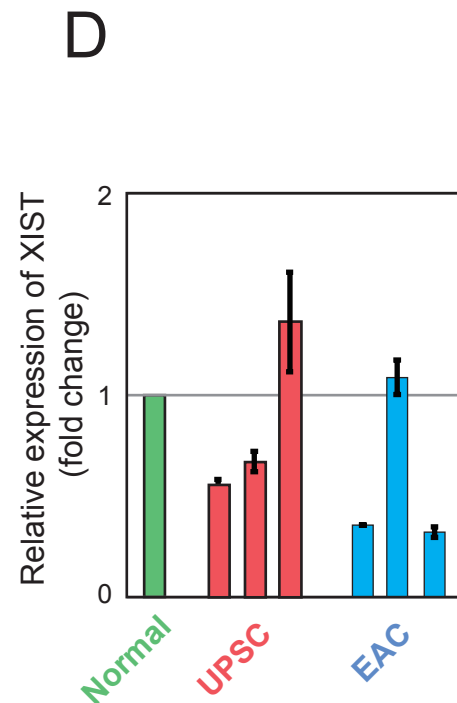
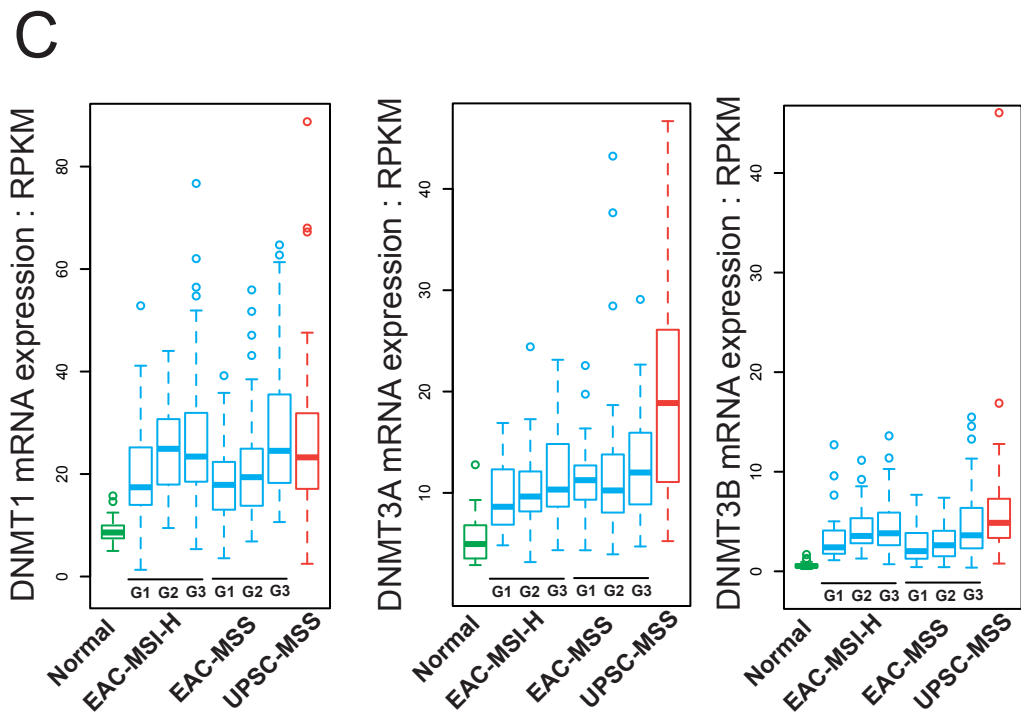
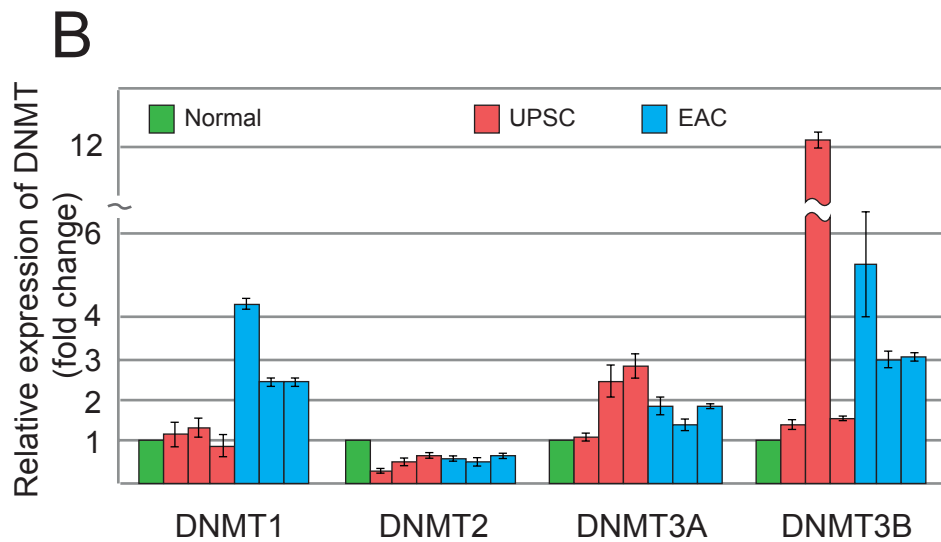
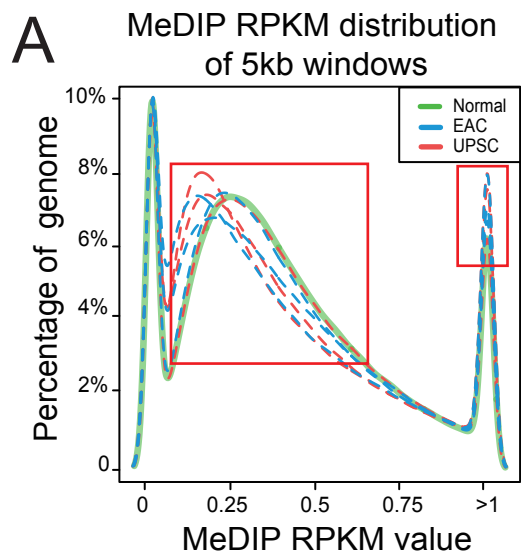
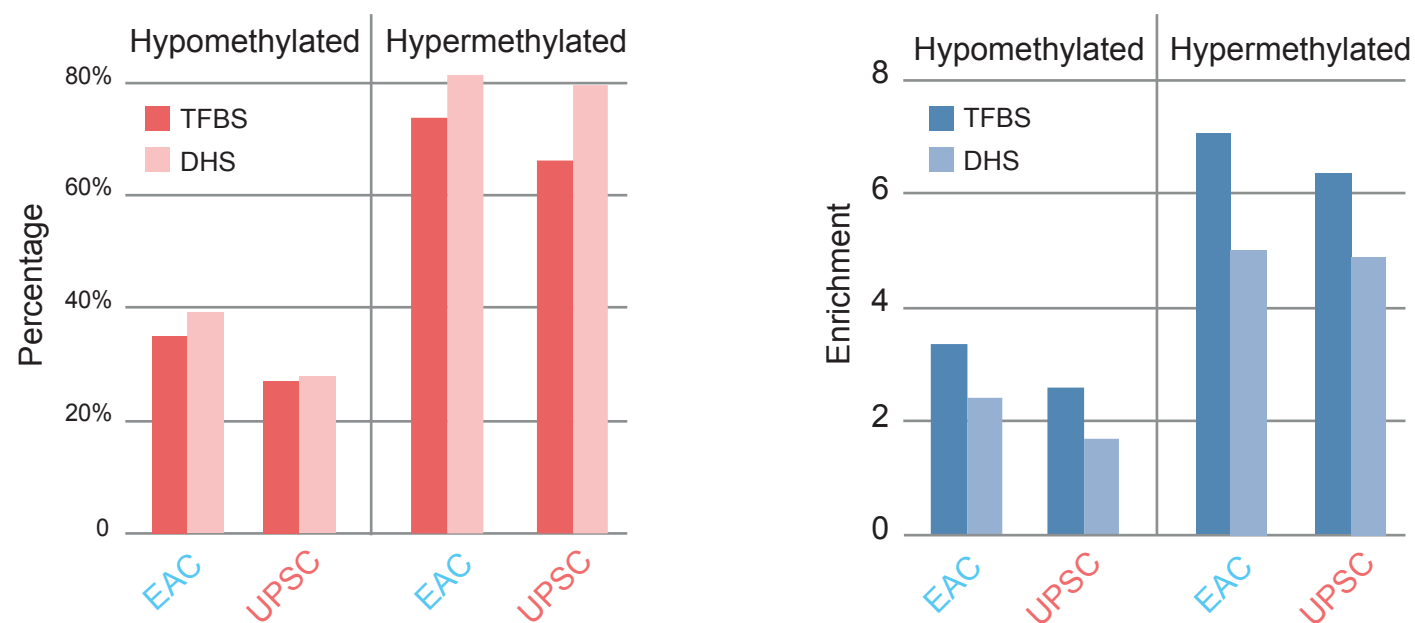


