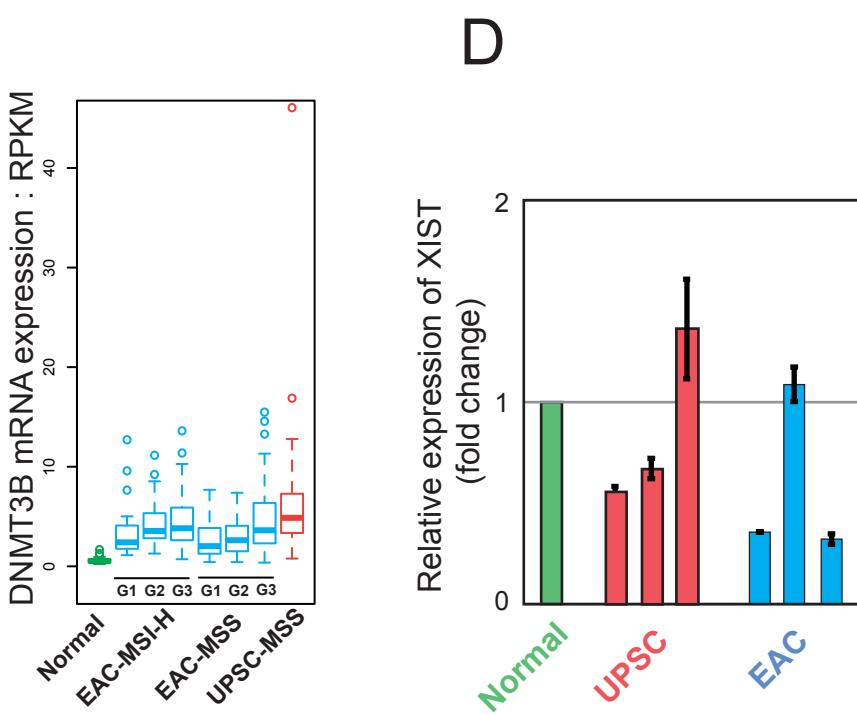
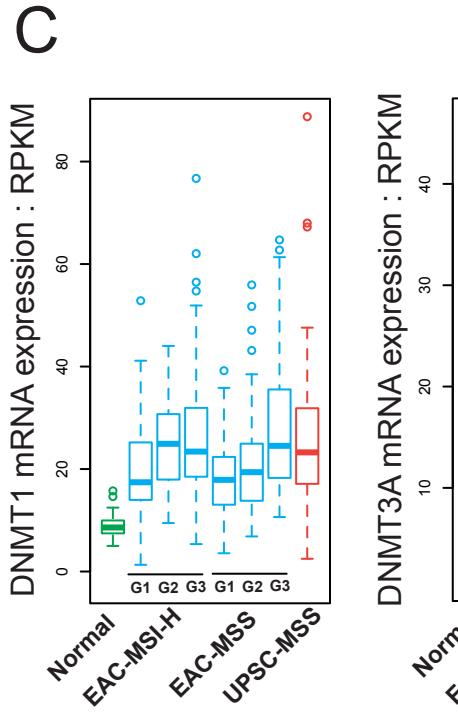
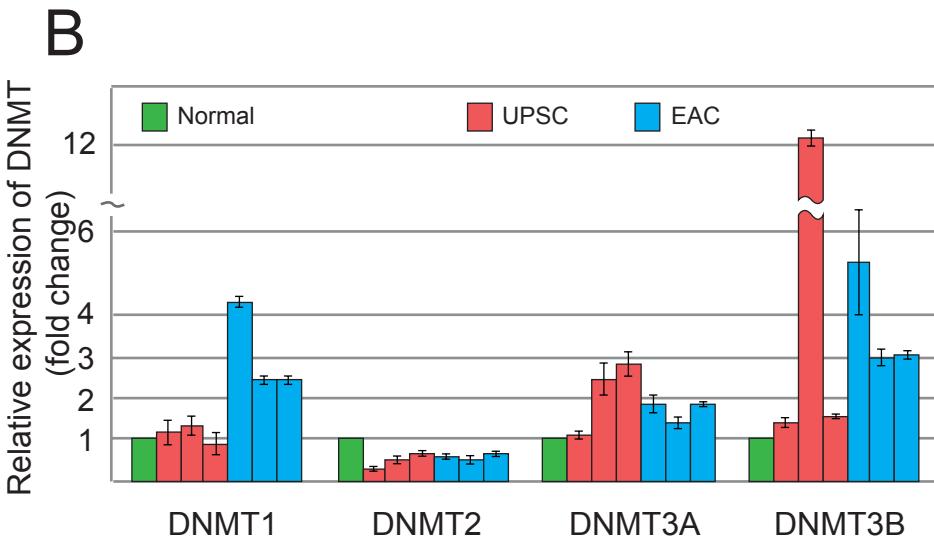
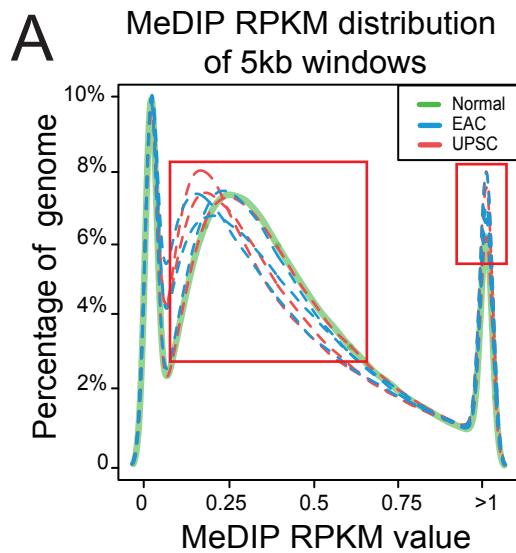
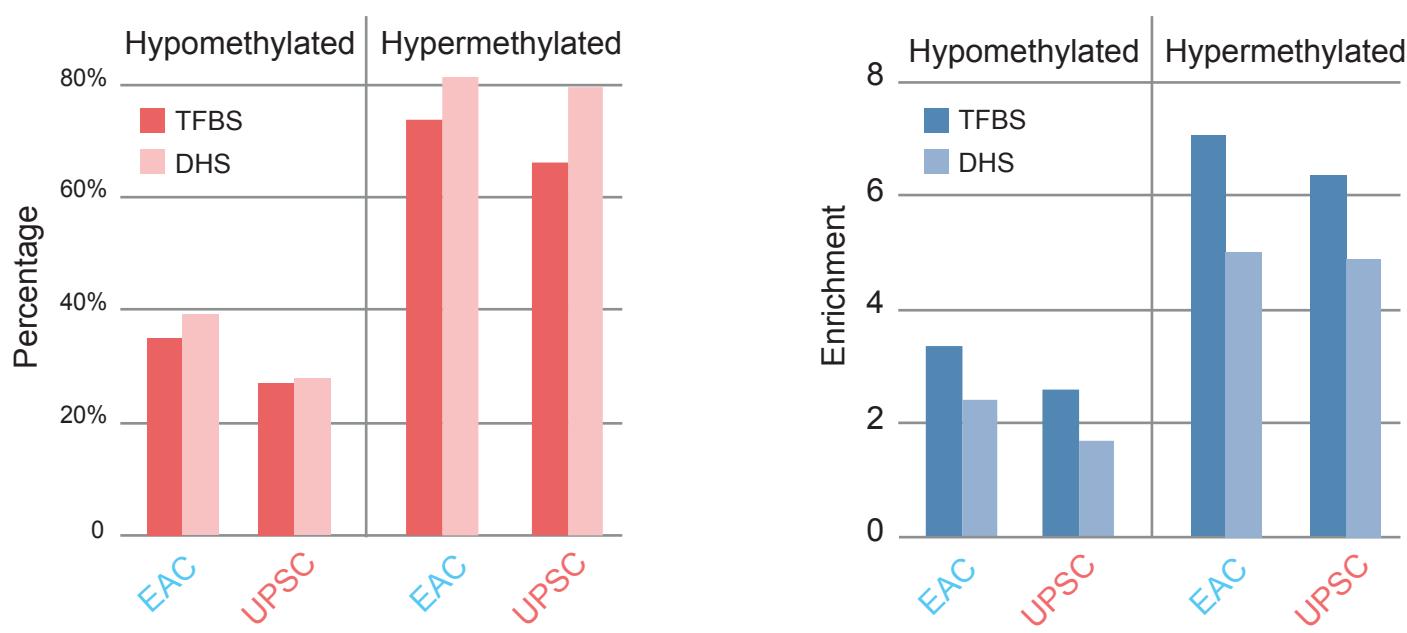


