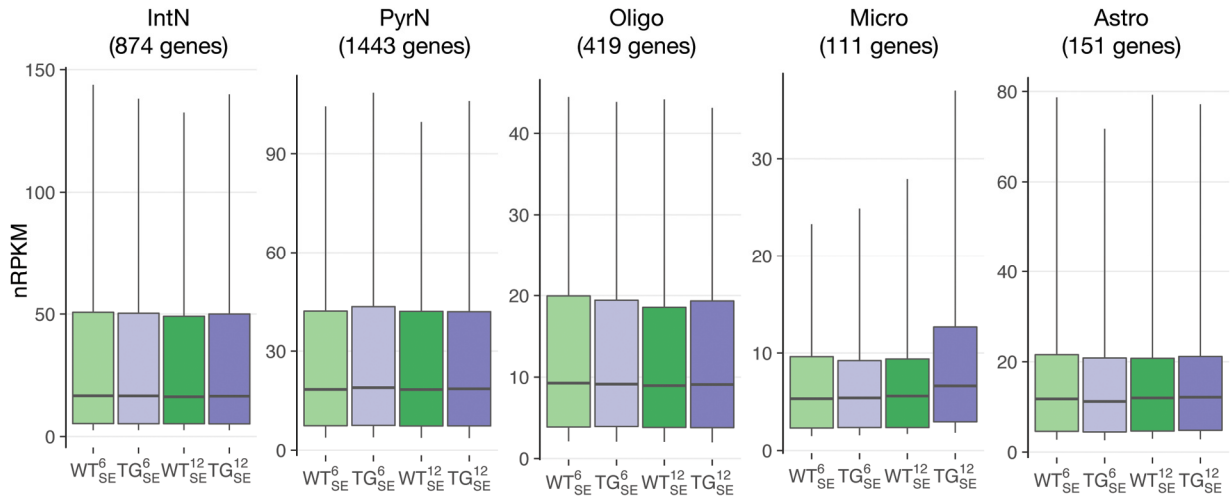
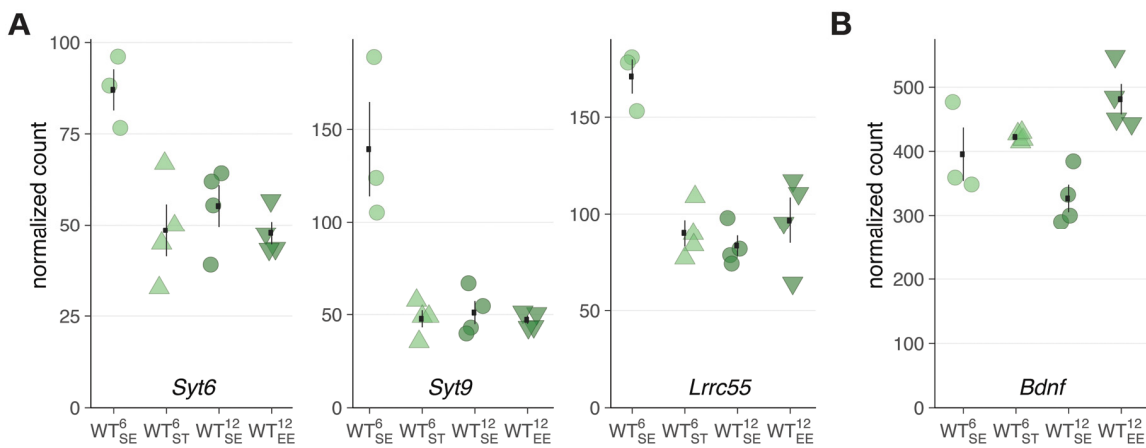


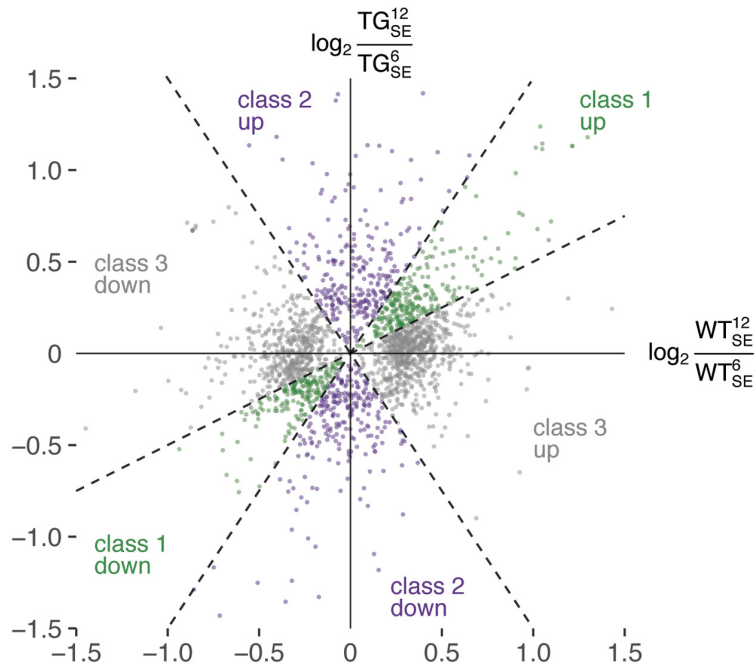
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Homogeneous cell type composition across genotype and age. Cell type-specific hippocampal gene expression in 6- and 12-month-old WT_{SE} and TG_{SE} animals. Boxplots show geometric mean as well as 10th, 25th, 75th, and 90th quantile of nRPKM values for all genes attributed to distinct cell types based on single-cell data [62]. Number of genes per cell type in brackets: Interneurons (IntN), pyramidal neurons (PyrN), oligodendrocytes (Oligo), microglia (Micro), and astrocytes (Astro). No significant compositional changes were observed (Mann-Whitney U test, two-tailed).



Supplementary Figure 2. Minor effect of chronic unpredictable mild stress on gene expression in wildtype animals. (A) Expression levels of three DEGs in WT_{ST}/WT_{SE} plotted as individual data points with mean ± SEM. (B) Expression level of *Bdnf* plotted as individual data points with mean ± SEM.



Supplementary Figure 3. Classification of DEGs based on their expression changes between 6- and 12-month-old wildtype and transgenic animals. Scatter plot of gene expression changes between 6- and 12-month-old WT (x-axis) and TG (y-axis) animals in SE. All 2162 DEGs summarized in Fig 3B are shown. DEGs were partitioned into three main classes such that class 1 represented genes with most similar expression changes for WT and TG animals (a 30° window around the standard diagonal), class 2 with prominent changes in TG animals only (a 30 + 30° window around the y-axis), and class 3 with prominent changes in WT animals only (a 30 + 60° window around the x-axis).