

Supplemental Fig S12. Motif enrichment score in a WGA sample (Alzheimer's disease Iso-seq dataset) as a negative control. **(a)** 2-mer motif enrichment score in the WGA sample. The barplot represents the motif enrichment score of all dinucleotide motifs. The putative methylated position is underscored. **(b)** 4-mer motif enrichment score in the WGA sample. Each 4x4 heatmap corresponds to all sixteen 4-mer motifs, for which 2nd and 3rd bases are fixed at the center/title. The rows and columns in the heatmaps represent the first and last bases of 4-mer motifs. Each cell in the following 4x4 heatmap shows the motif enrichment score based on the WGA sample. The motif enrichment scores for 2-mer motif <u>AG</u> and multiple 4-mer motifs with <u>AG</u> (e.g. A<u>A</u>GG, CA<u>A</u>G and TG<u>A</u>G) in the WGA are all much smaller than those in the native sample (Fig. 4f).