Supplementary Fig.S1

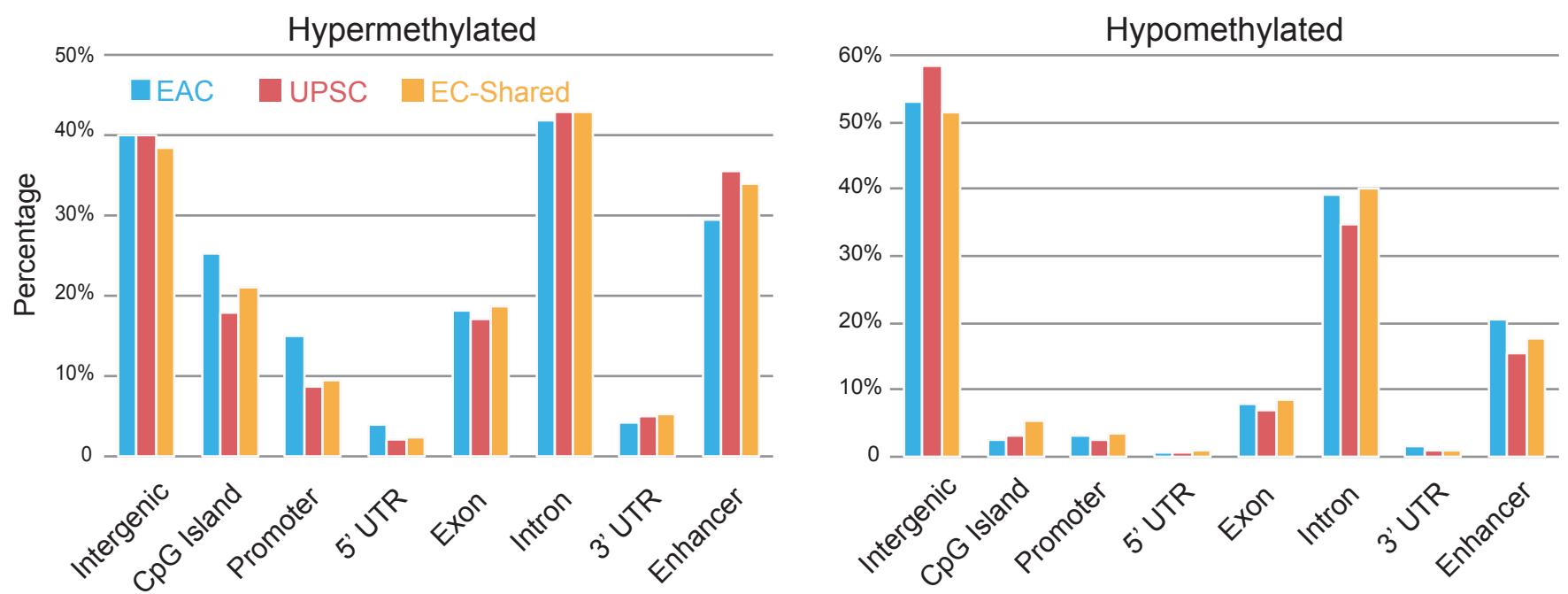
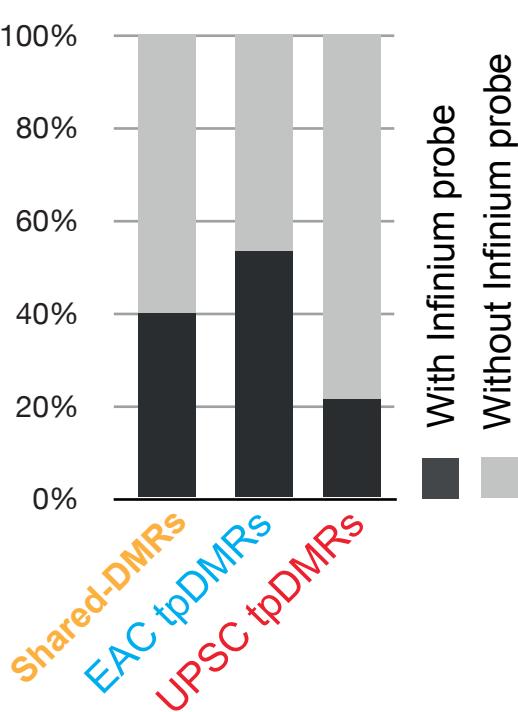
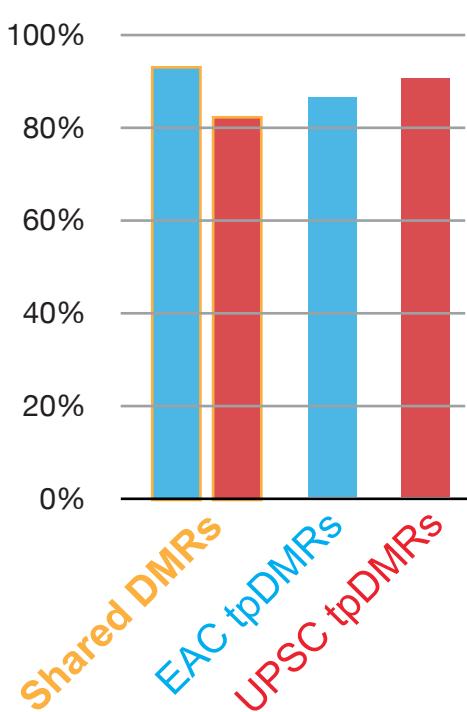
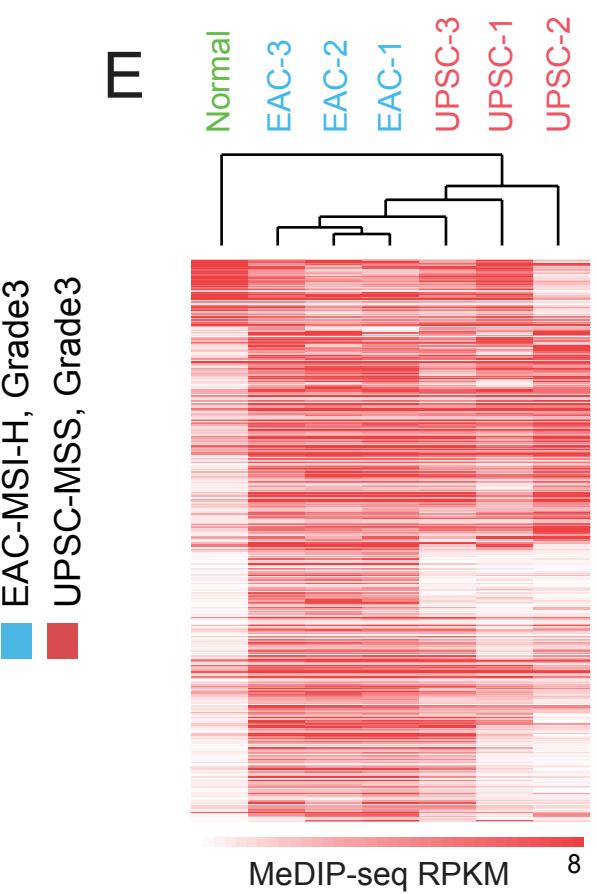


