supplement.pdf

Figure S1: Possible location of a CGI with regard to the CCDS.
Figures S2-S29: Histograms of read methylation of all 14 candidate CGIs (both methylomes).
Figures S30-S34: IGV screen shots of the five CGIs studied in detail (methylome 1).
Table S4: Primer sequences.
Table S5.1-S5.3: Deep bisulfite methylation analysis in monocyte DNA samples from heterozygous individuals (*ASRGL1*, *PARP11*, *PDXDC1*)

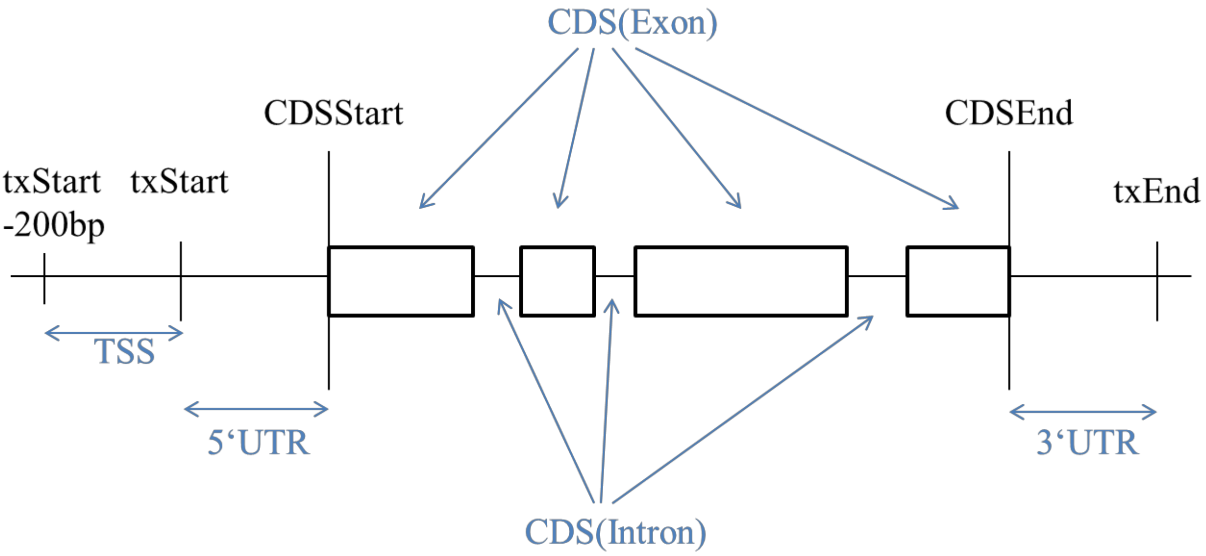

Fig. S1: Possible location of a CGI with regard to the CCDS. In black, a schematic view of a CCDS containing transcription start (txStart), start of the CDS (CDSStart), end of the CDS (CDSEnd) and the transcription end (txEnd). Five classes for CGI characterisation are defined, where a CGI can overlap no, one or more classes. The classes are (visualised in blue): TSS (the 200 bp region upstream of the transcription start site), 5’UTR, CDS(Exon), CDS(Intron) and 3’UTR.

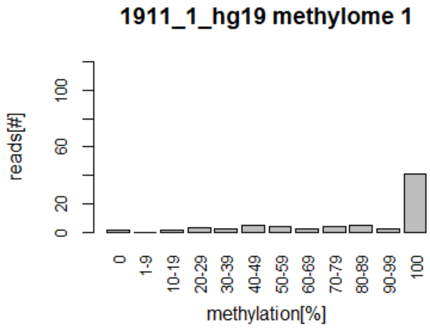
1911_1_hg19 methylome 1

Fig. S2: Read methylation 1911_1_hg19 (methylome 1)