Supplementary Fig.S1



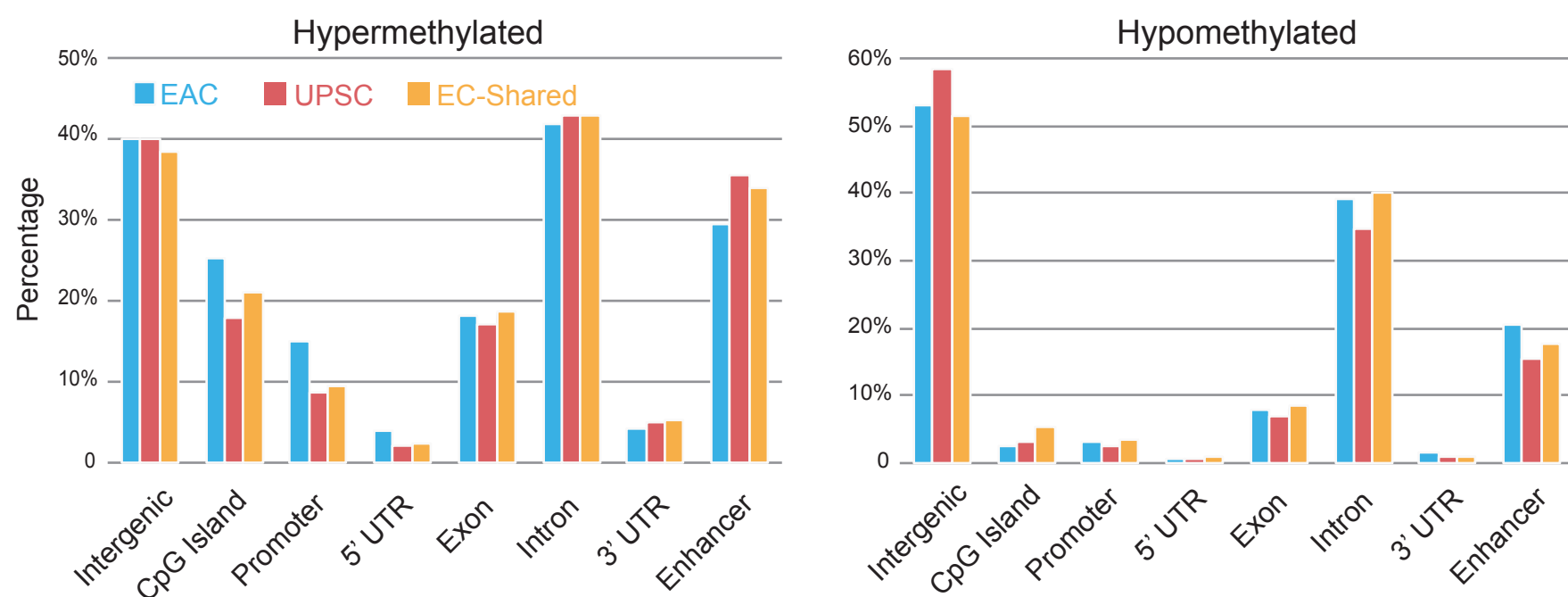
A

DMRs overlap ENCODE open chromatin features

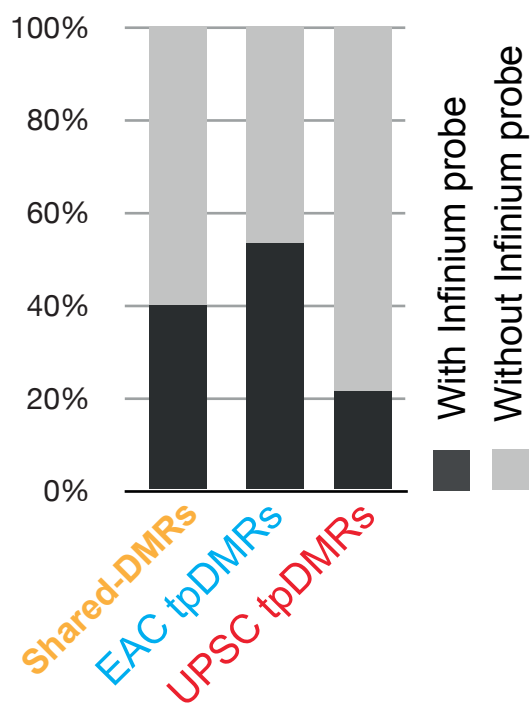


B

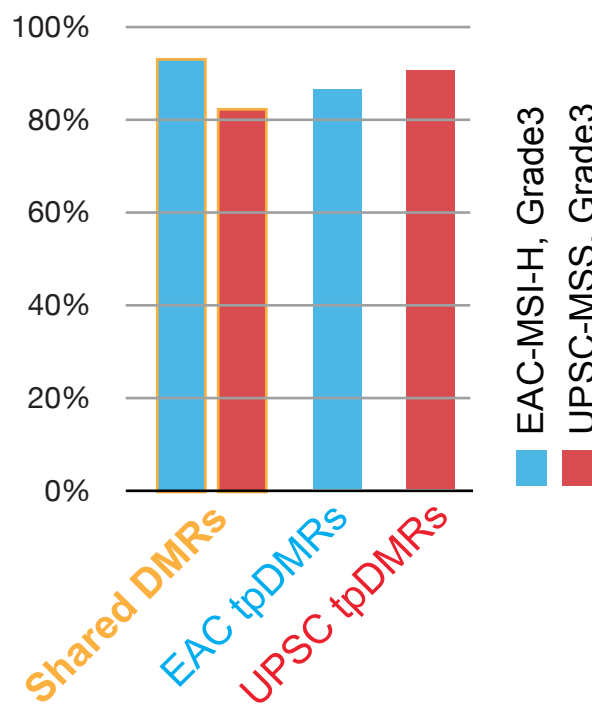
