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Increased epigenetic alterations at the promoters of transcriptional regulators following inadequate maternal gestational weight gain

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List of 2,521 hypermethylated outliers

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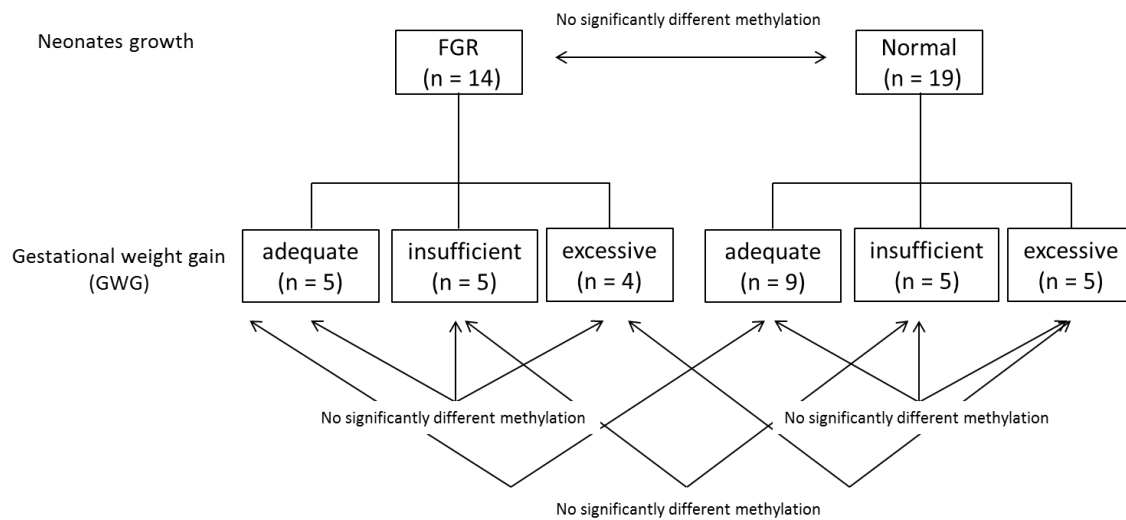
List of 977 hypomethylated outliers

Supplementary Table 3:

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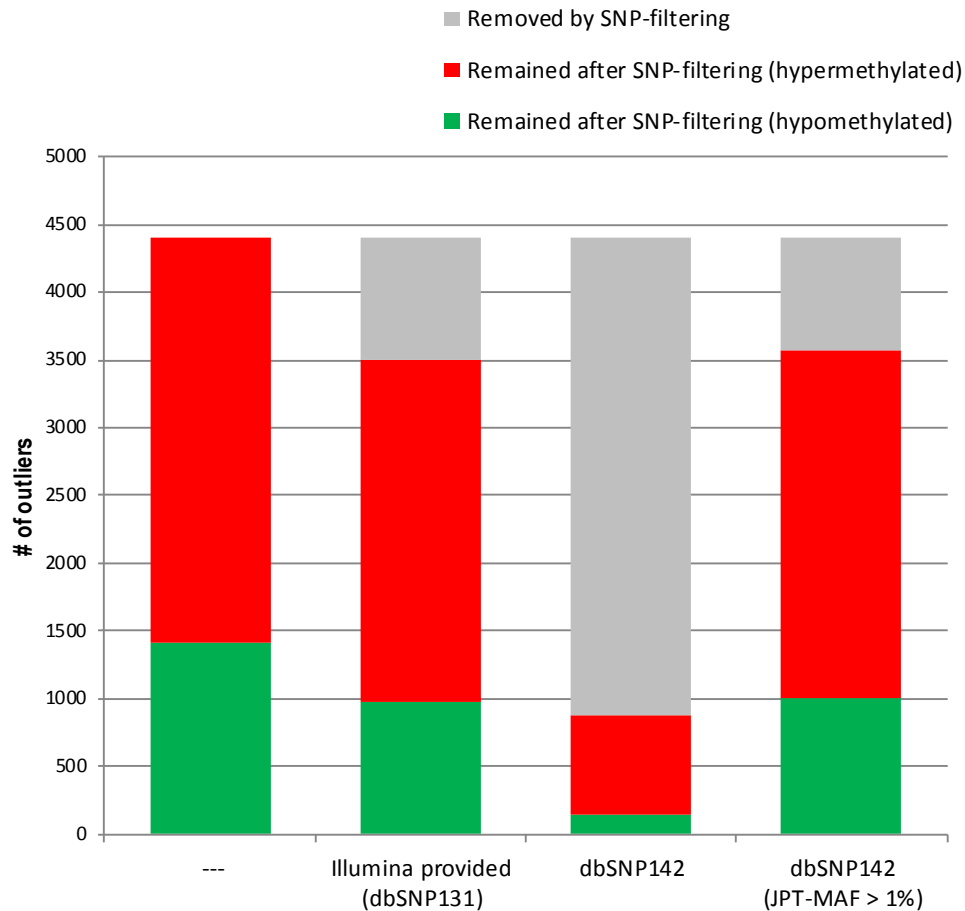
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Supplementary Figure 1:

Schematic representation of the group comparisons performed using Wilcoxon rank-sum test to detect differentially methylated CpG sites.

FGR (n=14) and Normal (n=19) birth groups were further categorized according to the extent of maternal gestational weight gain (GWG) (adequate, insufficient, or excessive). Among 449,848 CpG sites subjected to the statistical analysis, no sites showed statistically significant differential methylation in the comparison between FGR and Normal groups and in the seven comparisons between two subgroups (significance level = BH adjusted p -value 0.05).



	---	Illumina provided (dbSNP131)	dbSNP142	dbSNP142 (JPT-MAF > 1%)
Removed by SNP-filtering	---	901 / 4399 (20.5%)	3523 / 4399 (80.0%)	832 / 4399 (18.9%)
Remained after SNP-filtering	---	3498 / 4399 (79.5%)	876 / 4399 (20.0%)	3567 / 4399 (81.1%)
hypermethylated	2983 / 4399 (67.8%)	2521 / 3498 (72.1%)	729 / 876 (83.2%)	2569 / 3567 (72.0%)
hypomethylated	1416 / 4399 (32.2%)	977 / 3498 (27.9%)	147 / 876 (16.8%)	998 / 3567 (28.0%)

Supplementary Figure 2:

Evaluation of the numbers of SNP-containing probes among the probes corresponding to the 4,399 methylation outliers detected by the Smirnov-Grubbs' outlier test.

Illumina-provided list for SNP-containing probes were initially used to count the number of the outlying CpG sites whose beta value could possibly have been affected by sequence variation within the corresponding probe sequence. The Illumina probe annotation, HumanMethylation450_15017482_v.1.1.csv, lists 89,678 probes as SNP-containing in its "probe_SNP" and "probe_SNP_10" columns based on the information of NCBI dbSNP Build 131. Among the probes corresponding to the 4,399 outliers, 901 (20.5%) probes were found

to be annotated as SNP-containing. The numbers of remaining hyper- and hypomethylated outliers after SNP filtering were 2,521 and 977, respectively. Hypomethylated outliers tended to coincide with SNP-containing probes more often than hypermethylated outliers.

We also conducted SNP-filtering using the dbSNP142 dataset (the current second latest version). This SNP filtering removed an extremely high fraction of probes (80.0% removed). However, many of the SNPs located in the intervals of the probes removed were expected to be monomorphic (or with a very low minor allele frequency) in the Japanese population. Therefore, to keep the number of remaining probes after SNP-filtering appropriate for subsequent feature annotations, we also tested a filtering using only SNPs whose minor allele frequency is $>1\%$ in the Japanese population. In order to identify SNPs and short indels that are common (MAF $> 1\%$) in the Japanese population, we used datasets from dbSNP build 142

(ftp://ftp.wip.ncbi.nlm.nih.gov/snp/organisms/human_9606_b142_GRCh37p13/VCF/All_20150217.vcf.gz) and the 1000 Genomes Project (<ftp://ftp.ncbi.nih.gov/1000genomes/ftp/release/20130502/>). Allele frequency among the Japanese individuals (JPT samples) was calculated for each of refSNP entries when it was included in the variant list of the latter project. Genotypes of 48 female and 56 male JPT samples (from NA18939 to NA19091 with some missing data) were available in the release. The compiled list of refSNPs and their allele frequencies among the JPT samples is available upon request. Among 82,009,761 refSNPs registered in dbSNP142, 9,061,456 SNPs showing a MAF $> 1\%$ in the JPT population were used for SNP-filtering. As a result, 832 (18.9%) among 4,399 outlier probes were removed as SNP-containing probes.

We confirmed that approximately 90% of the probes were common between the two remaining outlier probe-sets after the SNP filtering using Illumina provided list (dbSNP131-based) and after the dbSNP142 filtering with the consideration of MAF ($> 1\%$), and that genomic and functional features (such as those shown in Fig.2, Table 2 and Table 3) were similar between them (data not shown).

Supplementary Table 1: list of 2,521 hypermethylated outliers

#	Sample_ID	Outlier-test P-value (adjusted)	Outlier's beta-value	Mean of the beta-values of all cells	delta-beta	CHR	MAPINFO_hg19	TargetID	UCSC_REFGENE_NAME	UCSC_REFGENE_GROUP	UCSC_CPG_ISLANDS_NAME	RELATION_TO_UCSC_CPG_ISLAND
hyper1	FGR_insufficient_1	2.9E-02	0.83	0.51	0.32	2	10152012	cg06819088				
hyper2	FGR_insufficient_1	1.9E-03	0.82	0.56	0.26	2	10152901	cg14811551				
hyper3	FGR_insufficient_1	1.5E-03	0.88	0.56	0.32	2	10155062	cg07951151				
hyper4	FGR_insufficient_1	5.4E-03	0.18	0.07	0.11	2	145277741	cg19123296	ZEB2;ZEB2;ZEB2;ZEB2	Body;5'UTR;1stExon;1stExon;5'UTR	chr2:145281736-145282269	N_Shelf
hyper5	FGR_insufficient_1	2.8E-03	0.51	0.26	0.25	2	241519705	cg13857354				
hyper6	FGR_insufficient_1	3.5E-04	0.29	0.05	0.24	3	145878177	cg00506629	PLOD2;PLOD2	Body;Body	chr3:145878430-145879287	N_Shore
hyper7	FGR_insufficient_1	1.9E-10	0.13	0.01	0.12	4	106630029	cg17197981	GSTCD;INTS12;INTS12;GSTCD	1stExon;TSS200;TSS200;5'UTR	chr4:106629575-106630214	Island
hyper8	FGR_insufficient_1	2.4E-05	0.26	0.09	0.17	4	113970660	cg01268541	ANK2;ANK2;ANK2	TSS200;Body;TSS200		
hyper9	FGR_insufficient_1	5.9E-03	0.33	0.15	0.19	5	168729558	cg21545840	SLIT3	TSS1500	chr5:168727429-168728275	S_Shore
hyper10	FGR_insufficient_1	1.5E-03	0.54	0.24	0.30	6	27661349	cg16615900				
hyper11	FGR_insufficient_1	1.4E-04	0.23	0.10	0.13	6	27661566	cg23078194				
hyper12	FGR_insufficient_1	5.7E-06	0.28	0.04	0.24	6	30071226	cg10102033				
hyper13	FGR_insufficient_1	5.1E-02	0.31	0.04	0.27	6	41605343	cg17094014	TRIM31	3'UTR	chr6:30071225-30071428	Island
hyper14	FGR_insufficient_1	1.9E-10	0.49	0.09	0.40	7	1272325	cg07765161	UNCX	TSS1500	chr6:41604583-41606663	Island
hyper15	FGR_insufficient_1	1.6E-03	0.50	0.08	0.41	8	11665843	cg00262122	FDFT1	Body	chr8:11665773-11666045	Island
hyper16	FGR_insufficient_1	5.1E-02	0.52	0.12	0.40	8	116660586	cg03277455	TRPS1	5'UTR	chr8:116660432-116660747	Island
hyper17	FGR_insufficient_1	1.3E-07	0.49	0.12	0.37	9	16829168	cg07941680	BNC2	Body	chr9:16828935-16829169	Island
hyper18	FGR_insufficient_1	5.9E-07	0.26	0.08	0.18	14	65007512	cg16319578	HSPA2;HSPA2	1stExon;5'UTR	chr14:65006874-65009197	Island
hyper19	FGR_insufficient_1	1.1E-02	0.38	0.18	0.20	14	65008641	cg10856875	HSPA2	1stExon	chr14:65006874-65009197	Island
hyper20	FGR_insufficient_1	1.1E-03	0.16	0.08	0.08	14	65009101	cg15802091	HSPA2	1stExon	chr14:65006874-65009197	Island
hyper21	FGR_insufficient_1	8.9E-03	0.30	0.07	0.23	15	88800510	cg04920689	NTRK3;NTRK3;NTRK3	TSS1500;TSS1500;TSS1500	chr15:88799522-88801017	Island
hyper22	FGR_insufficient_1	3.1E-05	0.15	0.04	0.11	16	699218	cg02734472	WDR90	TSS200	chr16:698826-700244	Island
hyper23	FGR_insufficient_1	1.1E-04	0.14	0.03	0.11	16	699293	cg08806263	WDR90	TSS200	chr16:698826-700244	Island
hyper24	FGR_insufficient_1	1.0E-07	0.40	0.13	0.28	17	26645325	cg10342447	TMEM97	TSS1500	chr17:26645290-26645614	Island
hyper25	FGR_insufficient_1	4.0E-06	0.47	0.05	0.42	17	26645466	cg19026207	TMEM97	TSS1500	chr17:26645290-26645614	Island
hyper26	FGR_insufficient_1	2.3E-08	0.45	0.07	0.38	17	26645861	cg01273840	TMEM97	TSS1500	chr17:26645860-26646055	Island
hyper27	FGR_insufficient_1	8.0E-08	0.48	0.06	0.42	17	26645865	cg03772856	TMEM97	TSS1500	chr17:26645860-26646055	Island
hyper28	FGR_insufficient_1	0.0E+00	0.32	0.01	0.31	17	26645920	cg07078622	TMEM97	TSS200	chr17:26645860-26646055	Island
hyper29	FGR_insufficient_1	7.5E-09	0.37	0.00	0.37	17	26645922	cg21784498	TMEM97	TSS200	chr17:26645860-26646055	Island
hyper30	FGR_insufficient_1	0.0E+00	0.34	0.02	0.31	17	26646013	cg12694510	TMEM97	TSS200	chr17:26645860-26646055	Island
hyper31	FGR_insufficient_1	2.9E-03	0.49	0.01	0.47	17	26646107	cg05898602	TMEM97	TSS200	chr17:26645860-26646055	Island
hyper32	FGR_insufficient_1	1.1E-04	0.48	0.03	0.45	17	26646373	cg07097636	TMEM97	1stExon	chr17:26645860-26646055	Island
hyper33	FGR_insufficient_1	2.8E-08	0.41	0.08	0.33	17	26646651	cg01438829	TMEM97	Body	chr17:26645290-26645614	S_Shore
hyper34	FGR_insufficient_1	3.7E-05	0.07	0.01	0.06	17	37213281	cg04029055				
hyper35	FGR_insufficient_1	9.0E-03	0.15	0.02	0.13	17	62658371	cg25704638	SMURF2;SMURF2	5'UTR;1stExon	chr17:62657409-62658858	Island
hyper36	FGR_insufficient_1	1.1E-02	0.30	0.08	0.22	17	62658750	cg04808672	SMURF2	TSS1500	chr17:62657409-62658858	Island
hyper37	FGR_insufficient_1	3.9E-02	0.24	0.10	0.14	17	62658827	cg22459320	SMURF2	TSS1500	chr17:62657409-62658858	Island
hyper38	FGR_insufficient_1	1.8E-08	0.30	0.05	0.25	19	9785295	cg09686889	ZNF562;ZNF562;ZNF562	5'UTR;5'UTR;5'UTR	chr19:9785480-9785806	N_Shore
hyper39	FGR_insufficient_1	1.1E-08	0.46	0.03	0.43	19	9785511	cg26110904	ZNF562;ZNF562;ZNF562	5'UTR;5'UTR;5'UTR	chr19:9785480-9785806	Island
hyper40	FGR_insufficient_1	0.0E+00	0.48	0.07	0.42	19	9785727	cg02487411	ZNF562;ZNF562;ZNF562;ZNF562	1stExon;5'UTR;5'UTR;5'UTR;1stExon	chr19:9785480-9785806	Island
hyper41	FGR_insufficient_1	0.0E+00	0.48	0.09	0.39	19	9785779	cg18587364	ZNF562;ZNF562;ZNF562	TSS200;TSS200;TSS200	chr19:9785480-9785806	Island
hyper42	FGR_insufficient_1	9.7E-08	0.46	0.08	0.38	19	9785805	cg20631204	ZNF562;ZNF562;ZNF562	TSS200;TSS200;TSS200	chr19:9785480-9785806	Island
hyper43	FGR_insufficient_1	0.0E+00	0.39	0.04	0.35	19	9785906	cg14073063	ZNF562;ZNF562;ZNF562	TSS200;TSS200;TSS200	chr19:9785480-9785806	S_Shore
hyper44	FGR_insufficient_1	0.0E+00	0.03	0.40	0.40	19	9785919	cg14306847	ZNF562;ZNF562;ZNF562	TSS200;TSS200;TSS200	chr19:9785480-9785806	S_Shore
hyper45	FGR_insufficient_1	0.0E+00	0.39	0.05	0.34	19	9786027	cg17704570	ZNF562;ZNF562;ZNF562	TSS1500;TSS1500;TSS1500	chr19:9785480-9785806	S_Shore
hyper46	FGR_insufficient_1	8.0E-09	0.27	0.07	0.20	19	9786115	cg17691880	ZNF562;ZNF562;ZNF562	TSS1500;TSS1500;TSS1500	chr19:9785480-9785806	S_Shore
hyper47	FGR_insufficient_1	4.4E-06	0.36	0.03	0.33	19	53758521	cg04154138	ZNF677	TSS1500	chr19:53757819-537578148	S_Shore
hyper48	FGR_insufficient_1	6.4E-03	0.48	0.12	0.36	19	57751591	cg03252986	ZNF805;ZNF805	TSS1500;TSS1500	chr19:57751888-57752286	N_Shore
hyper49	FGR_insufficient_1	3.4E-02	0.29	0.05	0.24	19	57751691	cg02446106	ZNF805;ZNF805	TSS1500;TSS1500	chr19:57751888-57752286	N_Shore
hyper50	FGR_insufficient_1	0.0E+00	0.29	0.06	0.23	20	14318152	cg23127998	FLRT3;MACROD2;FLRT3;FLRT3	5'UTR;Body;5'UTR;1stExon;1stExon		
hyper51	FGR_insufficient_1	1.1E-07	0.17	0.04	0.12	20	14318398	cg06722503	FLRT3;MACROD2;FLRT3	TSS200;Body;TSS200		
hyper52	FGR_insufficient_1	1.3E-03	0.17	0.07	0.11	20	14318410	cg26082638	FLRT3;MACROD2;FLRT3	TSS200;Body;TSS200		
hyper53	FGR_insufficient_1	4.1E-05	0.12	0.02	0.10	22	38221095	cg01961447	GALR3	Body	chr22:38220589-38221619	Island
hyper54	FGR_insufficient_2	7.9E-02	0.09	0.06	0.04	1	35496883	cg17343472	ZMYM6	5'UTR	chr1:35497121-35497587	N_Shore
hyper55	FGR_insufficient_2	6.4E-06	0.23	0.06	0.17	1	91172982	cg19731044			chr1:91172102-91172771	S_Shore
hyper56	FGR_insufficient_2	5.6E-04	0.14	0.04	0.10	1	111217406	cg26013553	KCNA3	1stExon	chr1:111216244-111217937	Island
hyper57	FGR_insufficient_2	0.0E+00	0.20	0.02	0.19	1	111217497	cg11595545	KCNA3;KCNA3	1stExon;5'UTR	chr1:111216244-111217937	Island
hyper58	FGR_insufficient_2	3.1E-02	0.17	0.09	0.08	1	111217715	cg09410234	KCNA3	TSS200	chr1:111216244-111217937	Island
hyper59	FGR_insufficient_2	4.2E-02	0.25	0.06	0.19	1	207818449	cg26750487	CRIL	TSS200	chr1:207818389-207818952	Island
hyper60	FGR_insufficient_2	8.0E-02	0.22	0.07	0.15	2	290317	cg03468249			chr2:287353-290099	S_Shore
hyper61	FGR_insufficient_2	2.2E-04	0.26	0.11	0.15	2	290382	cg11423790			chr2:287353-290099	S_Shore
hyper62	FGR_insufficient_2	3.5E-07	0.09	0.01	0.08	2	75874389	cg23889112	MRPL19	Body	chr2:75873981-75874420	Island
hyper63	FGR_insufficient_2	1.0E-03	0.17	0.07	0.11	2	145275139	cg17751438	ZEB2;ZEB2;ZEB2	Body;5'UTR;5'UTR	chr2:145273456-145275378	Island
hyper64	FGR_insufficient_2	9.2E-02	0.14	0.08	0.06	2	145275199	cg21701531	ZEB2;ZEB2;ZEB2	Body;5'UTR;5'UTR	chr2:145273456-145275378	Island
hyper65	FGR_insufficient_2	2.8E-07	0.10	0.01	0.09	2	176957842	cg04415176	HOXD13	1stExon	chr2:176957054-176958279	Island
hyper66	FGR_insufficient_2	4.0E-05	0.37	0.03	0.33	3	36805814	cg24144083			chr3:36805949-36806214	N_Shore
hyper67	FGR_insufficient_2	0.0E+00	0.38	0.05	0.32	3	42725643	cg13010797	KBTBD5	TSS1500	chr3:42727084-42727916	N_Shore
hyper68	FGR_insufficient_2	3.5E-04	0.08	0.02	0.06	3	194408845	cg09652652	FAM43A;FAM43A	3'UTR;1stExon	chr3:194406440-194409004	Island
hyper69	FGR_insufficient_2	1.5E-04	0.18	0.02	0.15	4	157997554	cg11163620	GLRB;GLRB;GLRB;GLRB	5'UTR;5'UTR;5'UTR;1stExon	chr4:157997166-157997686	Island
hyper70	FGR_insufficient_2	8.3E-02	0.12	0.07	0.05	5	6917229	cg22736718	TPPP	5'UTR	chr5:691080-691376	Island
hyper71	FGR_insufficient_2	4.0E-08	0.27	0.02	0.25	5	71404443	cg21952901	MAP1B	Body	chr5:71402877-71404868	Island
hyper72	FGR_insufficient_2	1.6E-02	0.12	0.02	0.10	5	132948217	cg04504441	FSTL4;FSTL4	1stExon;5'UTR	chr5:132946744-132948447	Island
hyper73	FGR_insufficient_2	2.0E-07	0.18	0.07	0.11	5	146257653	cg03225002	PPP2R2B;PPP2R2B;PPP2R2B;Pi	5'UTR;5'UTR;1stExon;Body;5'UTR	chr5:146257346-146258575	Island
hyper74	FGR_insufficient_2	1.6E-04	0.17	0.07	0.09	5	146258034	cg13693911	PPP2R2B;PPP2R2B;PPP2R2B;Pi	5'UTR;5'UTR;1stExon;Body;5'UTR	chr5:146257346-146258575	Island
hyper75	FGR_insufficient_2	3.1E-08	0.20	0.08	0.12	5	146258159	cg14693112	PPP2R2B;PPP2R2B;PPP2R2B;Pi	TSS200;5'UTR;Body;5'UTR;5'UTR	chr5:146257346-146258575	Island
hyper76	FGR_insufficient_2	3.1E-06	0.15	0.08	0.07	5	146258181	cg08771423	PPP2R2B;PPP2R2B;PPP2R2B;Pi	TSS200;5'UTR;Body;5'UTR;5'UTR	chr5:146257346-146258575	Island
hyper77	FGR_insufficient_2	1.9E-10	0.19	0.05	0.14	5	146258189	cg146583285	PPP2R2B;PPP2R2B;PPP2R2B;Pi	TSS200;5'UTR;Body;5'UTR;5'UTR	chr5:146257346-146258575	Island
hyper78	FGR_insufficient_2	3.9E-08	0.18	0.03	0.15	5	146258195	cg09528265	PPP2R2B;PPP2R2B;PPP2R2B;Pi	TSS200;5'UTR;Body;5'UTR;5'UTR	chr5:146257346-146258575	Island
hyper79	FGR_insufficient_2	1.3E-09	0.21	0.05	0.16	5	146258354	cg03851984	PPP2R2B;PPP2R2B;PPP2R2B;Pi	TSS200;5'UTR;Body;5'UTR;5'UTR	chr5:146257346-146258575	Island
hyper80	FGR_insufficient_2	3.6E-08	0.17	0.03	0.14	5	146258427	cg25149751	PPP2R2B;PPP2R2B;PPP2R2B;Pi	5'UTR;Body;5'UTR;5'UTR;Body;T	chr5:146257346-146258575	Island
hyper81	FGR_insufficient_2	5.3E-09	0.22	0.07	0.15	5	146258461	cg13659005	PPP2R2B;PPP2R2B;PPP2R2B;Pi	TSS200;5'UTR;Body;5'UTR;TSS2	chr5:146257346-146258575	Island
hyper82	FGR_insufficient_2	3.1E-09	0.24	0.03	0.21	5	146258					

hyper125	FGR_insufficient_2	1.5E-02	0.22	0.12	0.09	16	2196781	cg26112564	RAB26;RAB26	1stExon;5'UTR	chr16:2198455-2199129	Island
hyper126	FGR_insufficient_2	1.9E-10	0.15	0.01	0.14	16	28074384	cg03394150	GSGL1	Body	chr16:28073817-28075296	Island
hyper127	FGR_insufficient_2	5.8E-02	0.06	0.02	0.04	16	28074462	cg10471437	GSGL1	1stExon	chr16:28073817-28075296	Island
hyper128	FGR_insufficient_2	5.1E-02	0.09	0.03	0.07	16	52580987	cg26817217	TOX3;TOX3	5'UTR;TSS200	chr16:52581293-52581610	N_Shore
hyper129	FGR_insufficient_2	5.0E-04	0.17	0.01	0.16	16	56623390	cg08270206	MT3;MT3	5'UTR;1stExon	chr16:56623068-56623914	Island
hyper130	FGR_insufficient_2	3.2E-04	0.09	0.02	0.06	17	19648414	cg13453033	ALDH3A1;ALDH3A1	Body;Body;1stExon	chr17:19648139-19648492	Island
hyper131	FGR_insufficient_2	2.0E-02	0.24	0.11	0.13	17	79859932	cg22700894	NP8	TSS200	chr17:79859808-79860363	Island
hyper132	FGR_insufficient_2	8.2E-03	0.31	0.19	0.12	17	79859945	cg20081244	NP8	TSS200	chr17:79859808-79860363	Island
hyper133	FGR_insufficient_2	2.9E-05	0.25	0.07	0.18	17	79859947	cg08983997	NP8	TSS200	chr17:79859808-79860363	Island
hyper134	FGR_insufficient_2	1.4E-02	0.16	0.04	0.11	19	4247036	cg11358933	CCDC94	TSS200	chr19:4246828-4247222	Island
hyper135	FGR_insufficient_2	2.3E-02	0.22	0.10	0.12	19	31839734	cg06196755	TSZH3	Body	chr19:31839635-31843049	Island
hyper136	FGR_insufficient_2	1.3E-04	0.13	0.04	0.09	19	31841391	cg00545804	TSZH3	TSS1500	chr19:31839635-31843049	Island
hyper137	FGR_insufficient_2	4.1E-05	0.26	0.07	0.19	19	44302906	cg20110633	LYPD5;LYPD5	Body;Body	chr19:44302665-44303176	Island
hyper138	FGR_insufficient_2	0.0E+00	0.22	0.02	0.20	19	44303058	cg16900980	LYPD5;LYPD5	Body;Body	chr19:44302665-44303176	Island
hyper139	FGR_insufficient_2	3.6E-09	0.18	0.07	0.11	19	44405818	cg13933427			chr19:44405817-44406053	Island
hyper140	FGR_insufficient_2	4.7E-04	0.17	0.07	0.09	19	44529414	cg20254725	ZNF222;ZNF222	TSS200;TSS200	chr19:44529393-44529778	Island
hyper141	FGR_insufficient_2	1.6E-03	0.14	0.01	0.13	19	54599221	cg11196851	OSCAR;OSCAR;OSCAR;OSCAR	Body;Body;Body;Body	chr19:54599160-54599456	Island
hyper142	FGR_insufficient_2	8.1E-02	0.19	0.02	0.18	19	54599285	cg00606351	OSCAR;OSCAR;OSCAR;OSCAR	Body;Body;Body;Body	chr19:54599160-54599456	Island
hyper143	FGR_insufficient_2	3.4E-02	0.05	0.01	0.04	19	56953996	cg12137286	SHISA7	1stExon	chr19:56953371-56954641	Island
hyper144	FGR_insufficient_2	0.0E+00	0.34	0.03	0.31	19	56915622	cg02776314	ZNF583;ZNF583;ZNF583	5'UTR;TSS200;TSS200	chr19:56915356-56915856	Island
hyper145	FGR_insufficient_2	1.0E-07	0.28	0.08	0.20	19	56915650	cg00796360	ZNF583;ZNF583;ZNF583	5'UTR;TSS200;TSS200	chr19:56915356-56915856	Island
hyper146	FGR_insufficient_2	1.56E-03	0.27	0.08	0.18	19	56915653	cg21119079	ZNF583;ZNF583;ZNF583	5'UTR;TSS200;TSS200	chr19:56915356-56915856	Island
hyper147	FGR_insufficient_2	0.0E+00	0.28	0.01	0.27	19	56915655	cg02806624	ZNF583;ZNF583;ZNF583	5'UTR;TSS200;TSS200	chr19:56915356-56915856	Island
hyper148	FGR_insufficient_2	0.0E+00	0.27	0.03	0.24	19	56915658	cg20790208	ZNF583;ZNF583;ZNF583	5'UTR;TSS200;TSS200	chr19:56915356-56915856	Island
hyper149	FGR_insufficient_2	9.7E-11	0.45	0.06	0.39	19	56915732	cg01873234	ZNF583;ZNF583;ZNF583;ZNF583	1stExon;1stExon;5'UTR;5'UTR	chr19:56915356-56915856	Island
hyper150	FGR_insufficient_2	1.9E-03	0.22	0.19	0.20	20	13200930	cg04291219	ISM1	TSS1500	chr20:13200670-13202616	Island
hyper151	FGR_insufficient_2	1.2E-09	0.16	0.01	0.15	20	13200954	cg12664209	ISM1	TSS1500	chr20:13200670-13202616	Island
hyper152	FGR_insufficient_2	3.3E-05	0.18	0.05	0.13	20	13200973	cg06262346	ISM1	TSS1500	chr20:13200670-13202616	Island
hyper153	FGR_insufficient_2	4.3E-09	0.15	0.01	0.14	20	13200980	cg09491991	ISM1	TSS1500	chr20:13200670-13202616	Island
hyper154	FGR_insufficient_2	5.8E-09	0.09	0.01	0.08	20	13200982	cg26322248	ISM1	TSS1500	chr20:13200670-13202616	Island
hyper155	FGR_insufficient_2	6.9E-05	0.19	0.04	0.15	21	34442360	cg17016394	OLIG1	TSS200	chr21:34442206-34444543	Island
hyper156	FGR_insufficient_2	9.4E-09	0.11	0.01	0.10	21	34442511	cg05720454	OLIG1;OLIG1	1stExon;5'UTR	chr21:34442206-34444543	Island
hyper157	FGR_insufficient_2	3.9E-04	0.18	0.09	0.09	21	34442674	cg02736969	OLIG1	1stExon	chr21:34442206-34444543	Island
hyper158	FGR_insufficient_2	2.1E-07	0.21	0.06	0.15	21	34443010	cg03732762	OLIG1	1stExon	chr21:34442206-34444543	Island
hyper159	FGR_insufficient_2	4.0E-02	0.16	0.07	0.08	22	36323395	cg12797594	RBMY;RBMY;RBMY;RBMY;RBMY	5'UTR;Body;Body;5'UTR;5'UTR;1stExon;1stExon;1stExon;5'UTR;1stExon	chr1:1950411-1951479	Island
hyper160	FGR_insufficient_2	2.5E-02	0.28	0.10	0.18	1	1950616	cg09107007	GABRD	TSS200		
hyper161	FGR_insufficient_2	2.7E-04	0.21	0.07	0.14	1	35417078	cg00866953	KIAA1026	Body		
hyper162	FGR_insufficient_2	3.3E-03	0.17	0.07	0.10	1	36772006	cg03506609	C1orf113;C1orf113	TSS1500;Body	chr1:36771830-36773009	Island
hyper163	FGR_insufficient_2	1.5E-06	0.17	0.02	0.16	1	36772095	cg13446200	C1orf113;C1orf113	TSS1500;Body	chr1:36771830-36773009	Island
hyper164	FGR_insufficient_2	1.5E-04	0.21	0.06	0.15	1	36772417	cg05903806	C1orf113;C1orf113	TSS1500;Body	chr1:36771830-36773009	Island
hyper165	FGR_insufficient_2	1.2E-02	0.19	0.03	0.16	1	115632576	cg17131030	TSPAN2	TSS1500	chr1:115631850-115632584	Island
hyper166	FGR_insufficient_2	1.7E-02	0.19	0.03	0.16	1	166134282	cg18687774	FAM178B	Body	chr1:166134258-166136448	Island
hyper167	FGR_insufficient_2	3.9E-02	0.17	0.07	0.09	1	18236097	cg12535697	GLUL;GLUL;GLUL	5'UTR;TSS200;5'UTR	chr1:18235967-182361563	S_Shore
hyper168	FGR_insufficient_2	1.1E-07	0.20	0.08	0.12	1	209921370	cg06541795			chr1:209920953-209921345	S_Shore
hyper169	FGR_insufficient_2	2.6E-02	0.05	0.01	0.04	1	22956030	cg08090133	SRP9;SRP9	TSS200;TSS200	chr1:22956330-229565734	Island
hyper170	FGR_insufficient_2	3.6E-04	0.17	0.02	0.14	2	2636566	cg13354988	ACPI1;ACPI1;SH3YL1;ACPI1;SH3Y1	TSS1500;TSS1500;Body;TSS1500	chr2:2634040-265238	Island
hyper171	FGR_insufficient_2	1.1E-03	0.13	0.07	0.06	2	14775132	cg11533098	FAM64A	3'UTR	chr2:14773277-14775809	Island
hyper172	FGR_insufficient_2	0.0E+00	0.36	0.06	0.29	3	112931390	cg13765303	BOC;BOC	1stExon;5'UTR	chr3:112930437-112931506	Island
hyper173	FGR_insufficient_2	3.9E-02	0.57	0.33	0.25	3	166636307	cg15486124				
hyper174	FGR_insufficient_2	6.1E-07	0.23	0.07	0.16	3	197183416	cg26048523			chr3:197183404-197183724	Island
hyper175	FGR_insufficient_2	0.0E+00	0.30	0.02	0.27	3	197183582	cg25221442			chr3:197183404-197183724	Island
hyper176	FGR_insufficient_2	3.9E-10	0.31	0.03	0.27	3	197183662	cg11302533			chr3:197183404-197183724	Island
hyper177	FGR_insufficient_2	1.4E-05	0.28	0.09	0.19	4	4874548	cg17684202			chr4:487262-4873613	S_Shore
hyper178	FGR_insufficient_2	4.1E-02	0.19	0.09	0.10	4	48271107	cg17566936	TEC	5'UTR	chr4:48271362-48271846	N_Shore
hyper179	FGR_insufficient_2	1.6E-02	0.05	0.01	0.03	5	68485104	cg05567409	CENPH	TSS1500	chr5:6848515-68485577	N_Shore
hyper180	FGR_insufficient_2	3.8E-06	0.21	0.05	0.17	5	167000712	cg22554488	ODZ2	Body		
hyper181	FGR_insufficient_2	1.4E-04	0.31	0.03	0.28	5	178487123	cg08522107	ZNF354C	TSS1500	chr5:178487146-178487921	N_Shore
hyper182	FGR_insufficient_2	0.0E+00	0.32	0.02	0.37	5	178487310	cg15781115	ZNF354C	TSS1500	chr5:178487146-178487921	Island
hyper183	FGR_insufficient_2	4.7E-04	0.40	0.02	0.38	5	178487384	cg12623648	ZNF354C	TSS1500	chr5:178487146-178487921	Island
hyper184	FGR_insufficient_2	4.6E-05	0.25	0.05	0.20	5	178487465	cg07470489	ZNF354C	TSS200	chr5:178487146-178487921	Island
hyper185	FGR_insufficient_2	1.6E-04	0.28	0.04	0.24	5	178487481	cg11538128	ZNF354C	TSS200	chr5:178487146-178487921	Island
hyper186	FGR_insufficient_2	2.1E-05	0.30	0.05	0.24	5	178487485	cg08278489	ZNF354C	TSS200	chr5:178487146-178487921	Island
hyper187	FGR_insufficient_2	4.7E-03	0.35	0.07	0.28	5	178487500	cg10802132	ZNF354C	TSS200	chr5:178487146-178487921	Island
hyper188	FGR_insufficient_2	2.5E-02	0.37	0.06	0.31	5	178487576	cg007515940	ZNF354C	TSS200	chr5:178487146-178487921	Island
hyper189	FGR_insufficient_2	1.3E-05	0.06	0.01	0.05	6	13814565	cg18831738	CCDC90A	1stExon	chr6:13813943-13814946	Island
hyper190	FGR_insufficient_2	0.0E+00	0.31	0.03	0.28	7	12250161	cg06286300	TMEM106B;TMEM106B	TSS1500;TSS1500	chr7:12250720-12251214	N_Shore
hyper191	FGR_insufficient_2	0.0E+00	0.34	0.02	0.32	7	12250517	cg24949795	TMEM106B;TMEM106B	TSS1500;TSS1500	chr7:12250720-12251214	N_Shore
hyper192	FGR_insufficient_2	0.0E+00	0.24	0.01	0.23	7	12251200	cg27479937	TMEM106B;TMEM106B	5'UTR;5'UTR	chr7:12250720-12251214	Island
hyper193	FGR_insufficient_2	0.0E+00	0.38	0.05	0.33	7	12251342	cg21597649	TMEM106B;TMEM106B	5'UTR;5'UTR	chr7:12250720-12251214	S_Shore
hyper194	FGR_insufficient_2	1.8E-06	0.17	0.06	0.11	7	14028845	cg16805994	ETV1;ETV1;ETV1;ETV1	5'UTR;5'UTR;5'UTR;5'UTR	chr7:14029378-14029593	N_Shore
hyper195	FGR_insufficient_2	7.2E-05	0.11	0.04	0.07	7	14028954	cg21249126	ETV1;ETV1;ETV1;ETV1	5'UTR;5'UTR;5'UTR;5'UTR	chr7:14029378-14029593	N_Shore
hyper196	FGR_insufficient_2	3.4E-08	0.38	0.08	0.30	7	14029015	cg03932308	ETV1;ETV1;ETV1;ETV1	5'UTR;5'UTR;5'UTR;5'UTR	chr7:14029378-14029593	N_Shore
hyper197	FGR_insufficient_2	4.1E-05	0.22	0.07	0.15	7	14029057	cg30232919	ETV1;ETV1;ETV1;ETV1	5'UTR;5'UTR;5'UTR;5'UTR	chr7:14029378-14029593	N_Shore
hyper198	FGR_insufficient_2	0.0E+00	0.29	0.07	0.22	7	14029085	cg05164808	ETV1;ETV1;ETV1;ETV1	5'UTR;5'UTR;5'UTR;5'UTR	chr7:14029378-14029593	N_Shore
hyper199	FGR_insufficient_2	2.2E-08	0.18	0.05	0.14	7	14029265	cg31368779	ETV1;ETV1;ETV1;ETV1;ETV1	1stExon;5'UTR;5'UTR;5'UTR;1stExon	chr7:14029378-14029593	N_Shore
hyper200	FGR_insufficient_2	8.3E-04	0.34	0.08	0.25	7	14029514	cg11104510	ETV1;ETV1;ETV1;ETV1;ETV1;ET	1stExon;5'UTR;5'UTR;5'UTR;1stExon	chr7:14029378-14029593	Island
hyper201	FGR_insufficient_2	1.6E-05	0.24	0.07	0.17	7	42927968	cg00587042				
hyper202	FGR_insufficient_2	1.3E-05	0.42	0.05	0.37	7	42928245	cg16168014				
hyper203	FGR_insufficient_2	5.5E-02	0.08	0.01	0.06	7	44363536	cg16073349	CAMK2B;CAMK2B;CAMK2B	TSS1500;TSS1500;TSS1500;TSS	chr7:4436432-44365328	S_Shore
hyper204	FGR_insufficient_2	4.4E-02	0.27	0.11	0.16	7	101398152	cg14823389				
hyper205	FGR_insufficient_2	3.0E-04	0.27	0.09	0.18	7	101398177	cg221214489				
hyper206	FGR_insufficient_2	7.4E-08	0.43	0.11	0.32	7	142960387	cg				

hyper254	FGR_insufficient_3	0.0E+00	0.38	0.03	0.34	18	8367375	cg02996413	LOC100192426;PTRPM;PTRPM	TSS1500;Body;Body	chr18:8367273-8367599	Island
hyper255	FGR_insufficient_3	1.9E-10	0.45	0.05	0.40	18	8367425	cg25705486	LOC100192426;PTRPM;PTRPM	TSS1500;Body;Body	chr18:8367273-8367599	Island
hyper256	FGR_insufficient_3	4.8E-02	0.21	0.12	0.09	19	11533199	cg24185441	CCDC151	Body	chr19:11533198-11533619	Island
hyper257	FGR_insufficient_3	6.0E-05	0.09	0.02	0.07	19	38924182	cg02026160	RYR1;RYR1	TSS200;TSS200	chr19:38924239-38924519	N_Shore
hyper258	FGR_insufficient_3	5.5E-08	0.19	0.08	0.12	19	41882232	cg17831002	TMEM91;TMEM91;TMEM91;TMEM91	TSS1500;TSS1500;TSS1500;TSS1500	chr19:41882507-41882773	N_Shore
hyper259	FGR_insufficient_3	1.6E-09	0.15	0.05	0.10	19	41882324	cg12942614	TMEM91;TMEM91;TMEM91;TMEM91	TSS1500;TSS1500;TSS1500;TSS1500	chr19:41882507-41882773	N_Shore
hyper260	FGR_insufficient_3	1.4E-03	0.15	0.01	0.14	19	55973320	cg21753400	ISOC2;ISOC2;ISOC2	TSS1500;TSS1500;TSS1500	chr19:55972697-55973442	Island
hyper261	FGR_insufficient_3	4.0E-02	0.17	0.03	0.15	19	55973338	cg22563390	ISOC2;ISOC2;ISOC2	TSS1500;TSS1500;TSS1500	chr19:55972697-55973442	Island
hyper262	FGR_insufficient_3	6.4E-02	0.06	0.02	0.04	19	57049777	cg25680341	ZFP28	TSS1500	chr19:57049775-57050646	Island
hyper263	FGR_insufficient_3	2.9E-04	0.07	0.02	0.05	22	19132003	cg02080761	DGCR14	Body	chr22:19131992-19132297	Island
hyper264	FGR_insufficient_3	8.6E-03	0.07	0.02	0.05	22	50247415	cg20911168	ZBED4	TSS200	chr22:50246590-50248143	Island
hyper265	FGR_insufficient_4	7.2E-05	0.23	0.07	0.16	1	50488319	cg16260421	AGBL4	Body	chr1:50488417-50489846	N_Shore
hyper266	FGR_insufficient_4	3.9E-02	0.30	0.04	0.25	1	50513661	cg19098763	ELAVL4	TSS200	chr1:50513644-50514320	Island
hyper267	FGR_insufficient_4	3.6E-04	0.70	0.28	0.42	1	55504971	cg14993491	PCSK9	TSS1500	chr1:55505060-55506015	N_Shore
hyper268	FGR_insufficient_4	2.8E-06	0.13	0.03	0.10	1	76540574	cg21526205	ST6GALNAC3;ST6GALNAC3	Body;Body	chr1:76540147-76540653	Island
hyper269	FGR_insufficient_4	4.0E-05	0.20	0.05	0.15	1	76540641	cg21753866	ST6GALNAC3;ST6GALNAC3	Body;Body	chr1:76540147-76540653	Island
hyper270	FGR_insufficient_4	7.0E-06	0.23	0.09	0.14	2	11294738	cg09450367	PQLC3	TSS1500	chr2:11295559-11296006	N_Shore
hyper271	FGR_insufficient_4	2.7E-02	0.23	0.04	0.18	2	17721803	cg08031368	VSNL1	TSS200	chr2:17721537-17722021	Island
hyper272	FGR_insufficient_4	1.4E-06	0.09	0.01	0.07	2	51259493	cg08008931	NRXN1;NRXN1;NRXN1;NRXN1	1stExon;5'UTR;1stExon;5'UTR	chr2:51254522-51255498	S_Shelf
hyper273	FGR_insufficient_4	1.3E-02	0.16	0.08	0.08	2	85197811	cg21474384	KCMF1	TSS1500	chr2:85197445-85199321	Island
hyper274	FGR_insufficient_4	0.0E+00	0.42	0.06	0.35	2	88489792	cg18490616	THNSL2	TSS200	chr2:88486991-88470386	Island
hyper275	FGR_insufficient_4	0.0E+00	0.31	0.05	0.26	2	88470173	cg07952391	THNSL2	5'UTR	chr2:88469691-88470386	Island
hyper276	FGR_insufficient_4	0.0E+00	0.27	0.10	0.17	2	220083306	cg23547073	ABC86	1stExon	chr2:22008091-220084012	Island
hyper277	FGR_insufficient_4	0.0E+00	0.39	0.00	0.39	2	220083302	cg27486695	ABC86;ABC86	5'UTR;1stExon	chr2:22008299-220084012	Island
hyper278	FGR_insufficient_4	0.0E+00	0.23	0.04	0.19	2	220083665	cg26544277	ABC86	TSS200	chr2:22008299-220084012	Island
hyper279	FGR_insufficient_4	5.9E-10	0.07	0.05	0.27	2	220083916	cg2126680	ABC86	TSS1500	chr2:22008299-220084012	Island
hyper280	FGR_insufficient_4	0.0E+00	0.25	0.07	0.17	2	220083951	cg06716437	ABC86	TSS1500	chr2:22008299-220084012	Island
hyper281	FGR_insufficient_4	3.5E-02	0.38	0.06	0.32	3	35680980	cg24623247	EXOGE;EXOGE	Body;Body	chr3:35680509-35681628	Island
hyper282	FGR_insufficient_4	8.2E-02	0.38	0.11	0.27	3	38531868	cg16788250	EXOGE;EXOGE	Body;Body	chr3:38537682-38538071	S_Shore
hyper283	FGR_insufficient_4	7.4E-05	0.27	0.09	0.19	3	131246020	cg01966168			chr3:131245721-131246021	Island
hyper284	FGR_insufficient_4	6.6E-03	0.10	0.03	0.07	3	184971699	cg03414569	EHHADH;EHHADH;EHHADH	5'UTR;Body;1stExon	chr3:184971641-184972002	Island
hyper285	FGR_insufficient_4	7.8E-10	0.10	0.01	0.09	3	184971844	cg02738081	EHHADH;EHHADH;EHHADH;EHHADH	5'UTR;1stExon;1stExon;5'UTR	chr3:184971641-184972002	Island
hyper286	FGR_insufficient_4	1.1E-02	0.14	0.02	0.12	4	41883680	cg16146177			chr4:41883492-41884570	Island
hyper287	FGR_insufficient_4	4.8E-06	0.40	0.04	0.36	4	140952109	cg27341708	MAML3	Body		
hyper288	FGR_insufficient_4	2.2E-03	0.09	0.02	0.08	6	29600583	cg14128584	GABBR1;GABBR1	5'UTR;5'UTR	chr6:29600192-29600661	Island
hyper289	FGR_insufficient_4	6.5E-02	0.17	0.05	0.12	7	8473457	cg00852549	NXP1	TSS200	chr7:8473139-8475179	Island
hyper290	FGR_insufficient_4	3.0E-05	0.21	0.04	0.17	7	64712472	cg05841659			chr7:64712213-64712786	Island
hyper291	FGR_insufficient_4	4.0E-02	0.04	0.01	0.03	7	140714747	cg08522707	MRPS33;MRPS33;MRPS33	5'UTR;1stExon;TSS1500	chr7:140714478-140714943	Island
hyper292	FGR_insufficient_4	2.6E-06	0.16	0.02	0.14	8	12051240	cg21196034	FAM86B1;FAM86B1	Body;Body	chr8:12051096-12052607	Island
hyper293	FGR_insufficient_4	1.9E-04	0.21	0.08	0.13	8	30770121	cg070119143			chr8:30769264-30770122	Island
hyper294	FGR_insufficient_4	8.9E-02	0.30	0.09	0.21	9	97101029	cg12420162	DMRT3	1stExon	chr9:976162-977828	Island
hyper295	FGR_insufficient_4	4.1E-03	0.07	0.02	0.05	10	74202076	cg12795885			chr10:74202073-742021023	Island
hyper296	FGR_insufficient_4	4.8E-02	0.25	0.09	0.16	10	129705132	cg14325851	PTPRE	TSS200	chr10:129705217-129706237	N_Shore
hyper297	FGR_insufficient_4	6.7E-04	0.26	0.11	0.14	10	129705158	cg00355169	PTPRE	TSS200	chr10:129705217-129706237	N_Shore
hyper298	FGR_insufficient_4	4.7E-09	0.25	0.09	0.16	10	129705196	cg20299263	PTPRE	TSS200	chr10:129705217-129706237	N_Shore
hyper299	FGR_insufficient_4	1.9E-10	0.31	0.11	0.21	10	129705218	cg16442044	PTPRE	TSS200	chr10:129705217-129706237	N_Shore
hyper300	FGR_insufficient_4	1.3E-08	0.15	0.03	0.12	12	29938839	cg08729318	TMTCT1	5'UTR	chr12:29935995-29937433	Island
hyper301	FGR_insufficient_4	0.0E+00	0.23	0.07	0.15	12	29936845	cg20140110	TMTCT1	5'UTR	chr12:29935995-29937433	Island
hyper302	FGR_insufficient_4	4.1E-02	0.12	0.06	0.06	12	46890546	cg02021175				
hyper303	FGR_insufficient_4	5.8E-04	0.16	0.06	0.10	12	121533833	cg01556017			chr12:121533571-121533923	Island
hyper304	FGR_insufficient_4	1.9E-06	0.16	0.06	0.10	14	39630301	cg20553470	TRAPPC68;TRAPPC68	Body;Body	chr14:39633964-39639635	N_Shore
hyper305	FGR_insufficient_4	4.0E-04	0.26	0.10	0.16	14	62279702	cg10981009			chr14:62279476-62280019	Island
hyper306	FGR_insufficient_4	9.9E-03	0.08	0.03	0.05	16	3313947	cg23754665			chr16:3313946-3314789	Island
hyper307	FGR_insufficient_4	2.3E-02	0.20	0.10	0.10	16	4421654	cg02048412	VASN;CORO7	TSS200;Body	chr16:4421642-4422240	Island
hyper308	FGR_insufficient_4	1.9E-10	0.24	0.05	0.18	16	4422216	cg10102242	VASN;CORO7	5'UTR;Body	chr16:4421642-4422240	Island
hyper309	FGR_insufficient_4	1.1E-08	0.30	0.11	0.20	16	4422228	cg12071544	VASN;CORO7	5'UTR;Body	chr16:4421642-4422240	Island
hyper310	FGR_insufficient_4	7.9E-05	0.09	0.02	0.07	16	54962963	cg09293786			chr16:54962422-54969785	N_Shore
hyper311	FGR_insufficient_4	3.9E-10	0.05	0.01	0.26	17	27138003	cg17801691	C17orf63;C17orf63	5'UTR;5'UTR	chr17:27138185-27139671	N_Shore
hyper312	FGR_insufficient_4	0.0E+00	0.40	0.03	0.37	17	27138292	cg09684846	C17orf63;C17orf63	5'UTR;5'UTR	chr17:27138185-27139671	Island
hyper313	FGR_insufficient_4	0.0E+00	0.43	0.07	0.35	17	27139669	cg17613452	C17orf63;C17orf63	5'UTR;5'UTR	chr17:27138185-27139671	Island
hyper314	FGR_insufficient_4	0.0E+00	0.39	0.04	0.35	17	27139688	cg00977744	C17orf63;C17orf63	5'UTR;5'UTR	chr17:27138185-27139671	S_Shore
hyper315	FGR_insufficient_4	0.0E+00	0.40	0.05	0.35	19	30019369	cg09584454	VSTM2B	Body	chr19:30015781-30021367	Island
hyper316	FGR_insufficient_4	0.0E+00	0.24	0.03	0.21	19	41771748	cg01777748	HNRNPUL1;HNRNPUL1;HNRNPUL1	5'UTR;1stExon;5'UTR	chr19:41771713-41771113	Island
hyper317	FGR_insufficient_4	1.4E-03	0.13	0.05	0.08	19	44439215	cg09466880			chr19:44439200-44439612	Island
hyper318	FGR_insufficient_4	4.7E-02	0.26	0.03	0.23	19	44529683	cg09922628	ZNF222;ZNF222	5'UTR;Body	chr19:44529393-44529718	Island
hyper319	FGR_insufficient_4	5.7E-04	0.06	0.02	0.04	19	46405944	cg20152630	MYPOP	TSS200	chr19:46404537-46406455	Island
hyper320	FGR_insufficient_4	2.2E-03	0.43	0.04	0.39	19	56904945	cg02763101	ZNF582	TSS200	chr19:56904636-56905355	Island
hyper321	FGR_insufficient_4	3.1E-03	0.35	0.08	0.27	19	58095424	cg02653557	ZIK1	TSS1500	chr19:58094739-58095764	Island
hyper322	FGR_insufficient_4	2.1E-05	0.26	0.02	0.25	19	58095468	cg04342092	ZIK1	TSS200	chr19:58094739-58095764	Island
hyper323	FGR_insufficient_4	4.1E-04	0.56	0.16	0.40	19	58095588	cg12060744	ZIK1	TSS200	chr19:58094739-58095764	Island
hyper324	FGR_insufficient_4	2.7E-04	0.54	0.11	0.43	19	58095588	cg10461044	ZIK1	TSS200	chr19:58094739-58095764	Island
hyper325	FGR_insufficient_5	5.3E-03	0.35	0.04	0.31	2	43903582	cg09132607	PLEKH2;LOC728819	Body;TSS200		
hyper326	FGR_insufficient_5	3.1E-05	0.49	0.05	0.44	2	43903650	cg02111748	PLEKH2;LOC728819	Body;TSS200		
hyper327	FGR_insufficient_5	1.9E-10	0.15	0.01	0.15	3	46734981	cg1616841	ALS2CL	5'UTR	chr3:46734731-46735717	Island
hyper328	FGR_insufficient_5	8.4E-03	0.12	0.04	0.08	3	46735152	cg23444101	ALS2CL;ALS2CL	1stExon;5'UTR	chr3:46734731-46735717	Island
hyper329	FGR_insufficient_5	0.0E+00	0.27	0.02	0.25	3	46735315	cg03271029	ALS2CL	TSS200	chr3:46734731-46735717	Island
hyper330	FGR_insufficient_5	5.1E-06	0.09	0.02	0.07	3	46733319	cg07279281	ALS2CL	TSS200	chr3:46734731-46735717	Island
hyper331	FGR_insufficient_5	1.9E-10	0.23	0.04	0.20	3	46733335	cg19455322	ALS2CL	TSS200	chr3:46734731-46735717	Island
hyper332	FGR_insufficient_5	1.5E-05	0.26	0.10	0.16	3	46733338	cg21379004	ALS2CL	TSS200	chr3:46734731-46735717	Island
hyper333	FGR_insufficient_5	5.4E-04	0.16	0.04	0.12	3	46735454	cg25104512	ALS2CL	TSS1500	chr3:46734731-46735717	Island
hyper334	FGR_insufficient_5	9.4E-04	0.12	0.01	0.11	3	114866927	cg20784525	ZBTB20	TSS1500	chr3:114865436-114867124	Island
hyper335	FGR_insufficient_5	3.0E-03	0.24	0.05	0.18	5	134879818	cg14410395			chr5:134879443-134879819	Island
hyper336	FGR_insufficient_5	5.3E-03	0.36	0.03	0.32	5	134879961	cg18193764			chr5:134879443-134879819	