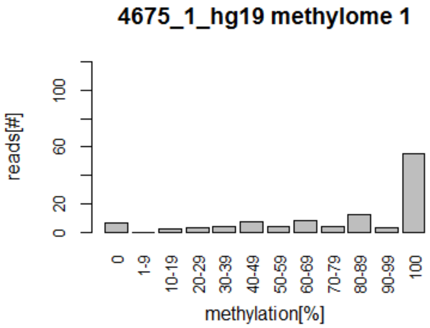
4675_1_hg19 methylome 1

Fig. S3: Read methylation 4675_1_hg19 (methylome 1)

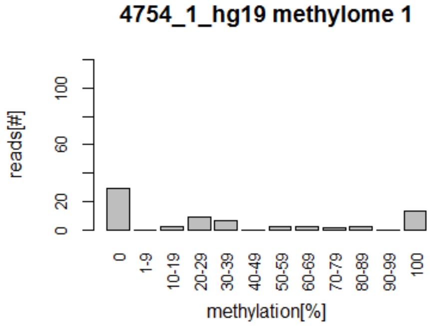
4754_1_hg19 methylome 1

Fig. S4: Read methylation 4754_1_hg19 (methylome 1)

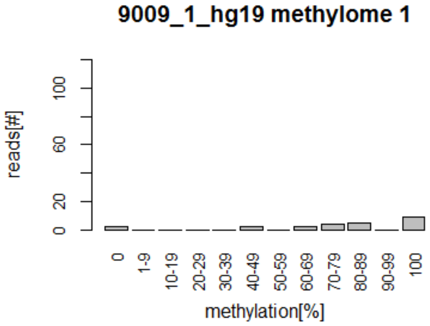
9009_1_hg19 methylome 1

Fig. S5: Read methylation 9009_1_hg19 (methylome 1)

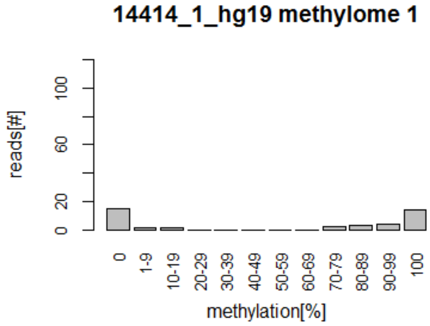
14414_1_hg19 methylome 1

Fig. S6: Read methylation 14414_1_hg19 (methylome 1)

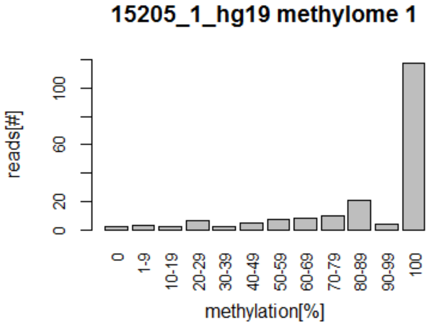
15205_1_hg19 methylome 1

Fig. S7: Read methylation 15205_1_hg19 (methylome 1)

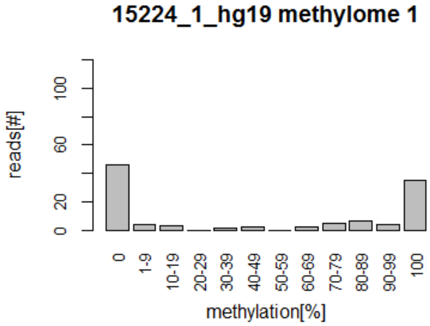
15224_1_hg19 methylome 1

Fig. S8: Read methylation 15224_1_hg19 (methylome 1)

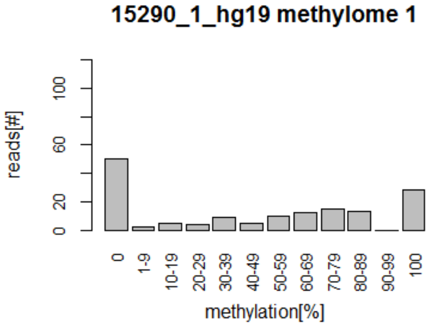
15290_1_hg19 methylome 1

Fig. S9: Read methylation 15290_1_hg19 (methylome 1)

