351088
cg22407458	chr6	35109121	rs78614904	TCP11;TCP11	5'UTR;1stExo	chr6:351088
cg15282732	chr6	150346863	NA	RAET1L	TSS200	
cg23008562	chr11	2891065	NA	KCNQ1DN	TSS200	chr11:28903
cg15414773	chr1	1100360	NA			chr1:109804
cg13885561	chr11	2890389	NA	KCNQ1DN	TSS1500	chr11:28903
cg19853760	chr22	38071677	NA	LGALS1;LGAL	1stExon;5'UT	chr22:38073
cg02929209	chr4	53588595	NA			chr4:535881
cg01647795	chr15	44969244	rs78276255	PATL2	TSS200	
cg14706162	chr4	1496411	rs73061856			chr4:149454
cg03983364	chr7	101272096	rs73415222	MYL10	Body	
cg17390106	chr6	32804555	NA	TAP2;TAP2	Body;Body	chr6:328062
cg03142586	chr19	58220080	NA	ZNF154	Body	chr19:58220
cg03876424	chr14	103569948	NA	C14orf73	Body	chr14:10356
cg05316463	chr14	95786663	rs114506181	CLMN	TSS1500	chr14:95785
cg27338957	chr6	33267265	NA	RGL2;RGL2	TSS200;TSS2	chr6:332663
cg15207422	chr19	19280969	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg02667348	chr16	88540992	NA	ZFPM1	Body	chr16:88539
cg26658272	chr5	1241765	NA	SLC6A18	Body	chr5:124244
cg01833923	chr17	47286719	NA	GNGT2;ABI3;	1stExon;TSS1500;TSS1500	
cg13104298	chr7	130131905	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg25203481	chr11	2891082	NA	KCNQ1DN	TSS200	chr11:28903

cg12699433	chr20	42142897	NA	L3MBTL;L3M	TSS200;TSS2	chr20:42143
cg04709900	chr2	97220393	NA			
cg09932405	chr2	121107495	NA	INHBB	3'UTR	chr2:121106
cg04319873	chr2	164205343	NA			chr2:164204
cg04255770	chr6	32804677	rs17583244	TAP2;TAP2	Body;Body	chr6:328062
cg10781814	chr19	19281559	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg24143221	chr6	31780526	NA	HSPA1L	5'UTR	chr6:317828
cg06212135	chr7	130131826	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg20073313	chr8	52322009	NA	PXDNL	Body	chr8:523211
cg27324426	chr19	58220837	NA	ZNF154	TSS1500	chr19:58220
cg08373989	chr6	31780239	NA	HSPA1L	5'UTR	chr6:317828
cg02145102	chr6	31276418	rs17192631			chr6:312762
cg04457979	chr11	2890647	NA	KCNQ1DN	TSS1500	chr11:28903
cg06778024	chr16	89408567	rs75540348	ANKRD11	5'UTR	chr16:89408
cg22705386	chr7	130131797	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg03438552	chr6	32805548	NA	TAP2;TAP2	Body;Body	chr6:328062
cg19550904	chr14	103569127	NA	C14orf73	Body	chr14:10356
cg05029822	chr11	2891118	NA	KCNQ1DN	TSS200	chr11:28903
cg00980784	chr17	47287577	NA	ABI3;GNGT2;	TSS200;TSS1500;TSS200	
cg03769055	chr6	30124804	NA	TRIM10;TRI	Body;Body	
cg27417677	chr7	130130918	NA	MESTIT1;ME	Body;TSS150	chr7:130130
cg24696183	chr11	2891360	NA	KCNQ1DN	Body	chr11:28903
cg22940798	chr6	32805554	NA	TAP2;TAP2	Body;Body	chr6:328062
cg23973272	chr8	52322169	NA	PXDNL	Body	chr8:523211
cg01208224	chr4	6383645	NA	PPP2R2C;PP	TSS200;Body	chr4:638023
cg12198813	chr11	2891077	NA	KCNQ1DN	TSS200	chr11:28903
cg27547543	chr6	31148524	NA			chr6:311483
cg20362817	chr6	30124687	rs115594810	TRIM10;TRI	Body;Body	
cg22960869	chr17	47287521	NA	ABI3;GNGT2;	TSS200;TSS1500;TSS200	
cg04251368	chr11	2890587	NA	KCNQ1DN	TSS1500	chr11:28903
cg06372850	chr2	164205188	NA			chr2:164204
cg20250981	chr11	2890644	NA	KCNQ1DN	TSS1500	chr11:28903
cg04953552	chr6	31276212	rs1634758			chr6:312762
cg21143587	chr14	103569397	NA	C14orf73	Body	chr14:10356
cg27513667	chr16	89408403	rs179504	ANKRD11	5'UTR	chr16:89408
cg17839611	chr17	47286802	NA	ABI3;ABI3;G	TSS1500;TSS1500;TSS200	
cg25451120	chr17	47287444	NA	ABI3;GNGT2;	TSS200;TSS1500;TSS200	
cg02611863	chr20	42143096	NA	L3MBTL;L3M	5'UTR;1stExo	chr20:42143
cg10249538	chr7	130131829	NA	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg09304357	chr2	97220596	NA			
cg13081704	chr11	2890457	NA	KCNQ1DN	TSS1500	chr11:28903
cg21667116	chr7	130131359	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg11708721	chr1	117530009	rs55948695	PTGFRN	3'UTR	
cg07592963	chr11	2890649	NA	KCNQ1DN	TSS1500	chr11:28903
cg11294513	chr19	58220295	NA	ZNF154	Body	chr19:58220

cg06478886	chr5	135416029	NA			chr5:135416
cg09554951	chr11	2890725	NA	KCNQ1DN	TSS1500	chr11:28903
cg23156962	chr7	130131367	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg24780501	chr11	2890450	NA	KCNQ1DN	TSS1500	chr11:28903
cg13563634	chr6	32805684	NA	TAP2;TAP2	Body;Body	chr6:328062
cg19340941	chr4	155702931	NA	RBM46	5'UTR	chr4:155702
cg19602728	chr4	1496334	rs73061856			chr4:149454
cg15937641	chr1	117529619	NA	PTGFRN	3'UTR	
cg21629528	chr7	130131921	rs116603785	MEST;MEST;	5'UTR;TSS20	chr7:130130
cg06797389	chr15	44969481	NA	PATL2	TSS1500	
cg10300188	chr11	2890577	NA	KCNQ1DN	TSS1500	chr11:28903
cg09357589	chr6	31148552	NA			chr6:311483
cg01107178	chr16	89408248	NA	ANKRD11	5'UTR	chr16:89408
cg03234186	chr19	58220657	NA	ZNF154	TSS200	chr19:58220
cg04786207	chr7	130131691	rs73724326	MEST;MEST;	TSS1500;5'U	chr7:130130
cg01268824	chr19	58220818	NA	ZNF154	TSS1500	chr19:58220
cg25629418	chr12	1929265	NA	LRTM2;LRTM	TSS200;TSS200;Body;TSS2	
cg26685246	chr6	32805692	NA	TAP2;TAP2	Body;Body	chr6:328062
cg08246619	chr11	2890454	NA	KCNQ1DN	TSS1500	chr11:28903
cg12506930	chr19	58220718	NA	ZNF154	TSS200	chr19:58220
cg26818629	chr6	31148516	NA			chr6:311483
cg26502817	chr6	31779953	NA	HSPA1L	5'UTR	chr6:317828
cg26334023	chr17	47287492	NA	ABI3;GNGT2;	TSS200;TSS1500;TSS200	
cg14582642	chr11	2890319	NA	KCNQ1DN	TSS1500	chr11:28903
cg02646491	chr11	2890710	rs7114157	KCNQ1DN	TSS1500	chr11:28903
cg15330298	chr20	42143174	NA	L3MBTL;L3M	5'UTR;1stExo	chr20:42143
cg09502866	chr11	2890473	NA	KCNQ1DN	TSS1500	chr11:28903
cg11805138	chr6	31148332	rs115103823			chr6:311483
cg12854186	chr6	32805398	rs56115039	TAP2;TAP2	Body;Body	chr6:328062
cg26504305	chr19	19281019	NA	LOC729991-	Body;5'UTR;	chr19:19280
cg21753226	chr11	2890668	rs7114157	KCNQ1DN	TSS1500	chr11:28903
cg06818047	chr1	1229105	rs7552099	ACAP3	Body	chr1:122878
cg23331653	chr12	1929348	NA	LRTM2;LRTM	TSS200;TSS200;Body;TSS2	
cg04678950	chr7	130131403	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg19386484	chr7	130131709	NA	MEST;MEST;	TSS1500;5'U	chr7:130130
cg18797653	chr5	135416613	NA	MIR886	TSS1500	chr5:135415
cg16615357	chr5	135416594	NA	MIR886	TSS1500	chr5:135415
cg12821804	chr11	2890705	rs7114157	KCNQ1DN	TSS1500	chr11:28903
cg11608150	chr5	135415948	NA			chr5:135416
cg17239974	chr11	2890629	NA	KCNQ1DN	TSS1500	chr11:28903
cg26457809	chr11	2890617	NA	KCNQ1DN	TSS1500	chr11:28903
cg12347392	chr7	130131676	rs73724326	MEST;MEST;	TSS1500;5'U	chr7:130130
cg26738614	chr12	1929588	NA	LRTM2;LRTM	1stExon;5'UTR;1stExon;5'	
cg08745965	chr5	135416529	rs9327740	MIR886	TSS1500	chr5:135415
cg08762424	chr6	31275881	rs1634760			chr6:312762

cg21746969	chr12	1929551	rs139835495	LRTM2;LRTM	1stExon;5'UTR;1stExon;5'U	
cg04481923	chr5	135416205	NA	MIR886	Body	chr5:135416
cg01515136	chr1	1229589	NA	ACAP3	Body	chr1:122878
cg26896946	chr5	135416405	NA	MIR886	TSS200	chr5:135416
cg25340688	chr5	135416398	NA	MIR886	TSS200	chr5:135416
cg06536614	chr5	135416381	NA	MIR886	TSS200	chr5:135416
cg00124993	chr5	135416412	NA	MIR886	TSS200	chr5:135416
cg18678645	chr5	135416331	NA	MIR886	TSS200	chr5:135416
cg22389375	chr11	2890670	rs7114157	KCNQ1DN	TSS1500	chr11:28903
cg07158503	chr5	135415693	NA			chr5:135416
cg26328633	chr5	135416394	NA	MIR886	TSS200	chr5:135416
cg23252259	chr6	31148612	rs6937752			chr6:311483
cg05290058	chr11	2890551	NA	KCNQ1DN	TSS1500	chr11:28903