A

DMRs overlap ENCODE open chromatin features

**B**

Genomic distribution of DMRs

**C****D****E**

Supplementary Fig.S3

A

GO Molecular Function

Transcription regulatory region sequence-specific DNA binding

Neurotransmitter transporter activity

Core promoter proximal region DNA binding

GO Biological Process

Regionalization

Neuron fate commitment

Cell differentiation in spinal cord

Anterior/posterior pattern specification

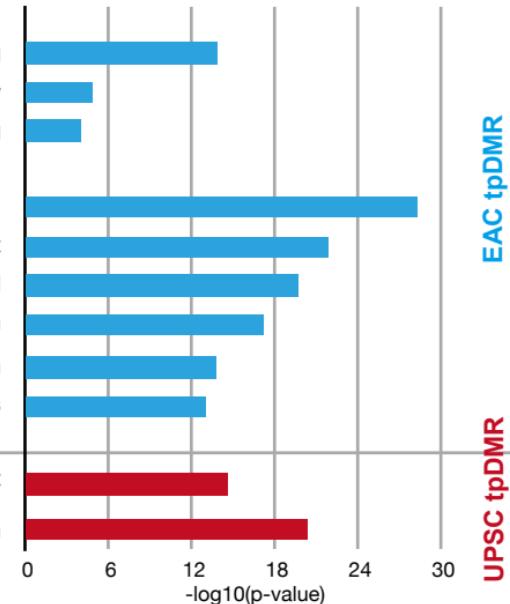
GO Biological Process

Cell fate specification

Forelimb morphogenesis

Regulation of cell development

Regulation of neuron differentiation



B

Hypermethylated promoter in EAC

Cell-cell adhesion

Cell-cell signaling

Transcription factor activity

Second-messenger-mediated signaling

Ion channel complex

Regulation of cAMP biosynthetic process

Endocrine system development

Glutamate receptor activity

Regulation of response to external stimulus

Morphogenesis of an epithelium

Embryonic morphogenesis

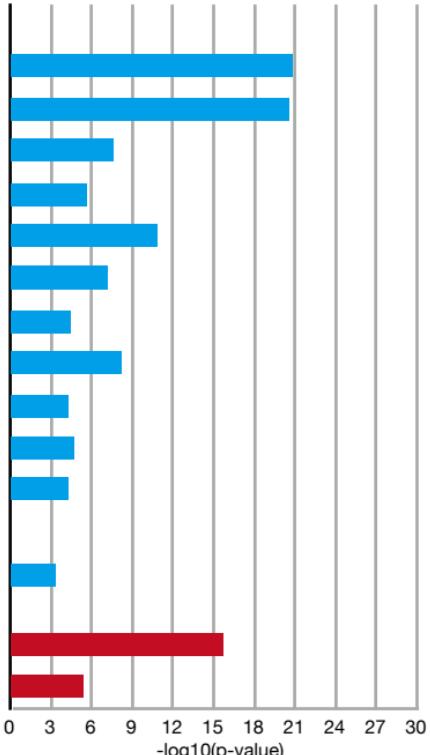
Hypomethylated promoter in EAC

Serine protease

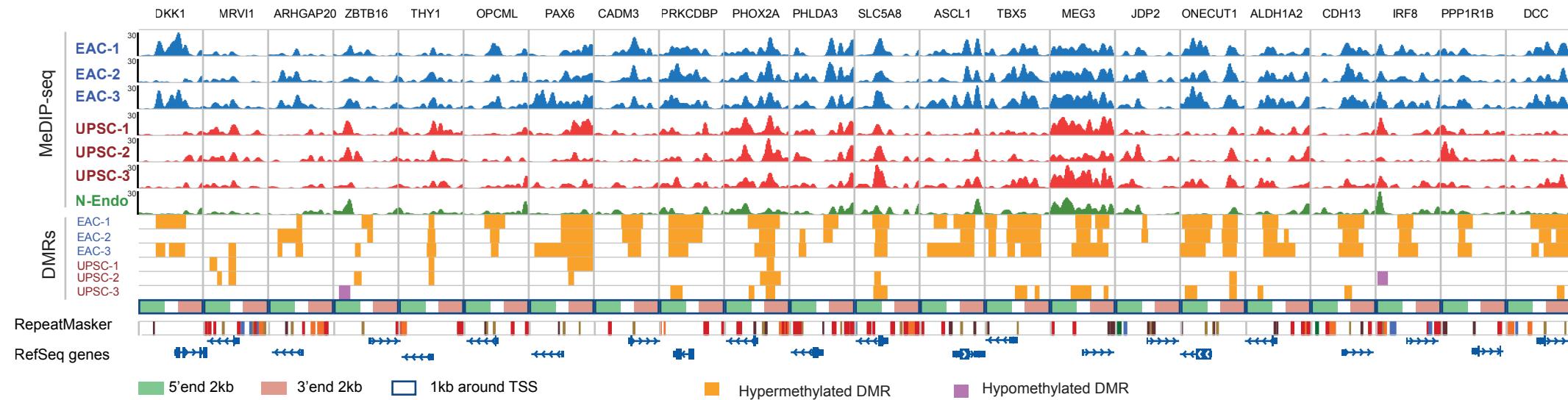
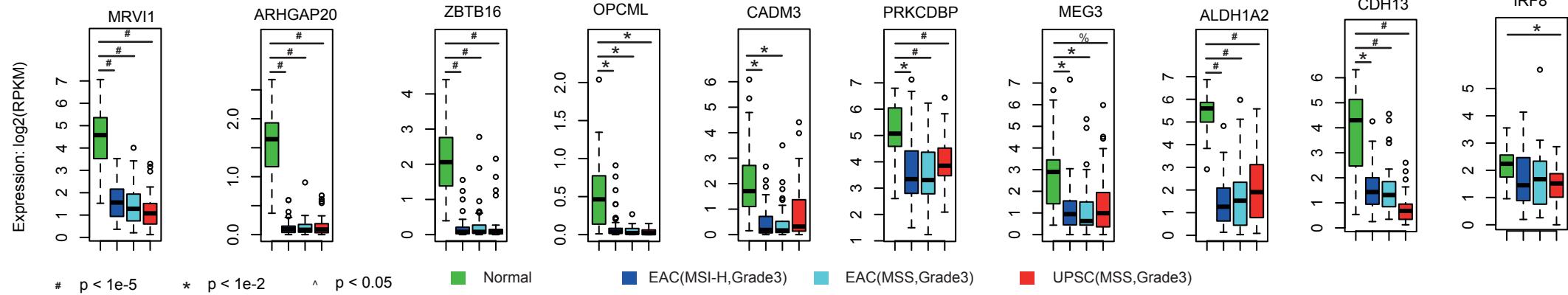
Hypermethylated promoter in UPSC