Genomic distribution of DMRs



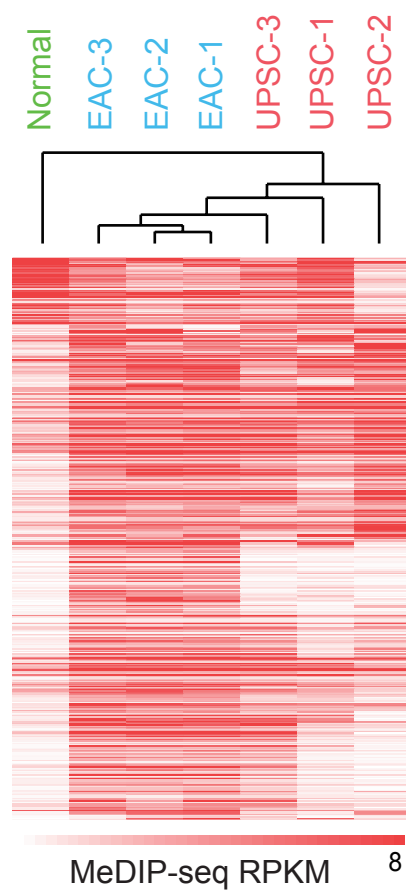
C



D

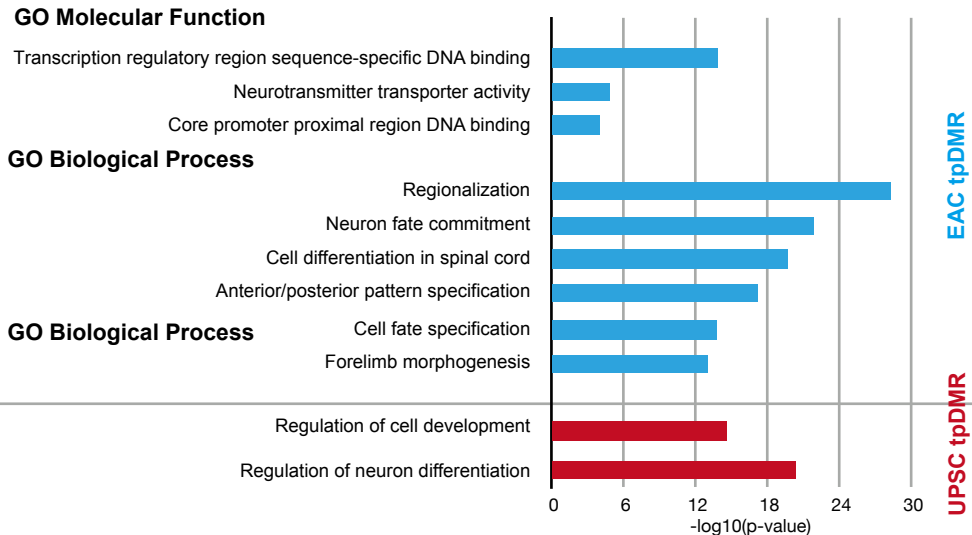


E

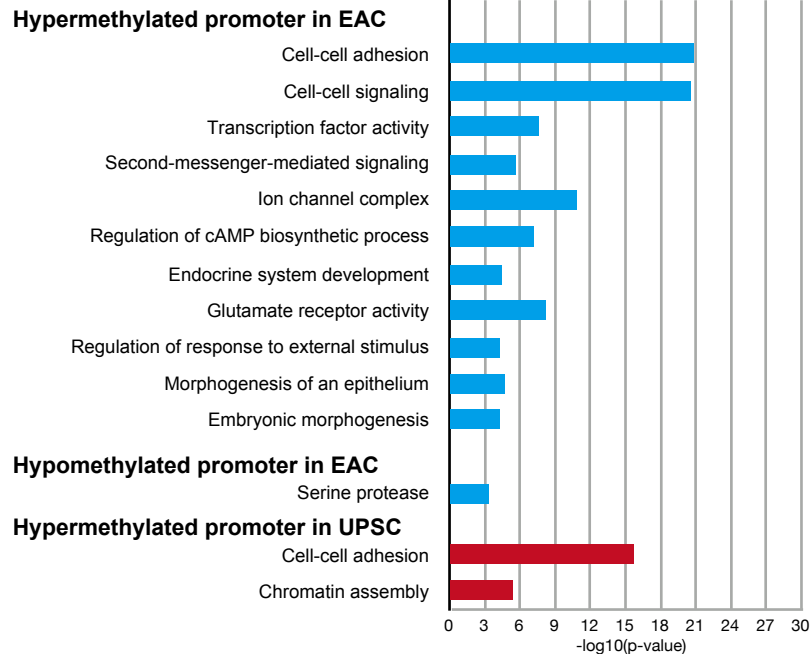


Supplementary Fig.S3

