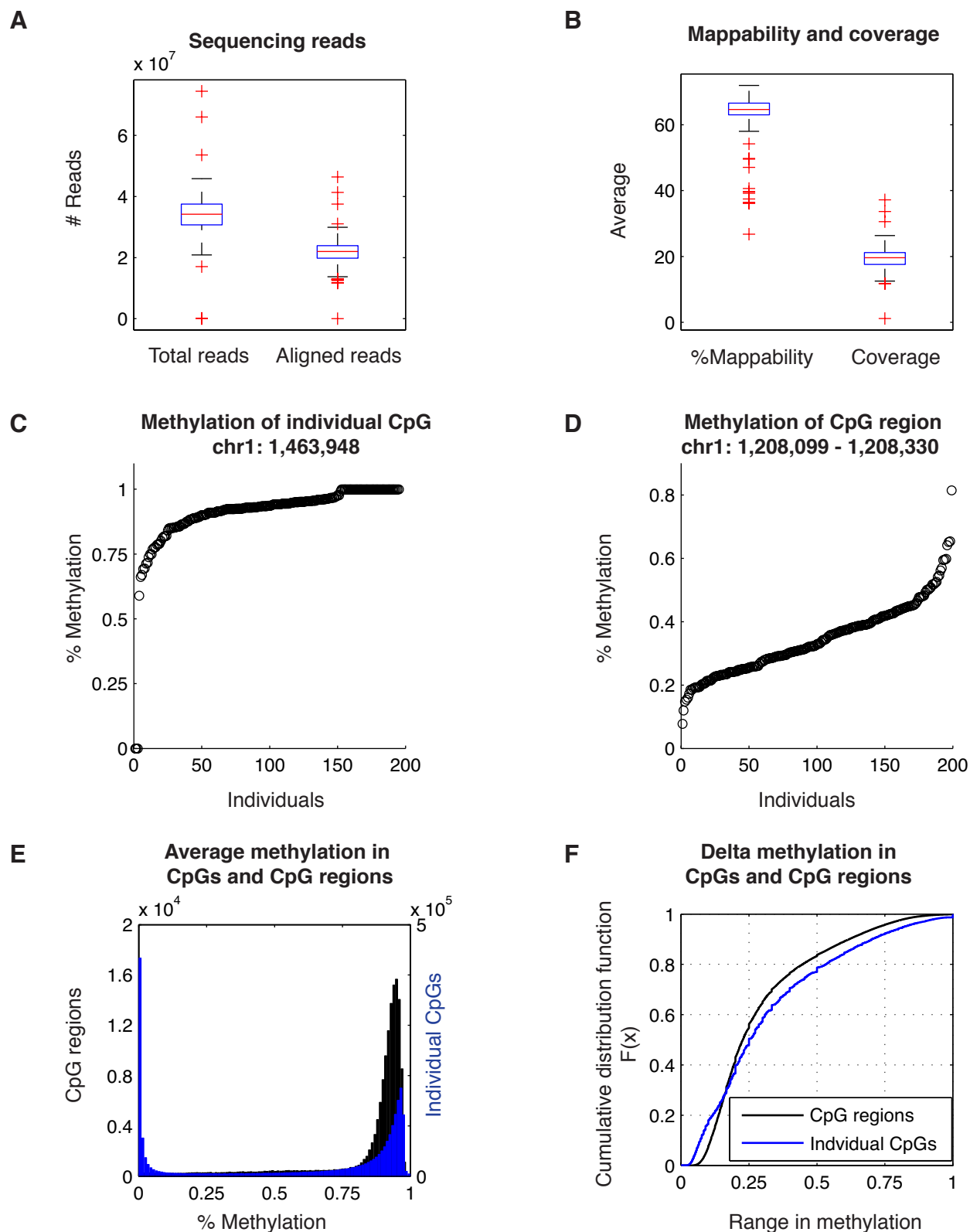


**Figure S1. Sample statistics**



**Figure S1.** Sample statistics. (A) Total number of reads and aligned reads in all RRBS libraries. (B) Mappability and coverage in all RRBS libraries. (C-D) Methylation patterns for an (C) individual CpG and (D) a CpG methylation region. The x-axes are individual samples, where each dot is a sample. The y-axes are the methylation levels for the CpG in that sample. (E) Histogram showing distribution of average methylation levels for individual CpGs (blue) and CpG regions (black). (F) Distribution of the range in methylation levels across samples for individual cytosines (blue) and methylation regions (black). The x-axis is delta methylation levels across individuals, and the y-axis is the cumulative distribution function  $F(x)$ .