



Figure 4 – figure supplement 1. Recovery of positive control genes regulated by sleep deprivation. Volcano plot of differential expression ($-\log_{10}$ P-value versus \log_2 fold change) caused by sleep deprivation in wild type animals (HC5 vs SD5). Genes with an $\text{FDR} < 0.05$ are highlighted in black. Positive controls (obtained from Gerstner et al. 2016 as described in Methods) are highlighted in red. Our RNA-seq analysis is able to detect 78% (454) of the 579 positive control genes obtained by microarrays as differentially expressed at $\text{FDR} < 0.05$.