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Group A mean	Group B mean	Group C mean	)ifference A-	ifference A-	Difference B-
0.262	**0.316**	**0.329**	-0.067	-0.054	-0.012
0.620	**0.670**	**0.679**	-0.059	-0.050	-0.009
0.222	**0.259**	**0.273**	-0.051	-0.038	-0.014
0.586	**0.621**	**0.636**	-0.050	-0.035	-0.015
0.580	**0.530**	**0.630**	-0.049	0.050	-0.099
0.522	**0.485**	**0.570**	-0.047	0.038	-0.085
0.206	**0.239**	**0.250**	-0.044	-0.033	-0.011
0.728	**0.662**	**0.767**	-0.039	0.067	-0.106
0.777	**0.718**	**0.814**	-0.037	0.059	-0.096
0.787	**0.804**	**0.823**	-0.037	-0.017	-0.019
0.644	**0.595**	**0.680**	-0.035	0.050	-0.085
0.649	**0.676**	**0.683**	-0.034	-0.027	-0.008
0.743	**0.677**	**0.778**	-0.034	0.066	-0.100
0.685	**0.623**	**0.718**	-0.034	0.062	-0.096
0.720	**0.663**	**0.754**	-0.034	0.058	-0.092
0.592	**0.608**	**0.625**	-0.033	-0.016	-0.017
0.398	**0.426**	**0.430**	-0.032	-0.028	-0.004
0.630	**0.571**	**0.661**	-0.032	0.059	-0.091
0.722	**0.744**	**0.753**	-0.031	-0.022	-0.009
0.826	**0.850**	**0.856**	-0.030	-0.024	-0.006
0.671	**0.675**	**0.699**	-0.028	-0.004	-0.025
0.544	**0.563**	**0.571**	-0.026	-0.019	-0.007
0.498	**0.515**	**0.522**	-0.024	-0.017	-0.007
0.367	**0.379**	**0.391**	-0.024	-0.012	-0.012
0.785	**0.803**	**0.809**	-0.024	-0.018	-0.006
0.152	**0.169**	**0.176**	-0.024	-0.017	-0.007
0.621	**0.643**	**0.645**	-0.024	-0.022	-0.002
0.830	**0.787**	**0.854**	-0.024	0.043	-0.067
0.711	**0.725**	**0.735**	-0.024	-0.014	-0.010
0.552	**0.560**	**0.576**	-0.024	-0.008	-0.015
0.586	**0.596**	**0.609**	-0.023	-0.011	-0.013
0.733	**0.745**	**0.757**	-0.023	-0.011	-0.012
0.159	**0.171**	**0.182**	-0.023	-0.013	-0.011
0.757	**0.772**	**0.780**	-0.023	-0.015	-0.008
0.673	**0.681**	**0.696**	-0.023	-0.008	-0.015
0.762	**0.780**	**0.785**	-0.023	-0.018	-0.004
0.854	**0.806**	**0.876**	-0.021	0.048	-0.069
0.881	**0.894**	**0.902**	-0.021	-0.013	-0.009
0.683	**0.698**	**0.704**	-0.021	-0.015	-0.006
0.489	**0.509**	**0.510**	-0.021	-0.019	-0.001
0.671	**0.621**	**0.691**	-0.021	0.050	-0.071

0.532	**0.550**	**0.552**	-0.021	-0.019	-0.002
0.812	**0.819**	**0.833**	-0.021	-0.007	-0.014
0.179	**0.208**	**0.199**	-0.020	-0.028	0.008
0.180	**0.189**	**0.199**	-0.020	-0.009	-0.010
0.786	**0.787**	**0.806**	-0.020	0.000	-0.019
0.144	**0.160**	**0.163**	-0.019	-0.017	-0.003
0.606	**0.619**	**0.625**	-0.019	-0.013	-0.006
0.756	**0.766**	**0.775**	-0.019	-0.010	-0.009
0.540	**0.557**	**0.559**	-0.019	-0.016	-0.003
0.426	**0.438**	**0.445**	-0.019	-0.012	-0.007
0.770	**0.780**	**0.788**	-0.019	-0.010	-0.008
0.760	**0.784**	**0.779**	-0.018	-0.024	0.005
0.672	**0.672**	**0.690**	-0.018	0.000	-0.018
0.168	**0.174**	**0.186**	-0.018	-0.006	-0.012
0.735	**0.748**	**0.752**	-0.017	-0.013	-0.004
0.649	**0.660**	**0.665**	-0.017	-0.011	-0.005
0.149	**0.152**	**0.165**	-0.017	-0.003	-0.013
0.767	**0.767**	**0.783**	-0.016	-0.001	-0.016
0.394	**0.399**	**0.410**	-0.016	-0.005	-0.011
0.773	**0.779**	**0.789**	-0.016	-0.006	-0.011
0.068	**0.079**	**0.085**	-0.016	-0.010	-0.006
0.463	**0.484**	**0.479**	-0.016	-0.022	0.006
0.651	**0.651**	**0.667**	-0.016	0.000	-0.016
0.476	**0.478**	**0.492**	-0.016	-0.002	-0.014
0.597	**0.619**	**0.612**	-0.016	-0.023	0.007
0.423	**0.435**	**0.439**	-0.016	-0.011	-0.005
0.422	**0.408**	**0.438**	-0.016	0.014	-0.030
0.221	**0.229**	**0.236**	-0.016	-0.008	-0.008
0.831	**0.834**	**0.846**	-0.015	-0.002	-0.013
0.567	**0.568**	**0.581**	-0.015	-0.001	-0.014
0.097	**0.110**	**0.111**	-0.015	-0.013	-0.001
0.785	**0.804**	**0.800**	-0.015	-0.019	0.005
0.314	**0.335**	**0.329**	-0.014	-0.021	0.006
0.748	**0.754**	**0.762**	-0.014	-0.006	-0.009
0.740	**0.742**	**0.754**	-0.014	-0.002	-0.012
0.090	**0.100**	**0.104**	-0.014	-0.011	-0.004
0.582	**0.589**	**0.596**	-0.014	-0.007	-0.007
0.672	**0.678**	**0.686**	-0.014	-0.006	-0.008
0.906	**0.886**	**0.920**	-0.014	0.020	-0.034
0.866	**0.868**	**0.880**	-0.014	-0.002	-0.012
0.123	**0.130**	**0.137**	-0.014	-0.007	-0.006
0.519	**0.528**	**0.533**	-0.014	-0.010	-0.004
0.528	**0.511**	**0.542**	-0.014	0.018	-0.031
0.094	**0.103**	**0.108**	-0.014	-0.008	-0.005
0.783	**0.798**	**0.797**	-0.014	-0.015	0.002

0.814	**0.824**	**0.827**	-0.013	-0.010	-0.003
0.653	**0.652**	**0.666**	-0.013	0.001	-0.014
0.272	**0.286**	**0.284**	-0.013	-0.014	0.001
0.310	**0.307**	**0.323**	-0.013	0.003	-0.016
0.708	**0.727**	**0.721**	-0.013	-0.018	0.006
0.742	**0.749**	**0.754**	-0.012	-0.007	-0.005
0.846	**0.858**	**0.858**	-0.012	-0.011	-0.001
0.592	**0.592**	**0.604**	-0.012	0.000	-0.013
0.698	**0.715**	**0.710**	-0.012	-0.016	0.004
0.702	**0.690**	**0.714**	-0.012	0.012	-0.024
0.069	**0.079**	**0.081**	-0.012	-0.010	-0.002
0.143	**0.151**	**0.155**	-0.012	-0.009	-0.003
0.870	**0.878**	**0.882**	-0.012	-0.008	-0.004
0.591	**0.609**	**0.603**	-0.012	-0.018	0.007
0.107	**0.127**	**0.119**	-0.011	-0.019	0.008
0.370	**0.374**	**0.381**	-0.011	-0.005	-0.007
0.653	**0.657**	**0.664**	-0.011	-0.004	-0.007
0.753	**0.757**	**0.765**	-0.011	-0.004	-0.008
0.351	**0.355**	**0.362**	-0.011	-0.004	-0.007
0.061	**0.065**	**0.071**	-0.011	-0.004	-0.006
0.703	**0.693**	**0.713**	-0.011	0.010	-0.021
0.811	**0.819**	**0.822**	-0.010	-0.008	-0.002
0.356	**0.377**	**0.367**	-0.010	-0.021	0.010
0.066	**0.073**	**0.076**	-0.010	-0.007	-0.003
0.095	**0.108**	**0.106**	-0.010	-0.013	0.003
0.588	**0.580**	**0.599**	-0.010	0.009	-0.019
0.571	**0.585**	**0.581**	-0.010	-0.014	0.004
0.680	**0.679**	**0.690**	-0.010	0.000	-0.010
0.608	**0.618**	**0.617**	-0.010	-0.010	0.001
0.880	**0.893**	**0.890**	-0.010	-0.013	0.003
0.919	**0.925**	**0.928**	-0.010	-0.007	-0.003
0.546	**0.553**	**0.556**	-0.010	-0.006	-0.003
0.085	**0.095**	**0.094**	-0.009	-0.011	0.001
0.264	**0.274**	**0.274**	-0.009	-0.009	0.000
0.134	**0.130**	**0.143**	-0.009	0.004	-0.013
0.097	**0.106**	**0.106**	-0.009	-0.010	0.001
0.306	**0.320**	**0.315**	-0.009	-0.014	0.005
0.815	**0.811**	**0.824**	-0.009	0.004	-0.013
0.909	**0.912**	**0.918**	-0.009	-0.002	-0.007
0.776	**0.797**	**0.785**	-0.009	-0.021	0.012
0.454	**0.456**	**0.463**	-0.009	-0.002	-0.007
0.554	**0.577**	**0.562**	-0.009	-0.023	0.015
0.790	**0.768**	**0.799**	-0.008	0.022	-0.031
0.203	**0.196**	**0.211**	-0.008	0.006	-0.015
0.074	**0.078**	**0.082**	-0.008	-0.004	-0.004

