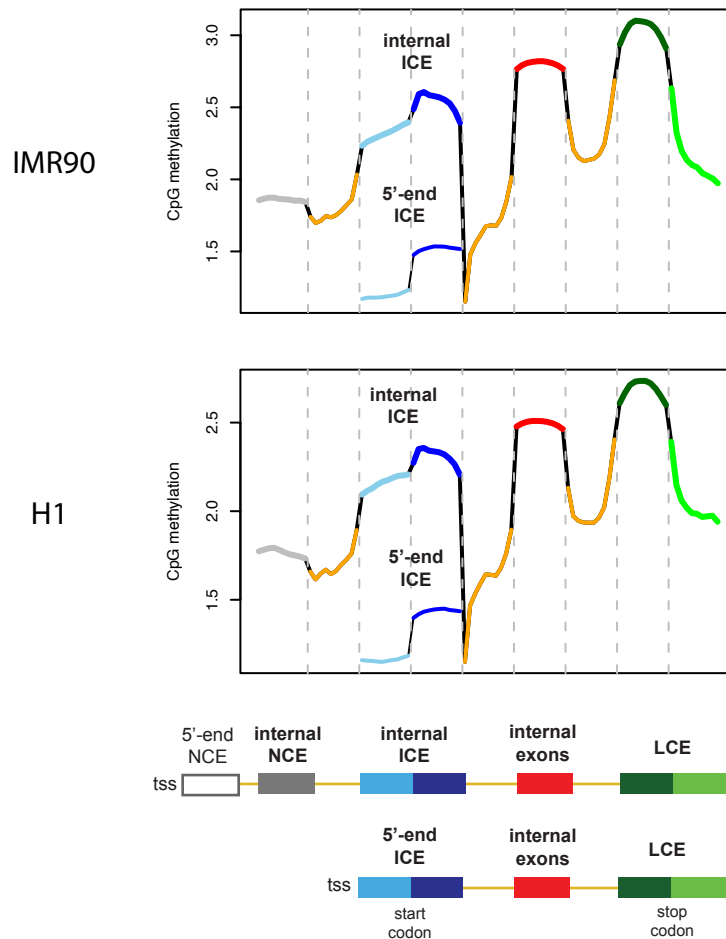


Supplementary Fig. 6



CpG methylation measured by bisulphite sequencing on exons and introns.

CpG methylation, measured as the average percentage of methylation of covered CpG sites, was 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).