



Figure S1: Pathway analysis from RNA-sequencing in toxin-exposed intestinal HT-29/B6-GR/MR epithelial cells. Panel plot of gene set enrichment results for the TcdA and TcdB compared to controls. Only gene sets significant at $FDR < 0.05$ are shown. Furthermore, only gene sets with $AUC > 0.55$ and $FDR < 0.01$ in at least one comparison are shown. Each row corresponds to one gene set. Each column corresponds to one comparison. The length of the bars corresponds to the effect size (AUC, area under the curve). Color strength corresponds to FDR (p -value adjusted for multiple testing using the Benjamini–Hochberg procedure). Colored fragments indicate the proportion of genes which are significantly up- (red) or down- (blue) regulated in the gene set. Grey fragments indicate the proportion of genes which are not significantly regulated in the gene set.