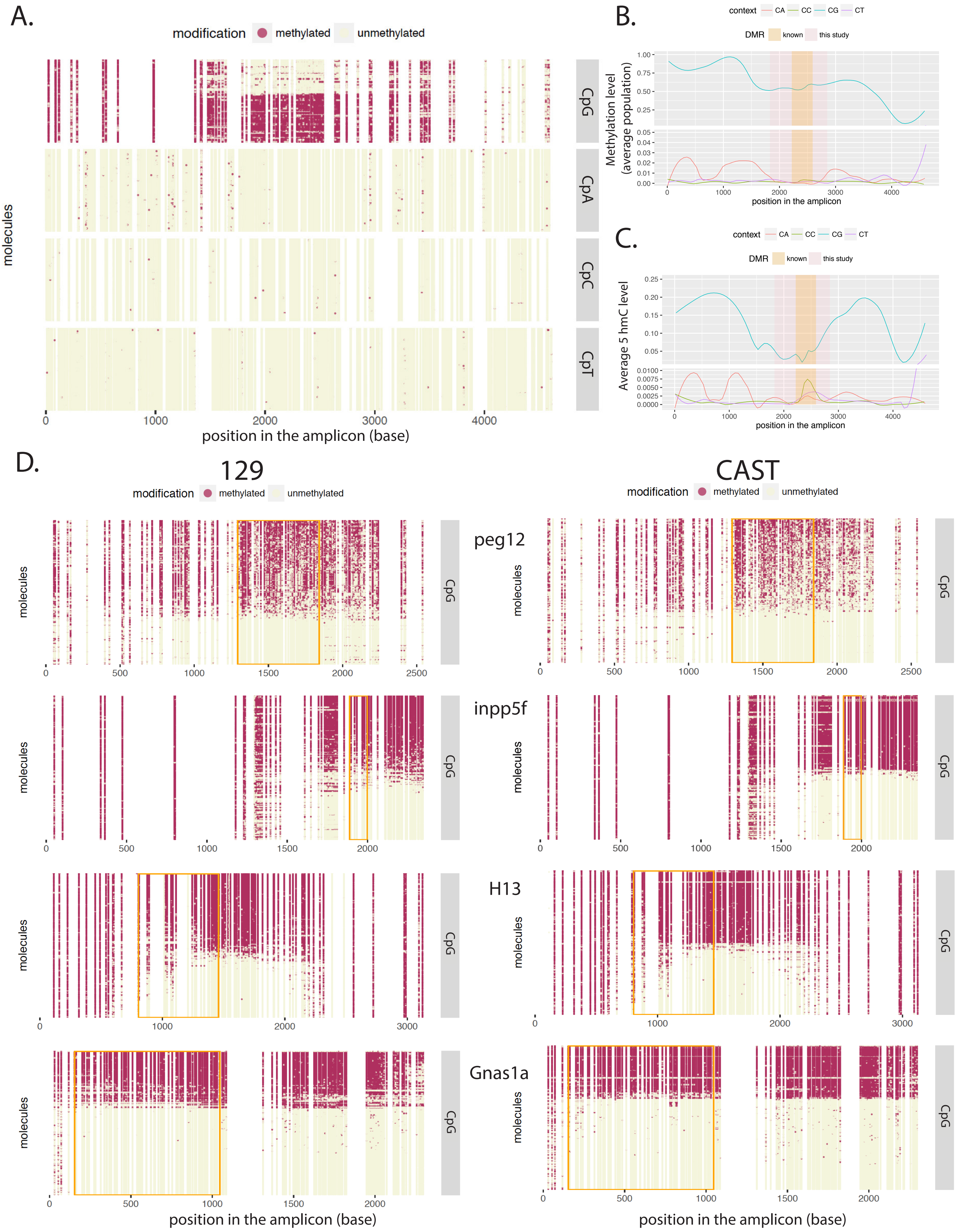

Supplemental Figure 5

(A) Methylation states (beige: unmethylated; red: methylated) of individual cytosines at each dinucleotide context (CpG, CpA, CpC, CpT) at single molecule level of the 4.6kb amplicon in the imprinted Inpp5f_v2 locus. CpA methylation (2nd panel) appears to be completely missing from the imprinted DMR (observable in the top panel). **(B)** Trend plot showing the population level methylation abundance of each cytosine dinucleotide context in the amplified region of Inpp5f_v2 gene. CpA methylation (red) appears to be lower in the DMR compared to the surrounding region. **(C)** Trend plot showing the population level hydroxymethylation abundance of each cytosine dinucleotide context in Inpp5f_v2 amplicon. **(D)** Methylation states (beige: unmethylated; red: methylated) of individual CpG sites at single molecule level of 4 previously reported DMR regions from two mouse inbred strains: Cast/EiJ (CAST, Right) and 129X1/SvJ (129, left).