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).