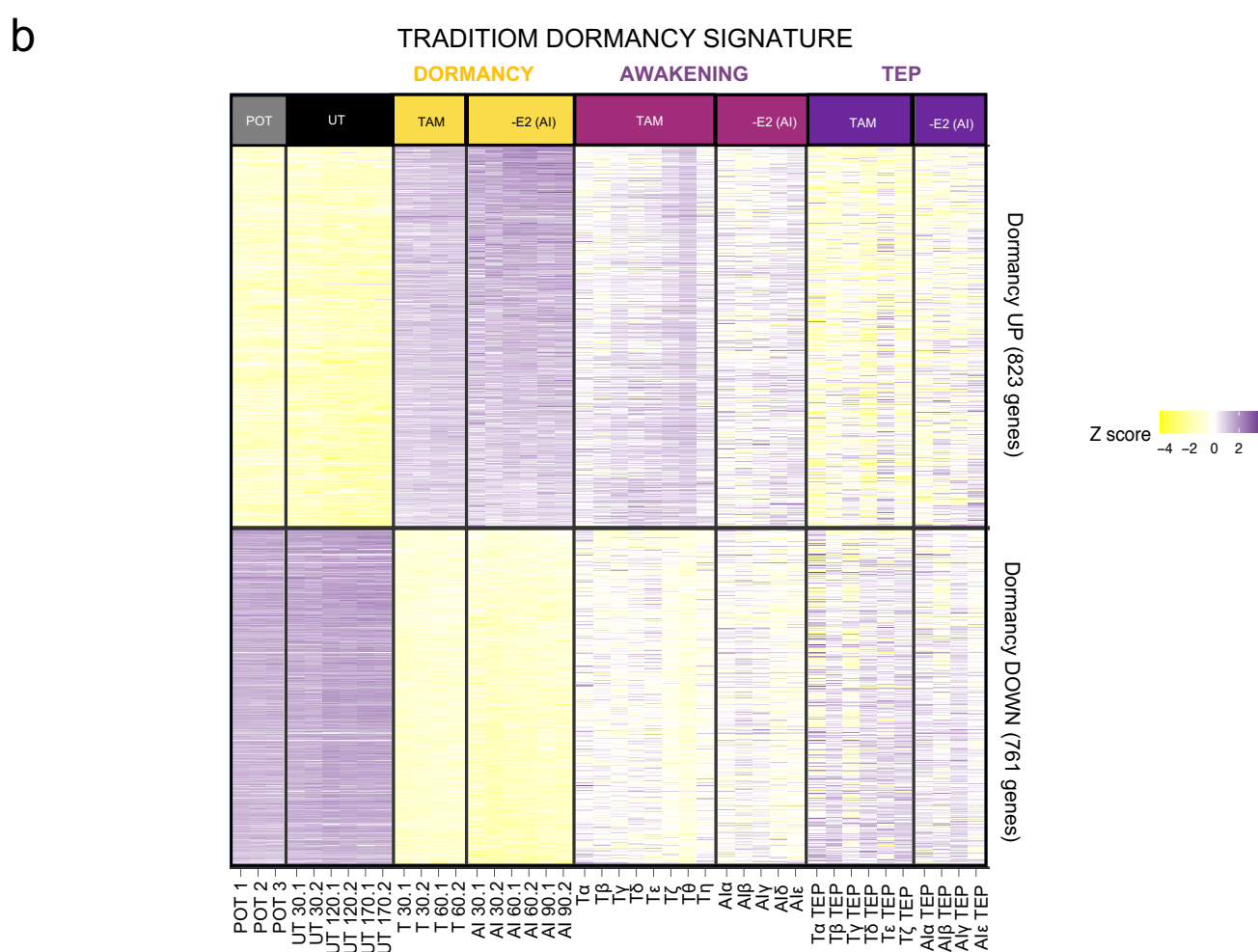
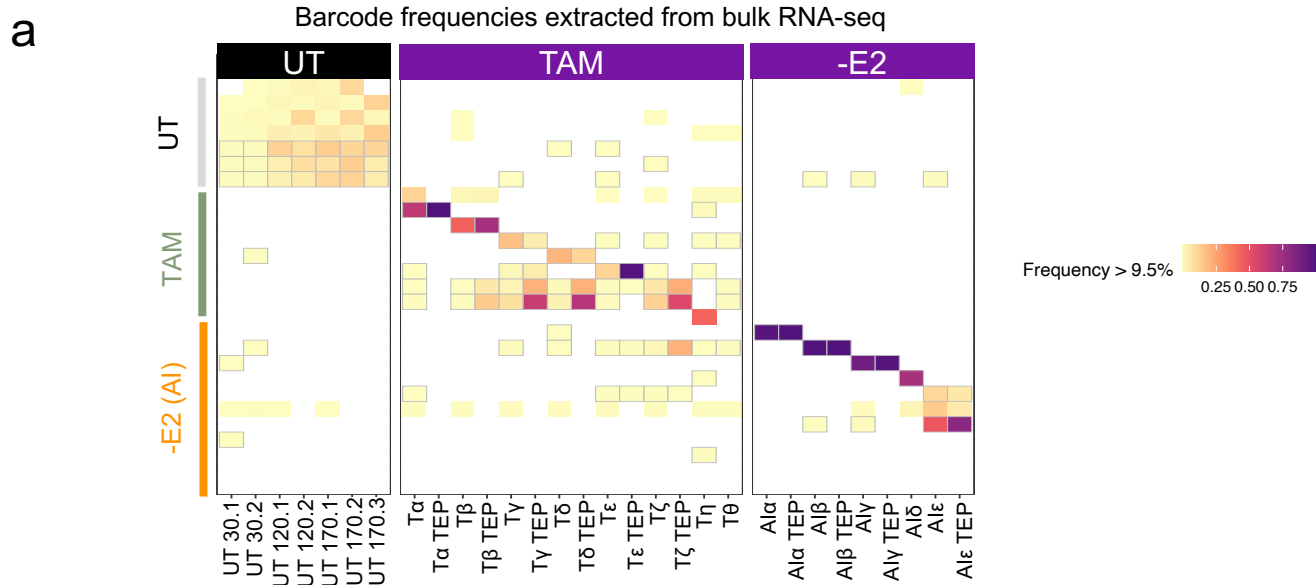


# Supplementary Figure S17. TRADITIOM MCF7 Bulk RNA-seq



**Supplementary Figure S17. TRADITIOM MCF7 Bulk RNA-seq. a)** Heatmap of high frequency barcodes (BC frequency > 10%) among UT (untreated) samples and TRADITIOM carbon-copies (replicates) for both TAM and -E2 (AI) arm at the time of awakening (early progression) and their corresponding TEPs (Terminal End Points, late progression) as determined by barcode calls from bulk RNA-seq data. **b)** Heatmap depicting significantly differentially expressed genes ( $abs(\log_2\text{FoldChange}) > 1$  &  $p_{adj} < 0.01$ ) at dormancy (AI day 30, 60, 90 and TAM day 30, 60) in comparison to the POT (pre-treatment). Dormancy specific gene list was created based on consensus of DEGs using z-score distributions across T0s and all dormancy samples from replicates of both TAM and -E2 (AI) treatment (dormancy up: dormancy z-score > 0 and  $\geq 0.1$ -quantile for at least 6 samples, dormancy down: dormancy z-score < 0 and  $\leq 0.9$ -quantile for at least 6 samples). The heatmap is further extended across UT (day 30, 120 and 170), awakening and TEPs of TAM and -E2 (AI) samples to report corresponding changes in transcriptional profile for rest of the samples.