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Supplementary Figure Legends

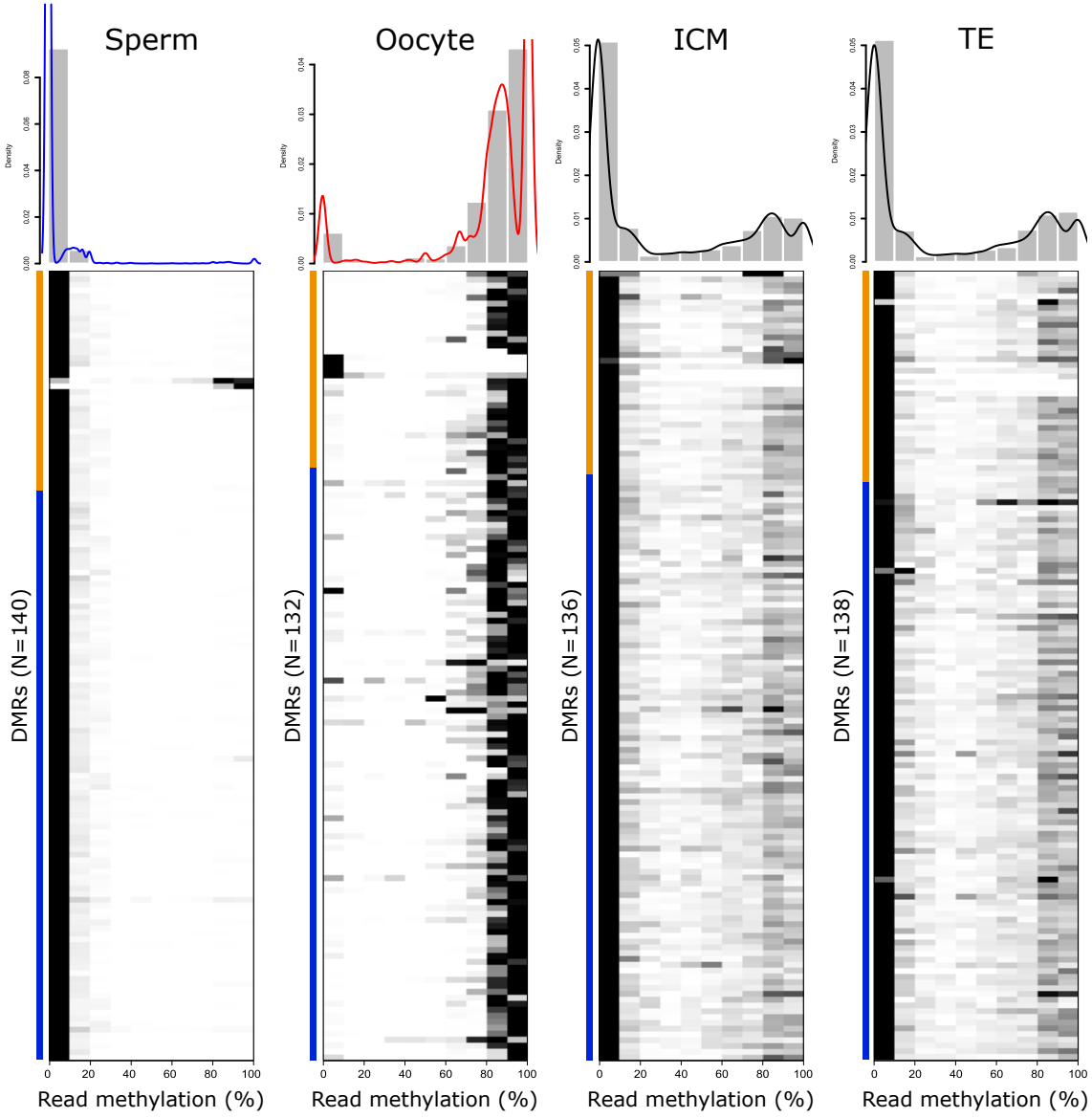
Supplementary Figure 1. DNA methylation was averaged across reads with ≥5 CpGs from RRBS in sperm, oocyte, inner cell mass (ICM) and trophectoderm (TE). Distribution of DNA methylation across DMRs (binned in 10% intervals) is shown in the density plot with a density heat map shows the distribution across each known (yellow) and novel (blue) DMR below in grey scale. DMRs with a minimum read depth of 5 were reported.

