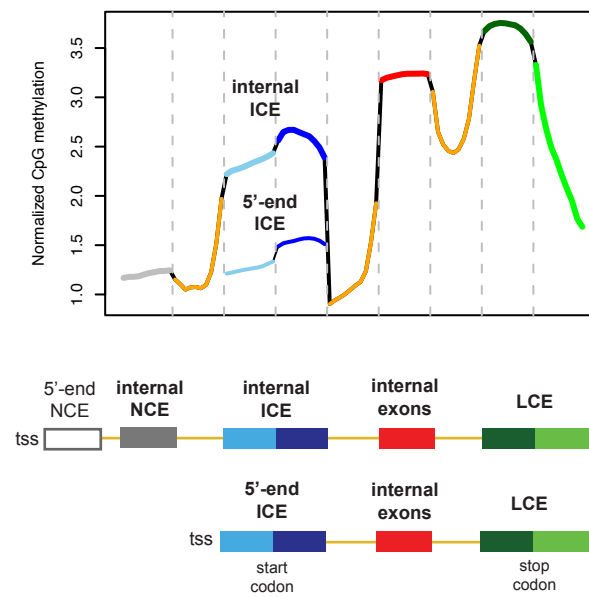


Supplementary Fig. 5



CpG methylation normalized by CpG density on exons and introns.

CpG methylation, measured as the NRC, was divided by CpG density and plotted within the transcript partitioned into non-coding exons, coding exons, and introns.

ICEs (initial coding exons) and LESs (last coding exons) are broken into the UTR (light blue or light green) and coding region (dark blue or dark green).