Figure S3

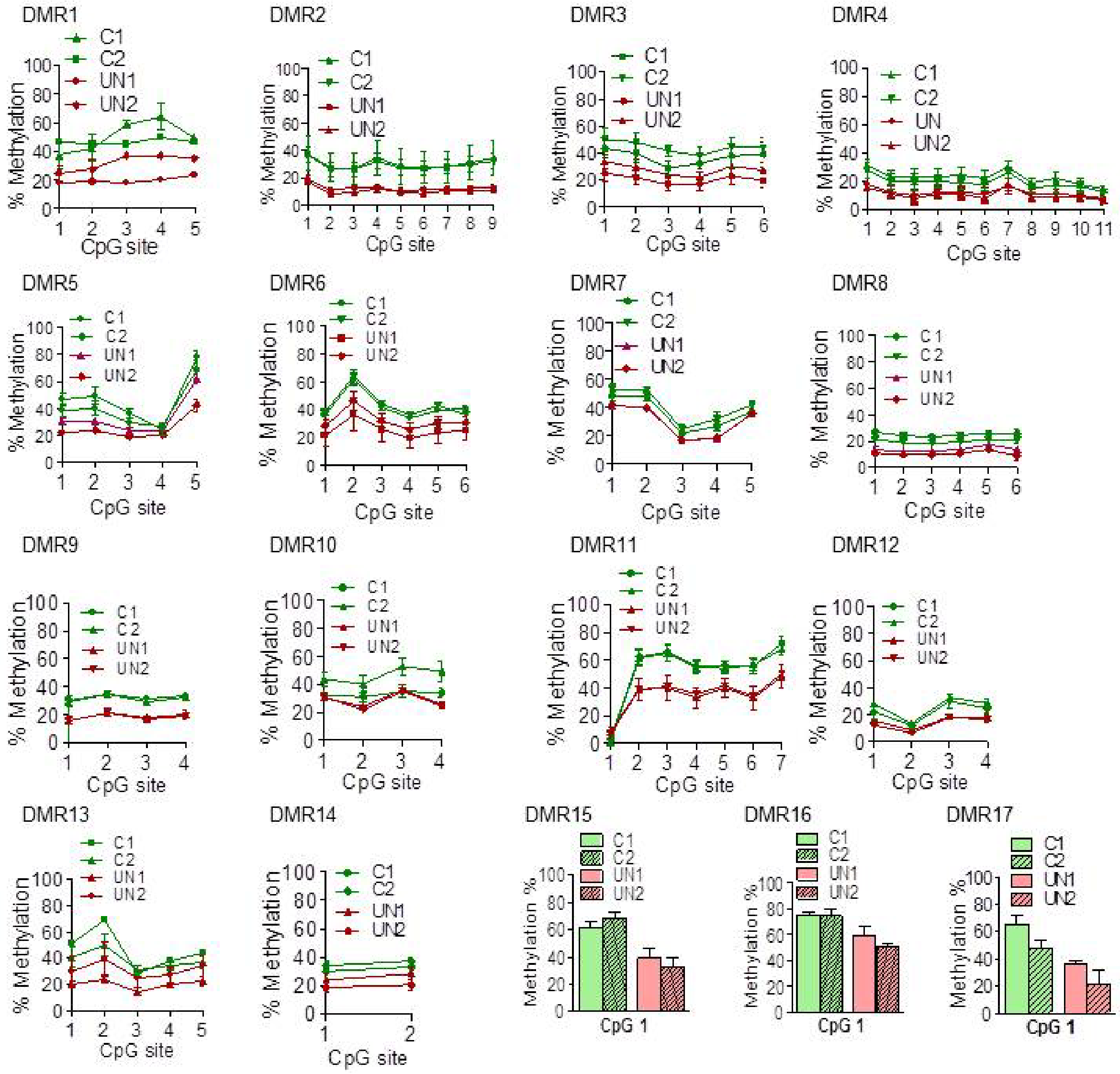

Fig.S3 DMRs identified by MeDIP-seq have the same absolute level of methylation in the two biological pooled replicate libraries.

To assess whether the DMRs had similar absolute methylation levels in the two pools assessed by MeDIP-seq, bisulphite validation data are shown for those samples which were represented in MeDIP-seq libraries 1 and 2 for Control (C) and Undernourished (UN) sperm samples. For each group n=4, 4 litters. All data expressed as mean +/- SEM.