Cell-cell adhesion

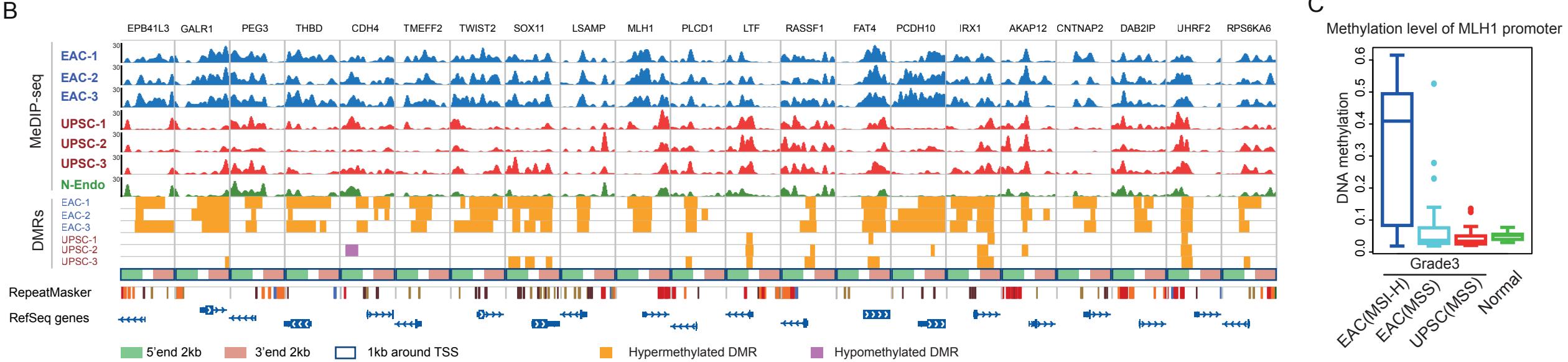
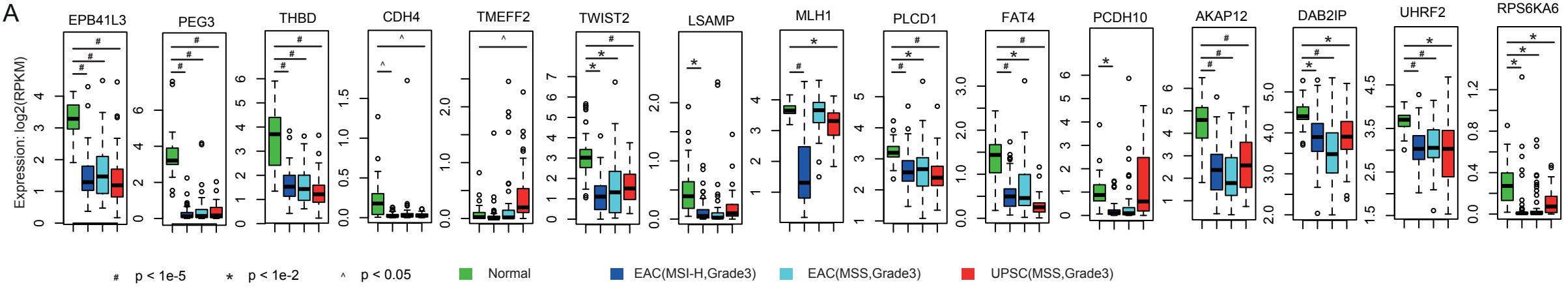
Chromatin assembly



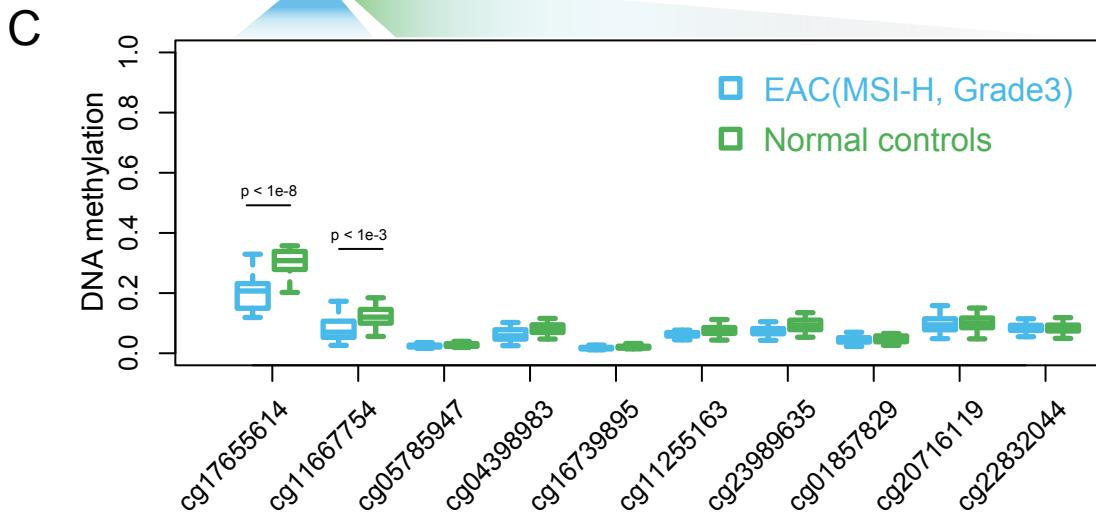
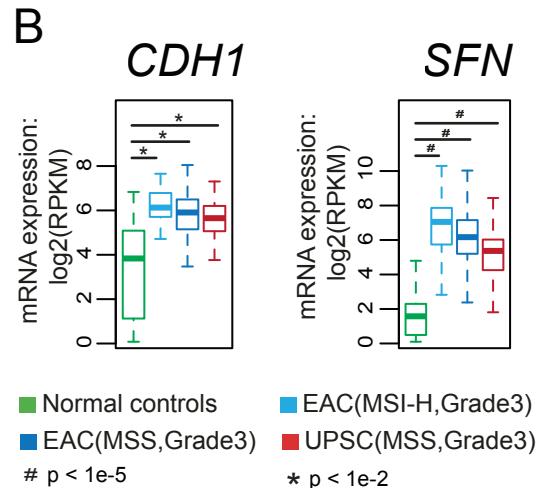
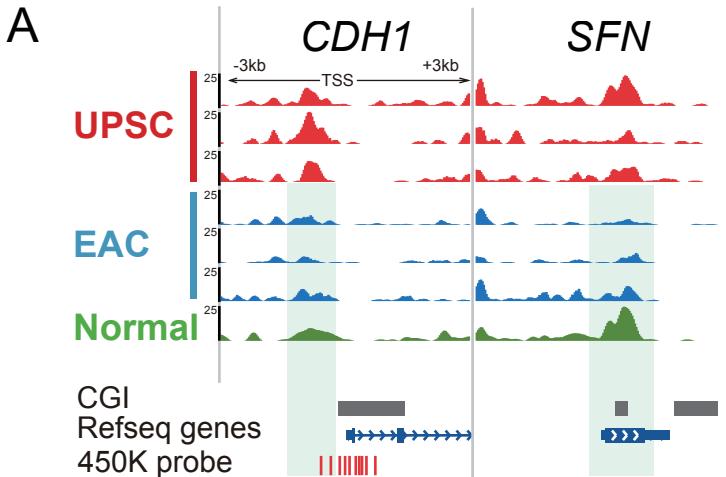
Supplementary Fig.S4



