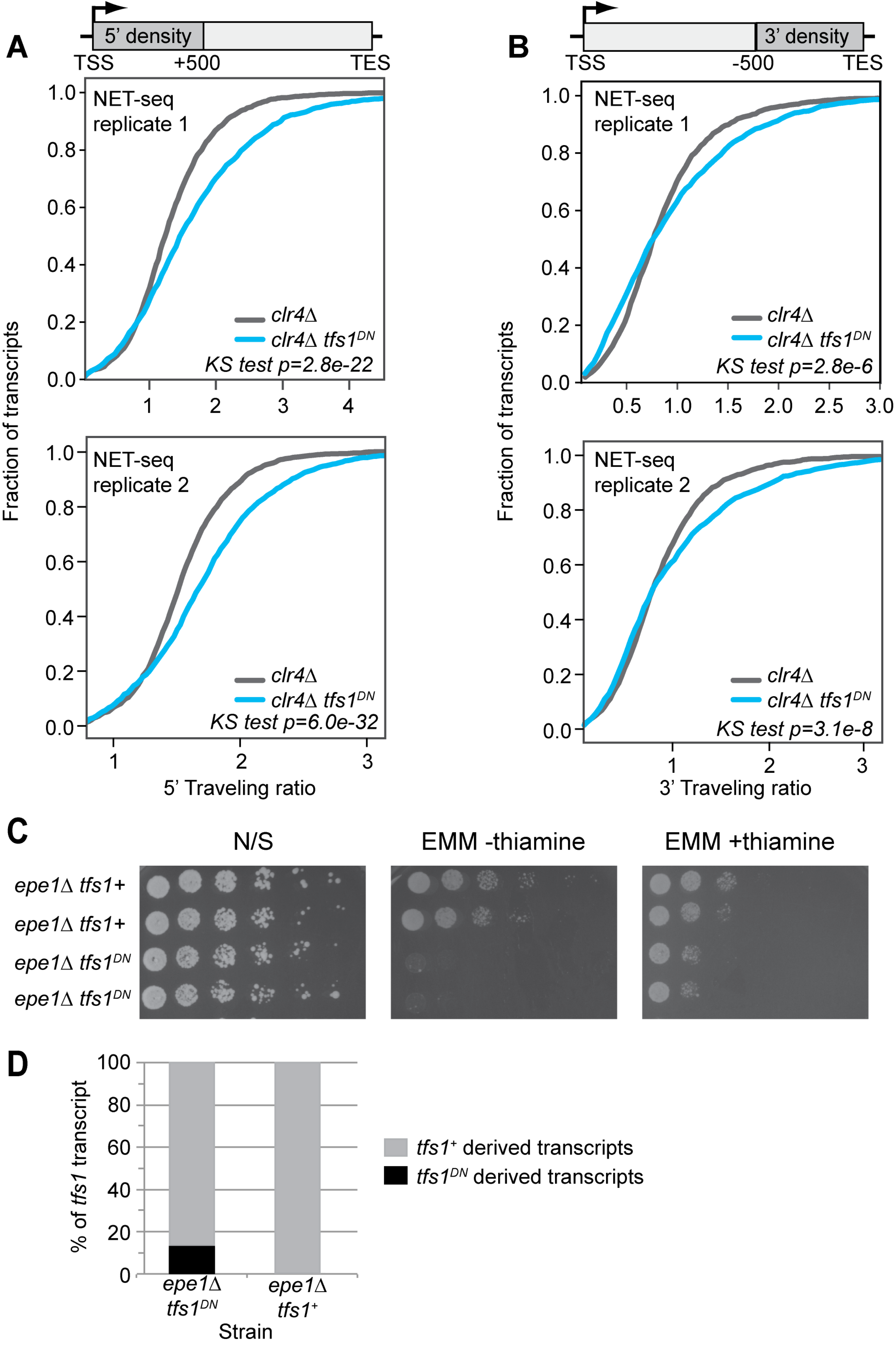
Supplemetal Figure S6.



Supplemental Figure S6. *pnmt1*$^{+}$-*tfs1*^{DN} expression impacts traveling ratios genome wide. A) Cumulative distribution function (cdf) plots of 5’ traveling ratios for *clr4*Δ (dark grey) to *clr4*Δ *tfs1*^{DN} (blue) NET-seq strains for two replicates. KS tests were conducted for p-values. **B)** Cumulative distribution function (cdf) plots of 3’ traveling ratios for *clr4*Δ (dark grey) to *clr4*Δ *tfs1*^{DN} (blue) NET-seq strains for two replicates. KS tests were conducted for p-values. **C)** Growth assays on *epe1*Δ *tfs1*$^{+}$ and *epe1*Δ *tfs1*^{DN} strains. Cells were plated on non-selective rich YS medium (N/S), EMM medium in the absence of thiamine (EMM -thiamine), and EMM medium containing 15uM thiamine (EMM +thiamine). **D)** Percent of total *tfs1* reads derived from the *tfs1*$^{+}$ (grey) and *tfs1*^{DN} alleles (black) in *pnmt1*+ repressible conditions (EMM 15uM thiamine) obtained from RNA-seq analysis of *epe1*Δ *tfs1*^{DN} and *epe1*Δ *tfs1*$^{+}$ strains (no reads corresponding to the *tfs1*^{DN} allele were observed in the *epe1*Δ *tfs1*$^{+}$ strain).