(A) Linnorm   (B) scone   (C) scran

(D) DESeq2   (E) logCPM   (F) TMM

(G) FTT   (H) none

S1 Fig: Heatmaps of normalized and denoised data on the RNAmix_CEL-seq2 dataset [36]. We use the R code provided in Tian et al. [37] to apply all normalization methods that we can successfully run on the RNAmix_CEL-seq2 dataset. We also apply our FTT-based preprocessing method on the data. We use the postprocessing and plotting scripts in [37] to generate plots for our analysis.