



Supplemental Figure 3: Distribution of hippocampal WT DhMRs. (A) A Manhattan plot shows the distribution of 5hmC sequenced data across the genome (x-axis; alternating black/grey for alternating chromosomes) and the level of significance (y-axis; $-\log_{10}(P\text{-value})$). Dots above the top blue line represent PS-WT-specific-(hyper) DhMRs, while dots below the bottom blue line represent Control-WT-specific-(hypo) DhMRs ($P\text{-value} < 0.05$). (B) A pie chart displays the proportion of WT-DhMRs across standard genomic structures. (C) Venn diagram showing the overlap of HET-DhMR-associated genes and WT-DhMR-associated genes. The asterisk (*) denotes a significant overlap (hypergeometric enrichment $P\text{-value} < 0.05$). (D) A 3-way Venn diagram showing the overlap of Control-HET, PS-HET, and PS-WT DhMR-associated genes. The asterisks (*) denote a significant overlap (hypergeometric enrichment $P\text{-value} < 0.05$). (E-F) Bar plots showing the top ten significantly over-represented ontological terms (y-axis) based on gene ontological analysis of PS-WT-specific DhMR-associated genes (E) and Control-WT-specific DhMR-associated genes (F). The number of DhMR-associated genes linked to the ontological terms are displayed on the x-axis. Bar color is based on $P\text{-value}$.