hyper383	FGR_adequate_1	0.0E+00	0.22	0.01	0.20	17	8055756	cg23363911	PER1	TSS200	chr17:8054550-8055835	Island
hyper384	FGR_adequate_1	0.0E+00	0.23	0.08	0.15	17	8055831	cg14158601	PER1	TSS200	chr17:8054550-8055835	Island
hyper385	FGR_adequate_1	1.9E-10	0.25	0.08	0.17	17	8055834	cg21093368	PER1	TSS200	chr17:8054550-8055835	Island
hyper386	FGR_adequate_1	1.2E-02	0.17	0.09	0.07	17	8055884	cg20503576	PER1	TSS200	chr17:8054550-8055835	S_Shore
hyper387	FGR_adequate_1	1.7E-06	0.26	0.12	0.14	17	8055888	cg16545079	PER1	TSS200	chr17:8054550-8055835	S_Shore
hyper388	FGR_adequate_1	2.8E-03	0.21	0.08	0.13	17	41116355	cg20848987	AARSD1;AARSD1	Body,Body	chr17:41116349-41116651	Island
hyper389	FGR_adequate_1	3.2E-02	0.28	0.04	0.24	17	41116479	cg25104488	AARSD1;AARSD1	Body,Body	chr17:41116349-41116651	Island
hyper390	FGR_adequate_1	0.0E+00	0.25	0.02	0.23	17	41116483	cg18658096	AARSD1;AARSD1	Body,Body	chr17:41116349-41116651	Island
hyper391	FGR_adequate_1	1.9E-02	0.23	0.08	0.15	17	41116517	cg16143763	AARSD1;AARSD1	Body,Body	chr17:41116349-41116651	Island
hyper392	FGR_adequate_1	1.3E-03	0.14	0.06	0.08	18	28621490	cg11814235	DSC3;DSC3	Body,Body	chr18:28621489-28623117	Island
hyper393	FGR_adequate_1	3.9E-05	0.19	0.04	0.15	19	17448797	cg09793057	GTPBP3;GTPBP3;GTPBP3	Body,Body,Body	chr19:17448735-17449043	Island
hyper394	FGR_adequate_1	3.8E-04	0.08	0.01	0.06	22	19754125	cg106719719	TBX1;TBX1;TBX1	Body,Body,Body	chr22:19753312-19755013	Island
hyper395	FGR_adequate_1	2.4E-02	0.15	0.08	0.07	22	19754448	cg21507095	TBX1;TBX1;TBX1	Body,3'UTR,Body	chr22:19753312-19755013	Island
hyper396	FGR_adequate_2	1.9E-04	0.15	0.05	0.10	1	151119109	cg00427454	SEMA6C	TSS200	chr1:151118049-151119373	Island
hyper397	FGR_adequate_2	6.3E-05	0.30	0.12	0.17	1	162792246	cg10588211			chr1:162792176-162792574	Island
hyper398	FGR_adequate_2	1.2E-07	0.16	0.04	0.11	2	24307701	cg08714407	TP53I3;TP53I3	Body;1stExon	chr2:24307026-24307678	Island
hyper399	FGR_adequate_2	6.0E-05	0.21	0.07	0.14	2	24307515	cg06005408	TP53I3;TP53I3;TP53I3	1stExon;5'UTR;5'UTR	chr2:24307026-24307678	Island
hyper400	FGR_adequate_2	4.8E-02	0.19	0.10	0.10	2	24307741	cg20763553	TP53I3;TP53I3	TSS200;TSS200	chr2:24307026-24307678	S_Shore
hyper401	FGR_adequate_2	7.5E-04	0.26	0.07	0.19	4	118006405	cg08145625	TRAM1L1	1stExon	chr4:118006538-118006859	N_Shore
hyper402	FGR_adequate_2	3.4E-03	0.24	0.07	0.18	4	118006429	cg07038423	TRAM1L1	1stExon	chr4:118006538-118006859	N_Shore
hyper403	FGR_adequate_2	9.4E-03	0.34	0.02	0.32	4	118006619	cg21599320	TRAM1L1;TRAM1L1	1stExon;5'UTR	chr4:118006538-118006859	Island
hyper404	FGR_adequate_2	2.1E-03	0.33	0.03	0.30	4	118006747	cg24183909	TRAM1L1	TSS200	chr4:118006538-118006859	Island
hyper405	FGR_adequate_2	5.4E-03	0.42	0.06	0.36	4	118006750	cg07837556	TRAM1L1	TSS200	chr4:118006538-118006859	Island
hyper406	FGR_adequate_2	1.1E-07	0.35	0.03	0.32	4	118006808	cg05807991	TRAM1L1	TSS200	chr4:118006538-118006859	Island
hyper407	FGR_adequate_2	2.6E-08	0.26	0.02	0.24	4	118006812	cg11163579	TRAM1L1	TSS200	chr4:118006538-118006859	Island
hyper408	FGR_adequate_2	4.9E-06	0.31	0.08	0.23	4	118006825	cg10271829	TRAM1L1	TSS200	chr4:118006538-118006859	Island
hyper409	FGR_adequate_2	8.5E-02	0.19	0.07	0.12	4	118006832	cg19041681	TRAM1L1	TSS200	chr4:118006538-118006859	Island
hyper410	FGR_adequate_2	8.6E-02	0.04	0.01	0.03	4	129209112	cg13841734	PGRMC2	TSS200	chr4:129208297-129209780	Island
hyper411	FGR_adequate_2	6.0E-04	0.19	0.07	0.12	4	163085081	cg22161476	FSTL5;FSTL5;FSTL5;FSTL5;FSTL5	1stExon;1stExon;5'UTR;5'UTR;1stExon;5'UTR		
hyper412	FGR_adequate_2	1.8E-03	0.15	0.08	0.07	4	163085311	cg18424393	FSTL5;FSTL5;FSTL5	TSS200;TSS200;TSS200		
hyper413	FGR_adequate_2	1.4E-09	0.30	0.12	0.18	4	163085318	cg14650167	FSTL5;FSTL5;FSTL5	TSS200;TSS200;TSS200		
hyper414	FGR_adequate_2	2.9E-06	0.19	0.07	0.12	4	163085342	cg18695917	FSTL5;FSTL5;FSTL5	TSS200;TSS200;TSS200		
hyper415	FGR_adequate_2	9.7E-10	0.27	0.06	0.21	4	163085348	cg03767310	FSTL5;FSTL5;FSTL5	TSS200;TSS200;TSS200		
hyper416	FGR_adequate_2	2.9E-10	0.24	0.06	0.18	4	163085403	cg26105150	FSTL5;FSTL5;FSTL5	TSS1500;TSS1500;TSS1500		
hyper417	FGR_adequate_2	9.7E-11	0.23	0.06	0.18	4	163085411	cg26883282	FSTL5;FSTL5;FSTL5	TSS1500;TSS1500;TSS1500		
hyper418	FGR_adequate_2	0.0E+00	0.22	0.06	0.17	4	163085663	cg01734786	FSTL5;FSTL5;FSTL5	TSS1500;TSS1500;TSS1500		
hyper419	FGR_adequate_2	0.0E+00	0.22	0.07	0.15	4	163085697	cg13808714	FSTL5;FSTL5;FSTL5	TSS1500;TSS1500;TSS1500		
hyper420	FGR_adequate_2	9.9E-05	0.12	0.03	0.09	5	18771335	cg18349911			chr5:1874907-1879032	Island
hyper421	FGR_adequate_2	1.0E-04	0.34	0.04	0.31	5	175793049	cg07352345	ARL10	Body	chr5:175792355-175793055	Island
hyper422	FGR_adequate_2	1.1E-02	0.09	0.01	0.08	8	17711561	cg04932639	ARHGEF10	TSS1500	chr8:17711361-1772760	Island
hyper423	FGR_adequate_2	1.0E-05	0.12	0.02	0.09	11	66824445	cg04420309	RNID	1stExon	chr11:66824118-66824621	Island
hyper424	FGR_adequate_2	4.6E-02	0.43	0.04	0.39	12	11653600	cg05659091			chr12:11653232-11653775	Island
hyper425	FGR_adequate_2	1.7E-04	0.17	0.04	0.13	13	42846195	cg12578287	AKAP11	TSS200	chr13:42845853-42846807	Island
hyper426	FGR_adequate_2	8.1E-02	0.36	0.07	0.29	13	42846648	cg08791849	AKAP11	5'UTR	chr13:42845853-42846807	Island
hyper427	FGR_adequate_2	5.5E-07	0.19	0.05	0.14	15	41805300	cg27496526	LTK;LTK;LTK	Body,Body,Body	chr15:41803443-41805331	Island
hyper428	FGR_adequate_2	1.9E-03	0.38	0.17	0.21	17	27277673	cg08657247	PHF12;PHF12	TSS1500;TSS1500	chr17:27276219-27278877	S_Shore
hyper429	FGR_adequate_2	1.2E-06	0.17	0.05	0.12	21	34638868	cg17943175	IL10RB	Body	chr21:34638515-34639075	Island
hyper430	FGR_adequate_2	6.0E-05	0.14	0.06	0.08	21	34638971	cg17506742	IL10RB	Body	chr21:34638515-34639075	Island
hyper431	FGR_adequate_2	5.8E-02	0.07	0.03	0.05	21	34639113	cg14280424	IL10RB	Body	chr21:34638515-34639075	S_Shore
hyper432	FGR_adequate_3	0.0E+00	0.23	0.02	0.21	1	714526	cg04231937			chr1:713984-714547	Island
hyper433	FGR_adequate_3	6.6E-07	0.22	0.08	0.14	1	714565	cg04496485			chr1:713984-714547	S_Shore
hyper434	FGR_adequate_3	0.0E+00	0.17	0.01	0.15	1	22140859	cg17456100	LDLRAD2	Body	chr1:22140891-22141407	N_Shore
hyper435	FGR_adequate_3	2.8E-05	0.11	0.02	0.09	1	22141014	cg15467466	LDLRAD2	Body	chr1:22140891-22141407	Island
hyper436	FGR_adequate_3	0.0E+00	0.41	0.05	0.36	1	23894874	cg07422195			chr1:23894640-23895064	Island
hyper437	FGR_adequate_3	0.0E+00	0.29	0.02	0.27	1	23894902	cg04567466			chr1:23894640-23895064	Island
hyper438	FGR_adequate_3	4.3E-03	0.10	0.04	0.06	1	25943438	cg26890920	MAN1C1	TSS1500	chr1:25944099-25944772	N_Shore
hyper439	FGR_adequate_3	1.2E-09	0.22	0.08	0.15	1	35450601	cg14517250			chr1:35450649-35451037	N_Shore
hyper440	FGR_adequate_3	1.9E-10	0.38	0.10	0.28	1	35450650	cg15190509			chr1:35450649-35451037	Island
hyper441	FGR_adequate_3	0.0E+00	0.38	0.01	0.37	1	35450787	cg26792589			chr1:35450649-35451037	Island
hyper442	FGR_adequate_3	4.9E-08	0.27	0.09	0.17	1	35451172	cg10379872			chr1:35450649-35451037	S_Shore
hyper443	FGR_adequate_3	1.4E-03	0.40	0.07	0.32	1	52195547	cg22812770	OSBP1L;OSBP1L;OSBP1L;OSBP1L	5'UTR;1stExon;Body;5'UTR;Body	chr1:52195028-52195821	Island
hyper444	FGR_adequate_3	6.5E-07	0.31	0.07	0.24	1	52195686	cg06327150	OSBP1L;OSBP1L;OSBP1L;OSBP1L	5'UTR;Body;Body;5'UTR;Body;Box	chr1:52195028-52195821	Island
hyper445	FGR_adequate_3	8.6E-02	0.14	0.02	0.12	1	228196227	cg26332740	WNT3A	Body	chr1:22819406-22819524	Island
hyper446	FGR_adequate_3	0.0E+00	0.75	0.03	0.72	2	28614638	cg11133114	FSO2L2	TSS1500	chr2:28612964-28616748	Island
hyper447	FGR_adequate_3	0.0E+00	0.33	0.04	0.28	2	227656248	cg19045733	IRS1	3'UTR	chr2:227655903-227656647	Island
hyper448	FGR_adequate_3	0.0E+00	0.44	0.06	0.38	2	227656261	cg07514207	IRS1	3'UTR	chr2:227655903-227656647	Island
hyper449	FGR_adequate_3	0.0E+00	0.34	0.07	0.27	2	227656408	cg02049847	IRS1	3'UTR	chr2:227655903-227656647	Island
hyper450	FGR_adequate_3	3.9E-10	0.34	0.05	0.29	2	227656417	cg08626939	IRS1	3'UTR	chr2:227655903-227656647	Island
hyper451	FGR_adequate_3	4.2E-02	0.07	0.03	0.04	2	237477186	cg12463851	CXCR7	TSS1500	chr2:237476311-237477263	Island
hyper452	FGR_adequate_3	5.8E-03	0.10	0.03	0.06	2	242673979	cg24430517	D2GHGD	TSS200	chr2:242673653-242675106	Island
hyper453	FGR_adequate_3	1.1E-05	0.33	0.12	0.20	3	40518595	cg22218636	ZNFB19;ZNFB19;ZNFB19;ZNFB19	TSS200;TSS200;TSS200;TSS200	chr3:40518517-40518848	Island
hyper454	FGR_adequate_3	2.3E-08	0.43	0.15	0.28	3	40518669	cg26132612	ZNFB19;ZNFB19;ZNFB19;ZNFB19	1stExon;Body;1stExon;5'UTR;5'UTR	chr3:40518517-40518848	Island
hyper455	FGR_adequate_3	1.3E-09	0.33	0.05	0.27	3	40518742	cg00417297	ZNFB19;ZNFB19;ZNFB19;ZNFB19	1stExon;Body;1stExon;5'UTR;5'UTR	chr3:40518517-40518848	Island
hyper456	FGR_adequate_3	4.3E-08	0.06	0.33	0.33	3	40518745	cg23713321	ZNFB19;ZNFB19;ZNFB19;ZNFB19	1stExon;Body;1stExon;5'UTR;5'UTR	chr3:40518517-40518848	Island
hyper457	FGR_adequate_3	1.8E-03	0.18	0.08	0.10	3	43731973	cg14121103	ABHD5	TSS1500	chr3:43731998-43733108	N_Shore
hyper458	FGR_adequate_3	1.9E-03	0.16	0.06	0.10	3	43732102	cg15150852	ABHD5	TSS1500	chr3:43731998-43733108	Island
hyper459	FGR_adequate_3	2.5E-04	0.21	0.10	0.11	3	122745685	cg10084513	SEMA5B	5'UTR	chr3:122745183-122746986	Island
hyper460	FGR_adequate_3	1.9E-05	0.36	0.04	0.32	3	134369939	cg22889573	KY	TSS200	chr3:134369464-134370242	Island
hyper461	FGR_adequate_3	7.6E-04	0.19	0.04	0.14	3	134369974	cg00060320	KY	TSS200	chr3:134369464-134370242	Island
hyper462	FGR_adequate_3	1.9E-03	0.30	0.07	0.23	3	134369987	cg12307306	KY	TSS200	chr3:134369464-134370242	Island
hyper463	FGR_adequate_3	8.7E-03	0.21	0.09	0.13	3	134370046	cg24370755	KY	TSS200	chr3:134369464-134370242	Island
hyper464	FGR_adequate_3	2.7E-07	0.19	0.06	0.13	4	4544010	cg16107224	STX18	TSS1500	chr4:4543437-4544104	Island
hyper465	FGR_adequate_3	1.2E-04	0.14	0.04</								

hyper512	FGR_adequate_3	1.3E-03	0.25	0.12	0.14	10	49813142	cg25290938	ARHGAP22	TSS200	chr10:49812852-49813352	Island
hyper513	FGR_adequate_3	1.3E-05	0.26	0.05	0.21	10	49813155	cg10242724	ARHGAP22	TSS200	chr10:49812852-49813352	Island
hyper514	FGR_adequate_3	3.7E-02	0.14	0.07	0.07	10	54073642	cg27411220	DDK1	TSS1500	chr10:54073989-54074827	N_Shore
hyper515	FGR_adequate_3	1.5E-02	0.05	0.01	0.04	10	111683345	cg06697697	XPNPEP1;XPNPEP1;XPNPEP1	TSS200;TSS200;TSS200	chr10:111682775-111683483	Island
hyper516	FGR_adequate_3	1.5E-02	0.14	0.04	0.10	11	790177	cg14183693	CEND1	TSS200	chr11:791953-792400	N_Shore
hyper517	FGR_adequate_3	2.1E-05	0.30	0.10	0.20	11	11643760	cg1975007	GALNTL4	TSS200	chr11:11642121-11643819	Island
hyper518	FGR_adequate_3	5.4E-02	0.54	0.14	0.40	11	69258203	cg06921552			chr11:69258149-69258544	Island
hyper519	FGR_adequate_3	1.4E-02	0.45	0.17	0.28	11	69259477	cg04729730			chr11:69258149-69258544	Island
hyper520	FGR_adequate_3	7.2E-06	0.08	0.28	0.20	12	49297569	cg22827806	CCDC65	TSS1500		
hyper521	FGR_adequate_3	2.4E-03	0.20	0.08	0.12	12	49297574	cg16869573	CCDC65;CCDC65	1stExon;5'UTR		
hyper522	FGR_adequate_3	2.9E-09	0.52	0.13	0.39	12	54567248	cg11426224				
hyper523	FGR_adequate_3	3.0E-03	0.28	0.09	0.19	12	54567476	cg15344914				
hyper524	FGR_adequate_3	7.4E-02	0.07	0.03	0.04	12	58145986	cg16716518	CDK4;CDK4	5'UTR;1stExon	chr12:58145853-58146360	Island
hyper525	FGR_adequate_3	1.4E-04	0.45	0.05	0.40	12	12268708	cg27049761	B3GNT4	5'UTR	chr12:122687800-122689106	Island
hyper526	FGR_adequate_3	6.6E-09	0.45	0.05	0.40	12	122688787	cg23445859	B3GNT4	5'UTR	chr12:122687800-122689106	Island
hyper527	FGR_adequate_3	7.5E-04	0.46	0.12	0.34	12	122688969	cg11970289	B3GNT4	5'UTR	chr12:122687800-122689106	Island
hyper528	FGR_adequate_3	1.3E-08	0.21	0.07	0.14	12	125411780	cg09234599			chr12:125412891-125413165	N_Shore
hyper529	FGR_adequate_3	8.4E-02	0.12	0.06	0.06	14	56568290	cg25465634	DLGAP5;DLGAP5;DLGAP5;DLGAP5	5'UTR;1stExon;5'UTR;1stExon	chr14:55658232-55658550	Island
hyper530	FGR_adequate_3	7.2E-05	0.38	0.05	0.33	14	70038884	cg18477200	C14orf162	TSS1500	chr14:70038108-70040302	Island
hyper531	FGR_adequate_3	4.0E-04	0.35	0.07	0.27	14	70038925	cg02380334	C14orf162	TSS1500	chr14:70038108-70040302	Island
hyper532	FGR_adequate_3	0.0E+00	0.71	0.07	0.65	14	77494451	cg02583546	C14orf4;C14orf4	5'UTR;1stExon	chr14:77491938-77492576	Island
hyper533	FGR_adequate_3	2.2E-02	0.80	0.50	0.30	15	62516405	cg03455316			chr15:62516324-62516805	Island
hyper534	FGR_adequate_3	1.9E-02	0.39	0.15	0.24	16	2844049	cg25618731	TESSP1	TSS200	chr16:284426-2849145	N_Shore
hyper535	FGR_adequate_3	3.3E-05	0.31	0.03	0.28	16	55699443	cg09321400	SLC6A2	TSS200	chr16:55699598-55699895	Island
hyper536	FGR_adequate_3	1.3E-03	0.31	0.03	0.28	16	89641296	cg24428821	CPNIE7;CPNIE7	TSS1500;TSS1500	chr16:89641053-89643415	Island
hyper537	FGR_adequate_3	2.1E-06	0.14	0.01	0.13	17	11708640	cg22122171	PLD6;PLD6	1stExon;5'UTR	chr17:11708673-11709301	Island
hyper538	FGR_adequate_3	5.3E-08	0.11	0.01	0.10	17	11708651	cg11392858	PLD6	TSS200	chr17:11708771-117109701	Island
hyper539	FGR_adequate_3	3.6E-05	0.09	0.02	0.07	17	11709678	cg23661344	PLD6	TSS200	chr17:11708771-117109701	Island
hyper540	FGR_adequate_3	3.0E-04	0.23	0.06	0.17	17	17109740	cg00572586	PLD6	TSS200	chr17:17109893-17110296	N_Shore
hyper541	FGR_adequate_3	3.4E-03	0.18	0.08	0.11	17	33760419	cg18587557	SLFN12	TSS1500		
hyper542	FGR_adequate_3	3.5E-02	0.16	0.09	0.07	17	46688490	cg09357097	H0XB7	TSS200	chr17:46687527-46688730	Island
hyper543	FGR_adequate_3	2.1E-04	0.31	0.04	0.28	17	46688593	cg24712277	H0XB7	TSS1500	chr17:46687527-46688730	Island
hyper544	FGR_adequate_3	2.7E-02	0.37	0.06	0.31	17	46688729	cg22291922	H0XB7	TSS1500	chr17:46687527-46688730	Island
hyper545	FGR_adequate_3	7.1E-02	0.33	0.06	0.27	17	46688845	cg23730436	H0XB7	TSS1500	chr17:46690390-46691055	N_Shore
hyper546	FGR_adequate_3	3.9E-02	0.04	0.01	0.03	17	61905144	cg22530822	FTSJ3;PSMCS	TSS200;Body	chr17:61904726-61905184	Island
hyper547	FGR_adequate_3	8.9E-06	0.25	0.10	0.15	17	66192411	cg25077430			chr17:66192363-66195873	Island
hyper548	FGR_adequate_3	1.3E-07	0.34	0.09	0.25	17	66192886	cg13537781			chr17:66192363-66195873	Island
hyper549	FGR_adequate_3	4.1E-03	0.38	0.09	0.30	17	79370518	cg06873452			chr17:79366806-79374742	Island
hyper550	FGR_adequate_3	3.7E-03	0.43	0.09	0.34	17	79371014	cg18549292			chr17:79366806-79374742	Island
hyper551	FGR_adequate_3	1.1E-03	0.10	0.03	0.07	18	11908803	cg16860267	MPPE1	TSS200	chr18:11908222-11909308	Island
hyper552	FGR_adequate_3	2.2E-02	0.20	0.09	0.11	19	17798325	cg26496291	UNC13A	TSS1500	chr19:17798679-17799329	Island
hyper553	FGR_adequate_3	9.9E-03	0.15	0.04	0.10	19	26227770	cg22456785			chr19:36822395-36822690	S_Shore
hyper554	FGR_adequate_3	4.5E-04	0.24	0.06	0.18	19	47742829	cg17384056			chr19:47742725-47743515	Island
hyper555	FGR_adequate_3	1.3E-02	0.10	0.03	0.07	19	55851052	cg18844304	SUV420H2	TSS200	chr19:55850495-55851493	Island
hyper556	FGR_adequate_3	4.1E-03	0.10	0.05	0.05	19	56136139	cg00766729	ZNF784	TSS200	chr19:56135773-56136007	S_Shore
hyper557	FGR_adequate_3	1.5E-02	0.11	0.04	0.08	20	36793705	cg08545268	TGM2;TGM2	TSS200;TSS200	chr20:36793549-36793867	Island
hyper558	FGR_adequate_3	2.3E-04	0.07	0.02	0.05	20	36793715	cg12947626	TGM2;TGM2	TSS200;TSS200	chr20:36793549-36793867	Island
hyper559	FGR_adequate_3	5.6E-04	0.05	0.01	0.04	20	36793726	cg11059239	TGM2;TGM2	TSS200;TSS200	chr20:36793549-36793867	Island
hyper560	FGR_adequate_3	2.2E-03	0.12	0.07	0.05	20	44440497	cg03408301	UBE2C;UBE2C;UBE2C;UBE2C;U	TSS1500;TSS1500;TSS1500;TSS	chr20:44440496-44441655	Island
hyper561	FGR_adequate_3	3.0E-04	0.27	0.09	0.18	20	45338122	cg08038974	SLC2A10	TSS200	chr20:45338071-45338663	Island
hyper562	FGR_adequate_3	0.0E+00	0.42	0.01	0.41	20	45338239	cg13690178	SLC2A10;SLC2A10	5'UTR;1stExon	chr20:45338071-45338663	Island
hyper563	FGR_adequate_3	0.0E+00	0.45	0.08	0.37	20	45338396	cg16117472	SLC2A10	Body	chr20:45338071-45338663	Island
hyper564	FGR_adequate_3	0.0E+00	0.34	0.06	0.28	20	45338652	cg17550582	SLC2A10	Body	chr20:45338071-45338663	Island
hyper565	FGR_adequate_3	7.3E-02	0.29	0.08	0.21	22	31002942	cg00788739	TGN2	TSS1500		
hyper566	FGR_adequate_3	0.0E+00	0.35	0.11	0.25	22	39378235	cg14194956	APOBEC3B	TSS200		
hyper567	FGR_adequate_3	1.9E-10	0.26	0.06	0.20	22	39378382	cg25787886	APOBEC3B	TSS200		
hyper568	FGR_adequate_3	6.5E-03	0.14	0.05	0.09	22	42095368	cg10296410	MEI1	TSS200	chr22:42095414-42096189	N_Shore
hyper569	FGR_adequate_4	7.9E-01	0.01	0.13	0.1	1	60529487	cg05933935	NHPHA;NHPHA	1stExon;5'UTR	chr1:6051505-6052955	Island
hyper570	FGR_adequate_4	0.0E+00	0.11	0.01	0.10	1	60529495	cg00931619	NHPHA;NHPHA	1stExon;5'UTR	chr1:6051505-6052955	Island
hyper571	FGR_adequate_4	0.0E+00	0.12	0.01	0.12	1	60529500	cg20797142	NHPHA;NHPHA	1stExon;5'UTR	chr1:6051505-6052955	Island
hyper572	FGR_adequate_4	4.9E-10	0.22	0.08	0.14	1	8483390	cg15889173	RERE;RERE;RERE	5'UTR;Body;Body	chr1:8483389-8484339	Island
hyper573	FGR_adequate_4	0.0E+00	0.20	0.03	0.17	1	8483475	cg22736444	RERE;RERE;RERE	5'UTR;Body;Body	chr1:8483389-8484339	Island
hyper574	FGR_adequate_4	0.0E+00	0.20	0.02	0.18	1	8484169	cg15492466	RERE;RERE;RERE	Body;TSS1500;Body	chr1:8483389-8484339	Island
hyper575	FGR_adequate_4	0.0E+00	0.21	0.02	0.19	1	8484310	cg23843414	RERE;RERE;RERE	Body;TSS1500;Body	chr1:8483389-8484339	Island
hyper576	FGR_adequate_4	7.7E-07	0.21	0.04	0.17	1	111097901	cg04780572			chr1:11109806-111098362	N_Shore
hyper577	FGR_adequate_4	6.8E-02	0.16	0.02	0.14	1	223316531	cg17598909	TLR5	5'UTR	chr1:223316185-223316689	Island
hyper578	FGR_adequate_4	4.6E-02	0.07	0.02	0.05	1	236305619	cg17269630	GPR137B	TSS1500	chr1:23630554-236306674	Island
hyper579	FGR_adequate_4	4.5E-02	0.05	0.01	0.04	1	236305663	cg07425541	GPR137B	TSS200	chr1:23630554-236306674	Island
hyper580	FGR_adequate_4	1.3E-08	0.15	0.06	0.10	1	236305785	cg21434251	GPR137B;GPR137B	1stExon;5'UTR	chr1:23630554-236306674	Island
hyper581	FGR_adequate_4	0.0E+00	0.16	0.01	0.15	1	236306000	cg09169938	GPR137B	1stExon	chr1:23630554-236306674	Island
hyper582	FGR_adequate_4	2.5E-02	0.18	0.09	0.09	1	236306311	cg26534058	GPR137B	1stExon	chr1:23630554-236306674	Island
hyper583	FGR_adequate_4	1.2E-02	0.24	0.08	0.17	2	121200503	cg21856256			chr2:121200503-121200788	Island
hyper584	FGR_adequate_4	4.7E-02	0.18	0.09	0.09	3	10857890	cg26836233	SLC6A11	TSS200	chr3:10857867-10858447	Island
hyper585	FGR_adequate_4	4.3E-05	0.06	0.18	0.3	3	11205189	cg21031025	CD200;CD200	TSS200;TSS200	chr3:112051893-112052406	Island
hyper586	FGR_adequate_4	9.7E-11	0.48	0.06	0.42	3	19665938	cg05938285	PIGZ	TSS1500	chr3:196659319-196670065	Island
hyper587	FGR_adequate_4	7.7E-02	0.55	0.04	0.51	3	196697064	cg00826889	PIGZ	TSS1500	chr3:196659319-196670065	Island
hyper588	FGR_adequate_4	4.2E-05	0.14	0.07	0.07	4	73433671	cg07044040	ADAMTS3	Body	chr4:73433783-73434289	N_Shore
hyper589	FGR_adequate_4	1.9E-06	0.11	0.02	0.09	4	73433788	cg18123319	ADAMTS3	Body	chr4:73433783-73434289	Island
hyper590	FGR_adequate_4	7.0E-07	0.27	0.09	0.18	4	73434035	cg08232905	ADAMTS3	Body	chr4:73433783-73434289	Island
hyper591	FGR_adequate_4	0.0E+00	0.24	0.04	0.20	4	73434209	cg13643796	ADAMTS3	Body	chr4:73433783-73434289	Island
hyper592	FGR_adequate_4	2.2E-04	0.13	0.03	0.09	4	73434487	cg25889750	ADAMTS3;ADAMTS3	1stExon;5'UTR	chr4:73434855-73435321	N_Shore
hyper593	FGR_adequate_4	4.3E-09	0.29	0.07	0.22	4	73434591	cg15102770	ADAMTS3	TSS200	chr4:73434855-73435321	N_Shore
hyper594	FGR_adequate_4	4.4E-06	0.32	0.12	0.20	4	73434820	cg27185819	ADAMTS3	TSS1500	chr4:73434855-73435321	N_Shore
hyper595	FGR_adequate_4	0.0E+00	0.26	0.04	0.21	4	73434856	cg11243196	ADAMTS3			

hyper641	FGR_adequate_4	2.9E-03	0.10	0.04	0.07	15	41952458	cg17178280	MGA,MGA	TSS200,TSS200	chr15:41952535-41953222	N_Shore
hyper642	FGR_adequate_4	5.7E-06	0.24	0.04	0.19	15	41952645	cg22546696	MGA,MGA,MGA,MGA	1stExon;5'UTR;5'UTR	chr15:41952535-41953222	Island
hyper643	FGR_adequate_4	5.7E-08	0.12	0.02	0.09	15	41952827	cg24856258	MGA,MGA	5'UTR;5'UTR	chr15:41952535-41953222	Island
hyper644	FGR_adequate_4	5.6E-02	0.29	0.05	0.23	15	41953061	cg25826226	MGA,MGA	5'UTR;5'UTR	chr15:41952535-41953222	Island
hyper645	FGR_adequate_4	9.4E-06	0.19	0.03	0.16	16	3079708	cg07868599	CCDC64B	Body	chr16:30795636-3079954	Island
hyper646	FGR_adequate_4	2.9E-05	0.20	0.06	0.13	17	70536484	cg09672890			chr17:70536483-70536687	Island
hyper647	FGR_adequate_4	8.4E-04	0.26	0.10	0.16	19	9517858	cg23891996			chr19:9517468-9517986	Island
hyper648	FGR_adequate_4	8.4E-03	0.25	0.09	0.16	19	38042472	cg03975694		5'UTR;1stExon	chr19:38039561-38040395	S_Shelf
hyper649	FGR_adequate_4	1.5E-05	0.18	0.04	0.14	19	54928734	cg23695837	TTYH1;TTYH1	1stExon;1stExon	chr19:54927902-54928225	Island
hyper650	FGR_adequate_4	8.2E-03	0.09	0.03	0.05	19	58352628	cg16615451	ZNF552	TSS200	chr19:58352655-58352830	Island
hyper651	FGR_adequate_4	1.6E-03	0.28	0.06	0.22	20	58508888	cg20800536			chr20:58507755-58509517	Island
hyper652	FGR_adequate_4	9.4E-04	0.34	0.07	0.27	20	58508922	cg02801359			chr20:58507755-58509517	Island
hyper653	FGR_adequate_4	4.7E-03	0.35	0.02	0.33	20	58508943	cg26690949			chr20:58507755-58509517	Island
hyper654	FGR_adequate_4	9.1E-04	0.25	0.09	0.16	20	58509242	cg00125414			chr20:58507755-58509517	Island
hyper655	FGR_adequate_4	7.6E-03	0.23	0.09	0.14	20	58509298	cg14536096			chr20:58507755-58509517	Island
hyper656	FGR_adequate_4	2.0E-03	0.09	0.01	0.08	21	47063285	cg01145054			chr21:47061773-47064308	Island
hyper657	FGR_adequate_5	0.0E+00	0.30	0.02	0.28	1	84464645	cg00773459	TLL7,TLL7	1stExon;5'UTR	chr1:84464223-84465232	Island
hyper658	FGR_adequate_5	1.6E-04	0.12	0.03	0.09	1	11326148	cg26044038			chr1:113261468-113261765	Island
hyper659	FGR_adequate_5	5.3E-05	0.09	0.02	0.07	1	11326163	cg10839663			chr1:113261468-113261765	Island
hyper660	FGR_adequate_5	4.5E-03	0.14	0.07	0.07	1	19657723	cg14664759	KCNT2	TSS1500	chr1:196577708-196580711	Island
hyper661	FGR_adequate_5	2.1E-02	0.07	0.02	0.05	1	23435003	cg10701282	SLC35F3	Body	chr1:234349884-234350471	Island
hyper662	FGR_adequate_5	8.3E-03	0.21	0.03	0.18	2	175201062	cg00153110	SP9	Body	chr2:175199463-175202639	Island
hyper663	FGR_adequate_5	0.0E+00	0.23	0.02	0.21	5	175792478	cg22424536	ARL10	TSS200	chr5:175792355-175793505	Island
hyper664	FGR_adequate_5	3.6E-03	0.26	0.02	0.24	5	175792498	cg09155701	ARL10	TSS200	chr5:175792355-175793505	Island
hyper665	FGR_adequate_5	4.4E-03	0.32	0.02	0.29	5	175792510	cg26720389	ARL10;ARL10	1stExon;5'UTR	chr5:175792355-175793505	Island
hyper666	FGR_adequate_5	7.9E-02	0.04	0.02	0.08	8	48100416	cg57467051			chr8:48100163-48100891	Island
hyper667	FGR_adequate_5	1.9E-08	0.10	0.01	0.09	8	48100429	cg02230854			chr8:48100163-48100891	Island
hyper668	FGR_adequate_5	0.0E+00	0.20	0.06	0.14	9	26956236	cg14408431	IFT74;IFT74;IFT74;IFT74	5'UTR;5'UTR;TSS200;TSS200	chr9:26956301-26956770	N_Shore
hyper669	FGR_adequate_5	3.6E-08	0.16	0.04	0.13	9	26956302	cg00415978	IFT74;IFT74;IFT74;IFT74	5'UTR;5'UTR;TSS200;TSS200	chr9:26956301-26956770	Island
hyper670	FGR_adequate_5	9.3E-04	0.07	0.02	0.05	13	38924368	cg004012509	UFM1	Body	chr13:38923957-38924413	Island
hyper671	FGR_adequate_5	4.8E-06	0.17	0.02	0.15	13	78493100	cg04390523	EDNRB;EDNRB;EDNRB	5'UTR;TSS200;TSS200	chr13:78492425-78493382	Island
hyper672	FGR_adequate_5	1.9E-02	0.19	0.09	0.10	13	78493182	cg001910869	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	Island
hyper673	FGR_adequate_5	1.6E-02	0.15	0.06	0.09	13	78493294	cg12602112	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	Island
hyper674	FGR_adequate_5	9.8E-03	0.18	0.07	0.11	13	78493297	cg19650157	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	Island
hyper675	FGR_adequate_5	3.1E-02	0.14	0.04	0.11	13	78493359	cg13434989	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	Island
hyper676	FGR_adequate_5	3.2E-02	0.16	0.06	0.10	13	78493313	cg10016380	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	Island
hyper677	FGR_adequate_5	6.9E-03	0.22	0.07	0.15	13	78493365	cg19742055	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	Island
hyper678	FGR_adequate_5	3.3E-04	0.20	0.07	0.13	13	78493561	cg06057566	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	S_Shore
hyper679	FGR_adequate_5	1.2E-04	0.20	0.03	0.16	13	78493561	cg25717994	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	S_Shore
hyper680	FGR_adequate_5	8.4E-07	0.15	0.02	0.14	13	78493561	cg09152886	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	S_Shore
hyper681	FGR_adequate_5	7.9E-02	0.18	0.08	0.10	13	78493561	cg16738796	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	S_Shore
hyper682	FGR_adequate_5	7.5E-05	0.17	0.05	0.11	13	78493574	cg1364111	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	S_Shore
hyper683	FGR_adequate_5	4.4E-02	0.19	0.08	0.12	13	78493590	cg12983394	EDNRB;EDNRB;EDNRB	TSS1500;5'UTR;TSS1500	chr13:78492425-78493382	S_Shore
hyper684	FGR_adequate_5	3.7E-03	0.05	0.01	0.04	13	108867893	cg05180121	LIG4;LIG4;LIG4	TSS1500;TSS200;5'UTR	chr13:108867107-108867364	S_Shore
hyper685	FGR_adequate_5	1.6E-03	0.33	0.05	0.28	15	83316223	cg27587811	CPEB1	Body	chr15:83315116-83317541	Island
hyper686	FGR_adequate_5	5.5E-02	0.23	0.11	0.12	15	83316911	cg24319381	CPEB1	TSS200	chr15:83315116-83317541	Island
hyper687	FGR_adequate_5	1.9E-05	0.33	0.12	0.21	16	85722694	cg27360527	GINS2	TSS200	chr16:85722209-85722941	Island
hyper688	FGR_adequate_5	0.0E+00	0.11	0.01	0.10	17	33569747	cg21383891	SLFN5	TSS1500	chr17:33569141-33570527	Island
hyper689	FGR_adequate_5	4.0E-05	0.20	0.03	0.17	19	46916741	cg06747432	CCDC8;CCDC8	1stExon;5'UTR	chr19:46916587-46916862	Island
hyper690	FGR_adequate_5	2.8E-03	0.19	0.05	0.14	20	22565240	cg06697267	FOXA2;FOXA2	5'UTR;TSS200	chr20:22562736-22566104	Island
hyper691	FGR_excessive_1	4.3E-07	0.32	0.12	0.20	1	47691158	cg10380348	TAL1	Body	chr1:47690980-47691727	Island
hyper692	FGR_excessive_1	2.0E-02	0.18	0.06	0.12	1	47691160	cg10810752	TAL1	Body	chr1:47690980-47691727	Island
hyper693	FGR_excessive_1	2.3E-08	0.22	0.07	0.15	1	77747875	cg17484154	AK5;AK5;AK5	1stExon;TSS1500;5'UTR	chr1:77747314-77748224	Island
hyper694	FGR_excessive_1	4.7E-07	0.32	0.02	0.31	1	77747987	cg04867733	AK5;AK5;AK5	1stExon;TSS1500;5'UTR	chr1:77747314-77748224	Island
hyper695	FGR_excessive_1	7.2E-03	0.21	0.03	0.18	1	91196332	cg14419975			chr1:91190489-91192804	S_Shelf
hyper696	FGR_excessive_1	4.9E-02	0.11	0.03	0.08	1	99470618	cg19365673	LPFR5;LPFR5	TSS200;TSS200	chr1:99469932-99470988	Island
hyper697	FGR_excessive_1	6.5E-04	0.24	0.12	0.13	1	116380316	cg11071826	NHLH2;NHLH2	3'UTR;3'UTR	chr1:116380359-116382364	N_Shore
hyper698	FGR_excessive_1	5.9E-03	0.13	0.03	0.20	1	116380417	cg21863110	NHLH2;NHLH2	3'UTR;3'UTR	chr1:116380359-116382364	Island
hyper699	FGR_excessive_1	0.0E+00	0.38	0.01	0.36	1	116380572	cg25979559	NHLH2;NHLH2	3'UTR;3'UTR	chr1:116380359-116382364	Island
hyper700	FGR_excessive_1	2.4E-04	0.21	0.08	0.13	1	116380946	cg00960552	NHLH2;NHLH2	Body;Body	chr1:116380359-116382364	Island
hyper701	FGR_excessive_1	9.2E-02	0.19	0.02	0.17	1	147624510	cg10127479			chr1:147623646-147624656	Island
hyper702	FGR_excessive_1	7.2E-08	0.30	0.11	0.19	1	239549830	cg08542090			chr1:239550108-239551339	N_Shore
hyper703	FGR_excessive_1	9.7E-03	0.12	0.07	0.06	1	239549853	cg23684246			chr1:239550108-239551339	N_Shore
hyper704	FGR_excessive_1	6.7E-04	0.16	0.05	0.11	1	239550177	cg22017581			chr1:239550108-239551339	Island
hyper705	FGR_excessive_1	1.1E-06	0.37	0.02	0.35	1	239550378	cg00371368			chr1:239550108-239551339	Island
hyper706	FGR_excessive_1	2.4E-03	0.33	0.08	0.25	2	37572289	cg17304496	QPCT	Body	chr2:37571676-37572397	Island
hyper707	FGR_excessive_1	9.0E-02	0.28	0.10	0.18	2	66803697	cg09902029			chr2:66802890-66804831	Island
hyper708	FGR_excessive_1	1.9E-10	0.26	0.07	0.18	2	69968558	cg19353425	ANXA4	TSS1500	chr2:69968749-69969592	N_Shore
hyper709	FGR_excessive_1	8.8E-10	0.23	0.04	0.19	2	69968602	cg17372745	ANXA4	TSS1500	chr2:69968749-69969592	N_Shore
hyper710	FGR_excessive_1	0.0E+00	0.30	0.01	0.29	2	69968853	cg09547034	ANXA4	TSS1500	chr2:69968749-69969592	Island
hyper711	FGR_excessive_1	0.0E+00	0.49	0.09	0.40	2	69968919	cg26034355	ANXA4	TSS1500	chr2:69968749-69969592	Island
hyper712	FGR_excessive_1	0.0E+00	0.43	0.09	0.35	2	69968926	cg03636174	ANXA4	TSS200	chr2:69968749-69969592	Island
hyper713	FGR_excessive_1	0.0E+00	0.38	0.03	0.35	2	69968926	cg03631172	ANXA4	TSS200	chr2:69968749-69969592	Island
hyper714	FGR_excessive_1	1.1E-09	0.42	0.08	0.43	2	699690229	cg10534459	ANXA4	TSS200	chr2:69968749-69969592	Island
hyper715	FGR_excessive_1	9.7E-11	0.42	0.08	0.35	2	69969033	cg10900124	ANXA4	TSS200	chr2:69968749-69969592	Island
hyper716	FGR_excessive_1	9.7E-11	0.39	0.06	0.33	2	69969052	cg20382057	ANXA4	TSS200	chr2:69968749-69969592	Island
hyper717	FGR_excessive_1	0.0E+00	0.47	0.02	0.46	2	69969063	cg08353937	ANXA4	TSS200	chr2:69968749-69969592	Island
hyper718	FGR_excessive_1	0.0E+00	0.36	0.01	0.35	2	69969079	cg05136786	ANXA4	TSS200	chr2:69968749-69969592	Island
hyper719	FGR_excessive_1	0.0E+00	0.35	0.05	0.30	2	69969221	cg11056435	ANXA4;ANXA4	5'UTR;1stExon	chr2:69968749-69969592	Island
hyper720	FGR_excessive_1	0.0E+00	0.39	0.05	0.34	2	69969227	cg21960922	ANXA4;ANXA4	5'UTR;1stExon	chr2:69968749-69969592	Island
hyper721	FGR_excessive_1	0.0E+00	0.41	0.04	0.37	2	69969370	cg19269713	ANXA4	5'UTR	chr2:69968749-69969592	Island
hyper722	FGR_excessive_1	1.1E-02	0.36	0.09	0.27	2	102090371	cg13274107	RFX8	5'UT		