Supplementary Fig.S5

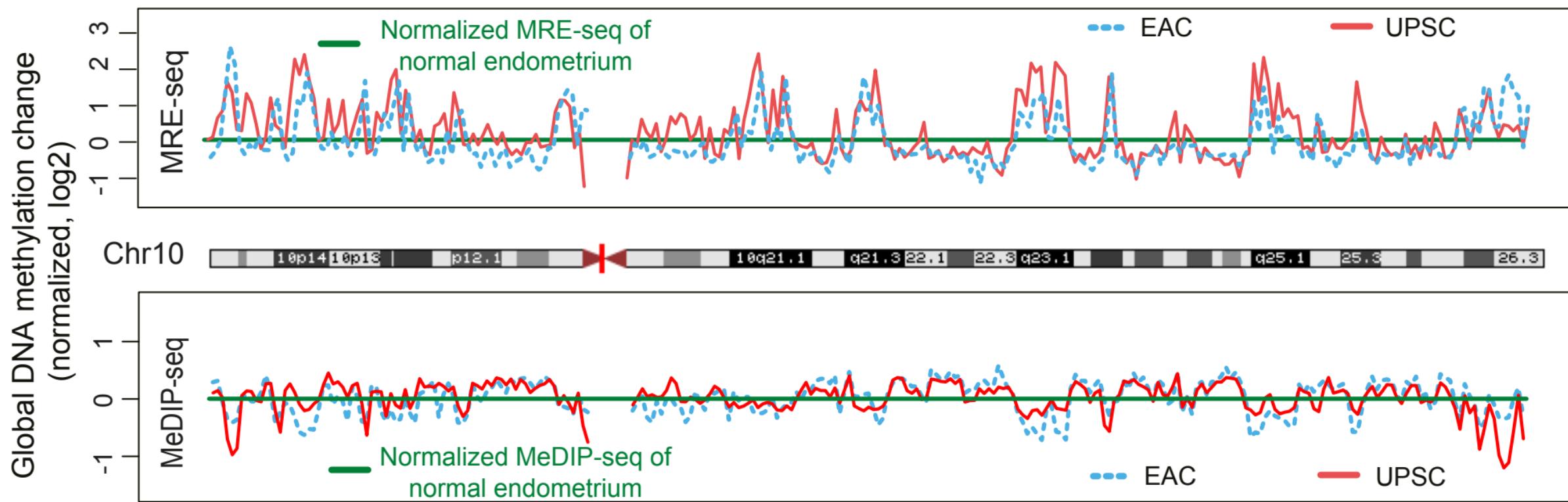


Supplementary Fig.S6



Supplementary Fig.S7

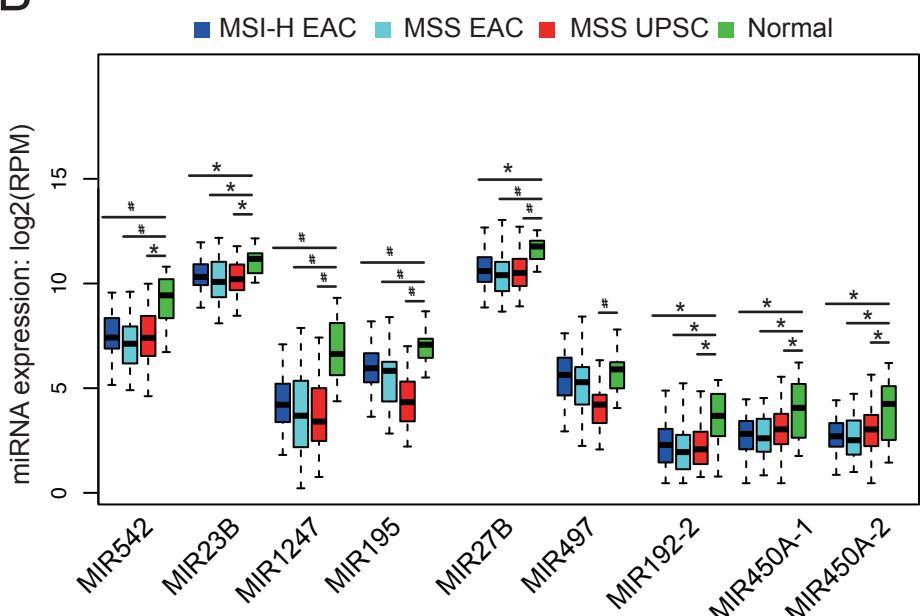
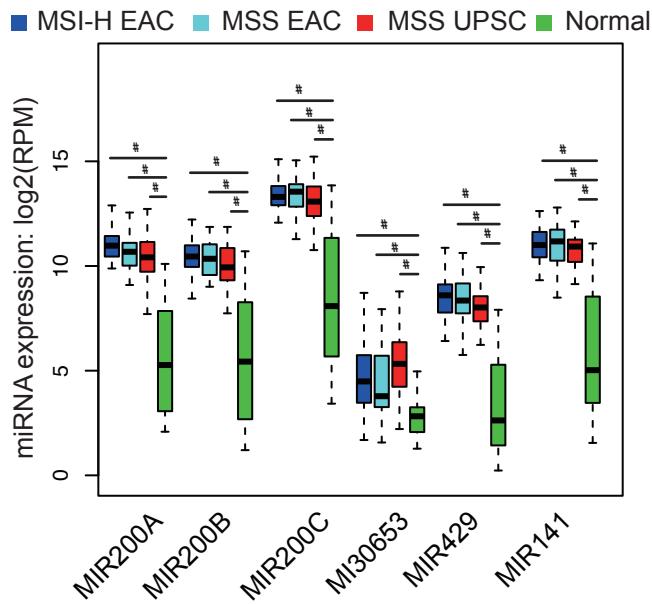
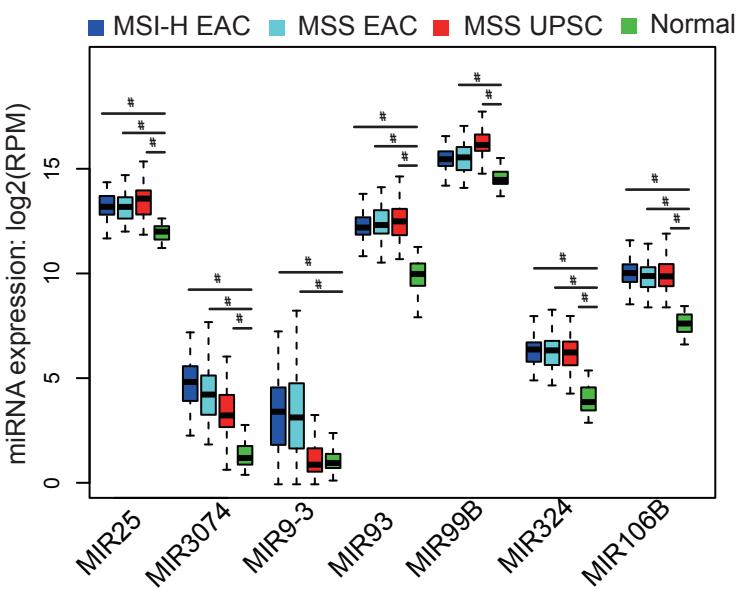
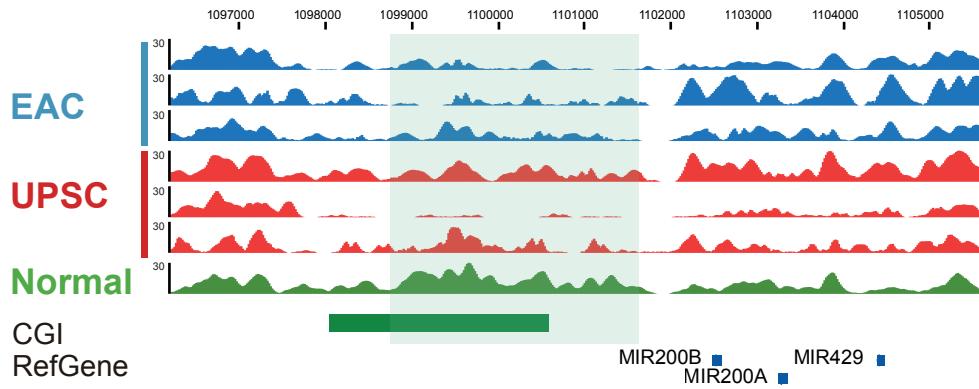
MeDIP and MRE RPKM fold change on chromosome 10 at 500kb resolution