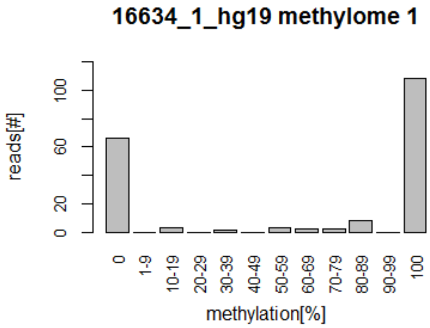

Fig. S10: Read methylation 16634_1_hg19 (methylome 1)

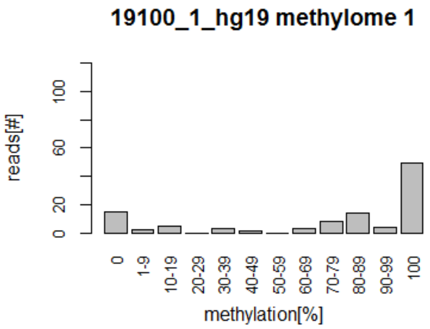

Fig. S11: Read methylation 19100_1_hg19 (methylome 1)

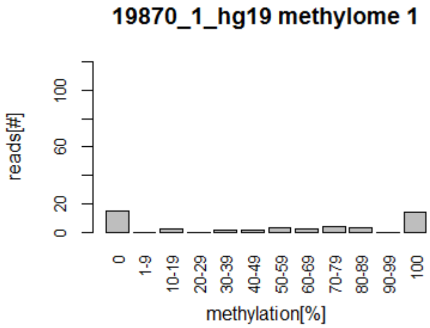

Fig. S12: Read methylation 19870_1_hg19 (methylome 1)

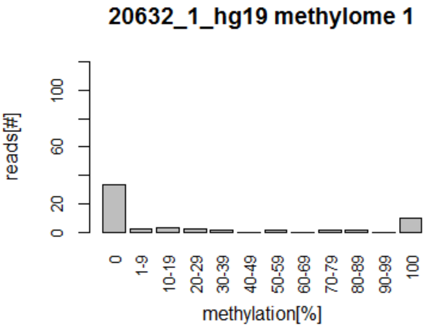

Fig. S13: Read methylation 20632_1_hg19 (methylome 1)

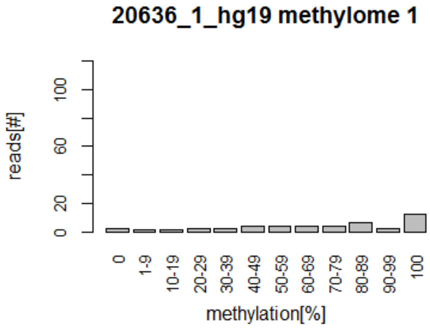

Fig. S14: Read methylation 20636_1_hg19 (methylome 1)

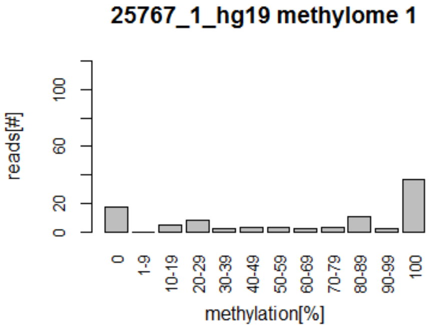

Fig. S15: Read methylation 25767_1_hg19 (methylome 1)

