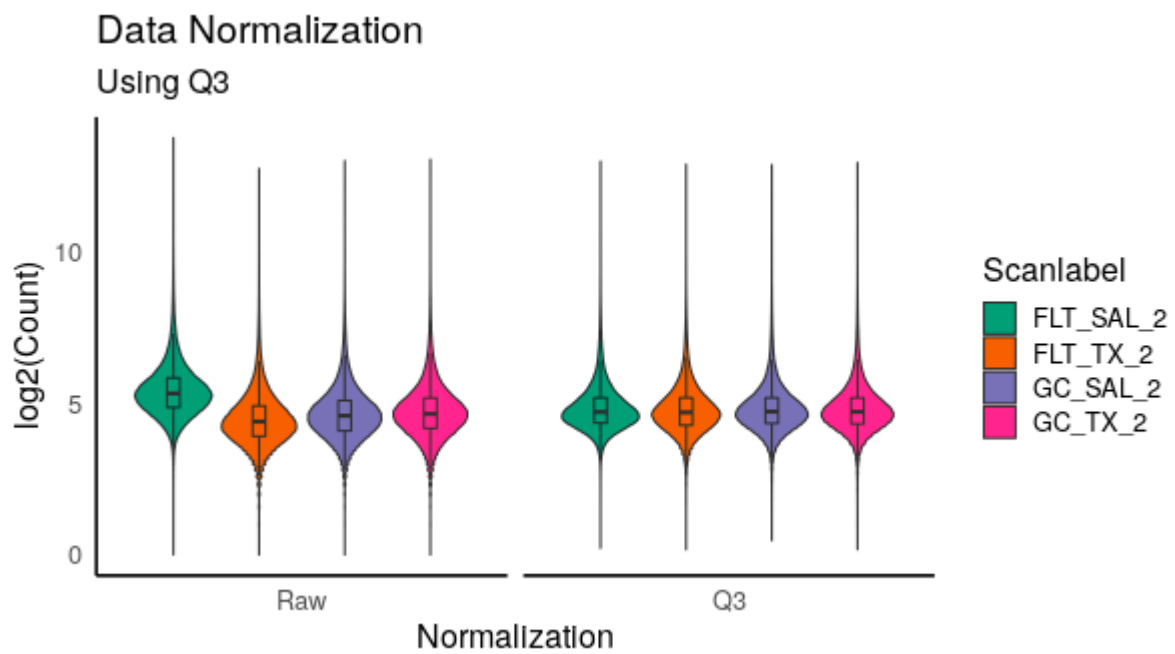
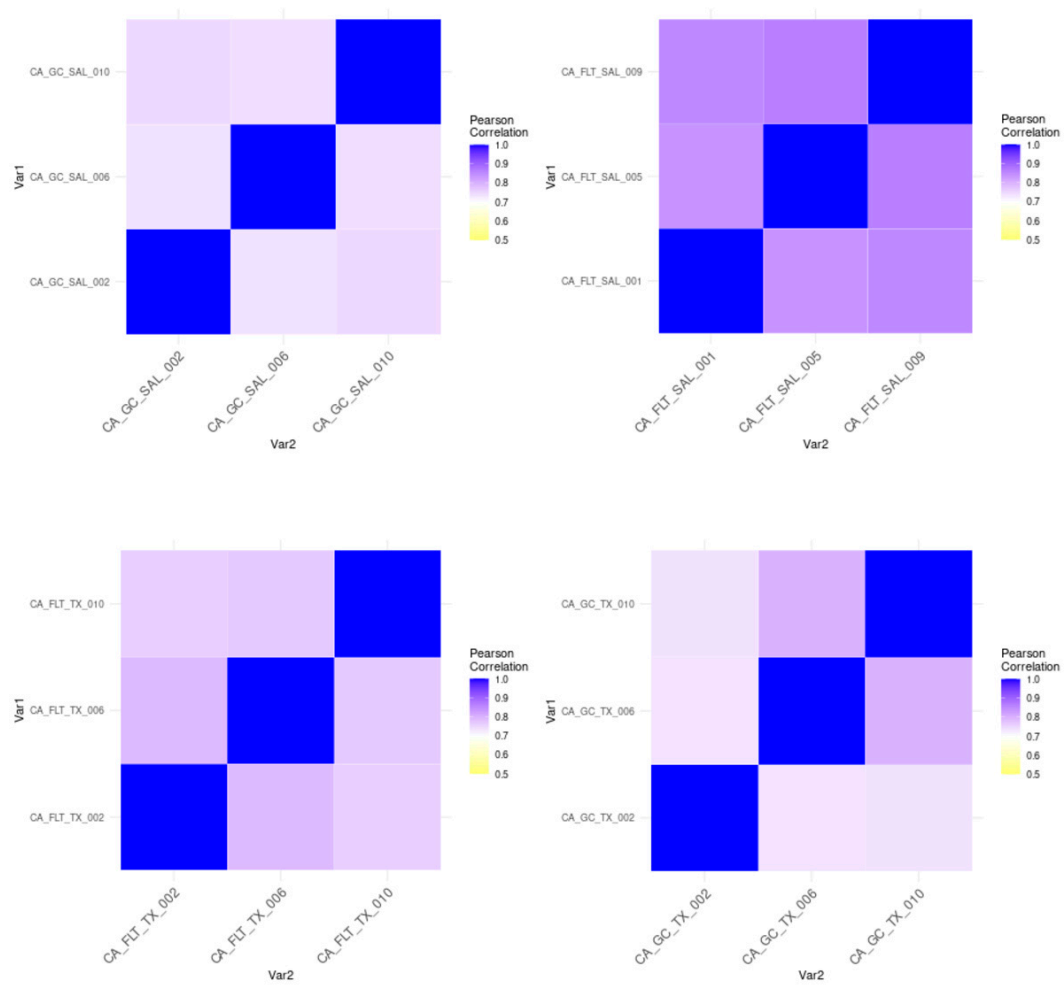


