

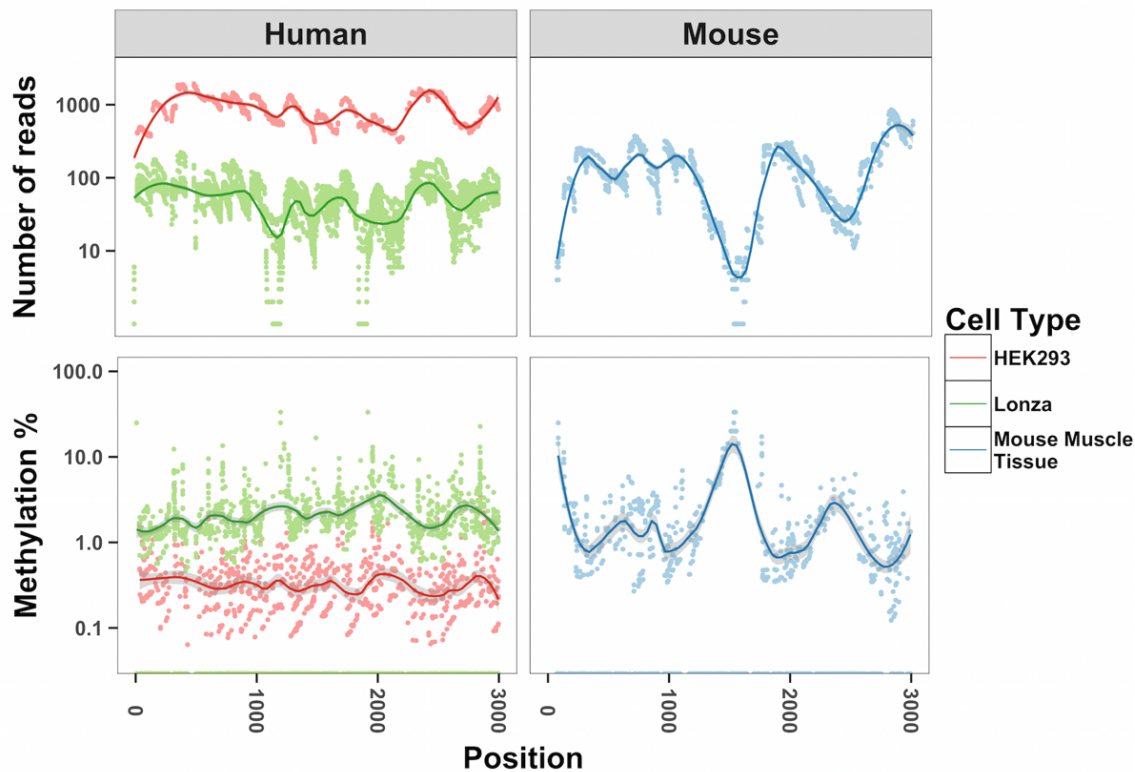
Supplementary Material

Evidence suggesting absence of mitochondrial DNA methylation

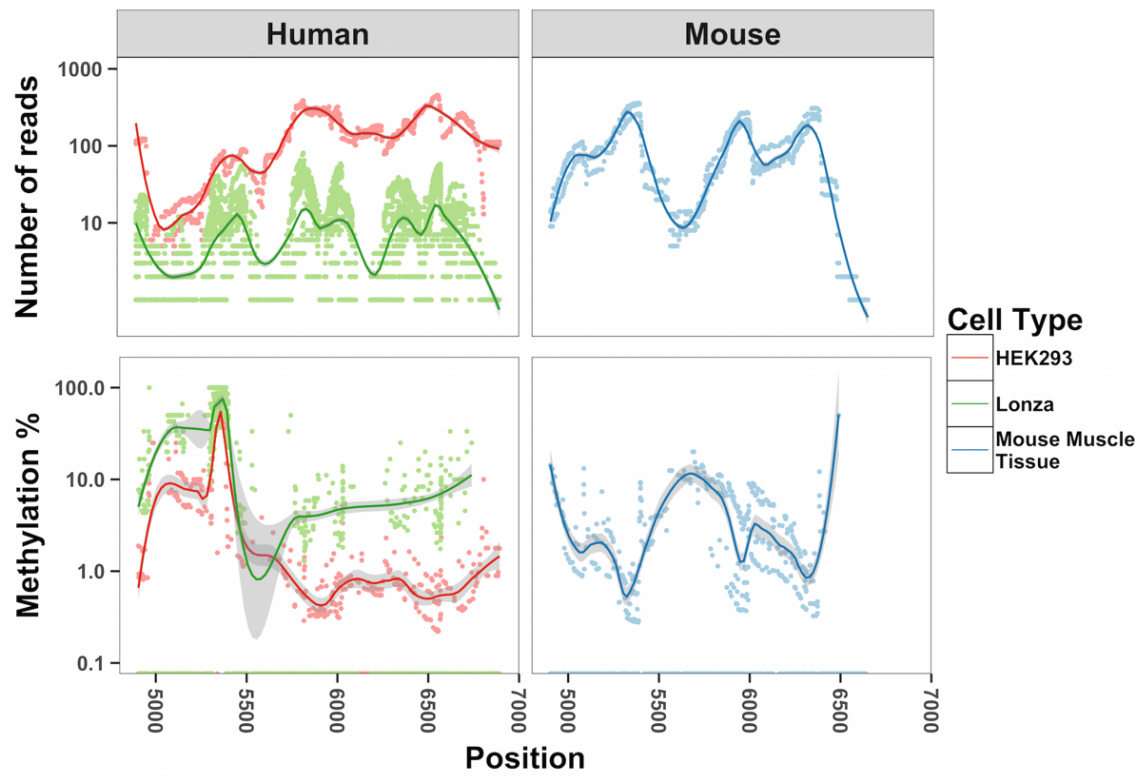
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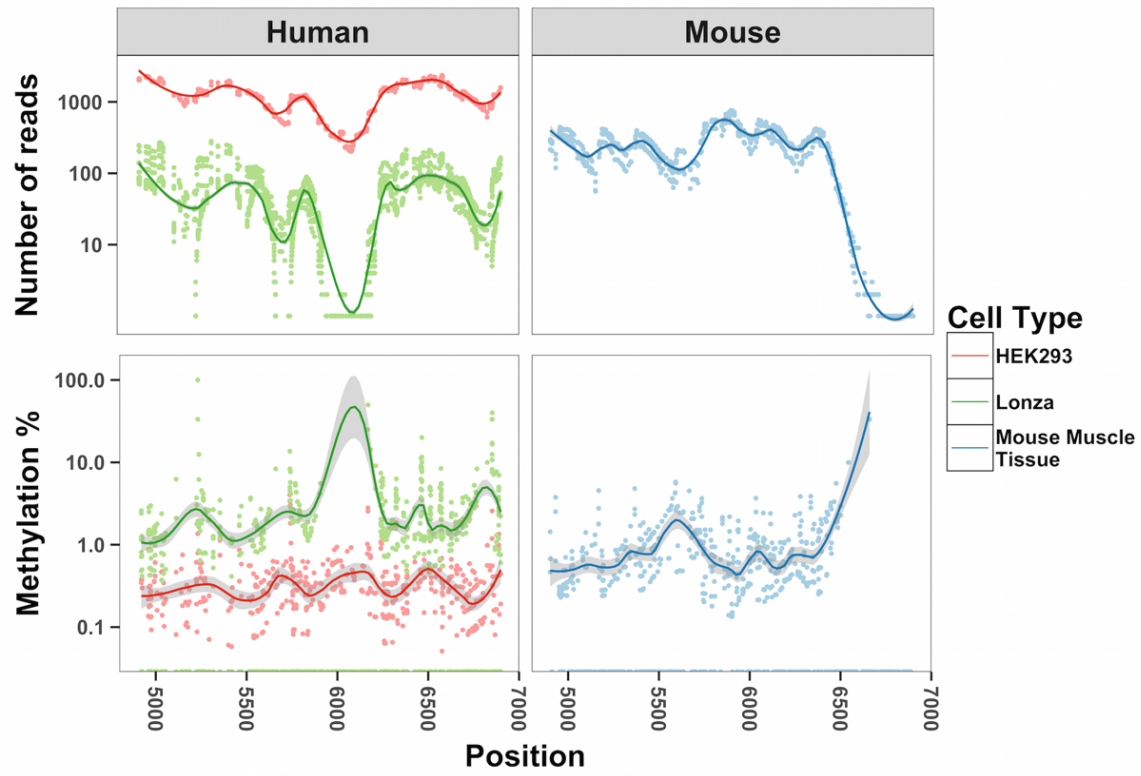
Supplementary Figure 1. Methylation of mtDNA and sequencing depth are inversely correlated in human cells and mouse skeletal muscle. The number of reads and methylation percentage are shown in the mitochondrial genome from position (A) 0-3000 antisense (B) 4900-6900 sense, (C) 4900-6900 antisense (D)14000-16000 sense and (E) 14000-16000 antisense. In red, human HEK293 cells; in green, human primary muscle cells (Lonza); in blue, mouse skeletal muscle. We analysed all cytosines in each of the samples corresponding to between 6,000-12,000 cytosines.