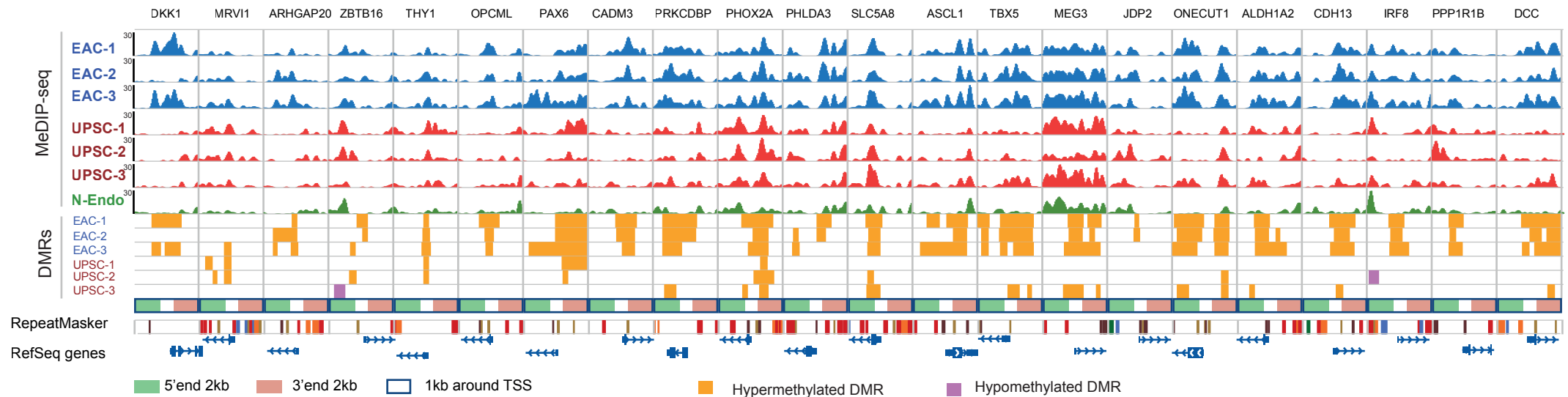
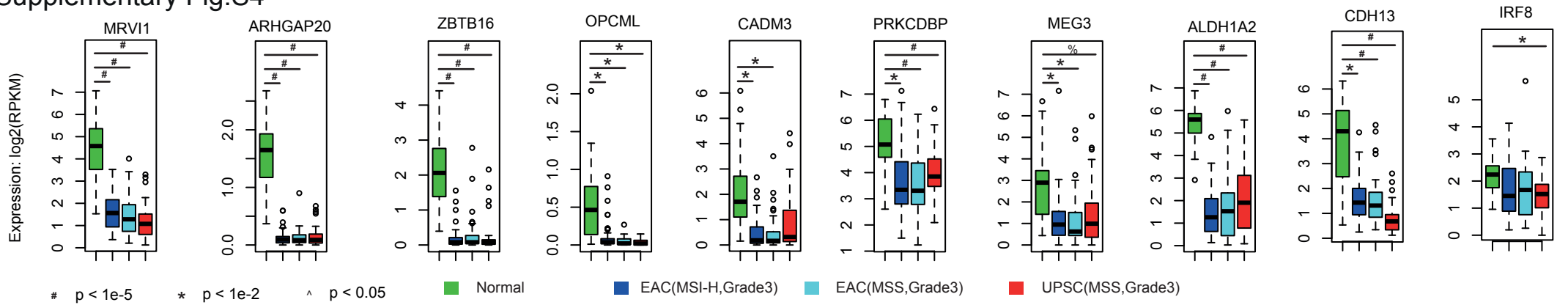
A



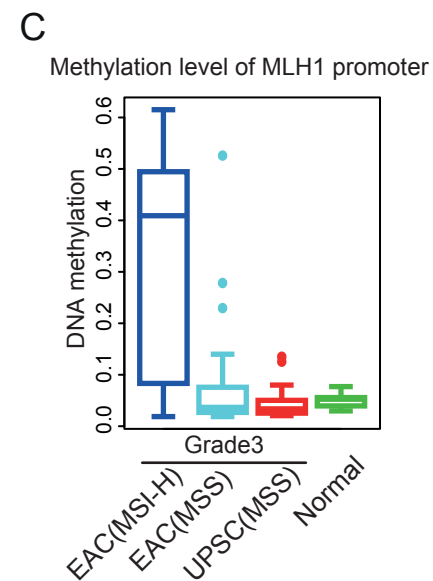
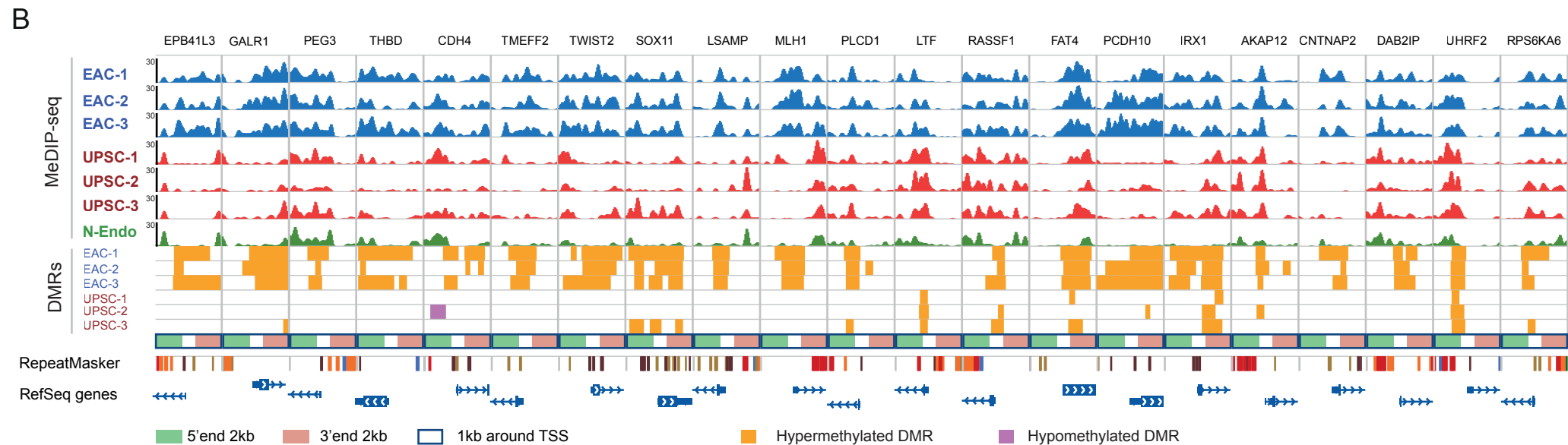
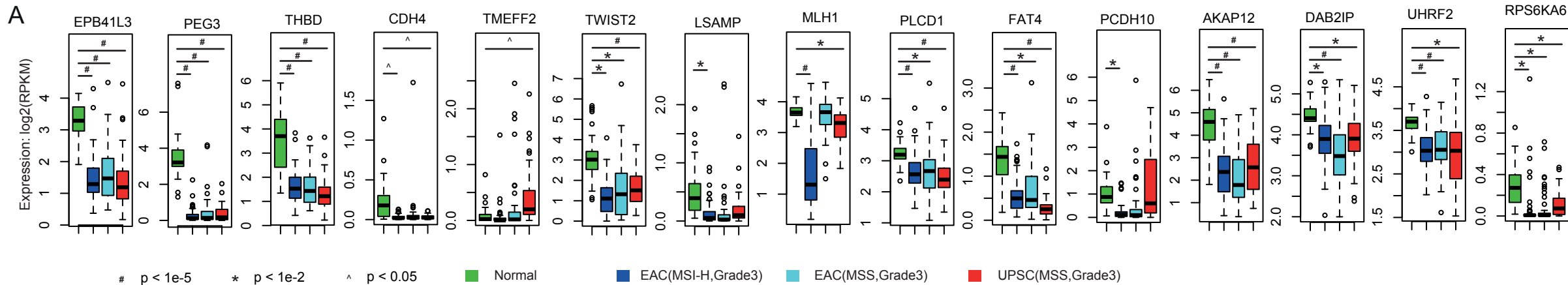
B