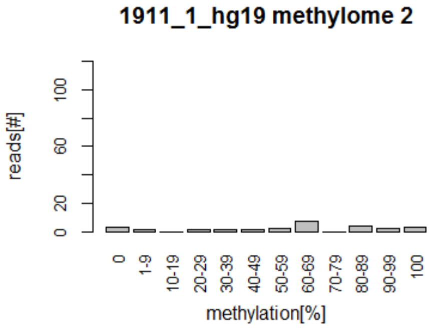

Fig. S16: Read methylation 1911_1_hg19 (methylome 2)

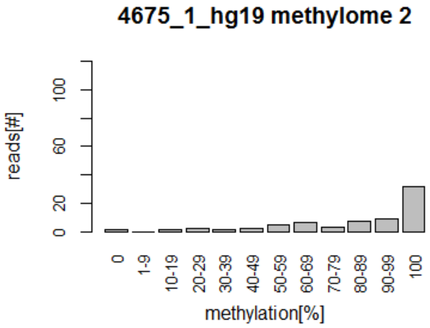

Fig. S17: Read methylation 4675_1_hg19 (methylome 2)

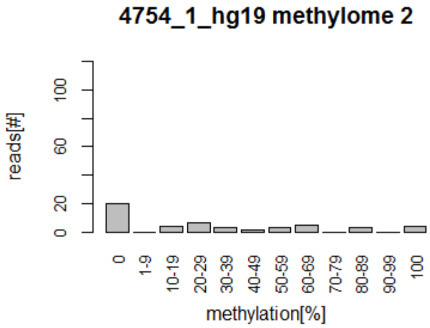

Fig. S18: Read methylation 4754_1_hg19 (methylome 2)

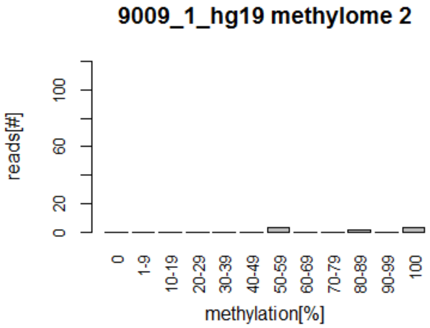

Fig. S19: Read methylation 9009_1_hg19 (methylome 2)

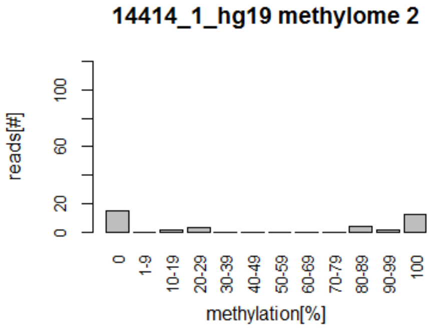

Fig. S20: Read methylation 14414_1_hg19 (methylome 2)

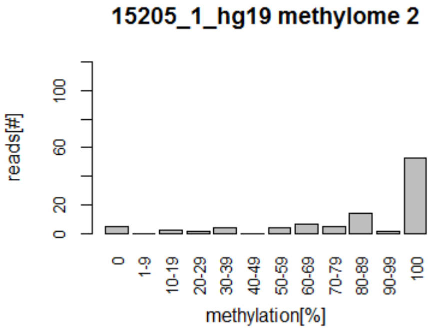

Fig. S21: Read methylation 15205_1_hg19 (methylome 2)

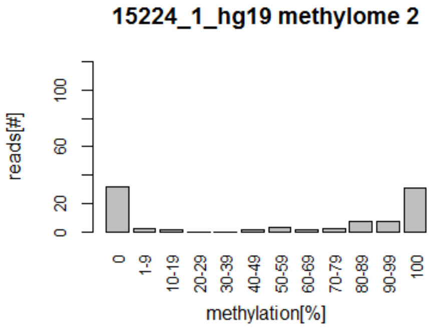

Fig. S22: Read methylation 15224_1_hg19 (methylome 2)