0.041	**0.045**	**0.050**	-0.008	-0.003	-0.005
0.526	**0.523**	**0.534**	-0.008	0.002	-0.010
0.135	**0.138**	**0.143**	-0.008	-0.003	-0.005
0.075	**0.073**	**0.083**	-0.008	0.001	-0.010
0.927	**0.926**	**0.935**	-0.008	0.001	-0.009
0.874	**0.878**	**0.882**	-0.008	-0.004	-0.004
0.587	**0.596**	**0.595**	-0.008	-0.009	0.001
0.097	**0.101**	**0.105**	-0.008	-0.004	-0.004
0.041	**0.043**	**0.049**	-0.008	-0.002	-0.006
0.918	**0.923**	**0.926**	-0.008	-0.005	-0.003
0.784	**0.781**	**0.792**	-0.008	0.003	-0.011
0.520	**0.525**	**0.528**	-0.008	-0.005	-0.002
0.041	**0.046**	**0.049**	-0.008	-0.005	-0.002
0.301	**0.292**	**0.308**	-0.008	0.009	-0.017
0.662	**0.661**	**0.669**	-0.008	0.000	-0.008
0.031	**0.030**	**0.039**	-0.008	0.002	-0.009
0.060	**0.067**	**0.067**	-0.007	-0.007	-0.001
0.926	**0.935**	**0.933**	-0.007	-0.009	0.002
0.422	**0.424**	**0.429**	-0.007	-0.002	-0.005
0.177	**0.180**	**0.185**	-0.007	-0.002	-0.005
0.067	**0.068**	**0.074**	-0.007	-0.001	-0.006
0.045	**0.047**	**0.053**	-0.007	-0.002	-0.006
0.401	**0.403**	**0.408**	-0.007	-0.002	-0.006
0.497	**0.508**	**0.504**	-0.007	-0.010	0.003
0.963	**0.966**	**0.970**	-0.007	-0.002	-0.005
0.027	**0.028**	**0.034**	-0.007	-0.001	-0.006
0.816	**0.838**	**0.823**	-0.007	-0.022	0.016
0.579	**0.584**	**0.585**	-0.007	-0.005	-0.002
0.425	**0.436**	**0.432**	-0.007	-0.011	0.004
0.351	**0.355**	**0.358**	-0.007	-0.005	-0.002
0.331	**0.348**	**0.337**	-0.007	-0.017	0.010
0.754	**0.759**	**0.761**	-0.007	-0.004	-0.002
0.931	**0.930**	**0.938**	-0.007	0.001	-0.008
0.110	**0.112**	**0.117**	-0.007	-0.001	-0.005
0.244	**0.235**	**0.250**	-0.007	0.008	-0.015
0.076	**0.079**	**0.082**	-0.007	-0.003	-0.003
0.802	**0.815**	**0.808**	-0.007	-0.013	0.006
0.859	**0.849**	**0.865**	-0.006	0.009	-0.016
0.843	**0.846**	**0.849**	-0.006	-0.003	-0.003
0.631	**0.636**	**0.638**	-0.006	-0.005	-0.001
0.881	**0.878**	**0.887**	-0.006	0.003	-0.009
0.046	**0.048**	**0.052**	-0.006	-0.002	-0.004
0.822	**0.828**	**0.828**	-0.006	-0.006	0.000
0.024	**0.028**	**0.030**	-0.006	-0.004	-0.002
0.099	**0.101**	**0.105**	-0.006	-0.003	-0.003

0.362	**0.368**	**0.368**	-0.006	-0.006	0.000
0.036	**0.039**	**0.042**	-0.006	-0.003	-0.003
0.058	**0.064**	**0.064**	-0.005	-0.006	0.001
0.505	**0.511**	**0.510**	-0.005	-0.006	0.001
0.900	**0.901**	**0.905**	-0.005	-0.001	-0.004
0.740	**0.744**	**0.745**	-0.005	-0.004	-0.001
0.109	**0.114**	**0.115**	-0.005	-0.004	-0.001
0.202	**0.196**	**0.207**	-0.005	0.005	-0.010
0.040	**0.040**	**0.045**	-0.005	0.000	-0.005
0.069	**0.071**	**0.074**	-0.005	-0.002	-0.003
0.471	**0.478**	**0.476**	-0.005	-0.006	0.001
0.118	**0.123**	**0.123**	-0.005	-0.005	-0.001
0.711	**0.724**	**0.716**	-0.005	-0.013	0.008
0.496	**0.507**	**0.501**	-0.005	-0.011	0.006
0.112	**0.116**	**0.117**	-0.005	-0.004	-0.001
0.029	**0.026**	**0.034**	-0.005	0.003	-0.008
0.092	**0.095**	**0.097**	-0.005	-0.003	-0.002
0.385	**0.389**	**0.390**	-0.005	-0.004	0.000
0.510	**0.520**	**0.515**	-0.005	-0.011	0.006
0.624	**0.629**	**0.628**	-0.005	-0.005	0.000
0.790	**0.799**	**0.794**	-0.005	-0.010	0.005
0.030	**0.038**	**0.034**	-0.005	-0.008	0.004
0.281	**0.290**	**0.286**	-0.005	-0.009	0.004
0.326	**0.337**	**0.330**	-0.005	-0.012	0.007
0.596	**0.603**	**0.601**	-0.004	-0.007	0.002
0.154	**0.156**	**0.159**	-0.004	-0.002	-0.002
0.490	**0.492**	**0.494**	-0.004	-0.002	-0.003
0.569	**0.582**	**0.573**	-0.004	-0.013	0.009
0.034	**0.037**	**0.038**	-0.004	-0.003	-0.002
0.087	**0.087**	**0.092**	-0.004	0.000	-0.004
0.052	**0.055**	**0.057**	-0.004	-0.002	-0.002
0.876	**0.878**	**0.880**	-0.004	-0.002	-0.002
0.951	**0.955**	**0.955**	-0.004	-0.004	0.000
0.672	**0.692**	**0.676**	-0.004	-0.020	0.016
0.259	**0.247**	**0.263**	-0.004	0.012	-0.016
0.037	**0.033**	**0.041**	-0.004	0.004	-0.008
0.554	**0.556**	**0.558**	-0.004	-0.002	-0.002
0.057	**0.058**	**0.061**	-0.004	-0.001	-0.003
0.162	**0.164**	**0.166**	-0.004	-0.001	-0.003
0.925	**0.926**	**0.928**	-0.004	-0.001	-0.002
0.298	**0.302**	**0.302**	-0.004	-0.004	0.000
0.912	**0.914**	**0.916**	-0.004	-0.001	-0.002
0.922	**0.923**	**0.926**	-0.004	-0.001	-0.003
0.181	**0.185**	**0.185**	-0.004	-0.004	0.000
0.404	**0.398**	**0.408**	-0.004	0.006	-0.010

0.501	**0.508**	**0.505**	-0.004	-0.007	0.003
0.088	**0.093**	**0.092**	-0.004	-0.004	0.001
0.753	**0.748**	**0.756**	-0.003	0.005	-0.008
0.160	**0.162**	**0.163**	-0.003	-0.002	-0.001
0.231	**0.245**	**0.234**	-0.003	-0.014	0.011
0.036	**0.035**	**0.040**	-0.003	0.001	-0.004
0.094	**0.093**	**0.097**	-0.003	0.001	-0.004
0.955	**0.957**	**0.958**	-0.003	-0.003	-0.001
0.032	**0.031**	**0.035**	-0.003	0.001	-0.004
0.042	**0.045**	**0.046**	-0.003	-0.003	0.000
0.911	**0.910**	**0.914**	-0.003	0.001	-0.004
0.069	**0.075**	**0.073**	-0.003	-0.006	0.003
0.959	**0.959**	**0.962**	-0.003	0.000	-0.003
0.041	**0.042**	**0.045**	-0.003	-0.001	-0.002
0.031	**0.034**	**0.035**	-0.003	-0.003	0.000
0.034	**0.036**	**0.037**	-0.003	-0.002	-0.001
0.829	**0.830**	**0.832**	-0.003	-0.001	-0.002
0.049	**0.046**	**0.052**	-0.003	0.003	-0.006
0.723	**0.671**	**0.726**	-0.003	0.052	-0.055
0.073	**0.074**	**0.076**	-0.003	-0.001	-0.002
0.905	**0.904**	**0.908**	-0.003	0.001	-0.004
0.031	**0.032**	**0.034**	-0.003	-0.001	-0.002
0.652	**0.664**	**0.654**	-0.003	-0.012	0.009
0.049	**0.058**	**0.052**	-0.003	-0.008	0.006
0.655	**0.661**	**0.658**	-0.003	-0.005	0.003
0.052	**0.058**	**0.055**	-0.003	-0.006	0.003
0.130	**0.135**	**0.133**	-0.003	-0.005	0.002
0.041	**0.043**	**0.043**	-0.003	-0.003	0.000
0.044	**0.046**	**0.046**	-0.003	-0.002	0.000
0.491	**0.479**	**0.493**	-0.003	0.012	-0.015
0.924	**0.925**	**0.927**	-0.003	0.000	-0.002
0.038	**0.039**	**0.041**	-0.003	-0.001	-0.002
0.026	**0.025**	**0.028**	-0.003	0.000	-0.003
0.930	**0.937**	**0.933**	-0.003	-0.007	0.004
0.195	**0.177**	**0.197**	-0.002	0.018	-0.020
0.025	**0.025**	**0.027**	-0.002	0.000	-0.002
0.885	**0.884**	**0.887**	-0.002	0.001	-0.004
0.611	**0.610**	**0.614**	-0.002	0.001	-0.003
0.034	**0.034**	**0.036**	-0.002	-0.001	-0.002
0.031	**0.032**	**0.034**	-0.002	0.000	-0.002
0.055	**0.059**	**0.058**	-0.002	-0.004	0.002
0.557	**0.560**	**0.559**	-0.002	-0.004	0.001
0.511	**0.482**	**0.514**	-0.002	0.030	-0.032
0.485	**0.488**	**0.487**	-0.002	-0.003	0.001
0.962	**0.966**	**0.965**	-0.002	-0.004	0.001