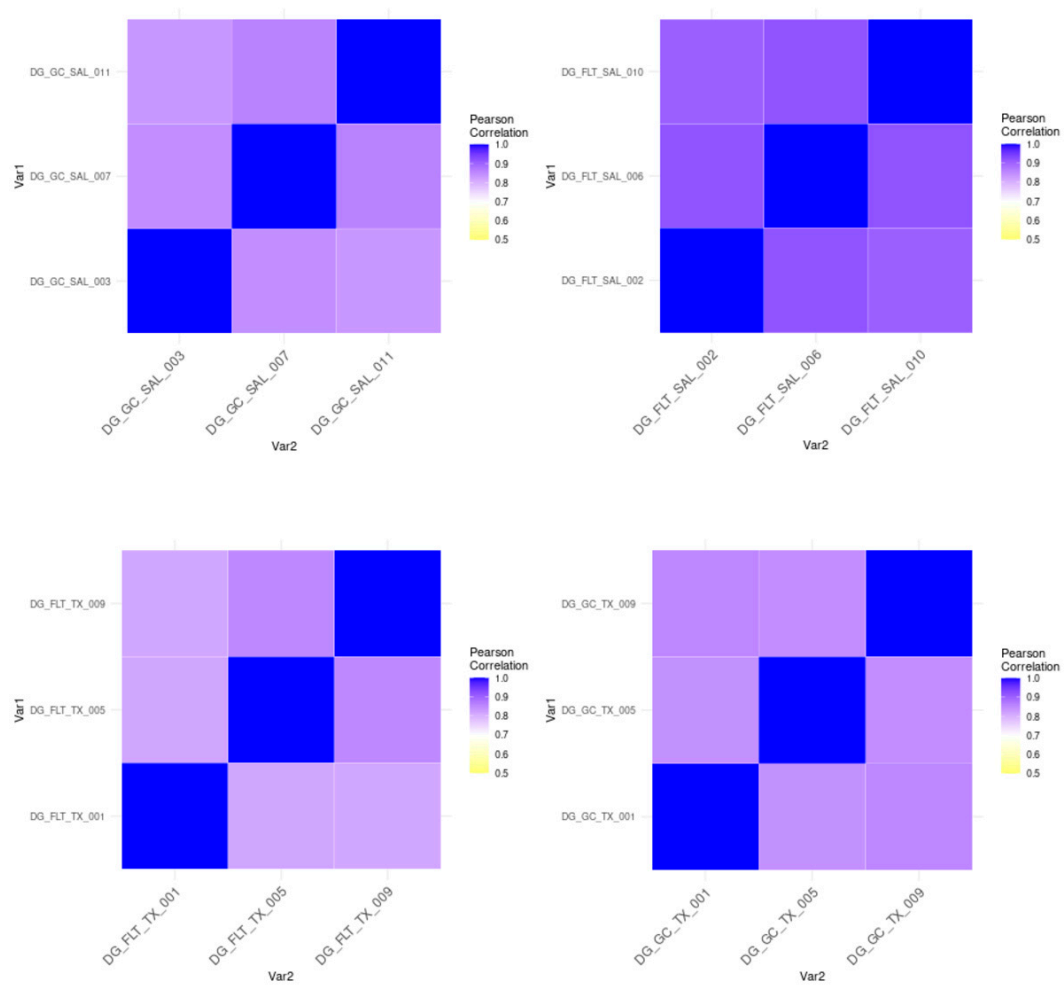
(A)