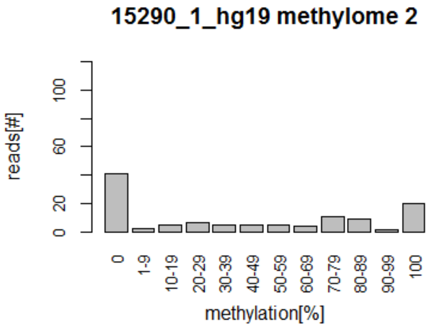

Fig. S23: Read methylation 15290_1_hg19 (methylome 2)

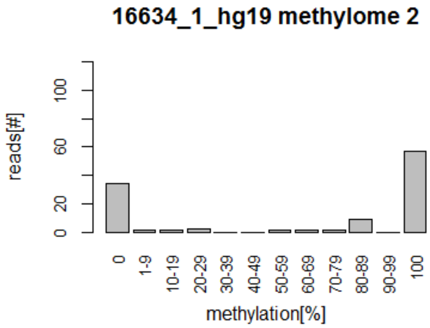

Fig. S24: Read methylation 16634_1_hg19 (methylome 2)

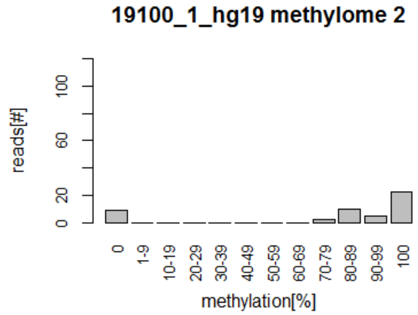

Fig. S25: Read methylation 19100_1_hg19 (methylome 2)

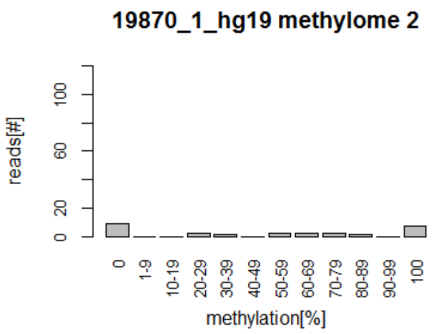

Fig. S26: Read methylation 19870_1_hg19 (methylome 2)

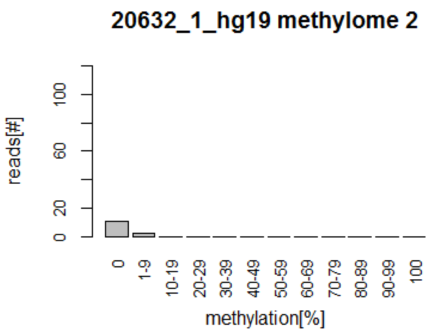

Fig. S27: Read methylation 20632_1_hg19 (methylome 2)

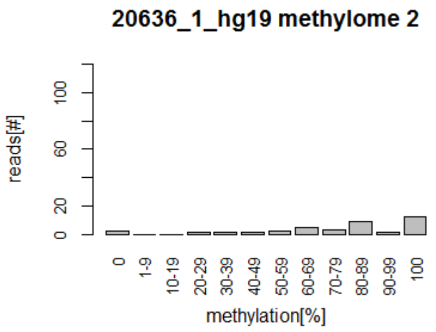

Fig. S28: Read methylation 20636_1_hg19 (methylome 2)

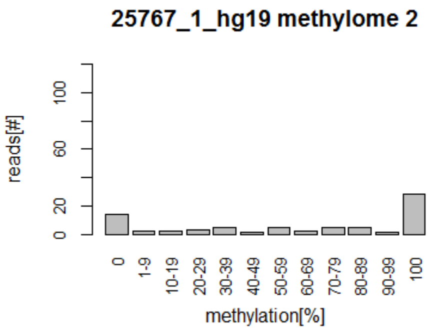

Fig. S29: Read methylation 25767_1_hg19 (methylome 2)