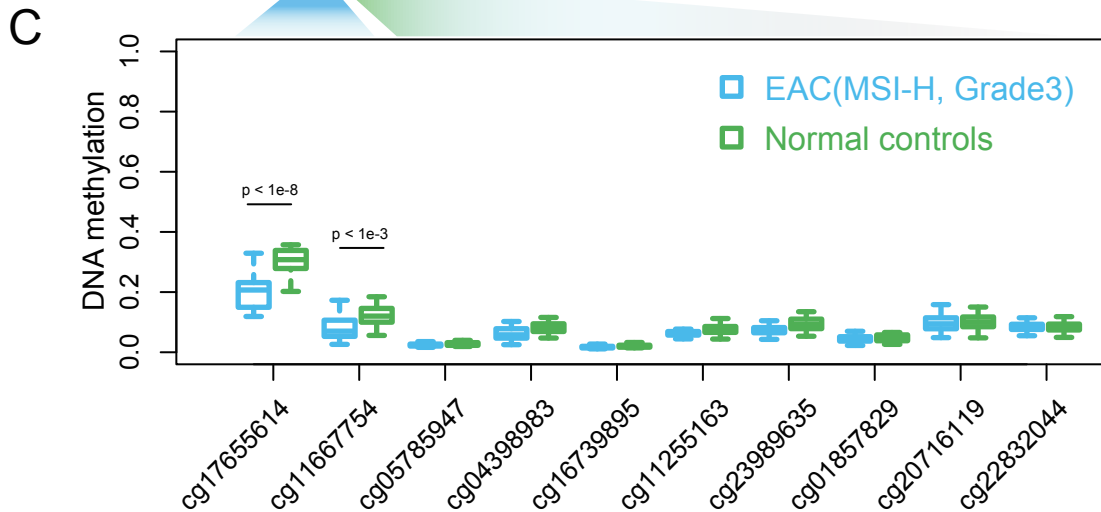
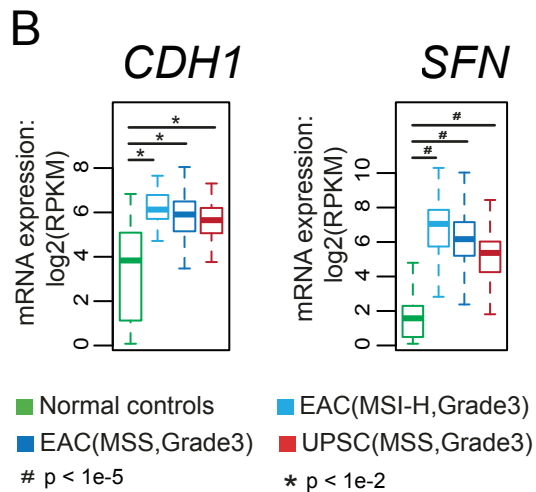
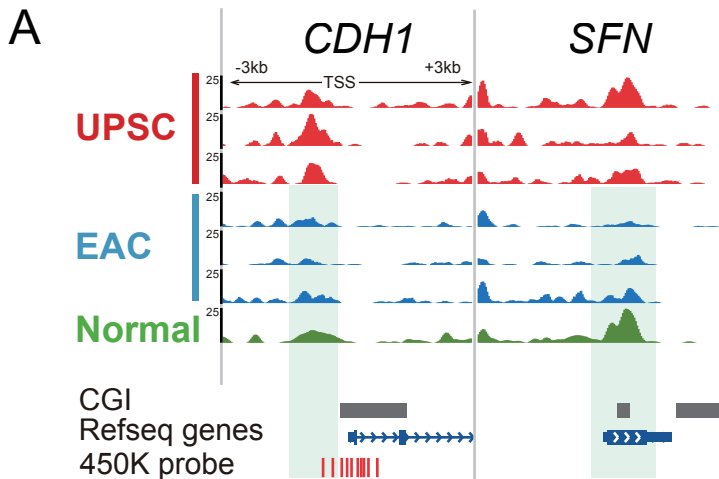


