Figure S32

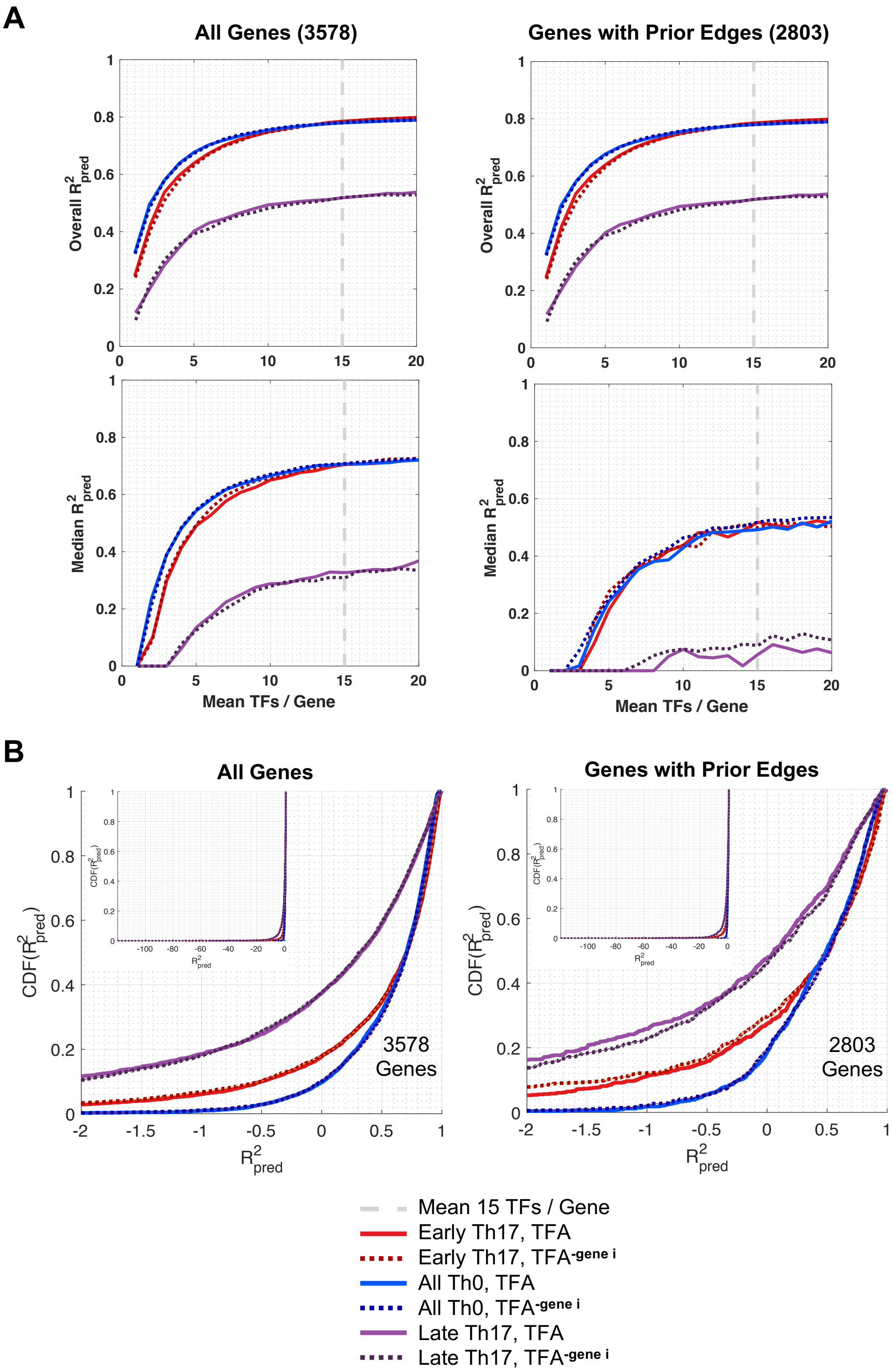

Figure S32. **Effect of individual target genes on prediction using prior-based TFA.** For the three out-of-sample prediction challenges, gene models were built using **Equation 2** ("TFA") or **Equation 6** ("TFA$^{\text{-gene i}}$"), using mLASSO-StARS, Th17 ATAC prior, and moderate prior reinforcement. **(A)** Overall R^2_{pred} and median per-gene R^2_{pred} for all genes or limited to those genes with edges in the prior. **(B)** The CDFs of per-gene R^2_{pred} are plotted for average model size of 15 TFs/gene. Thus, in this context, evaluation of out-of-sample gene expression prediction can be accomplished using **Equation 2** (versus the more computationally intensive **Equation 6**).