hyper770	FGR_excessive_1	4.7E-06	0.16	0.05	0.11	8	63999003	cg04163863	TTPA	TSS1500	chr8:63998227-63998737	S_Shore
hyper771	FGR_excessive_1	4.7E-02	0.18	0.06	0.11	8	7523407	cg03608002	JPH1	TSS1500	chr8:75232649-75234101	Island
hyper772	FGR_excessive_1	1.5E-04	0.44	0.22	0.22	9	114287300	cg13570660	ZNF483,ZNF483	TSS200,TSS200	chr9:114287380-114287695	N_Shore
hyper773	FGR_excessive_1	9.7E-10	0.24	0.07	0.17	9	114287380	cg02612963	ZNF483,ZNF483	TSS200,TSS200	chr9:114287380-114287695	Island
hyper774	FGR_excessive_1	0.0E+00	0.31	0.03	0.29	10	22540745	cg16663900			chr10:22540707-22542739	Island
hyper775	FGR_excessive_1	2.1E-06	0.23	0.06	0.17	10	22540824	cg16782935			chr10:22540707-22542739	Island
hyper776	FGR_excessive_1	1.6E-08	0.30	0.05	0.25	10	22541366	cg03167951			chr10:22540707-22542739	Island
hyper777	FGR_excessive_1	1.2E-07	0.19	0.07	0.12	10	52751119	cg26337884	PRKG1,PRKG1	1stExon,5'UTR	chr10:52750595-52751765	Island
hyper778	FGR_excessive_1	0.0E+00	0.17	0.01	0.17	10	52751341	cg15603623	PRKG1	1stExon	chr10:52750595-52751765	Island
hyper779	FGR_excessive_1	1.5E-05	0.17	0.06	0.11	10	13173388	cg01137532	ZNF365,ZNF365,ZNF365	TSS200,TSS200,TSS200	chr10:64133789-64134422	Island
hyper780	FGR_excessive_1	3.7E-02	0.09	0.02	0.07	10	94352821	cg05019463	KIF11	TSS200	chr10:94352667-94351159	Island
hyper781	FGR_excessive_1	7.3E-02	0.18	0.05	0.13	11	93063692	cg14750263			chr11:10324353-10324882	Island
hyper782	FGR_excessive_1	5.8E-07	0.24	0.02	0.22	11	93063692	cg18766355	CCDC67	TSS200	chr11:93063598-93064076	Island
hyper783	FGR_excessive_1	1.1E-03	0.23	0.02	0.21	12	7023515	cg02297254	ENO2	TSS200	chr12:7023261-7024089	Island
hyper784	FGR_excessive_1	5.1E-06	0.19	0.07	0.12	12	21680409	cg05161082	C12orf39	Body	chr12:21680408-21680982	Island
hyper785	FGR_excessive_1	1.1E-03	0.16	0.04	0.13	12	21680426	cg06347047	C12orf39	Body	chr12:21680408-21680982	Island
hyper786	FGR_excessive_1	2.5E-08	0.11	0.02	0.09	12	21680508	cg10437806	C12orf39	Body	chr12:21680408-21680982	Island
hyper787	FGR_excessive_1	2.5E-04	0.26	0.09	0.18	12	21681006	cg08828403	C12orf39	Body	chr12:21680408-21680982	S_Shore
hyper788	FGR_excessive_1	1.0E-06	0.20	0.03	0.17	12	66683048	cg26415547	IRAK3,IRAK3,IRAK3,IRAK3	1stExon;1stExon;5'UTR;5'UTR	chr12:66682695-66683345	Island
hyper789	FGR_excessive_1	2.5E-03	0.29	0.03	0.26	12	66683203	cg10389229	IRAK3,IRAK3	1stExon;1stExon	chr12:66682695-66683345	Island
hyper790	FGR_excessive_1	4.3E-02	0.25	0.09	0.16	12	85306474	cg14449051	SLC6A15,SLC6A15,SLC6A15,SLC	1stExon;5'UTR;5'UTR;1stExon;1st	chr12:85306282-85306829	Island
hyper791	FGR_excessive_1	2.4E-04	0.33	0.08	0.25	12	96183791	cg25253534	NTN4	Body	chr12:96183873-96185199	N_Shore
hyper792	FGR_excessive_1	2.7E-02	0.49	0.06	0.43	12	96184020	cg16829450	NTN4	Body	chr12:96183873-96185199	Island
hyper793	FGR_excessive_1	1.1E-02	0.47	0.04	0.44	12	96184558	cg15367106	NTN4	TSS200	chr12:96183873-96185199	Island
hyper794	FGR_excessive_1	7.7E-05	0.45	0.13	0.31	12	96184787	cg22828090	NTN4	TSS1500	chr12:96183873-96185199	Island
hyper795	FGR_excessive_1	3.3E-05	0.06	0.06	0.12	12	96184965	cg07461313	NTN4	TSS1500	chr12:96183873-96185199	Island
hyper796	FGR_excessive_1	9.7E-04	0.20	0.06	0.14	12	96185437	cg013100449	NTN4	TSS1500	chr12:96183873-96185199	S_Shore
hyper797	FGR_excessive_1	2.9E-03	0.05	0.01	0.04	12	109251281	cg10817500	SSH1,SSH1,SSH1,SSH1	5'UTR;5'UTR;1stExon;1stExon	chr12:109251205-109251586	Island
hyper798	FGR_excessive_1	7.4E-07	0.28	0.09	0.19	13	25746767	cg18815647	FAM123A,FAM123A	Body;1stExon	chr13:25743998-25746127	Island
hyper799	FGR_excessive_1	0.0E+00	0.17	0.01	0.16	14	52535758	cg13592399	NID2,NID2	5'UTR;1stExon	chr14:52534581-52536722	Island
hyper800	FGR_excessive_1	0.0E+00	0.28	0.06	0.22	14	52535887	cg102131779	NID2,NID2	5'UTR;1stExon	chr14:52534581-52536722	Island
hyper801	FGR_excessive_1	6.0E-08	0.22	0.09	0.13	14	52535949	cg16066272	NID2	TSS200	chr14:52534581-52536722	Island
hyper802	FGR_excessive_1	9.7E-11	0.26	0.08	0.18	14	52535953	cg10149976	NID2	TSS200	chr14:52534581-52536722	Island
hyper803	FGR_excessive_1	1.9E-03	0.20	0.08	0.12	14	52535964	cg06782686	NID2	TSS200	chr14:52534581-52536722	Island
hyper804	FGR_excessive_1	7.0E-06	0.18	0.04	0.14	14	52535973	cg01781974	NID2	TSS200	chr14:52534581-52536722	Island
hyper805	FGR_excessive_1	4.3E-05	0.25	0.12	0.13	14	52536022	cg00766845	NID2	TSS200	chr14:52534581-52536722	Island
hyper806	FGR_excessive_1	0.0E+00	0.42	0.06	0.35	14	52536147	cg22881914	NID2	TSS1500	chr14:52534581-52536722	Island
hyper807	FGR_excessive_1	9.1E-07	0.36	0.03	0.32	14	52536175	cg04701034	NID2	TSS1500	chr14:52534581-52536722	Island
hyper808	FGR_excessive_1	7.3E-02	0.32	0.11	0.21	14	76842507	cg09329564	ESRRB	5'UTR	chr14:76842506-76843846	Island
hyper809	FGR_excessive_1	1.3E-03	0.33	0.11	0.22	14	90849959	cg00870057			chr14:90849994-90850331	Island
hyper810	FGR_excessive_1	3.9E-03	0.01	0.01	0.09	14	102022086	cg16368843			chr14:102025989-102031567	Island
hyper811	FGR_excessive_1	2.2E-03	0.63	0.24	0.38	15	33034966	cg13821077	TLN2	Body		
hyper812	FGR_excessive_1	4.6E-07	0.13	0.02	0.11	16	56623132	cg16336272	MT3,MT3	5'UTR;1stExon	chr16:56623068-56623914	Island
hyper813	FGR_excessive_1	3.6E-09	0.24	0.04	0.20	16	80574553	cg07732115	DYNLRB2	TSS1500	chr16:80574741-80575090	N_Shore
hyper814	FGR_excessive_1	3.4E-03	0.17	0.05	0.11	16	80574580	cg02656308	DYNLRB2	TSS1500	chr16:80574741-80575090	N_Shore
hyper815	FGR_excessive_1	3.1E-04	0.21	0.03	0.19	16	80574757	cg027254295	DYNLRB2	TSS200	chr16:80574741-80575090	Island
hyper816	FGR_excessive_1	0.0E+00	0.34	0.01	0.32	16	80574926	cg06395091	DYNLRB2,DYNLRB2	1stExon;5'UTR	chr16:80574741-80575090	Island
hyper817	FGR_excessive_1	1.8E-05	0.36	0.07	0.29	16	80575018	cg00720137	DYNLRB2	Body	chr16:80574741-80575090	Island
hyper818	FGR_excessive_1	1.6E-04	0.36	0.07	0.29	17	11144509	cg18160402	SHISA6	TSS1500	chr17:11143487-11145416	Island
hyper819	FGR_excessive_1	0.0E+00	0.19	0.01	0.17	17	80477962	cg18242682	FOXK2	1stExon	chr17:80477098-80478553	Island
hyper820	FGR_excessive_1	1.4E-06	0.21	0.09	0.12	18	12076435	cg02272280			chr18:12076434-12076799	Island
hyper821	FGR_excessive_1	1.9E-08	0.24	0.07	0.17	19	24269890	cg09777776	ZNF254	TSS200		
hyper822	FGR_excessive_1	0.0E+00	0.30	0.03	0.27	19	24270007	cg04571847	ZNF254,ZNF254	1stExon;5'UTR		
hyper823	FGR_excessive_1	2.8E-08	0.31	0.09	0.22	19	24270073	cg02286642	ZNF254,ZNF254	1stExon;5'UTR		
hyper824	FGR_excessive_1	2.8E-03	0.16	0.03	0.13	19	24270468	cg01000657	ZNF254	Body		
hyper825	FGR_excessive_1	7.2E-04	0.25	0.06	0.19	19	36478250	cg18812980			chr19:36478097-36478330	Island
hyper826	FGR_excessive_1	6.9E-08	0.29	0.08	0.21	19	51831274	cg08874512	IGLON5	Body		
hyper827	FGR_excessive_1	1.0E-08	0.28	0.10	0.18	19	51843601	cg03352428	YSYG10L	Body	chr19:51830064-51831145	S_Shore
hyper828	FGR_excessive_1	0.0E+00	0.43	0.05	0.39	19	51843654	cg18563413	YSYG10L	Body	chr19:51830064-51831145	Island
hyper829	FGR_excessive_1	8.9E-08	0.24	0.09	0.15	19	51869353	cg10219093	ETFB	Body	chr19:51869400-51871587	N_Shore
hyper830	FGR_excessive_1	1.6E-02	0.22	0.08	0.13	19	51869678	cg08854169	ETFB	TSS200	chr19:51869400-51871587	Island
hyper831	FGR_excessive_1	0.0E+00	0.22	0.01	0.21	19	51869680	cg02666184	ETFB	TSS200	chr19:51869400-51871587	Island
hyper832	FGR_excessive_1	1.1E-05	0.18	0.06	0.11	19	51869687	cg20367072	ETFB	TSS200	chr19:51869400-51871587	Island
hyper833	FGR_excessive_1	0.0E+00	0.27	0.06	0.21	19	51870581	cg19319774	CLDN2D,ETFB	Body,TSS1500	chr19:51869400-51871587	Island
hyper834	FGR_excessive_1	0.0E+00	0.31	0.06	0.25	19	51870612	cg07757224	CLDN2D,ETFB	Body,TSS1500	chr19:51869400-51871587	Island
hyper835	FGR_excessive_1	0.0E+00	0.20	0.04	0.16	19	51870714	cg101226447	CLDN2D,ETFB	Body,TSS1500	chr19:51869400-51871587	Island
hyper836	FGR_excessive_1	0.0E+00	0.33	0.10	0.24	19	51871466	cg05562817	CLDN2D	Body	chr19:51869400-51871587	Island
hyper837	FGR_excessive_1	2.9E-03	0.21	0.05	0.17	20	10153355	cg23022785			chr20:10152768-10153193	S_Shore
hyper838	FGR_excessive_1	6.9E-02	0.18	0.03	0.15	20	32803935	cg21747188			chr20:32803823-32804181	Island
hyper839	FGR_excessive_1	1.4E-02	0.33	0.12	0.21	20	57268419	cg10073706	NPEP1	Body	chr20:57267527-57268420	Island
hyper840	FGR_excessive_1	1.1E-04	0.16	0.05	0.11	22	42062693	cg10474712			chr22:42062790-42063002	N_Shore
hyper841	FGR_excessive_1	1.8E-07	0.19	0.06	0.13	22	42062791	cg10113544			chr22:42062790-42063002	Island
hyper842	FGR_excessive_1	2.1E-07	0.18	0.06	0.12	22	42062938	cg14458955			chr22:42062790-42063002	Island
hyper843	FGR_excessive_1	6.4E-05	0.16	0.05	0.15	22	42063028	cg10077671			chr22:42062790-42063002	S_Shore
hyper844	FGR_excessive_1	7.0E-02	0.23	0.04	0.18	22	42631615	cg22688623			chr22:4262065-42623747	Island
hyper845	FGR_excessive_2	9.1E-04	0.15	0.06	0.08	1	6052177	cg07420961	NPNHP4	5'UTR	chr1:60511595-6052955	Island
hyper846	FGR_excessive_2	0.0E+00	0.25	0.01	0.25	1	84764278	cg24002839	SAMD13	Body	chr1:84764108-84764906	Island
hyper847	FGR_excessive_2	1.3E-09	0.25	0.07	0.17	1	84764375	cg16026299	SAMD13	Body	chr1:84764108-84764906	Island
hyper848	FGR_excessive_2	7.3E-02	0.14	0.06	0.08	1	165567358	cg16599568			chr1:165567265-165567330	Island
hyper849	FGR_excessive_2	9.7E-11	0.37	0.09	0.28	1	182758324	cg027583088			chr1:182758395-182759097	N_Shore
hyper850	FGR_excessive_2	0.0E+00	0.46	0.07	0.39	1	182758421	cg03994069			chr1:182758395-182759097	Island
hyper851	FGR_excessive_2	0.0E+00	0.39	0.12	0.27	1	182758699	cg06676233			chr1:182758395-182759097	Island
hyper852	FGR_excessive_2	0.0E+00	0.23	0.02	0.22	1	182758764	cg14844172			chr1:182758395-182759097	Island
hyper853	FGR_excessive_2	0.0E+00	0.35	0.01	0.34	1	182758792	cg07202210			chr1:182758395-182759097	Island
hyper854	FGR_excessive_2	0.0E+00	0.42	0.02	0.40	1	182758953	cg13559225			chr1:182758395-182759097	Island
hyper8												

hyper899	FGR_excessive_2	0.0E+00	0.42	0.01	0.41	19	52391166	cg24794228	ZNF577,ZNF577,ZNF577,ZNF577	Body,5'UTR,5'UTR;1stExon;1stEx	chr19:52390841-52391368	Island
hyper900	FGR_excessive_2	0.0E+00	0.49	0.05	0.45	19	52391304	cg11269599	ZNF577,ZNF577,ZNF577	TSS200,TSS200,TSS200	chr19:52390841-52391368	Island
hyper901	FGR_excessive_2	9.7E-11	0.42	0.09	0.33	19	52391350	cg22331349	ZNF577,ZNF577,ZNF577	TSS200,TSS200,TSS200	chr19:52390841-52391368	Island
hyper902	FGR_excessive_2	6.4E-05	0.18	0.06	0.12	21	39288941	cg23909031	KCNJ9	TSS1500	chr21:39287946-39289267	Island
hyper903	FGR_excessive_2	9.1E-03	0.15	0.06	0.09	21	47010461	cg02983163			chr21:47009996-47011163	Island
hyper904	FGR_excessive_3	3.7E-03	0.54	0.21	0.33	1	15242180	cg17598058	KIAA1026,KIAA1026	Body,Body		
hyper905	FGR_excessive_3	8.8E-02	0.30	0.08	0.23	1	110453914	cg22621745	CSF1,CSF1,CSF1,CSF1	Body,Body,Body,Body	chr1:110453143-110453889	S_Shore
hyper906	FGR_excessive_3	4.4E-03	0.22	0.06	0.16	1	160001329	cg24523950	PIGM	1stExon	chr1:160001295-160001989	Island
hyper907	FGR_excessive_3	0.0E+00	0.36	0.01	0.35	2	019045309	cg06350814	C2orf88,C2orf88,C2orf88,C2orf88	TSS1500,5'UTR,TSS1500,5'UTR	chr2:191044979-191045829	Island
hyper908	FGR_excessive_3	7.9E-07	0.17	0.02	0.17	2	191045430	cg26532037	C2orf88,C2orf88,C2orf88,C2orf88	TSS1500,TSS1500,TSS200,5'UTR	chr2:191044979-191045829	Island
hyper909	FGR_excessive_3	0.0E+00	0.43	0.10	0.33	2	191045632	cg14210694	C2orf88,C2orf88,C2orf88,C2orf88	5'UTR,5'UTR;1stExon,5'UTR,TSS	chr2:191044979-191045829	Island
hyper910	FGR_excessive_3	0.0E+00	0.45	0.13	0.31	2	191045635	cg11097717	C2orf88,C2orf88,C2orf88,C2orf88	5'UTR,5'UTR;1stExon,5'UTR,TSS	chr2:191044979-191045829	Island
hyper911	FGR_excessive_3	0.0E+00	0.38	0.02	0.36	2	191045668	cg15313226	C2orf88,C2orf88,C2orf88,C2orf88	5'UTR,5'UTR;1stExon,5'UTR,TSS	chr2:191044979-191045829	Island
hyper912	FGR_excessive_3	8.0E-06	0.39	0.14	0.25	2	191045693	cg19906093	C2orf88,C2orf88,C2orf88,C2orf88	5'UTR;1stExon,5'UTR,5'UTR;1stEx	chr2:191044979-191045829	Island
hyper913	FGR_excessive_3	1.9E-10	0.24	0.05	0.19	2	191045885	cg22003435	C2orf88,C2orf88,C2orf88,C2orf88	5'UTR,5'UTR,5'UTR,5'UTR	chr2:191044979-191045829	S_Shore
hyper914	FGR_excessive_3	6.3E-07	0.29	0.09	0.21	3	89164038	cg05475667	EPHA3,EPHA3	Body,Body	chr3:89163635-89164107	Island
hyper915	FGR_excessive_3	1.3E-08	0.16	0.02	0.14	4	42659536	cg24533989	ATP8A1,ATP8A1	TSS1500,TSS1500	chr4:42658748-42659550	Island
hyper916	FGR_excessive_3	3.7E-02	0.25	0.11	0.14	5	95297364	cg10774586	ELL2	1stExon	chr5:95296368-95297438	Island
hyper917	FGR_excessive_3	4.3E-04	0.46	0.25	0.21	5	139554307	cg05598363	C5orf32	TSS1500	chr5:139554389-139555457	N_Shore
hyper918	FGR_excessive_3	2.6E-09	0.17	0.05	0.13	5	139554488	cg22434226	C5orf32	TSS200	chr5:139554389-139555457	Island
hyper919	FGR_excessive_3	4.0E-02	0.47	0.09	0.38	7	99155739	cg05165378	ZNF655,ZNF655,ZNF655,ZNF655	TSS1500,TSS1500,TSS1500,TSS	chr7:99155871-99156699	N_Shore
hyper920	FGR_excessive_3	3.0E-02	0.36	0.04	0.32	7	99155767	cg21950525	ZNF655,ZNF655,ZNF655,ZNF655	TSS1500,TSS1500,TSS1500,TSS	chr7:99155871-99156699	N_Shore
hyper921	FGR_excessive_3	2.3E-02	0.23	0.05	0.18	7	99156011	cg07121182	ZNF655,ZNF655,ZNF655,ZNF655	TSS200,TSS1500,TSS1500,TSS2	chr7:99155871-99156699	Island
hyper922	FGR_excessive_3	1.5E-05	0.61	0.08	0.53	9	140512455	cg14485934	C9orf37,EHMT1,EHMT1	5'UTR,TSS1500,TSS1500	chr9:140512692-140513420	N_Shore
hyper923	FGR_excessive_3	2.3E-09	0.36	0.10	0.26	11	22646597	cg03784550	FANCF	1stExon	chr11:22646706-22647441	N_Shore
hyper924	FGR_excessive_3	3.0E-07	0.22	0.14	0.11	11	22646591	cg03006551	FANCF	1stExon	chr11:22646706-22647441	Island
hyper925	FGR_excessive_4	3.3E-03	0.06	0.02	0.05	1	1407183	cg04286729	ATAD3B,ATAD3B	1stExon,5'UTR	chr1:1406844-1407821	Island
hyper926	FGR_excessive_4	6.7E-02	0.11	0.04	0.07	1	196137378	ch.1.194404001R				
hyper927	FGR_excessive_4	3.0E-03	0.29	0.03	0.26	1	197881540	cg13501359	LHX9	TSS200	chr1:197880016-197881637	Island
hyper928	FGR_excessive_4	4.6E-03	0.33	0.09	0.24	2	79738639	cg22350070	CTNNA2,CTNNA2	TSS1500,TSS1500	chr2:79739696-79740243	N_Shore
hyper929	FGR_excessive_4	4.7E-02	0.54	0.21	0.33	2	82120996	cg01296927				
hyper930	FGR_excessive_4	6.9E-04	0.23	0.12	0.11	2	223184510	cg16975959			chr2:223183013-223185468	Island
hyper931	FGR_excessive_4	3.2E-08	0.21	0.07	0.14	2	223184557	cg27506462			chr2:223183013-223185468	Island
hyper932	FGR_excessive_4	9.1E-03	0.09	0.03	0.06	2	233497957	cg26148236	EFHD1,EFHD1	TSS1500,Body	chr2:233497826-233499727	Island
hyper933	FGR_excessive_4	1.2E-03	0.15	0.05	0.09	6	32952826	cg25435686				
hyper934	FGR_excessive_4	4.6E-04	0.12	0.06	0.06	6	150184345	cg24761195	LRP11	Body	chr6:150184344-150185505	Island
hyper935	FGR_excessive_4	1.7E-07	0.16	0.06	0.11	6	160211790	cg10634217	TC1P1,TC1P1,MRPL18	TSS1500,TSS1500,Body	chr6:160209941-160212015	Island
hyper936	FGR_excessive_4	1.8E-04	0.18	0.07	0.10	6	160212014	cg16346065	TC1P1,TC1P1,MRPL18	TSS1500,TSS1500,Body	chr6:160209941-160212015	Island
hyper937	FGR_excessive_4	1.5E-02	0.21	0.10	0.11	6	160212070	cg22313322	TC1P1,TC1P1,MRPL18	TSS1500,TSS1500,Body	chr6:160209941-160212015	S_Shore
hyper938	FGR_excessive_4	1.6E-02	0.31	0.10	0.21	7	25988618	cg07184013	MIR148A	TSS200	chr7:259890012-25991320	N_Shore
hyper939	FGR_excessive_4	8.6E-07	0.43	0.08	0.34	7	25988735	cg25771013	MIR148A	TSS200	chr7:259890012-25991320	N_Shore
hyper940	FGR_excessive_4	3.9E-06	0.44	0.12	0.32	7	25988763	cg38535208	MIR148A	TSS200	chr7:259890012-25991320	N_Shore
hyper941	FGR_excessive_4	2.1E-09	0.38	0.07	0.31	7	25990013	cg16291657	MIR148A	TSS1500	chr7:259900012-25991320	Island
hyper942	FGR_excessive_4	0.0E+00	0.44	0.08	0.35	7	25990026	cg0956116	MIR148A	TSS1500	chr7:259900012-25991320	Island
hyper943	FGR_excessive_4	0.0E+00	0.55	0.07	0.48	7	25990079	cg12693702	MIR148A	TSS1500	chr7:259900012-25991320	Island
hyper944	FGR_excessive_4	0.0E+00	0.28	0.05	0.23	7	25990086	cg00399596	MIR148A	TSS1500	chr7:259900012-25991320	Island
hyper945	FGR_excessive_4	2.5E-07	0.06	0.01	0.05	7	25991025	cg18188200	MIR148A	TSS1500	chr7:259900012-25991320	Island
hyper946	FGR_excessive_4	2.8E-08	0.11	0.02	0.09	7	25991027	cg16872086	MIR148A	TSS1500	chr7:259900012-25991320	Island
hyper947	FGR_excessive_4	7.0E-09	0.27	0.08	0.19	7	25991107	cg15263946			chr7:259900012-25991320	Island
hyper948	FGR_excessive_4	5.0E-02	0.09	0.04	0.04	7	100807410	cg14814333	VGF	Body	chr7:100806279-100809064	Island
hyper949	FGR_excessive_4	2.3E-03	0.30	0.07	0.23	8	104310713	cg24115571	FZD6,FZD6,FZD6,FZD6	TSS1500,TSS1500,5'UTR;1stExon	chr8:104310809-104311620	N_Shore
hyper950	FGR_excessive_4	3.8E-02	0.44	0.06	0.38	8	104310808	cg00487870	FZD6,FZD6,FZD6	TSS200,5'UTR,TSS200	chr8:104310809-104311620	Island
hyper951	FGR_excessive_4	2.0E-03	0.06	0.01	0.04	9	140195998	cg13897564	NRARP,NRARP	1stExon,3'UTR	chr9:140195601-140197475	Island
hyper952	FGR_excessive_4	1.2E-03	0.15	0.06	0.09	13	31736577	cg12292402	HSPH1	TSS1500	chr13:31735109-31736670	Island
hyper953	FGR_excessive_4	3.8E-06	0.32	0.08	0.24	13	31736727	cg04454913	HSPH1	TSS1500	chr13:31735109-31736670	S_Shore
hyper954	FGR_excessive_4	2.6E-02	0.39	0.10	0.29	13	102068296	cg11621911	NALCN	TSS1500	chr13:102068116-102069258	S_Shore
hyper955	FGR_excessive_4	2.3E-02	0.33	0.09	0.24	16	31724470	cg22198868	ZNF720	TSS200	chr16:31724651-31725071	N_Shore
hyper956	FGR_excessive_4	1.0E-02	0.47	0.04	0.43	16	31724503	cg14747222	ZNF720	Body	chr16:31724651-31725071	Island
hyper957	FGR_excessive_4	1.4E-04	0.18	0.05	0.13	19	1020409	cg14165328	C19orf6,C19orf6	Body,Body	chr19:10205111-1021385	N_Shore
hyper958	FGR_excessive_4	7.2E-05	0.28	0.05	0.23	19	42681512	cg1029613			chr19:42681304-42681513	Island
hyper959	FGR_excessive_4	1.7E-02	0.05	0.02	0.03	19	49014774	cg26739378	LMTK3	Body	chr19:49014611-49014940	Island
hyper960	FGR_excessive_4	2.0E-02	0.37	0.05	0.32	20	9819697	cg02167438	PAK7,PAK7	TSS200,TSS200	chr20:9819271-9819861	Island
hyper961	FGR_excessive_4	2.0E-08	0.23	0.07	0.16	20	33297179	cg01118078	TP53NP2	Body	chr20:33296514-33298248	Island
hyper962	FGR_excessive_4	3.3E-04	0.22	0.09	0.13	20	33297218	cg26204638	TP53NP2	Body	chr20:33296514-33298248	Island
hyper963	FGR_excessive_4	2.7E-02	0.03	0.01	0.02	20	62393231	cg16400469	ARFRP1,ZGPAT,ZGPAT,ARFRP1	5'UTR,TSS200,5'UTR;1stExon;1st	chr20:62388659-62340274	Island
hyper964	FGR_excessive_4	1.7E-02	0.24	0.03	0.22	20	62496620	cg27655620	TPD52L2,TPD52L2,TPD52L2,TPC	1stExon;5'UTR,5'UTR;1stEx	chr20:62496243-62497196	Island
hyper965	FGR_excessive_4	1.7E-06	0.10	0.02	0.08	22	24093429	cg18803171	ZNF70	TSS200	chr22:24093026-24093621	Island
hyper966	N_insufficient_1	0.0E+00	0.53	0.07	0.46	1	567747	cg18024865	MIR1977	TSS1500		
hyper967	N_insufficient_1	2.1E-02	0.04	0.01	0.03	1	4716537	cg02483484	AJAP1,AJAP1	Body,Body	chr1:4713989-4716555	Island
hyper968	N_insufficient_1	5.3E-07	0.28	0.10	0.18	1	9242937	cg03521358			chr1:9242167-9243827	Island
hyper969	N_insufficient_1	3.3E-05	0.24	0.08	0.16	1	9242956	cg06658816			chr1:9242167-9243827	Island
hyper970	N_insufficient_1	3.5E-02	0.31	0.07	0.24	1	13910667	cg05140089	PDPN,PDPN,PDPN,PDPN	TSS1500,TSS1500,Body,Body	chr1:13910137-13910888	Island
hyper971	N_insufficient_1	9.8E-07	0.17	0.03	0.14	1	29891576	cg05654606			chr1:2989129-298970251	Island
hyper972	N_insufficient_1	2.5E-06	0.20	0.15	0.06	1	39269995	cg21841643			chr1:39269729-39270251	Island
hyper973	N_insufficient_1	3.0E-02	0.17	0.10	0.07	1	39270050	cg24827214			chr1:39269729-39270251	Island
hyper974	N_insufficient_1	7.1E-08	0.24	0.06	0.18	1	39270149	cg17834155			chr1:39269729-39270251	Island
hyper975	N_insufficient_1	9.6E-04	0.17	0.08	0.09	1	40157480	cg01775082	HPCAL4	TSS1500	chr1:40156930-40158514	Island
hyper976	N_insufficient_1	6.0E-03	0.18	0.05	0.14	1	45956974	cg00609097	TESK2	TSS200	chr1:45956345-45956893	S_Shore
hyper977	N_insufficient_1	2.1E-02	0.11	0.01	0.10	1	47697948	cg25764899			chr1:47696504-47698197	Island
hyper978	N_insufficient_1	2.2E-03	0.19	0.07	0.12	1	59248148	cg15156614	JUN	1stExon	chr1:59247461-59250590	Island
hyper979	N_insufficient_1	0.0E+00	0.18	0.01	0.18	1	63790044	cg18279094	FOXO3	1stExon	chr1:63782394-63790471	Island
hyper980	N_insufficient_1	4.5E-02	0.11	0.06</								

hyper1028	N_insufficient_1	4.0E-03	0.47	0.13	0.34	3	45883628	cg05485520	LZTFL1	TSS200	chr3:45883221-45883860	Island
hyper1029	N_insufficient_1	5.3E-04	0.55	0.06	0.49	3	45883734	cg05648986	LZTFL1	TSS200	chr3:45883221-45883860	Island
hyper1030	N_insufficient_1	2.1E-04	0.17	0.07	0.11	3	67704629	cg07703372	SUCLG2	Body	chr3:67704628-67705051	Island
hyper1031	N_insufficient_1	5.8E-10	0.38	0.03	0.35	3	67704890	cg11151121	SUCLG2	Body	chr3:67704628-67705051	Island
hyper1032	N_insufficient_1	0.0E+00	0.35	0.03	0.32	3	67704970	cg05555772	SUCLG2	1stExon	chr3:67704628-67705051	Island
hyper1033	N_insufficient_1	1.2E-08	0.19	0.02	0.16	3	67705044	cg11161853	SUCLG2	TSS200	chr3:67704628-67705051	Island
hyper1034	N_insufficient_1	1.9E-10	0.21	0.03	0.19	3	67705048	cg24673788	SUCLG2	TSS200	chr3:67704628-67705051	Island
hyper1035	N_insufficient_1	2.1E-09	0.21	0.05	0.15	3	67705222	cg19435306	SUCLG2	TSS200	chr3:67704628-67705051	S_Shore
hyper1036	N_insufficient_1	0.0E+00	0.21	0.09	0.12	3	67705228	cg08376549	SUCLG2	TSS200	chr3:67704628-67705051	S_Shore
hyper1037	N_insufficient_1	3.3E-02	0.17	0.10	0.08	3	67705285	cg11197418	SUCLG2	TSS1500	chr3:67704628-67705051	S_Shore
hyper1038	N_insufficient_1	7.1E-04	0.16	0.08	0.09	3	125932279	cg06827562	TMEM22		chr3:125931735-12593235	Island
hyper1039	N_insufficient_1	2.5E-04	0.12	0.02	0.10	3	136539834	cg18740893	TMEM22;TMEM22;TMEM22	5'UTR;5'UTR;5'UTR	chr3:136537559-136539204	Island
hyper1040	N_insufficient_1	7.3E-02	0.15	0.08	0.07	3	138665006	cg10641721	FOXL2;C3orf72	1stExon;TSS1500	chr3:138663718-138666346	Island
hyper1041	N_insufficient_1	2.9E-08	0.33	0.07	0.26	3	138665654	cg05386493	FOXL2;C3orf72;FOXL2	1stExon;TSS1500;5'UTR	chr3:138663718-138666346	Island
hyper1042	N_insufficient_1	8.8E-04	0.28	0.09	0.20	3	138665930	cg13894046	FOXL2;C3orf72;FOXL2	1stExon;TSS200;5'UTR	chr3:138663718-138666346	Island
hyper1043	N_insufficient_1	7.3E-03	0.37	0.12	0.25	3	138665957	cg19592439	FOXL2;C3orf72;FOXL2	1stExon;TSS200;5'UTR	chr3:138663718-138666346	Island
hyper1044	N_insufficient_1	5.5E-08	0.31	0.02	0.29	3	138665984	cg25670330	FOXL2;C3orf72	TSS200;TSS200	chr3:138663718-138666346	Island
hyper1045	N_insufficient_1	0.0E+00	0.28	0.02	0.26	3	138666040	cg15720669	FOXL2;C3orf72	TSS200;TSS200	chr3:138663718-138666346	Island
hyper1046	N_insufficient_1	5.2E-07	0.18	0.03	0.15	3	138666048	cg04111064	FOXL2;C3orf72	TSS200;TSS200	chr3:138663718-138666346	Island
hyper1047	N_insufficient_1	0.0E+00	0.23	0.02	0.21	3	138666050	cg17802942	FOXL2;C3orf72	TSS200;TSS200	chr3:138663718-138666346	Island
hyper1048	N_insufficient_1	3.9E-10	0.36	0.08	0.28	3	138666054	cg17503456	FOXL2;C3orf72	TSS200;TSS200	chr3:138663718-138666346	Island
hyper1049	N_insufficient_1	0.0E+00	0.35	0.02	0.32	3	138666118	cg06186698	C3orf72;FOXL2;C3orf72	5'UTR;TSS200;1stExon	chr3:138663718-138666346	Island
hyper1050	N_insufficient_1	0.0E+00	0.35	0.02	0.33	3	138666144	cg01379240	C3orf72;FOXL2;C3orf72	5'UTR;TSS200;1stExon	chr3:138663718-138666346	Island
hyper1051	N_insufficient_1	5.3E-07	0.19	0.05	0.14	3	138666318	cg10838925	FOXL2;C3orf72	TSS1500;Body	chr3:138663718-138666346	Island
hyper1052	N_insufficient_1	4.8E-06	0.19	0.01	0.18	3	142682288	cg15852572	PAQR9	TSS200	chr3:142681137-142683268	Island
hyper1053	N_insufficient_1	4.5E-04	0.20	0.04	0.16	3	142682291	cg14062317	PAQR9	TSS200	chr3:142681137-142683268	Island
hyper1054	N_insufficient_1	3.9E-10	0.30	0.04	0.26	3	142682652	cg04912999	PAQR9	TSS1500	chr3:142681137-142683268	Island
hyper1055	N_insufficient_1	4.6E-08	0.26	0.06	0.20	3	142682682	cg17627617	PAQR9	TSS1500	chr3:142681137-142683268	Island
hyper1056	N_insufficient_1	2.0E-03	0.27	0.13	0.14	3	142839837	cg23749856	CHST2	Body	chr3:142837885-142840388	Island
hyper1057	N_insufficient_1	0.0E+00	0.41	0.03	0.38	3	182896670	cg17323383	MCF2L2	3'UTR	chr3:182896920-182897381	N_Shore
hyper1058	N_insufficient_1	0.0E+00	0.45	0.07	0.38	3	182896920	cg02929310	MCF2L2	3'UTR	chr3:182896920-182897381	N_Shore
hyper1059	N_insufficient_1	0.0E+00	0.35	0.08	0.27	3	182896995	cg21857959	MCF2L2	3'UTR	chr3:182896920-182897381	Island
hyper1060	N_insufficient_1	0.0E+00	0.43	0.01	0.42	3	182897196	cg20724810	MCF2L2	Body	chr3:182896920-182897381	Island
hyper1061	N_insufficient_1	0.0E+00	0.46	0.03	0.43	3	182897283	cg00794178	MCF2L2	Body	chr3:182896920-182897381	Island
hyper1062	N_insufficient_1	0.0E+00	0.46	0.05	0.41	3	182970833	cg17701886	MCF2L2;B3GN5	Body;TSS200	chr3:182971429-182972635	N_Shore
hyper1063	N_insufficient_1	0.0E+00	0.37	0.06	0.31	3	182970846	cg01720186	MCF2L2;B3GN5	Body;TSS200	chr3:182971429-182972635	N_Shore
hyper1064	N_insufficient_1	0.0E+00	0.40	0.05	0.35	3	182970850	cg15510249	MCF2L2;B3GN5	Body;TSS200	chr3:182971429-182972635	N_Shore
hyper1065	N_insufficient_1	6.2E-09	0.46	0.08	0.38	3	182970903	cg19996875	MCF2L2;B3GN5	Body;TSS200	chr3:182971429-182972635	N_Shore
hyper1066	N_insufficient_1	0.0E+00	0.35	0.01	0.34	3	182970927	cg20585088	MCF2L2;B3GN5	Body;TSS200	chr3:182971429-182972635	N_Shore
hyper1067	N_insufficient_1	0.0E+00	0.42	0.02	0.40	3	182971009	cg12930573	MCF2L2;B3GN5	Body;TSS200	chr3:182971429-182972635	N_Shore
hyper1068	N_insufficient_1	0.0E+00	0.51	0.01	0.50	3	182971025	cg19368490	MCF2L2;B3GN5	Body;TSS200	chr3:182971429-182972635	N_Shore
hyper1069	N_insufficient_1	0.0E+00	0.44	0.05	0.40	3	182971069	cg22338826	MCF2L2;B3GN5;B3GN5	Body;1stExon;5'UTR	chr3:182971429-182972635	N_Shore
hyper1070	N_insufficient_1	0.0E+00	0.50	0.08	0.41	3	182971430	cg27034902	MCF2L2;B3GN5	Body;5'UTR	chr3:182971429-182972635	Island
hyper1071	N_insufficient_1	0.0E+00	0.44	0.07	0.37	3	182971442	cg05685893	MCF2L2;B3GN5	Body;5'UTR	chr3:182971429-182972635	Island
hyper1072	N_insufficient_1	0.0E+00	0.46	0.07	0.39	3	182971483	cg16579594	MCF2L2;B3GN5	Body;5'UTR	chr3:182971429-182972635	Island
hyper1073	N_insufficient_1	0.0E+00	0.40	0.02	0.38	3	182972408	cg02958321	MCF2L2;B3GN5	Body;5'UTR	chr3:182971429-182972635	Island
hyper1074	N_insufficient_1	0.0E+00	0.56	0.01	0.55	3	182972326	cg03657573	MCF2L2;B3GN5	Body;5'UTR	chr3:182971429-182972635	Island
hyper1075	N_insufficient_1	3.6E-03	0.37	0.14	0.24	3	182972742	cg23655039	MCF2L2;B3GN5	Body;5'UTR	chr3:182971429-182972635	S_Shore
hyper1076	N_insufficient_1	4.7E-04	0.22	0.10	0.12	3	186544945	cg09516202			chr3:186544916-186545471	Island
hyper1077	N_insufficient_1	2.7E-02	0.13	0.05	0.09	3	194406450	cg23670932	FAM43A	TSS200	chr3:194406440-194409045	Island
hyper1078	N_insufficient_1	1.9E-02	0.07	0.01	0.06	3	194406572	cg04689082	FAM43A	TSS200	chr3:194406440-194409045	Island
hyper1079	N_insufficient_1	3.2E-08	0.21	0.08	0.13	3	194407750	cg17064907	FAM43A	1stExon	chr3:194406440-194409045	Island
hyper1080	N_insufficient_1	8.8E-05	0.42	0.16	0.25	4	10458454	cg17524637	ZNF518B	5'UTR	chr4:10458129-10459353	Island
hyper1081	N_insufficient_1	0.0E+00	0.40	0.02	0.38	4	10458531	cg18795809	ZNF518B	5'UTR	chr4:10458129-10459353	Island
hyper1082	N_insufficient_1	0.0E+00	0.19	0.03	0.16	4	10458667	cg13425964	ZNF518B	5'UTR	chr4:10458129-10459353	Island
hyper1083	N_insufficient_1	1.6E-07	0.40	0.12	0.28	4	10458918	cg09534159	ZNF518B	5'UTR	chr4:10458129-10459353	Island
hyper1084	N_insufficient_1	1.9E-04	0.37	0.16	0.21	4	104589141	cg21098470	ZNF518B	TSS200	chr4:10458129-10459353	Island
hyper1085	N_insufficient_1	0.0E+00	0.26	0.07	0.18	4	104589167	cg12016437	ZNF518B	TSS200	chr4:10458129-10459353	Island
hyper1086	N_insufficient_1	0.0E+00	0.25	0.05	0.20	4	104589183	cg21667325	ZNF518B	TSS200	chr4:10458129-10459353	Island
hyper1087	N_insufficient_1	7.3E-05	0.34	0.02	0.32	4	15495219	cg16295725	ZNF518B	TSS200	chr4:10458129-10459353	Island
hyper1088	N_insufficient_1	1.7E-02	0.13	0.06	0.07	4	15402686	cg03290977	C10TNF7;C10TNF7	Body;5'UTR		
hyper1089	N_insufficient_1	5.6E-04	0.20	0.05	0.15	4	37245514	cg09259573	KIAA1239	TSS1500	chr4:37245520-37246979	Island
hyper1090	N_insufficient_1	5.0E-03	0.19	0.04	0.15	4	38869650	cg25943096	MIR574;FAM114A1	TSS200;5'UTR	chr4:38869401-38869780	Island
hyper1091	N_insufficient_1	5.6E-03	0.11	0.03	0.08	4	55094999	cg13002399	PDGFRA	TSS1500	chr4:55094321-55094993	Island
hyper1092	N_insufficient_1	2.3E-02	0.34	0.08	0.26	4	85419557	cg18589016	NKX6-1	TSS200	chr4:85417659-85420799	Island
hyper1093	N_insufficient_1	1.4E-02	0.17	0.02	0.16	4	122873018	cg12087304	TRPC3	TSS200	chr4:122871142-122871382	Island
hyper1094	N_insufficient_1	2.6E-03	0.25	0.15	0.11	4	123748753	cg12632152	FGF2	Body	chr4:123747740-123748980	Island
hyper1095	N_insufficient_1	3.1E-03	0.12	0.03	0.09	4	176923544	cg22478591	GPM6A;GPM6A;GPM6A;GPM6A	5'UTR;5'UTR;1stExon;1stExon	chr4:176923075-176923630	Island
hyper1096	N_insufficient_1	1.8E-08	0.20	0.09	0.11	5	19988706	cg19693760	CDH18;CDH18	TSS1500;TSS1500		
hyper1097	N_insufficient_1	0.0E+00	0.28	0.09	0.20	5	76011127	cg04528371	F2R	TSS1500	chr5:76011120-76012292	Island
hyper1098	N_insufficient_1	3.9E-10	0.18	0.03	0.15	5	76011138	cg24678700	F2R	TSS1500	chr5:76011120-76012292	Island
hyper1099	N_insufficient_1	9.7E-11	0.29	0.04	0.25	5	76011404	cg14718568	F2R	TSS1500	chr5:76011120-76012292	Island
hyper1100	N_insufficient_1	1.8E-05	0.14	0.06	0.08	5	76011328	cg13436055	F2R	TSS1500	chr5:76011120-76012292	Island
hyper1101	N_insufficient_1	3.9E-04	0.23	0.05	0.18	5	89178572	cg05948405	MEF2C;MEF2C	5'UTR;5'UTR	chr5:89179866-89180258	N_Shore
hyper1102	N_insufficient_1	7.0E-08	0.32	0.04	0.28	5	98104747	cg20275296	RGMB	TSS1500	chr5:98104578-98106270	Island
hyper1103	N_insufficient_1	1.8E-02	0.12	0.07	0.05	5	110409196	cg08354104	TSLP;TSLP;TSLP	1stExon;5'UTR;Body	chr5:110408704-110409039	S_Shore
hyper1104	N_insufficient_1	6.9E-03	0.28	0.11	0.17	5	113697861	cg07713533	KCNN2	TSS200	chr5:113696516-113699195	Island
hyper1105	N_insufficient_1	4.5E-02	0.16	0.09	0.07	5	114598137	cg02001558	PGGT1B	Body	chr5:114598301-114598657	N_Shore
hyper1106	N_insufficient_1	5.1E-04	0.15	0.08	0.08	5	114598306	cg07242620	PGGT1B	Body	chr5:114598301-114598657	Island
hyper1107	N_insufficient_1	0.0E+00	0.30	0.07	0.23	5	114598433	cg03966541	PGGT1B	1stExon	chr5:114598301-114598657	Island
hyper1108	N_insufficient_1	3.0E-04	0.11	0.05	0.06	5	114598574	cg26173203	PGGT1B	TSS200	chr5:114598301-114598657	Island
hyper1109	N_insufficient_1	1.8E-05	0.12	0.03	0.08	5</						