0.029	**0.029**	**0.031**	-0.002	0.000	-0.002
0.120	**0.120**	**0.122**	-0.002	0.000	-0.003
0.036	**0.038**	**0.039**	-0.002	-0.002	0.000
0.129	**0.126**	**0.131**	-0.002	0.003	-0.005
0.439	**0.437**	**0.441**	-0.002	0.002	-0.004
0.578	**0.582**	**0.581**	-0.002	-0.003	0.001
0.040	**0.040**	**0.042**	-0.002	0.000	-0.002
0.614	**0.629**	**0.616**	-0.002	-0.015	0.013
0.120	**0.121**	**0.122**	-0.002	-0.001	-0.001
0.603	**0.604**	**0.605**	-0.002	-0.001	-0.001
0.061	**0.065**	**0.063**	-0.002	-0.004	0.002
0.037	**0.042**	**0.039**	-0.002	-0.004	0.002
0.244	**0.251**	**0.246**	-0.002	-0.007	0.005
0.788	**0.785**	**0.790**	-0.002	0.003	-0.005
0.046	**0.049**	**0.048**	-0.002	-0.003	0.001
0.070	**0.074**	**0.072**	-0.002	-0.004	0.002
0.043	**0.042**	**0.045**	-0.002	0.001	-0.003
0.104	**0.103**	**0.106**	-0.002	0.002	-0.003
0.687	**0.684**	**0.688**	-0.002	0.002	-0.004
0.048	**0.050**	**0.050**	-0.002	-0.002	0.001
0.969	**0.971**	**0.971**	-0.002	-0.002	0.000
0.021	**0.021**	**0.023**	-0.002	0.000	-0.002
0.831	**0.829**	**0.833**	-0.002	0.002	-0.004
0.071	**0.078**	**0.073**	-0.002	-0.007	0.005
0.024	**0.026**	**0.026**	-0.002	-0.002	0.000
0.027	**0.028**	**0.028**	-0.002	-0.001	0.000
0.026	**0.025**	**0.027**	-0.002	0.000	-0.002
0.032	**0.034**	**0.034**	-0.002	-0.001	0.000
0.076	**0.076**	**0.078**	-0.002	0.000	-0.002
0.064	**0.064**	**0.066**	-0.002	0.000	-0.002
0.069	**0.071**	**0.071**	-0.002	-0.001	0.000
0.030	**0.035**	**0.032**	-0.002	-0.005	0.003
0.956	**0.956**	**0.958**	-0.002	0.000	-0.002
0.910	**0.911**	**0.912**	-0.002	-0.001	0.000
0.923	**0.922**	**0.925**	-0.002	0.001	-0.002
0.778	**0.774**	**0.779**	-0.002	0.004	-0.005
0.032	**0.033**	**0.034**	-0.002	-0.001	-0.001
0.026	**0.030**	**0.027**	-0.002	-0.004	0.002
0.905	**0.910**	**0.907**	-0.002	-0.005	0.003
0.963	**0.963**	**0.965**	-0.002	0.000	-0.001
0.899	**0.900**	**0.900**	-0.002	-0.001	-0.001
0.045	**0.046**	**0.046**	-0.002	-0.001	-0.001
0.025	**0.028**	**0.027**	-0.002	-0.003	0.001
0.553	**0.553**	**0.555**	-0.001	0.001	-0.002
0.044	**0.044**	**0.046**	-0.001	0.001	-0.002

0.280	**0.273**	**0.281**	-0.001	0.007	-0.008
0.046	**0.046**	**0.047**	-0.001	0.000	-0.002
0.981	**0.979**	**0.983**	-0.001	0.002	-0.004
0.033	**0.033**	**0.034**	-0.001	-0.001	-0.001
0.069	**0.073**	**0.070**	-0.001	-0.005	0.003
0.022	**0.025**	**0.024**	-0.001	-0.003	0.002
0.022	**0.026**	**0.024**	-0.001	-0.004	0.002
0.960	**0.960**	**0.961**	-0.001	0.000	-0.001
0.948	**0.949**	**0.949**	-0.001	-0.001	0.000
0.391	**0.406**	**0.393**	-0.001	-0.014	0.013
0.871	**0.858**	**0.873**	-0.001	0.013	-0.014
0.189	**0.187**	**0.191**	-0.001	0.002	-0.003
0.110	**0.116**	**0.112**	-0.001	-0.005	0.004
0.040	**0.044**	**0.041**	-0.001	-0.004	0.003
0.037	**0.038**	**0.038**	-0.001	-0.001	0.000
0.038	**0.040**	**0.039**	-0.001	-0.002	0.001
0.113	**0.122**	**0.114**	-0.001	-0.009	0.008
0.145	**0.156**	**0.146**	-0.001	-0.011	0.009
0.035	**0.036**	**0.036**	-0.001	-0.001	0.000
0.095	**0.097**	**0.097**	-0.001	-0.001	0.000
0.034	**0.035**	**0.035**	-0.001	0.000	-0.001
0.028	**0.027**	**0.029**	-0.001	0.000	-0.001
0.034	**0.034**	**0.036**	-0.001	0.001	-0.002
0.022	**0.023**	**0.023**	-0.001	-0.001	0.000
0.958	**0.955**	**0.959**	-0.001	0.003	-0.004
0.304	**0.308**	**0.305**	-0.001	-0.004	0.003
0.048	**0.047**	**0.049**	-0.001	0.001	-0.002
0.844	**0.844**	**0.845**	-0.001	0.000	-0.001
0.245	**0.248**	**0.246**	-0.001	-0.003	0.002
0.061	**0.065**	**0.062**	-0.001	-0.004	0.003
0.040	**0.041**	**0.041**	-0.001	-0.001	0.000
0.294	**0.288**	**0.295**	-0.001	0.006	-0.007
0.512	**0.510**	**0.513**	-0.001	0.002	-0.003
0.036	**0.038**	**0.037**	-0.001	-0.002	0.001
0.028	**0.028**	**0.029**	-0.001	-0.001	0.000
0.033	**0.034**	**0.034**	-0.001	-0.001	0.000
0.414	**0.408**	**0.415**	-0.001	0.006	-0.007
0.309	**0.305**	**0.310**	-0.001	0.004	-0.005
0.035	**0.036**	**0.036**	-0.001	-0.001	0.000
0.011	**0.014**	**0.012**	-0.001	-0.003	0.002
0.875	**0.873**	**0.875**	-0.001	0.001	-0.002
0.016	**0.015**	**0.016**	-0.001	0.001	-0.002
0.014	**0.014**	**0.015**	-0.001	0.000	-0.001
0.028	**0.029**	**0.029**	-0.001	-0.001	0.000
0.026	**0.027**	**0.027**	-0.001	-0.001	0.000

0.159	**0.157**	**0.160**	-0.001	0.002	-0.002
0.035	**0.036**	**0.036**	-0.001	-0.001	0.000
0.030	**0.031**	**0.031**	-0.001	-0.001	0.000
0.054	**0.052**	**0.055**	-0.001	0.003	-0.004
0.782	**0.780**	**0.783**	-0.001	0.003	-0.003
0.030	**0.031**	**0.031**	-0.001	0.000	0.000
0.038	**0.038**	**0.039**	-0.001	0.000	-0.001
0.063	**0.063**	**0.064**	-0.001	0.001	-0.002
0.026	**0.025**	**0.027**	-0.001	0.001	-0.002
0.027	**0.027**	**0.027**	-0.001	0.000	-0.001
0.141	**0.136**	**0.141**	-0.001	0.004	-0.005
0.387	**0.397**	**0.388**	-0.001	-0.010	0.009
0.119	**0.123**	**0.120**	-0.001	-0.004	0.003
0.524	**0.524**	**0.524**	-0.001	-0.001	0.000
0.028	**0.033**	**0.029**	-0.001	-0.004	0.004
0.909	**0.913**	**0.909**	-0.001	-0.004	0.003
0.896	**0.896**	**0.897**	-0.001	0.000	0.000
0.018	**0.018**	**0.018**	-0.001	0.000	0.000
0.016	**0.017**	**0.017**	-0.001	-0.001	0.000
0.014	**0.014**	**0.014**	0.000	-0.001	0.000
0.846	**0.845**	**0.847**	0.000	0.001	-0.001
0.953	**0.953**	**0.953**	0.000	0.000	-0.001
0.965	**0.966**	**0.965**	0.000	-0.001	0.000
0.975	**0.975**	**0.976**	0.000	0.000	-0.001
0.030	**0.030**	**0.030**	0.000	-0.001	0.000
0.042	**0.040**	**0.042**	0.000	0.002	-0.002
0.932	**0.928**	**0.933**	0.000	0.004	-0.004
0.041	**0.039**	**0.042**	0.000	0.002	-0.003
0.014	**0.016**	**0.015**	0.000	-0.001	0.001
0.029	**0.029**	**0.029**	0.000	0.000	0.000
0.041	**0.042**	**0.041**	0.000	-0.001	0.001
0.037	**0.041**	**0.038**	0.000	-0.003	0.003
0.678	**0.628**	**0.678**	0.000	0.050	-0.050
0.015	**0.016**	**0.016**	0.000	0.000	0.000
0.043	**0.047**	**0.044**	0.000	-0.003	0.003
0.457	**0.462**	**0.458**	0.000	-0.005	0.005
0.201	**0.201**	**0.202**	0.000	0.001	-0.001
0.020	**0.020**	**0.021**	0.000	0.001	-0.001
0.020	**0.022**	**0.021**	0.000	-0.002	0.001
0.056	**0.056**	**0.056**	0.000	0.000	0.000
0.926	**0.931**	**0.927**	0.000	-0.005	0.005
0.019	**0.018**	**0.020**	0.000	0.001	-0.001
0.527	**0.539**	**0.528**	0.000	-0.012	0.011
0.020	**0.020**	**0.021**	0.000	0.000	0.000
0.028	**0.029**	**0.028**	0.000	0.000	0.000