Supplementary Fig.S4

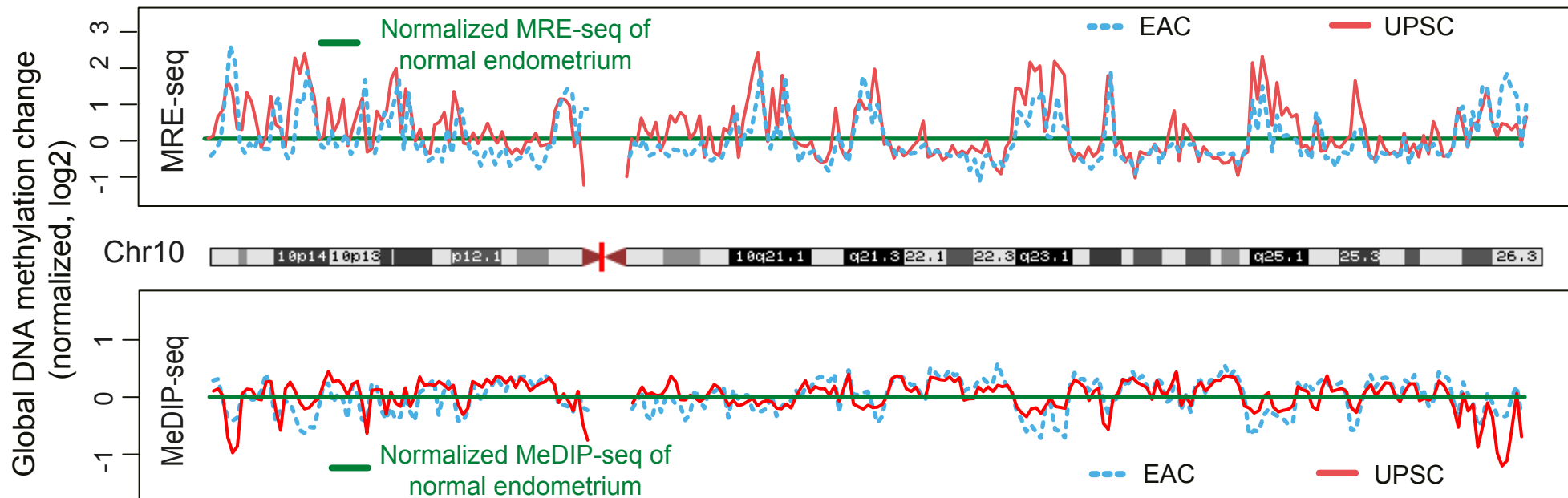


Supplementary Fig.S5





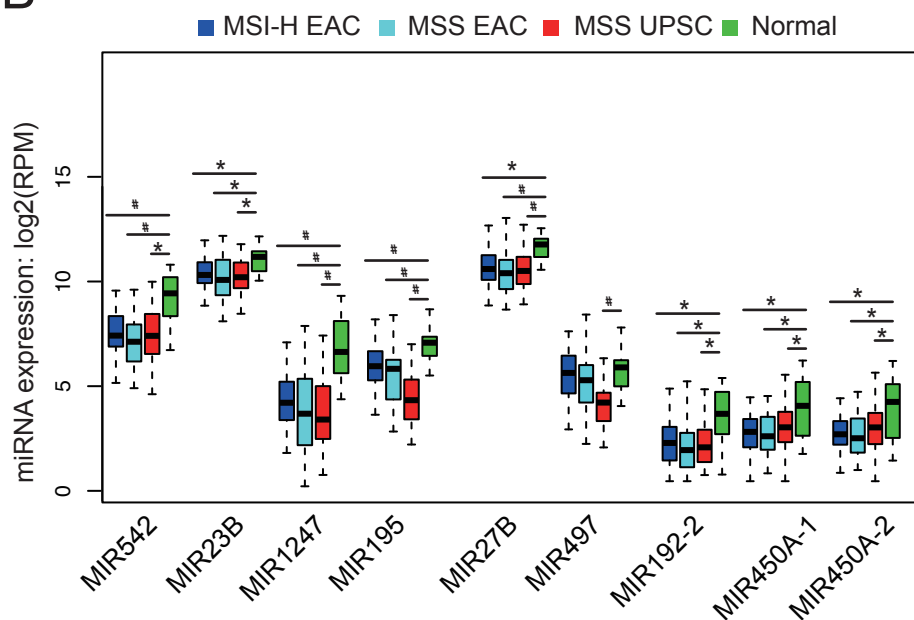
MeDIP and MRE RPKM fold change on chromosome 10 at 500kb resolution



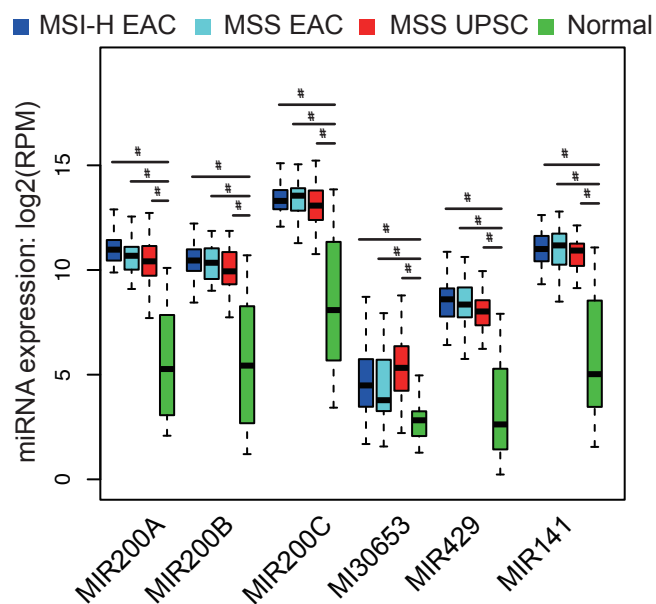
A

		EAC	UPSC
MiRNA-cluster	Hypermethylated	24	9
	Hypomethylated	6	2
lncRNA	Hypermethylated	621	168
	Hypomethylated	207	245