hyper1157	N_insufficient_1	1.5E-09	0.09	0.02	0.07	8	97507595	cg07146119	SDC2	Body	chr8:97505747-97507607	Island
hyper1158	N_insufficient_1	8.7E-04	0.21	0.09	0.12	8	97507666	cg20594401	SDC2	Body	chr8:97505747-97507607	S_Shore
hyper1159	N_insufficient_1	1.4E-09	0.23	0.03	0.19	8	143696133	cg04321580	ARC	TSS1500	chr8:143694430-143696166	Island
hyper1160	N_insufficient_1	3.8E-02	0.41	0.05	0.37	9	14313526	cg13518604	NFIB,NFIB	5'UTR,1stExon	chr9:14312952-14315351	Island
hyper1161	N_insufficient_1	4.4E-03	0.45	0.09	0.36	9	14313762	cg09965258	NFIB,NFIB	5'UTR,1stExon	chr9:14312952-14315351	Island
hyper1162	N_insufficient_1	2.9E-10	0.28	0.04	0.24	9	14314158	cg14455636	NFIB	TSS1500	chr9:14312952-14315351	Island
hyper1163	N_insufficient_1	5.8E-08	0.19	0.04	0.15	9	21974704	cg13601799	CDKN2A,CDKN2A,CDKN2A	1stExon,Body,1stExon	chr9:21974578-21975306	Island
hyper1164	N_insufficient_1	2.0E-05	0.19	0.04	0.15	9	96708224	cg13867237			chr9:96708116-96708487	Island
hyper1165	N_insufficient_1	1.7E-09	0.31	0.03	0.28	9	125109046	cg13655281			chr9:125109007-125109644	Island
hyper1166	N_insufficient_1	4.9E-10	0.28	0.08	0.19	9	125109120	cg12675848			chr9:125109007-125109644	Island
hyper1167	N_insufficient_1	0.0E+00	0.27	0.02	0.24	9	125109458	cg13802840			chr9:125109007-125109644	Island
hyper1168	N_insufficient_1	5.0E-07	0.20	0.07	0.14	9	125109542	cg03246694			chr9:125109007-125109644	Island
hyper1169	N_insufficient_1	1.6E-05	0.42	0.11	0.31	9	125133121	cg10493166	PTGS1,PTGS1	TSS200,TSS200		
hyper1170	N_insufficient_1	4.2E-03	0.47	0.05	0.42	9	125133318	cg12927153	PTGS1,PTGS1,PTGS1,PTGS1	5'UTR,5'UTR,1stExon,1stExon		
hyper1171	N_insufficient_1	2.0E-04	0.21	0.06	0.15	9	137533141	cg01753595	COL5A1	TSS1500	chr9:137533359-137534397	N_Shore
hyper1172	N_insufficient_1	1.4E-04	0.17	0.04	0.13	10	7451314	cg09060610	SFMBT2	5'UTR	chr10:7449376-7455339	Island
hyper1173	N_insufficient_1	8.3E-09	0.31	0.06	0.25	10	7451822	cg25291138	SFMBT2	5'UTR	chr10:7449376-7455339	Island
hyper1174	N_insufficient_1	6.4E-02	0.26	0.09	0.16	10	28287388	cg17862332	ARMC4	5'UTR	chr10:28287447-28288057	N_Shore
hyper1175	N_insufficient_1	3.1E-05	0.20	0.08	0.12	10	28287707	cg08555772	ARMC4	5'UTR	chr10:28287447-28288057	Island
hyper1176	N_insufficient_1	9.7E-11	0.31	0.04	0.28	10	28287879	cg0366818	ARMC4	5'UTR	chr10:28287447-28288057	Island
hyper1177	N_insufficient_1	3.2E-05	0.06	0.01	0.05	10	31609882	cg12758366	ZEB1,ZEB1,ZEB1,ZEB1,ZEB1	TSS200,Body,Body,Body,Body	chr10:31607227-31610094	Island
hyper1178	N_insufficient_1	9.8E-05	0.18	0.05	0.14	10	31609891	cg04403381	ZEB1,ZEB1,ZEB1,ZEB1,ZEB1	TSS200,Body,Body,Body,Body	chr10:31607227-31610094	Island
hyper1179	N_insufficient_1	9.4E-08	0.22	0.06	0.16	10	31609896	cg18465286	ZEB1,ZEB1,ZEB1,ZEB1,ZEB1	TSS200,Body,Body,Body,Body	chr10:31607227-31610094	Island
hyper1180	N_insufficient_1	6.4E-06	0.13	0.02	0.11	10	31609919	cg04667277	ZEB1,ZEB1,ZEB1,ZEB1,ZEB1	TSS200,Body,Body,Body,Body	chr10:31607227-31610094	Island
hyper1181	N_insufficient_1	6.6E-03	0.29	0.05	0.24	10	50887616	cg14520447	C10orf53,C10orf53	TSS200,TSS200	chr10:50887555-50887682	Island
hyper1182	N_insufficient_1	0.0E+00	0.44	0.02	0.25	10	89120809	cg0393674	GRD1	1stExon	chr10:89122924-89127364	Island
hyper1183	N_insufficient_1	6.4E-06	0.21	0.07	0.14	10	88126104	cg03370738	GRD1	1stExon	chr10:88122924-89127364	Island
hyper1184	N_insufficient_1	0.0E+00	0.19	0.01	0.18	10	88126299	cg03052869	GRD1	TSS200	chr10:88122924-89127364	Island
hyper1185	N_insufficient_1	0.0E+00	0.14	0.01	0.13	10	88126306	cg20649951	GRD1	TSS200	chr10:88122924-89127364	Island
hyper1186	N_insufficient_1	2.5E-02	0.11	0.05	0.05	10	90967189	cg10092652	CH25H	TSS200	chr10:90967555-90967900	N_Shore
hyper1187	N_insufficient_1	2.2E-03	0.39	0.14	0.25	10	97802829	cg26268044	CCNJ,CCNJ,CCNJ	TSS1500,TSS1500,TSS1500	chr10:97802871-97804262	Island
hyper1188	N_insufficient_1	6.8E-06	0.30	0.11	0.19	10	97802941	cg04509078	CCNJ,CCNJ,CCNJ	TSS1500,TSS1500,TSS1500	chr10:97802871-97804262	Island
hyper1189	N_insufficient_1	4.1E-03	0.43	0.25	0.18	10	97802959	cg01016800	CCNJ,CCNJ,CCNJ	TSS200,TSS200,TSS200	chr10:97802871-97804262	Island
hyper1190	N_insufficient_1	8.7E-05	0.18	0.07	0.10	10	97802977	cg08461586	CCNJ,CCNJ,CCNJ	TSS200,TSS200,TSS200	chr10:97802871-97804262	Island
hyper1191	N_insufficient_1	1.9E-10	0.26	0.09	0.18	10	97803045	cg00015024	CCNJ,CCNJ,CCNJ	TSS200,TSS200,TSS200	chr10:97802871-97804262	Island
hyper1192	N_insufficient_1	0.0E+00	0.29	0.09	0.20	10	97803048	cg11930665	CCNJ,CCNJ,CCNJ	TSS200,TSS200,TSS200	chr10:97802871-97804262	Island
hyper1193	N_insufficient_1	4.4E-04	0.35	0.20	0.16	10	97803058	cg08379212	CCNJ,CCNJ,CCNJ	TSS200,TSS200,TSS200	chr10:97802871-97804262	Island
hyper1194	N_insufficient_1	0.0E+00	0.36	0.01	0.35	10	97803386	cg05739190	CCNJ,CCNJ,CCNJ,CCNJ,CCNJ,CCNJ	1stExon,1stExon,5'UTR,5'UTR,1st	chr10:97802871-97804262	Island
hyper1195	N_insufficient_1	0.0E+00	0.31	0.02	0.30	10	97803525	cg22864416	CCNJ,CCNJ,CCNJ	5'UTR,5'UTR,5'UTR	chr10:97802871-97804262	Island
hyper1196	N_insufficient_1	4.6E-09	0.24	0.08	0.16	10	97804045	cg13017807	CCNJ,CCNJ,CCNJ	5'UTR,5'UTR,5'UTR	chr10:97802871-97804262	Island
hyper1197	N_insufficient_1	0.7E-02	0.14	0.05	0.09	10	102553365	cg04235519	PAX2,PAX2,PAX2,PAX2,PAX2	TSS200,TSS200,TSS200,TSS200	chr10:10253913-10256146	Island
hyper1198	N_insufficient_1	3.3E-02	0.14	0.07	0.07	10	116163160	cg20048434	AFAP1L2,AFAP1L2	Body,Body	chr10:116163391-116164599	N_Shore
hyper1199	N_insufficient_1	4.4E-06	0.22	0.09	0.13	10	116163392	cg20663200	AFAP1L2,AFAP1L2	Body,Body	chr10:116163391-116164599	Island
hyper1200	N_insufficient_1	0.0E+00	0.35	0.05	0.30	10	121652004	cg25418309	SEC23P	TSS1500	chr10:121652003-121652507	Island
hyper1201	N_insufficient_1	0.0E+00	0.37	0.01	0.36	10	121652003	cg09776153	SEC23P	TSS200	chr10:121652003-121652507	Island
hyper1202	N_insufficient_1	0.0E+00	0.40	0.01	0.39	10	121652237	cg04622176	SEC23P,SEC23P	1stExon,5'UTR	chr10:121652003-121652507	Island
hyper1203	N_insufficient_1	4.4E-09	0.51	0.07	0.45	10	123873748	cg23828763	TACC2,TACC2	Body,Body	chr10:123872119-123873462	S_Shore
hyper1204	N_insufficient_1	5.7E-03	0.23	0.04	0.19	10	124907540	cg17498296	HMX2	TSS200	chr10:124907283-124911035	Island
hyper1205	N_insufficient_1	5.5E-07	0.30	0.02	0.28	10	124907553	cg22603247	HMX2	TSS200	chr10:124907283-124911035	Island
hyper1206	N_insufficient_1	9.8E-05	0.17	0.08	0.08	10	124909415	cg04820634	HMX2	Body	chr10:124907283-124911035	Island
hyper1207	N_insufficient_1	7.6E-03	0.17	0.08	0.09	10	128076260	cg08602190	ADAM12,ADAM12	Body,Body	chr10:128076155-128077482	Island
hyper1208	N_insufficient_1	7.0E-05	0.28	0.08	0.20	10	128077080	cg00922781	ADAM12,ADAM12,ADAM12,ADAM12	1stExon,5'UTR,5'UTR,1stExon	chr10:128076155-128077482	Island
hyper1209	N_insufficient_1	1.9E-02	0.38	0.09	0.29	10	133805404	cg16447865			chr10:133849676-133850826	Island
hyper1210	N_insufficient_1	7.5E-02	0.18	0.05	0.13	11	12031097	cg05106294	DKK3,DKK3,DKK3	TSS1500,TSS200,TSS1500	chr11:12029737-12030084	S_Shore
hyper1211	N_insufficient_1	1.8E-02	0.25	0.09	0.16	11	12031099	cg01286655	DKK3,DKK3,DKK3	TSS1500,TSS200,TSS1500	chr11:12029737-12030084	S_Shore
hyper1212	N_insufficient_1	6.7E-04	0.18	0.09	0.09	11	44971593	cg24061542	TP53I11,TP53I11	5'UTR,5'UTR	chr11:44971048-44972685	Island
hyper1213	N_insufficient_1	6.5E-08	0.18	0.07	0.11	11	44971602	cg07916486	TP53I11,TP53I11	5'UTR,5'UTR	chr11:44971048-44972685	Island
hyper1214	N_insufficient_1	1.1E-07	0.13	0.01	0.11	11	44971833	cg07913112	TP53I11,TP53I11	5'UTR,5'UTR	chr11:44971048-44972685	Island
hyper1215	N_insufficient_1	2.6E-05	0.13	0.02	0.11	11	44971894	cg07301180	TP53I11,TP53I11	5'UTR,5'UTR	chr11:44971048-44972685	Island
hyper1216	N_insufficient_1	6.5E-08	0.12	0.02	0.10	11	44972293	cg22623062	TP53I11,TP53I11,TP53I11,TP53I11	5'UTR,1stExon,5'UTR,1stExon	chr11:44971048-44972685	Island
hyper1217	N_insufficient_1	2.5E-03	0.35	0.12	0.23	11	56059643	cg22629065	ORH1	TSS1500		
hyper1218	N_insufficient_1	1.6E-05	0.22	0.04	0.18	11	59333490	cg14665813				
hyper1219	N_insufficient_1	1.3E-06	0.14	0.06	0.08	11	59333608	cg18442286				
hyper1220	N_insufficient_1	5.8E-05	0.16	0.03	0.12	11	69590113	cg23964057	FGF4,FGF4	1stExon,5'UTR	chr11:69588826-69590546	Island
hyper1221	N_insufficient_1	1.6E-06	0.16	0.03	0.14	11	69590282	cg18947739	FGF4	TSS200	chr11:69588826-69590546	Island
hyper1222	N_insufficient_1	4.1E-03	0.10	0.03	0.07	11	110583036	cg03813168	ARHGAP20	Body	chr11:110581839-110583883	Island
hyper1223	N_insufficient_1	1.8E-02	0.13	0.06	0.07	11	111411756	cg04610224	LAYN	5'UTR	chr11:111410932-111412199	Island
hyper1224	N_insufficient_1	7.2E-06	0.39	0.05	0.34	11	113930340	cg09719477	ZBTB16,ZBTB16,ZBTB16	1stExon,TSS1500,5'UTR	chr11:113929633-113932190	Island
hyper1225	N_insufficient_1	1.1E-04	0.49	0.19	0.30	11	113931305	cg09890653	ZBTB16,ZBTB16,ZBTB16	5'UTR,1stExon,5'UTR	chr11:113929633-113932190	Island
hyper1226	N_insufficient_1	2.1E-09	0.32	0.01	0.31	11	120894801	cg06747745	TBCEL,TBCEL	TSS200,TSS200	chr11:120894689-120895082	Island
hyper1227	N_insufficient_1	1.3E-03	0.27	0.02	0.24	11	128563634	cg08590601	FLI1,FLI1	TSS200,5'UTR	chr11:128562671-128565011	Island
hyper1228	N_insufficient_1	1.2E-03	0.12	0.04	0.08	12	1639527	cg05998639			chr12:1639033-1640750	Island
hyper1229	N_insufficient_1	3.0E-05	0.18	0.06	0.12	12	1639534	cg05941033			chr12:1639033-1640750	Island
hyper1230	N_insufficient_1	8.6E-04	0.15	0.08	0.07	12	83332881	cg18584732	FAM66C	Body	chr12:8332788-8333188	Island
hyper1231	N_insufficient_1	2.1E-02	0.38	0.21	0.27	12	8217763	cg10605804	LOC144571	TSS200	chr12:9213738-9217715	S_Shore
hyper1232	N_insufficient_1	5.0E-02	0.14	0.02	0.12	12	54144855	cg0385164			chr12:54144562-54145470	Island
hyper1233	N_insufficient_1	3.8E-04	0.31	0.11	0.20	12	54144921	cg06858186			chr12:54144562-54145470	Island
hyper1234	N_insufficient_1	7.0E-08	0.30	0.07	0.24	12	64062564	cg04455164	DPY19L2	TSS1500	chr12:64061836-64062774	Island
hyper1235	N_insufficient_1	7.6E-03	0.13	0.04	0.09	12	66217818	cg16409497	HMGGA2,RPSAP52,HMGGA2	TSS1500,Body,TSS1500	chr12:66217627-66220181	Island
hyper1236	N_insufficient_1	7.0E-03	0.33	0.12	0.22	12	92538822	cg08832261	BTG1	3'UTR	chr12:92538710-92540333	N_Shelf
hyper1237	N_insufficient_1	3.7E-02	0.30	0.06	0.24	12	113941511	cg05412058			chr12:113914440-113914567	Island
hyper1238	N_insufficient_1</											

hyper1286	N_insufficient_1	0.0E+00	0.26	0.04	0.22	17	6939282	cg09543792	SLC16A13	TSS200	chr17:6939137-6940090	Island
hyper1287	N_insufficient_1	0.0E+00	0.33	0.05	0.27	17	6939299	cg22884899	SLC16A13	TSS200	chr17:6939137-6940090	Island
hyper1288	N_insufficient_1	5.8E-10	0.27	0.03	0.24	17	6939304	cg25241322	SLC16A13	TSS200	chr17:6939137-6940090	Island
hyper1289	N_insufficient_1	1.3E-04	0.31	0.12	0.19	17	6939665	cg02805871	SLC16A13,SLC16A13	5'UTR,1stExon	chr17:6939137-6940090	Island
hyper1290	N_insufficient_1	1.7E-02	0.19	0.08	0.11	17	8906601	cg07848706			chr17:8906236-8908080	Island
hyper1291	N_insufficient_1	4.1E-06	0.13	0.06	0.06	17	19437003	cg10514549	SLC47A1	TSS200	chr17:19436788-19437692	Island
hyper1292	N_insufficient_1	1.9E-04	0.14	0.06	0.08	17	19437013	cg07829432	SLC47A1	TSS200	chr17:19436788-19437692	Island
hyper1293	N_insufficient_1	0.0E+00	0.18	0.03	0.16	17	19437157	cg13004927	ACCN1	TSS200	chr17:19436788-19437692	Island
hyper1294	N_insufficient_1	9.9E-05	0.38	0.07	0.31	17	31619231	cg03977243	ACCN1,ACCN1,ACCN1	1stExon,5'UTR,Body	chr17:31618345-31620465	Island
hyper1295	N_insufficient_1	2.0E-02	0.23	0.07	0.15	17	31620378	cg12373736	ACCN1,ACCN1	TSS1500,Body	chr17:31618345-31620465	Island
hyper1296	N_insufficient_1	2.1E-02	0.10	0.06	0.04	17	35014438	cg00371418			chr17:35014272-35014596	Island
hyper1297	N_insufficient_1	6.1E-06	0.12	0.02	0.10	17	39890494	cg01777228	HAP1,HAP1,HAP1	1stExon,1stExon,1stExon	chr17:39898956-39891489	Island
hyper1298	N_insufficient_1	2.0E-03	0.19	0.04	0.16	17	40913055	cg01101510	LOC100190938,RAMP2,LOC1001	Body,TSS200,Body	chr17:40912816-40913553	Island
hyper1299	N_insufficient_1	3.9E-03	0.17	0.05	0.12	17	40913076	cg12627273	LOC100190938,RAMP2,LOC1001	Body,TSS200,Body	chr17:40912816-40913553	Island
hyper1300	N_insufficient_1	5.4E-04	0.08	0.02	0.05	17	42061083	cg27375198	PYY	5'UTR	chr17:42061046-42061643	Island
hyper1301	N_insufficient_1	1.6E-02	0.07	0.02	0.05	17	47307743	cg03259494	PHOSPHO1,PHOSPHO1	5'UTR,5'UTR	chr17:47307740-47308276	Island
hyper1302	N_insufficient_1	2.1E-02	0.36	0.07	0.30	17	54991064	cg20613151	TRIM25	1stExon	chr17:54990832-54991771	Island
hyper1303	N_insufficient_1	2.8E-04	0.07	0.02	0.05	17	54991616	cg19695198	TRIM25	TSS1500	chr17:54990832-54991771	Island
hyper1304	N_insufficient_1	3.9E-02	0.11	0.05	0.07	17	54991697	cg00938453	TRIM25	TSS1500	chr17:54990832-54991771	Island
hyper1305	N_insufficient_1	9.8E-03	0.12	0.03	0.08	17	58227265	cg23010302	CA4	TSS200	chr17:58227241-58227720	Island
hyper1306	N_insufficient_1	4.9E-07	0.11	0.02	0.09	17	58227267	cg05248618	CA4	TSS200	chr17:58227241-58227720	Island
hyper1307	N_insufficient_1	0.0E+00	0.62	0.12	0.50	17	58494866	cg06531671	C17orf64	TSS1500	chr17:58498711-58499332	N_Shore
hyper1308	N_insufficient_1	0.0E+00	0.45	0.06	0.38	17	58498712	cg22191510	C17orf64	TSS1500	chr17:58498711-58499332	Island
hyper1309	N_insufficient_1	0.0E+00	0.61	0.10	0.51	17	58498871	cg10179315	C17orf64	TSS1500	chr17:58498711-58499332	Island
hyper1310	N_insufficient_1	0.0E+00	0.62	0.01	0.61	17	58498977	cg09695735	C17orf64	TSS1500	chr17:58498711-58499332	Island
hyper1311	N_insufficient_1	5.4E-03	0.03	0.03	0.09	18	25610871	cg09697114	CABLES1,CABLES1	1stExon,Body	chr18:25714968-25714971	Island
hyper1312	N_insufficient_1	1.9E-10	0.32	0.05	0.27	18	18514555	cg26697111	OSBPL1A,OSBPL1A	Body,5'UTR	chr18:21851399-21852169	Island
hyper1313	N_insufficient_1	0.0E+00	0.40	0.07	0.34	18	21852118	cg19925062	OSBPL1A,OSBPL1A,OSBPL1A	Body,1stExon,5'UTR	chr18:21851399-21852169	Island
hyper1314	N_insufficient_1	1.9E-08	0.25	0.01	0.24	18	21852333	cg03384992	OSBPL1A,OSBPL1A	Body,TSS200	chr18:21851399-21852169	S_Shore
hyper1315	N_insufficient_1	1.6E-09	0.29	0.04	0.25	18	21852337	cg26398656	OSBPL1A,OSBPL1A	Body,TSS200	chr18:21851399-21852169	S_Shore
hyper1316	N_insufficient_1	7.8E-10	0.37	0.05	0.32	18	21852333	cg06593258	OSBPL1A,OSBPL1A	Body,TSS200	chr18:21851399-21852169	S_Shore
hyper1317	N_insufficient_1	6.0E-03	0.34	0.12	0.23	18	21852436	cg21840153	OSBPL1A,OSBPL1A	Body,TSS1500	chr18:21851399-21852169	S_Shore
hyper1318	N_insufficient_1	6.4E-04	0.22	0.03	0.19	18	22929808	cg25015867	ZNF521	Body	chr18:22930018-22930904	N_Shore
hyper1319	N_insufficient_1	1.5E-04	0.24	0.05	0.19	18	22930283	cg21678445	ZNF521	Body	chr18:22930018-22930904	Island
hyper1320	N_insufficient_1	1.3E-09	0.21	0.05	0.17	18	43651686	cg22038796	PSTPIP2	Body	chr18:43651796-43652455	N_Shore
hyper1321	N_insufficient_1	0.0E+00	0.20	0.02	0.19	18	43651835	cg13768737	PSTPIP2	Body	chr18:43651796-43652455	Island
hyper1322	N_insufficient_1	0.0E+00	0.24	0.02	0.22	18	43652232	cg11864882	PSTPIP2,PSTPIP2	1stExon,5'UTR	chr18:43651796-43652455	Island
hyper1323	N_insufficient_1	0.0E+00	0.32	0.01	0.31	18	43652255	cg17329670	PSTPIP2	TSS200	chr18:43651796-43652455	Island
hyper1324	N_insufficient_1	5.8E-10	0.27	0.07	0.20	18	43652366	cg21949781	PSTPIP2	TSS200	chr18:43651796-43652455	Island
hyper1325	N_insufficient_1	0.0E+00	0.22	0.05	0.17	18	43652398	cg24026435	PSTPIP2	TSS200	chr18:43651796-43652455	Island
hyper1326	N_insufficient_1	1.5E-08	0.22	0.04	0.18	18	43652430	cg13405114	PSTPIP2	TSS200	chr18:43651796-43652455	Island
hyper1327	N_insufficient_1	3.9E-10	0.20	0.06	0.14	18	43652437	cg14304186	PSTPIP2	TSS200	chr18:43651796-43652455	Island
hyper1328	N_insufficient_1	4.1E-08	0.19	0.06	0.12	18	43652454	cg28226511	PSTPIP2	TSS1500	chr18:43651796-43652455	Island
hyper1329	N_insufficient_1	3.2E-02	0.24	0.12	0.12	18	43652592	cg16730908	PSTPIP2	TSS1500	chr18:43651796-43652455	S_Shore
hyper1330	N_insufficient_1	1.3E-06	0.19	0.07	0.12	18	70211835	cg27376271	CBLN2	TSS200	chr18:70208974-70211790	S_Shore
hyper1331	N_insufficient_1	3.6E-02	0.12	0.05	0.08	19	35853507	cg26797585	GIPC3	1stExon	chr19:35853557-3585947	Island
hyper1332	N_insufficient_1	6.8E-02	0.17	0.06	0.11	19	7795619	cg13950603	CLEC4G	Body	chr19:7794793-7796410	Island
hyper1333	N_insufficient_1	1.1E-02	0.19	0.04	0.15	19	30017829	cg18777119	VSTM2B	Body	chr19:30015781-30021367	Island
hyper1334	N_insufficient_1	1.5E-04	0.16	0.05	0.11	19	45281236	cg18612786	CBLCL,CBLCL	1stExon,1stExon	chr19:45281133-45281355	Island
hyper1335	N_insufficient_1	3.6E-02	0.20	0.05	0.15	19	55690876	cg14047019	SYT5	5'UTR	chr19:55690182-55691623	Island
hyper1336	N_insufficient_1	3.9E-05	0.25	0.06	0.19	19	58629828	cg03145999	ZSCAN18,ZSCAN18	TSS200,TSS200	chr19:58629309-58630241	Island
hyper1337	N_insufficient_1	1.2E-03	0.27	0.07	0.19	20	10199536	cg16564824	SNAP25,SNAP25,SNAP25,SNAP	1stExon,5'UTR,1stExon,5'UTR	chr20:10200088-10200384	N_Shore
hyper1338	N_insufficient_1	4.4E-03	0.09	0.03	0.07	20	13201328	cg15577927	ISM1	TSS1500	chr20:13200670-13202616	Island
hyper1339	N_insufficient_1	5.8E-02	0.11	0.03	0.07	20	30458044	cg21578322	TTLL9,DUSP15,DUSP15,DUSP15	TSS1500,TSS200,TSS1500,Body	chr20:30457907-30458712	Island
hyper1340	N_insufficient_1	7.9E-06	0.06	0.01	0.05	20	30480601	cg16313728	TTLL9,DUSP15,DUSP15,DUSP15	TSS1500,TSS200,TSS1500,Body	chr20:30457907-30458712	Island
hyper1341	N_insufficient_1	5.8E-02	0.42	0.25	0.17	20	61080903	cg02065637	MIR124-3	TSS1500	chr20:61080254-61810867	Island
hyper1342	N_insufficient_1	2.0E-08	0.17	0.01	0.16	20	62103627	cg08003150	KCNQ2,KCNQ2,KCNQ2,KCNQ2	1stExon,1stExon,1stExon,1stExon	chr20:62102541-62103995	Island
hyper1343	N_insufficient_1	5.4E-03	0.08	0.08	0.11	21	21833859	cg18075077	ADAMTS,ADAMTS5	1stExon,5'UTR	chr21:28333856-28409237	Island
hyper1344	N_insufficient_1	6.0E-06	0.11	0.02	0.09	22	19510977	cg21872764	CLDN5,CLDN5,CLDN5	1stExon,5'UTR,5'UTR	chr22:19510871-19512254	Island
hyper1345	N_insufficient_1	2.1E-03	0.17	0.08	0.08	22	21311670	cg10785109			chr22:21311336-21312201	Island
hyper1346	N_insufficient_1	3.0E-04	0.21	0.08	0.13	22	47133964	cg27326469	CERK	1stExon	chr22:50241735-50243918	Island
hyper1347	N_insufficient_1	5.0E-03	0.06	0.01	0.05	22	50242492	cg15219689			chr21:16173889-16175396	Island
hyper1348	N_insufficient_1	1.1E-02	0.07	0.02	0.05	1	16174780	cg06526137	SPEN,FLJ37453	Body,TSS200	chr1:38510102-38513642	Island
hyper1349	N_insufficient_1	4.9E-03	0.09	0.02	0.07	1	38512238	cg05336094	POU3F1	1stExon	chr1:14772377-14775808	Island
hyper1350	N_insufficient_1	6.8E-02	0.06	0.02	0.04	2	14772731	cg20720059	FAM84A	TSS200	chr2:29033351-29034041	Island
hyper1351	N_insufficient_1	6.6E-03	0.21	0.04	0.17	2	29033897	cg04786857	SPDYA,SPDYA	5'UTR,5'UTR	chr2:219723702-219725010	Island
hyper1352	N_insufficient_1	6.4E-05	0.11	0.02	0.09	2	219724539	cg06157334	WNT6	TSS200		
hyper1353	N_insufficient_1	2.2E-02	0.41	0.23	0.19	2	23340434	cg27382389	CHRG	TSS200		
hyper1354	N_insufficient_1	5.7E-03	0.05	0.01	0.04	2	242626259	cg18361031	DTYMK,DTYMK,DTYMK,DTYMK	5'UTR,5'UTR,1stExon,Body,1stEx	chr2:242625961-24262760	Island
hyper1355	N_insufficient_1	4.4E-05	0.05	0.01	0.05	2	242641384	cg15561235	ING5	TSS200	chr2:24264043-24264246	Island
hyper1356	N_insufficient_1	1.9E-02	0.04	0.01	0.03	3	11024379	cg11021744	SLC6A1	TSS200	chr3:11034446-11035384	N_Shore
hyper1357	N_insufficient_1	8.1E-05	0.05	0.01	0.04	3	10780993	cg12363543	CD47,CD47,CD47	TSS200,TSS200,TSS200	chr3:10809375-107810543	Island
hyper1358	N_insufficient_1	1.3E-02	0.16	0.08	0.08	3	102527499	cg08602596			chr3:128326397-128327507	Island
hyper1359	N_insufficient_1	5.4E-03	0.23	0.07	0.13	3	167813154	cg03036482	GOLIM4,GOLIM4	TSS200	chr3:167813829-167814102	Island
hyper1360	N_insufficient_1	3.0E-06	0.22	0.08	0.13	4	164253938	cg11064073	NPY1R	TSS200	chr4:164252954-164253471	S_Shore
hyper1361	N_insufficient_1	4.6E-04	0.18	0.08	0.09	4	164254082	cg17500103	NPY1R	TSS1500	chr4:164252954-164253471	S_Shore
hyper1362	N_insufficient_1	2.7E-09	0.24	0.05	0.19	4	164254111	cg06734271	NPY1R	TSS1500	chr4:164252954-164253471	S_Shore
hyper1363	N_insufficient_1	8.7E-03	0.04	0.02	0.03	4	166244807	cg27324455	SCAMOL,SCAMOL	TSS200,TSS200	chr4:16624454-166249063	Island
hyper1364	N_insufficient_1	5.7E-02	0.29	0.11	0.18	4	172734347	cg05295006	GALNTL6	TSS1500	chr4:17273374-17273518	Island
hyper1365	N_insufficient_1	1.1E-04	0.22	0.07	0.15	4	172734718	cg26588943	GALNTL6,GALNTL6	1stExon,5'UTR	chr4:17273374-17273518	Island
hyper1366	N_insufficient_1	2.6E-02	0.25	0.04	0.21	4	172734718	cg03413465	GALNTL6,GALNTL6	1stExon,5'UTR	chr4:17273374-17273518	Island
hyper1367	N_insufficient_1	2.4E-02	0.09	0.03	0.06	5	893022	cg0193570				

hyper1415	N_insufficient_2	5.9E-02	0.11	0.03	0.08	18	5296031	cg07305215	ZFP161,ZFP161,ZFP161,ZFP161;1stExon;5'UTR;1stExon;TSS1500;chr18:5295323-5297099	Island
hyper1416	N_insufficient_2	5.5E-06	0.41	0.17	0.24	18	15197867	cg00279001	chr18:15197650-15198309	Island
hyper1417	N_insufficient_2	2.4E-07	0.54	0.14	0.40	18	15198067	cg01301382	chr18:15197650-15198309	Island
hyper1418	N_insufficient_2	1.6E-04	0.03	0.00	0.02	19	4909554	cg09317102	chr19:4909262-4910256	Island
hyper1419	N_insufficient_2	7.0E-04	0.14	0.04	0.10	19	6464082	cg25637722	chr19:6463991-6464780	Island
hyper1420	N_insufficient_2	2.7E-05	0.17	0.09	0.08	19	56904755	cg11740788	chr19:56904636-56905355	Island
hyper1421	N_insufficient_2	1.6E-03	0.21	0.05	0.17	19	56905032	cg20984085	chr19:56904636-56905355	Island
hyper1422	N_insufficient_2	9.0E-02	0.06	0.02	0.04	20	61847713	cg08514185	chr20:61846843-61848103	Island
hyper1423	N_insufficient_2	4.7E-04	0.08	0.01	0.07	20	63288574	cg13628982	chr20:63275589-63289476	Island
hyper1424	N_insufficient_2	2.4E-06	0.06	0.01	0.05	22	30753142	cg18031436	chr22:30752583-30753214	Island
hyper1425	N_insufficient_2	7.1E-05	0.05	0.01	0.03	22	42915677	cg13919496	chr22:42915512-42915999	Island
hyper1426	N_insufficient_3	7.6E-04	0.05	0.01	0.04	1	26793635	cg13064914	chr1:26793666-26799842	Island
hyper1427	N_insufficient_3	6.9E-02	0.10	0.03	0.07	1	70033739	cg23730181	chr1:70032967-70034495	Island
hyper1428	N_insufficient_3	2.3E-02	0.15	0.09	0.06	1	70033902	cg21004042	chr1:70032967-70034495	Island
hyper1429	N_insufficient_3	7.5E-04	0.18	0.10	0.08	1	115632038	cg03614513	chr1:115631850-115632584	Island
hyper1430	N_insufficient_3	9.6E-04	0.04	0.00	0.03	1	115632306	cg01522456	chr1:115631850-115632584	Island
hyper1431	N_insufficient_3	9.4E-05	0.13	0.04	0.09	1	115632455	cg06043114	chr1:115631850-115632584	Island
hyper1432	N_insufficient_3	8.7E-05	0.12	0.04	0.09	1	154297643	cg06824583	chr1:154298205-154298544	N_Shore
hyper1433	N_insufficient_3	3.0E-02	0.28	0.11	0.18	1	154297985	cg12644885	chr1:154298205-154298544	N_Shore
hyper1434	N_insufficient_3	3.3E-02	0.30	0.04	0.25	1	214160848	cg23992410	chr1:214160798-214161034	Island
hyper1435	N_insufficient_3	2.9E-10	0.11	0.01	0.10	1	214161251	cg25347098	chr1:214161197-214161415	Island
hyper1436	N_insufficient_3	3.8E-02	0.18	0.09	0.09	1	214161306	cg214019317	chr1:214161197-214161415	Island
hyper1437	N_insufficient_3	7.4E-05	0.11	0.02	0.09	1	214161371	cg23265047	chr1:214161197-214161415	Island
hyper1438	N_insufficient_3	4.1E-03	0.20	0.08	0.12	1	218520325	cg06899755	chr1:218520287-218520506	Island
hyper1439	N_insufficient_3	5.6E-04	0.13	0.03	0.10	1	218520468	cg22021178	chr1:218520287-218520506	Island
hyper1440	N_insufficient_3	5.7E-09	0.26	0.02	0.24	1	239550303	cg123955108	chr1:239550108-239551339	Island
hyper1441	N_insufficient_3	1.4E-09	0.10	0.01	0.10	1	245317971	cg11586800	chr1:245316547-245320247	Island
hyper1442	N_insufficient_3	1.0E-04	0.12	0.02	0.10	1	245317980	cg09065617	chr1:245316547-245320247	Island
hyper1443	N_insufficient_3	1.2E-06	0.18	0.01	0.16	1	245318209	cg01787565	chr1:245316547-245320247	Island
hyper1444	N_insufficient_3	1.5E-03	0.14	0.04	0.10	1	245318229	cg12054521	chr1:245316547-245320247	Island
hyper1445	N_insufficient_3	1.2E-06	0.15	0.04	0.11	1	245318245	cg13888026	chr1:245316547-245320247	Island
hyper1446	N_insufficient_3	5.8E-09	0.14	0.02	0.12	1	245318335	cg19252551	chr1:245316547-245320247	Island
hyper1447	N_insufficient_3	5.2E-03	0.10	0.04	0.06	1	245318734	cg03284440	chr1:245316547-245320247	Island
hyper1448	N_insufficient_3	2.6E-06	0.08	0.02	0.07	1	245318817	cg02054059	chr1:245316547-245320247	Island
hyper1449	N_insufficient_3	3.1E-06	0.09	0.02	0.07	2	60776713	cg18674579	chr2:60776596-60778157	Island
hyper1450	N_insufficient_3	1.6E-06	0.20	0.03	0.17	2	60777051	cg26580134	chr2:60776596-60778157	Island
hyper1451	N_insufficient_3	1.9E-05	0.21	0.09	0.12	2	60777279	cg00732907	chr2:60776596-60778157	Island
hyper1452	N_insufficient_3	2.4E-05	0.28	0.05	0.23	2	159173778	cg21514997	chr2:60776596-60778157	Island
hyper1453	N_insufficient_3	2.5E-04	0.28	0.05	0.24	2	239140169	cg07323141	chr2:239140096-239140659	Island
hyper1454	N_insufficient_3	5.1E-04	0.36	0.02	0.34	2	239140182	cg23497383	chr2:239140096-239140659	Island
hyper1455	N_insufficient_3	6.5E-03	0.32	0.02	0.30	2	239140190	cg13530938	chr2:239140096-239140659	Island
hyper1456	N_insufficient_3	1.5E-03	0.12	0.05	0.07	3	380807586	cg00807586	chr3:38080628-38081187	Island
hyper1457	N_insufficient_3	5.3E-02	0.14	0.08	0.06	3	48700245	cg12091542	chr3:48698353-48701667	Island
hyper1458	N_insufficient_3	5.8E-10	0.25	0.01	0.24	3	115503520	cg18176703	chr3:115502725-115503581	Island
hyper1459	N_insufficient_3	3.4E-08	0.19	0.03	0.16	3	132757741	cg19430967	chr3:132756985-132757895	Island
hyper1460	N_insufficient_3	9.4E-04	0.12	0.03	0.09	3	142833578	cg08774368	chr3:142837885-142840838	Island
hyper1461	N_insufficient_3	9.0E-04	0.05	0.01	0.04	4	926294	cg19987229	chr4:925808-926488	Island
hyper1462	N_insufficient_3	1.2E-06	0.06	0.01	0.05	4	85504501	cg03403966	chr4:85503546-85504893	Island
hyper1463	N_insufficient_3	3.8E-03	0.25	0.06	0.19	4	109088990	cg03534432	chr4:109087747-109090407	Island
hyper1464	N_insufficient_3	2.9E-04	0.19	0.05	0.14	4	113436625	cg08929548	chr4:113435898-113438002	Island
hyper1465	N_insufficient_3	2.3E-05	0.20	0.06	0.15	5	53545	cg05648010	chr5:53111-54264	Island
hyper1466	N_insufficient_3	0.0E+00	0.27	0.03	0.23	5	53564	cg22807585	chr5:53111-54264	Island
hyper1467	N_insufficient_3	2.0E-03	0.17	0.08	0.09	5	53886	cg10411494	chr5:53111-54264	Island
hyper1468	N_insufficient_3	3.5E-03	0.21	0.06	0.14	5	60627447	cg02486078	chr5:60626505-60629809	Island
hyper1469	N_insufficient_3	3.3E-06	0.31	0.09	0.22	5	60629795	cg07939285	chr5:60626505-60629809	Island
hyper1470	N_insufficient_3	3.5E-02	0.31	0.09	0.22	5	159200479	cg00028918	chr5:159200237-159200692	Island
hyper1471	N_insufficient_3	2.8E-08	0.29	0.06	0.23	6	1603827	cg03085948	chr6:1604606-1615866	Island
hyper1472	N_insufficient_3	5.9E-02	0.28	0.11	0.16	6	1610101	cg02020480	chr6:1604606-1615866	Island
hyper1473	N_insufficient_3	4.4E-07	0.26	0.05	0.21	6	1610120	cg23572376	chr6:1604606-1615866	Island
hyper1474	N_insufficient_3	6.2E-05	0.13	0.06	0.07	6	1610197	cg23867624	chr6:1604606-1615866	Island
hyper1475	N_insufficient_3	0.0E+00	0.25	0.02	0.23	6	1610699	cg04780909	chr6:1604606-1615866	Island
hyper1476	N_insufficient_3	3.1E-07	0.32	0.13	0.20	6	1610673	cg11815762	chr6:1604606-1615866	Island
hyper1477	N_insufficient_3	1.1E-05	0.37	0.11	0.26	6	1611451	cg20491838	chr6:1604606-1615866	Island
hyper1478	N_insufficient_3	1.9E-10	0.17	0.02	0.16	6	1611712	cg01912921	chr6:1604606-1615866	Island
hyper1479	N_insufficient_3	1.6E-03	0.25	0.10	0.15	6	1611850	cg10365447	chr6:1604606-1615866	Island
hyper1480	N_insufficient_3	4.6E-08	0.17	0.02	0.15	6	3227755	cg11522018	chr6:3227025-3229688	Island
hyper1481	N_insufficient_3	1.0E-02	0.13	0.03	0.10	6	3227949	cg10926113	chr6:3227025-3229688	Island
hyper1482	N_insufficient_3	6.3E-02	0.08	0.03	0.05	6	13486415	cg21348771	chr6:13486324-13488792	Island
hyper1483	N_insufficient_3	8.4E-03	0.13	0.05	0.09	6	32939317	cg17013193	chr6:32939275-32940594	Island
hyper1484	N_insufficient_3	9.1E-05	0.12	0.02	0.10	6	32939335	cg110061292	chr6:32939275-32940594	Island
hyper1485	N_insufficient_3	1.1E-05	0.10	0.02	0.08	6	32939364	cg07211678	chr6:32939275-32940594	Island
hyper1486	N_insufficient_3	6.6E-07	0.14	0.02	0.11	6	32939456	cg26226566	chr6:32939275-32940594	Island
hyper1487	N_insufficient_3	3.0E-03	0.16	0.08	0.08	6	32939507	cg21174644	chr6:32939275-32940594	Island
hyper1488	N_insufficient_3	1.7E-07	0.14	0.02	0.09	6	46702683	cg14645023	chr6:46702736-46703316	N_Shore
hyper1489	N_insufficient_3	4.6E-09	0.22	0.06	0.16	6	46702790	cg12863300	chr6:46702736-46703316	N_Shore
hyper1490	N_insufficient_3	0.0E+00	0.20	0.00	0.20	6	46702983	cg18630040	chr6:46702736-46703316	N_Shore
hyper1491	N_insufficient_3	2.2E-03	0.19	0.05	0.14	6	110679107	cg10259748	chr6:110678854-110679108	Island
hyper1492	N_insufficient_3	3.4E-05	0.16	0.02	0.14	6	166401700	cg02465374	chr6:166401526-166402659	Island
hyper1493	N_insufficient_3	7.8E-03	0.31	0.09	0.22	6	166419641	cg12856646	chr6:166421891-166422241	N_Shelf
hyper1494	N_insufficient_3	1.1E-02	0.22	0.09	0.13	6	168719564	cg05070558	chr6:168719681-168720495	Island
hyper1495	N_insufficient_3	3.4E-02	0.16	0.08	0.08	7	64734517	cg26337123	chr7:64734488-64734692	Island
hyper1496	N_insufficient_3	4.0E-02	0.25	0.08	0.17	7	98226035	cg19329121	chr7:98225503-98226194	Island
hyper1497	N_insufficient_3	2.9E-02	0.10	0.04	0.06	7	100291184	cg05401159	chr7:100291183-100292266	Island
hyper1498	N_insufficient_3	1.2E-02	0.20	0.03	0.17	7	112726653	cg03119639	chr7:140772358-140774560	Island
hyper1499	N_insufficient_3	2.1E-02	0.22	0.04	0.18	7	140773578	cg15928538	chr7:140772358-140774560	Island
hyper1500	N_insufficient_3	1.4E-07	0.19	0.03	0.16	7	140773905	cg07028821	chr7:140772358-140774560	Island
hyper1501	N_insufficient_3	2.0E-07	0.31	0.11	0.20	7	140774104	cg093044986	chr7:140772358-140774560	Island
hyper1502	N_insufficient_3	2.3E-09	0.26	0.02	0.25	7	140774161	cg18750086	chr7:140772358-140774560	Island
hyper1503	N_insufficient_3	2.8E-04	0.27	0.03	0.23	7	140774522	cg17554604	chr7:140772358-140774560	Island
hyper1504	N_insufficient_3	1.3E-07	0.20	0.04	0.16	8	6691787	cg21493703	chr8:6691833-6693135	Island
hyper1505	N_insufficient_3	3.6E-02	0.28	0.08	0.20	8	6692470	cg15234760	chr8:6691833-6693135	Island
hyper1506	N_insufficient_3	4.4E-02	0.14	0.09	0.06	8	16859451	cg11152975	chr8:168594044-168594542	Island
hyper1507	N_insufficient_3	9.6E-04	0.04	0.01	0.03	8	22014129	cg10309695	chr8:22014152-22014559	N_Shore
hyper1508	N_insufficient_3	1.0E-05	0.13	0.03	0.10	8	41166990	cg24319902	chr8:41165852-41167140	Island
hyper1509	N_insufficient_3	1.0E-02	0.19	0.09	0.11	8	41167087	cg10495122	chr8:41165852-41167140	Island
hyper1510	N_insufficient_3	1.1E-03	0.09	0.02	0.07	8	41167107	cg215		

hyper1544	N_insufficient_3	7.2E-02	0.22	0.04	0.18	15	40212176	cg08364767	GPR176	1stExon	chr15:40211961-40213444	Island
hyper1545	N_insufficient_3	6.9E-02	0.24	0.10	0.14	15	40212188	cg11119742	GPR176	1stExon	chr15:40211961-40213444	Island
hyper1546	N_insufficient_3	3.9E-03	0.16	0.04	0.12	15	60296159	cg2628621	FOXB1	TSS1500	chr15:60296135-60298520	Island
hyper1547	N_insufficient_3	6.4E-09	0.24	0.02	0.22	15	60296169	cg16611005	FOXB1	TSS1500	chr15:60296135-60298520	Island
hyper1548	N_insufficient_3	9.1E-05	0.09	0.02	0.06	15	84034416	cg06842989				
hyper1549	N_insufficient_3	4.2E-07	0.15	0.05	0.10	15	96960214	cg11862671			chr15:96959341-96960531	Island
hyper1550	N_insufficient_3	6.7E-07	0.22	0.05	0.17	15	96960331	cg26470794			chr15:96959341-96960531	Island
hyper1551	N_insufficient_3	6.4E-07	0.20	0.09	0.11	15	96960392	cg20382758			chr15:96959341-96960531	Island
hyper1552	N_insufficient_3	7.5E-06	0.18	0.06	0.11	15	96960574	cg18496247			chr15:96959341-96960531	S_Shore
hyper1553	N_insufficient_3	8.1E-03	0.18	0.09	0.10	16	257303018	cg23290209	HS3ST4	TSS1500	chr16:25720295-25704631	Island
hyper1554	N_insufficient_3	2.3E-06	0.19	0.06	0.13	16	54320670	cg24662961	IRX3	TSS1500	chr16:54317821-54324604	Island
hyper1555	N_insufficient_3	3.3E-04	0.03	0.00	0.03	16	67694967	cg06287927	ACD;ACD;PARD6A;ACD;PARD6B	TSS1500;TSS1500;1stExon;TSS1	chr16:67693451-67695602	Island
hyper1556	N_insufficient_3	7.0E-04	0.18	0.02	0.15	17	35293930	cg24761507	LHX1	TSS1500	chr17:35291899-35300875	Island
hyper1557	N_insufficient_3	7.4E-05	0.22	0.04	0.18	17	35294230	cg12279877	LHX1	TSS1500	chr17:35291899-35300875	Island
hyper1558	N_insufficient_3	0.0E+00	0.24	0.03	0.21	17	40333464	cg26949289	KCNH4	TSS200	chr17:40332597-40333471	Island
hyper1559	N_insufficient_3	6.3E-05	0.17	0.06	0.12	17	45056008	cg22674412	RPRML;RPRML	3'UTR;1stExon	chr17:45055317-45056838	Island
hyper1560	N_insufficient_3	0.0E+00	0.29	0.03	0.26	17	54991456	cg20675642	TRIM25	TSS200	chr17:54990832-54991771	Island
hyper1561	N_insufficient_3	1.5E-03	0.22	0.08	0.14	17	71898264	cg13990321			chr17:71897970-71898240	Island
hyper1562	N_insufficient_3	2.3E-05	0.11	0.02	0.09	18	78005649	cg05872073	PARD6G	TSS1500	chr18:78004028-78005438	S_Shore
hyper1563	N_insufficient_3	5.7E-03	0.14	0.05	0.09	18	78005665	cg00870662	PARD6G	TSS1500	chr18:78004028-78005438	S_Shore
hyper1564	N_insufficient_3	2.7E-07	0.28	0.08	0.20	19	10120092	cg12122464	COL5A3	Body	chr19:10120750-10121231	N_Shore
hyper1565	N_insufficient_3	4.8E-02	0.19	0.12	0.07	19	17536024	cg22641093	FAM125A	3'UTR		
hyper1566	N_insufficient_3	1.4E-06	0.23	0.07	0.17	19	35615444	cg09478274	LG4	3'UTR	chr19:35615412-35615665	Island
hyper1567	N_insufficient_3	5.9E-03	0.20	0.08	0.12	19	35615579	cg11620066	LG4	3'UTR	chr19:35615412-35615665	Island
hyper1568	N_insufficient_3	0.0E+00	0.14	0.01	0.13	19	35615638	cg27316970	LG4	3'UTR	chr19:35615412-35615665	Island
hyper1569	N_insufficient_3	4.3E-02	0.15	0.08	0.15	19	58917778	cg24369702	ZNF132	TSS200	chr19:58915214-58922260	Island
hyper1570	N_insufficient_3	2.3E-02	0.05	0.01	0.03	19	58951814	cg00868383	ZNF132	TSS1500	chr19:58951214-58952250	Island
hyper1571	N_insufficient_3	6.8E-03	0.18	0.05	0.13	19	58951885	cg07878486	ZNF132	TSS1500	chr19:58951214-58952250	Island
hyper1572	N_insufficient_4	5.9E-06	0.23	0.03	0.20	1	35247397	cg18262616	GJB3;GJB3	TSS1500;5'UTR	chr1:35246876-35247599	Island
hyper1573	N_insufficient_4	2.1E-04	0.18	0.05	0.13	1	240161249	cg13239420			chr1:24016037-24016116	Island
hyper1574	N_insufficient_4	0.0E+00	0.16	0.01	0.15	1	240161445	cg21854408			chr1:24016037-24016116	Island
hyper1575	N_insufficient_4	2.4E-07	0.25	0.09	0.16	2	133174094	cg23410738	GPR39	TSS200	chr2:133173532-133174369	Island
hyper1576	N_insufficient_4	3.5E-03	0.32	0.11	0.21	2	133174117	cg13136510	GPR39	TSS200	chr2:133173532-133174369	Island
hyper1577	N_insufficient_4	0.0E+00	0.24	0.02	0.22	2	133174136	cg22866015	GPR39	TSS200	chr2:133173532-133174369	Island
hyper1578	N_insufficient_4	2.8E-06	0.16	0.04	0.12	2	133174168	cg02570563	GPR39;GPR39	1stExon;5'UTR	chr2:133173532-133174369	Island
hyper1579	N_insufficient_4	1.9E-03	0.07	0.02	0.05	2	175547399	cg25075147	WIPF1	5'UTR	chr2:175546862-17554780	Island
hyper1580	N_insufficient_4	7.9E-02	0.13	0.07	0.06	3	79067337	cg01793933	ROBO1;ROBO1;ROBO1;ROBO1	Body;Body;Body;Body	chr3:79067882-79068566	N_Shore
hyper1581	N_insufficient_4	1.3E-02	0.10	0.02	0.07	3	79067920	cg07467520	ROBO1;ROBO1;ROBO1;ROBO1	1stExon;1stExon;1stExon;5'UTR;5	chr3:79067882-79068566	Island
hyper1582	N_insufficient_4	3.4E-02	0.14	0.06	0.08	3	79068292	cg15709235	ROBO1;ROBO1;ROBO1;ROBO1	1stExon;1stExon;1stExon;5'UTR;5	chr3:79067882-79068566	Island
hyper1583	N_insufficient_4	2.5E-02	0.14	0.09	0.05	3	79068813	cg27221334	ROBO1;ROBO1;ROBO1;ROBO1	TSS1500;TSS1500;Body;TSS1500	chr3:79067882-79068566	S_Shore
hyper1584	N_insufficient_4	1.6E-07	0.13	0.04	0.10	3	79068831	cg24787494	ROBO1;ROBO1;ROBO1;ROBO1	TSS1500;TSS1500;Body;TSS1500	chr3:79067882-79068566	S_Shore
hyper1585	N_insufficient_4	6.9E-02	0.14	0.09	0.04	3	79068857	cg28233589	ROBO1;ROBO1;ROBO1;ROBO1	TSS1500;TSS1500;Body;TSS1500	chr3:79067882-79068566	S_Shore
hyper1586	N_insufficient_4	1.6E-06	0.44	0.06	0.38	4	39448975	cg13732582	KLB	Body	chr4:39448184-39449054	Island
hyper1587	N_insufficient_4	1.2E-04	0.14	0.02	0.12	4	141419169	cg09643034			chr4:141419007-141419504	Island
hyper1588	N_insufficient_4	1.4E-05	0.09	0.02	0.07	5	1931251	cg03595755			chr5:19307544-1931986	Island
hyper1589	N_insufficient_4	4.9E-02	0.30	0.05	0.25	5	5140646	cg22784954	ADAMTS16	1stExon	chr5:5139441-5140941	Island
hyper1590	N_insufficient_4	1.4E-02	0.10	0.04	0.06	5	149682233	cg25780607	ARSI;ARSI	5'UTR;1stExon	chr5:149681702-149682601	Island
hyper1591	N_insufficient_4	6.9E-04	0.12	0.06	0.05	6	30180785	cg02957918	TRIM26	5'UTR	chr6:30180933-30182187	N_Shore
hyper1592	N_insufficient_4	7.6E-03	0.15	0.07	0.08	6	30180804	cg26560341	TRIM26	5'UTR	chr6:30180933-30182187	N_Shore
hyper1593	N_insufficient_4	3.2E-04	0.17	0.08	0.09	6	30180820	cg13083523	TRIM26	5'UTR	chr6:30180933-30182187	N_Shore
hyper1594	N_insufficient_4	7.1E-04	0.11	0.04	0.07	6	30180863	cg16392144	TRIM26	5'UTR	chr6:30180933-30182187	N_Shore
hyper1595	N_insufficient_4	2.5E-04	0.13	0.02	0.11	6	30180962	cg18068919	TRIM26	5'UTR	chr6:30180933-30182187	N_Shore
hyper1596	N_insufficient_4	2.8E-06	0.22	0.05	0.18	6	30181014	cg10793756	TRIM26	5'UTR	chr6:30180933-30182187	Island
hyper1597	N_insufficient_4	1.1E-05	0.30	0.05	0.24	6	30181025	cg16797983	TRIM26	5'UTR	chr6:30180933-30182187	Island
hyper1598	N_insufficient_4	1.1E-04	0.32	0.07	0.25	6	30181032	cg18556540	TRIM26	5'UTR	chr6:30180933-30182187	Island
hyper1599	N_insufficient_4	8.7E-06	0.28	0.06	0.23	6	30181036	cg16808910	TRIM26	5'UTR	chr6:30180933-30182187	Island
hyper1600	N_insufficient_4	3.4E-05	0.03	0.00	0.03	6	30181173	cg12103149	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1601	N_insufficient_4	0.0E+00	0.16	0.01	0.15	6	30181175	cg05864692	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1602	N_insufficient_4	3.8E-04	0.09	0.02	0.07	6	30181183	cg20674777	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1603	N_insufficient_4	2.9E-06	0.12	0.02	0.10	6	30181189	cg26937613	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1604	N_insufficient_4	3.7E-07	0.15	0.03	0.12	6	30181194	cg13118072	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1605	N_insufficient_4	2.3E-02	0.25	0.11	0.13	6	30181212	cg01962105	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1606	N_insufficient_4	3.8E-05	0.24	0.07	0.17	6	30181302	cg09084877	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1607	N_insufficient_4	6.0E-09	0.28	0.04	0.25	6	30181335	cg02210602	TRIM26	TSS200	chr6:30180933-30182187	Island
hyper1608	N_insufficient_4	1.9E-08	0.25	0.03	0.23	6	30181383	cg24243375	TRIM26	TSS1500	chr6:30180933-30182187	Island
hyper1609	N_insufficient_4	1.7E-08	0.22	0.08	0.14	6	30181425	cg10037053	TRIM26	TSS1500	chr6:30180933-30182187	Island
hyper1610	N_insufficient_4	1.5E-05	0.15	0.05	0.09	6	30181448	cg14694232	TRIM26	TSS1500	chr6:30180933-30182187	Island
hyper1611	N_insufficient_4	5.7E-06	0.19	0.06	0.13	6	30181488	cg04274844	TRIM26	TSS1500	chr6:30180933-30182187	Island
hyper1612	N_insufficient_4	1.2E-06	0.13	0.04	0.08	6	30181645	cg18841691	TRIM26	TSS1500	chr6:30180933-30182187	Island
hyper1613	N_insufficient_4	3.9E-04	0.12	0.02	0.09	6	43970084	cg25360181	C6orf223	Body	chr6:43970073-43970923	Island
hyper1614	N_insufficient_4	5.2E-05	0.14	0.06	0.08	6	46097650	cg14225611	ENPP4	TSS200	chr6:46097694-46097953	N_Shore
hyper1615	N_insufficient_4	2.6E-03	0.32	0.15	0.17	6	46097671	cg23634318	ENPP4	TSS200	chr6:46097694-46097953	N_Shore
hyper1616	N_insufficient_4	9.3E-05	0.03	0.02	0.25	6	46097695	cg06768203	ENPP4	TSS200	chr6:46097694-46097953	Island
hyper1617	N_insufficient_4	1.7E-02	0.03	0.12	0.11	6	46097788	cg28211309	ENPP4;ENPP4	Body;1stExon	chr6:46097694-46097953	Island
hyper1618	N_insufficient_4	1.1E-03	0.13	0.02	0.11	6	100062572	cg18600649	PRDM13	5'UTR	chr6:100060979-100062657	Island
hyper1619	N_insufficient_4	1.2E-02	0.16	0.05	0.11	6	170604676	cg20745457			chr6:170604411-170606479	Island
hyper1620	N_insufficient_4	1.3E-08	0.19	0.05	0.14	6	170605003	cg02134248			chr6:170604411-170606479	Island
hyper1621	N_insufficient_4	1.9E-10	0.31	0.03	0.28	6	170605623	cg12123671			chr6:170604411-170606479	Island
hyper1622	N_insufficient_4	3.7E-02	0.12	0.04	0.08	7	24796881	cg07320646	DFNA5;DFNA5;DFNA5	5'UTR;5'UTR;5'UTR	chr7:24796541-24797487	Island
hyper1623	N_insufficient_4	8.2E-02	0.24	0.05	0.19	7	24797192	cg07283520	DFNA5;DFNA5;DFNA5	5'UTR;5'UTR;TSS200	chr7:24796541-24797487	Island
hyper1624	N_insufficient_4	8.8E-03	0.16	0.01	0.14	7	91510198	cg00309769	MTERF	TSS200	chr7:91509997-91510427	Island
hyper1625	N_insufficient_4	1.2E-04	0.15	0.03	0.12	8	21923840	cg23897733	EPB49;EPB49;EPB49;EPB49	5'UTR;5'UTR;5'UTR;5'UTR	chr8:21923840-21924633	Island
hyper1626	N_insufficient_4	2.8E-07	0.16	0.04	0.12	8	27629759	cg02032552	CCDC25	Body	chr8:27629753-27630234	Island
hyper1627	N_insufficient_4	0.0E+00	0.26	0.02	0.24	8	2					