0.122	**0.128**	**0.122**	0.000	-0.006	0.006
0.040	**0.040**	**0.040**	0.000	0.000	-0.001
0.672	**0.676**	**0.673**	0.000	-0.003	0.003
0.029	**0.029**	**0.029**	0.000	0.000	0.000
0.024	**0.024**	**0.024**	0.000	0.000	0.000
0.025	**0.025**	**0.025**	0.000	0.000	0.000
0.029	**0.030**	**0.029**	0.000	-0.001	0.001
0.025	**0.027**	**0.025**	0.000	-0.002	0.002
0.029	**0.030**	**0.029**	0.000	-0.001	0.001
0.021	**0.022**	**0.021**	0.000	-0.001	0.001
0.031	**0.029**	**0.031**	0.000	0.002	-0.002
0.023	**0.023**	**0.023**	0.000	0.000	0.000
0.020	**0.020**	**0.020**	0.000	0.000	0.000
0.960	**0.955**	**0.960**	0.000	0.005	-0.005
0.016	**0.018**	**0.016**	0.000	-0.002	0.002
0.051	**0.053**	**0.051**	0.000	-0.002	0.001
0.033	**0.032**	**0.033**	0.000	0.001	-0.001
0.544	**0.546**	**0.544**	0.000	-0.003	0.003
0.027	**0.027**	**0.028**	0.000	0.000	0.000
0.028	**0.026**	**0.028**	0.000	0.002	-0.002
0.192	**0.183**	**0.192**	0.000	0.009	-0.009
0.037	**0.037**	**0.037**	0.000	0.000	0.000
0.039	**0.041**	**0.039**	0.000	-0.002	0.002
0.961	**0.963**	**0.961**	0.000	-0.001	0.001
0.018	**0.018**	**0.018**	0.000	0.000	0.000
0.042	**0.043**	**0.042**	0.000	-0.001	0.001
0.353	**0.352**	**0.353**	0.000	0.002	-0.002
0.881	**0.885**	**0.881**	0.000	-0.004	0.004
0.069	**0.067**	**0.069**	0.000	0.002	-0.002
0.028	**0.029**	**0.028**	0.000	0.000	0.001
0.080	**0.080**	**0.080**	0.000	0.000	0.000
0.028	**0.029**	**0.028**	0.000	-0.001	0.001
0.441	**0.455**	**0.441**	0.000	-0.014	0.014
0.033	**0.035**	**0.033**	0.000	-0.002	0.002
0.025	**0.024**	**0.025**	0.000	0.001	-0.001
0.040	**0.043**	**0.040**	0.000	-0.003	0.003
0.019	**0.019**	**0.019**	0.000	0.000	0.000
0.023	**0.024**	**0.023**	0.000	0.000	0.001
0.026	**0.026**	**0.025**	0.000	-0.001	0.001
0.041	**0.041**	**0.040**	0.000	-0.001	0.001
0.020	**0.018**	**0.020**	0.000	0.002	-0.001
0.033	**0.034**	**0.033**	0.000	-0.001	0.001
0.073	**0.072**	**0.073**	0.000	0.002	-0.001
0.052	**0.052**	**0.052**	0.000	0.000	0.001
0.083	**0.081**	**0.083**	0.000	0.002	-0.002

0.030	**0.031**	**0.030**	0.000	-0.001	0.001
0.024	**0.025**	**0.023**	0.000	-0.002	0.002
0.040	**0.039**	**0.039**	0.000	0.000	0.000
0.899	**0.902**	**0.899**	0.000	-0.003	0.003
0.038	**0.038**	**0.038**	0.000	0.000	0.000
0.746	**0.770**	**0.746**	0.000	-0.024	0.025
0.041	**0.040**	**0.040**	0.000	0.001	0.000
0.017	**0.017**	**0.017**	0.000	0.000	0.000
0.885	**0.890**	**0.885**	0.000	-0.005	0.005
0.041	**0.042**	**0.041**	0.000	-0.001	0.001
0.048	**0.046**	**0.047**	0.000	0.002	-0.001
0.011	**0.010**	**0.011**	0.000	0.001	0.000
0.020	**0.019**	**0.019**	0.000	0.001	-0.001
0.037	**0.039**	**0.037**	0.000	-0.001	0.002
0.036	**0.034**	**0.035**	0.000	0.001	-0.001
0.033	**0.031**	**0.033**	0.001	0.002	-0.001
0.042	**0.043**	**0.041**	0.001	-0.001	0.002
0.963	**0.963**	**0.962**	0.001	-0.001	0.001
0.512	**0.512**	**0.511**	0.001	0.000	0.001
0.045	**0.044**	**0.044**	0.001	0.001	0.000
0.016	**0.017**	**0.015**	0.001	-0.001	0.001
0.019	**0.018**	**0.018**	0.001	0.001	0.000
0.040	**0.040**	**0.039**	0.001	0.000	0.001
0.063	**0.062**	**0.062**	0.001	0.001	0.000
0.028	**0.029**	**0.027**	0.001	-0.001	0.002
0.550	**0.550**	**0.549**	0.001	0.000	0.000
0.016	**0.016**	**0.016**	0.001	0.000	0.000
0.020	**0.021**	**0.020**	0.001	0.000	0.001
0.903	**0.906**	**0.902**	0.001	-0.003	0.004
0.017	**0.017**	**0.016**	0.001	0.000	0.001
0.816	**0.823**	**0.816**	0.001	-0.007	0.008
0.022	**0.021**	**0.022**	0.001	0.001	0.000
0.389	**0.367**	**0.389**	0.001	0.022	-0.021
0.054	**0.054**	**0.053**	0.001	0.000	0.001
0.046	**0.048**	**0.045**	0.001	-0.002	0.002
0.089	**0.086**	**0.088**	0.001	0.003	-0.002
0.021	**0.023**	**0.020**	0.001	-0.002	0.003
0.964	**0.963**	**0.963**	0.001	0.001	0.000
0.027	**0.027**	**0.026**	0.001	0.000	0.001
0.028	**0.027**	**0.027**	0.001	0.001	-0.001
0.023	**0.021**	**0.022**	0.001	0.002	-0.001
0.017	**0.016**	**0.016**	0.001	0.001	0.000
0.969	**0.970**	**0.968**	0.001	0.000	0.001
0.055	**0.057**	**0.054**	0.001	-0.002	0.003
0.017	**0.019**	**0.017**	0.001	-0.001	0.002

0.017	**0.016**	**0.016**	0.001	0.001	0.000
0.033	**0.034**	**0.032**	0.001	-0.001	0.002
0.047	**0.048**	**0.046**	0.001	-0.001	0.002
0.016	**0.016**	**0.015**	0.001	0.000	0.001
0.045	**0.044**	**0.044**	0.001	0.001	0.000
0.042	**0.042**	**0.041**	0.001	-0.001	0.002
0.051	**0.048**	**0.050**	0.001	0.002	-0.001
0.021	**0.022**	**0.020**	0.001	-0.002	0.003
0.024	**0.023**	**0.023**	0.001	0.001	0.000
0.870	**0.858**	**0.869**	0.001	0.012	-0.011
0.031	**0.030**	**0.029**	0.001	0.000	0.001
0.014	**0.013**	**0.013**	0.001	0.001	0.000
0.030	**0.030**	**0.029**	0.001	-0.001	0.002
0.030	**0.029**	**0.029**	0.001	0.001	0.000
0.510	**0.503**	**0.509**	0.001	0.007	-0.006
0.055	**0.053**	**0.053**	0.001	0.002	-0.001
0.017	**0.017**	**0.016**	0.001	0.000	0.002
0.086	**0.100**	**0.085**	0.001	-0.014	0.015
0.942	**0.947**	**0.940**	0.001	-0.006	0.007
0.028	**0.029**	**0.027**	0.001	0.000	0.001
0.022	**0.022**	**0.021**	0.001	0.001	0.001
0.026	**0.025**	**0.024**	0.001	0.001	0.000
0.019	**0.018**	**0.017**	0.001	0.001	0.000
0.044	**0.042**	**0.042**	0.001	0.002	0.000
0.028	**0.027**	**0.027**	0.001	0.001	0.000
0.024	**0.022**	**0.023**	0.001	0.002	-0.001
0.200	**0.207**	**0.198**	0.001	-0.008	0.009
0.602	**0.553**	**0.601**	0.001	0.049	-0.048
0.049	**0.049**	**0.048**	0.001	0.000	0.001
0.048	**0.047**	**0.047**	0.001	0.000	0.001
0.220	**0.231**	**0.219**	0.001	-0.010	0.012
0.970	**0.969**	**0.969**	0.001	0.001	0.000
0.045	**0.042**	**0.044**	0.001	0.003	-0.002
0.022	**0.020**	**0.021**	0.001	0.001	0.000
0.067	**0.068**	**0.065**	0.001	-0.001	0.003
0.063	**0.063**	**0.062**	0.001	0.000	0.001
0.024	**0.022**	**0.022**	0.001	0.002	0.000
0.018	**0.018**	**0.017**	0.001	0.000	0.001
0.025	**0.026**	**0.023**	0.001	-0.001	0.002
0.085	**0.089**	**0.083**	0.001	-0.004	0.006
0.909	**0.904**	**0.907**	0.001	0.004	-0.003
0.013	**0.013**	**0.012**	0.001	0.000	0.001
0.018	**0.017**	**0.016**	0.002	0.000	0.001
0.260	**0.267**	**0.259**	0.002	-0.007	0.008
0.064	**0.063**	**0.062**	0.002	0.001	0.001

0.032	**0.032**	**0.031**	0.002	0.001	0.001
0.706	**0.705**	**0.705**	0.002	0.001	0.000
0.062	**0.061**	**0.060**	0.002	0.000	0.001
0.926	**0.924**	**0.925**	0.002	0.002	-0.001
0.107	**0.103**	**0.106**	0.002	0.005	-0.003
0.945	**0.947**	**0.943**	0.002	-0.002	0.003
0.127	**0.128**	**0.126**	0.002	-0.001	0.003
0.030	**0.028**	**0.028**	0.002	0.001	0.000
0.044	**0.046**	**0.042**	0.002	-0.002	0.004
0.040	**0.038**	**0.038**	0.002	0.001	0.000
0.498	**0.498**	**0.496**	0.002	0.000	0.002
0.016	**0.017**	**0.014**	0.002	-0.002	0.003
0.937	**0.926**	**0.935**	0.002	0.011	-0.009
0.077	**0.075**	**0.075**	0.002	0.001	0.000
0.902	**0.893**	**0.900**	0.002	0.009	-0.007
0.024	**0.025**	**0.023**	0.002	-0.001	0.003
0.015	**0.014**	**0.014**	0.002	0.002	0.000
0.041	**0.040**	**0.039**	0.002	0.001	0.001
0.085	**0.085**	**0.083**	0.002	0.000	0.002
0.031	**0.030**	**0.029**	0.002	0.001	0.001
0.037	**0.036**	**0.035**	0.002	0.001	0.001
0.960	**0.957**	**0.958**	0.002	0.003	-0.001
0.017	**0.015**	**0.015**	0.002	0.002	0.000
0.023	**0.024**	**0.021**	0.002	-0.001	0.003
0.891	**0.891**	**0.889**	0.002	0.000	0.002
0.958	**0.953**	**0.956**	0.002	0.004	-0.003
0.036	**0.038**	**0.034**	0.002	-0.001	0.003
0.902	**0.891**	**0.900**	0.002	0.010	-0.008
0.228	**0.230**	**0.226**	0.002	-0.002	0.004
0.957	**0.953**	**0.955**	0.002	0.005	-0.003
0.151	**0.146**	**0.149**	0.002	0.005	-0.003
0.820	**0.826**	**0.818**	0.002	-0.006	0.008
0.274	**0.280**	**0.272**	0.002	-0.005	0.007
0.834	**0.836**	**0.832**	0.002	-0.002	0.004
0.952	**0.956**	**0.950**	0.002	-0.004	0.006
0.095	**0.093**	**0.093**	0.002	0.002	0.000
0.052	**0.050**	**0.050**	0.002	0.002	0.000
0.102	**0.100**	**0.100**	0.002	0.002	0.000
0.977	**0.977**	**0.975**	0.002	0.001	0.002
0.031	**0.028**	**0.029**	0.002	0.003	-0.001
0.958	**0.956**	**0.956**	0.002	0.002	0.001
0.477	**0.474**	**0.475**	0.002	0.003	0.000
0.571	**0.562**	**0.569**	0.002	0.010	-0.007
0.020	**0.020**	**0.018**	0.002	0.000	0.002
0.029	**0.028**	**0.026**	0.002	0.001	0.002

