Table S1

DMR coordinates	MeDIP UN hypo/hyper methylated	Sperm methylation	Blastocyst methylation (*26*)
DMR18:MMU12:109478201-109478700	Hypo	Ctrl=90% UN=91%	25.8%
DMR19:MMU12:112549801-112550300	Hypo	Ctrl=99% UN=99%	23.1%
DMR20:MMU12:109475001-109475500	Hypo	Ctrl=74% UN=85%	33.5%
DMR21: MMU2:167694001-167694500	Hypo	Ctrl=96% UN=96%	6.3%
DMR22: MMU18:80774801-80775300	Hypo	Ctrl=97% UN=96%	5.7%
DMR23: MMU15:4809001-4809500	Hypo	Ctrl=75% UN=75%	Not assessed
DMR24: MMU2:127151801-127152300	Hypo	Ctrl=76% UN=87%	19.9%
DMR25: MMU12:71964401-71964900	Hyper	Ctrl=74% UN=74%	33.3%
DMR26: MMU7:53400801-53401300	Hyper	Ctrl=98% UN=97%	9.2%
DMR27: MMU1:170174001-170174300	Hyper	Ctrl=94% UN=94%	19.6%
DMR28: MMU2:126409801-126410300	Hyper	Ctrl=100% UN=100%	3.3%
DMR29: MMU2:126435401-126435700	Hyper	Ctrl=95% UN=97%	25
DMR30: MMU1:187298601-187299100	Hyper	Ctrl=95% UN=95%	5.6%
DMR31: MMU5:137955601-137956100	Hyper	Ctrl=50% UN=51%	22.8%
DMR32: MMU4:106155201-106155700	Hyper	Ctrl=93% UN=93%	11.4%

Table S1: Bisulphite mutagenesis analysis of putative DMRs that failed to validate.
Bisulphite mutagenesis combined with pyrosequencing was used to calculate the absolute level of methylation in C and UN F1 sperm at putative DMRs identified by MeDIP-seq. Controls n=12, 5 litters; UN n=11, 4 litters. Note that those loci verified to have differential methylation are provided in Table 1; the above putative DMRs did not demonstrate differential methylation using pyrosequencing analysis. (Blastocyst methylation level extracted from data presented by Kobayashi *et al. 2012*.)