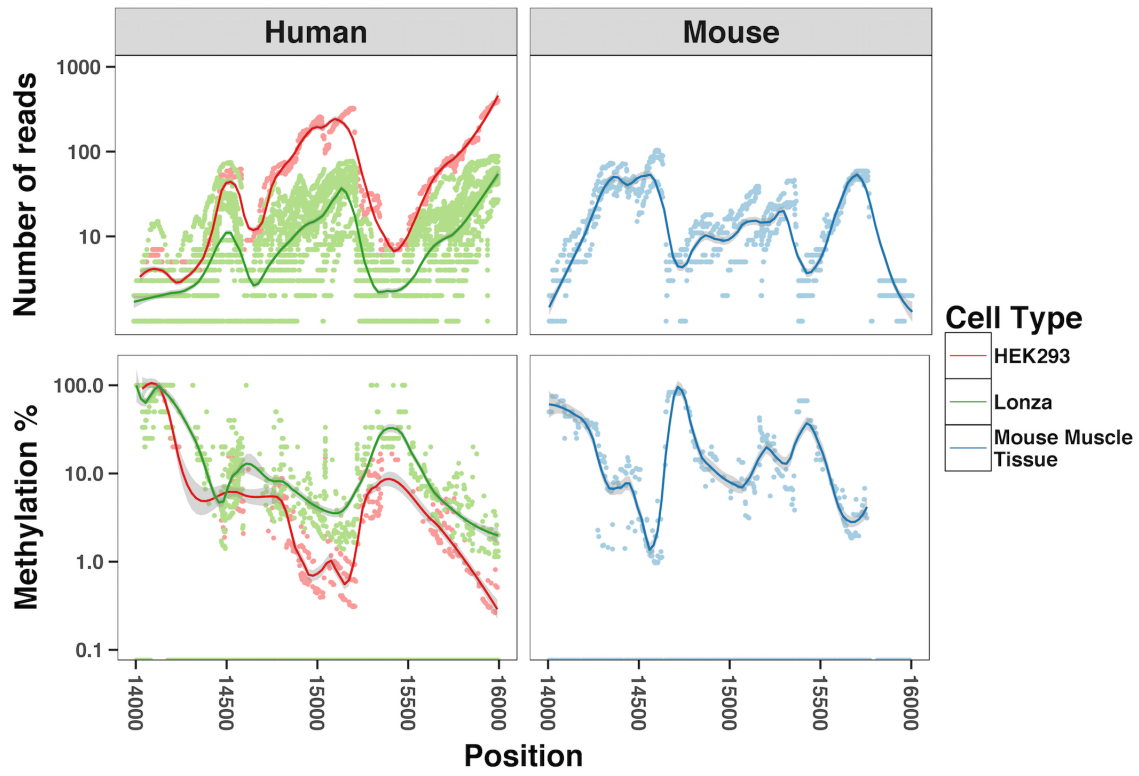
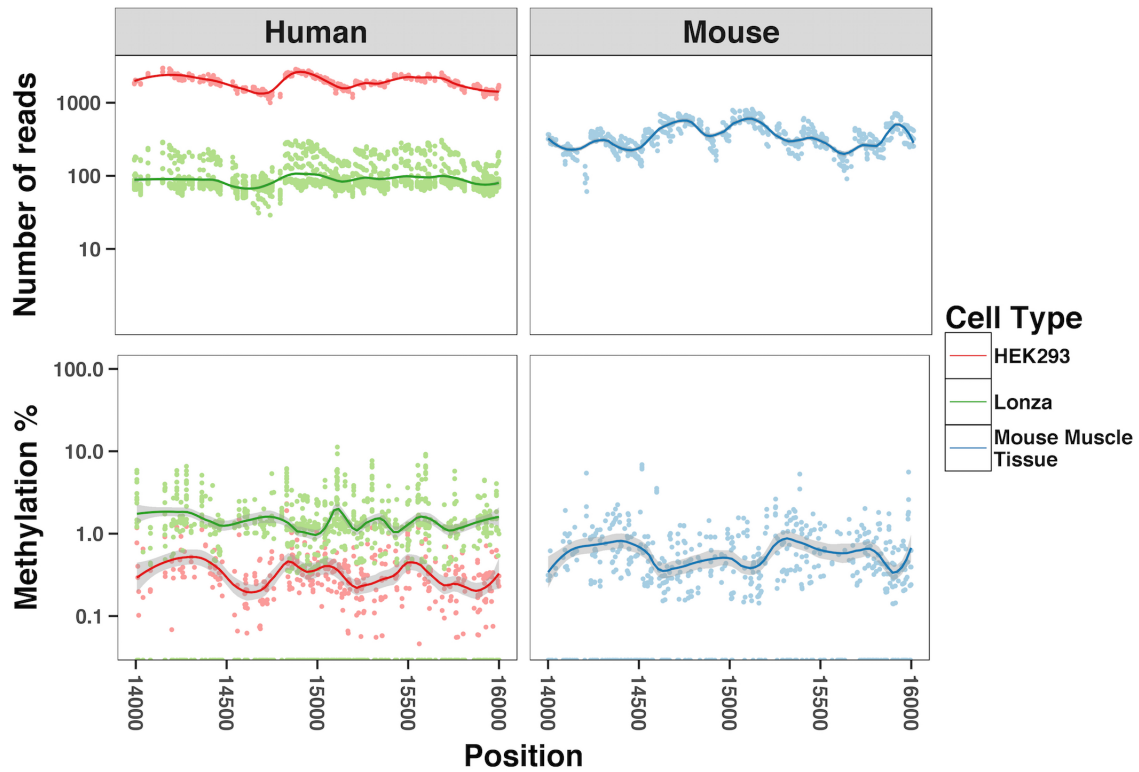
A