Supplementary Fig.S8

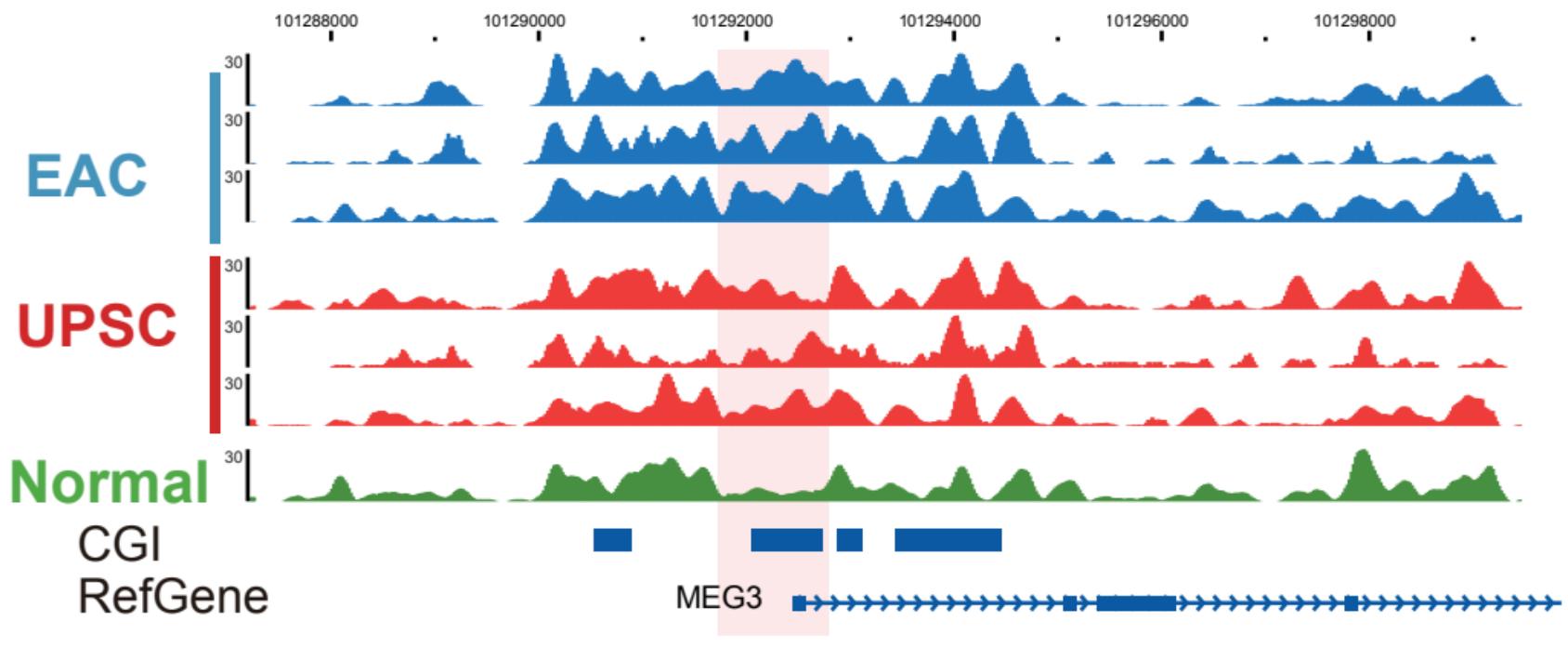
A

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

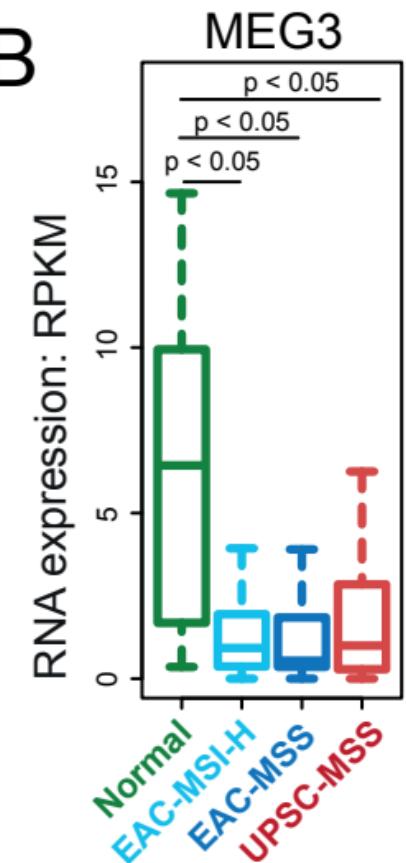
B**C****E****D**

Supplementary Fig.S9

A



B

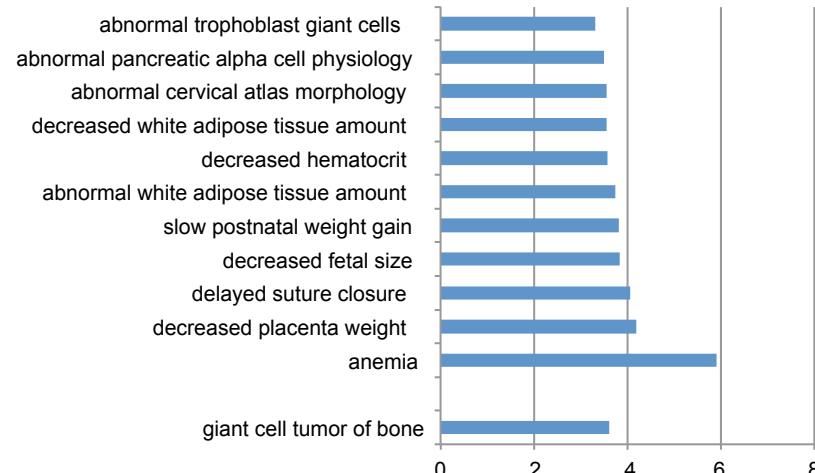


Supplementary Fig.S10

A

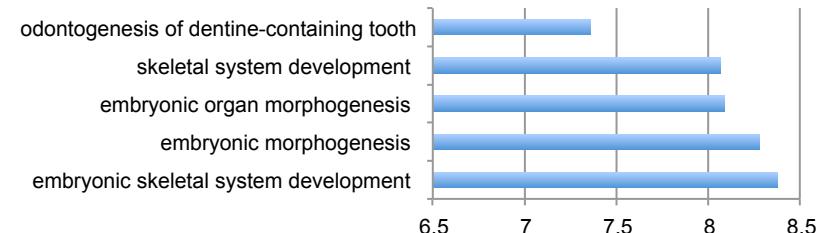
Methylation pattern MMU: EAC DMR with promoter state

Disease Ontology & Mouse Phenotype : -log10(p-value)