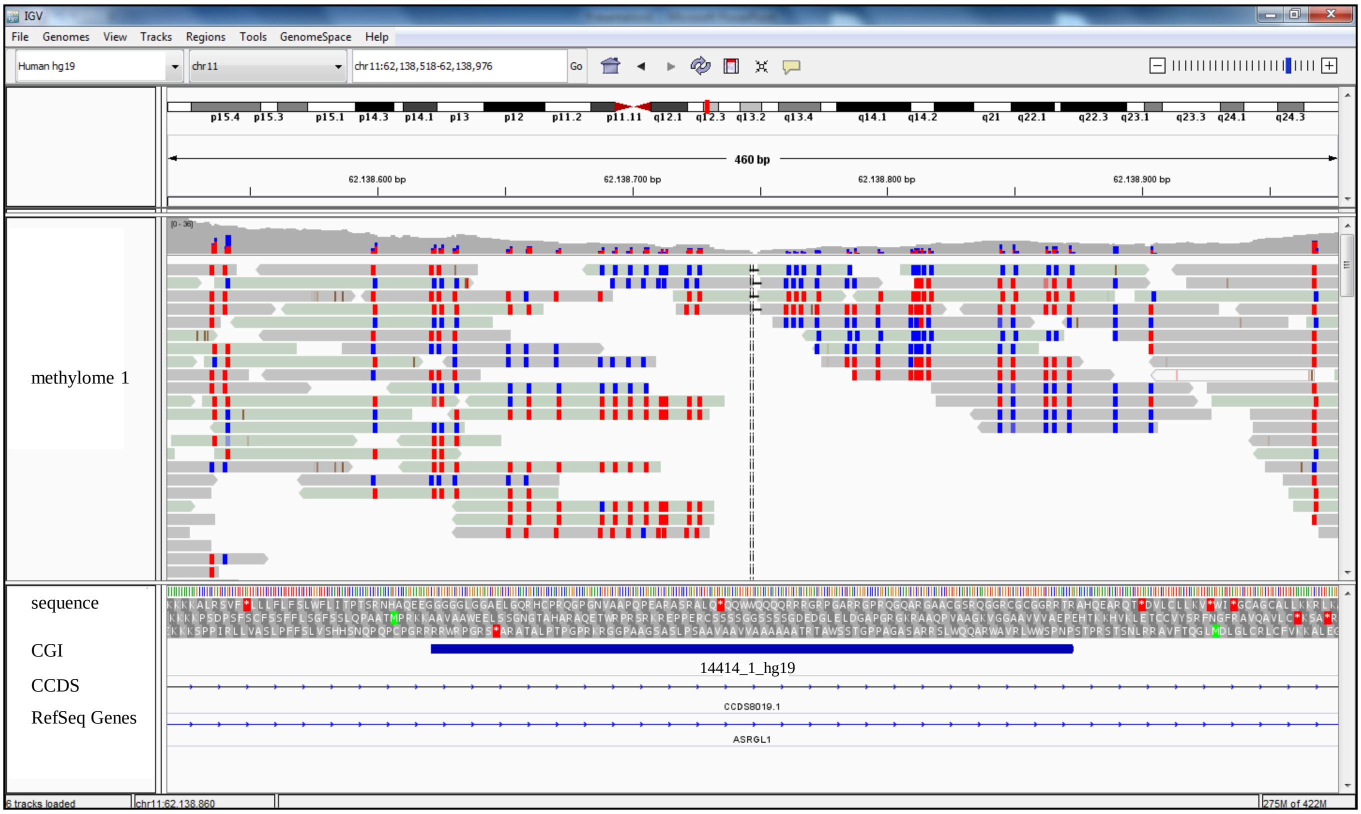

Fig. S30: Screenshot IGV Browser of CGI 14414_1_hg19 (*ASRGL1*)

