



Figure S1: Principal component analysis (PCA) of MB and WH RNA sequencing data.

PCA was performed on variance stabilized transformed counts using the plotPCA function within DESeq2 for the top 150 variable genes for (A) WH and MB samples (B) WH samples between experimental conditions and (C) MB samples between experimental conditions. Plots display the top two principal components accounting for the majority of sample variance. Generally, WH and MB samples do cluster apart from each other (A). WH and MB 24h-AR samples are tightly clustered, while the 1h-AR and Naïve samples show considerable spread (B-C). Generally, the different experimental conditions do cluster separately, but there is more overlap between the 24h-AR and Naïve samples, which is reflected in the low number of differential expressed genes between these two groups.