



Supplementary Figure S1. Comparison of the two DESeq2 differential expression analysis approaches. **(a)** Analysis separately for each PNI model and its time points, contrasted to naïve; **(b)** Multivariate analysis design including all PNI models together, contrasted to naïve; **(c)** Pathways with highest enrichment in the SpNT (left) and Crush (right) groups using DEGs from DESeq2 analysis separately for each PNI model as in **(a)**. Volcano plots in **(a)** and **(b)** show the annotation for the 10 genes with lowest adjusted p value with multivariate analysis **(b)** which was used in the analysis of the main text.