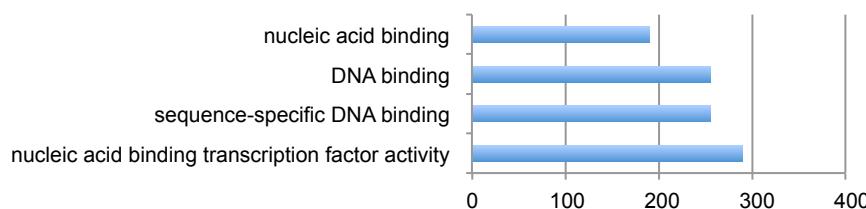
Methylation pattern UMU: EAC DMR with promoter state

GO Biological Process: -log10(p-value)



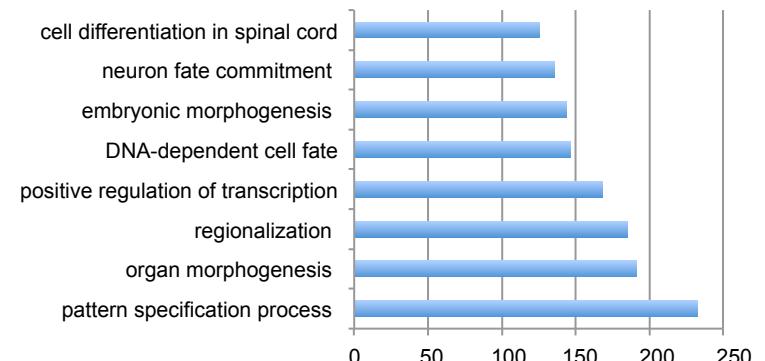
Methylation pattern UUM: UPSC DMR with promoter state

GO Molecular Function: -log10(p-value)

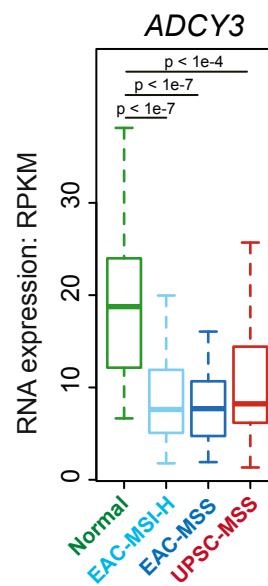


Methylation pattern UUM: EAC DMR with promoter state

GO Molecular Function: -log10(p-value)