Supplementary Figure 2. Distribution of DNA methylation at orthologous regions to the human known DMRs (yellow) and novel (blue) placental-specific DMRs is shown in mouse gametes, inner cell mass, trophectoderm, epiblast, extra-embryonic ectoderm, placenta and somatic tissues (heart, liver, brain). Orthologous regions in the mouse genome were identified using the LiftOver tool in the UCSC Genome Browser. White boxes in the heat map indicate DMRs for which there was no data; DMRs with no data in ≥9 (80%) samples were omitted.

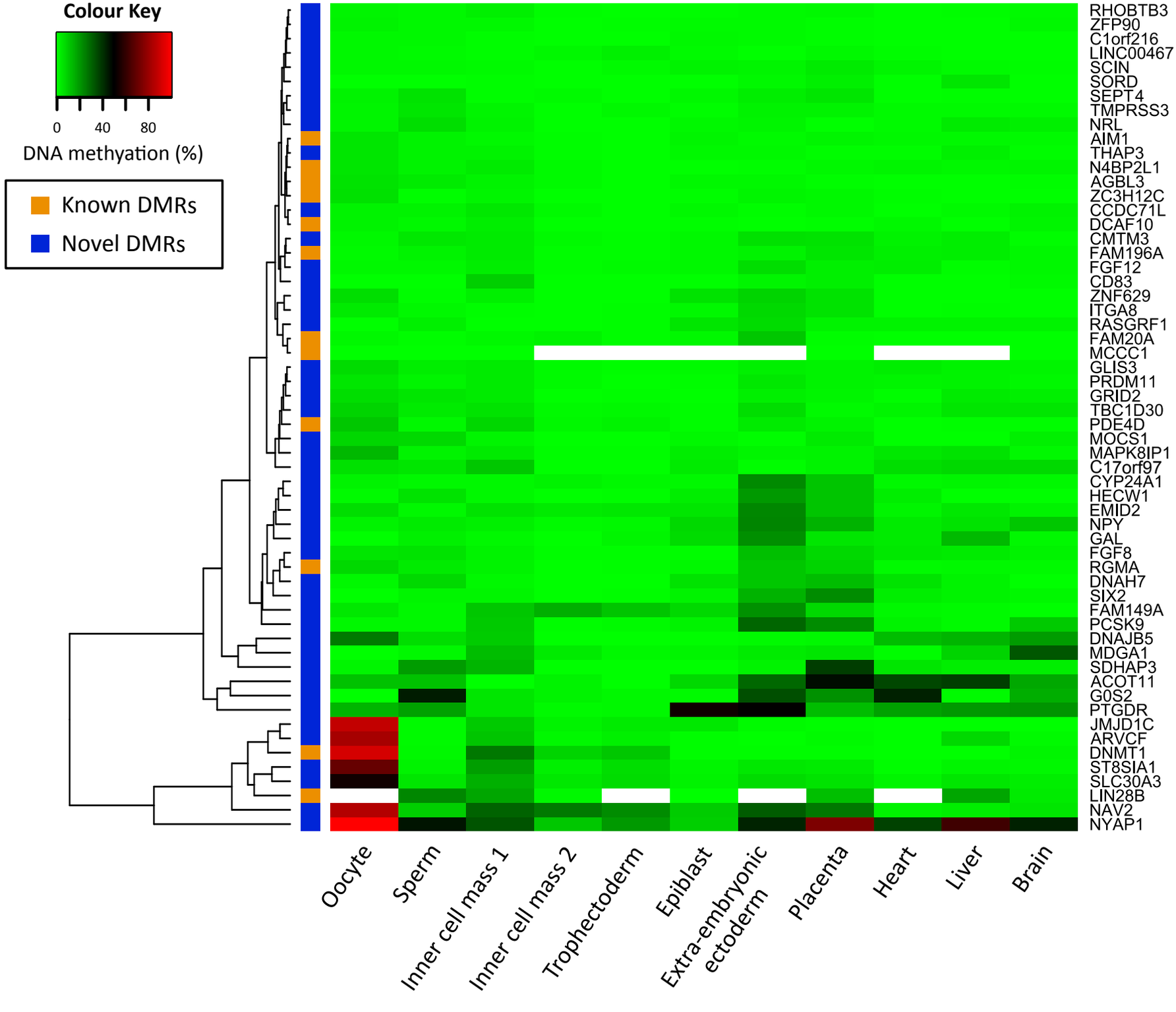
Supplementary Figure 3. A) The heat map shows DNA methylation across early human development for all CGIs that were >75% methylated in both oocytes and sperm (and therefore not imprinted), with an intermediate methylation (15-60%) in the ICM and TE of the blastocyst. White boxes in the heat map indicate DMRs for which there was no data. **B)** The Venn diagram shows the number of placental-specific DMRs that are adjacent to (±1000bp) a placental-specific partially methylated domain (Schroeder et al. 2013).