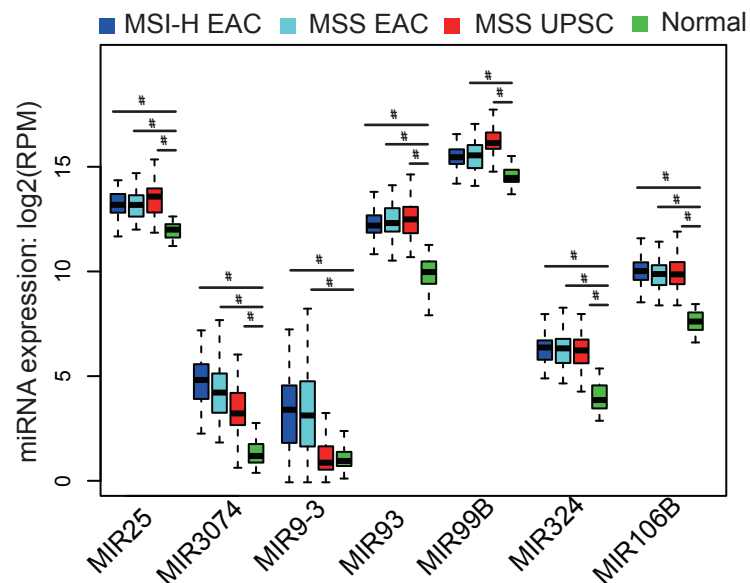
B



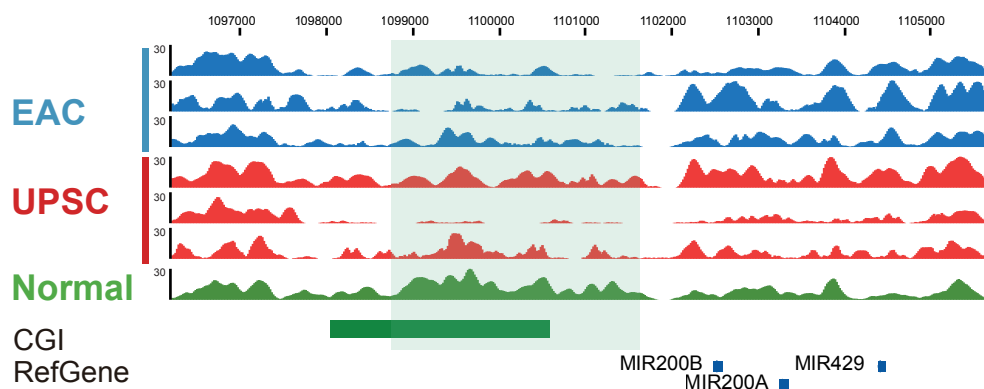
C



E

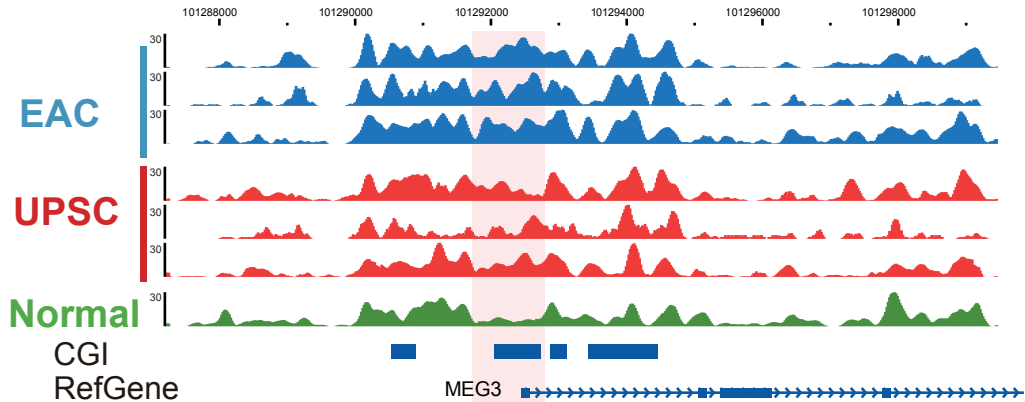


D

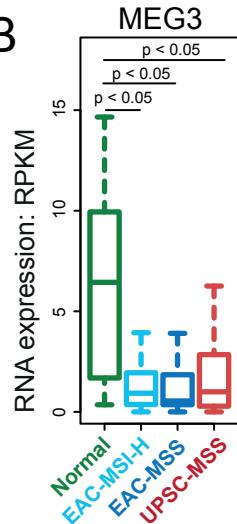


Supplementary Fig.S9

A



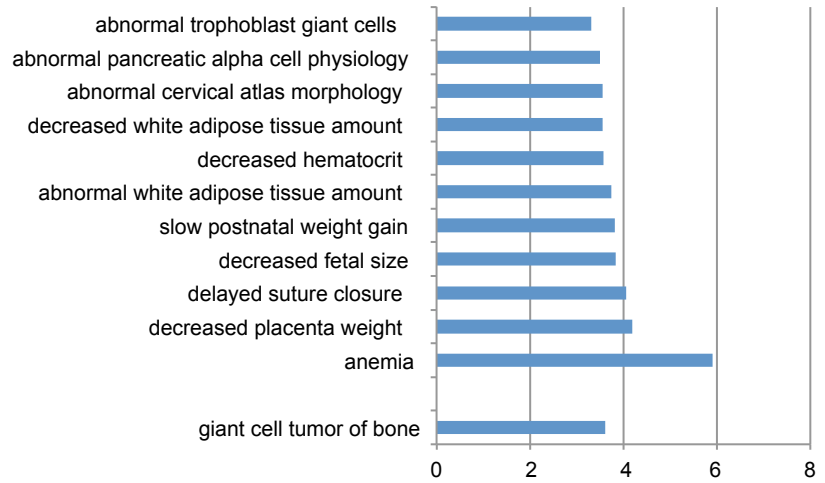
B



A

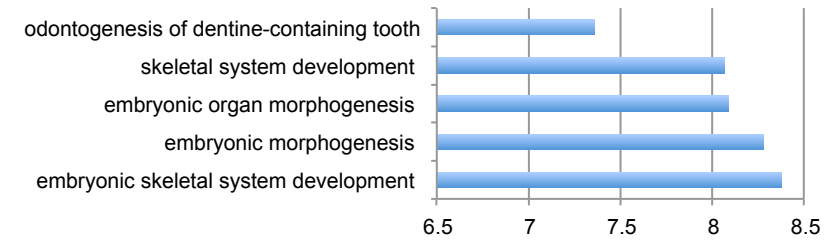
Methylation pattern MMU: EAC DMR with promoter state

Disease Ontology & Mouse Phenotype : $-\log_{10}(p\text{-value})$



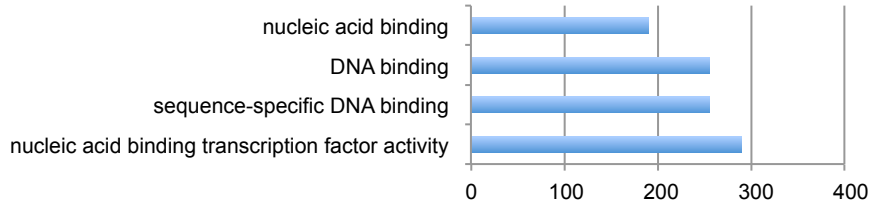
Methylation pattern UUM: EAC DMR with promoter state

GO Biological Process: $-\log_{10}(p\text{-value})$



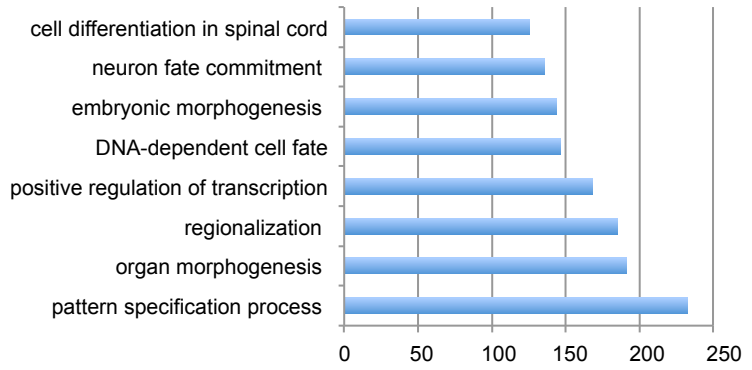
Methylation pattern UUM: UPSC DMR with promoter state