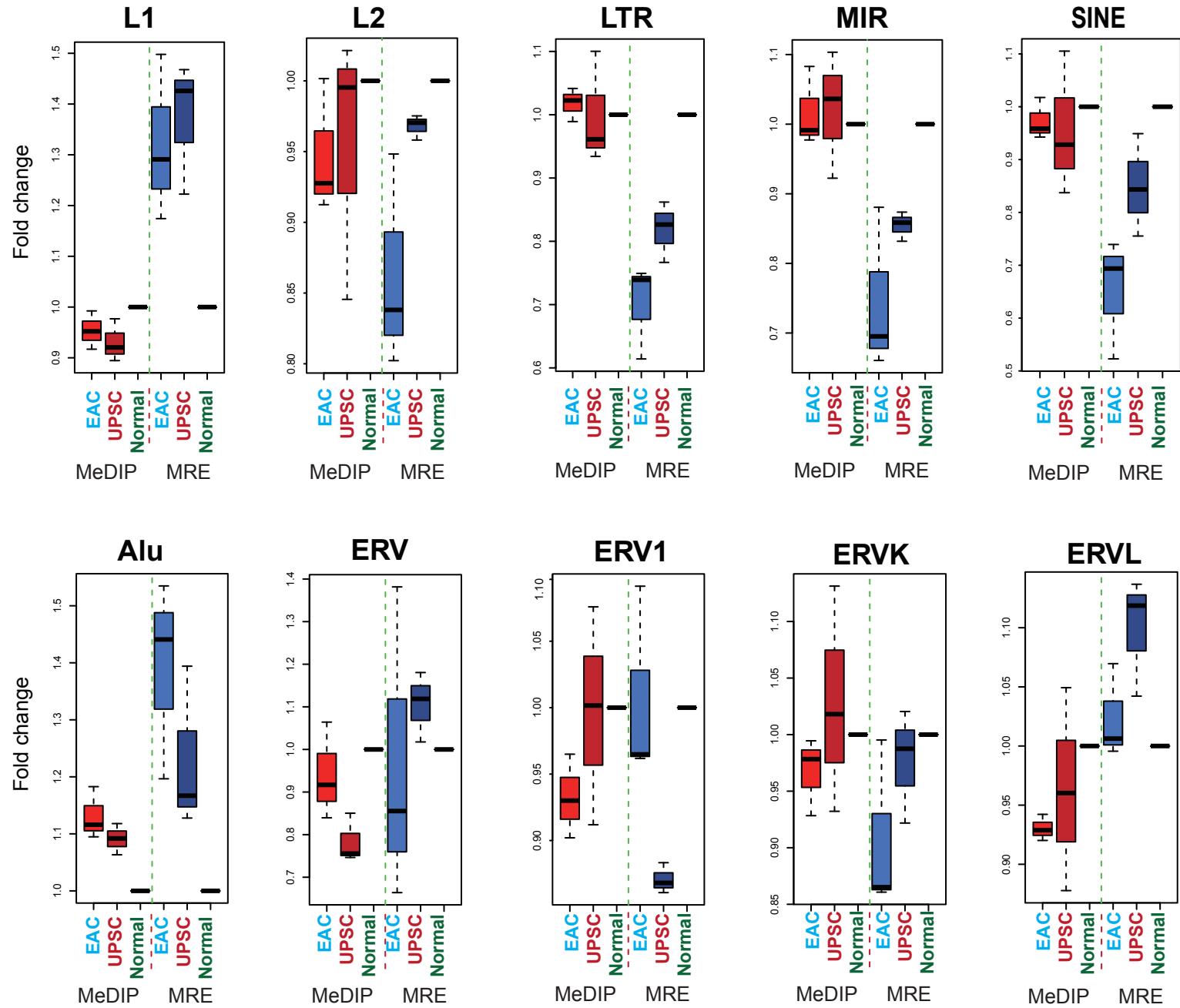


B



Supplementary Fig.S11

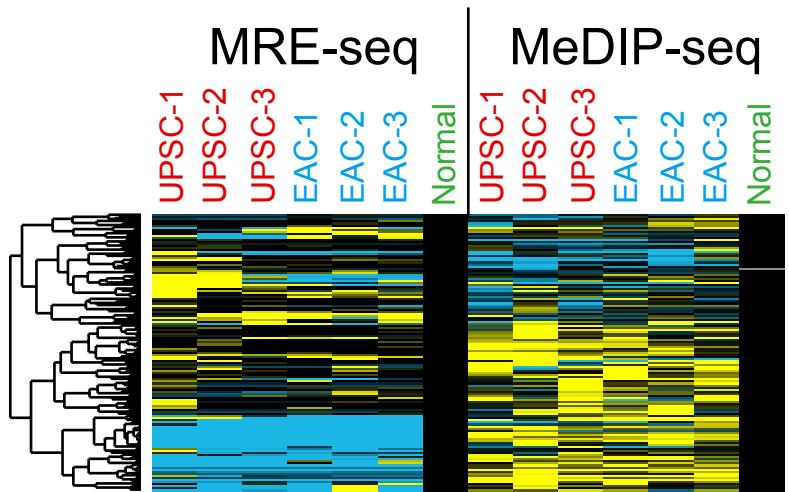
DNA methylation change of transposable element families



Supplementary Fig.S12

A

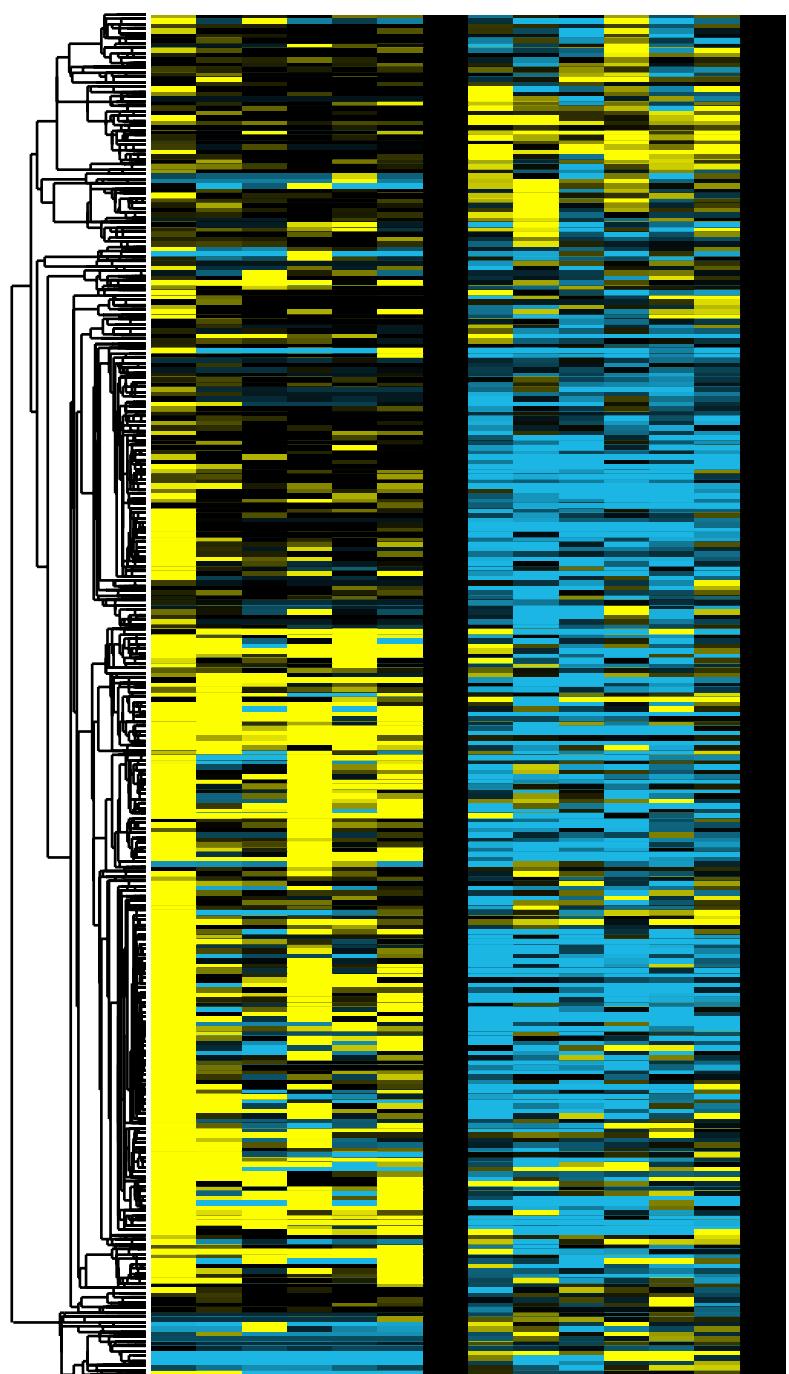
LTR6A
(136 copies)



Hyper-methylated

B

MER52A
(1413 copies)



Hypomethylated

Δ RPKM: -1 0 1