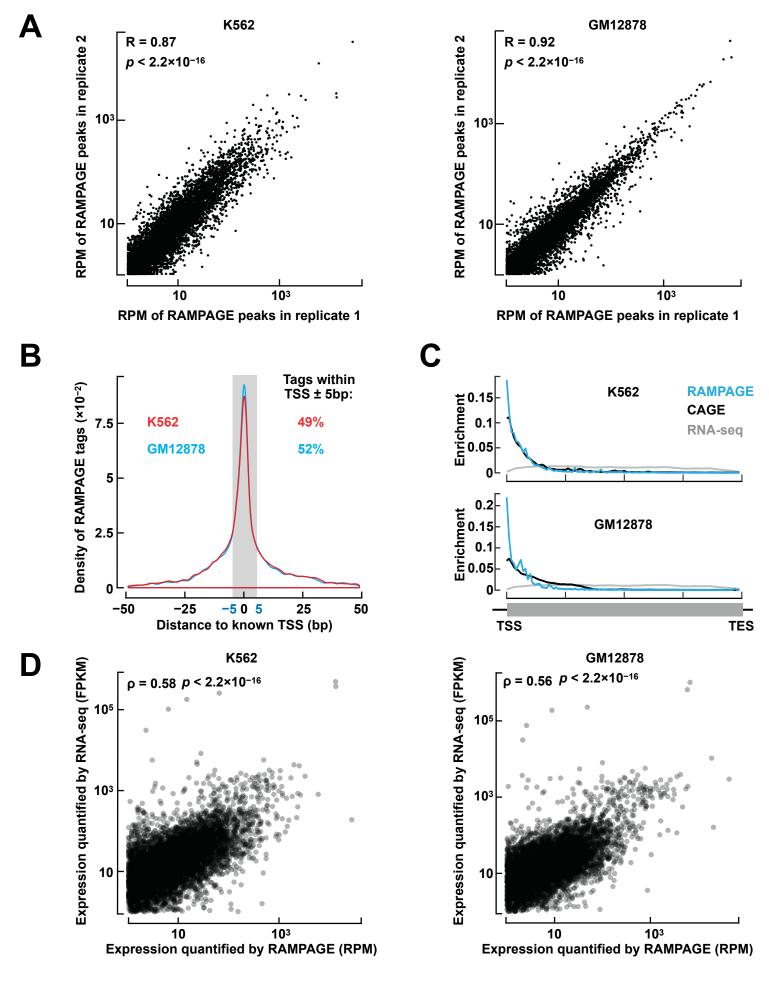# Zhang et al., Supplemental Figure S1

**Supplemental Figure S1. RAMPAGE data facilitate the identification of TSSs.**

A. High correlation of RAMPAGE signal levels between biological replicates. Pearson correlation coefficients (R) are 0.87 for K562 and 0.92 for GM12878. The mean ± sd for R across 70 RAMPAGE biosamples each with two biological replicates are 0.79 ± 0.16.

B. Roughly 50% of RAMPAGE peaks are located within the ± 5 bp window (grey box) of known TSSs.

C. RAMPAGE reads (blue line) show a stronger enrichment than CAGE reads (black line) at the 5′-ends of genes. In contrast, RNA-seq reads (grey line) show an even distribution over the entire gene body.

D. Expression quantification by RAMPAGE is positively correlated with expression quantification by RNA-seq—Spearman's rank correlation coefficients are 0.56 and 0.58 in two cell lines: K562 and GM12878.