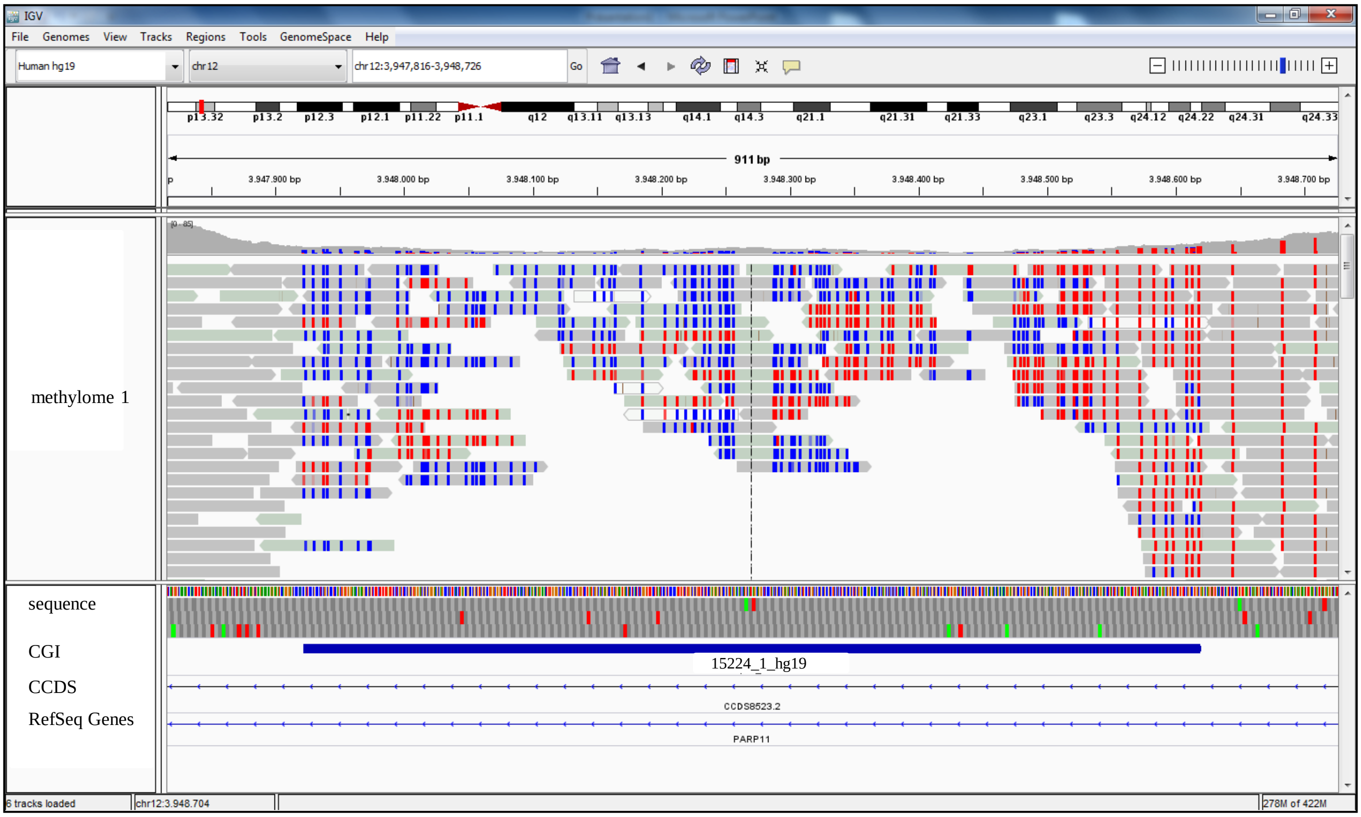

Fig. S31: Screenshot IGV Browser of CGI 15224_1_hg19 (*PARP11*)

Fig. S32: Screenshot IGV Browser of CGI 16634_1_hg19 (*RB1*)

Fig. S33: Screenshot IGV Browser of CGI 19100_1_hg19 (*PDXDC1*)

Fig. S34: Screenshot IGV Browser of CGI 20632_1_hg19 (*MYO1D*)

Table S4: Primer sequences.

