

Supplementary Materials

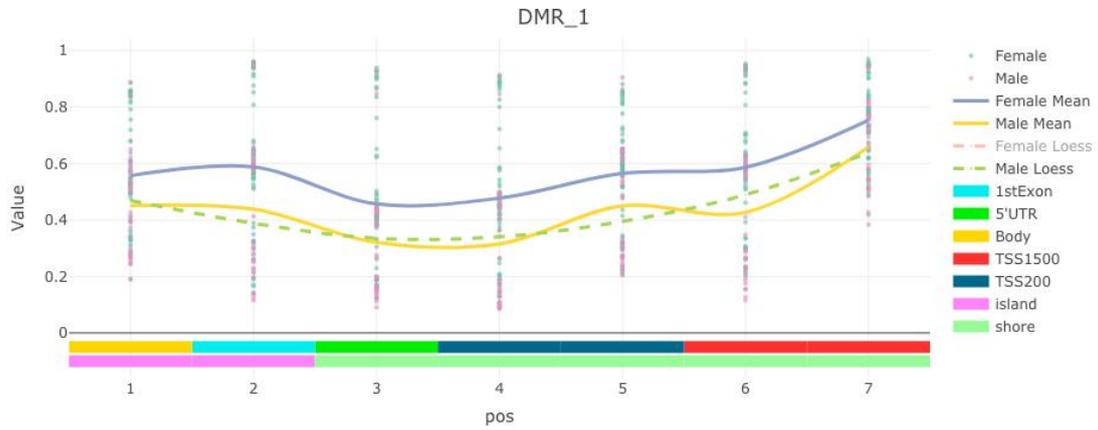
Blood-based sex-differential DNA methylation in Alzheimer's disease

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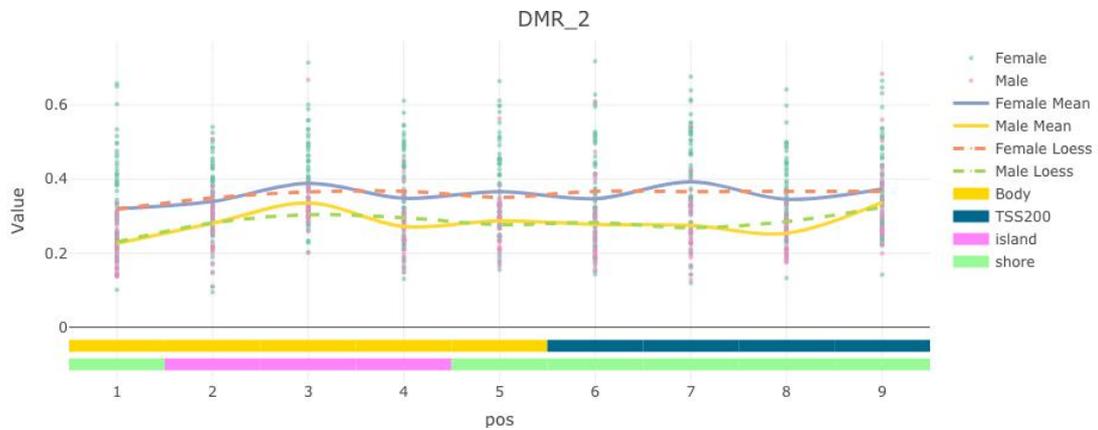
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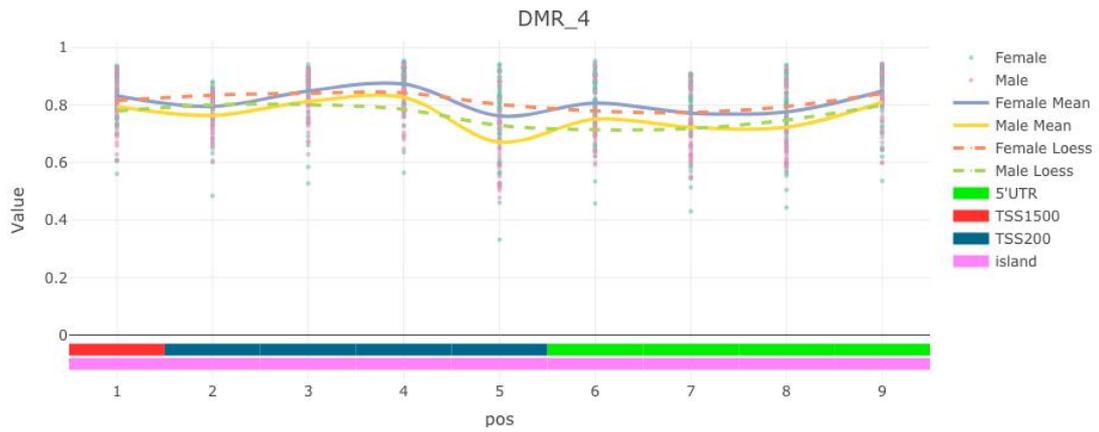
Supplementary Figures 1-6. Sex-differential methylated regions (DMRs) significant in both the two Alzheimer's disease datasets, but not significant in any healthy control datasets.