0.045	**0.048**	**0.043**	0.002	-0.003	0.005
0.968	**0.966**	**0.966**	0.002	0.002	0.000
0.107	**0.113**	**0.105**	0.002	-0.006	0.009
0.039	**0.039**	**0.037**	0.002	0.001	0.002
0.984	**0.981**	**0.981**	0.002	0.003	-0.001
0.014	**0.013**	**0.012**	0.002	0.001	0.001
0.033	**0.031**	**0.031**	0.002	0.002	0.000
0.033	**0.034**	**0.031**	0.002	0.000	0.003
0.336	**0.339**	**0.333**	0.002	-0.003	0.006
0.981	**0.980**	**0.979**	0.002	0.001	0.001
0.297	**0.291**	**0.295**	0.002	0.006	-0.003
0.589	**0.582**	**0.586**	0.002	0.007	-0.005
0.635	**0.635**	**0.632**	0.002	0.000	0.003
0.024	**0.024**	**0.021**	0.002	0.000	0.003
0.119	**0.113**	**0.117**	0.003	0.006	-0.003
0.029	**0.027**	**0.026**	0.003	0.002	0.001
0.092	**0.091**	**0.090**	0.003	0.001	0.001
0.053	**0.051**	**0.050**	0.003	0.002	0.001
0.032	**0.032**	**0.030**	0.003	0.000	0.003
0.042	**0.043**	**0.040**	0.003	0.000	0.003
0.033	**0.029**	**0.031**	0.003	0.005	-0.002
0.212	**0.199**	**0.210**	0.003	0.014	-0.011
0.907	**0.901**	**0.905**	0.003	0.006	-0.004
0.030	**0.030**	**0.027**	0.003	0.000	0.002
0.076	**0.075**	**0.073**	0.003	0.001	0.001
0.369	**0.373**	**0.367**	0.003	-0.004	0.006
0.212	**0.203**	**0.209**	0.003	0.008	-0.005
0.368	**0.365**	**0.365**	0.003	0.003	0.000
0.110	**0.110**	**0.107**	0.003	0.000	0.003
0.030	**0.036**	**0.027**	0.003	-0.007	0.009
0.041	**0.038**	**0.038**	0.003	0.003	0.000
0.026	**0.021**	**0.023**	0.003	0.005	-0.002
0.037	**0.035**	**0.034**	0.003	0.002	0.001
0.084	**0.082**	**0.081**	0.003	0.002	0.000
0.035	**0.034**	**0.032**	0.003	0.001	0.002
0.022	**0.020**	**0.020**	0.003	0.002	0.001
0.093	**0.087**	**0.090**	0.003	0.006	-0.003
0.118	**0.114**	**0.115**	0.003	0.004	-0.001
0.946	**0.945**	**0.943**	0.003	0.001	0.002
0.048	**0.050**	**0.045**	0.003	-0.002	0.005
0.182	**0.182**	**0.179**	0.003	0.000	0.003
0.036	**0.036**	**0.033**	0.003	0.000	0.003
0.033	**0.032**	**0.030**	0.003	0.001	0.002
0.253	**0.257**	**0.250**	0.003	-0.004	0.007
0.055	**0.055**	**0.052**	0.003	0.000	0.003

0.601	**0.596**	**0.598**	0.003	0.005	-0.002
0.032	**0.032**	**0.029**	0.003	0.000	0.003
0.215	**0.212**	**0.211**	0.003	0.002	0.001
0.920	**0.915**	**0.917**	0.003	0.005	-0.002
0.051	**0.049**	**0.048**	0.003	0.002	0.001
0.050	**0.043**	**0.046**	0.003	0.007	-0.003
0.021	**0.018**	**0.017**	0.003	0.002	0.001
0.031	**0.032**	**0.028**	0.003	0.000	0.004
0.048	**0.048**	**0.045**	0.003	0.000	0.003
0.042	**0.042**	**0.038**	0.003	0.000	0.003
0.028	**0.027**	**0.024**	0.003	0.001	0.002
0.932	**0.929**	**0.928**	0.004	0.003	0.000
0.039	**0.040**	**0.036**	0.004	-0.001	0.005
0.949	**0.945**	**0.945**	0.004	0.003	0.000
0.289	**0.292**	**0.286**	0.004	-0.003	0.007
0.853	**0.851**	**0.850**	0.004	0.002	0.001
0.105	**0.116**	**0.102**	0.004	-0.011	0.015
0.034	**0.033**	**0.030**	0.004	0.001	0.003
0.588	**0.573**	**0.584**	0.004	0.015	-0.011
0.021	**0.020**	**0.018**	0.004	0.001	0.003
0.894	**0.889**	**0.890**	0.004	0.004	0.000
0.027	**0.025**	**0.023**	0.004	0.002	0.002
0.032	**0.030**	**0.028**	0.004	0.002	0.002
0.179	**0.179**	**0.175**	0.004	0.000	0.004
0.044	**0.042**	**0.040**	0.004	0.002	0.002
0.033	**0.032**	**0.029**	0.004	0.002	0.002
0.060	**0.061**	**0.056**	0.004	-0.001	0.005
0.049	**0.048**	**0.045**	0.004	0.001	0.003
0.084	**0.080**	**0.080**	0.004	0.004	0.000
0.616	**0.620**	**0.612**	0.004	-0.004	0.009
0.685	**0.683**	**0.681**	0.004	0.003	0.001
0.233	**0.235**	**0.229**	0.004	-0.002	0.006
0.515	**0.514**	**0.511**	0.004	0.001	0.003
0.030	**0.028**	**0.026**	0.004	0.002	0.002
0.301	**0.296**	**0.296**	0.004	0.004	0.000
0.192	**0.185**	**0.188**	0.004	0.007	-0.003
0.135	**0.127**	**0.131**	0.004	0.008	-0.004
0.405	**0.401**	**0.400**	0.004	0.004	0.000
0.132	**0.140**	**0.127**	0.004	-0.009	0.013
0.026	**0.025**	**0.021**	0.004	0.001	0.003
0.045	**0.043**	**0.041**	0.004	0.002	0.002
0.046	**0.045**	**0.042**	0.004	0.001	0.004
0.918	**0.916**	**0.914**	0.004	0.002	0.002
0.059	**0.056**	**0.054**	0.005	0.002	0.002
0.350	**0.353**	**0.345**	0.005	-0.003	0.008

0.362	**0.361**	**0.358**	0.005	0.001	0.004
0.532	**0.531**	**0.527**	0.005	0.001	0.004
0.924	**0.921**	**0.919**	0.005	0.003	0.002
0.637	**0.635**	**0.632**	0.005	0.003	0.002
0.147	**0.148**	**0.142**	0.005	0.000	0.005
0.933	**0.927**	**0.928**	0.005	0.005	0.000
0.075	**0.073**	**0.069**	0.005	0.001	0.004
0.066	**0.063**	**0.061**	0.005	0.003	0.002
0.043	**0.042**	**0.038**	0.005	0.001	0.004
0.943	**0.939**	**0.938**	0.005	0.004	0.001
0.023	**0.022**	**0.017**	0.005	0.000	0.005
0.213	**0.227**	**0.207**	0.005	-0.014	0.019
0.057	**0.057**	**0.052**	0.005	0.000	0.006
0.108	**0.105**	**0.103**	0.005	0.003	0.002
0.488	**0.466**	**0.483**	0.005	0.022	-0.017
0.826	**0.836**	**0.821**	0.005	-0.009	0.015
0.113	**0.108**	**0.107**	0.005	0.005	0.000
0.277	**0.273**	**0.271**	0.006	0.004	0.002
0.042	**0.041**	**0.037**	0.006	0.002	0.004
0.060	**0.062**	**0.055**	0.006	-0.002	0.008
0.051	**0.046**	**0.045**	0.006	0.005	0.000
0.343	**0.315**	**0.337**	0.006	0.028	-0.022
0.708	**0.698**	**0.702**	0.006	0.010	-0.005
0.711	**0.698**	**0.705**	0.006	0.012	-0.006
0.267	**0.257**	**0.261**	0.006	0.010	-0.004
0.054	**0.053**	**0.048**	0.006	0.001	0.005
0.029	**0.026**	**0.023**	0.006	0.003	0.003
0.911	**0.896**	**0.905**	0.006	0.016	-0.010
0.042	**0.039**	**0.036**	0.006	0.002	0.004
0.932	**0.924**	**0.926**	0.006	0.008	-0.001
0.918	**0.913**	**0.912**	0.006	0.005	0.001
0.061	**0.058**	**0.055**	0.006	0.003	0.003
0.102	**0.097**	**0.096**	0.006	0.005	0.001
0.923	**0.915**	**0.917**	0.006	0.008	-0.002
0.188	**0.196**	**0.182**	0.006	-0.007	0.014
0.432	**0.432**	**0.425**	0.006	0.000	0.007
0.067	**0.058**	**0.061**	0.007	0.009	-0.003
0.077	**0.073**	**0.070**	0.007	0.004	0.003
0.083	**0.079**	**0.077**	0.007	0.004	0.003
0.046	**0.044**	**0.039**	0.007	0.001	0.006
0.068	**0.064**	**0.061**	0.007	0.004	0.003
0.040	**0.029**	**0.033**	0.007	0.011	-0.004
0.870	**0.865**	**0.864**	0.007	0.005	0.002
0.724	**0.715**	**0.717**	0.007	0.009	-0.002
0.434	**0.433**	**0.427**	0.007	0.001	0.006