hyper1673	N_insufficient_5	4.8E-02	0.18	0.05	0.13	7	14030351	cg05918135	ETV1.ETV1.ETV1.ETV1	5UTR,TSS1500.5UTR,TSS1500	chr7:14030965-14031213	N_Shore
hyper1674	N_insufficient_5	2.4E-03	0.22	0.08	0.14	7	14030466	cg11897145	ETV1.ETV1.ETV1.ETV1	5UTR,TSS1500.5UTR,TSS1500	chr7:14030965-14031213	N_Shore
hyper1675	N_insufficient_5	5.8E-10	0.13	0.02	0.12	7	14030482	cg06566166	ETV1.ETV1.ETV1.ETV1	5UTR,TSS1500.5UTR,TSS1500	chr7:14030965-14031213	N_Shore
hyper1676	N_insufficient_5	1.1E-03	0.11	0.02	0.09	7	14030807	cg03028693	ETV1.ETV1.ETV1.ETV1.ETV1	5UTR,TSS1500.5UTR,TSS1500	chr7:14030965-14031213	N_Shore
hyper1677	N_insufficient_5	8.9E-04	0.15	0.05	0.10	7	19155806	cg04043691	TWIST1	3UTR	chr7:19156060-19158202	N_Shore
hyper1678	N_insufficient_5	0.0E+00	0.31	0.08	0.23	7	121512875	cg21423724	PTPRZ1	TSS1500	chr7:121513046-121513911	N_Shore
hyper1679	N_insufficient_5	0.0E+00	0.42	0.05	0.37	7	121513078	cg05931096	PTPRZ1	TSS200	chr7:121513046-121513911	Island
hyper1680	N_insufficient_5	0.0E+00	0.34	0.08	0.25	7	121513065	cg08026368	PTPRZ1	TSS200	chr7:121513046-121513911	Island
hyper1681	N_insufficient_5	0.0E+00	0.38	0.09	0.29	7	121513704	cg07757261	PTPRZ1	Body	chr7:121513046-121513911	Island
hyper1682	N_insufficient_5	0.0E+00	0.23	0.02	0.22	7	121513910	cg06631603	PTPRZ1	Body	chr7:121513046-121513911	Island
hyper1683	N_insufficient_5	1.1E-09	0.29	0.04	0.25	7	121513944	cg22410750	PTPRZ1	Body	chr7:121513046-121513911	S_Shore
hyper1684	N_insufficient_5	1.5E-09	0.22	0.05	0.17	8	23584098	cg19719133			chr8:23584001-23584761	Island
hyper1685	N_insufficient_5	9.7E-11	0.46	0.14	0.32	9	79792074	cg10975354	VPS13A.VPS13A.LOC100286938	TSS1500.TSS1500.Body.TSS1500	chr9:79792070-79793328	Island
hyper1686	N_insufficient_5	0.0E+00	0.32	0.08	0.24	9	127703551	cg14452096	GOLGA1	TSS200	chr9:127703131-127703629	Island
hyper1687	N_insufficient_5	0.0E+00	0.31	0.06	0.26	9	127703617	cg09227136	GOLGA1	TSS1500	chr9:127703131-127703629	Island
hyper1688	N_insufficient_5	2.1E-03	0.49	0.17	0.32	12	39538854	cg20762480			chr12:39538383-39539500	Island
hyper1689	N_insufficient_5	0.0E+00	0.27	0.05	0.22	12	39538408	cg09788416			chr12:39538383-39539500	Island
hyper1690	N_insufficient_5	6.0E-09	0.27	0.08	0.19	12	39532422	cg03468072			chr12:39538383-39539500	Island
hyper1691	N_insufficient_5	2.4E-02	0.10	0.04	0.06	12	125534403	cg13938881			chr12:125534060-125534527	N_Shore
hyper1692	N_insufficient_5	5.4E-02	0.14	0.05	0.09	12	125534110	cg21265540			chr12:125534060-125534527	Island
hyper1693	N_insufficient_5	1.1E-06	0.20	0.08	0.12	12	125534526	cg15701313			chr12:125534060-125534527	Island
hyper1694	N_insufficient_5	4.7E-09	0.15	0.02	0.14	14	105116681	cg23656707			chr14:105116496-105116623	Island
hyper1695	N_insufficient_5	5.0E-07	0.37	0.13	0.23	15	51386254	cg06813578	TNFAIP8L3	Body	chr15:51385861-51387203	Island
hyper1696	N_insufficient_5	0.0E+00	0.31	0.10	0.21	15	51386452	cg17180386	TNFAIP8L3	Body	chr15:51385861-51387203	Island
hyper1697	N_insufficient_5	0.0E+00	0.41	0.04	0.37	15	51386759	cg07218022	TNFAIP8L3	Body	chr15:51385861-51387203	Island
hyper1698	N_insufficient_5	2.9E-07	0.03	0.28	0.15	15	51387571	cg06421871	TNFAIP8L3	Body	chr15:51387532-51387765	Island
hyper1699	N_insufficient_5	1.2E-02	0.03	0.01	0.03	16	12009700	cg15711407	GSPT1.GSPT1.GSPT1.G	1stExon.5UTR;1stExon.5UTR;5UTR	chr16:12008880-12011014	S_Shore
hyper1700	N_insufficient_5	6.5E-03	0.20	0.09	0.11	17	19015961	cg16919567			chr17:19014144-19014604	S_Shore
hyper1701	N_insufficient_5	6.1E-02	0.19	0.09	0.10	18	5542879	cg26790372	EPB41L3	5UTR	chr18:5542847-5543054	Island
hyper1702	N_insufficient_5	1.2E-02	0.29	0.08	0.21	18	47088306	cg27631427	LIPG	TSS200	chr18:47087879-47088528	Island
hyper1703	N_insufficient_5	7.1E-04	0.27	0.07	0.20	18	47088309	cg21574400	LIPG	TSS200	chr18:47087879-47088528	Island
hyper1704	N_insufficient_5	1.1E-06	0.30	0.06	0.25	18	47088343	cg14320593	LIPG	TSS200	chr18:47087879-47088528	Island
hyper1705	N_insufficient_5	1.0E-05	0.22	0.06	0.16	18	47088373	cg00692763	LIPG	TSS200	chr18:47087879-47088528	Island
hyper1706	N_insufficient_5	9.7E-04	0.22	0.08	0.13	18	47088421	cg11038073	LIPG	TSS200	chr18:47087879-47088528	Island
hyper1707	N_insufficient_5	8.1E-04	0.23	0.08	0.16	18	47088432	cg14254867	LIPG.LIPG	5UTR;1stExon	chr18:47087879-47088528	Island
hyper1708	N_insufficient_5	3.9E-10	0.25	0.04	0.20	19	9648995	cg25227274	ZNF426	5UTR	chr19:9648934-9649410	Island
hyper1709	N_insufficient_5	1.9E-10	0.17	0.03	0.14	19	9649241	cg11845033	ZNF426	5UTR	chr19:9648934-9649410	Island
hyper1710	N_insufficient_5	1.5E-06	0.28	0.10	0.18	19	9649376	cg21285525	ZNF426	TSS200	chr19:9648934-9649410	Island
hyper1711	N_adequate_1	1.1E-02	0.13	0.04	0.09	1	110453107	cg05005301	CSF1.CSF1.CSF1.CSF1	TSS200.TSS200.TSS200.TSS200	chr1:110453143-110453889	N_Shore
hyper1712	N_adequate_1	4.2E-02	0.13	0.07	0.06	2	211341126	cg20604466	LANCL1.LANCL1.CPS1.LANCL1	5UTR.5UTR.TSS1500.5UTR	chr2:211341181-211341536	N_Shore
hyper1713	N_adequate_1	3.5E-03	0.08	0.01	0.07	2	211341199	cg21574953	LANCL1.LANCL1.CPS1.LANCL1	5UTR.5UTR.TSS1500.5UTR	chr2:211341181-211341536	Island
hyper1714	N_adequate_1	7.2E-08	0.10	0.02	0.08	2	119861150	cg14506391			chr2:119860927-119861242	Island
hyper1715	N_adequate_1	0.0E+00	0.18	0.02	0.16	3	9957221	cg23350106	IL17RE.IL17RE.IL17RE	Body.Body.Body	chr3:9956822-9957664	Island
hyper1716	N_adequate_1	4.2E-03	0.13	0.06	0.07	3	9957373	cg05845178	IL17RE.IL17RC.IL17RE.IL17RE.IL	3UTR.TSS1500.3UTR.3UTR.TSS	chr3:9956822-9957664	Island
hyper1717	N_adequate_1	1.4E-09	0.25	0.08	0.17	3	154797083	cg07862554	MME.MME.MME.MME	TSS1500.TSS1500.TSS1500.TSS	chr3:154797398-154797988	N_Shore
hyper1718	N_adequate_1	8.8E-10	0.20	0.08	0.12	3	154797399	cg08085954	MME.MME.MME.MME	TSS200.TSS1500.TSS1500.TSS1	chr3:154797398-154797988	Island
hyper1719	N_adequate_1	0.0E+00	0.27	0.08	0.19	3	154797508	cg03648334	MME.MME.MME.MME.MME	TSS1500;1stExon.TSS200.TSS15	chr3:154797398-154797988	Island
hyper1720	N_adequate_1	0.0E+00	0.24	0.05	0.19	3	154797563	cg17344755	MME.MME.MME.MME	TSS1500.TSS200.TSS1500.5UTR	chr3:154797398-154797988	Island
hyper1721	N_adequate_1	1.6E-09	0.27	0.09	0.18	3	154797589	cg16580737	MME.MME.MME.MME	TSS1500.TSS200.TSS1500.5UTR	chr3:154797398-154797988	Island
hyper1722	N_adequate_1	0.0E+00	0.37	0.05	0.31	3	154797767	cg21496658	MME.MME.MME.MME	TSS1500.TSS200.TSS1500.5UTR	chr3:154797398-154797988	Island
hyper1723	N_adequate_1	5.8E-10	0.29	0.09	0.26	3	154797779	cg22471320	MME.MME.MME.MME.MME	5UTR.TSS1500.TSS200;1stExon	chr3:154797398-154797988	Island
hyper1724	N_adequate_1	0.0E+00	0.36	0.02	0.27	3	154797867	cg201208850	MME.MME.MME.MME	5UTR.TSS1500.TSS200.5UTR	chr3:154797398-154797988	Island
hyper1725	N_adequate_1	0.0E+00	0.34	0.07	0.27	3	154797892	cg26872138	MME.MME.MME.MME	TSS200.5UTR.TSS200.5UTR	chr3:154797398-154797988	Island
hyper1726	N_adequate_1	0.0E+00	0.31	0.02	0.29	3	154797917	cg23209255	MME.MME.MME.MME	TSS200.5UTR.TSS200.5UTR	chr3:154797398-154797988	Island
hyper1727	N_adequate_1	0.0E+00	0.29	0.02	0.26	3	154797947	cg22955973	MME.MME.MME.MME	TSS200.5UTR.TSS200.5UTR	chr3:154797398-154797988	Island
hyper1728	N_adequate_1	0.0E+00	0.26	0.01	0.25	3	154797958	cg20216802	MME.MME.MME.MME.MME	TSS200.5UTR;1stExon.5UTR;5UTR	chr3:154797398-154797988	Island
hyper1729	N_adequate_1	5.8E-10	0.24	0.07	0.17	3	154798079	cg05862239	MME.MME.MME.MME.MME.MME	5UTR.5UTR;1stExon.5UTR;1stExon	chr3:154797398-154797988	S_Shore
hyper1730	N_adequate_1	1.9E-03	0.08	0.01	0.07	4	56502116	cg07943185	NMU	Body	chr4:56501912-56502247	Island
hyper1731	N_adequate_1	0.0E+00	0.23	0.01	0.21	4	56502392	cg17191517	NMU.NMU	1stExon.5UTR	chr4:56501912-56502253	Island
hyper1732	N_adequate_1	3.1E-08	0.25	0.09	0.16	4	56502469	cg2653813	NMU	TSS200	chr4:56501912-56502253	Island
hyper1733	N_adequate_1	1.4E-03	0.09	0.04	0.05	4	56502664	cg04427852	NMU	TSS200	chr4:56501912-56502253	S_Shore
hyper1734	N_adequate_1	1.4E-02	0.16	0.05	0.10	10	8374293	cg08860067				
hyper1735	N_adequate_1	6.9E-04	0.29	0.11	0.18	10	44880236	cg25721625	CXCL12.CXCL12.CXCL12	Body.Body.Body	chr10:44879714-44882391	Island
hyper1736	N_adequate_1	0.0E+00	0.17	0.01	0.16	10	44880542	cg06048524	CXCL12.CXCL12.CXCL12	TSS200.TSS200.TSS200	chr10:44879714-44882391	Island
hyper1737	N_adequate_1	0.0E+00	0.22	0.02	0.20	10	44880545	cg17267805	CXCL12.CXCL12.CXCL12	TSS200.TSS200.TSS200	chr10:44879714-44882391	Island
hyper1738	N_adequate_1	2.3E-03	0.03	0.00	0.03	10	44880559	cg23407507	CXCL12.CXCL12.CXCL12	TSS200.TSS200.TSS200	chr10:44879714-44882391	Island
hyper1739	N_adequate_1	0.0E+00	0.11	0.01	0.10	10	45496482	cg19185955	C10orf25.ZNF22	TSS200.5UTR	chr10:45496275-45496550	Island
hyper1740	N_adequate_1	1.6E-02	0.07	0.01	0.06	10	45496672	cg14260521	ZNF22.C10orf25	5UTR.TSS1500	chr10:45496275-45496550	S_Shore
hyper1741	N_adequate_1	2.2E-02	0.76	0.55	0.21	11	2722407	cg28963277	KCNQ1OT1.KCNQ1.KCNQ1	TSS1500.Body.Body	chr11:2722010-2722087	S_Shore
hyper1742	N_adequate_1	6.9E-04	0.16	0.02	0.14	15	82555113	cg13512069	EFTUD1.EFTUD1.FAM154B	TSS200.TSS200.TSS200	chr15:82554785-82555476	Island
hyper1743	N_adequate_1	5.5E-02	0.19	0.08	0.11	15	84749130	cg16444883			chr15:84748593-84749285	Island
hyper1744	N_adequate_1	2.9E-03	0.17	0.07	0.10	16	74655916	cg1684049R	GLG1.GLG1.GLG1.GLG1.GLG1	Body.Body.Body.Body.Body		
hyper1745	N_adequate_1	4.8E-08	0.14	0.03	0.11	17	16310359	cg03781505			chr17:16310306-16310914	Island
hyper1746	N_adequate_1	4.4E-03	0.26	0.13	0.13	17	42633120	cg2529126	FZD2	1stExon	chr17:42633429-42636961	Island
hyper1747	N_adequate_1	1.5E-04	0.13	0.02	0.11	17	46659318	cg24672833			chr17:46658948-46660003	Island
hyper1748	N_adequate_1	7.2E-03	0.78	0.63	0.15	20	57427146	cg24617313	GNAS.GNAS.GNAS.GNASAS	TSS1500.TSS1500.3UTR.TSS15	chr20:57427691-57427995	N_Shore
hyper1749	N_adequate_1	3.9E-10	0.34	0.06	0.28	22	33197338	cg20502037	SYN3.TIMP3.TIMP3.SYN3.SYN3	Body;1stExon.5UTR.Body.Body	chr22:33197380-33198267	Island
hyper1750	N_adequate_1	0.0E+00	0.31	0.07	0.24	22	33197605	cg05288803	SYN3.TIMP3.SYN3.SYN3	Body;1stExon.Body.Body	chr22:33197380-33198267	Island
hyper1751	N_adequate_2	1.3E-03	0.09	0.02	0.06	2	101435167	cg00581731	NPAS2	TSS1500	chr2:101434979-101437453	Island
hyper1752	N_adequate_2	1.5E-02	0.39	0.10	0.30	2	157292132	cg20233586	GPD2.GPD2.GPD2	1stExon.TSS1500.5UTR	chr2:157292102-157292646	

hyper1802	N_adequate_3	7.4E-05	0.27	0.06	0.21	7	64466808	cg14059817											
hyper1803	N_adequate_3	9.3E-04	0.35	0.06	0.29	7	64466846	cg04321566											
hyper1804	N_adequate_3	1.1E-04	0.30	0.09	0.21	7	64467056	cg26268843											
hyper1805	N_adequate_3	2.4E-03	0.07	0.03	0.04	8	22722817	cg10611863	PEBP4	Body		chr8:22722313-22723562	Island						
hyper1806	N_adequate_3	4.6E-05	0.05	0.01	0.04	10	99393498	cg06124827	MORNA;MORNA	TSS200;5'UTR		chr10:99392786-99393375	S_Shore						
hyper1807	N_adequate_3	1.3E-02	0.32	0.13	0.19	11	75917251	cg20633317	WNT11	Body		chr11:75917271-75917926	N_Shore						
hyper1808	N_adequate_3	0.0E+00	0.29	0.06	0.23	15	95388002	cg26237512				chr15:95388001-95388438	Island						
hyper1809	N_adequate_3	0.0E+00	0.32	0.10	0.23	19	24097753	cg20642963											
hyper1810	N_adequate_3	0.0E+00	0.71	0.14	0.57	19	45909099	cg23584739	CD3EAP;CD3EAP;PPR1913L	5'UTR;1stExon;TSS1500		chr19:45909062-45910124	Island						
hyper1811	N_adequate_3	1.5E-04	0.27	0.13	0.14	19	523082027	cg20280027	ZNF880	TSS1500		chr19:52307304-523073572	N_Shore						
hyper1812	N_adequate_3	3.3E-08	0.12	0.02	0.11	19	56015301	cg27303646	SSC5D	Body		chr19:56014811-56015333	Island						
hyper1813	N_adequate_3	4.0E-03	0.10	0.02	0.08	20	61051438	cg18278265	GATA5	TSS1500		chr20:61049361-61051897	Island						
hyper1814	N_adequate_4	1.2E-02	0.27	0.09	0.19	1	55462126	cg18384681				chr1:55462688-55463010	N_Shore						
hyper1815	N_adequate_4	1.1E-06	0.28	0.04	0.24	1	55462274	cg02392553				chr1:55462688-55463010	N_Shore						
hyper1816	N_adequate_4	0.0E+00	0.29	0.07	0.22	1	155231827	cg02768471	SCAMP3;SCAMP3	Body;Body		chr1:155231812-155232312	Island						
hyper1817	N_adequate_4	3.2E-02	0.11	0.04	0.07	1	155232227	cg18279150	SCAMP3;SCAMP3	TSS200;TSS200		chr1:155231812-155232312	Island						
hyper1818	N_adequate_4	2.9E-08	0.26	0.06	0.19	1	155232251	cg20795117	SCAMP3;SCAMP3	TSS200;TSS200		chr1:155231812-155232312	Island						
hyper1819	N_adequate_4	3.4E-05	0.18	0.05	0.13	1	155232344	cg24034289	SCAMP3;SCAMP3	TSS200;TSS200		chr1:155231812-155232312	S_Shore						
hyper1820	N_adequate_4	1.6E-08	0.18	0.06	0.12	1	155232379	cg01745448	SCAMP3;SCAMP3	TSS200;TSS200		chr1:155231812-155232312	S_Shore						
hyper1821	N_adequate_4	1.9E-02	0.30	0.09	0.21	2	45029285	cg19893751				chr2:45029855-45029318	Island						
hyper1822	N_adequate_4	3.0E-05	0.22	0.07	0.15	2	45029729	cg13732857				chr2:45029728-45030035	Island						
hyper1823	N_adequate_4	6.4E-05	0.32	0.06	0.26	4	124342	cg12717203	ZNF718	Body		chr4:124332-124841	Island						
hyper1824	N_adequate_4	2.4E-02	0.19	0.04	0.16	4	125112	cg10197305	ZNF718	Body		chr4:124332-124841	S_Shore						
hyper1825	N_adequate_4	2.1E-02	0.17	0.09	0.08	4	467407	cg05856015	ZNF721;ABCA11P	5'UTR;Body		chr4:467471-467839	N_Shore						
hyper1826	N_adequate_4	3.1E-02	0.28	0.04	0.24	4	3464874	cg25237365	DOCK7;DOCK7	TSS200;TSS200		chr4:3464799-3465440	Island						
hyper1827	N_adequate_4	1.3E-02	0.25	0.04	0.24	4	3464887	cg25757524	DOCK7;DOCK7	TSS200;TSS200		chr4:3464799-3465440	Island						
hyper1828	N_adequate_4	3.6E-07	0.36	0.04	0.31	4	3464966	cg24034289	DOCK7;DOCK7	TSS200;TSS200		chr4:3464799-3465440	Island						
hyper1829	N_adequate_4	3.8E-03	0.33	0.10	0.23	4	3464998	cg20622300	DOCK7;DOCK7	TSS200;TSS200		chr4:3464799-3465440	Island						
hyper1830	N_adequate_4	4.6E-02	0.30	0.08	0.22	4	3465004	cg17960516	DOCK7;DOCK7	TSS200;TSS200		chr4:3464799-3465440	Island						
hyper1831	N_adequate_4	4.2E-06	0.40	0.04	0.36	5	169064451	cg08862890	DOCK2	Body		chr5:169064270-169064702	Island						
hyper1832	N_adequate_4	1.0E-03	0.17	0.02	0.15	7	91808503	cg17063962				chr7:91808331-91808632	Island						
hyper1833	N_adequate_4	0.0E+00	0.15	0.00	0.14	8	143751204	cg10279794	JRK;JRK	5'UTR;5'UTR		chr8:143750759-143751448	Island						
hyper1834	N_adequate_4	1.2E-06	0.09	0.02	0.07	8	143751325	cg26325135	JRK;JRK	5'UTR;5'UTR		chr8:143750759-143751448	Island						
hyper1835	N_adequate_4	3.6E-02	0.42	0.04	0.38	10	75531995	cg17426063	FUT11	TSS200		chr10:75531970-75532817	Island						
hyper1836	N_adequate_4	7.4E-02	0.43	0.06	0.37	10	75532169	cg23588893	FUT11	1stExon		chr10:75531970-75532817	Island						
hyper1837	N_adequate_4	2.7E-02	0.45	0.09	0.36	10	75533025	cg12419678	FUT11	Body		chr10:75531970-75532817	S_Shore						
hyper1838	N_adequate_4	2.4E-03	0.22	0.05	0.17	10	75533400	cg15838173	FUT11	Body		chr10:75531970-75532817	S_Shore						
hyper1839	N_adequate_4	1.7E-08	0.20	0.01	0.19	10	98480463	cg12362864	PIK3AP1	TSS200		chr10:98479725-98480487	Island						
hyper1840	N_adequate_4	1.1E-03	0.32	0.11	0.21	10	98480465	cg24478788	PIK3AP1	TSS200		chr10:98479725-98480487	Island						
hyper1841	N_adequate_4	3.3E-03	0.26	0.08	0.18	10	98480474	cg07316170	PIK3AP1	TSS200		chr10:98479725-98480487	Island						
hyper1842	N_adequate_4	2.5E-07	0.22	0.05	0.16	11	60733865	cg07588442	PRPF19;PRPF19	1stExon;5'UTR		chr11:60733597-60674184	Island						
hyper1843	N_adequate_4	4.9E-10	0.50	0.09	0.42	12	64203034	cg20678225	PLEKHG6;PLEKHG6	TSS200;TSS200		chr12:6419603-6420024	S_Shore						
hyper1844	N_adequate_4	1.6E-06	0.15	0.06	0.09	14	23938784	cg05833251	NGDN;NGDN	TSS200;TSS200									
hyper1845	N_adequate_4	0.0E+00	0.24	0.07	0.16	14	23938824	cg05873158	NGDN;NGDN	TSS200;TSS200									
hyper1846	N_adequate_4	0.0E+00	0.28	0.07	0.21	14	23938846	cg26122402	NGDN;NGDN	TSS200;TSS200									
hyper1847	N_adequate_4	2.1E-03	0.17	0.03	0.14	14	23938929	cg05200925	NGDN;NGDN	1stExon;1stExon									
hyper1848	N_adequate_4	1.6E-05	0.16	0.05	0.11	14	23938996	cg04960285	NGDN;NGDN	Body;Body									
hyper1849	N_adequate_4	2.9E-06	0.16	0.05	0.11	14	23939157	cg10235955	NGDN;NGDN	Body;Body									
hyper1850	N_adequate_4	4.1E-02	0.21	0.09	0.12	16	5121709	cg05407018	ALG1	TSS200		chr16:5121749-5122192	N_Shore						
hyper1851	N_adequate_4	5.8E-02	0.35	0.11	0.24	18	67067721	cg05588496	DOCK6	TSS1500		chr18:67067509-67069168	Island						
hyper1852	N_adequate_4	5.7E-02	0.44	0.08	0.36	18	67067867	cg27347269	DOCK6	TSS1500		chr18:67067509-67069168	Island						
hyper1853	N_adequate_4	1.7E-03	0.13	0.04	0.09	19	40950431	cg14150973	SERTAD3	TSS200		chr19:40950025-40950777	Island						
hyper1854	N_adequate_4	7.4E-05	0.34	0.10	0.24	19	49925720	cg08567644	PTH2	3'UTR		chr19:49925626-49926012	Island						
hyper1855	N_adequate_4	2.1E-05	0.31	0.10	0.20	19	49925731	cg05248581	PTH2	Body		chr19:49925626-49926012	Island						
hyper1856	N_adequate_4	2.6E-02	0.31	0.18	0.13	19	49925920	cg13115979	PTH2	Body		chr19:49925626-49926012	Island						
hyper1857	N_adequate_5	3.2E-05	0.14	0.02	0.12	1	49242757	cg03603214	AGBL4;BEND5	Body;TSS1500		chr1:49242371-49242810	Island						
hyper1858	N_adequate_5	0.0E+00	0.24	0.03	0.20	1	184006265	cg05777716	GLT2SD2	1stExon		chr1:184005359-184006766	Island						
hyper1859	N_adequate_5	0.0E+00	0.36	0.04	0.26	1	184006496	cg15358901	GLT2SD2;GLT2SD2	5'UTR;1stExon		chr1:184005359-184006766	Island						
hyper1860	N_adequate_5	3.2E-02	0.22	0.10	0.12	1	184006765	cg18073907	GLT2SD2;GLT2SD2	5'UTR;1stExon		chr1:184005359-184006766	Island						
hyper1861	N_adequate_5	2.2E-03	0.13	0.06	0.08	1	223302861	cg16586333	TLR5	5'UTR									
hyper1862	N_adequate_5	5.5E-03	0.10	0.03	0.07	3	160822494	cg12349858	B3GALNT1;B3GALNT1;B3GALNT1	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR		chr3:160822494-160823260	Island						
hyper1863	N_adequate_5	5.2E-04	0.19	0.11	0.09	3	160822661	cg23252387	B3GALNT1;B3GALNT1;B3GALNT1	5'UTR;5'UTR;5'UTR;1stExon;5'UTR		chr3:160822494-160823260	Island						
hyper1864	N_adequate_5	7.8E-10	0.19	0.09	0.11	3	160822711	cg25469234	B3GALNT1;B3GALNT1;B3GALNT1	5'UTR;5'UTR;5'UTR;TSS200;5'UTR		chr3:160822494-160823260	Island						
hyper1865	N_adequate_5	5.7E-09	0.18	0.05	0.13	3	160822728	cg16496687	B3GALNT1;B3GALNT1;B3GALNT1	5'UTR;5'UTR;5'UTR;TSS200;5'UTR		chr3:160822494-160823260	Island						
hyper1866	N_adequate_5	0.0E+00	0.19	0.02	0.18	3	160822911	cg20841906	B3GALNT1;B3GALNT1;B3GALNT1	5'UTR;5'UTR;5'UTR;5'UTR;TSS1500		chr3:160822494-160823260	Island						
hyper1867	N_adequate_5	2.2E-03	0.04	0.00	0.04	4	57976561	cg01959562	IGFBP7	TSS200		chr4:57975860-57976916	Island						
hyper1868	N_adequate_5	1.4E-04	0.04	0.01	0.04	4	57976573	cg03357180	IGFBP7	TSS200		chr4:57975860-57976916	Island						
hyper1869	N_adequate_5	3.7E-04	0.06	0.01	0.05	5	16795364	cg14743594	FBL1	TSS200		chr5:167956219-167957371	Island						
hyper1870	N_adequate_5	4.7E-04	0.20	0.05	0.15	6	116601073	cg15056247	DSE;TSPYL1;TSPYL1	TSS1500;1stExon;5'UTR		chr6:116600044-116601174	Island						
hyper1871	N_adequate_5	3.2E-05	0.18	0.06	0.12	8	95732141	cg14329673	DPY19L4;DPY19L4	1stExon;5'UTR		chr8:95731798-95732449	Island						
hyper1872	N_adequate_5	5.8E-02	0.11	0.07	0.05	8	146126807	cg04151839	ZNF250;ZNF250;ZNF250;ZNF250	5'UTR;1stExon;1stExon;5'UTR		chr8:146126088-146128055	Island						
hyper1873	N_adequate_5	5.2E-05	0.04	0.01	0.03	8	146126815												

hyper1931	N_adequate_7	2.7E-06	0.22	0.09	0.12	4	15704795	cg13528854	BST1	1stExon	chr4:15704640-15705000	Island
hyper1932	N_adequate_7	1.3E-06	0.22	0.10	0.12	4	15704844	cg17924813	BST1	1stExon	chr4:15704640-15705000	Island
hyper1933	N_adequate_7	5.2E-02	0.24	0.09	0.15	5	42995369	cg24676817			chr5:42995122-42995415	Island
hyper1934	N_adequate_7	8.0E-05	0.14	0.06	0.08	5	43042108	cg16970804	LOC153684	TSS200	chr5:43042107-43043477	Island
hyper1935	N_adequate_7	0.0E+00	0.16	0.02	0.14	5	43042177	cg16628484	LOC153684	TSS200	chr5:43042107-43043477	Island
hyper1936	N_adequate_7	2.6E-03	0.22	0.12	0.10	5	43042233	cg22196610	LOC153684	TSS200	chr5:43042107-43043477	Island
hyper1937	N_adequate_7	0.0E+00	0.21	0.01	0.20	5	43042288	cg04711080	LOC153684	Body	chr5:43042107-43043477	Island
hyper1938	N_adequate_7	2.0E-02	0.19	0.09	0.11	5	17236894	cg17360560	RPL26L1,LOC100268166,LOC100	Body,TSS1500,TSS1500	chr5:17236893-172387102	Island
hyper1939	N_adequate_7	4.6E-08	0.03	0.14	0.11	5	4189478629	cg02051512	BTNL9	Body	chr5:18047585-180480959	Island
hyper1940	N_adequate_7	0.0E+00	0.16	0.02	0.14	5	180480234	cg02660602	BTNL9	Body	chr5:18047585-180480959	Island
hyper1941	N_adequate_7	1.0E-06	0.26	0.03	0.24	7	138720287	cg11590647	ZC3HAV1L	Body	chr7:138720044-138721019	Island
hyper1942	N_adequate_7	3.1E-04	0.34	0.08	0.26	7	138720988	cg14347989	ZC3HAV1L	TSS200	chr7:138720044-138721019	Island
hyper1943	N_adequate_7	7.6E-04	0.44	0.07	0.37	7	138720909	cg02657292	ZC3HAV1L	TSS200	chr7:138720044-138721019	Island
hyper1944	N_adequate_7	1.5E-04	0.23	0.09	0.14	7	138721065	cg24251035	ZC3HAV1L	TSS1500	chr7:138720044-138721019	S_Shore
hyper1945	N_adequate_7	1.3E-02	0.18	0.07	0.11	8	38614832	cg11071960	TACC1	5UTR	chr8:38614414-38615236	Island
hyper1946	N_adequate_7	2.2E-05	0.21	0.10	0.11	8	146176331	cg08699181	ZNF16,ZNF16	TSS200,TSS200	chr8:146175835-146176337	Island
hyper1947	N_adequate_7	6.8E-10	0.18	0.04	0.13	8	146176336	cg07534467	ZNF16,ZNF16	TSS200,TSS200	chr8:146175835-146176337	Island
hyper1948	N_adequate_7	1.9E-10	0.25	0.07	0.18	8	146176420	cg11914370	ZNF16,ZNF16	TSS200,TSS200	chr8:146175835-146176337	S_Shore
hyper1949	N_adequate_7	5.5E-02	0.38	0.17	0.21	8	146176436	cg13734177	ZNF16,ZNF16	TSS200,TSS200	chr8:146175835-146176337	S_Shore
hyper1950	N_adequate_7	1.4E-02	0.06	0.01	0.04	10	15413437	cg18375586	FAM171A1	TSS1500	chr10:15412419-15413040	S_Shore
hyper1951	N_adequate_7	4.8E-02	0.21	0.07	0.15	11	2161892	cg13791131	IGF2AS,INS-IGF2,IGF2,IGF1	Body,Body,5UTR,5UTR,Body	chr11:2158951-2162484	Island
hyper1952	N_adequate_7	1.4E-03	0.22	0.08	0.14	11	60775233	cg08177332	CD6	Body	chr11:60775036-60776307	Island
hyper1953	N_adequate_7	7.8E-02	0.38	0.04	0.34	13	33590273	cg05855588	KL	TSS1500	chr13:33589928-33591428	Island
hyper1954	N_adequate_7	3.5E-02	0.34	0.03	0.30	13	33590495	cg05116906	KL	TSS200	chr13:33589928-33591428	Island
hyper1955	N_adequate_7	1.8E-05	0.23	0.03	0.20	14	27060404	cg07559273	NOVA1,NOVA1,NOVA1	Body,Body,Body	chr14:27060313-27060578	Island
hyper1956	N_adequate_7	9.7E-10	0.28	0.08	0.19	15	55790446	cg15903790	DYX1C1,DYX1C1,DYX1C1	Body,Body,Body	chr15:55790301-55790754	Island
hyper1957	N_adequate_7	0.0E+00	0.27	0.01	0.26	15	55790509	cg01053602	DYX1C1,DYX1C1,DYX1C1	Body,Body,Body	chr15:55790301-55790754	Island
hyper1958	N_adequate_7	0.0E+00	0.29	0.08	0.21	15	55790608	cg18344452	DYX1C1,DYX1C1,DYX1C1	5UTR,5UTR,5UTR	chr15:55790301-55790754	Island
hyper1959	N_adequate_7	0.0E+00	0.26	0.06	0.20	15	557903615	cg07033615	DYX1C1,DYX1C1,DYX1C1	5UTR,5UTR,5UTR	chr15:55790301-55790754	Island
hyper1960	N_adequate_7	2.3E-05	0.26	0.07	0.19	15	101458615	cg24163563	LRRK1	TSS1500	chr15:101458286-101460223	Island
hyper1961	N_adequate_7	3.0E-07	0.35	0.04	0.30	15	101458783	cg06679538	LRRK1	TSS1500	chr15:101458286-101460223	Island
hyper1962	N_adequate_7	2.4E-08	0.32	0.04	0.28	15	101459283	cg25331703	LRRK1	TSS200	chr15:101458286-101460223	Island
hyper1963	N_adequate_7	2.9E-02	0.36	0.08	0.28	15	101460077	cg10253457	LRRK1	5UTR	chr15:101458286-101460223	Island
hyper1964	N_adequate_7	1.0E-03	0.31	0.10	0.21	16	71518618	cg03711682	ZNF19	5UTR		
hyper1965	N_adequate_7	0.0E+00	0.31	0.03	0.28	16	90085722	cg11239016	DBND1	1stExon	chr16:90085109-90086419	Island
hyper1966	N_adequate_7	7.2E-08	0.07	0.01	0.06	17	6555443	cg24184221	MED31,C17orf100	TSS1500,1stExon	chr17:6554832-6555585	Island
hyper1967	N_adequate_7	1.2E-02	0.14	0.07	0.07	19	45931688	cg26322788		Body	chr19:45931687-45932295	Island
hyper1968	N_adequate_7	0.0E+00	0.23	0.01	0.21	19	47933586	cg01263386	SLC8A2	Body	chr19:47933295-47933827	Island
hyper1969	N_adequate_7	2.8E-02	0.28	0.10	0.18	20	61005060	cg15749748	GATA5	Body	chr20:61049361-61051897	Island
hyper1970	N_adequate_7	7.9E-03	0.39	0.04	0.35	22	31218629	cg17330672	OSBP2	Body	chr22:31218626-31218693	Island
hyper1971	N_adequate_8	3.6E-03	0.08	0.20	0.12	1	14922656	cg01855656	KIAA1026,KIAA1026	Body,Body	chr1:14924610-14925993	Island
hyper1972	N_adequate_8	3.0E-08	0.31	0.10	0.20	1	15850417	cg56061016	CASP9,CASP9	Body,Body	chr1:15850493-15850699	N_Shore
hyper1973	N_adequate_8	2.6E-03	0.33	0.03	0.30	1	21766547	cg10019095	NBP3	TSS200	chr1:21766272-21767224	Island
hyper1974	N_adequate_8	1.5E-03	0.26	0.09	0.17	1	101071734	cg05160678	S1PR1	TSS1500	chr1:101071785-101072068	N_Shore
hyper1975	N_adequate_8	3.6E-02	0.35	0.11	0.24	1	101071965	cg05338680	S1PR1	TSS1500	chr1:101071785-101072068	Island
hyper1976	N_adequate_8	1.8E-05	0.13	0.04	0.09	1	148556046	cg18376472		Body	chr1:148556640-148556626	Island
hyper1977	N_adequate_8	0.0E+00	0.12	0.02	0.11	1	148556049	cg06616806		Body,Body,Body	chr1:148556640-148556626	Island
hyper1978	N_adequate_8	6.3E-02	0.28	0.18	0.11	1	156096301	cg03946955	LMNA,LMNA,LMNA	Body,Body,Body		
hyper1979	N_adequate_8	4.9E-04	0.07	0.01	0.06	2	30144547	cg13562710	ALK	TSS200	chr2:30142831-30144624	Island
hyper1980	N_adequate_8	7.2E-05	0.08	0.02	0.06	2	43202474	cg04011671				
hyper1981	N_adequate_8	2.7E-07	0.16	0.02	0.14	2	43202481	cg03717364				
hyper1982	N_adequate_8	2.3E-02	0.18	0.07	0.11	2	145277843	cg26522240	ZEB2,ZEB2,ZEB2,ZEB2	Body,5UTR,1stExon,1stExon,5UT	chr2:145281736-145282269	N_Shelf
hyper1983	N_adequate_8	1.2E-06	0.24	0.09	0.16	2	228736089	cg14646075	WDR69	TSS1500	chr2:228736230-228736544	N_Shore
hyper1984	N_adequate_8	4.0E-05	0.29	0.10	0.18	2	228736135	cg14329157	WDR69	TSS200	chr2:228736230-228736544	N_Shore
hyper1985	N_adequate_8	9.6E-09	0.33	0.08	0.25	2	228736145	cg22072947	WDR69	TSS200	chr2:228736230-228736544	N_Shore
hyper1986	N_adequate_8	3.8E-06	0.32	0.02	0.30	2	228736253	cg00063174	WDR69	TSS200	chr2:228736230-228736544	Island
hyper1987	N_adequate_8	6.9E-08	0.29	0.02	0.28	2	228736258	cg20647610	WDR69	TSS200	chr2:228736230-228736544	Island
hyper1988	N_adequate_8	6.0E-08	0.02	0.21	0.29	2	228736357	cg23807890	WDR69,WDR69	1stExon,5UTR	chr2:228736230-228736544	Island
hyper1989	N_adequate_8	9.1E-07	0.28	0.08	0.21	2	228736449	cg21577049	WDR69	Body	chr2:228736230-228736544	Island
hyper1990	N_adequate_8	2.9E-06	0.14	0.02	0.12	2	228736459	cg0216370	WDR69	Body	chr2:228736230-228736544	Island
hyper1991	N_adequate_8	3.1E-03	0.19	0.05	0.14	3	27756844	cg16700000			chr3:27756660-27756941	Island
hyper1992	N_adequate_8	1.8E-02	0.19	0.04	0.14	3	27756851	cg05409218			chr3:27756660-27756941	Island
hyper1993	N_adequate_8	2.9E-07	0.28	0.05	0.22	9	69786306	cg14346461			chr9:69785274-69787720	Island
hyper1994	N_adequate_8	2.9E-05	0.08	0.02	0.07	11	64059037	cg10028227	KCNK4	5UTR	chr11:64058808-64060118	Island
hyper1995	N_adequate_8	6.2E-07	0.32	0.12	0.19	12	122231455	cg09088508	RHOE	1stExon	chr12:122230903-122232359	Island
hyper1996	N_adequate_8	3.9E-09	0.13	0.03	0.10	12	122231626	cg03341523	RHOE	TSS200	chr12:122230903-122232359	Island
hyper1997	N_adequate_8	2.2E-05	0.18	0.10	0.07	12	122231757	cg25776635	RHOE	TSS200	chr12:122230903-122232359	Island
hyper1998	N_adequate_8	1.4E-07	0.16	0.06	0.09	12	122231765	cg24097153	RHOE	TSS200	chr12:122230903-122232359	Island
hyper1999	N_adequate_8	1.9E-10	0.16	0.05	0.11	12	122231866	cg02539714	RHOE	TSS1500	chr12:122230903-122232359	Island
hyper2000	N_adequate_8	0.0E+00	0.31	0.08	0.23	12	122231927	cg26269863	RHOE	TSS1500	chr12:122230903-122232359	Island
hyper2001	N_adequate_8	8.0E-02	0.33	0.10	0.23	15	72565042	cg08294267	PARP6	TSS1500	chr15:72564442-72565165	Island
hyper2002	N_adequate_8	1.5E-06	0.29	0.05	0.24	16	744681	cg03349020	FBXL16	Body	chr16:743924-745943	Island
hyper2003	N_adequate_8	1.5E-02	0.39	0.10	0.30	16	32057551	cg08781853			chr16:32057241-32058277	Island
hyper2004	N_adequate_9	4.1E-02	0.01	0.04	0.03	1	15339849	cg22238339			chr1:15339843-15339980	Island
hyper2005	N_adequate_9	2.0E-08	0.25	0.02	0.23	2	242823485	cg23370306			chr2:24282346-242823970	Island
hyper2006	N_adequate_9	9.6E-04	0.12	0.02	0.10	2	242823679	cg16595261			chr2:24282346-242823970	Island
hyper2007	N_adequate_9	6.7E-07	0.25	0.03	0.22	3	14643854	cg22981512			chr3:14643718-14644830	Island
hyper2008	N_adequate_9	9.0E-03	0.15	0.02	0.13	3	14643925	cg12146386			chr3:14643718-14644830	Island
hyper2009	N_adequate_9	2.6E-05	0.20	0.11	0.09	3	139258822	cg06543018	RBP1,RBP1,RBP1	TSS200,TSS200,TSS200	chr3:139257712-139257949	S_Shore
hyper2010	N_adequate_9	9.0E-06	0.16	0.03	0.13	3	139258939	cg23363832	RBP1,RBP1,RBP1	TSS1500,TSS1500,TSS1500	chr3:139257712-139257949	S_Shore
hyper2011	N_adequate_9	2.7E-02	0.07	0.01	0.05	4	4387917	cg20460797	D4S234E,D4S234E	TSS200,TSS200	chr4:4387593-4389919	Island
hyper2012	N_adequate_9	2.8E-02	0.07	0.01	0.07	4	113436232	cg10511618	NEUROG2	Body	chr4:113435898-113438002	Island
hyper2013	N_adequate_9	1.6E-02	0.14	0.08	0.06	5	140893101	cg00980731			chr5:140892913-140893189	Island
hyper2014	N_adequate_9	4.3E-05	0.1									