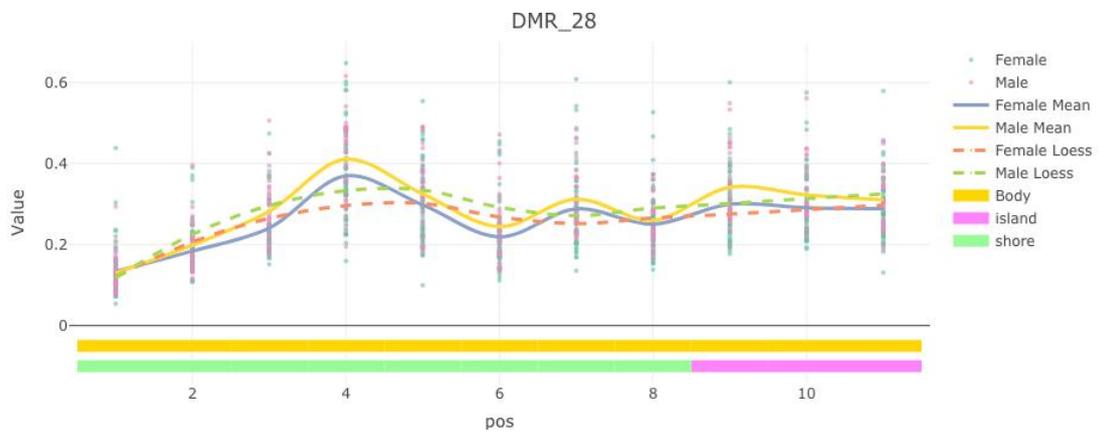
Supplementary Figure 1. DMR_1 (chr1: 205818956-205819609).



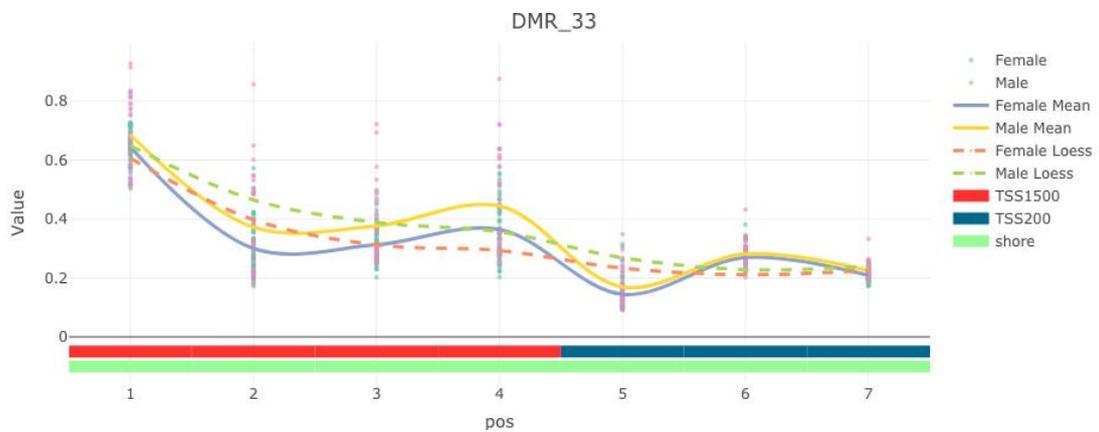
Supplementary Figure 2. DMR_2 (chr10: 42862876-42863594).