0.076	**0.070**	**0.069**	0.007	0.006	0.001
0.581	**0.568**	**0.574**	0.007	0.013	-0.006
0.089	**0.088**	**0.082**	0.007	0.001	0.006
0.601	**0.596**	**0.594**	0.007	0.005	0.002
0.099	**0.095**	**0.091**	0.007	0.003	0.004
0.868	**0.851**	**0.861**	0.007	0.017	-0.009
0.719	**0.716**	**0.712**	0.007	0.003	0.005
0.037	**0.033**	**0.030**	0.007	0.004	0.004
0.052	**0.050**	**0.045**	0.007	0.003	0.005
0.347	**0.326**	**0.339**	0.007	0.021	-0.014
0.035	**0.032**	**0.027**	0.007	0.003	0.005
0.072	**0.068**	**0.065**	0.007	0.004	0.003
0.531	**0.522**	**0.524**	0.007	0.009	-0.002
0.777	**0.776**	**0.769**	0.007	0.001	0.006
0.884	**0.899**	**0.877**	0.008	-0.015	0.022
0.041	**0.036**	**0.033**	0.008	0.005	0.003
0.896	**0.889**	**0.888**	0.008	0.006	0.001
0.541	**0.532**	**0.533**	0.008	0.009	-0.001
0.077	**0.083**	**0.069**	0.008	-0.006	0.015
0.104	**0.099**	**0.096**	0.008	0.005	0.004
0.678	**0.650**	**0.670**	0.008	0.028	-0.020
0.565	**0.569**	**0.556**	0.008	-0.004	0.012
0.038	**0.035**	**0.030**	0.008	0.004	0.005
0.055	**0.044**	**0.047**	0.009	0.012	-0.003
0.067	**0.062**	**0.059**	0.009	0.005	0.003
0.222	**0.217**	**0.213**	0.009	0.004	0.004
0.313	**0.309**	**0.304**	0.009	0.004	0.004
0.717	**0.713**	**0.708**	0.009	0.004	0.005
0.371	**0.367**	**0.362**	0.009	0.004	0.005
0.558	**0.552**	**0.549**	0.009	0.006	0.003
0.145	**0.140**	**0.136**	0.009	0.005	0.004
0.855	**0.854**	**0.846**	0.009	0.001	0.008
0.769	**0.765**	**0.760**	0.009	0.004	0.005
0.886	**0.876**	**0.877**	0.009	0.010	-0.001
0.931	**0.921**	**0.921**	0.009	0.009	0.000
0.082	**0.084**	**0.073**	0.009	-0.002	0.011
0.067	**0.072**	**0.058**	0.009	-0.004	0.014
0.390	**0.384**	**0.381**	0.009	0.006	0.003
0.110	**0.103**	**0.101**	0.009	0.007	0.002
0.123	**0.125**	**0.113**	0.010	-0.003	0.012
0.863	**0.860**	**0.853**	0.010	0.003	0.007
0.808	**0.806**	**0.798**	0.010	0.003	0.008
0.526	**0.529**	**0.516**	0.010	-0.003	0.013
0.620	**0.615**	**0.610**	0.010	0.005	0.005
0.218	**0.223**	**0.207**	0.011	-0.005	0.016

0.420	**0.414**	**0.409**	0.011	0.005	0.005
0.122	**0.112**	**0.111**	0.011	0.010	0.000
0.810	**0.783**	**0.799**	0.011	0.027	-0.016
0.257	**0.259**	**0.246**	0.011	-0.002	0.013
0.892	**0.890**	**0.881**	0.011	0.002	0.009
0.710	**0.708**	**0.699**	0.011	0.001	0.009
0.750	**0.743**	**0.739**	0.011	0.007	0.004
0.600	**0.590**	**0.589**	0.011	0.011	0.000
0.812	**0.780**	**0.801**	0.011	0.033	-0.022
0.167	**0.159**	**0.156**	0.011	0.008	0.003
0.855	**0.855**	**0.843**	0.011	-0.001	0.012
0.079	**0.086**	**0.068**	0.011	-0.006	0.018
0.135	**0.134**	**0.123**	0.011	0.001	0.010
0.893	**0.882**	**0.881**	0.012	0.011	0.000
0.551	**0.550**	**0.539**	0.012	0.001	0.011
0.532	**0.539**	**0.520**	0.012	-0.007	0.019
0.205	**0.207**	**0.193**	0.012	-0.003	0.015
0.308	**0.297**	**0.296**	0.012	0.011	0.001
0.235	**0.233**	**0.223**	0.012	0.002	0.010
0.910	**0.905**	**0.898**	0.012	0.005	0.007
0.559	**0.551**	**0.546**	0.013	0.008	0.005
0.747	**0.746**	**0.734**	0.013	0.001	0.012
0.398	**0.406**	**0.385**	0.013	-0.008	0.021
0.746	**0.724**	**0.733**	0.013	0.022	-0.009
0.836	**0.823**	**0.822**	0.013	0.013	0.001
0.299	**0.297**	**0.285**	0.014	0.002	0.012
0.657	**0.665**	**0.643**	0.014	-0.008	0.022
0.863	**0.856**	**0.850**	0.014	0.008	0.006
0.237	**0.230**	**0.223**	0.014	0.007	0.007
0.126	**0.121**	**0.112**	0.014	0.005	0.009
0.216	**0.221**	**0.202**	0.014	-0.005	0.019
0.299	**0.298**	**0.285**	0.014	0.001	0.013
0.214	**0.208**	**0.199**	0.015	0.006	0.009
0.766	**0.753**	**0.751**	0.015	0.013	0.002
0.671	**0.662**	**0.656**	0.015	0.009	0.006
0.615	**0.612**	**0.600**	0.015	0.003	0.012
0.629	**0.627**	**0.614**	0.015	0.002	0.013
0.525	**0.513**	**0.510**	0.015	0.012	0.003
0.607	**0.592**	**0.592**	0.015	0.015	0.000
0.267	**0.253**	**0.252**	0.016	0.014	0.001
0.446	**0.446**	**0.430**	0.016	0.000	0.016
0.444	**0.433**	**0.429**	0.016	0.011	0.005
0.528	**0.533**	**0.512**	0.016	-0.004	0.020
0.133	**0.126**	**0.117**	0.016	0.007	0.009
0.145	**0.143**	**0.129**	0.016	0.001	0.015

0.331	**0.318**	**0.315**	0.016	0.013	0.003
0.250	**0.239**	**0.234**	0.017	0.011	0.005
0.413	**0.399**	**0.396**	0.017	0.014	0.003
0.460	**0.461**	**0.443**	0.017	-0.001	0.018
0.545	**0.548**	**0.528**	0.017	-0.003	0.019
0.648	**0.643**	**0.631**	0.017	0.005	0.012
0.828	**0.808**	**0.811**	0.018	0.021	-0.003
0.657	**0.656**	**0.639**	0.018	0.001	0.016
0.426	**0.431**	**0.408**	0.018	-0.005	0.023
0.793	**0.775**	**0.775**	0.018	0.018	0.000
0.400	**0.395**	**0.382**	0.018	0.005	0.013
0.684	**0.687**	**0.665**	0.019	-0.004	0.022
0.643	**0.638**	**0.624**	0.019	0.005	0.014
0.170	**0.156**	**0.150**	0.019	0.014	0.005
0.565	**0.559**	**0.546**	0.019	0.006	0.014
0.232	**0.219**	**0.212**	0.020	0.012	0.007
0.358	**0.335**	**0.338**	0.020	0.023	-0.003
0.406	**0.398**	**0.386**	0.020	0.007	0.013
0.425	**0.420**	**0.405**	0.020	0.005	0.015
0.229	**0.213**	**0.208**	0.021	0.016	0.005
0.648	**0.646**	**0.626**	0.021	0.002	0.019
0.890	**0.873**	**0.869**	0.022	0.018	0.004
0.472	**0.459**	**0.450**	0.022	0.013	0.009
0.214	**0.205**	**0.191**	0.022	0.008	0.014
0.252	**0.248**	**0.230**	0.023	0.005	0.018
0.568	**0.547**	**0.546**	0.023	0.021	0.001
0.373	**0.368**	**0.350**	0.023	0.005	0.018
0.702	**0.702**	**0.678**	0.024	0.000	0.024
0.487	**0.485**	**0.463**	0.024	0.002	0.022
0.271	**0.259**	**0.247**	0.024	0.012	0.012
0.237	**0.233**	**0.213**	0.024	0.004	0.020
0.875	**0.878**	**0.850**	0.024	-0.003	0.028
0.389	**0.355**	**0.365**	0.025	0.034	-0.010
0.529	**0.516**	**0.504**	0.025	0.013	0.012
0.517	**0.502**	**0.491**	0.026	0.015	0.012
0.432	**0.406**	**0.405**	0.027	0.026	0.000
0.489	**0.462**	**0.462**	0.027	0.026	0.000
0.279	**0.266**	**0.251**	0.027	0.013	0.014
0.341	**0.304**	**0.314**	0.027	0.037	-0.010
0.350	**0.339**	**0.323**	0.027	0.011	0.016
0.307	**0.294**	**0.279**	0.028	0.013	0.015
0.491	**0.474**	**0.463**	0.029	0.018	0.011
0.206	**0.174**	**0.177**	0.029	0.032	-0.004
0.311	**0.297**	**0.282**	0.029	0.014	0.015
0.347	**0.332**	**0.316**	0.030	0.015	0.016

0.229	**0.193**	**0.197**	0.032	0.036	-0.004
0.376	**0.350**	**0.344**	0.032	0.025	0.007
0.837	**0.838**	**0.805**	0.032	-0.001	0.033
0.425	**0.407**	**0.391**	0.034	0.018	0.016
0.418	**0.392**	**0.383**	0.035	0.026	0.009
0.408	**0.392**	**0.373**	0.036	0.016	0.019
0.376	**0.353**	**0.339**	0.036	0.023	0.014
0.369	**0.340**	**0.332**	0.037	0.029	0.008
0.322	**0.310**	**0.284**	0.038	0.012	0.026
0.476	**0.441**	**0.437**	0.039	0.034	0.004
0.432	**0.412**	**0.392**	0.039	0.020	0.020
0.640	**0.622**	**0.601**	0.039	0.018	0.021
0.299	**0.282**	**0.256**	0.043	0.017	0.026

DNA methylation signatures link prenatal famine exposure to growth and metabolism. Tobi,
http://www.ncbi.nlm.nih.gov/pubmed/25424739