B

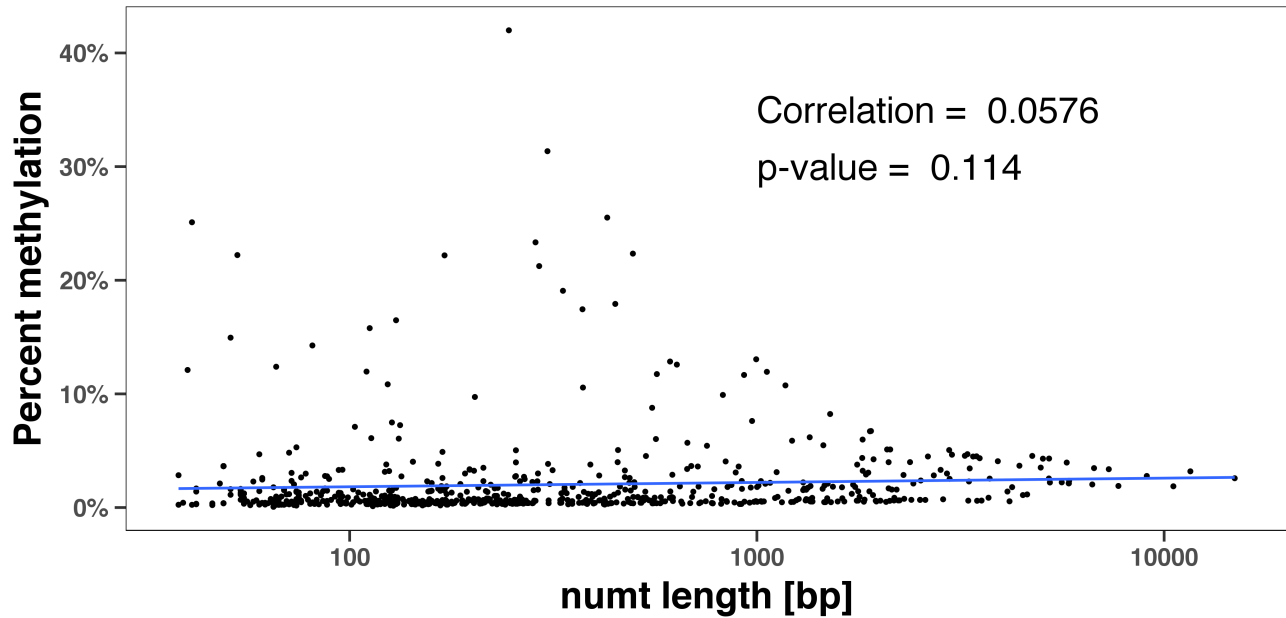
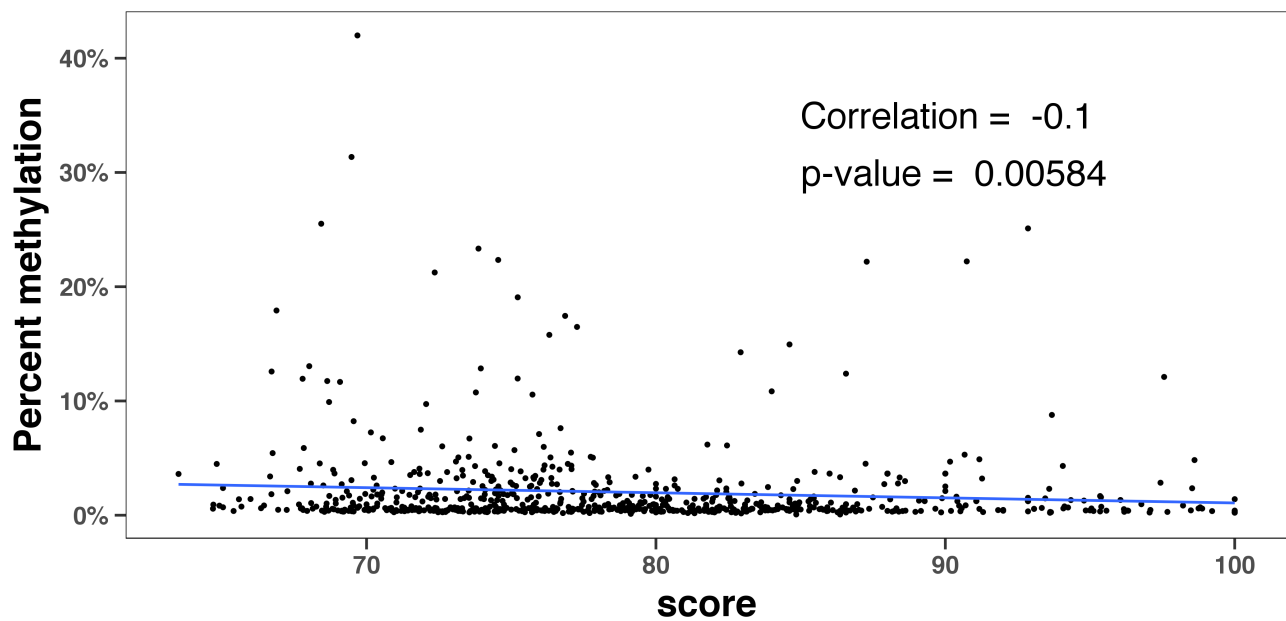


C



D**E**

Supplementary Figure 2. Role of NUMTs in mtDNA methylation levels. (A) Correlation between mtDNA methylation and NUMT length ($R=0.06$, $P=0.11$). (B) Correlation between mtDNA methylation and NUMT score ($R=-0.1$, $P=0.006$). The NUMT score is described elsewhere (Ramos et al. 2011) and is a score representing how well each NUMTs align to mtDNA.

A**B**

REFERENCE

Ramos, A. et al., 2011. Nuclear insertions of mitochondrial origin: Database updating and usefulness in cancer studies. *Mitochondrion*, 11(6), pp.946–953.