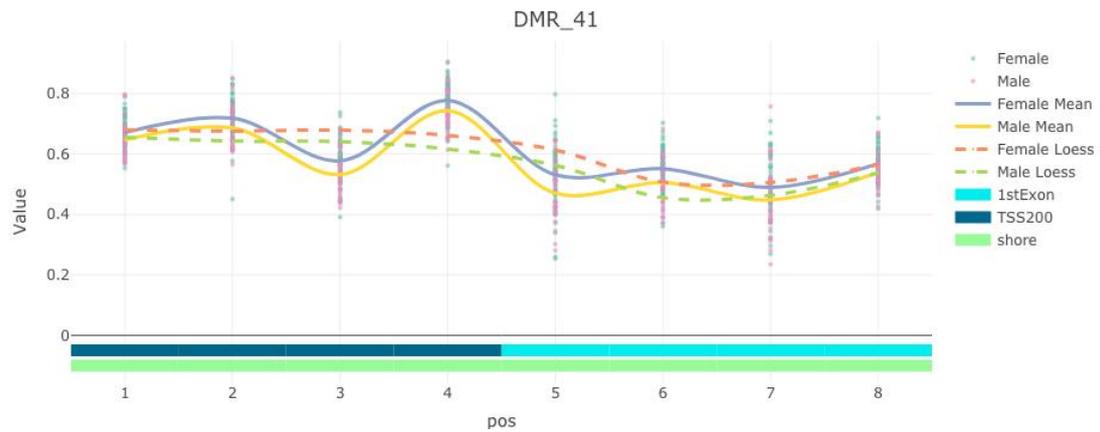
Supplementary Figure 3. DMR_4 (chr19: 57742112-57742444).



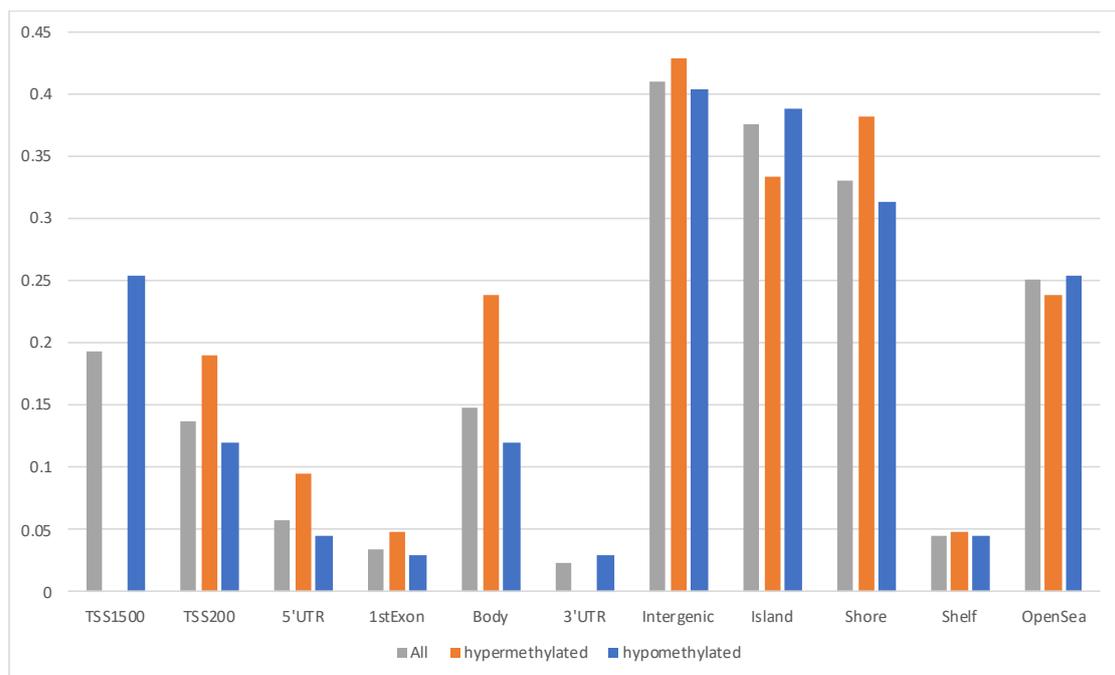
Supplementary Figure 4. DMR_28 (chr5: 140810051-140810920).



