FigS16

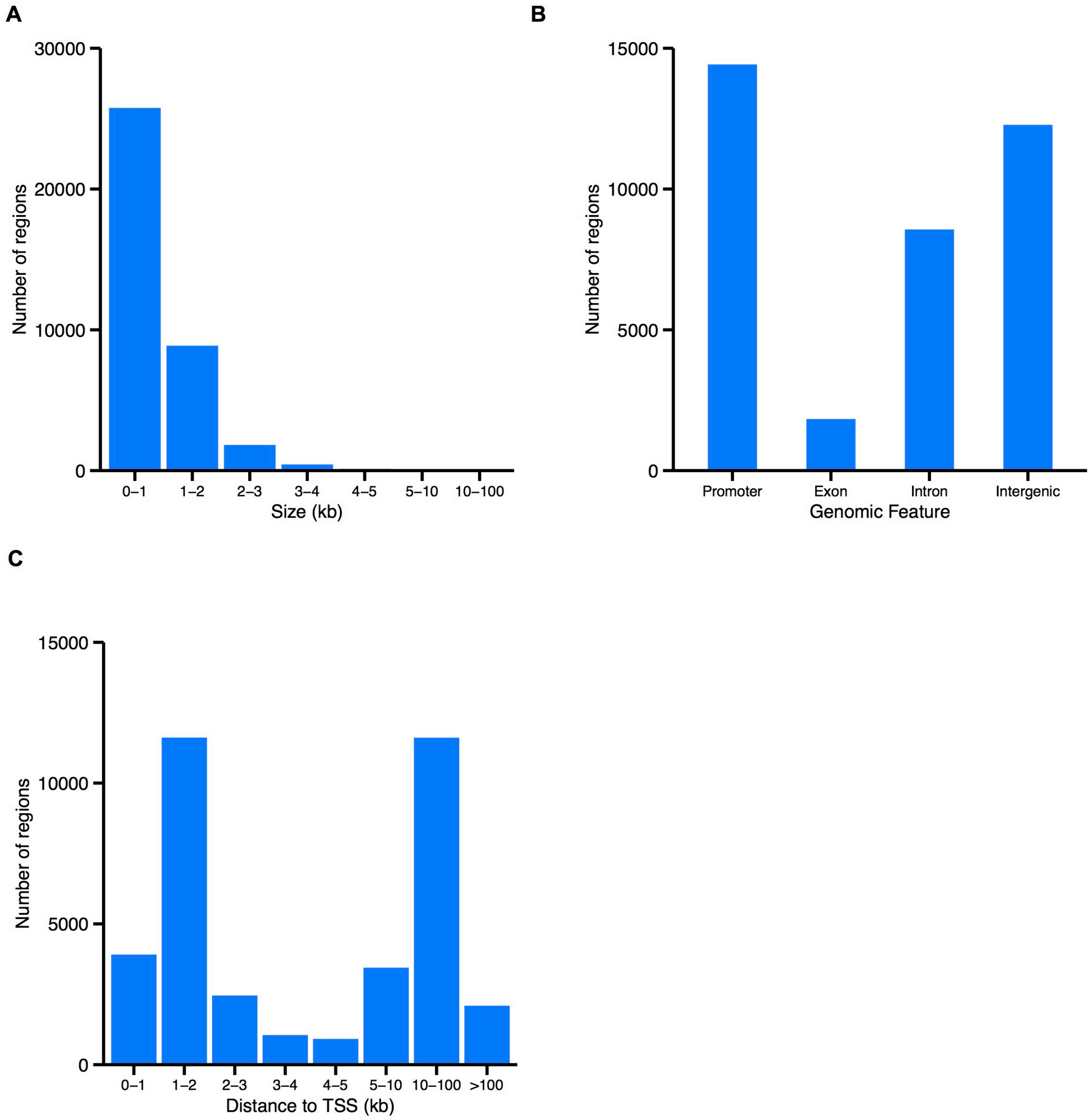

Figure S16. Characterization of constitutively unmethylated regions (UMRs).

A. Distribution of UMR lengths at each range. B. Percentage of UMRs at each length range. C. Distance of UMRs to the nearest transcription start sites (TSSs).