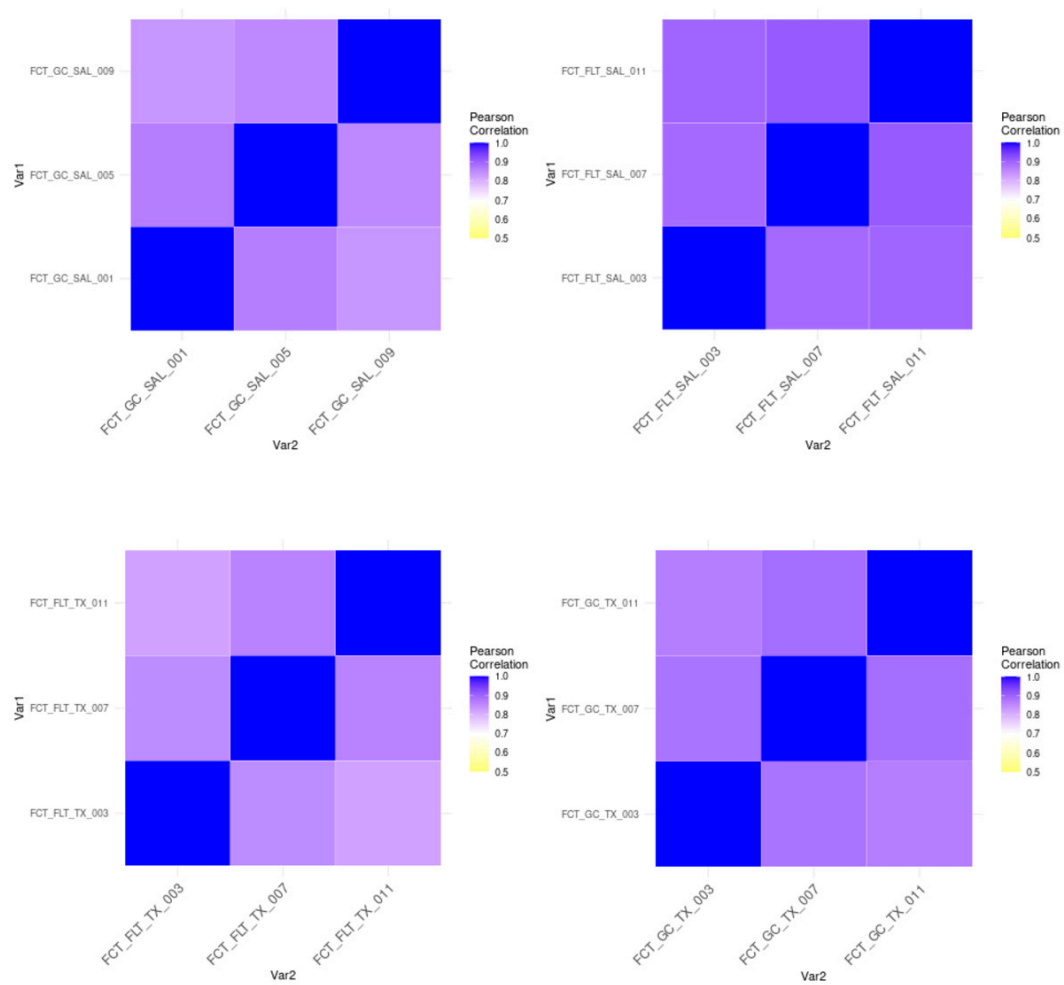
(B)