hyper2060	N_excessive_1	0.0E+00	0.41	0.04	0.37	2	198364115	cg05654645	HSPD1;HSPD1;HSP1	5UTR;5UTR;TSS1500	chr2:198363689-198365405	Island	
hyper2061	N_excessive_1	0.0E+00	0.57	0.10	0.48	2	198364282	cg08602604	HSPD1;HSPD1;HSP1	5UTR;5UTR;TSS1500	chr2:198363689-198365405	Island	
hyper2062	N_excessive_1	0.0E+00	0.46	0.01	0.45	2	198364585	cg05767788	HSPD1;HSPD1;HSPD1;HSP1	1stExon;5UTR;5UTR;TSS200	chr2:198363689-198365405	Island	
hyper2063	N_excessive_1	0.0E+00	0.40	0.02	0.38	2	198364596	cg23159081	HSPD1;HSPD1;HSPD1;HSP1	1stExon;5UTR;5UTR;TSS200	chr2:198363689-198365405	Island	
hyper2064	N_excessive_1	0.0E+00	0.35	0.05	0.30	2	198364743	cg00437134	HSPD1;HSP1;HSPD1;HSPD1	1stExon;5UTR;5UTR;TSS200	chr2:198363689-198365405	Island	
hyper2065	N_excessive_1	5.8E-10	0.36	0.09	0.28	2	198364931	cg25273507	HSPD1;HSP1;HSPD1;HSPD1;H	1stExon;5UTR;5UTR;1stExon;TSS200	chr2:198363689-198365405	Island	
hyper2066	N_excessive_1	0.0E+00	0.46	0.04	0.42	2	198365065	cg10884341	HSPD1;HSP1;HSPD1;HSPD1	1stExon;5UTR;TSS1500;TSS200	chr2:198363689-198365405	Island	
hyper2067	N_excessive_1	0.0E+00	0.46	0.01	0.45	2	198365119	cg02208776	HSPD1;HSPD1;HSPD1;HSPD1	1stExon;5UTR;TSS1500;TSS200	chr2:198363689-198365405	Island	
hyper2068	N_excessive_1	0.0E+00	0.38	0.03	0.38	2	198365139	cg27005655	HSP1;HSP1;HSPD1;HSPD1	1stExon;5UTR;TSS1500;TSS200	chr2:198363689-198365405	Island	
hyper2069	N_excessive_1	1.1E-07	0.21	0.03	0.18	2	237078726	cg16023545	GBX2	TSS200	chr2:237071794-237078762	Island	
hyper2070	N_excessive_1	3.8E-05	0.28	0.03	0.26	2	237078811	cg14216003	GBX2	TSS200	chr2:237071794-237078762	Island	
hyper2071	N_excessive_1	2.5E-04	0.36	0.04	0.32	2	237078815	cg19761848	GBX2	TSS200	chr2:237071794-237078762	Island	
hyper2072	N_excessive_1	0.0E+00	0.31	0.07	0.24	3	59035660	cg19830192	C3orf67;C3orf67	5UTR;1stExon	chr3:59035406-59035944	Island	
hyper2073	N_excessive_1	0.0E+00	0.12	0.01	0.11	3	59035796	cg03187299	C3orf67	TSS200	chr3:59035406-59035944	Island	
hyper2074	N_excessive_1	0.0E+00	0.82	0.07	0.75	5	38557386	cg18848688	LIFR;LIFR	TSS1500;5UTR	chr5:3856222-38567563	Island	
hyper2075	N_excessive_1	1.3E-02	0.31	0.10	0.20	5	95159614	cg10949007	GLRX;GLRX	TSS1500;TSS1500			
hyper2076	N_excessive_1	1.1E-05	0.14	0.05	0.09	6	29720641	cg01426208			chr6:2972061-29721101	Island	
hyper2077	N_excessive_1	3.9E-10	0.47	0.10	0.38	6	32941126	cg02448295	BRD2;BRD2	Body;Body	chr6:32939275-32940954	S_Shore	
hyper2078	N_excessive_1	0.0E+00	0.25	0.07	0.18	7	56119028	cg03532005	CCT6A;PSPH;CCT6A;PSPH	TSS1500;5UTR;TSS1500;1stExon	chr7:56119045-56119963	N_Shore	
hyper2079	N_excessive_1	2.3E-09	0.27	0.08	0.19	7	56119046	cg02753865	CCT6A;PSPH;CCT6A;PSPH	TSS1500;5UTR;TSS1500;1stExon	chr7:56119045-56119963	Island	
hyper2080	N_excessive_1	0.0E+00	0.33	0.05	0.28	7	56119079	cg01830765	CCT6A;PSPH;CCT6A;PSPH	TSS1500;5UTR;TSS1500;1stExon	chr7:56119045-56119963	Island	
hyper2081	N_excessive_1	1.6E-09	0.29	0.05	0.24	7	56119212	cg22128468	PSPH;PSPH;CCT6A;CCT6A	5UTR;1stExon;TSS200;TSS200	chr7:56119045-56119963	Island	
hyper2082	N_excessive_1	8.6E-06	0.14	0.03	0.12	7	56119218	cg10749792	PSPH;PSPH;CCT6A;CCT6A	5UTR;1stExon;TSS200;TSS200	chr7:56119045-56119963	Island	
hyper2083	N_excessive_1	7.6E-05	0.86	0.36	0.50	9	138413253	cg00040426	LCN1	TSS200			
hyper2084	N_excessive_1	1.5E-06	0.15	0.05	0.11	10	26822390	cg00955200	WAC;WAC;WAC	TSS200;Body;TSS200	chr10:26821189-26823092	Island	
hyper2085	N_excessive_1	6.9E-10	0.07	0.03	0.33	11	61878966	cg135891		1stExon	chr12:81330608-81331514	Island	
hyper2086	N_excessive_1	0.0E+00	0.35	0.07	0.28	12	81331457	cg28480223	LINTA	1stExon	chr12:81330608-81331514	Island	
hyper2087	N_excessive_1	0.0E+00	0.31	0.08	0.23	12	81331469	cg17061244	LINTA	1stExon	chr12:81330608-81331514	Island	
hyper2088	N_excessive_1	0.0E+00	0.38	0.06	0.33	12	81331486	cg23441441	LINTA	1stExon	chr12:81330608-81331514	Island	
hyper2089	N_excessive_1	8.6E-03	0.33	0.05	0.28	12	81331660	cg21152690	LINTA;LINTA	1stExon;5UTR	chr12:81330608-81331514	S_Shore	
hyper2090	N_excessive_1	6.9E-02	0.27	0.06	0.21	12	81331845	cg14874351	LINTA	TSS200	chr12:81330608-81331514	S_Shore	
hyper2091	N_excessive_1	4.3E-02	0.18	0.08	0.10	14	100438957	cg21054473			chr14:100437381-100438863	S_Shore	
hyper2092	N_excessive_1	8.0E-02	0.25	0.08	0.17	16	49518414	cg09231171					
hyper2093	N_excessive_1	5.1E-07	0.36	0.08	0.28	19	52489783	cg24162630	ZNF350	5UTR			
hyper2094	N_excessive_1	5.9E-03	0.31	0.03	0.28	19	52490058	cg02573825	ZNF350;ZNF350	1stExon;5UTR			
hyper2095	N_excessive_1	5.8E-10	0.36	0.08	0.29	19	52490069	cg27565719	ZNF350;ZNF350	1stExon;5UTR			
hyper2096	N_excessive_1	1.9E-10	0.42	0.07	0.35	19	52490101	cg27654641	ZNF350	TSS200			
hyper2097	N_excessive_1	4.3E-07	0.34	0.07	0.27	19	52490173	cg03577153	ZNF350	TSS200			
hyper2098	N_excessive_1	1.5E-08	0.42	0.07	0.35	19	52490199	cg25835225	ZNF350	TSS200			
hyper2099	N_excessive_1	1.0E-08	0.33	0.05	0.28	19	52490211	cg05011753	ZNF350	TSS200			
hyper2100	N_excessive_1	0.0E+00	0.40	0.07	0.33	19	52490223	cg18649745	ZNF350	TSS200			
hyper2101	N_excessive_1	8.2E-02	0.23	0.04	0.19	22	13385914	cg05684406	SLC7A4	TSS200	chr22:13386493-21387000	Island	
hyper2102	N_excessive_1	1.1E-06	0.22	0.07	0.16	22	33453893	cg14062468	SYN3	5UTR	chr22:33453892-33454050	Island	
hyper2103	N_excessive_1	4.2E-07	0.09	0.02	0.08	22	33454324	cg05206884	SYN3;SYN3	5UTR;1stExon	chr22:33453892-33454050	Island	
hyper2104	N_excessive_2	3.5E-03	0.07	0.02	0.05	1	21058625	cg04902671	SH2D5;SH2D5	5UTR;5UTR	chr1:21058006-21059366	Island	
hyper2105	N_excessive_2	0.0E+00	0.08	0.00	0.08	1	100503596	cg24955406	HIAT1	TSS200	chr1:100503482-100504404	Island	
hyper2106	N_excessive_2	6.6E-03	0.04	0.01	0.03	1	154377970	cg03957204	IL6R;IL6R;IL6R;IL6R	5UTR;1stExon;1stExon;5UTR	chr1:154377670-154378445	Island	
hyper2107	N_excessive_2	8.7E-03	0.23	0.03	0.20	1	166853578	cg26248173			chr1:166853253-166853710	Island	
hyper2108	N_excessive_2	1.9E-08	0.07	0.01	0.06	2	24583331	cg18920904	ITSN2;ITSN2;ITSN2;ITSN2;ITSN2	1stExon;1stExon;5UTR;5UTR;5UTR	chr2:24582620-24583611	Island	
hyper2109	N_excessive_2	6.3E-03	0.11	0.02	0.08	2	25149977	cg15423357					
hyper2110	N_excessive_2	5.0E-07	0.40	0.16	0.25	3	186826590	cg17466567	ETV5	5UTR	chr3:185825462-185827003	Island	
hyper2111	N_excessive_2	3.4E-04	0.06	0.01	0.05	4	10118516	cg10699215	WDR1;WDR1;WDR1;WDR1	1stExon;5UTR;5UTR;1stExon	chr4:10117575-10118952	Island	
hyper2112	N_excessive_2	9.7E-09	0.73	0.46	0.27	4	14361291	cg05036183					
hyper2113	N_excessive_2	7.6E-04	0.22	0.08	0.14	4	40751770	cg19786920	NSUN7	TSS200	chr4:40751842-40752493	N_Shore	
hyper2114	N_excessive_2	1.3E-04	0.18	0.01	0.17	4	40751845	cg01143804	NSUN7	TSS200	chr4:40751842-40752493	Island	
hyper2115	N_excessive_2	1.2E-04	0.30	0.05	0.25	4	40752415	cg08508988	NSUN7	5UTR	chr4:40751842-40752493	Island	
hyper2116	N_excessive_2	5.1E-09	0.05	0.01	0.04	5	16935695	cg19510792	MYO10	Body	chr5:16935555-16936408	Island	
hyper2117	N_excessive_2	8.3E-03	0.08	0.02	0.28	5	57879402	cg26589061	RAB3C	Body	chr5:57878725-57879177	S_Shore	
hyper2118	N_excessive_2	6.4E-08	0.14	0.04	0.10	5	70883065	cg16320199	MCCC2	TSS200	chr5:70882936-70883413	Island	
hyper2119	N_excessive_2	0.0E+00	0.12	0.01	0.12	5	70883072	cg18788891	MCCC2	TSS200	chr5:70882936-70883413	Island	
hyper2120	N_excessive_2	1.3E-08	0.08	0.01	0.07	5	70883087	cg24034966	MCCC2	TSS200	chr5:70882936-70883413	Island	
hyper2121	N_excessive_2	2.4E-04	0.16	0.08	0.08	5	70883173	cg18359921	MCCC2;MCCC2	5UTR;1stExon	chr5:70882936-70883413	Island	
hyper2122	N_excessive_2	9.7E-11	0.26	0.07	0.19	5	70883341	cg24558977	MCCC2	1stExon	chr5:70882936-70883413	Island	
hyper2123	N_excessive_2	7.8E-10	0.22	0.03	0.20	5	72598965	cg17595854			chr5:72598958-72599656	Island	
hyper2124	N_excessive_2	4.1E-06	0.18	0.07	0.11	5	72599143	cg02495823			chr5:72598958-72599656	Island	
hyper2125	N_excessive_2	6.4E-09	0.33	0.08	0.25	5	72599282	cg15168727			chr5:72598958-72599656	Island	
hyper2126	N_excessive_2	2.7E-02	0.16	0.05	0.11	6	10415653	cg11063729	TFAP2A;TFAP2A	Body;TSS200	chr6:10417384-10417842	N_Shore	
hyper2127	N_excessive_2	5.6E-03	0.18	0.10	0.09	6	26271587	cg02909790	HIST1H3G	1stExon	chr6:26271345-26271588	Island	
hyper2128	N_excessive_2	2.4E-02	0.17	0.07	0.10	6	26271822	cg14273822	HIST1H3G;HIST1H2BI	TSS200;TSS1500	chr6:26272470-26272696	N_Shore	
hyper2129	N_excessive_2	1.5E-03	0.21	0.08	0.13	6	26271718	cg00306311	HIST1H3G;HIST1H2BI	TSS200;TSS1500	chr6:26272470-26272696	N_Shore	
hyper2130	N_excessive_2	1.3E-03	0.17	0.08	0.09	6	26272695	cg23233200	HIST1H3G;HIST1H2BI	TSS1500;TSS1500	chr6:26272470-26272696	Island	
hyper2131	N_excessive_2	2.6E-02	0.23	0.11	0.12	6	28956312	cg16622920			chr6:28956106-28956578	Island	
hyper2132	N_excessive_2	3.2E-03	0.24	0.03	0.21	6	32145342	cg06529658	RNF6P1;RNF5;AGPAT1;AGPAT1	TSS1500;TSS1500;TSS1500;5UTR			
hyper2133	N_excessive_2	5.9E-02	0.30	0.07	0.23	6	32145470	cg03237395	RNF6P1;RNF5;AGPAT1	TSS1500;TSS1500;5UTR			
hyper2134	N_excessive_2	8.4E-02	0.22	0.05	0.18	6	32145543	cg10774928	RNF6P1;RNF5;AGPAT1	TSS1500;TSS1500;5UTR			
hyper2135	N_excessive_2	7.0E-02	0.24	0.06	0.18	6	32145904	cg08049198	AGPAT1;RNF6P1;RNF5	TSS200;TSS1500;TSS1500			
hyper2136	N_excessive_2	5.8E-02	0.31	0.06	0.25	6	32146548	cg02973270	AGPAT1;RNF5;RNF5P1	TSS1500;Body;Body			
hyper2137	N_excessive_2	1.3E-02	0.43	0.14	0.29	6	163746175	cg21229979	LOC285796	TSS1500			
hyper2138	N_excessive_2	1.7E-02	0.09	0.02	0.06	7	30029238	cg20554228	SCRN1;SCRN1;SCRN1;SCRN1	5UTR;Body;5UTR;5UTR	chr7:30028518-30029822	Island	
hyper2139	N_excessive_2	4.5E-03	0.05	0.02	0.03	7	30029390	cg18003762	SCRN1;SCRN1;SCRN1;SCRN1;5UTR;Body;5UTR;5UTR	1stExon;5UTR;5UTR;5UTR	chr7:30028518-30029822	Island	
hyper2140	N_excessive_2	3.1E-08	0.07	0.01	0.07	7	44925112	cg16770798	PURB	TSS200			
hyper2141	N_excessive_2	4.5E-02	0.13	0.06	0.06	7	131377089	cg20816493					
hyper2142	N_excessive_2	8.2E-02	0.29	0.06	0.24	8	43131353	cg01754525					

hyper2189	N_excessive_3	6.6E-05	0.18	0.06	0.12	4	8582101	cg06643298	GPR78	TSS200	chr4:8582036-8583364	Island
hyper2190	N_excessive_3	6.3E-06	0.13	0.04	0.09	4	8582110	cg21523251	GPR78	TSS200	chr4:8582036-8583364	Island
hyper2191	N_excessive_3	4.2E-08	0.26	0.08	0.19	4	8582565	cg06568182	GPR78,GPR78	1stExon,5'UTR	chr4:8582036-8583364	Island
hyper2192	N_excessive_3	2.9E-10	0.18	0.03	0.15	4	8393173	cg20451727	LN54, LN54, LN54, LN54, LN54	1stExon,5'UTR,5'UTR,5'UTR,1stExon	chr4:83931642-83932194	Island
hyper2193	N_excessive_3	2.1E-09	0.32	0.10	0.21	4	83931902	cg16854524	LN54, LN54, LN54, LN54, LN54	1stExon,5'UTR,5'UTR,5'UTR,1stExon	chr4:83931642-83932194	Island
hyper2194	N_excessive_3	2.1E-02	0.16	0.05	0.11	4	83932010	cg03421743	LN54, LN54, LN54	5'UTR,TSS200,TSS200	chr4:83931642-83932194	Island
hyper2195	N_excessive_3	1.9E-10	0.15	0.01	0.14	4	83932058	cg19517378	LN54, LN54, LN54	5'UTR,TSS200,TSS200	chr4:83931642-83932194	Island
hyper2196	N_excessive_3	3.3E-07	0.19	0.03	0.16	4	83932168	cg10724425	LN54, LN54, LN54	5'UTR,TSS200,TSS200	chr4:83931642-83932194	Island
hyper2197	N_excessive_3	3.2E-06	0.10	0.05	0.15	4	83932170	cg23895666	LN54, LN54, LN54	5'UTR,TSS200,TSS200	chr4:83931642-83932194	Island
hyper2198	N_excessive_3	1.9E-09	0.18	0.05	0.13	4	83932193	cg21787596	LN54, LN54, LN54	TSS1500,5'UTR,TSS1500	chr4:83931642-83932194	Island
hyper2199	N_excessive_3	5.8E-10	0.19	0.10	0.09	4	83932227	cg07406821	LN54, LN54, LN54	TSS1500,5'UTR,TSS1500	chr4:8393332-83934370	N_Shore
hyper2200	N_excessive_3	0.0E+00	0.33	0.06	0.28	4	119786577	cg02064368				
hyper2201	N_excessive_3	1.1E-05	0.18	0.04	0.14	5	1931376	cg11439596			chr5:1930754-1931986	Island
hyper2202	N_excessive_3	9.8E-03	0.25	0.07	0.18	5	2038899	cg00213479			chr5:2038527-2038949	Island
hyper2203	N_excessive_3	2.1E-08	0.23	0.05	0.17	5	78429774	cg22188827				
hyper2204	N_excessive_3	9.5E-03	0.06	0.01	0.05	5	179125478	cg08691740	CANX,CANX	TSS1500,TSS1500	chr5:179125341-179126340	Island
hyper2205	N_excessive_3	0.0E+00	0.72	0.04	0.68	7	130353515	cg04678743	TSGA13,COPG2,COPG2	3'UTR,5'UTR,1stExon	chr7:130353070-130353979	Island
hyper2206	N_excessive_3	2.6E-04	0.27	0.10	0.17	8	144635260	cg08688335	GSMD	TSS1500	chr8:144635308-144636026	N_Shore
hyper2207	N_excessive_3	0.0E+00	0.38	0.06	0.32	8	144691562	cg26507094	PYCLR	Body	chr8:144691400-144692269	Island
hyper2208	N_excessive_3	1.1E-03	0.16	0.08	0.08	9	27528300	cg14173147	MOBK12B	5'UTR	chr9:27528357-27528725	N_Shore
hyper2209	N_excessive_3	2.1E-02	0.29	0.05	0.23	10	51572300	cg25794402	NCOA4,NCOA4,NCOA4,NCOA4	TSS200,5'UTR,Body,Body	chr10:51572198-51572620	Island
hyper2210	N_excessive_3	1.2E-02	0.30	0.05	0.25	10	51572303	cg07588964	NCOA4,NCOA4,NCOA4,NCOA4	TSS200,5'UTR,Body,Body	chr10:51572198-51572620	Island
hyper2211	N_excessive_3	2.2E-02	0.30	0.12	0.18	10	103539953	cg20653518			chr10:103538815-103539988	Island
hyper2212	N_excessive_3	2.2E-02	0.93	0.68	0.25	10	127464165	cg11254426	MMP21	Body	chr10:127464156-127464385	Island
hyper2213	N_excessive_3	3.0E-03	0.26	0.03	0.23	11	61062837	cg27175288	WVCE	TSS200	chr11:61061751-61063063	Island
hyper2214	N_excessive_3	2.4E-03	0.48	0.27	0.48	11	61062870	cg25818574	KCNK4	TSS200	chr11:64058808-64061118	N_Shore
hyper2215	N_excessive_3	1.3E-05	0.11	0.01	0.09	12	121975423	cg17474126	KDM2B,KDM2B	Body,Body	chr12:121975028-121976140	Island
hyper2216	N_excessive_3	7.8E-04	0.10	0.01	0.09	12	124086727	cg06061698	DDX55	1stExon	chr12:124086217-124087015	Island
hyper2217	N_excessive_3	1.1E-04	0.16	0.07	0.08	15	79576298	cg22694275	ANKRD34C	5'UTR	chr15:79574830-79575211	S_Shore
hyper2218	N_excessive_3	8.7E-02	0.15	0.02	0.13	16	725543	cg07847424	RHBDL1	TSS1500	chr16:729438-735815	N_Shelf
hyper2219	N_excessive_3	3.3E-05	0.25	0.10	0.14	16	1660153	cg20322611	IFT140	5'UTR	chr16:1660054-1660595	Island
hyper2220	N_excessive_3	2.5E-04	0.21	0.05	0.16	16	15982174	cg06490162	C16orf63	Body	chr16:15982245-15982672	N_Shore
hyper2221	N_excessive_3	7.3E-05	0.15	0.01	0.14	16	15982478	cg16401214	C16orf63	TSS200	chr16:15982245-15982672	Island
hyper2222	N_excessive_3	7.2E-04	0.23	0.01	0.22	16	15982508	cg06879630	C16orf63	TSS200	chr16:15982245-15982672	Island
hyper2223	N_excessive_3	1.7E-05	0.21	0.03	0.18	16	15982637	cg09516144	C16orf63	TSS200	chr16:15982245-15982672	Island
hyper2224	N_excessive_3	1.0E-02	0.85	0.32	0.53	16	89809557	cg07630078	CBFA2T3	Body	chr16:89066334-89068600	S_Shore
hyper2225	N_excessive_3	4.2E-03	0.08	0.01	0.07	16	89788335	cg25719439	C16orf7,ZNF726,ZNF726,ZNF726	TSS1500,5'UTR,1stExon,5'UTR	chr16:89786837-89789089	Island
hyper2226	N_excessive_3	2.4E-02	0.11	0.04	0.07	17	4871094	cg02111792	SPAG7	1stExon	chr17:48710189-4871710	Island
hyper2227	N_excessive_3	1.3E-02	0.20	0.02	0.18	17	42083989	cg22241593	NAGS	Body	chr17:42082027-42084972	Island
hyper2228	N_excessive_3	6.9E-03	0.21	0.08	0.13	17	42084612	cg00483503	NAGS	Body	chr17:42082027-42084972	Island
hyper2229	N_excessive_3	1.1E-04	0.16	0.04	0.12	17	64962417	cg20410810	CACNG4	Body	chr17:64961007-64962321	S_Shore
hyper2230	N_excessive_3	1.3E-03	0.21	0.08	0.13	18	52495796	cg14135988	RAB27B	TSS200	chr18:52495604-52496607	Island
hyper2231	N_excessive_3	3.7E-02	0.16	0.08	0.08	19	1470810	cg13368085	APC2	3'UTR	chr19:1465206-1471241	Island
hyper2232	N_excessive_3	4.3E-06	0.26	0.08	0.18	19	5536532	cg12542584			chr19:5536531-5536789	Island
hyper2233	N_excessive_3	1.3E-02	0.34	0.07	0.27	19	5536626	cg23229259			chr19:5536531-5536789	Island
hyper2234	N_excessive_3	1.3E-05	0.31	0.07	0.24	19	10541267	cg14965524	PDE4A,PDE4A	Body,TSS1500	chr19:10542662-10543120	N_Shore
hyper2235	N_excessive_3	1.1E-04	0.17	0.02	0.14	19	10541304	cg02605007	PDE4A,PDE4A	Body,TSS1500	chr19:10542662-10543120	N_Shore
hyper2236	N_excessive_3	0.0E+00	0.37	0.00	0.36	19	10541478	cg18345115	PDE4A,PDE4A	TSS200,Body	chr19:10542662-10543120	N_Shore
hyper2237	N_excessive_3	8.9E-02	0.21	0.11	0.10	19	10542000	cg09997271	PDE4A,PDE4A,PDE4A	Body,Body,TSS1500	chr19:10542662-10543120	N_Shore
hyper2238	N_excessive_3	0.0E+00	0.30	0.04	0.26	19	10543210	cg19355182	PDE4A,PDE4A,PDE4A	Body,TSS200,Body	chr19:10542662-10543120	Island
hyper2239	N_excessive_3	2.4E-08	0.32	0.10	0.22	19	10543504	cg11863536	PDE4A,PDE4A,PDE4A	Body,TSS200,Body	chr19:10542662-10543120	Island
hyper2240	N_excessive_3	4.0E-06	0.36	0.12	0.24	19	10543100	cg05240570	PDE4A,PDE4A,PDE4A	Body,1stExon,Body	chr19:10542662-10543120	S_Shore
hyper2241	N_excessive_3	3.4E-03	0.12	0.02	0.10	19	19754386	cg20038169	GMIP,GMIP	1stExon,5'UTR	chr19:19754284-19754507	Island
hyper2242	N_excessive_3	3.9E-10	0.34	0.09	0.25	19	53073422	cg20125424	ZNF701	TSS1500	chr19:53073308-53074039	N_Shore
hyper2243	N_excessive_3	3.9E-10	0.11	0.01	0.10	20	60718612	cg11012980	PSMAT,SS18L1	TSS200,TSS1500	chr20:60717598-60719667	Island
hyper2244	N_excessive_3	4.0E-02	0.13	0.03	0.10	20	62205648	cg19131103	PRIC285	TSS200	chr20:62205585-62205857	Island
hyper2245	N_excessive_3	2.4E-04	0.12	0.02	0.11	21	45759228	cg11105585	C21orf2,C21orf2	1stExon,5'UTR	chr21:45758975-45759252	Island
hyper2246	N_excessive_4	0.0E+00	0.13	0.01	0.03	1	64534542	cg23461619	ACOT7	1stExon	chr1:6452814-6454185	Island
hyper2247	N_excessive_4	1.0E-00	0.42	0.07	0.35	1	28975167	cg00956350	RNU11	Body		
hyper2248	N_excessive_4	1.4E-09	0.37	0.08	0.29	1	152080471	cg14661959	TCHH	Body	chr1:152079997-152081705	Island
hyper2249	N_excessive_4	1.2E-04	0.38	0.05	0.33	1	152080543	cg04938315	TCHH	Body	chr1:152079997-152081705	Island
hyper2250	N_excessive_4	9.7E-10	0.44	0.04	0.40	1	152081002	cg05523911	TCHH	Body	chr1:152079997-152081705	Island
hyper2251	N_excessive_4	7.4E-09	0.07	0.01	0.06	1	160175286	cg23659592	PEA15,PEA15	5'UTR,1stExon	chr1:160175132-160175702	Island
hyper2252	N_excessive_4	1.3E-06	0.11	0.02	0.09	1	160175429	cg27510197	PEA15	5'UTR	chr1:160175132-160175702	Island
hyper2253	N_excessive_4	5.2E-03	0.15	0.08	0.07	1	160175593	cg18177682	PEA15	5'UTR	chr1:160175132-160175702	Island
hyper2254	N_excessive_4	3.8E-08	0.25	0.08	0.16	2	27319374	cg23562406	KHK,KHK	Body,Body		
hyper2255	N_excessive_4	1.8E-04	0.17	0.02	0.15	2	101767891	cg00420922	TBC1D8	TSS200	chr2:101767042-101768259	Island
hyper2256	N_excessive_4	2.0E-02	0.04	0.01	0.03	2	241938321	cg21384492	SNED1	1stExon	chr2:241937716-241938468	Island
hyper2257	N_excessive_4	5.7E-05	0.20	0.04	0.16	3	146262421	cg10679755	PLSCR1,PLSCR1	1stExon,5'UTR	chr3:146262126-146262505	Island
hyper2258	N_excessive_4	9.4E-06	0.22	0.07	0.15	4	108910565	cg08356168	HADH	TSS1500	chr4:108910770-108911370	N_Shore
hyper2259	N_excessive_4	1.9E-10	0.14	0.01	0.13	4	108910787	cg21721155	HADH	TSS200	chr4:108910770-108911370	Island
hyper2260	N_excessive_4	0.0E+00	0.23	0.01	0.21	4	108910774	cg19932974	HADH,HADH	5'UTR,1stExon	chr4:108910770-108911370	Island
hyper2261	N_excessive_4	9.7E-11	0.32	0.09	0.23	4	108910777	cg0612467	HADH,HADH	5'UTR,1stExon	chr4:108910770-108911370	Island
hyper2262	N_excessive_4	1.0E-00	0.34	0.10	0.24	4	108911341	cg17156290	HADH	Body	chr4:108910770-108911370	Island
hyper2263	N_excessive_4	0.0E+00	0.28	0.10	0.19	4	108911521	cg18523371	HADH	Body	chr4:108910770-108911370	S_Shore
hyper2264	N_excessive_4	1.9E-03	0.41	0.02	0.39	4	140216770	cg11373049	NDUFC1	Body	chr4:140216727-140217078	Island
hyper2265	N_excessive_4	1.5E-03	0.54	0.04	0.50	4	140216885	cg07830416	NDUFC1	1stExon	chr4:140216727-140217078	Island
hyper2266	N_excessive_4	5.5E-06	0.44	0.04	0.40	4	140216998	cg07723855	NDUFC1	TSS200	chr4:140216727-140217078	Island
hyper2267	N_excessive_4	0.0E+00	0.35	0.01	0.34	4	140217063	cg22127491	NDUFC1	TSS200	chr4:140216727-140217078	Island
hyper2268	N_excessive_4	1.9E-08	0.42	0.04	0.38	4	140217077	cg25491088	NDUFC1	TSS200	chr4:140216727-140217078	Island
hyper2269	N_excessive_4	2.5E-02	0.32	0.08	0.24	6	10694962	cg23811837	C6orf52,PAK1IP1,C6orf52,C6orf52	Body,TSS1500,TSS200,TSS200	chr6:10694617-10695352	Island
hyper2270	N_excessive_4	6.7E-02	0.28	0.07	0.22	6	10695044	cg22249279	C6orf52,C6orf52,PAK1IP1,C6orf52	TSS1500,TSS1500,TSS200,TSS200	chr6:10694617-10695352	Island
hyper2271	N_excessive_4	9.7E-03										

hyper2318	N_excessive_5	1.2E-07	0.61	0.10	0.51	1	206786174	cg16966520	LGTN	TSS1500	chr1:206785804-206786030	S_Shore
hyper2319	N_excessive_5	1.5E-06	0.66	0.15	0.52	1	206786178	cg16639185	LGTN	TSS1500	chr1:206785804-206786030	S_Shore
hyper2320	N_excessive_5	8.8E-07	0.70	0.14	0.56	1	206786180	cg21936179	LGTN	TSS1500	chr1:206785804-206786030	S_Shore
hyper2321	N_excessive_5	2.2E-05	0.36	0.03	0.32	1	213124896	cg04907523	VASH2;VASH2;VASH2	Body;5'UTR;5'UTR	chr1:213123647-213125092	Island
hyper2322	N_excessive_5	3.7E-05	0.19	0.06	0.12	1	218338772	cg11537367			chr1:218337780-218339033	Island
hyper2323	N_excessive_5	3.0E-08	0.05	0.00	0.05	2	9614578	cg05986044	IAH1	TSS200	chr2:9614194-9615235	Island
hyper2324	N_excessive_5	1.1E-03	0.22	0.08	0.14	2	17721764	cg18735601	VSNL1	TSS200	chr2:17721537-1772201	Island
hyper2325	N_excessive_5	1.6E-02	0.21	0.06	0.15	2	17721988	cg01307387	VSNL1;VSNL1	1stExon;5'UTR	chr2:17721537-1772201	Island
hyper2326	N_excessive_5	5.6E-04	0.29	0.02	0.27	2	201011779	cg26693520	TTCC2	TSS200	chr2:201011004-20102067	Island
hyper2327	N_excessive_5	3.2E-03	0.27	0.03	0.16	2	210210266	cg17420218	TTCC2	TSS1500	chr2:201011004-20102067	Island
hyper2328	N_excessive_5	2.2E-07	0.21	0.07	0.14	2	44395004	cg04920474	PPM1B;PPM1B;PPM1B;PPM1B;F	TSS1500;TSS1500;TSS1500;TSS	chr2:44394983-44396629	Island
hyper2329	N_excessive_5	5.7E-06	0.36	0.11	0.25	2	71115994	cg08793877			chr2:71115927-71116412	Island
hyper2330	N_excessive_5	3.6E-03	0.07	0.02	0.05	2	121070622	cg24072013				
hyper2331	N_excessive_5	2.1E-02	0.16	0.06	0.10	2	131099469	cg20670292	IMP4;CCDC115	TSS1500;Body	chr2:131099469-131100863	Island
hyper2332	N_excessive_5	3.8E-06	0.38	0.04	0.34	2	142887886	cg20443778	LRP1B	Body	chr2:142887724-142888553	Island
hyper2333	N_excessive_5	1.1E-02	0.39	0.11	0.28	2	142888052	cg10634922	LRP1B	Body	chr2:142887724-142888553	Island
hyper2334	N_excessive_5	1.5E-06	0.24	0.07	0.17	2	142888598	cg02322989	LRP1B;LRP1B	5'UTR;1stExon	chr2:142887724-142888553	S_Shore
hyper2335	N_excessive_5	3.2E-05	0.07	0.02	0.05	2	154333184	cg17942639	RPRM;RPRM	1stExon;5'UTR	chr2:154334449-154335458	Island
hyper2336	N_excessive_5	1.9E-04	0.24	0.05	0.19	2	162094118	cg21211367			chr2:162094460-162096195	N_Shore
hyper2337	N_excessive_5	4.6E-06	0.14	0.03	0.11	2	162094696	cg00322319			chr2:162094460-162096195	Island
hyper2338	N_excessive_5	4.4E-06	0.20	0.06	0.15	2	162094836	cg09064687			chr2:162094460-162096195	Island
hyper2339	N_excessive_5	1.3E-09	0.26	0.02	0.24	2	162094867	cg26915774			chr2:162094460-162096195	Island
hyper2340	N_excessive_5	2.0E-03	0.24	0.06	0.18	2	171674437	cg01763173	GAD1;GAD1	5'UTR;5'UTR	chr2:171672310-171675447	Island
hyper2341	N_excessive_5	3.9E-07	0.20	0.06	0.13	2	172951501	cg16347858	DLX1;DLX1	Body;Body	chr2:172951289-172952159	Island
hyper2342	N_excessive_5	5.6E-06	0.19	0.03	0.16	2	176046185	cg18684400	ATP5G3;ATP5G3;ATP5G3	5'UTR;1stExon;5'UTR	chr2:176045989-176046594	Island
hyper2343	N_excessive_5	6.5E-03	0.06	0.13	0.07	2	176045495	cg131308	ATP5G3;ATP5G3	TSS200;TSS200	chr2:176045989-176046594	Island
hyper2344	N_excessive_5	6.5E-02	0.14	0.06	0.08	2	176867400	cg23322292	KIAA1715	TSS1500	chr2:176866993-176867188	S_Shore
hyper2345	N_excessive_5	9.0E-03	0.09269903	0.02	0.07	2	192110021	cg04692993	MYO1B;MYO1B;MYO1B	TSS200;TSS1500;TSS200	chr2:192109828-192110940	Island
hyper2346	N_excessive_5	4.2E-02	0.2548827	0.07	0.18	2	230933543	cg16273133	SLC16A14;SLC16A14	1stExon;5'UTR	chr2:230933468-230933550	Island
hyper2347	N_excessive_5	4.2E-06	0.1448195	0.04	0.10	3	8543014	cg20595215	LMCD1	TSS1500	chr3:8543201-8543579	N_Shore
hyper2348	N_excessive_5	2.5E-02	0.3731982	0.08	0.30	3	44754398	cg04974323	ZNF502;ZNF502;ZNF502	5'UTR;5'UTR;5'UTR	chr3:44754099-44754399	Island
hyper2349	N_excessive_5	2.6E-02	0.0830604	0.02	0.06	3	50242735	cg16468914	SLC38A3;SLC38A3	1stExon;5'UTR	chr3:50242550-50243589	Island
hyper2350	N_excessive_5	3.9E-02	0.3980304	0.17	0.23	3	109128982	cg20382831	FLJ25363;FLJ25363	1stExon;5'UTR		
hyper2351	N_excessive_5	2.3E-04	0.1539849	0.02	0.13	3	142837995	cg19442495	CHST2	TSS1500	chr3:142837885-142840388	Island
hyper2352	N_excessive_5	4.5E-08	0.6302117	0.22	0.41	3	170408349	cg01092546				
hyper2353	N_excessive_5	6.7E-03	0.2839854	0.02	0.26	3	192959176	cg07068191	HRASL3;HRASL3;MCC289	1stExon;5'UTR;TSS1500	chr3:192958709-192959373	Island
hyper2354	N_excessive_5	6.5E-03	0.322541	0.03	0.29	3	196366437	cg08026502	LRR3C3	TSS1500	chr3:196366394-196366919	Island
hyper2355	N_excessive_5	4.1E-02	0.37211	0.14	0.24	4	30720741	cg15322330	PCDH7;PCDH7;PCDH7	TSS1500;TSS1500;TSS1500	chr4:30721204-3072482	N_Shore
hyper2356	N_excessive_5	5.9E-06	0.0953128	0.01	0.08	4	44728642	cg09662896	GNPDA2	TSS200	chr4:44728033-44728719	Island
hyper2357	N_excessive_5	1.5E-05	0.1430921	0.02	0.13	4	44728647	cg25512518	GNPDA2	TSS200	chr4:44728033-44728719	Island
hyper2358	N_excessive_5	2.5E-03	0.1023535	0.04	0.07	4	90031989	cg17656165			chr4:90031934-90033005	Island
hyper2359	N_excessive_5	1.0E-02	0.3038339	0.02	0.29	4	113437909	cg10871779			chr4:113435898-113438002	Island
hyper2360	N_excessive_5	2.1E-06	0.1784283	0.06	0.12	4	129474594	cg17714665	NEUROG2	TSS1500		
hyper2361	N_excessive_5	2.3E-02	0.2049494	0.04	0.16	4	156874415	cg10592446	CTSO	Body	chr4:156874740-156875083	N_Shore
hyper2362	N_excessive_5	7.9E-03	0.3603713	0.06	0.30	4	156874602	cg11754095	CTSO	Body	chr4:156874740-156875083	N_Shore
hyper2363	N_excessive_5	6.3E-04	0.2381632	0.09	0.15	4	180979522	cg21229339			chr4:180979038-180980619	Island
hyper2364	N_excessive_5	1.6E-05	0.1827952	0.05	0.13	4	187646301	cg18894055	FAT1	TSS1500	chr4:187644319-187648253	Island
hyper2365	N_excessive_5	6.7E-07	0.2982114	0.09	0.21	4	187647344	cg22501604			chr4:187644319-187648253	Island
hyper2366	N_excessive_5	4.5E-06	0.1669849	0.03	0.14	4	187647402	cg20274950			chr4:187644319-187648253	Island
hyper2367	N_excessive_5	4.9E-02	0.2716151	0.12	0.15	5	2722023	cg21748578	PDCD6	Body	chr5:272139-272485	Island
hyper2368	N_excessive_5	2.4E-02	0.1278426	0.05	0.07	5	1633830	cg18250340	LOC728613	Body	chr5:1633901-1634224	N_Shore
hyper2369	N_excessive_5	1.0E-03	0.394485	0.11	0.29	5	1875058	cg06654549			chr5:1874907-1879032	Island
hyper2370	N_excessive_5	4.0E-03	0.2432682	0.02	0.22	5	50679151	cg11039614	ISL1;ISL1	5'UTR;1stExon	chr5:50678632-50679375	Island
hyper2371	N_excessive_5	3.0E-05	0.1745401	0.05	0.12	5	54516372	cg15334364			chr5:54516267-54516919	Island
hyper2372	N_excessive_5	4.0E-02	0.1477816	0.04	0.11	5	54516879	cg14608384			chr5:54516267-54516919	Island
hyper2373	N_excessive_5	9.6E-03	0.3335182	0.13	0.20	5	60921535	cg04569837			chr5:60921534-60922472	Island
hyper2374	N_excessive_5	4.6E-02	0.2951182	0.10	0.20	5	63461930	cg10372047	RNF190;RNF180	5'UTR;5'UTR	chr5:63461448-63462106	Island
hyper2375	N_excessive_5	2.4E-02	0.2431545	0.08	0.16	5	113697632	cg23615676	CKN2	TSS1500	chr5:113695516-113699195	Island
hyper2376	N_excessive_5	2.2E-03	0.3856588	0.04	0.34	5	114515916	cg10569615	TRIM36;TRIM36;TRIM36;TRIM36;TRIM36	1stExon;1stExon;1stExon;5'UTR;5'UTR	chr5:114514716-114516220	Island
hyper2377	N_excessive_5	2.1E-04	0.1663377	0.03	0.13	5	114516141	cg09463882	TRIM36;TRIM36;TRIM36;TRIM36;TRIM36	1stExon;1stExon;1stExon;5'UTR;5'UTR	chr5:114514716-114516220	Island
hyper2378	N_excessive_5	1.4E-04	0.2375454	0.04	0.20	5	114516315	cg04450862	TRIM36;TRIM36;TRIM36	TSS200;TSS200;TSS200	chr5:114514716-114516220	S_Shore
hyper2379	N_excessive_5	4.4E-04	0.3764512	0.06	0.32	5	128796168	cg15034135	ADAMTS19	1stExon	chr5:128795503-128797417	Island
hyper2380	N_excessive_5	2.7E-02	0.3254394	0.09	0.23	5	128796266	cg25309017	ADAMTS19	Body	chr5:128795503-128797417	Island
hyper2381	N_excessive_5	1.9E-03	0.2215271	0.09	0.14	5	146833171	cg20564764	DYSL3;DYSLS3	5'UTR;1stExon	chr5:146832560-146833938	Island
hyper2382	N_excessive_5	7.5E-03	0.4342609	0.10	0.33	5	178368123	cg203234732	ZNF454	TSS200	chr5:178367620-178368725	Island
hyper2383	N_excessive_5	4.5E-08	0.4941208	0.02	0.47	6	27064769	cg11183365			chr6:27064628-27065004	Island
hyper2384	N_excessive_5	2.9E-10	0.4338505	0.03	0.41	6	27064698	cg22058855			chr6:27064628-27065004	Island
hyper2385	N_excessive_5	1.0E-07	0.3363522	0.05	0.29	6	27065003	cg12298212			chr6:27064628-27065004	Island
hyper2386	N_excessive_5	1.9E-07	0.2929942	0.08	0.21	6	39760416	cg14135551	DAAM2	TSS1500	chr6:39760066-39760426	Island
hyper2387	N_excessive_5	7.8E-02	0.3056509	0.05	0.26	6	42949692	cg04457536	PEX6;PEX6	1stExon;5'UTR	chr6:42946310-42947127	Island
hyper2388	N_excessive_5	6.3E-03	0.1780632	0.05	0.13	6	42947056	cg26304593	PEX6	TSS200	chr6:42946310-42947127	Island
hyper2389	N_excessive_5	1.2E-03	0.4510594	0.26	0.19	6	87832220	cg08192165			chr6:87832219-87832610	Island
hyper2390	N_excessive_5	2.6E-08	0.4899381	0.10	0.39	6	87832609	cg18625538			chr6:87832219-87832610	Island
hyper2391	N_excessive_5	5.9E-02	0.4132885	0.10	0.31	6	87832686	cg13164087			chr6:87832219-87832610	S_Shore
hyper2392	N_excessive_5	9.0E-03	0.3094874	0.10	0.21	6	88875622	cg28565436			chr6:88875397-88877449	Island
hyper2393	N_excessive_5	1.7E-08	0.2795798	0.04	0.24	6	88875836	cg07251193	CNR1;CNR1;CNR1;CNR1;CNR1	TSS200;TSS200;TSS200;TSS200;TSS200	chr6:88875397-88877449	Island
hyper2394	N_excessive_5	1.1E-07	0.3570535	0.03	0.33	6	88875840	cg20622089	CNR1;CNR1;CNR1;CNR1	TSS200;TSS200;TSS200;TSS200	chr6:88875397-88877449	Island
hyper2395	N_excessive_5	4.4E-04	0.1834499	0.08	0.10	6	100061504	cg08933939	PROM13	Body	chr6:100060979-100062657	Island
hyper2396	N_excessive_5	1.5E-07	0.1526267	0.02	0.13	7	5633086	cg22447539	FSCN1	1stExon	chr7:5632335-5634555	Island
hyper2397	N_excessive_5	8.2E-03	0.432141	0.13	0.30	7	27213966	cg01397139	HOXA10;HOXA10	TSS200;Body	chr7:27212416-27214396	Island
hyper2398	N_excessive_5	2.6E-03	0.07853214	0.03	0.05	7	29724905	cg12042055	LOC46762	TSS200	chr7:29724188-29725436	Island
hyper2399	N_excessive_5	8.3E-02	0.1697295									

hyper2447	N_excessive_5	4.1E-02	0.5226871	0.03	0.49	11	13690702	cg04012924	FAR1	5UTR	chr11:13689588-13690724	Island
hyper2448	N_excessive_5	1.6E-05	0.3570966	0.10	0.25	11	24518737	cg06931933	LUZP2;LUZP2	5UTR;1stExon	chr11:24518224-24518738	Island
hyper2449	N_excessive_5	3.2E-03	0.2827678	0.02	0.27	11	31831974	cg18270629	PAX6;PAX6;PAX6	5UTR;5UTR;5UTR	chr11:31831620-31839038	Island
hyper2450	N_excessive_5	1.3E-04	0.2192658	0.03	0.19	11	31832246	cg28848086	PAX6;PAX6;PAX6	5UTR;5UTR;5UTR	chr11:31831620-31839038	Island
hyper2451	N_excessive_5	3.3E-03	0.09628962	0.03	0.07	11	32112632	cg03576787	RCN1;RCN1	5UTR;1stExon	chr11:32112394-32113277	Island
hyper2452	N_excessive_5	4.5E-02	0.1013444	0.03	0.07	11	32112634	cg04677061	RCN1;RCN1	5UTR;1stExon	chr11:32112394-32113277	Island
hyper2453	N_excessive_5	2.9E-03	0.4632607	0.06	0.40	11	44331108	cg24335138	ALX4	Body	chr11:44330542-44331761	Island
hyper2454	N_excessive_5	1.2E-07	0.07647201	0.01	0.07	11	62105152	cg13799206	ASRGL1;ASRGL1	5UTR;5UTR	chr11:62104779-62105636	Island
hyper2455	N_excessive_5	0.0E+00	0.534848	0.03	0.50	11	63438716	cg14589563	ATL3	Body	chr11:63438301-63439314	Island
hyper2456	N_excessive_5	3.0E-03	0.2878025	0.07	0.22	11	63438816	cg27568631	ATL3;ATL3	5UTR;1stExon	chr11:63438301-63439314	Island
hyper2457	N_excessive_5	2.6E-04	0.05754682	0.01	0.05	11	63439157	cg02761940	ATL3	TSS200	chr11:63438301-63439314	Island
hyper2458	N_excessive_5	3.3E-03	0.102944	0.04	0.07	11	63439207	cg27042081	ATL3	TSS200	chr11:63438301-63439314	Island
hyper2459	N_excessive_5	3.6E-02	0.3285916	0.01	0.32	11	66336125	cg17381565	CTSF	TSS200	chr11:66335575-66336151	Island
hyper2460	N_excessive_5	4.7E-09	0.4028866	0.07	0.33	11	94884121	cg22049858			chr11:94883647-94884811	Island
hyper2461	N_excessive_5	6.4E-02	0.3171716	0.11	0.21	11	124736661	cg05086956	ROBO3	Body	chr11:124735069-124736465	S_Shore
hyper2462	N_excessive_5	3.5E-03	0.1544504	0.09	0.07	11	12536803	cg06309855	FEZ1;FEZ1	5UTR;5UTR	chr11:125365137-125366319	Island
hyper2463	N_excessive_5	1.4E-02	0.1349568	0.05	0.08	12	58027199	cg14905909	B4GALNT1	TSS1500	chr12:58025661-58027056	S_Shore
hyper2464	N_excessive_5	5.3E-02	0.1880773	0.08	0.11	12	94542156	cg13488680	PLXNC1	TSS1500	chr12:94541727-94544000	Island
hyper2465	N_excessive_5	9.1E-02	0.07511911	0.02	0.06	12	121904973	cg15340887	KDM2B;KDM2B	Body;Body	chr12:121905463-121905956	N_Shore
hyper2466	N_excessive_5	1.6E-06	0.322732	0.07	0.26	12	124246391	cg06745944	DNAH10	TSS1500	chr12:124246524-124247254	N_Shore
hyper2467	N_excessive_5	1.5E-02	0.4567332	0.17	0.29	12	124246434	cg27125645	DNAH10	TSS1500	chr12:124246524-124247254	N_Shore
hyper2468	N_excessive_5	3.6E-06	0.3757852	0.04	0.34	12	124246446	cg10575376	DNAH10	TSS1500	chr12:124246524-124247254	N_Shore
hyper2469	N_excessive_5	1.8E-04	0.3378074	0.07	0.27	12	124246525	cg26986180	DNAH10	TSS1500	chr12:124246524-124247254	Island
hyper2470	N_excessive_5	4.8E-02	0.5462338	0.12	0.42	12	124247047	cg12044044	DNAH10;DNAH10	1stExon;5UTR	chr12:124246524-124247254	Island
hyper2471	N_excessive_5	4.6E-03	0.4382882	0.07	0.37	12	124247223	cg11026555	DNAH10	Body	chr12:124246524-124247254	Island
hyper2472	N_excessive_5	2.9E-03	0.03126758	0.00	0.03	13	20532920	cg21004366	ZMYM2;ZMYM2;ZMYM2;ZMYM2	1stExon;5UTR;5UTR;1stExon	chr13:20531548-20533630	Island
hyper2473	N_excessive_5	3.2E-02	0.6270647	0.41	0.21	13	33002597	cg19807326	N4BP2L1;N4BP2L1	TSS1500;TSS1500	chr13:33001249-33002078	S_Shore
hyper2474	N_excessive_5	7.0E-02	0.1672384	0.04	0.13	13	96743895	cg27513979	HSST3	Body	chr13:96742138-96744162	Island
hyper2475	N_excessive_5	7.9E-04	0.3528457	0.08	0.27	14	27066771	cg15602241	NOVA1;NOVA1;NOVA1;NOVA1	5UTR;5UTR;5UTR;1stExon;1stExon	chr14:27066313-27066578	S_Shore
hyper2476	N_excessive_5	2.8E-03	0.3130897	0.08	0.23	14	60097124	cg19490868	RTN1;RTN1;RTN1	Body;Body;Body	chr14:60097208-60097553	N_Shore
hyper2477	N_excessive_5	3.5E-03	0.3025842	0.08	0.23	14	60097209	cg05565239	RTN1;RTN1;RTN1	Body;Body;1stExon	chr14:60097208-60097553	Island
hyper2478	N_excessive_5	3.1E-06	0.1833213	0.09	0.10	14	71288541	cg12919976			chr14:71288403-71288957	Island
hyper2479	N_excessive_5	0.0E+00	0.3638572	0.02	0.35	14	77422934	cg00998665			chr14:77422842-77423094	Island
hyper2480	N_excessive_5	1.2E-05	0.3124688	0.10	0.22	14	77423080	cg18366782			chr14:77422842-77423094	Island
hyper2481	N_excessive_5	0.0E+00	0.2817187	0.07	0.21	14	77423093	cg25555279			chr14:77422842-77423094	Island
hyper2482	N_excessive_5	2.9E-07	0.2139657	0.08	0.14	14	77423234	cg14260355			chr14:77422842-77423094	S_Shore
hyper2483	N_excessive_5	2.4E-03	0.08729123	0.03	0.06	15	42565700	cg27313857	GANC;TMEM87A;TMEM87A	TSS1500;TSS200;TSS200	chr15:42565452-42565791	Island
hyper2484	N_excessive_5	7.7E-06	0.1738459	0.03	0.14	15	61520001	cg04132917	RORA	Body	chr15:61519621-61520031	Island
hyper2485	N_excessive_5	6.0E-08	0.4490493	0.10	0.35	15	61520931	cg18136062	RORA	Body	chr15:61520423-61521716	Island
hyper2486	N_excessive_5	5.4E-03	0.3362514	0.09	0.25	15	61521000	cg09112687	RORA	Body	chr15:61520423-61521716	Island
hyper2487	N_excessive_5	2.9E-08	0.3144593	0.08	0.23	16	3415077	cg19989114			chr16:3414964-3415167	Island
hyper2488	N_excessive_5	8.3E-04	0.2037538	0.07	0.14	16	3415256	cg12898051			chr16:3414964-3415167	S_Shore
hyper2489	N_excessive_5	6.9E-04	0.1955134	0.09	0.11	16	30194484	cg06030619	CORO1A	TSS1500	chr16:3019477-30195357	N_Shore
hyper2490	N_excessive_5	2.4E-04	0.2374803	0.04	0.20	16	79634723	cg02962380		TSS200;TSS200	chr16:79632619-79633537	Island
hyper2491	N_excessive_5	1.7E-03	0.2770669	0.04	0.24	16	84002237	cg20070685	NECA82	1stExon	chr16:84002269-84002860	Island
hyper2492	N_excessive_5	7.2E-04	0.3457963	0.11	0.24	16	84002599	cg02899772	NECA82	Body	chr16:84002269-84002860	Island
hyper2493	N_excessive_5	3.0E-04	0.1223969	0.02	0.10	17	8925203	cg07616990	NTN1	5UTR	chr17:8924167-8926920	Island
hyper2494	N_excessive_5	4.9E-03	0.1575761	0.03	0.13	17	15244482	cg22264930	TEKT3	5UTR	chr17:15244705-15245126	N_Shore
hyper2495	N_excessive_5	1.6E-09	0.3591559	0.05	0.31	17	36102740	cg03433642	HNF1B;HNF1B	Body;Body	chr17:36102033-36104766	Island
hyper2496	N_excessive_5	6.4E-03	0.2660848	0.05	0.22	17	66286791	cg07407787	ARSG;SLC16A6	5UTR;5UTR	chr17:66286541-66288532	Island
hyper2497	N_excessive_5	2.6E-03	0.07689697	0.02	0.05	17	78010476	cg07441156	CCDC40;TBC1D16	1stExon;TSS1500	chr17:78009076-78011084	Island
hyper2498	N_excessive_5	4.4E-05	0.05211311	0.01	0.05	18	8706720	cg19669959			chr18:8704721-8707557	Island
hyper2499	N_excessive_5	6.6E-05	0.1645087	0.08	0.08	18	20139442	cg07114353			chr18:20139484-20140246	N_Shore
hyper2500	N_excessive_5	1.2E-04	0.1597035	0.07	0.09	18	20139642	cg12429953			chr18:20139484-20140246	Island
hyper2501	N_excessive_5	5.2E-05	0.1740218	0.06	0.11	18	20139875	cg01676182			chr18:20139484-20140246	Island
hyper2502	N_excessive_5	2.5E-08	0.2212508	0.08	0.14	18	20139913	cg05760402		TSS1500	chr18:20139484-20140246	Island
hyper2503	N_excessive_5	9.9E-08	0.6008995	0.03	0.57	18	47087108	cg20486897	LIPG		chr18:47087075-47087446	Island
hyper2504	N_excessive_5	3.7E-05	0.6212655	0.07	0.55	18	47087215	cg07277041	LIPG	TSS1500	chr18:47087075-47087446	Island
hyper2505	N_excessive_5	6.1E-02	0.05973423	0.01	0.05	19	925903	cg07752304	ARID3A	TSS200	chr19:925120-926816	Island
hyper2506	N_excessive_5	3.8E-02	0.2198596	0.11	0.11	19	9434523	cg23179379	ZNF559	TSS1500	chr19:9434784-9435144	N_Shore
hyper2507	N_excessive_5	4.8E-03	0.4124852	0.06	0.35	19	12203029	cg20773651	ZNF788	TSS200	chr19:12203028-12203503	Island
hyper2508	N_excessive_5	6.6E-03	0.5352734	0.08	0.46	19	12203066	cg09489445	ZNF788	TSS200	chr19:12203028-12203503	Island
hyper2509	N_excessive_5	4.8E-04	0.4198285	0.05	0.37	19	12203198	cg06384763	ZNF788	Body	chr19:12203028-12203503	Island
hyper2510	N_excessive_5	1.0E-07	0.4003082	0.04	0.36	19	12203315	cg01172903	ZNF788	Body	chr19:12203028-12203503	Island
hyper2511	N_excessive_5	4.2E-06	0.4638691	0.04	0.42	19	12203349	cg11767984	ZNF788	Body	chr19:12203028-12203503	Island
hyper2512	N_excessive_5	2.3E-07	0.2869674	0.07	0.22	19	12203644	cg01404753	ZNF788	Body	chr19:12203028-12203503	S_Shore
hyper2513	N_excessive_5	1.9E-06	0.4323865	0.06	0.37	19	37997730	cg07482795	ZNF793	TSS200	chr19:37997790-37998125	N_Shore
hyper2514	N_excessive_5	1.9E-08	0.2388238	0.09	0.15	20	18118240	cg18396157	PET117	TSS1500	chr20:18117962-18118989	Island
hyper2515	N_excessive_5	2.8E-09	0.06624232	0.00	0.06	20	30795610	cg25987077	POFUT1;PLAGL2;POFUT1	TSS200;TSS200;TSS200	chr20:30795282-30795841	Island
hyper2516	N_excessive_5	2.6E-03	0.1446201	0.04	0.11	20	37434950	cg25932164	PPP1R16B	5UTR	chr20:37434206-37435592	Island
hyper2517	N_excessive_5	2.7E-04	0.08435883	0.02	0.06	21	22370758	cg25818292	NCAM2;NCAM2	5UTR;1stExon	chr21:22369423-22370582	S_Shore
hyper2518	N_excessive_5	2.1E-04	0.1008918	0.03	0.08	21	38935991	cg23484755			chr21:38935854-38936546	Island
hyper2519	N_excessive_5	8.7E-04	0.114774	0.03	0.08	22	31090747	cg08170140	OSBP2	TSS200	chr22:31090200-31091334	Island
hyper2520	N_excessive_5	6.4E-09	0.1356723	0.01	0.12	22	39268508	cg04215348	CBX6	TSS1500	chr22:39267539-39269160	Island
hyper2521	N_excessive_5	2.5E-06	0.06268803	0.01	0.05	22	45404843	cg01033463	PHF21B;PHF21B	Body;Body	chr22:45403036-45406372	Island