Primer name	Primer sequence (5‘-3‘)	Tm (°C)	Product size (bp)
Genomic sequence analysis			
PDXDC1-CpG69-F	TGCACGAAGGGCACAAAGTC	68	382
PDXDC1-CpG69-R	CGATGTGGCTACAGCAGG		
PARP11-CpG88-F2	CTGGCCATGTGGGGCTAG	64	353
PARP11-CpG88-R	ACCCATTCCTGTGGATTTTC		
ASRGL1-CpG28-F	TCAAAAGCTCCCCTTTGCAC	64	516
ASRGL1-CpG28-R3	CTGGTTTCTCATCACTCCAA		
Deep bisulfite sequencing (universal tags in **bold**)			
PDXDC1-CpG69-Ftag	**CTTGCTTCCTGGCACGAG**GTTGTAYGAAGGGTATAAAGTT	50	421
PDXDC1-CpG69-RM13	**CAGGAAACAGCTATGAC**CCCRATATAACTACAACAAAA		
PARP11-CpG88-Ftag	**CTTGCTTCCTGGCACGAG**TTGGTTATGTGGGGTTAGTTTT	56	388
PARP11-CpG88-RM13	**CAGGAAACAGCTATGAC**ACCCATTCCTATAAATTTTCCA		
ASRGL1-CpG28-Ftag	**CTTGCTTCCTGGCACGAG**TTTTTTGTATTTTGTGAGGAAGT	56	543
ASRGL1-CpG28-RM13	**CAGGAAACAGCTATGAC**CTCTAATTTCTCATCACTCCAA		

Table S5.1: Methylation levels in heterozygous monocyte samples for *ASRGL1*

ASRGL1				
sample	**genotype**	**methylation level**		
		total	**allele G**	**allele A**
R2	A/G	90%	93%	79%
R4	A/G	93%	93%	94%
R6	A/G	96%	96%	97%
R8	A/G	90%	92%	86%
R10	A/G	88%	85%	91%
R11	A/G	78%	77%	82%
R14	A/G	95%	94%	97%
R15	A/G	78%	36%	93%
R17	A/G	93%	93%	94%
P1	A/G	76%	73%	78%
P2	A/G	73%	54%	90%
P3	A/G	90%	82%	93%
K1	A/G	75%	63%	92%
K2	A/G	90%	89%	91%

Table S5.2: Methylation levels in heterozygous monocyte samples for *PARP11*

PARP11				
sample	**genotype**	**methylation level**		
		total	**allele G**	**allele A**
R1	A/G	83%	84%	83%
R2	A/G	68%	75%	59%
R3	A/G	79%	81%	77%
R4	A/G	80%	81%	78%
R7	A/G	72%	71%	73%
R9	A/G	70%	74%	65%
R10	A/G	84%	82%	87%
R11	A/G	74%	73%	75%
R13	A/G	76%	71%	79%
R16	A/G	80%	80%	79%
K1	A/G	73%	73%	72%
K2	A/G	72%	73%	72%

Table S5.3: Methylation levels in heterozygous monocyte samples for *PDXDC1*

PDXDC1				
sample	**genotype**	**methylation level**		
		total	**allele A**	**allele C**
R1	A/C	68%	91%	4%
R2	A/C	61%	66%	57%
R3	A/C	70%	87%	55%
R6	A/C	61%	75%	15%
R7	A/C	54%	77%	61%
R8	A/C	73%	77%	62%
R9	A/C	55%	90%	31%
R10	A/C	80%	90%	71%
R11	A/C	69%	79%	48%
R13	A/C	61%	90%	42%
R14	A/C	77%	70%	83%
R17	A/C	76%	90%	63%
K1	A/C	59%	87%	28%
K2	A/C	53%	90%	19%