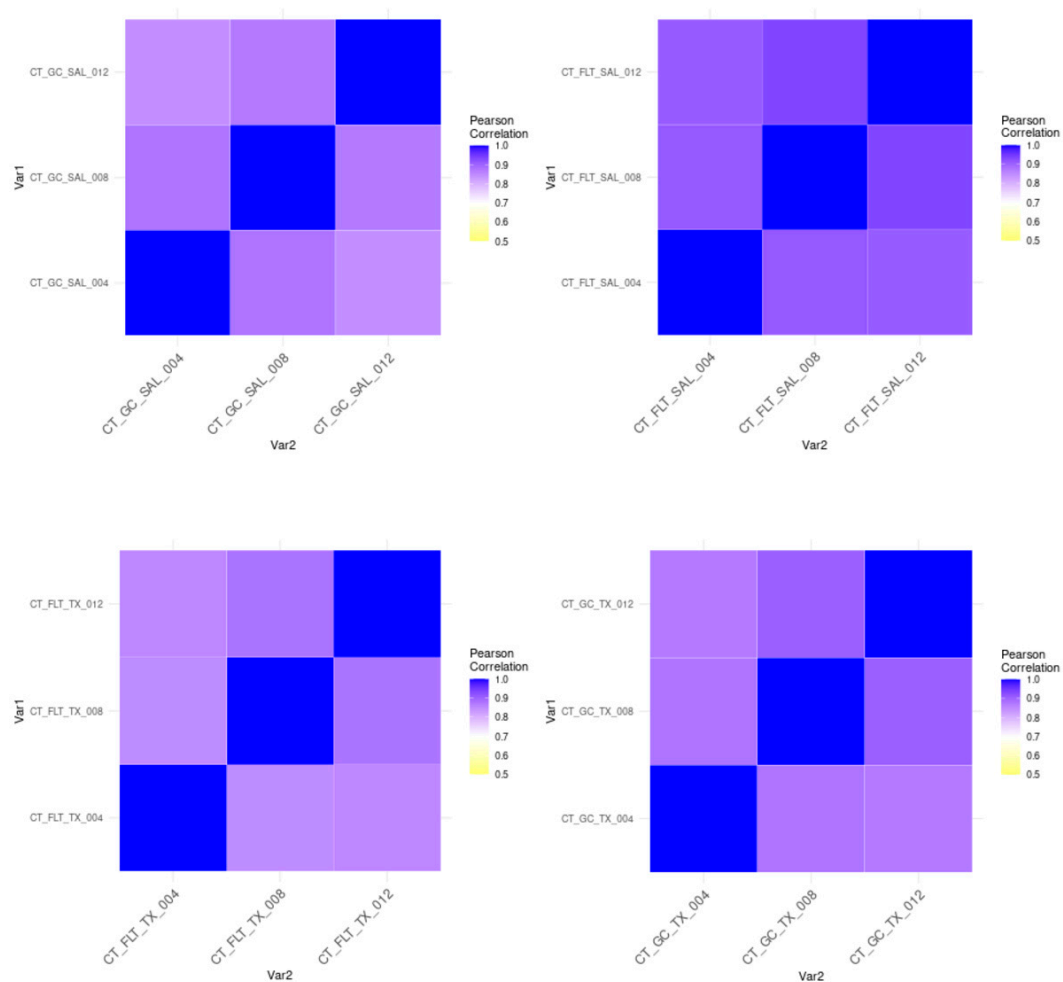
(C) Replicate correlations CA (TX=BuOE)



