



S5 Fig. Normalized coverage depth near the TSS, ESS, and EES in the 1000 Genome Project.

Coverage depth at each nucleotide normalized to regional mean depth within ± 1000 bp of the TSS and ± 500 bp of the ESS and EES in randomly selected samples from the 1000 Genome Project. Each grey line represents a sample. Red lines represent the mean value of all samples.