Supplementary Figure 4. Enrichment for H3K9me3, using 1000bp running window probes with a 1000bp step, was compared between human placenta and amnion. The absolute difference between placenta and amnion showed a significant enrichment for placental-specific DMRs (p=2.2E-16, *t*-test) and CGIs (p=3.1E-14, *t*-test) in placenta compared to all other probes. Placental-specific DMRs were not significantly different from CGIs (p=0.82, *t*-test).

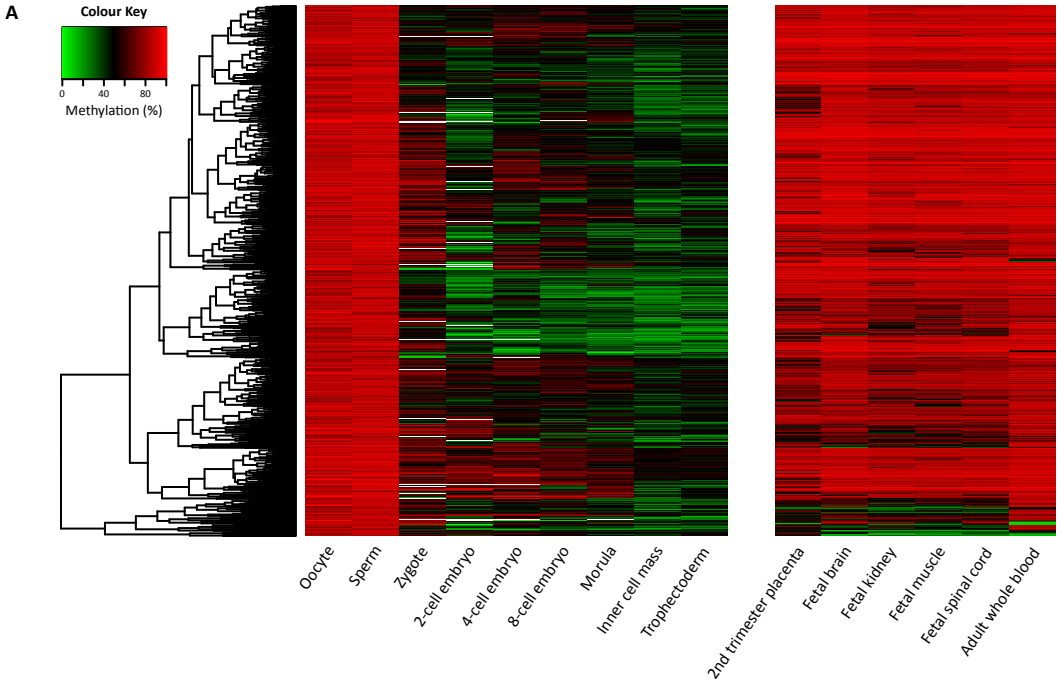
Supplementary Figure 1

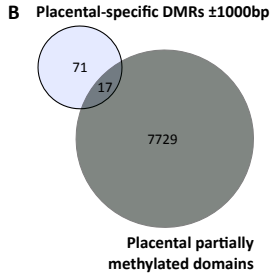


Supplementary Figure 2

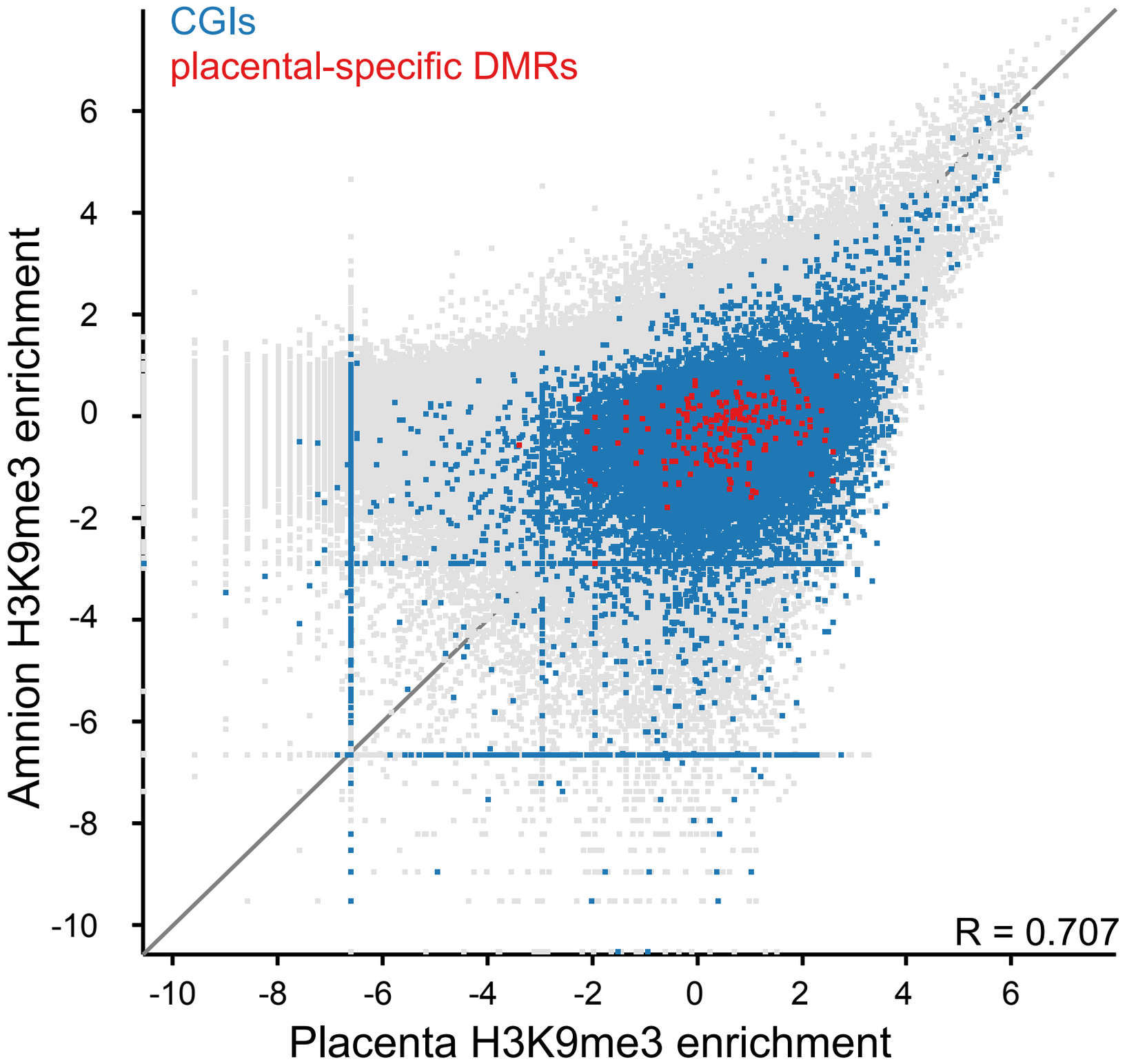


Supplementary Figure 3





Supplementary Figure 4



Supplementary Tables

Supplementary Table 1. List of 882 DMRs identified between diandric and digynic triploid placentas generated by DMRFinder in the CHARM Bioconductor package, using the default parameters: ≥3 differentially methylated probes within a 500bp window and *t*-statistic cutoff of 0.995.

Supplementary Table 2. Imprinted DMRs in humans that were significantly different when comparing DNA methylation between diandric and digynic triploid placental villi and male and female gametes, including 43 known DMRs and 101 novel DMRs. DMRs were merged into one representative region if they were within 1200bp of an adjacent DMR, which included DMRs for *TRAPPC9*, *SNRPN*, *GNAS*, and *NNAT*.

Supplementary Table 3. DNA methylation for allele 1 and 2 for all heterozygous samples with ≥5 reads per allele, assayed by multiplex bisulfite sequencing.

Supplementary Table 4. Quality metrics for remapped RRBS libraries

Supplementary Table 5. List of primers, hg19 coordinates and SNPs for all assayed regions for multiplex bisulfite sequencing.

Supplementary Table 6. List of placental-specific DMR associated genes, based on the closest TSS,hg19 coordinates used for DAVID and gene expression analyses, and RPKM values for each gene in trophectoderm, 2nd and 3rd trimester placenta. Additional categories added to the default analysis included UP_tissue.

Supplementary Table 7. Gene Ontology terms enriched among genes associated with placental-specific DMR (N=88).

Supplementary Table 8. Average DNA methylation for each read, with at least 5 informative CpGs, corresponding to allele 1 or allele 2 of SNPs for each assayed region in each sample, measured by multiplex bisulfite sequencing.

Supplementary Table 9. Number of reads per allele for each SNP in assayed regions for all samples, assayed by multiplex bisulfite sequencing.

Supplementary File Legend

Supplementary file 1. Custom script to assess allelic methylation levels and distributions on reads extracted from the Bismark BAM files.