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Supplementary Material

Genome-wide analysis of sperm DNA methylation from monozygotic twin bulls

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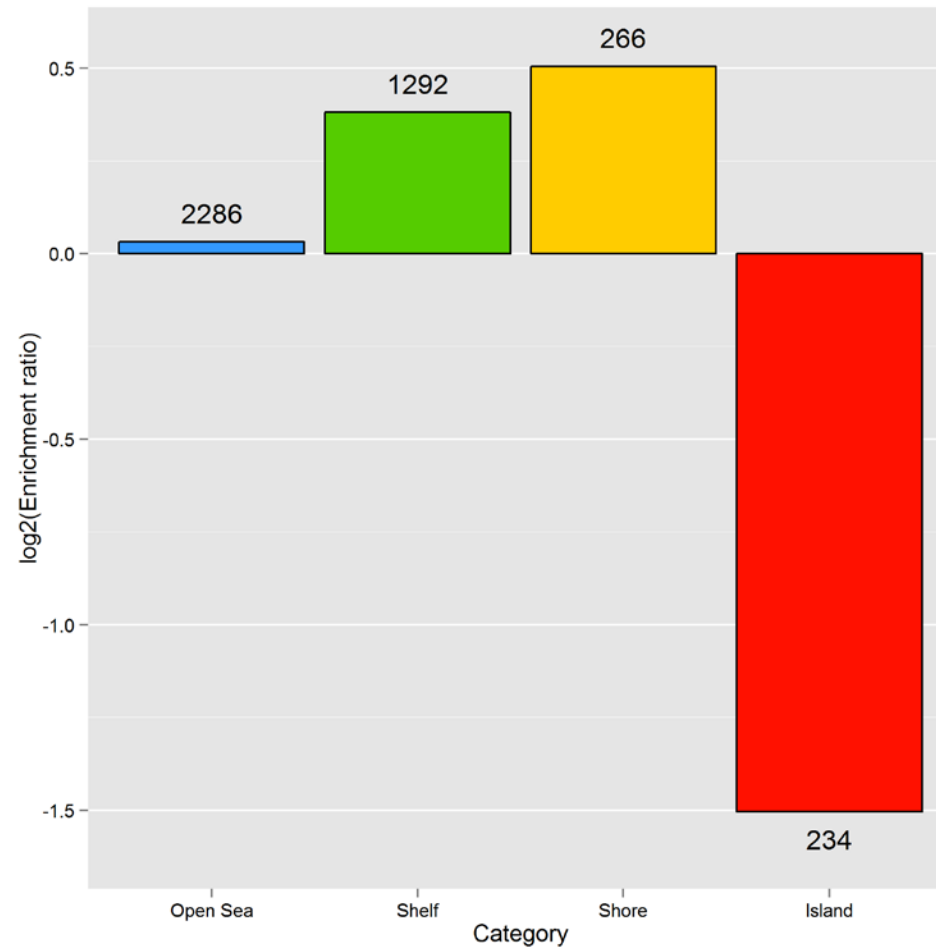


Fig. S1. The proportion of the detected top 1% of the DMRs in MZ twin bulls sperm based on their distance from CpG islands. Approximately 40% of changes occurred at CpG shore and shelf regions of the MZ bulls' sperm genome.