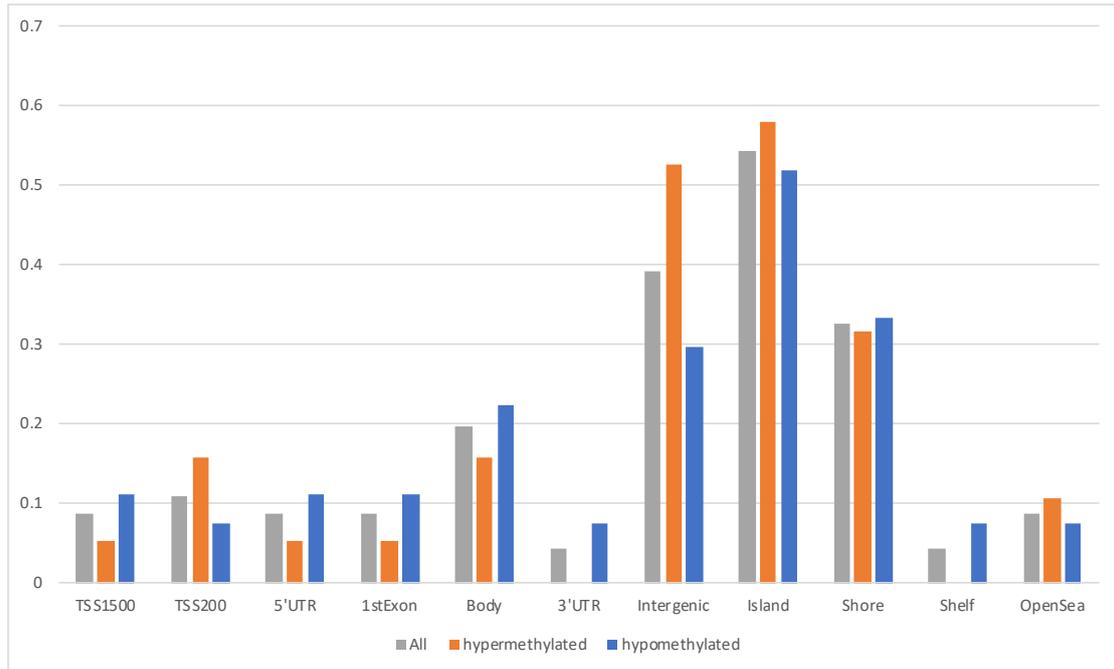
Supplementary Figure 5. DMR_33 (chr12: 14926572-14927099).



