

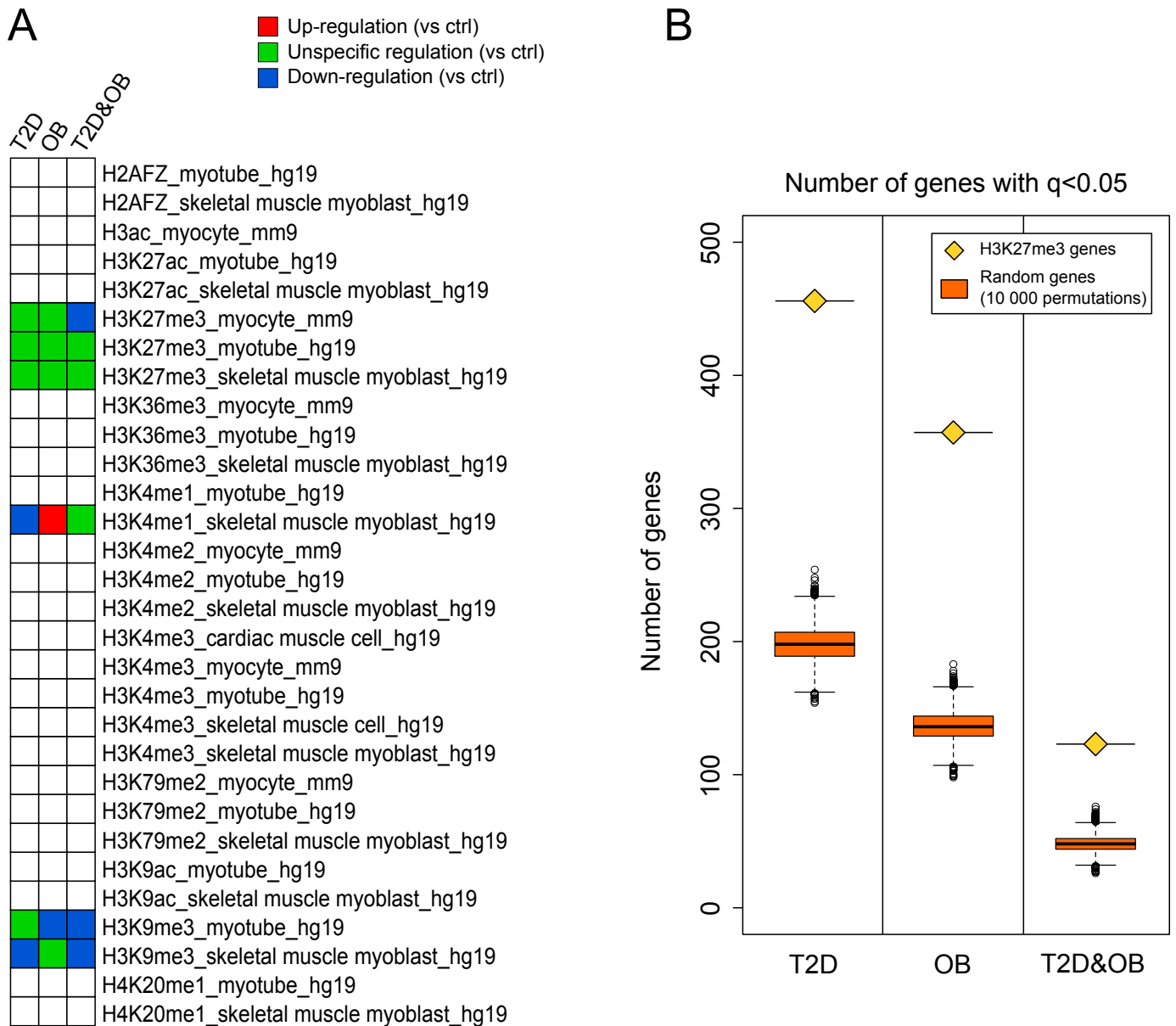


Figure S4. (A) A heatmap showing all investigated ENCODE histone modification gene-sets. Significant gene-sets are marked as either red (up-regulated), blue (down-regulated), or green (unspecifically regulated). **(B)** A plot showing the number of significantly differentially expressed H3K27me3 genes (i.e. belonging to one of the H3K27me3 gene-sets in Figure 2). These numbers are distinctively higher than the number of significant genes among randomly permuted genes (repeated 10,000 times).