GO Molecular Function: $-\log_{10}(p\text{-value})$

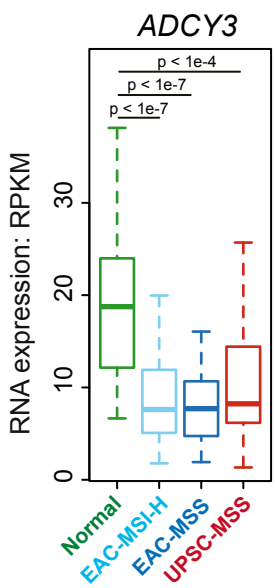


Methylation pattern UUM: EAC DMR with promoter state

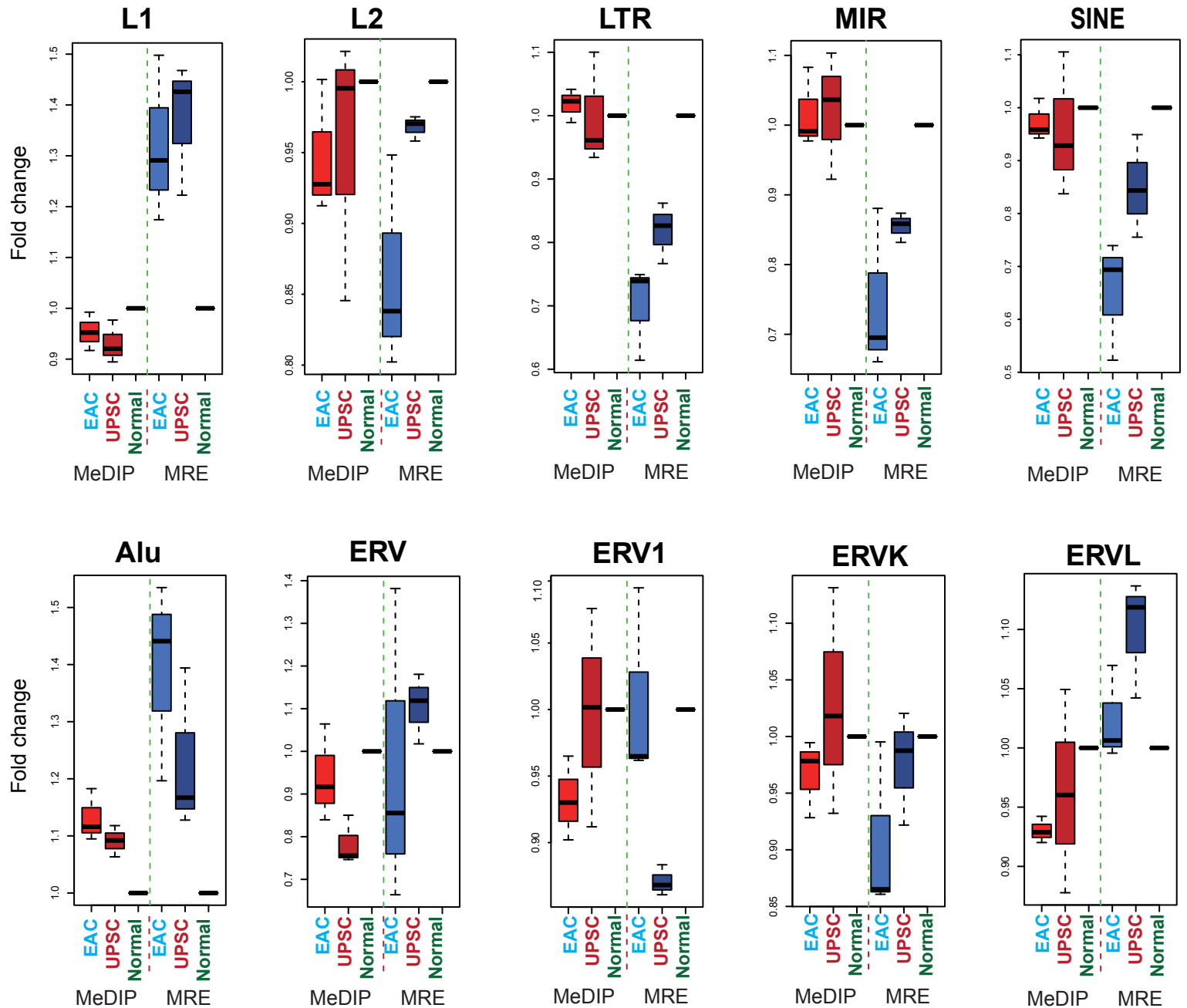
GO Molecular Function: $-\log_{10}(p\text{-value})$



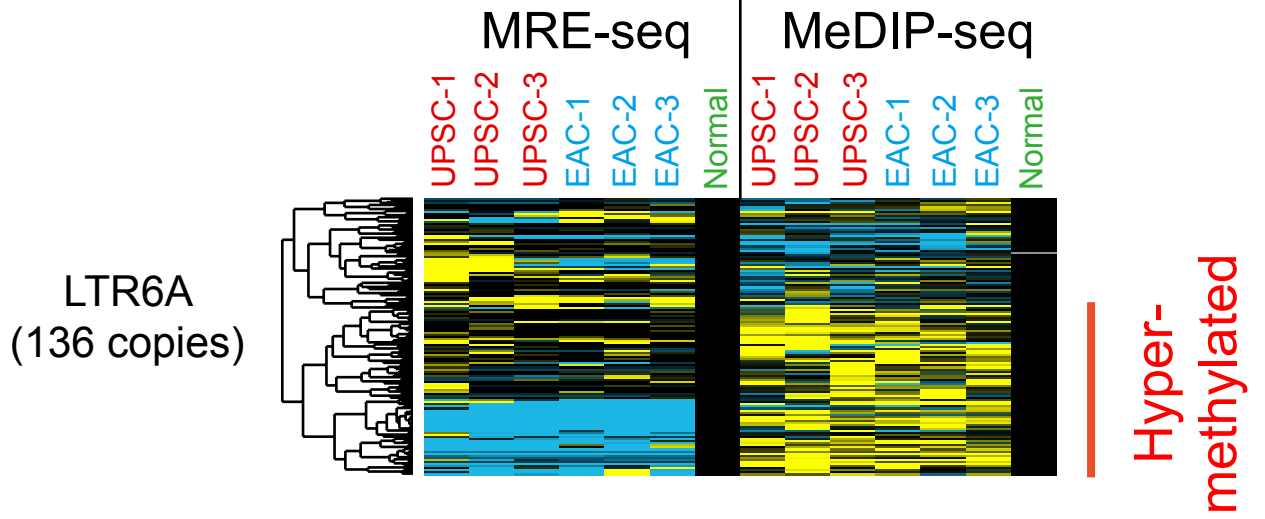
B



DNA methylation change of transposable element families



A



B