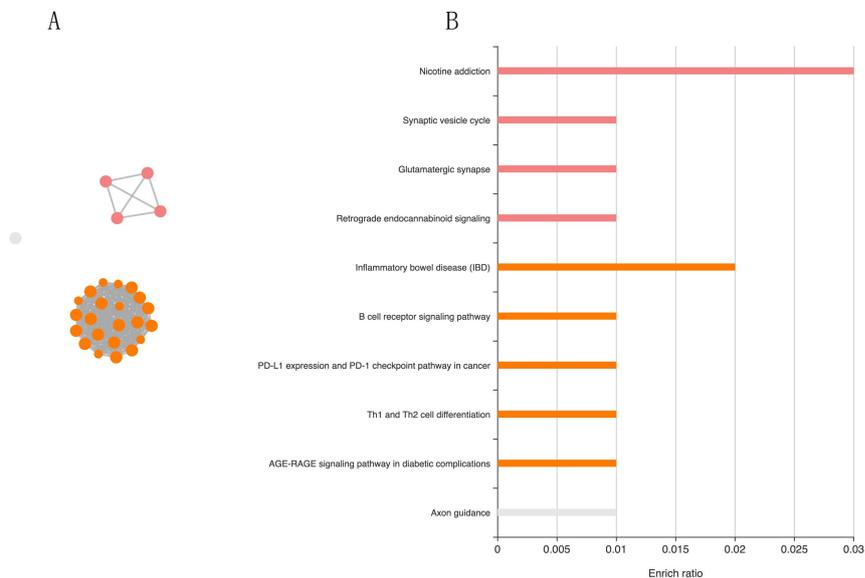
Supplementary Figure 6. DMR_41 (chr16: 3062349-3062975).



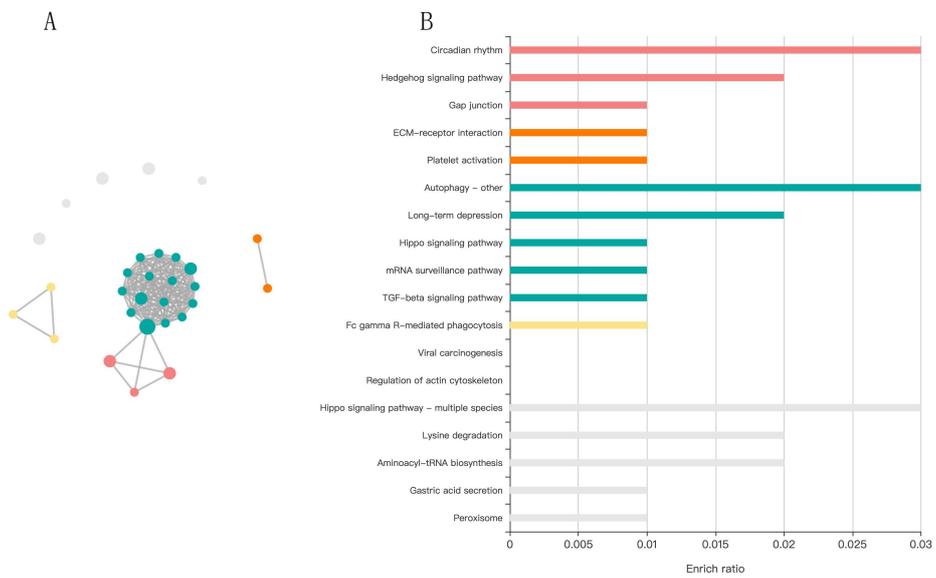
Supplementary Figure 7. Annotation in gene features (TSS1500, TSS200, 5'UTR, 1stExon, body, 3'UTR, intergenic) and CpG features (island, shore, shelf, open sea) of 88 AD-sex-DMPs.



Supplementary Figure 8. Annotation in gene features (TSS1500, TSS200, 5'UTR, 1stExon, body, 3'UTR, intergenic) and CpG features (island, shore, shelf, open sea) of 46 AD-HC-sex-DMPs.



Supplementary Figure 9. cirFunMap visualization of KEGG pathway enrichment analysis for hypermethylated genes mapped from AD-sex-DMPs. The immune-related cluster (cluster 2) was replicated.



Supplementary Figure 10. cirFunMap visualization of KEGG pathway enrichment analysis for hypomethylated genes mapped from AD-sex-DMPs. The immune-related cluster was absent.