Supplementary Table 2: list of 977 hypomethylated outliers

#	Sample_ID	Outlier-test P-value (adjusted)	Outlier's beta-value	Mean of the beta-values of others	delta-beta	CHR	MAPINFO_hg19	TargetID	UCSC_REFGENE_NAME	UCSC_REFGENE_GROUP	UCSC_CPG_ISLANDS_NAME	RELATION_TO_ UCSC_CPG_ISLAND
hypo1	FGR_insufficient_1	6.1E-16	0.41	0.90	-0.49	1	1415868	cq00695214	ATAD3B	Body	chr1:1417285-1417753	N_Shore
hypo2	FGR_insufficient_1	6.5E-03	0.25	0.62	-0.37	1	91190620	cq15452970			chr1:91190489-91192804	Island
hypo3	FGR_insufficient_1	7.1E-03	0.57	0.86	-0.29	1	223565773	cq26572518	C1orf65	TSS1500	chr1:223566642-223567268	N_Shore
hypo4	FGR_insufficient_1	1.1E-03	0.20	0.70	-0.50	2	30478251	cq26176018	LBH	Body		
hypo5	FGR_insufficient_1	3.5E-05	0.33	0.54	-0.21	2	62732892	cq10848792	TMEM17	Body	chr2:62732758-62733497	Island
hypo6	FGR_insufficient_1	4.7E-03	0.13	0.46	-0.32	2	62733114	cq107290273	TMEM17	Body	chr2:62732758-62733497	Island
hypo7	FGR_insufficient_1	4.0E-04	0.22	0.54	-0.31	2	62733485	cq17444943	TMEM17;TMEM17	5'UTR;1stExon	chr2:62732758-62733497	Island
hypo8	FGR_insufficient_1	1.9E-02	0.17	0.54	-0.37	2	62733576	cq12385425	TMEM17;TMEM17	5'UTR;1stExon	chr2:62732758-62733497	S_Shore
hypo9	FGR_insufficient_1	6.8E-04	0.64	0.87	-0.23	2	67387038	cq07850407				
hypo10	FGR_insufficient_1	2.0E-02	0.63	0.92	-0.28	2	128956533	cq04724176				
hypo11	FGR_insufficient_1	8.8E-02	0.13	0.56	-0.44	2	134024093	cq12915892	NCKAP5;NCKAP5	Body;Body	chr2:134023947-134024467	Island
hypo12	FGR_insufficient_1	2.5E-03	0.28	0.64	-0.36	2	134024266	cq22325000	NCKAP5;NCKAP5	Body;Body	chr2:134023947-134024467	Island
hypo13	FGR_insufficient_1	1.9E-02	0.66	0.90	-0.24	2	184125416	cq07423985			chr2:184125343-184125583	Island
hypo14	FGR_insufficient_1	6.2E-03	0.55	0.84	-0.29	3	10202595	cq18073702			chr3:10206449-10207024	N_Shelf
hypo15	FGR_insufficient_1	1.4E-04	0.75	0.95	-0.20	3	134758333	cq07048323	EPHB1	Body		
hypo16	FGR_insufficient_1	1.2E-02	0.39	0.75	-0.36	3	197842485	cq01392017			chr3:197840490-197840783	S_Shore
hypo17	FGR_insufficient_1	6.5E-02	0.43	0.83	-0.40	4	14926897	cq04581571				
hypo18	FGR_insufficient_1	6.9E-06	0.81	0.96	-0.14	5	6749408	cq00530298	POLS	Body		
hypo19	FGR_insufficient_1	3.6E-02	0.55	0.82	-0.27	5	97971808	cq06803420				
hypo20	FGR_insufficient_1	6.5E-06	0.58	0.85	-0.27	5	138842004	cq08331427	ECSCR	Body		
hypo21	FGR_insufficient_1	5.4E-02	0.62	0.86	-0.25	5	140871464	cq18032518	PCDHGA4;PCDHGC3;PCDHGA1	Body;Body;Body;Body;Body;Body	chr5:140871064-140872335	Island
hypo22	FGR_insufficient_1	9.3E-02	0.68	0.84	-0.16	5	140871590	cq17297328	PCDHGA4;PCDHGC3;PCDHGA1	Body;Body;Body;Body;Body;Body	chr5:140871064-140872335	Island
hypo23	FGR_insufficient_1	3.8E-07	0.64	0.93	-0.29	6	28874479	cq20544852	TRIM27	Body		
hypo24	FGR_insufficient_1	2.4E-03	0.49	0.82	-0.34	6	32034322	cq08895562	TNXB	Body		
hypo25	FGR_insufficient_1	1.5E-03	0.76	0.88	-0.12	6	72294420	cq07816653			chr6:72294372-72294988	Island
hypo26	FGR_insufficient_1	2.0E-02	0.06	0.59	-0.52	6	170338591	cq12173150			chr6:170338214-170339677	Island
hypo27	FGR_insufficient_1	9.7E-10	0.54	0.85	-0.31	7	27070361	cq26572901				
hypo28	FGR_insufficient_1	2.7E-02	0.69	0.90	-0.21	8	70312598	cq25827124				
hypo29	FGR_insufficient_1	2.5E-02	0.78	0.95	-0.17	9	135432492	cq13725340	C9orf171	Body		
hypo30	FGR_insufficient_1	3.2E-02	0.30	0.65	-0.35	10	50887049	cq05834477	C10orf53;C10orf53	TSS1500;TSS1500	chr10:50887565-50887862	N_Shore
hypo31	FGR_insufficient_1	1.0E-02	0.53	0.88	-0.34	10	134992080	cq3580836	KNDCC1	Body	chr10:134993121-134993324	N_Shore
hypo32	FGR_insufficient_1	9.8E-04	0.66	0.86	-0.20	11	503807	cq19223782	RNH1;RNH1;RNH1;RNH1;RNH1	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR	chr11:504189-504659	N_Shore
hypo33	FGR_insufficient_1	6.9E-02	0.77	0.94	-0.17	11	3435091	cq04128776			chr11:3435033-3435239	Island
hypo34	FGR_insufficient_1	5.3E-02	0.77	0.95	-0.18	11	36596040	cq26154599	RAG1	Body		
hypo35	FGR_insufficient_1	3.0E-04	0.61	0.86	-0.25	12	33585954	cq06721860	SYT10	Body		
hypo36	FGR_insufficient_1	2.6E-03	0.45	0.79	-0.34	12	52800873	cq20679157	KRT82	TSS1500	chr12:33591763-33593050	N_Shelf
hypo37	FGR_insufficient_1	5.2E-04	0.73	0.96	-0.22	13	112905745	cq01562175				
hypo38	FGR_insufficient_1	2.5E-05	0.90	0.98	-0.07	14	20786069	cq25091820	CENB1IP1;CCNB1IP1;CCNB1IP1	5'UTR;5'UTR;5'UTR;5'UTR		
hypo39	FGR_insufficient_1	8.9E-11	0.52	0.85	-0.33	16	2239275	cq03524868	CASKIN1	Body	chr16:2236712-2236939	S_Shelf
hypo40	FGR_insufficient_1	5.1E-08	0.57	0.87	-0.30	17	3872291	cq11252995				
hypo41	FGR_insufficient_1	9.1E-04	0.33	0.73	-0.40	18	55095177	cq05735180			chr18:55094825-55096310	Island
hypo42	FGR_insufficient_1	1.6E-04	0.25	0.71	-0.47	18	55092429	cq15222899			chr18:55094825-55096310	Island
hypo43	FGR_insufficient_1	8.8E-02	0.04	0.39	-0.35	18	55102005	cq25800170	ONECUT2	TSS1500	chr18:55102427-55102708	N_Shore
hypo44	FGR_insufficient_1	1.9E-05	0.30	0.98	-0.68	21	47344376	cq10125522	PCBP3;PCBP3	Body;Body	chr21:47343715-47345139	Island
hypo45	FGR_insufficient_1	2.2E-06	0.59	0.84	-0.26	1	1344064	cq25893543	MRPL20	TSS1500	chr1:1342004-1342952	S_Shore
hypo46	FGR_insufficient_2	2.1E-06	0.43	0.84	-0.41	1	10388646	cq19773385	KIF1B	Body	chr1:10386183-10386390	S_Shelf
hypo47	FGR_insufficient_2	3.7E-13	0.49	0.86	-0.37	1	161009463	cq22110569	TSTD1;TSTD1;USF1;USF1	TSS1500;TSS1500;TSS1500;3'UTR	chr1:161008377-161008830	S_Shore
hypo48	FGR_insufficient_2	2.1E-15	0.48	0.88	-0.40	2	8593963	cq07903001			chr2:8596907-8597573	N_Shelf
hypo49	FGR_insufficient_2	4.8E-02	0.45	0.80	-0.36	2	32483267	cq24608304	NLRCA	5'UTR		
hypo50	FGR_insufficient_2	2.9E-03	0.47	0.73	-0.27	2	32483392	cq23459416	NLRCA	5'UTR		
hypo51	FGR_insufficient_2	2.0E-14	0.49	0.91	-0.41	2	236864888	cq13192735	AGAP1;AGAP1	Body;Body	chr2:236867652-236867906	N_Shelf
hypo52	FGR_insufficient_2	2.5E-07	0.54	0.88	-0.34	4	3444147	cq07364841	HGFC	Body		
hypo53	FGR_insufficient_2	7.3E-09	0.34	0.73	-0.39	4	6306335	cq18764836			chr4:6303353-6304210	S_Shelf
hypo54	FGR_insufficient_2	3.5E-02	0.42	0.68	-0.25	4	83674694	cq18948646	SCD5;MIR575;SCD5	Body;TSS200;Body		
hypo55	FGR_insufficient_2	1.8E-06	0.43	0.74	-0.31	5	864385	cq15052217	BRD9;BRD9;BRD9	Body;3'UTR;3'UTR	chr5:865317-865642	N_Shore
hypo56	FGR_insufficient_2	2.5E-02	0.43	0.66	-0.23	6	31936565	cq22098742	SKIVL2	Body	chr6:31939370-31940559	N_Shore
hypo57	FGR_insufficient_2	6.7E-15	0.50	0.93	-0.43	7	1949247	cq03530573	MAD1L1;MAD1L1;MAD1L1	Body;Body;Body	chr7:1950279-1950482	N_Shore
hypo58	FGR_insufficient_2	2.2E-05	0.42	0.76	-0.34	7	66307208	cq22789911	LOC729156	Body	chr7:6630503-66310040	N_Shelf
hypo59	FGR_insufficient_2	1.9E-05	0.14	0.65	-0.52	7	66308541	cq07448840	LOC729156	Body	chr7:6630503-66310040	N_Shore
hypo60	FGR_insufficient_2	6.9E-04	0.71	0.83	-0.12	8	80544644	cq13511293			chr7:80546966-80547234	N_Shelf
hypo61	FGR_insufficient_2	3.9E-02	0.40	0.68	-0.28	7	80544479	cq15566990	SEMA3C	Body	chr7:80548306-80548726	N_Shelf
hypo62	FGR_insufficient_2	5.2E-14	0.60	0.93	-0.33	8	42306711	cq18334848	SLC20A2	Body		
hypo63	FGR_insufficient_2	2.8E-07	0.55	0.83	-0.28	8	129073877	cq24146714	PVT1	Body		
hypo64	FGR_insufficient_2	4.2E-14	0.53	0.90	-0.37	10	13696795	cq04686117	FRMD4A	Body	chr10:13698562-13699540	N_Shore
hypo65	FGR_insufficient_2	2.3E-11	0.59	0.92	-0.33	10	27146906	cq10311020	ABI1;ABI1;ABI1;ABI1	Body;Body;Body;Body	chr10:27149166-27150229	N_Shelf
hypo66	FGR_insufficient_2	2.0E-06	0.53	0.78	-0.25	10	32639458	cq20306821			chr10:32635217-32636655	S_Shelf
hypo67	FGR_insufficient_2	4.3E-10	0.61	0.92	-0.30	10	127571375	cq08199003	DHX32	TSS1500		
hypo68	FGR_insufficient_2	1.6E-04	0.56	0.88	-0.32	11	18271401	cq03687333	SAA2;SAA2	TSS1500;TSS1500		
hypo69	FGR_insufficient_2	7.6E-10	0.54	0.87	-0.33	12	68056168	cq19968199	DYRK2;DYRK2	3'UTR;3'UTR		
hypo70	FGR_insufficient_2	2.0E-02	0.42	0.79	-0.37	12	77260534	cq26994885	CSRP2	5'UTR		
hypo71	FGR_insufficient_2	1.2E-14	0.50	0.88	-0.38	15	101567894	cq24950894	LRK1	Body		
hypo72	FGR_insufficient_2	5.9E-07	0.86	0.97	-0.10	16	50613442	cq09930155	NKD1	Body	chr16:50613108-50613701	Island
hypo73	FGR_insufficient_2	1.1E-03	0.70	0.86	-0.15	16	67757411	cq01114989	RANBP10	3'UTR	chr16:67752849-67753446	S_Shelf
hypo74	FGR_insufficient_2	6.8E-03	0.30	0.46	-0.15	20	52209811	cq09123431			chr20:52209590-52211360	Island
hypo75	FGR_insufficient_2	3.3E-03	0.41	0.54	-0.14	22	17090962	cq26581886	psTPT22	Body	chr22:17090455-17091224	Island
hypo76	FGR_insufficient_2	2.8E-09	0.55	0.88	-0.34	22	38225114	cq22082700			chr22:38220589-38221619	S_Shelf
hypo77	FGR_insufficient_3	1.1E-09	0.65	0.92	-0.27	1	33744259	cq20206116	ZNF362	Body	chr1:33745741-33745990	N_Shore
hypo78	FGR_insufficient_3	1.9E-05	0.62	0.83	-0.22	2	239403239	cq17850055				
hypo79	FGR_insufficient_3	9.8E-08	0.48	0.83	-0.35	3	13864471	cq21224025	WNT7A	Body	chr3:13860434-13860882	S_Shelf
hypo80	FGR_insufficient_3	1.7E-08	0.51	0.79	-0.28	4	184686701	cq16039660				
hypo81	FGR_insufficient_3	2.2E-02	0.57	0.88	-0.31	4	187418419	cq12937770			chr4:187422034-187422244	N_Shelf
hypo82	FGR_insufficient_3	1.4E-03	0.09	0.51	-0.42	5	92178	cq10165894			chr5:92007-92438	Island
hypo83	FGR_insufficient_3	1.8E-02	0.16	0.55	-0.39	5	92376	cq25622036			chr5:92007-92438	Island
hypo84	FGR_insufficient_3	3.1E-04	0.74	0.89	-0.16	5	663787	cq22936884	TPPP	3'UTR	chr5:665187-665401	N_Shore
hypo85	FGR_insufficient_3	1.5E-10	0.59	0.91	-0.32	5	31361135	cq20539449				
hypo86	FGR_insufficient_3	1.4E-04	0.70	0.88	-0.18	5	165513101	cq14069726				
hypo87	FGR_insufficient_3	1.7E-12	0.60	0.94	-0.35	6	30156892	cq23814883	TRIM26	Body		
hypo88	FGR_insufficient_3	2.5E-09	0.50	0.86	-0.37	6	91003200	cq03035849	BACH2;BACH2	5'UTR;5'UTR	chr6:91004795-91006944	N_Shore
hypo89	FGR_insufficient_3	1.2E-12	0.34	0.88	-0.55	6	110504754	cq10512408	CDC40	Body	chr6:110500025-110500966	S_Shelf
hypo90	FGR_insufficient_3	1.4E-05	0.65	0.85	-0.21	7	11468680	cq05232241	THSD7A	Body		

hypo126	FGR_insufficient_4	7.3E-13	0.52	0.90	-0.37	11	35644854	cg13916633			chr11:35639629-35641485	S_Shelf
hypo126	FGR_insufficient_4	4.3E-04	0.59	0.88	-0.30	11	129683974	cg08524015			chr11:129685737-129686211	N_Shore
hypo127	FGR_insufficient_4	7.4E-09	0.57	0.89	-0.31	15	33188759	cg27158011	FMN1	Body		
hypo128	FGR_insufficient_4	2.9E-13	0.53	0.90	-0.38	16	22189495	cg27166767	TRAF7	Body	chr16:2214222-2215518	
hypo129	FGR_insufficient_4	1.4E-02	0.94	0.98	-0.04	16	57416074	cg05410102	CX3CL1	Body	chr16:57415974-57416338	S_Shelf
hypo130	FGR_insufficient_4	8.0E-13	0.55	0.89	-0.34	17	56069567	cg24008395			chr17:56064830-56066051	S_Shelf
hypo131	FGR_insufficient_4	3.6E-03	0.84	0.94	-0.10	19	11754404	cg15556222			chr19:11750529-11751006	S_Shelf
hypo132	FGR_insufficient_4	8.2E-04	0.55	0.82	-0.27	19	47158242	cg06454084	DACT3	Body		
hypo133	FGR_insufficient_4	2.7E-02	0.47	0.78	-0.31	20	23470274	cg11897976	CST8	TSS1500		
hypo134	FGR_insufficient_4	2.1E-06	0.41	0.70	-0.29	20	36975083	cg08351331	LBP	Body		
hypo135	FGR_insufficient_4	3.4E-08	0.43	0.78	-0.35	21	47803078	cg03165002	PCNT	Body	chr21:47802465-47804760	Island
hypo136	FGR_insufficient_5	2.8E-10	0.43	0.80	-0.37	1	1597086	cg08484848	CDK11B,CDK11B,CDK11B,CDK11B,ECE1,ECE1,ECE1,ECE1	Body,Body,Body,Body,Body,3'UTR	chr1:16009811-1601231	N_Shelf
hypo137	FGR_insufficient_5	4.8E-04	0.56	0.82	-0.26	1	21552839	cg07114751			chr2:21551574-21551931	S_Shore
hypo138	FGR_insufficient_5	1.0E-04	0.71	0.50	-0.21	1	44686794	cg23599716	ERIC3	3'UTR		
hypo139	FGR_insufficient_5	0.3E-03	0.70	0.23	-0.20	2	cg03368204					
hypo140	FGR_insufficient_5	1.6E-04	0.61	0.88	-0.27	2	26098817	cg00844078	ASXL2	Body	chr2:25142472-25143689	S_Shelf
hypo141	FGR_insufficient_5	2.1E-08	0.51	0.84	-0.32	2	99081350	cg11555067	INPP4A,INPP4A,INPP4A,INPP4A	5'UTR,5'UTR,5'UTR,5'UTR	chr2:26100513-26101653	N_Shore
hypo142	FGR_insufficient_5	3.0E-02	0.55	0.80	-0.24	2	223765655	cg22909085	ACSL3,ACSL3	5'UTR,5'UTR		
hypo143	FGR_insufficient_5	4.3E-04	0.17	0.83	-0.66	2	242580471	cg11574665	ATG4B,ATG4B	Body,Body	chr2:24257506-242577492	S_Shelf
hypo144	FGR_insufficient_5	2.6E-10	0.60	0.90	-0.30	4	75020915	cg12718874			chr4:75023577-75023403	N_Shelf
hypo145	FGR_insufficient_5	3.3E-03	0.60	0.86	-0.26	4	109115092	cg15508749				
hypo146	FGR_insufficient_5	7.4E-03	0.47	0.74	-0.27	6	144329887	cg23460430	PLAGL1,PLAGL1,PLAGL1,PLAGL1	TSS1500,TSS1500,5'UTR,TSS1500	chr6:144328916-144329847	S_Shore
hypo147	FGR_insufficient_5	6.3E-08	0.49	0.79	-0.30	7	1575737	cg246467108	MAFK	5'UTR	chr7:1575736-1575993	
hypo148	FGR_insufficient_5	2.5E-05	0.48	0.77	-0.29	7	133056105	cg12826833	EXOC4,EXOC4	Body		
hypo149	FGR_insufficient_5	4.1E-02	0.50	0.80	-0.29	8	102221396	cg22009239			chr8:102217317-102218461	S_Shelf
hypo150	FGR_insufficient_5	3.2E-03	0.61	0.83	-0.22	10	71876389	cg13908507	AIFM2			
hypo151	FGR_insufficient_5	3.4E-04	0.16	0.74	-0.58	11	65685316	cg19648728	DRAP1,C11orf6B,C11orf6B	TSS1500,Body,Body	chr11:65685100-65685364	Island
hypo152	FGR_insufficient_5	5.0E-02	0.61	0.90	-0.09	11	75063831	cg07225648			chr11:75062224-75062377	S_Shelf
hypo153	FGR_insufficient_5	1.2E-06	0.61	0.86	-0.28	11	94467433	cg05103613				
hypo154	FGR_insufficient_5	6.4E-06	0.58	0.88	-0.30	12	341431	cg04647176	SLOC613	Body		
hypo155	FGR_insufficient_5	3.3E-06	0.48	0.72	-0.24	12	132516068	cg00089214	EP400	Body	chr12:132514283-132514525	S_Shore
hypo156	FGR_insufficient_5	7.1E-03	0.20	0.60	-0.40	13	51417469	cg17241776	DLEU7	1stExon	chr13:51417371-51418149	Island
hypo157	FGR_insufficient_5	1.1E-06	0.51	0.79	-0.27	17	757312494	cg16722931	SEPT9,SEPT9	5'UTR,Body		
hypo158	FGR_insufficient_5	3.1E-16	0.29	0.87	-0.58	17	79792936	cg18470662	DYSFIP1	TSS200	chr17:79790530-79791553	S_Shore
hypo159	FGR_insufficient_5	5.4E-02	0.55	0.83	-0.29	19	3355151	cg25919177			chr19:3358495-3361248	N_Shelf
hypo160	FGR_insufficient_5	5.6E-04	0.57	0.81	-0.24	19	54327780	cg25866075	NLRP12	TSS200		
hypo161	FGR_insufficient_5	6.7E-02	0.13	0.45	-0.33	20	44880006	cg07676002	CDH22,CDH22	1stExon,5'UTR	chr20:44879699-44880288	Island
hypo162	FGR_insufficient_5	8.8E-03	0.15	0.38	-0.23	20	52789646	cg24582168	CYP24A1,CYP24A1	Body,Body	chr20:52789252-52790986	Island
hypo163	FGR_insufficient_5	3.8E-07	0.26	0.57	-0.31	20	52790063	cg23685712	CYP24A1,CYP24A1	1stExon,1stExon	chr20:52789252-52790986	Island
hypo164	FGR_insufficient_5	4.4E-08	0.37	0.81	-0.44	1	1159106	cg09819798	SDF4,SDF4	Body,Body	chr21:1159168-1159528	N_Shore
hypo165	FGR_insufficient_5	7.2E-04	0.58	0.82	-0.24	3	30733753	cg05074709	TGFBF2,TGFBF2	3'UTR,3'UTR		
hypo166	FGR_insufficient_5	4.9E-03	0.86	0.62	-0.24	3	16181434	cg03263676	TT3B	Body		
hypo167	FGR_insufficient_5	2.6E-05	0.61	0.86	-0.26	3	190043045	cg25704745			chr3:190039817-190040465	S_Shelf
hypo168	FGR_insufficient_5	4.1E-08	0.70	0.87	-0.17	4	730453	cg20823529	PCGF3	Body	chr4:730282-731005	Island
hypo169	FGR_insufficient_5	2.0E-02	0.38	0.81	-0.44	5	33794720	cg07784793	ADAMT3	Body		
hypo170	FGR_insufficient_5	2.3E-02	0.59	0.82	-0.23	5	66123702	cg17606548	MAST4,MAST4,MAST4	TSS1500,Body,Body		
hypo171	FGR_insufficient_5	2.5E-10	0.68	0.93	-0.25	5	130497746	cg01175503	HINT1,HINT1,HINT1	Body,Body,Body	chr5:130500226-130501095	N_Shelf
hypo172	FGR_insufficient_5	7.6E-09	0.34	0.85	-0.51	6	4923095	cg24589893	CDYL,CDYL,CDYL,CDYL	Body,Body,Body,Body		
hypo173	FGR_insufficient_5	3.5E-12	0.63	0.92	-0.29	6	31854545	cg05425464	EHMT2,EHMT2	Body,Body	chr6:31856896-31857104	N_Shelf
hypo174	FGR_insufficient_5	2.7E-09	0.71	0.94	-0.23	6	149367279	cg06827883	URST	Body		
hypo175	FGR_insufficient_5	7.3E-10	0.61	0.92	-0.31	8	124031034	cg11604216	DERL1,DERL1	Body		
hypo176	FGR_insufficient_5	4.7E-04	0.64	0.86	-0.23	11	63990575	cg02160996	FERM3,FERM3	Body,Body	chr11:63993589-63993834	N_Shelf
hypo177	FGR_insufficient_5	1.0E-06	0.84	0.91	-0.27	11	63990595	cg02191933	FERM3,FERM3	Body,Body	chr11:63993589-63993834	N_Shelf
hypo178	FGR_insufficient_5	3.3E-10	0.70	0.97	-0.27	11	63990629	cg24634304	FERM3,FERM3	Body,Body	chr11:63993589-63993834	N_Shelf
hypo179	FGR_insufficient_5	4.7E-03	0.62	0.85	-0.23	11	71915177	cg16082721	FOLR2,FOLR2,FOLR2,FOLR2	Body,Body,Body,Body	chr11:71934247-71936321	N_Shelf
hypo180	FGR_insufficient_5	1.5E-02	0.81	0.95	-0.23	11	12257343	cg10227827	DOX8	5'UTR	chr11:118661305-118663026	N_Shelf
hypo181	FGR_insufficient_5	9.2E-04	0.61	0.83	-0.21	12	110836588	cg13557301	ANAPC7,ANAPC7	Body,Body	chr12:110841021-110841548	N_Shelf
hypo182	FGR_insufficient_5	5.9E-09	0.66	0.91	-0.24	14	62021555	cg18703243				
hypo183	FGR_insufficient_5	3.2E-09	0.57	0.81	-0.24	14	103556656	cg03007309			chr14:103557606-103558235	N_Shore
hypo184	FGR_insufficient_5	4.8E-11	0.65	0.92	-0.27	16	57484979	cg06578063	COQ9	Body	chr16:57480995-57481666	S_Shelf
hypo185	FGR_insufficient_5	2.8E-11	0.57	0.89	-0.32	19	46198630	cg08182826	QPCTL,QPCTL	Body,Body	chr19:46195482-46196292	S_Shelf
hypo186	FGR_insufficient_5	8.6E-04	0.80	0.94	-0.14	19	49611733	cg19281603	SNRNP70	3'UTR	chr19:494610928-49611410	S_Shelf
hypo187	FGR_insufficient_5	6.2E-04	0.51	0.73	-0.22	1	1234367	cg22675767	ACAP3	Body		
hypo188	FGR_insufficient_5	2.7E-10	0.61	0.89	-0.28	1	6267579	cg19694465	RNF207	Body		
hypo189	FGR_insufficient_5	4.7E-06	0.60	0.84	-0.24	1	15764869	cg03096785	CTRC	TSS200	chr1:6268802-6269688	N_Shore
hypo190	FGR_insufficient_5	8.9E-11	0.61	0.89	-0.28	1	119715385	cg18451982				
hypo191	FGR_insufficient_5	9.9E-05	0.63	0.84	-0.21	1	231838098	cg10116456	TSNAX,DISC1,DISC			

hypo254	FGR_adequate_4	6.4E-10	0.72	0.94	-0.22	6	146051934	cg00077566	EPM2A;EPM2A	Body;Body	chr6:146055896-146056981	N_Shelf
hypo255	FGR_adequate_4	2.1E-10	0.75	0.97	-0.22	10	99278449	cg10989317	UBTD1	Body		
hypo256	FGR_adequate_4	2.1E-09	0.22	0.56	-0.34	11	2019732	cg11735853	H19	TSS1500	chr11:2019565-2019863	Island
hypo257	FGR_adequate_4	3.1E-06	0.60	0.83	-0.22	12	64360878	cg26897521	SRGAP1	Body		
hypo258	FGR_adequate_4	5.5E-04	0.84	0.97	-0.12	12	124798985	cg18124134	FAM101A	Body	chr12:124798796-124799224	Island
hypo259	FGR_adequate_4	6.3E-07	0.62	0.87	-0.25	16	2794914	cg16392797	LOC100128788;LOC100128788	TSS200;Body		
hypo260	FGR_adequate_4	4.4E-06	0.59	0.85	-0.26	16	89620074	cg16677432	SPG7	Body		
hypo261	FGR_adequate_4	3.3E-09	0.65	0.92	-0.27	17	80902556	cg073431961	B3GNTL1	3'UTR	chr17:80898965-80899313	S_Shelf
hypo262	FGR_adequate_5	8.2E-05	0.54	0.79	-0.25	1	17328620	cg05064739	ATP13A2;ATP13A2;ATP13A2	Body;Body;Body	chr1:17331885-17332093	N_Shelf
hypo263	FGR_adequate_5	7.3E-11	0.56	0.84	-0.28	1	19209709	cg07787591	ALDH4A1;ALDH4A1;ALDH4A1	Body;Body;Body	chr1:16206826-19206914	Island
hypo264	FGR_adequate_5	2.2E-08	0.60	0.87	-0.26	1	36931973	cg11577454	CSF3R;CSF3R;CSF3R;CSF3R	Body;3'UTR;Body;Body	chr1:36929414-36930131	S_Shore
hypo265	FGR_adequate_5	5.2E-02	0.63	0.84	-0.22	6	119252835	cg26771384	MC9R	Body	chr6:119255738-119256331	N_Shelf
hypo266	FGR_adequate_5	1.8E-06	0.68	0.91	-0.23	6	143891455	cg20298778	LOC285740	TSS1500		
hypo267	FGR_adequate_5	7.3E-02	0.61	0.82	-0.22	10	127779842	cg24194674	ADAM12;ADAM12	Body;Body		
hypo268	FGR_adequate_5	3.3E-08	0.65	0.88	-0.23	11	977931	cg27445792	AP2A2	Body	chr11:976949-977193	S_Shore
hypo269	FGR_adequate_5	1.9E-05	0.53	0.77	-0.24	11	2423571	cg27135510	TSSC4;TSSC4	5'UTR;1stExon	chr11:2421040-2422474	S_Shore
hypo270	FGR_adequate_5	4.5E-09	0.64	0.91	-0.27	11	92577553	cg24168798	FAT3	Body		
hypo271	FGR_adequate_5	3.0E-10	0.68	0.93	-0.25	12	3950698	cg07023594	PARP11	Body	chr12:3947922-3948620	S_Shelf
hypo272	FGR_adequate_5	3.9E-07	0.57	0.79	-0.23	14	24032626	cg04882359	AP1G2	Body	chr14:24036399-24037076	N_Shelf
hypo273	FGR_adequate_5	7.0E-04	0.69	0.91	-0.22	14	71250264	cg01022840	MAP3K9	Body		
hypo274	FGR_adequate_5	4.4E-03	0.81	0.90	-0.08	15	25301930	cg20568038	SNORD116;3;SNORD116;9	TSS200;TSS200		
hypo275	FGR_adequate_5	2.4E-04	0.88	0.96	-0.09	16	1706201	cg04908586	GRAMP1L	Body	chr16:1705866-1706244	Island
hypo276	FGR_adequate_5	9.6E-03	0.48	0.73	-0.25	16	3613509	cg02719221	NLR3C	Body	chr16:3613100-3613546	Island
hypo277	FGR_adequate_5	3.8E-04	0.69	0.89	-0.21	17	78748471	cg00523683	RPTOR;RPTOR	Body;Body		
hypo278	FGR_adequate_5	1.0E-06	0.54	0.91	-0.37	19	53269486	cg05619639	ZNF600	Body		
hypo279	FGR_adequate_5	9.7E-04	0.69	0.91	-0.22	22	39109522	cg05816914	TOMM22	3'UTR	chr22:39077816-39078400	S_Shelf
hypo280	FGR_excessive_1	1.3E-02	0.71	0.89	-0.18	1	6339954	cg11690194	ACOT7;ACOT7;ACOT7;ACOT7	Body;Body;Body;Body	chr1:6339948-6340268	Island
hypo281	FGR_excessive_1	2.1E-11	0.52	0.87	-0.35	1	9005474	cg23738308	CAB	TSS1500		
hypo282	FGR_excessive_1	1.7E-02	0.62	0.85	-0.24	2	183123847	cg07496624	PDE1A;PDE1A	Body;Body		
hypo283	FGR_excessive_1	4.3E-03	0.73	0.89	-0.15	2	183498282	cg26192279		Body		
hypo284	FGR_excessive_1	5.3E-03	0.60	0.79	-0.19	2	192891657	cg22742965	TMEFF2	Body		
hypo285	FGR_excessive_1	1.1E-11	0.25	0.77	-0.52	2	237028669	cg13018278	AGAP1;AGAP1	Body;Body	chr2:237028848-237029121	Island
hypo286	FGR_excessive_1	5.6E-07	0.57	0.84	-0.27	3	126744035	cg13631725	PLXNA1	Body		
hypo287	FGR_excessive_1	2.5E-02	0.37	0.65	-0.29	3	196908930	cg12594803	DLG1;DLG1	Body;Body		
hypo288	FGR_excessive_1	7.2E-02	0.83	0.92	-0.08	4	295862	cg20241375		Body;Body;Body	chr4:298803-299312	N_Shelf
hypo289	FGR_excessive_1	1.1E-04	0.49	0.81	-0.32	4	119826303	cg08774280	SYNPO2;SYNPO2;SYNPO2	Body;Body;Body		
hypo290	FGR_excessive_1	9.6E-04	0.63	0.88	-0.25	4	138468381	cg14017444		Body		
hypo291	FGR_excessive_1	8.1E-02	0.63	0.87	-0.24	4	138535339	cg11920765		Body		
hypo292	FGR_excessive_1	8.5E-03	0.79	0.92	-0.13	4	140619779	cg21634993	MGST2	Body	chr4:140619547-140619780	Island
hypo293	FGR_excessive_1	1.4E-02	0.72	0.88	-0.16	5	41071990	cg01900397	HEATR7B2	TSS1500		
hypo294	FGR_excessive_1	2.3E-04	0.85	0.89	-0.24	5	150054944	cg15696933	MYO23;MYO23	Body;Body	chr5:150051116-150052107	S_Shelf
hypo295	FGR_excessive_1	1.6E-11	0.57	0.87	-0.31	6	36462140	cg13528479	STK38	3'UTR		
hypo296	FGR_excessive_1	1.9E-02	0.19	0.60	-0.41	6	37617124	cg00807871	MDGA1	Body	chr6:37616722-37617179	Island
hypo297	FGR_excessive_1	1.3E-14	0.52	0.92	-0.39	6	107021926	cg25216682	RTN4IP1	Body		
hypo298	FGR_excessive_1	4.5E-05	0.44	0.68	-0.24	7	2261337	cg12577003	MAD1L1;MAD1L1;MAD1L1	Body;Body;Body		
hypo299	FGR_excessive_1	2.8E-11	0.54	0.90	-0.36	7	108055705	cg06002804	NRCAM;NRCAM	5'UTR;5'UTR		
hypo300	FGR_excessive_1	3.7E-05	0.57	0.83	-0.26	7	142659378	cg26806603	KEL;KEL	1stExon;5'UTR		
hypo301	FGR_excessive_1	1.4E-02	0.76	0.94	-0.17	7	158883968	cg23540020	VIPR2	Body	chr7:158886367-158886595	N_Shelf
hypo302	FGR_excessive_1	2.2E-02	0.64	0.83	-0.20	8	61227705	cg10796022		Body		
hypo303	FGR_excessive_1	6.0E-05	0.50	0.80	-0.30	10	3280494	cg04678570		Body		
hypo304	FGR_excessive_1	2.6E-05	0.51	0.85	-0.34	10	87426906	cg15209053	GRID1	Body		
hypo305	FGR_excessive_1	1.7E-11	0.52	0.84	-0.32	10	126856869	cg07341129	CTBP2;CTBP2;CTBP2	Body;Body;Body	chr10:126686551-126686892	N_Shore
hypo306	FGR_excessive_1	9.4E-10	0.60	0.92	-0.32	10	128932004	cg22909333	DOCK1	Body		
hypo307	FGR_excessive_1	2.1E-05	0.77	0.90	-0.13	11	78380599	cg12051260	OD24	Body		
hypo308	FGR_excessive_1	2.4E-02	0.73	0.84	-0.11	11	83372714	cg27373604	DLG2;DLG2;DLG2;DLG2	5'UTR;Body;Body;Body		
hypo309	FGR_excessive_1	1.3E-11	0.52	0.87	-0.35	11	105010531	cg20120939	CARD18	TSS200		
hypo310	FGR_excessive_1	1.6E-04	0.49	0.84	-0.34	11	117063002	cg27273731	SIDT2	Body		
hypo311	FGR_excessive_1	4.3E-02	0.74	0.89	-0.15	11	130536540	cg08193293		Body		
hypo312	FGR_excessive_1	1.2E-05	0.53	0.81	-0.27	12	38045811	cg19250083	IPO8	Body	chr12:30848264-30849016	N_Shelf
hypo313	FGR_excessive_1	3.2E-02	0.78	0.88	-0.10	12	89118099	cg09154414		Body		
hypo314	FGR_excessive_1	4.2E-08	0.81	0.95	-0.14	12	96389483	cg09636302	HAL	Body	chr12:96389405-96389675	Island
hypo315	FGR_excessive_1	3.7E-09	0.57	0.87	-0.31	12	109046825	cg06251181	CORO1C	Body		
hypo316	FGR_excessive_1	5.9E-03	0.50	0.82	-0.32	14	51137626	cg18406010		Body	chr14:51134480-51135304	S_Shelf
hypo317	FGR_excessive_1	2.1E-14	0.65	0.94	-0.29	14	105836263	cg18853010	PACS2;PACS2	Body;Body	chr14:105836031-105836386	Island
hypo318	FGR_excessive_1	8.6E-06	0.47	0.74	-0.27	15	101645225	cg02346706		Body		
hypo319	FGR_excessive_1	9.6E-07	0.65	0.87	-0.21	16	88032157	cg10637565	BANP;BANP	Body;Body	chr16:88032156-88034968	Island
hypo320	FGR_excessive_1	2.3E-02	0.91	0.98	-0.07	16	88550450	cg02071579	ZFPM1	Body	chr16:88554354-88554847	N_Shelf
hypo321	FGR_excessive_1	3.4E-03	0.92	0.98	-0.06	16	89177789	cg04388767	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89173704-89173905	S_Shelf
hypo322	FGR_excessive_1	4.5E-03	0.80	0.96	-0.16	16	89187106	cg26656884	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89186198-89186551	S_Shore
hypo323	FGR_excessive_1	2.3E-03	0.97	0.99	-0.02	17	27903940	cg06013127	GIT1;GIT1	Body;Body	chr17:27899511-27900067	S_Shelf
hypo324	FGR_excessive_1	1.4E-03	0.61	0.83	-0.22	17	88980107	cg15979932	CUEDC1	5'UTR		
hypo325	FGR_excessive_1	2.9E-06	0.70	0.90	-0.19	17	80540666	cg15014089	FOXK2	Body	chr17:80541548-80541754	N_Shore
hypo326	FGR_excessive_1	7.0E-02	0.57	0.85	-0.22	17	80540696	cg08697578	FOXK2	Body	chr17:80541548-80541754	N_Shore
hypo327	FGR_excessive_1	2.3E-05	0.78	0.90	-0.13	17	80542006	cg26986438	FOXK2	Body	chr17:80541912-80542119	Island
hypo328	FGR_excessive_1	1.2E-02	0.74	0.89	-0.14	17	80559449	cg13362683	FOXK2	3'UTR	chr17:80559025-80559450	Island
hypo329	FGR_excessive_1	6.2E-02	0.37	0.62	-0.25	18	32957127	cg06475288	ZNF396	5'UTR	chr18:32956764-32957406	Island
hypo330	FGR_excessive_1	5.1E-03	0.87	0.97	-0.09	20	61472147	cg06598544	COL9A3	3'UTR	chr20:61471903-61472256	Island
hypo331	FGR_excessive_1	6.3E-03	0.61	0.89	-0.28	21	34957259	cg08911536	DONSON	Body	chr21:34960388-34961252	N_Shelf
hypo332	FGR_excessive_2	1.1E-04	0.82	0.97	-0.15	1	5943388	cg26791536	NPHP4	Body		
hypo333	FGR_excessive_2	3.0E-05	0.76	0.95	-0.20	1	5950833	cg21451253	NPHP4	Body	chr1:5950824-5951029	Island
hypo334	FGR_excessive_2	2.2E-05	0.82	0.94	-0.12	1	5951028	cg05463119	NPHP4	Body	chr1:5950824-5951029	Island
hypo335	FGR_excessive_2	7.6E-02	0.66	0.91	-0.24	1	5955929	cg15598789	NPHP4	Body		
hypo336	FGR_excessive_2	7.2E-10	0.47	0.80	-0.33	1	27185941	cg10817520		Body	chr17:27189912-27190128	N_Shelf
hypo337	FGR_excessive_2	1.8E-08	0.52	0.85	-0.33	1	160769081	cg07106927	LY9;LY9	Body;Body	chr1:160771683-160771953	N_Shelf
hypo338	FGR_excessive_2	5.4E-05	0.68	0.92	-0.24	2	219754840	cg26449951	WNT10A	Body	chr2:219757458-219758001	N_Shelf
hypo339	FGR_excessive_2	9.1E-12	0.53	0.90	-0.37	2	231584368	cg20724690	CAB39;CAB39;CAB39	5'UTR;5'UTR;5'UTR		
hypo340	FGR_excessive_2	4.5E-02	0.75	0.96	-0.21	4	3735986	cg03469578		Body		
hypo341	FGR_excessive_2	7.2E-13	0.56	0.92	-0.36	6	32394046	cg00326788	CNCD3;CNCD3	5'UTR;5'UTR	chr6:32395896-32397692	N_Shore
hypo342	FGR_excessive_2	3.9E-14	0.56	0.91	-0.34	6	41913381	cg16323359	TBTK1	Body	chr6:41908745-41909711	S_Shelf
hypo343	FGR_excessive_2	8.4E-02	0.37	0.59	-0.21	6	43230751	cg25020820	LAMA2;LAMA2	Body;Body	chr4:43230670-43231064	Island
hypo344	FGR_excessive_2	3.1E-03	0.55</									

