

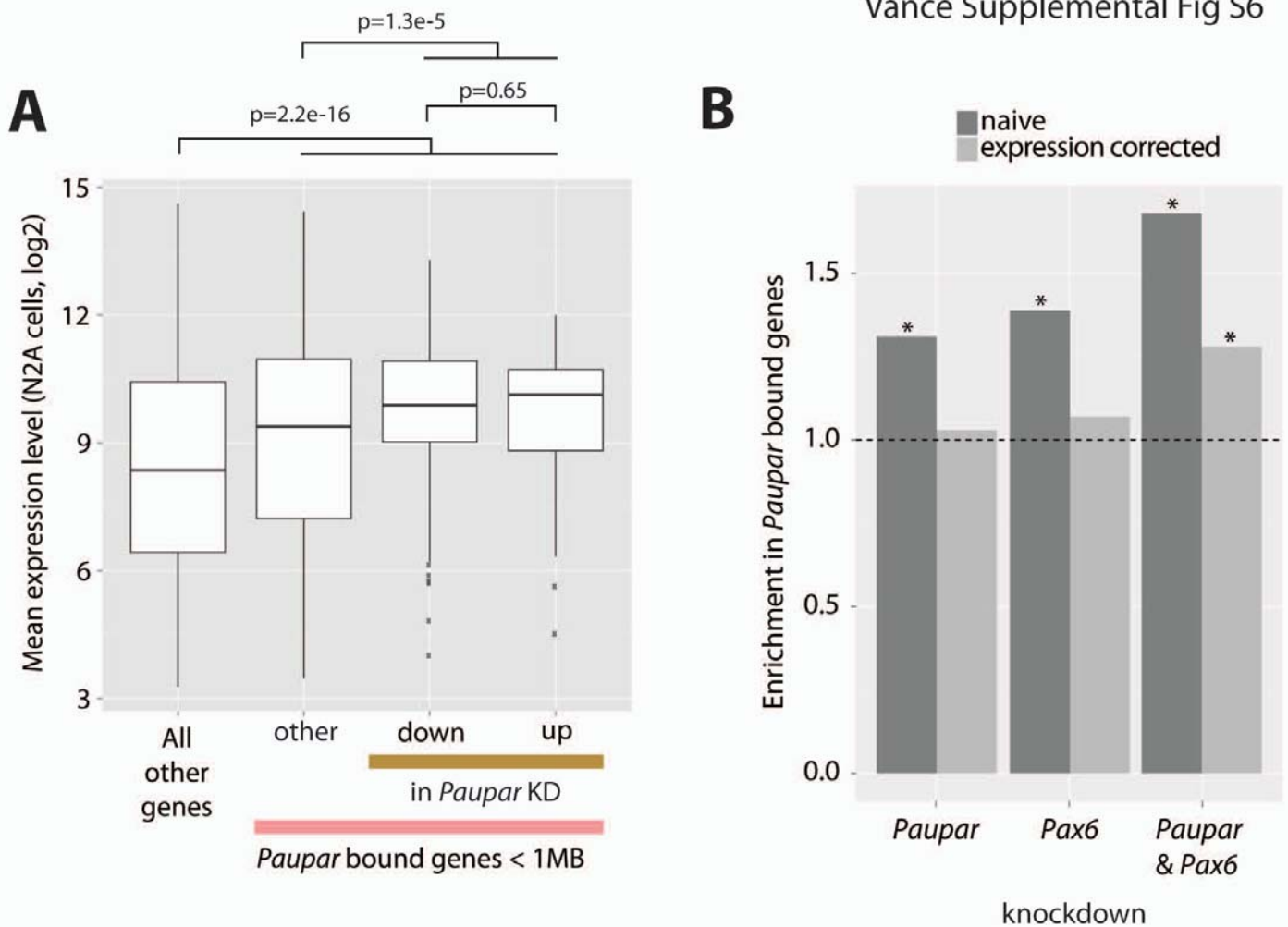


Figure S6 Expression levels and enrichments of *Paupar* associated genes for *Paupar* and/or *Pax6* regulated genes. *Paupar* bound genes were identified using the GREAT definition of gene promoters as described in the methods. (A) Genes bound and regulated by *Paupar* are more highly expressed in N2A cells based on the control microarray data from the *Paupar* and *Pax6* knock-down experiments (p-values for the indicated comparisons were calculated using a two-sided Mann-Whitney U test). (B) The enrichment of *Paupar* and/or *Pax6* regulated genes among genes associated with *Paupar* binding was tested using the Genomic Association Tester (GAT). Both naive (only mapability corrected) and gene expression level corrected scores reveal a significant enrichment of *Paupar* and *Pax6* regulated genes among those associated with *Paupar* binding. For the expression level correction, the analysis was stratified by gene expression level using six equal bins of expression level. Asterisks indicate a significant enrichment (BH corrected p value < 0.05).