		CHR	MAPINFO	Probe_SNPs	UCSC_RefGe	UCSC_RefGe
SMAD7	cg14785810	18	44676983		HDHD2	TSS200
SMAD7	cg18936800	18	44676962		HDHD2	TSS200
SMAD7	cg20581250	18	44676959		HDHD2	TSS200
SMAD7	cg05830870	18	44677236		HDHD2	TSS1500
SMAD7	cg05848120	18	44676992		HDHD2	TSS200
SMAD7	cg12344490	18	44677139		HDHD2	TSS1500
SMAD7	cg17192377	18	44677553		HDHD2	TSS1500
KLF13	cg11166299	15	29424391		FAM189A1	Body
KLF13	cg17051704	15	29424197	rs7162625	FAM189A1	Body
KLF13	cg16264249	15	29424512		FAM189A1	Body
RFTN1	cg00822591	3	16306489	rs2271078	DPH3;OXNA	5'UTR;TSS15
RFTN1	cg13262419	3	16306634		OXNAD1;DP	TSS200;TSS2
RFTN1	cg13470477	3	16306636		OXNAD1;DP	TSS200;TSS2
RFTN1	cg14877820	3	16306698		OXNAD1;DP	TSS200;TSS1
RFTN1	cg19424343	3	16306684		OXNAD1;DP	TSS200;TSS2
RFTN1	cg20846042	3	16306509	rs2271078	OXNAD1;DP	TSS1500;TSS
RFTN1	cg23474789	3	16306055		DPH3;OXNA	Body;TSS150
RFTN1	cg23969669	3	16306450		DPH3;OXNA	5'UTR;TSS15
RFTN1	cg25096193	3	16306690		OXNAD1;DP	TSS200;TSS2
RFTN1	cg00203037	3	16360321	rs689716	RFTN1	Body
RFTN1	cg00641792	3	16306543		OXNAD1;DP	TSS200;TSS2
RFTN1	cg01133779	3	16371295		RFTN1	Body
RFTN1	cg01798391	3	16306595		OXNAD1;DP	TSS200;TSS2
RFTN1	cg02255107	3	16347334		OXNAD1	3'UTR
RFTN1	cg08523978	3	16394492		RFTN1	Body
RFTN1	cg10579246	3	16305290		DPH3;OXNA	Body;TSS150
RFTN1	cg10895687	3	16289098			
RFTN1	cg11208165	3	16308357		OXNAD1	5'UTR
RFTN1	cg12172478	3	16357591	rs79146591	RFTN1	3'UTR
RFTN1	cg13026795	3	16379963		RFTN1	Body
RFTN1	cg13601096	3	16303382		DPH3;DPH3	Body;Body
RFTN1	cg16456087	3	16343197		OXNAD1	Body
RFTN1	cg17886536	3	16320218		OXNAD1	Body
RFTN1	cg18276599	3	16393023	rs78610660	RFTN1	Body
RFTN1	cg21761922	3	16309088		OXNAD1	5'UTR
RFTN1	cg22230912	3	16331335		OXNAD1	Body
RFTN1	cg22688260	3	16306809		OXNAD1;DP	1stExon;TSS1
RFTN1	cg25809215	3	16306823		OXNAD1;DP	1stExon;TSS1

RFTN1	ch.3.373140	3	16361589	rs79063464	RFTN1	Body
CDH23	no informative data					
INSR	no informative data					
KLF13	no informative data					
CPT1A	no informative data					

Dutch Winter Hunger – Tobi, IJE 2015 http://ije.oxfordjournals.org/content/early/2015/05/

		CHR	MAPINFO	Probe_SNP	UCSC_RefG	UCSC_RefG
	cg20823026	chr2	366113	rs6548229		
	cg11496778	chr11	3225076	NA		
	cg10354880	chr12	46737123	NA		
	cg27370573	chr19	292167	NA	PPAP2C;PPA	TSS1500;TSS

		CHR	MAPINFO	Probe_SNP	UCSC_RefG	UCSC_RefG
	cg15659713	chr8	38586183	NA	TACC1;TACC	1stExon;5'UT
	cg26199857	chr12	54764265	NA	ZNF385A;ZN	Body;Body;B

		CHR	MAPINFO	Probe_SNP	UCSC_RefG	UCSC_RefG
	1	chr17	79283915	NA	C17orf55	TSS1500

ism. Tobi, Nat Comm 2014

	Group A		**Group B**		**Group C**
UCSC_CpG_Islands_Name	**Average**	SD	**Average**	SD	**Average**
chr18:44676470-4467705	**0.021**	0.004	**0.019**	0.004	**0.019**
chr18:44676470-4467705	**0.060**	0.010	**0.059**	0.010	**0.061**
chr18:44676470-4467705	**0.022**	0.005	**0.022**	0.006	**0.022**
chr18:44676470-4467705	**0.014**	0.003	**0.013**	0.003	**0.013**
chr18:44676470-4467705	**0.025**	0.004	**0.027**	0.005	**0.029**
chr18:44676470-4467705	**0.017**	0.003	**0.016**	0.004	**0.017**
chr18:44676470-4467705	**0.393**	0.028	**0.392**	0.037	**0.390**
	0.079	**0.008**	**0.078**	**0.010**	**0.079**
	0.610	0.025	**0.596**	0.024	**0.594**
	0.134	0.051	**0.135**	0.046	**0.126**
	0.874	0.020	**0.864**	0.025	**0.869**
	0.539	**0.032**	**0.532**	**0.032**	**0.530**
chr3:16306136-16306986	**0.019**	0.004	**0.019**	0.005	**0.022**
chr3:16306136-16306986	**0.031**	0.007	**0.030**	0.005	**0.032**
chr3:16306136-16306986	**0.019**	0.006	**0.020**	0.006	**0.019**
chr3:16306136-16306986	**0.017**	0.005	**0.017**	0.005	**0.018**
chr3:16306136-16306986	**0.023**	0.006	**0.022**	0.005	**0.024**
chr3:16306136-16306986	**0.012**	0.005	**0.010**	0.004	**0.011**
chr3:16306136-16306986	**0.060**	0.011	**0.057**	0.010	**0.057**
chr3:16306136-16306986	**0.039**	0.008	**0.037**	0.007	**0.039**
chr3:16306136-16306986	**0.018**	0.004	**0.018**	0.005	**0.018**
	0.515	0.108	**0.525**	0.083	**0.550**
chr3:16306136-16306986	**0.098**	0.014	**0.095**	0.010	**0.100**
	0.896	0.015	**0.902**	0.019	**0.897**
chr3:16306136-16306986	**0.013**	0.004	**0.013**	0.003	**0.013**
	0.915	0.031	**0.916**	0.025	**0.908**
	0.910	0.017	**0.914**	0.020	**0.908**
chr3:16306136-16306986	**0.943**	0.015	**0.930**	0.021	**0.932**
	0.030	0.007	**0.032**	0.007	**0.035**
chr3:16306136-16306986	**0.830**	0.028	**0.825**	0.025	**0.819**
	0.738	0.053	**0.731**	0.050	**0.717**
	0.017	0.003	**0.017**	0.004	**0.017**
chr3:16306136-16306986	**0.932**	0.018	**0.943**	0.014	**0.941**
	0.580	0.063	**0.575**	0.071	**0.577**
	0.787	0.035	**0.804**	0.038	**0.804**
	0.974	0.008	**0.971**	0.011	**0.969**
chr3:16306136-16306986	**0.947**	0.013	**0.950**	0.013	**0.947**
	0.732	0.075	**0.735**	0.065	**0.738**
chr3:16306136-16306986	**0.013**	0.003	**0.013**	0.002	**0.012**
chr3:16306136-16306986	**0.033**	0.006	**0.032**	0.010	**0.034**

0.045	0.016	**0.053**	0.018	**0.049**
0.386	**0.020**	**0.386**	**0.019**	**0.386**

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UCSC_CpG_Islands_N	**Mean**	SD	**Mean**	SD	**Mean**
	0.906	0.097	**0.884**	0.170	**0.910**
chr11:3224524-3225077	**0.192**	0.034	**0.186**	0.049	**0.192**
	0.889	0.016	**0.865**	0.164	**0.894**
chr19:290594-292249	**0.835**	0.044	**0.817**	0.155	**0.837**

UCSC_CpG_Islands_Name					
tExon;5'UTR	**0.280**	0.032	**0.264**	0.063	**0.280**
chr12:54764065-5476451	**0.587**	0.072	**0.568**	0.124	**0.606**

UCSC_CpG_Islands_Name					
chr17:79283863-7928413	**0.692**	0.035	**0.676**	0.134	**0.689**

	Difference A-C	Difference B-C	Difference B-A
SD			
0.005	0.002	0.000	-0.002
0.009	0.000	-0.001	-0.001
0.006	0.000	-0.001	0.000
0.004	0.000	0.000	-0.001
0.007	-0.004	-0.002	0.002
0.004	0.001	-0.001	-0.001
0.040	0.003	0.001	-0.002
0.011	**0.000**	**-0.001**	**-0.001**
0.019	0.016	0.002	-0.014
0.042	0.008	0.010	0.002
0.023	0.006	-0.004	-0.010
0.028	**0.010**	**0.002**	**-0.007**
0.005	-0.003	-0.003	0.000
0.005	-0.001	-0.002	-0.001
0.005	0.000	0.001	0.001
0.005	0.000	-0.001	-0.001
0.007	-0.001	-0.002	-0.001
0.004	0.000	-0.001	-0.002
0.012	0.004	0.000	-0.004
0.007	0.000	-0.002	-0.002
0.003	0.000	0.000	0.000
0.088	-0.034	-0.024	0.010
0.012	-0.002	-0.005	-0.003
0.018	-0.001	0.005	0.006
0.004	-0.001	-0.001	0.000
0.029	0.007	0.008	0.001
0.017	0.002	0.007	0.005
0.024	0.010	-0.002	-0.012
0.009	-0.005	-0.003	0.002
0.022	0.011	0.006	-0.005
0.060	0.021	0.014	-0.007
0.003	0.000	0.000	0.001
0.015	-0.010	0.001	0.011
0.071	0.003	-0.002	-0.005
0.032	-0.016	0.000	0.016
0.011	0.005	0.002	-0.003
0.010	0.000	0.002	0.002
0.061	-0.006	-0.004	0.003
0.004	0.001	0.001	-0.001
0.006	-0.001	-0.002	-0.001

0.017	-0.003	0.005	0.008
0.020	**-0.001**	**0.000**	**0.001**

SD	**Difference A-C**	**Difference B-C**	**Difference B-A**
0.092	-0.004	-0.026	-0.022
0.047	0.000	-0.006	-0.007
0.017	-0.005	-0.030	-0.025
0.044	-0.001	-0.020	-0.019

0.027	0.000	-0.016	-0.016
0.058	-0.020	-0.039	-0.019

0.050	0.003	-0.013	-0.016