hypo383	FGR_excessive_3	7.1E-09	0.04	0.48	-0.44	7	151328924	cg18334211	PRKAG2;PRKAG2;PRKAG2	Body;Body;Body			
hypo384	FGR_excessive_3	6.6E-03	0.32	0.56	-0.24	7	151330008	cg01108370	PRKAG2;PRKAG2;PRKAG2	Body;TSS1500;Body			
hypo385	FGR_excessive_3	9.2E-09	0.57	0.89	-0.31	10	72113560	cg09504384	LRRC20;LRRC20;LRRC20	Body;Body;Body			
hypo386	FGR_excessive_3	5.5E-08	0.65	0.90	-0.25	11	35817123	cg07271405	TRIM44	Body			
hypo387	FGR_excessive_3	4.3E-07	0.70	0.82	-0.12	16	84693437	cg09145053	KLHL36	Body	chr16:84695169-84695681	N_Shore	
hypo388	FGR_excessive_3	1.3E-06	0.47	0.75	-0.28	17	58169865	cg03120558	LOC645638	TSS200			
hypo389	FGR_excessive_4	1.2E-02	0.52	0.79	-0.27	1	167902728	cg19777644	BRP44;BRP44;BRP44	Body;Body;Body	chr1:167905027-167906801	N_Shelf	
hypo390	FGR_excessive_4	1.4E-05	0.36	0.67	-0.31	1	203605590	cg13808058	ATP2B4;ATP2B4	5'UTR;5'UTR			
hypo391	FGR_excessive_4	2.4E-15	0.55	0.91	-0.35	3	39429575	cg14528273	SLC25A38	Body	chr3:39424696-39426058	S_Shelf	
hypo392	FGR_excessive_4	3.3E-03	0.62	0.90	-0.28	3	48705266	cg13293227			chr3:48698335-48701667	S_Shelf	
hypo393	FGR_excessive_4	6.6E-12	0.56	0.92	-0.36	3	64080488	cg07990808	PRICKLE2	3'UTR			
hypo394	FGR_excessive_4	7.7E-13	0.25	0.81	-0.56	3	119420208	cg25188166			chr3:119421855-119422334	N_Shore	
hypo395	FGR_excessive_4	1.4E-06	0.64	0.90	-0.26	4	74854214	cg21398186	PPBP	TSS1500			
hypo396	FGR_excessive_4	1.2E-09	0.78	0.96	-0.18	5	1329669	cg26947723	CLPTM1L	Body			
hypo397	FGR_excessive_4	4.5E-10	0.86	0.97	-0.11	5	138737437	cg11570383	SPATA24	Body	chr5:138739492-138739912	N_Shelf	
hypo398	FGR_excessive_4	4.8E-02	0.79	0.89	-0.10	6	13365510	cg14949271	GFD01	Body	chr6:13364999-13365949	N_Shore	
hypo399	FGR_excessive_4	3.3E-04	0.75	0.90	-0.15	6	13365826	cg26738980	GFD01	Body	chr6:13364999-13365949	Island	
hypo400	FGR_excessive_4	1.9E-14	0.53	0.90	-0.37	6	101306732	cg09392911	ASCC3;ASCC3	3'UTR;Body			
hypo401	FGR_excessive_4	1.5E-02	0.85	0.93	-0.08	8	104315598	cg14645926	FZD6;FZD6;FZD6	Body;Body;Body	chr8:104310089-104311620	S_Shelf	
hypo402	FGR_excessive_4	1.4E-09	0.43	0.78	-0.35	8	140990001	cg25699417	TRAPPC9;TRAPPC9	Body;Body			
hypo403	FGR_excessive_4	6.6E-16	0.13	0.84	-0.71	9	99264127	cg14155501	CDC14B;CDC14B;CDC14B	3'UTR;3'UTR;3'UTR			
hypo404	FGR_excessive_4	7.6E-02	0.74	0.92	-0.18	10	81444403	cg10452333	LOC650623		chr10:81444163-81444474	Island	
hypo405	FGR_excessive_4	2.8E-11	0.49	0.86	-0.37	10	125624685	cg01512466	CPXM2	Body			
hypo406	FGR_excessive_4	2.3E-02	0.57	0.84	-0.27	11	69949353	cg15767218	ANO1;ANO1	Body;Body			
hypo407	FGR_excessive_4	2.0E-11	0.51	0.88	-0.37	12	76277069	cg15007809					
hypo408	FGR_excessive_4	4.7E-02	0.71	0.92	-0.21	13	31732963	cg02309157	HSRPH1	Body	chr13:31735109-31736670	N_Shelf	
hypo409	FGR_excessive_4	3.2E-08	0.72	0.91	-0.19	15	25415399	cg02241833	SNORD115-1	TSS1500			
hypo410	FGR_excessive_4	4.5E-10	0.57	0.89	-0.32	17	15415649	cg15374027	FAM18B2	Body			
hypo411	FGR_excessive_4	1.3E-02	0.43	0.66	-0.23	17	16381219	cg11624993	C17orf76;C17orf76	Body;Body			
hypo412	FGR_excessive_4	8.0E-05	0.32	0.92	-0.61	17	78093132	cg11469818	GAA;GAA;GAA	3'UTR;3'UTR;3'UTR			
hypo413	FGR_excessive_4	7.1E-04	0.54	0.81	-0.27	18	60260226	cg07429775			chr18:60263380-60264248	N_Shelf	
hypo414	FGR_excessive_4	2.1E-02	0.69	0.88	-0.19	19	2586206	cg04696890	GN7	5'UTR	chr19:2588375-2588590	N_Shelf	
hypo415	FGR_excessive_4	8.7E-02	0.86	0.97	-0.11	19	4956786	cg00033371	UHRF1;UHRF1	Body;Body	chr19:4954453-4954870	S_Shore	
hypo416	FGR_excessive_4	5.5E-05	0.48	0.72	-0.25	19	10222409	cg18910313	PPAN-P2RY11;P2RY11	Body;1stExon	chr19:10220612-10221147	S_Shore	
hypo417	FGR_excessive_4	8.7E-02	0.27	0.49	-0.22	22	46367703	cg13458651	WNT7B	Body	chr22:46366726-46368726	Island	
hypo418	FGR_excessive_4	2.9E-04	0.43	0.75	-0.33	22	50909668	cg19800640	C22orf41	Body	chr22:50984972-50988141	S_Shelf	
hypo419	N_insufficient_1	2.9E-13	0.57	0.93	-0.36	1	246942431	cg25350722					
hypo420	N_insufficient_1	1.3E-06	0.47	0.80	-0.33	2	98349537	cg27280787	ZAP70;ZAP70	Body;TSS1500	chr2:9835094-98351257	N_Shore	
hypo421	N_insufficient_1	3.8E-06	0.44	0.75	-0.31	2	164471195	cg14448393	FIGN	Body			
hypo422	N_insufficient_1	1.5E-03	0.50	0.85	-0.35	4	66650395	cg09867452			chr4:6665671-6666089	N_Shore	
hypo423	N_insufficient_1	4.3E-10	0.55	0.92	-0.37	4	59231727	cg08891829	SRD5A3	Body			
hypo424	N_insufficient_1	1.6E-05	0.59	0.88	-0.30	5	77917917	cg07228402	LHFPL2	5'UTR			
hypo425	N_insufficient_1	1.2E-11	0.51	0.86	-0.35	5	149115085	cg26876242	PPARGC1B	Body	chr5:149109570-149111750	S_Shelf	
hypo426	N_insufficient_1	2.3E-04	0.12	0.78	-0.66	6	13560875	cg12487153			chr6:30852102-30852676	N_Shelf	
hypo427	N_insufficient_1	7.3E-13	0.44	0.78	-0.34	6	30848807	cg06642647					
hypo428	N_insufficient_1	1.3E-02	0.50	0.72	-0.22	6	36492993	cg07986413	STK38	Body			
hypo429	N_insufficient_1	4.8E-10	0.62	0.91	-0.29	7	120455697	cg16969077	TSPAN12	Body			
hypo430	N_insufficient_1	1.1E-07	0.63	0.89	-0.27	7	150079014	cg15362480	ZNF775	5'UTR	chr7:150075939-150076856	S_Shelf	
hypo431	N_insufficient_1	2.5E-05	0.50	0.84	-0.34	10	3600710	cg14380840			chr10:3598475-3598930	S_Shore	
hypo432	N_insufficient_1	1.5E-05	0.09	0.89	-0.80	11	43391688	cg07515919	TTCT17	Body			
hypo433	N_insufficient_1	3.3E-04	0.41	0.78	-0.37	15	65665635	cg13614617	IGDCC3	Body	chr15:65654077-65654334	S_Shelf	
hypo434	N_insufficient_1	2.9E-05	0.77	0.93	-0.16	16	89161567	cg06419212	ACSF3;ACSF3;ACSF3	Body;5'UTR;5'UTR	chr16:89160018-89160706	S_Shore	
hypo435	N_insufficient_1	8.0E-02	0.62	0.85	-0.23	16	89162196	cg01427313	ACSF3;ACSF3;ACSF3	Body;5'UTR;5'UTR	chr16:89160018-89160706	N_Shore	
hypo436	N_insufficient_1	4.8E-02	0.65	0.89	-0.23	16	89165765	cg08316009	ACSF3;ACSF3;ACSF3	Body;5'UTR;5'UTR	chr16:89167116-89167482	N_Shore	
hypo437	N_insufficient_1	5.2E-05	0.58	0.79	-0.20	16	89167154	cg27424853	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89167116-89167482	Island	
hypo438	N_insufficient_1	3.7E-04	0.71	0.95	-0.24	16	89168371	cg01083549	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89167116-89167482	S_Shore	
hypo439	N_insufficient_1	4.0E-06	0.66	0.92	-0.26	16	89168508	cg02098559	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89167116-89167482	S_Shore	
hypo440	N_insufficient_1	2.8E-02	0.59	0.83	-0.24	16	89168599	cg04262928	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89167116-89167482	S_Shore	
hypo441	N_insufficient_1	7.7E-12	0.64	0.86	-0.22	16	89168963	cg04069539	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89167116-89167482	S_Shore	
hypo442	N_insufficient_1	1.2E-04	0.65	0.93	-0.28	16	89169744	cg01942849	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:8916763-89167991	S_Shore	
hypo443	N_insufficient_1	3.2E-03	0.88	0.98	-0.11	16	89173855	cg07116312	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89173704-89173905	Island	
hypo444	N_insufficient_1	8.5E-06	0.69	0.91	-0.22	16	89174012	cg02204831	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89173704-89173905	S_Shore	
hypo445	N_insufficient_1	3.7E-06	0.68	0.97	-0.29	16	89177293	cg00623015	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89173704-89173905	S_Shelf	
hypo446	N_insufficient_1	7.3E-02	0.65	0.95	-0.30	16	89180742	cg06934654	ACSF3;ACSF3;ACSF3	Body;Body;Body			
hypo447	N_insufficient_1	6.4E-03	0.69	0.90	-0.21	16	89183453	cg03573961	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89186198-89186551	N_Shelf	
hypo448	N_insufficient_1	8.3E-03	0.64	0.86	-0.21	16	89186454	cg00759803	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89186198-89186551	Island	
hypo449	N_insufficient_1	4.3E-02	0.66	0.84	-0.19	16	89187002	cg07235885	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89186198-89186551	S_Shore	
hypo450	N_insufficient_1	2.5E-03	0.68	0.88	-0.20	16	89189383	cg04033022	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89186198-89186551	S_Shelf	
hypo451	N_insufficient_1	3.8E-02	0.82	0.92	-0.10	16	89202817	cg02747280	ACSF3;ACSF3;ACSF3	Body;Body;Body			
hypo452	N_insufficient_1	1.5E-06	0.75	0.94	-0.19	16	89203153	cg00144414	ACSF3;ACSF3;ACSF3	Body;Body;Body			
hypo453	N_insufficient_1	8.1E-04	0.70	0.94	-0.24	16	89205832	cg00739608	ACSF3;ACSF3;ACSF3	Body;Body;Body			
hypo454	N_insufficient_1	1.8E-03	0.67	0.91	-0.23	16	89217849	cg07882423	ACSF3;ACSF3;ACSF3	Body;Body;Body	chr16:89219333-89219651	N_Shore	
hypo455	N_insufficient_1	1.6E-13	0.64	0.94	-0.30	17	80880952	cg02870816	TBCD	Body			
hypo456	N_insufficient_1	7.7E-13	0.52	0.89	-0.37	20	23584367	cg07473985	CST9	Body			
hypo457	N_insufficient_1	7.7E-12	0.60	0.91	-0.31	20	62492694	cg07272402	C20orf135;C20orf135	5'UTR;1stExon	chr20:62492649-62494249	N_Shore	
hypo458	N_insufficient_2	1.9E-04	0.82	0.93	-0.12	1	5931389	cg26661089	NHPH4	Body			
hypo459	N_insufficient_2	1.8E-02	0.85	0.98	-0.13	1	5947386	cg16430402	NHPH4	Body	chr1:5950824-5951029	N_Shelf	
hypo460	N_insufficient_2	1.1E-04	0.43	0.75	-0.32	1	12241073	cg05599723	TNFRSF1B	Body			
hypo461	N_insufficient_2	3.6E-04	0.47	0.73	-0.26	1	47688728	cg16006738	TAL1	Body	chr1:47680980-47691727	N_Shelf	
hypo462	N_insufficient_2	9.4E-06	0.76	0.92	-0.16	2	54855588	cg01502208	SPTBN1;SPTBN1	Body;Body	chr2:54856098-54856487	N_Shore	
hypo463	N_insufficient_2	1.3E-03	0.40	0.68	-0.28	3	32934782	cg22985281					
hypo464	N_insufficient_2	2.8E-10	0.50	0.81	-0.31	4	89299173	cg08684066	HERC6;HERC6	TSS1500;TSS1500	chr4:8929990-89300429	N_Shore	
hypo465	N_insufficient_2	3.0E-07	0.90	0.97	-0.07	4	188924752	cg14725631	ZFP42	Body			
hypo466	N_insufficient_2	1.7E-10	0.60	0.91	-0.30	5	5479496	cg00235313	PPAP2A;PPAP2A	Body;Body			
hypo467	N_insufficient_2	7.5E-03	0.48	0.81	-0.33	5	110088130	cg02061660	SLC25A46	Body			
hypo468	N_insufficient_2	2.0E-07	0.61	0.90	-0.28	5	157115228	cg15122603			chr5:157117149-157118379	N_Shore	
hypo469	N_insufficient_2	7.7E-11	0.51	0.88	-0.37	6	170593078	cg27614489	DLL1				

hypo512	N_insufficient_4	3.3E-06	0.87	0.97	-0.10	6	30153882	cg16012536	TRIM26	Body			
hypo513	N_insufficient_4	2.7E-04	0.79	0.90	-0.11	6	30157507	cg24443629	TRIM26	Body			
hypo514	N_insufficient_4	2.6E-03	0.83	0.94	-0.11	6	30158249	cg04110164	TRIM26	Body			
hypo515	N_insufficient_4	6.9E-02	0.78	0.87	-0.10	6	30164320	cg01782500	TRIM26	Body			
hypo516	N_insufficient_4	5.3E-02	0.79	0.90	-0.11	6	30166517	cg18901633	TRIM26	Body			
hypo517	N_insufficient_4	1.4E-02	0.78	0.87	-0.09	6	30172433	cg22272129	TRIM26	5'UTR			
hypo518	N_insufficient_4	1.2E-06	0.64	0.93	-0.28	6	74126975	cg24868643	DDX43	3'UTR			
hypo519	N_insufficient_4	3.8E-02	0.89	0.97	-0.07	7	4245514	cg26734522	SDK1,SDK1	BodyBody			
hypo520	N_insufficient_4	1.6E-05	0.10	0.47	-0.37	7	143153223	cg17045801	HECW1	Body	chr7:43152020-43153340	Island	
hypo521	N_insufficient_4	8.4E-02	0.82	0.97	-0.15	8	39380341	cg01911981	ADAM3A,ADAM3A,ADAM3A	BodyBody,Body	chr8:39330252-39380533	Island	
hypo522	N_insufficient_4	1.4E-08	0.58	0.86	-0.28	9	94178668	cg14193653	NFIL3	5'UTR			
hypo523	N_insufficient_4	6.0E-03	0.51	0.81	-0.30	10	4822998	cg23445945					
hypo524	N_insufficient_4	8.0E-10	0.52	0.83	-0.31	10	89116779	cg18516898	FAM22D	TSS1500	chr10:89114863-89115182	S_Shore	
hypo525	N_insufficient_4	3.8E-06	0.42	0.70	-0.28	10	105215053	cg09083688	CALHM1	Body	chr10:105215052-105215460	N_Shelf	
hypo526	N_insufficient_4	4.3E-04	0.87	0.97	-0.10	11	72465959	cg12598767	STAR10	Body	chr11:72465884-72466209	Island	
hypo527	N_insufficient_4	7.4E-02	0.89	0.97	-0.08	11	72466028	cg03697509	STAR10	Body	chr11:72465884-72466209	Island	
hypo528	N_insufficient_4	2.3E-06	0.45	0.77	-0.32	12	68720057	cg24599943	MDM1,MDM1	Body,3'UTR			
hypo529	N_insufficient_4	1.8E-08	0.60	0.90	-0.31	12	95048009	cg24950506			chr12:95043551-95044312	S_Shelf	
hypo530	N_insufficient_4	1.8E-08	0.66	0.89	-0.22	13	100776866	cg11183144	PCCA,PCCA	BodyBody			
hypo531	N_insufficient_4	3.7E-02	0.93	0.97	-0.04	13	100803190	cg14630369	PCCA,PCCA	BodyBody			
hypo532	N_insufficient_4	2.1E-06	0.72	0.91	-0.19	13	100927476	cg26574777	PCCA,PCCA	BodyBody			
hypo533	N_insufficient_4	8.7E-02	0.53	0.76	-0.23	13	100944053	cg11312087	PCCA,PCCA	BodyBody			
hypo534	N_insufficient_4	8.7E-09	0.76	0.93	-0.17	13	101010186	cg23228451	PCCA,PCCA	BodyBody			
hypo535	N_insufficient_4	5.3E-04	0.77	0.87	-0.10	13	101168039	cg04154116	PCCA,PCCA	BodyBody			
hypo536	N_insufficient_4	1.6E-08	0.78	0.92	-0.15	13	101171765	cg15589490	PCCA,PCCA	BodyBody			
hypo537	N_insufficient_4	2.9E-04	0.71	0.88	-0.10	13	101174098	cg08985988	PCCA,PCCA	BodyBody			
hypo538	N_insufficient_4	3.7E-02	0.86	0.94	-0.08	13	101175894	cg05327509	PCCA,PCCA	BodyBody			
hypo539	N_insufficient_4	8.1E-03	0.85	0.93	-0.08	13	101179286	cg10894626	PCCA,PCCA	BodyBody			
hypo540	N_insufficient_4	1.3E-07	0.52	0.83	-0.32	14	65104174	cg13142949					
hypo541	N_insufficient_4	3.2E-02	0.54	0.81	-0.26	14	67828531	cg11076181	EIF2S1	5'UTR	chr14:67826139-67827526	S_Shore	
hypo542	N_insufficient_4	1.8E-06	0.20	0.69	-0.49	15	30861172	cg23804921			chr15:30864782-30865586	N_Shelf	
hypo543	N_insufficient_4	7.4E-02	0.08	0.35	-0.27	15	79383852	cg25673084	RASGRF1,RASGRF1	TSS1500,TSS1500	chr15:79381804-79384209	Island	
hypo544	N_insufficient_4	2.1E-02	0.08	0.40	-0.31	15	79383858	cg11806630	RASGRF1,RASGRF1	TSS1500,TSS1500	chr15:79381804-79384209	Island	
hypo545	N_insufficient_4	3.4E-04	0.08	0.40	-0.32	15	79383980	cg13571707	RASGRF1,RASGRF1	TSS1500,TSS1500	chr15:79381804-79384209	Island	
hypo546	N_insufficient_4	4.1E-04	0.42	0.70	-0.27	16	48468609	cg03977385					
hypo547	N_insufficient_4	4.2E-11	0.57	0.89	-0.32	17	53470397	cg24943737	MMD	3'UTR			
hypo548	N_insufficient_4	9.3E-15	0.47	0.88	-0.41	17	80006003	cg27206903	RNFNG	3'UTR	chr17:80008514-80010567	N_Shelf	
hypo549	N_insufficient_4	1.9E-05	0.49	0.80	-0.30	19	49115456	cg10736770	FAM83E	Body	chr19:49116245-49116641	N_Shore	
hypo550	N_insufficient_4	2.8E-08	0.49	0.81	-0.31	19	58372914	cg11949533	ZNF587	3'UTR			
hypo551	N_insufficient_5	9.3E-03	0.57	0.79	-0.22	2	175169039	cg001330528			chr2:175190866-175192123	N_Shore	
hypo552	N_insufficient_5	6.1E-03	0.09	0.50	-0.40	3	11680536	cg22078057	VGLL4,VGLL4	BodyBody	chr3:11684132-11684930	N_Shelf	
hypo553	N_insufficient_5	2.2E-06	0.37	0.74	-0.36	3	194119885	cg13185177	GPS	5'UTR	chr3:194117601-194119898	S_Shore	
hypo554	N_insufficient_5	6.3E-03	0.41	0.73	-0.32	4	8277560	cg19303305	HTRA3	Body			
hypo555	N_insufficient_5	8.7E-04	0.20	0.45	-0.25	5	180486604	cg22418829	BTNL9	Body	chr5:180486154-180486892	Island	
hypo556	N_insufficient_5	8.8E-02	0.34	0.59	-0.25	5	180486679	cg18049690	BTNL9	Body	chr5:180486154-180486892	Island	
hypo557	N_insufficient_5	3.7E-05	0.71	0.89	-0.19	6	21078941	cg19130313	CKKAL1	Body			
hypo558	N_insufficient_5	6.8E-03	0.47	0.76	-0.29	6	97325863	cg27617159					
hypo559	N_insufficient_5	1.9E-06	0.10	0.86	-0.75	6	154821545	cg07896329	CNKSR3	Body			
hypo560	N_insufficient_5	5.1E-05	0.76	0.93	-0.17	7	1970646	cg17593934	MAD1L1,MAD1L1,MAD1L1	BodyBody,Body	chr7:1970627-1970924	Island	
hypo561	N_insufficient_5	1.4E-08	0.54	0.91	-0.38	8	71182802	cg14656774	NCOA2	5'UTR			
hypo562	N_insufficient_5	1.2E-05	0.15	0.85	-0.70	9	37780478	cg13441107	EXOSC3,EXOSC3	3'UTR,3'UTR			
hypo563	N_insufficient_5	1.6E-13	0.57	0.93	-0.36	11	2222912	cg07146321					
hypo564	N_insufficient_5	3.9E-04	0.08	0.83	-0.75	11	17825098	cg08849813	SERGEF	Body			
hypo565	N_insufficient_5	1.1E-04	0.59	0.87	-0.28	11	70305696	cg20454213			chr11:70309696-70310121	N_Shelf	
hypo566	N_insufficient_5	8.0E-11	0.50	0.86	-0.36	16	69368667	cg04413148	CTRL	TSS200	chr16:67969290-67970418	N_Shelf	
hypo567	N_insufficient_5	1.5E-17	0.13	0.83	-0.71	16	69385761	cg08627125	TMED8	TSS200			
hypo568	N_insufficient_5	7.5E-08	0.47	0.80	-0.33	17	43220208	cg19172143	ACBD4,ACBD4,ACBD4,ACBD4,A	BodyBody,Body,3'UTR,Body	chr17:43221927-43222388	N_Shore	
hypo569	N_insufficient_5	2.8E-08	0.58	0.88	-0.30	17	48251798	cg10296810	SCGA,SCGA	BodyBody			
hypo570	N_insufficient_5	3.9E-16	0.67	0.96	-0.28	17	8692024	cg21306321	MED16	Body	chr19:870774-871318	N_Shore	
hypo571	N_insufficient_5	1.4E-13	0.58	0.92	-0.34	19	44040457	cg27337277			chr19:44039232-44039756	S_Shore	
hypo572	N_insufficient_5	2.9E-07	0.48	0.81	-0.33	19	48641011	cg15550049	LIG1	Body	chr19:48640718-48641014	Island	
hypo573	N_insufficient_5	2.7E-02	0.09	0.38	-0.30	22	50164437	cg14884760			chr22:50164864-50165513	N_Shore	
hypo574	N_aequate_1	2.6E-05	0.59	0.86	-0.27	1	3810632	cg09757127	C1orf174	Body	chr1:3809490-3809236	S_Shore	
hypo575	N_aequate_1	1.6E-03	0.62	0.86	-0.24	2	16816994	cg10288578	FAM49A	5'UTR			
hypo576	N_aequate_1	8.3E-03	0.51	0.77	-0.25	4	6284031	cg16417416	WFS1,WFS1	BodyBody			
hypo577	N_aequate_1	1.8E-03	0.17	0.40	-0.23	4	187065417	cg10032668	FAM149A	TSS1500	chr4:187066155-187066460	N_Shore	
hypo578	N_aequate_1	3.4E-03	0.17	0.39	-0.21	4	187065516	cg05911003	FAM149A	TSS1500	chr4:187066155-187066460	N_Shore	
hypo579	N_aequate_1	3.3E-03	0.18	0.43	-0.25	4	187065713	cg04081326	FAM149A	TSS1500	chr4:187066155-187066460	N_Shore	
hypo580	N_aequate_1	2.7E-07	0.23	0.61	-0.38	4	187065831	cg13208832	FAM149A	TSS200	chr4:187066155-187066460	N_Shore	
hypo581	N_aequate_1	1.8E-07	0.24	0.59	-0.34	4	187065846	cg16289355	FAM149A	TSS200	chr4:187066155-187066460	N_Shore	
hypo582	N_aequate_1	4.9E-05	0.26	0.59	-0.33	4	187065940	cg08055910	FAM149A	TSS200	chr4:187066155-187066460	N_Shore	
hypo583	N_aequate_1	5.7E-04	0.21	0.57	-0.36	4	187065944	cg13136036	FAM149A	TSS200	chr4:187066155-187066460	N_Shore	
hypo584	N_aequate_1	1.7E-07	0.22	0.54	-0.33	4	187065950	cg1873491	FAM149A	TSS200	chr4:187066155-187066460	N_Shore	
hypo585	N_aequate_1	1.2E-07	0.27	0.59	-0.32	4	187065955	cg08644841	FAM149A	TSS200	chr4:187066155-187066460	N_Shore	
hypo586	N_aequate_1	1.4E-05	0.70	0.91	-0.21	5	10226648	cg08989888	FAM173B	3'UTR	chr4:187066155-187066460	N_Shore	
hypo587	N_aequate_1	1.9E-10	0.50	0.87	-0.37	6	32267990	cg21819211	PSMG4,PSMG4	3'UTR,3'UTR			
hypo588	N_aequate_1	6.2E-04	0.63	0.85	-0.23	6	70507787	cg07062388	LMBRD1	TSS1500	chr6:70506622-70507024	S_Shore	
hypo589	N_aequate_1	2.8E-04	0.81	0.91	-0.10	8	18387969	cg24613644	PSD3,PSD3	3'UTR,3'UTR			
hypo590	N_aequate_1	4.4E-05	0.53	0.79	-0.26	8	126438567	cg1889252			chr8:126441471-126443552	N_Shelf	
hypo591	N_aequate_1	9.0E-02	0.39	0.67	-0.27	10	75336540	cg15134506	USP54	TSS1500			
hypo592	N_aequate_1	3.2E-09	0.63	0.91	-0.28	10	103813206	cg04946551	C10orf76	5'UTR	chr10:103815502-103816105	N_Shelf	
hypo593	N_aequate_1	8.9E-02	0.74	0.88	-0.14	12	22688743	cg10052400	KIAA0528	Body			
hypo594	N_aequate_1	2.9E-07	0.56	0.82	-0.26	12	72246108	cg10833114	MRS2P2,TBC1D15,TBC1D15,TBK	TSS1500,Body,Body,5'UTR,Body			
hypo595	N_aequate_1	2.4E-07	0.57	0.81	-0.24	17	55540412	cg13790810	MSI2,MSI2	BodyBody			
hypo596	N_aequate_1	4.5E-03	0.56	0.80	-0.24	17	78834710	cg05249744	RPTOR,RPTOR	BodyBody	chr17:78831505-78831864	S_Shelf	
hypo597	N_aequate_1	5.3E-06	0.59	0.85	-0.26	19	49204782	cg06594736	FUT2,FUT2	5'UTR,5'UTR	chr19:49206443-49206818	N_Shore	
hypo598	N_aequate_2	6.5E-04	0.67	0.86	-0.19	1	180069210	cg24865482	CEP350	Body			
hypo599	N_aequate_2	9.8E-08	0.60	0.89	-0.29	1	211668429	cg08753273	RD3,RD3	TSS200,TSS200			
hypo600	N_aequate_2	4.0E-02	0.44	0.61	-0.18	2	44313980	cg01101677			chr2:44314288-44314564	N_Shore	
hypo601	N_aequate_2	3.4E-02											

[illegible]

[illegible]

hyp089	N_excessive_3	4.8E-02	0.66	0.82	-0.16	11	134212891	cg12128119	GLB1L2	Body		chr11:134211759-134212611	S_Shore
hyp090	N_excessive_3	9.2E-02	0.87	0.96	-0.10	13	25740027	cg02592025				chr13:25743998-25746127	N_Shelf
hyp901	N_excessive_3	2.7E-02	0.48	0.78	-0.30	13	95711745	cg14808360	ABCC4	Body			
hyp902	N_excessive_3	6.7E-02	0.91	0.97	-0.07	13	110386152	cg26573274					
hyp903	N_excessive_3	5.1E-02	0.89	0.96	-0.07	13	114023282	cg15660684				chr13:114023638-114023919	Island
hyp904	N_excessive_3	2.6E-08	0.46	0.82	-0.36	15	42162712	cg16590643	SPTBN5	Body			
hyp905	N_excessive_3	7.0E-03	0.78	0.88	-0.10	15	45412590	cg26387667	DUOX1	Body		chr15:45408573-45409528	S_Shelf
hyp906	N_excessive_3	2.3E-03	0.76	0.92	-0.17	15	57611481	cg03904104					
hyp907	N_excessive_3	1.3E-02	0.75	0.87	-0.12	16	75563114	cg025421069	CHST5	Body		chr16:75563113-75564112	Island
hyp908	N_excessive_3	3.4E-05	0.91	0.98	-0.08	17	8012578	cg11310756	ALOXE3;ALOXE3	Body,Body		chr17:8012474-8012846	Island
hyp909	N_excessive_3	1.6E-06	0.50	0.86	-0.36	17	19617253	cg16569407	SLC47A2;SLC47A2	Body,Body		chr17:19617083-19617424	Island
hyp910	N_excessive_3	8.3E-02	0.72	0.87	-0.15	17	29818175	cg24174232	RAB11FIP4	Body		chr17:29814614-29815662	S_Shelf
hyp911	N_excessive_3	3.8E-04	0.90	0.97	-0.07	17	79792777	cg26066277	DYSFIP1	1stExon		chr17:79790530-79791553	S_Shore
hyp912	N_excessive_3	7.8E-11	0.51	0.86	-0.36	17	80772942	cg06796120	TBCD	Body		chr17:80772792-80773003	Island
hyp913	N_excessive_3	1.4E-09	0.57	0.89	-0.32	18	60245587	cg13863769	ZCCHC2	3'UTR			
hyp914	N_excessive_3	7.6E-08	0.91	0.99	-0.08	19	5455843	cg22894548	ZNRF4	1stExon		chr19:5455481-5456262	Island
hyp915	N_excessive_3	3.1E-02	0.78	0.90	-0.12	19	41630815	cg07701518	CYP2F1	Body		chr19:41630485-41630794	N_Shore
hyp916	N_excessive_3	7.0E-10	0.11	0.68	-0.57	19	47123947	cg19043207	PTGIR	3'UTR		chr19:47126782-47127478	S_Shelf
hyp917	N_excessive_3	1.7E-11	0.45	0.78	-0.33	19	47341466	cg25230305	AP2S1;AP2S1	3'UTR;3'UTR			
hyp918	N_excessive_3	1.1E-05	0.91	0.98	-0.07	19	52216726	cg02261174	HAS1	Body		chr19:52216659-52217389	Island
hyp919	N_excessive_3	1.2E-06	0.45	0.73	-0.28	22	18366798	cg21563049	MICAL3;MICAL3;MICAL3	Body,Body,Body			
hyp920	N_excessive_3	4.9E-10	0.53	0.67	-0.34	22	38155575	cg22811910	TRIOBP;TRIOBP;TRIOBP	Body;3'UTR;Body			
hyp921	N_excessive_3	5.8E-03	0.88	0.97	-0.09	22	46770644	cg24986829	CELSR1	Body		chr22:46770433-46770871	Island
hyp922	N_excessive_4	4.7E-09	0.51	0.87	-0.36	1	26394001	cg44695973	TRIM63;TRIM63	1stExon;5'UTR			
hyp923	N_excessive_4	0.8E-02	0.68	0.77	-0.18	1	20186181	cg20119970				chr2:70188511-70188726	N_Shelf
hyp924	N_excessive_4	1.3E-10	0.55	0.91	-0.35	2	176042976	cg04528892	ATP5G3;ATP5G3	3'UTR;3'UTR		chr2:176045968-176046504	N_Shelf
hyp925	N_excessive_4	1.3E-02	0.79	0.89	-0.09	2	242664612	cg14409746	ING5	3'UTR		chr2:242664207-242665154	Island
hyp926	N_excessive_4	2.6E-02	0.47	0.77	-0.30	3	108191083	cg01135165	MYH15	Body			
hyp927	N_excessive_4	9.2E-10	0.60	0.90	-0.29	3	156546908	cg17778101	LEKR1	5'UTR		chr3:156543891-156544405	S_Shelf
hyp928	N_excessive_4	9.7E-10	0.51	0.85	-0.34	3	182694617	cg13265572	DCUN1D1	Body		chr3:182697749-182698731	N_Shore
hyp929	N_excessive_4	3.4E-03	0.71	0.88	-0.17	5	20306611	cg022831264				chr5:20305562-20305936	S_Shelf
hyp930	N_excessive_4	6.1E-14	0.56	0.93	-0.36	6	30026181	cg06193668	NCRNA00171	Body		chr6:30028936-30029195	N_Shelf
hyp931	N_excessive_4	9.0E-05	0.47	0.77	-0.30	6	31761062	cg10807309	VARS	Body		chr6:31763240-31763905	N_Shelf
hyp932	N_excessive_4	5.0E-05	0.59	0.93	-0.34	6	68535378	cg12086421					
hyp933	N_excessive_4	7.2E-02	0.70	0.83	-0.13	8	21937728	cg16782396	EPB49;EPB49;EPB49;EPB49;EPB49;EPB49;EPB49;EPB49	Body,Body,Body,Body,Body,Body,Body,Body			
hyp934	N_excessive_4	1.5E-14	0.51	0.90	-0.39	8	145089594	cg03722185	SPATC1;SPATC1	TSS1500;TSS1500			
hyp935	N_excessive_4	3.3E-08	0.55	0.87	-0.32	9	95993065	cg14655900	WNK2	Body			
hyp936	N_excessive_4	2.8E-04	0.60	0.85	-0.24	9	104147168	cg05770171	BAAT;BAAT;BAAT	TSS1500;1stExon;5'UTR			
hyp937	N_excessive_4	2.0E-02	0.54	0.88	-0.34	10	10202925	cg05201317					
hyp938	N_excessive_4	3.7E-02	0.12	0.84	-0.73	10	111912029	cg24051234					
hyp939	N_excessive_4	6.9E-09	0.53	0.83	-0.30	11	8761869	cg08592104	ST5;ST5;ST5	Body,Body,Body			
hyp940	N_excessive_4	1.4E-04	0.51	0.80	-0.29	12	14765994	cg27486692	GUCY2C	3'UTR			
hyp941	N_excessive_4	7.4E-12	0.55	0.91	-0.36	14	24683542	cg26407029	MDP1;CHMP4A	TSS1500		chr14:24682402-24682837	S_Shore
hyp942	N_excessive_4	5.4E-07	0.53	0.85	-0.32	14	73073497	cg18263767					
hyp943	N_excessive_4	1.6E-08	0.61	0.88	-0.26	16	31515409	cg27592424	C16orf58	Body		chr16:31519381-31519940	N_Shelf
hyp944	N_excessive_4	1.3E-07	0.59	0.93	-0.24	17	1839591	cg18059303	RTN4RL1	3'UTR		chr17:1839589-1841209	N_Shore
hyp945	N_excessive_4	0.9E-05	0.92	0.96	-0.46	19	20151528	cg13689497	NCLN	Body		chr19:3201455-3201681	Island
hyp946	N_excessive_4	1.4E-07	0.52	0.83	-0.31	20	28473327	cg13630574	VPS16;PTPRA;VPS16	Body,Body;3'UTR			
hyp947	N_excessive_5	1.1E-05	0.45	0.86	-0.41	1	9308197	cg1150353	H6PD	Body			
hyp948	N_excessive_5	4.6E-07	0.59	0.89	-0.30	2	101635691	cg07294677	RPL31;TBC1D8	3'UTR;Body			
hyp949	N_excessive_5	2.8E-06	0.52	0.82	-0.31	3	155458975	cg04078644				chr3:155461917-155462561	N_Shelf
hyp950	N_excessive_5	1.6E-10	0.54	0.87	-0.33	4	24567220	cg04436083	DHX15	Body			
hyp951	N_excessive_5	1.0E-03	0.75	0.90	-0.15	4	187524686	cg24997677	FAT1	Body			
hyp952	N_excessive_5	6.3E-03	0.72	0.89	-0.17	4	187527265	cg11972666	FAT1	Body			
hyp953	N_excessive_5	1.3E-07	0.49	0.77	-0.28	5	131599890	cg02484352	PDLM4;PDLM4	Body,Body			
hyp954	N_excessive_5	7.4E-05	0.55	0.82	-0.27	6	89340909	cg15692086	RNGTT	Body			
hyp955	N_excessive_5	5.5E-06	0.57	0.87	-0.31	6	161432631	cg25138713	MAP3K4;MAP3K4	Body,Body			
hyp956	N_excessive_5	1.2E-02	0.60	0.88	-0.28	7	3298343	cg27443265	POU6F2;POU6F2	Body,Body			
hyp957	N_excessive_5	1.6E-04	0.66	0.86	-0.20	7	39305238	cg10874881	POU6F2;POU6F2	Body,Body			
hyp958	N_excessive_5	1.9E-12	0.14	0.56	-0.42	7	94286267	cg27001184	SGCE;PEG10;SGCE;PEG10;SGT	TSS1500;5'UTR;TSS1500;5'UTR;	chr7:94284858-94286527	Island	
hyp959	N_excessive_5	3.7E-07	0.68	0.87	-0.19	7	149557121	cg01844514	ZNF862	Body		chr7:149558420-149558665	N_Shore
hyp960	N_excessive_5	2.4E-14	0.57	0.91	-0.35	8	39950015	cg10139476					
hyp961	N_excessive_5	5.5E-05	0.14	0.44	-0.30	9	86153568	cg121197878	FRMD3	TSS1500		chr9:86152533-86153777	Island
hyp962	N_excessive_5	1.1E-11	0.55	0.85	-0.30	10	71570779	cg23366779	COL13A1;COL13A1;COL13A1;CT	Body,Body			

Supplementary Table3: Full results of Gene ontology term analysis for the full and partial lists of hyper- and hypo-methylated outliers using DAVID

Hypomethylated_at [272]-outliers in Table S2: 556-genes														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0050900-regulation of defense response to virus by virus	4	0.66	1.4E-03	AP2B1, AP2A2, COB8, AP2S1	414	6	13528	16.34	9.3E-01	9.5E-01	2.1E-01		
GOTERM_BP_FAT	GO:0030329-actin cytoskeleton organization	7	2.89	1.6E-03	TROPB, PRKCZ, SHROOM2, TI	414	228	13528	2.46	9.7E-01	8.1E-01	2.7E-01		
GOTERM_BP_FAT	GO:0030329-actin filament-based process	127	2.82	3.0E-03	TROPB, PRKCZ, SHROOM2, TI	414	241	13528	2.30	1.0E-00	8.8E-01	5.4E-01		
GOTERM_BP_FAT	GO:0031333-negative regulation of protein complex assembly	6	1.00	3.5E-03	TROPB, PRKCZ, SPTBNS, SPTB1	414	34	13528	9.77	1.0E-00	8.4E-01	5.8E-01		
GOTERM_BP_FAT	GO:0030329-actin filament capping	414	22	1.35E-03	TROPB, SPTBNS, SPTBNS, SPTB1	414	22	13528	7.4	1.0E-00	8.2E-01	6.1E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0019629-actin cytoskeleton	379	16	3.4	1.3E-04	TROPB, PRKCZ, MHH1S, SPTB	379	659	12782	2.71	5.4E-01	6.5E-01	2.1E-01	
GOTERM_CC_FAT	GO:0008586-extracellular matrix	63	10.45	5.1E-04	MDM1L1, MHH1S, INTN1, FERB	379	1381	12782	1.54	1.7E-01	9.1E-02	7.0E-01		
GOTERM_CC_FAT	GO:0044443-cytosolic vesicle part	15	2.49	1.3E-03	AP2B1, AP2S1, ACTN1, SPAC	379	187	12782	2.71	4.6E-01	1.5E-01	2.6E-01		
GOTERM_CC_FAT	GO:0009991-spectrin	4	0.66	1.8E-03	EPH4L2, SPTBNS, SPTBNS, SPTB1	379	187	12782	6.80	5.1E-01	2.6E-01	2.6E-01		
GOTERM_CC_FAT	GO:0043292-contraction fiber	11	1.82	3.1E-03	HDAC4, MHH1S, NEN, SORBS2	379	121	12782	3.07	6.9E-01	2.1E-01	4.2E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0008092-cytoskeletal protein binding	37	6.14	4.1E-06	TROPB, MHH1S, SHROOM2, AI	411	504	12983	2.32	2.5E-03	2.5E-03	6.1E-01		
GOTERM_MF_FAT	GO:0003719-actin binding	23	3.81	6.9E-02	TROPB, SHROOM2, MHH1S, S	411	305	12983	2.32	1.4E-01	1.0E-01	1.0E-01		
GOTERM_MF_FAT	GO:0003719-actin binding	24	3.98	6.7E-02	GIT1, SERGEF, ABR, ARHGEP1	411	305	12983	1.88	9.5E-01	6.2E-01	1.0E-01		
GOTERM_MF_FAT	GO:0060289-nucleoside-triphosphatase regulator activity	41	6.38	6.1E-03	GIT1, SERGEF, ABR, ARHGEP1	411	413	12983	1.84	9.8E-01	6.1E-01	1.0E-01		
GOTERM_MF_FAT	GO:0005000-actin GTPase regulator activity	18	2.99	6.3E-03	GIT1, SERGEF, ABR, ARHGEP1	411	274	12983	2.08	9.8E-01	5.4E-01	8.2E-01		
Hypomethylated_delta-beta >0.2-729-outliers_483-genes														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0030329-actin cytoskeleton organization	16	3.33	4.1E-04	PRKCZ, TROPB, SHROOM2, TI	329	138	13528	2.71	5.4E-01	6.4E-01	2.1E-01		
GOTERM_BP_FAT	GO:0050900-regulation of defense response to virus by virus	4	0.83	7.2E-03	AP2B1, AP2A2, COB8, AP2S1	329	8	13528	20.56	7.4E-01	4.8E-01	1.2E-01		
GOTERM_BP_FAT	GO:0030329-actin filament-based process	16	3.33	8.1E-04	TROPB, PRKCZ, SHROOM2, TI	329	241	13528	2.73	7.8E-01	4.0E-01	4.4E-01		
GOTERM_BP_FAT	GO:0030329-actin filament capping	20	4.16	3.8E-03	DNAH1, SHROOM2, KTNBL1	329	307	13528	2.07	1	8.4E-01	6.4E-01		
GOTERM_BP_FAT	GO:0003231-regulation of response to biotic stimulus	5	1.04	5.0E-03	PVR, AP2B1, AP2A2, COB8, AP	329	29	13528	7.09	1	8.8E-01	8.2E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0019629-actin cytoskeleton	18	3.74	2.0E-04	TROPB, PRKCZ, MHH1S, SPTB	300	269	12782	2.85	7.0E-02	7.0E-02	2.8E-01		
GOTERM_CC_FAT	GO:0044443-cytosolic vesicle part	13	2.70	1.5E-03	AP2B1, AP2S1, ACTN1, SPAC	300	187	12782	4.96	4.2E-01	2.4E-01	2.0E-01		
GOTERM_CC_FAT	GO:0009991-spectrin	10	10.40	1.8E-03	MDM1L1, MHH1S, INTN1, FERB	300	1381	12782	1.54	4.5E-01	2.0E-01	2.0E-01		
GOTERM_CC_FAT	GO:0043292-contraction fiber	10	2.08	2.1E-03	HDAC4, MHH1S, NEN, SORBS2	300	121	12782	3.52	5.9E-01	1.7E-01	2.6E-01		
GOTERM_CC_FAT	GO:0030376-myofibril	9	1.87	4.5E-03	HDAC4, MHH1S, NEN, SORBS2	300	111	12782	3.45	8.0E-01	2.8E-01	6.0E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0008092-cytoskeletal protein binding	30	6.23	3.3E-05	TROPB, MHH1S, SHROOM2, AI	330	407	12983	2.34	1.9E-02	1.9E-02	8.9E-01		
GOTERM_MF_FAT	GO:0030329-actin/bonded/cytoskeleton binding	59	12.27	6.1E-04	ACDYL1, SPOT1, MHH1S, STK38.1	330	1407	12983	1.55	2.9E-01	1.6E-01	8.9E-01		
GOTERM_MF_FAT	GO:0037197-actin binding	34	6.40	6.6E-04	TROPB, SHROOM2, MHH1S, S	330	326	12983	2.41	3.1E-01	2.1E-01	8.9E-01		
GOTERM_MF_FAT	GO:0003719-actin binding	34	6.40	6.6E-04	ACDYL1, SPOT1, MHH1S, STK38.1	330	1407	12983	1.55	2.9E-01	1.6E-01	8.9E-01		
GOTERM_MF_FAT	GO:0005224-ATP binding	58	12.06	7.6E-04	ACDYL1, SPOT1, MHH1S, STK38.1	330	1477	12983	1.54	3.5E-01	8.2E-02	1.1E-01		
Hypomethylated_TSS-188-outliers_155-genes														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0030310-regulation of BMP signaling pathway	3	1.94	1.8E-02	RGMA, SOST, PCSK6	89	30	13528	15.20	1	1	2.2E-01		
GOTERM_BP_FAT	GO:0022037-metamorphosis development	8	3.14	2.2E-02	HOBX1, NDC80, CACNA1A	89	35	13528	13.03	1	1	2.5E-01		
GOTERM_BP_FAT	GO:0007016-actin polymerization	8	5.16	3.3E-02	ATN1, SNA2, NPY, PPP2R	89	63	13528	2.59	1	1	3.1E-01		
GOTERM_BP_FAT	GO:0021638-icosahedron binding	6	3.87	3.3E-02	ATN1, SNA2, PPP2R, CACNA1A	89	274	13528	3.33	1	1	4.0E-01		
GOTERM_BP_FAT	GO:0021548-pore binding	2	1.29	3.8E-02	HOBX1, CACNA1A	89	6	13528	50.67	1	1	4.0E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0005000-neuron projection	8	3.87	7.4E-02	NRXN1, CANX1, ANK3, RASGRF	85	242	12782	2.54	1	1	6.2E-01		
GOTERM_CC_FAT	GO:0042101-1-cell receptor complex	2	1.29	7.6E-02	CD84, COB8	85	12	12782	25.06	1	1	6.2E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0008267-enzyme inhibitor activity	7	4.52	1.2E-02	CSTF1, SRSF10, SNAI2, CACNA1A	93	270	12983	3.12	9.8E-01	3.8E-01	1.5E-01		
GOTERM_MF_FAT	GO:0008092-cytoskeletal protein binding	8	5.16	6.6E-02	FRMD3, NRXN1, SNAI2, SNAI2	93	504	12983	2.22	1	1	5.9E-01		
Hypomethylated_clustered_105-outliers_26-genes														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0000210-cell death	4	14.29	3.6E-02	NLRP3, RASGRF1, ARHGEP1	17	719	13528	4.43	1	1	5.2E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0005759-mitochondrial associated complex	9	2.9	2.5E-02	DNAH11, DNAH10, NPNP4, SP9	193	234	12782	2.55	1	9.9E-01	2.8E-01		
GOTERM_CC_FAT	GO:0031980-mitochondrial lumen	8	2.5	5.5E-02	MCCO2, NAGS, SLCUG2, HSPE	193	227	12782	2.33	1	9.9E-01	5.2E-01		
GOTERM_CC_FAT	GO:0005759-mitochondrial matrix	8	2.5	5.5E-02	MCCO2, NAGS, SLCUG2, HSPE	193	227	12782	2.33	1	9.9E-01	5.2E-01		
GOTERM_CC_FAT	GO:0031012-extracellular matrix	10	3.2	7.8E-02	FLRT3, COL4A3, ADAMT19, P	193	345	12782	1.92	1	9.9E-01	6.4E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0037000-transcription factor activity	34	10.8	4.4E-05	HMO2, ZNF132, PA6B, MYEF2, L	212	975	12983	2.14	1.6E-02	1.6E-02	6.0E-02		
GOTERM_MF_FAT	GO:0043565-sequence-specific DNA binding	21	7.3	2.6E-04	FOSL2, HMO2, ESR1, PA6B, ZH	212	607	12983	2.32	1.2E-01	6.2E-02	1.5E-01		
GOTERM_MF_FAT	GO:0036771-DNA binding	59	18.7	3.7E-04	HMO2, ZNF518B, ZNF583, PA6B	212	2331	12983	1.55	1.3E-01	4.6E-02	5.1E-01		
GOTERM_MF_FAT	GO:0030528-transcription regulator activity	40	12.7	2.2E-03	HMO2, ZNF132, PA6B, MYEF2, L	212	1512	12983	1.62	5.7E-01	1.9E-01	3.1E-01		
GOTERM_MF_FAT	GO:0051598-insulin receptor binding	4	1.3	1.0E-02	IRS2, DOK6, DOK7, IRS1	212	28	12983	8.75	9.8E-01	5.4E-01	1.3E-01		
Hypomethylated_delta-beta >0.2&TSS&clustered_419-outliers_163-genes														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0006355-regulation of transcription, DNA-dependent	36	22.1	3.3E-06	HMO2, ZNF583, ZNF585, PA6B	122	1773	13528	2.25	3.8E-03	3.8E-03	5.2E-03		
GOTERM_BP_FAT	GO:0051252-regulation of RNA metabolic process	36	22.1	4.4E-06	HMO2, ZNF583, ZNF585, PA6B	122	1813	13528	2.20	4.5E-03	4.5E-03	6.0E-03		
GOTERM_BP_FAT	GO:0045449-regulation of transcription	44	27.0	1.7E-05	HMO2, ZNF583, ZNF518B, ZNF8	122	2601	13528	1.85	2.0E-02	6.8E-03	2.6E-02		
GOTERM_BP_FAT	GO:0006350-transcription	38	23.3	2.2E-05	HMO2, ZNF518B, ZNF583, ZNF8	122	2101	13528	2.01	2.6E-02	6.5E-03	3.6E-02		
GOTERM_BP_FAT	GO:0051785-response to protein stimulus	5	3.1	1.6E-02	HSPA2, MAP1B, HSPA1F, HSPD1	122	107	13528	5.18	1	9.7E-01	2.2E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0005759-mitochondrial associated complex	9	2.9	2.5E-02	DNAH11, DNAH10, NPNP4, SP9	193	234	12782	2.55	1	9.9E-01	2.8E-01		
GOTERM_CC_FAT	GO:0031980-mitochondrial lumen	8	2.5	5.5E-02	MCCO2, NAGS, SLCUG2, HSPE	193	227	12782	2.33	1	9.9E-01	5.2E-01		
GOTERM_CC_FAT	GO:0005759-mitochondrial matrix	8	2.5	5.5E-02	MCCO2, NAGS, SLCUG2, HSPE	193	227	12782	2.33	1	9.9E-01	5.2E-01		
GOTERM_CC_FAT	GO:0031012-extracellular matrix	10	3.2	7.8E-02	FLRT3, COL4A3, ADAMT19, P	193	345	12782	1.92	1	9.9E-01	6.4E-01		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0037000-transcription factor activity	34	10.8	4.4E-05	HMO2, ZNF132, PA6B, MYEF2, L	212	975	12983	2.14	1.6E-02	1.6E-02	6.0E-02		
GOTERM_MF_FAT	GO:0043565-sequence-specific DNA binding	21	7.3	2.6										

Supplementary Table 4: additional clinical informaton of the subjects

Subject ^a	BMI		Body weight (kg)		Gestational weght gain (kg)	Maternal complication ^b	Gestational week ^c	Caesarean section ^d		Newborn's gender	# of methylated outliers	
	pre-pregnancy	at delivery	pre-pregnancy	at delivery				Yes/No	Reason		hyper	hypo
FGR_insufficient_1	8.0	18.3	43.0	45.1	2.1		37	N		female	53	44
FGR_insufficient_2	20.0	21.1	57.0	60.4	3.4		35	Y	growth arrest	male	106	32
FGR_insufficient_3	17.6	19.6	44.0	49.0	5.0		37	N		male	105	30
FGR_insufficient_4	19.5	21.3	53.0	58.1	5.1		34	Y	growth arrest	female	60	29
FGR_insufficient_5	19.1	21.7	50.0	56.9	6.9		36	N		female	27	28
FGR_adequate_1	20.0	23.3	45.0	52.5	7.5		37	Y	due to previous caesarean delivery	female	44	23
FGR_adequate_2	17.9	21.0	43.0	50.5	7.5		37	Y	due to previous caesarean delivery	female	36	21
FGR_adequate_3	18.7	21.6	51.0	58.7	7.7		35	N		male	137	40
FGR_adequate_4	22.6	25.8	56.5	64.5	8.0		37	N		male	88	14
FGR_adequate_5	22.0	26.6	49.6	59.8	10.2		39	Y	request without clinical indication	female	34	18
FGR_excesive_1	18.4	23.5	46.0	58.8	12.8		32	Y	subamniotic hematoma	female	154	52
FGR_excesive_2	19.0	24.4	45.0	57.8	12.8		37	N		female	59	34
FGR_excesive_3	20.1	25.8	49.0	62.8	13.8		37	Y	breech presentation	female	21	23
FGR_excesive_4	20.7	27.3	46.0	60.5	14.5		39	N		female	41	30
Normal_insufficient_1	20.8	23.2	48.0	53.6	5.6	depression	41	N		female	382	39
Normal_insufficient_2	23.0	25.3	59.0	64.7	5.7		41	Y	arrest of labor	female	78	24
Normal_insufficient_3	19.1	21.6	49.0	55.2	6.2		37	N		female	146	22
Normal_insufficient_4	17.5	20.5	41.0	47.9	6.9		39	N		male	84	47
Normal_insufficient_5	18.1	21.1	43.0	50.0	7.0		40	N		female	55	23
Normal_adequate_1	22.6	25.5	56.5	63.6	7.1		40	N		male	40	24
Normal_adequate_2	20.1	23.0	51.5	59.0	7.5		38	N		female	40	28
Normal_adequate_3	22.9	26.2	55.0	63.0	8.0		35	N		male	23	23
Normal_adequate_4	20.7	24.1	53.0	61.6	8.6		38	N		male	43	24
Normal_adequate_5	18.0	21.0	52.0	60.7	8.7		39	N		male	42	18
Normal_adequate_6	20.1	23.3	54.0	62.8	8.8		37	Y	congenital dislocation of the hip	female	18	38
Normal_adequate_7	17.3	21.5	39.0	48.4	9.4		40	N		female	54	9
Normal_adequate_8	19.4	23.7	46.0	56.2	10.2		39	N		male	33	23
Normal_adequate_9	19.6	23.4	52.0	62.2	10.2		36	Y	due to previous caesarean delivery	male	46	28
Normal_excesive_1	20.5	26.1	50.0	63.5	13.5		40	N		male	54	43
Normal_excesive_2	19.2	24.8	48.0	61.8	13.8		41	N		male	80	27
Normal_excesive_3	20.7	26.1	57.0	71.9	14.9	autoimmune hepatitis	38	N		male	62	63
Normal_excesive_4	20.4	26.7	49.0	64.2	15.2		40	N		female	54	25
Normal_excesive_5	18.0	23.8	49.0	64.9	15.9	pituitary adenoma	39	Y	request without clinical indication	female	222	31

^a All subjects did not smoke or drink alcohol during pregnancy.

^b Women with pregnancy complications of gestational diabetes, pre-eclampsia, and pregnancy-induced hypertension were not enrolled in this study. Maternal complications other than GDM, PE, and PIH are listed.

^c No statistically significant correlation was detected between gestational weeks and the numbers of hyper- and hypomethylated outliers. The preason's correlation coefficient (and p-value) were 0.094 (0.602) for hypermethylated outliers and 0.038 (0.832) for hypomethylated outliers.

^d No statistically dignificant difference was detected for the numbers of hyper- and hypomethylated outliers between the C-section group (n=11) and vaginal delivery group (n=22). The Wilcoxon rank sum test p-values were 0.479 for hypermethylated outliers and 0.632 for hypomethyltaed outliers.