**(D) Replicate correlations DG (TX=BuOE)**

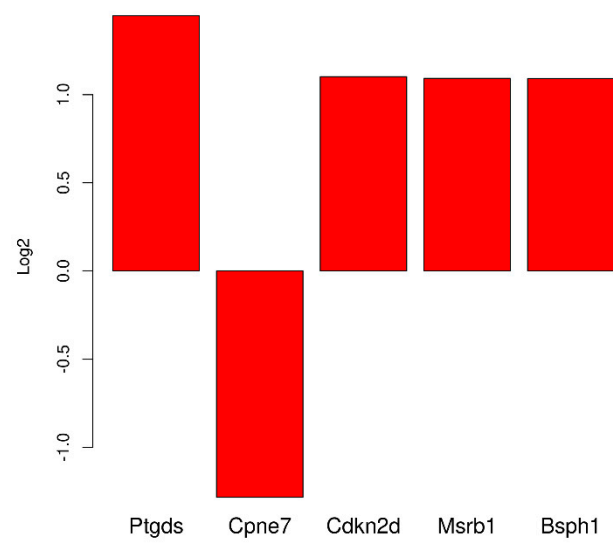


**(E) Replicate correlations FCT (TX=BuOE)**

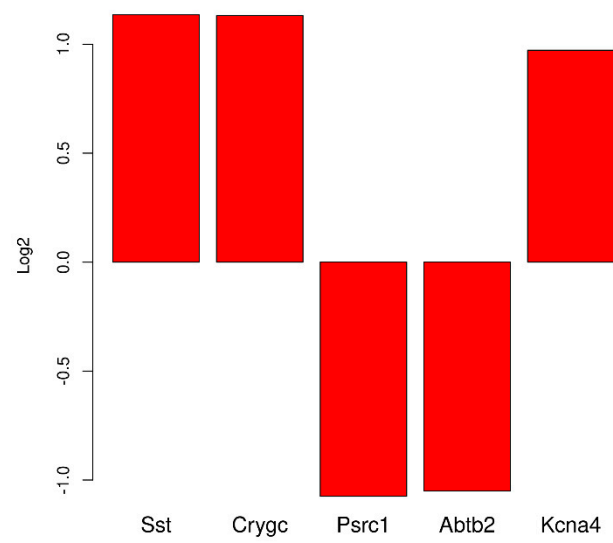


#### (F) Replicate correlations CT (TX=BuOE)

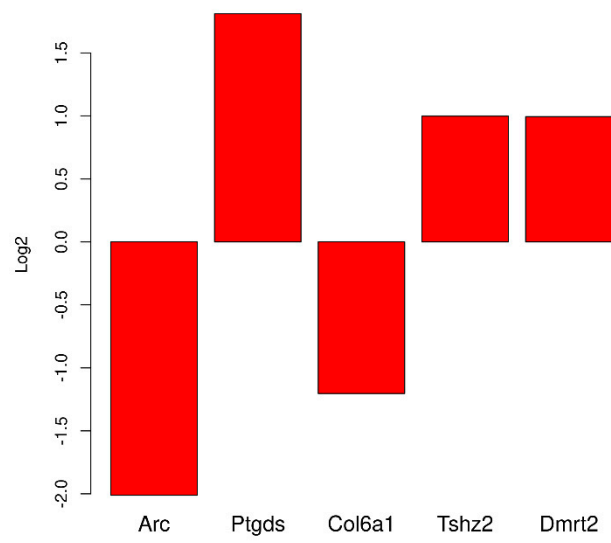
**Figure S1. Validation of DSP data.** **A** Plot of sequencing saturation, as generated by the online GeoMx DSP Control Center. **B** Violin plots showing the distributions of raw and normalized read counts for each sample, as provided by Nanostring. **C-F** Heatmaps showing Pearson's correlation coefficient when comparing log-transformed, normalized gene expression values ( $\ln(\text{normalized expression} + 1)$ ) between replicates of the indicated samples and regions.



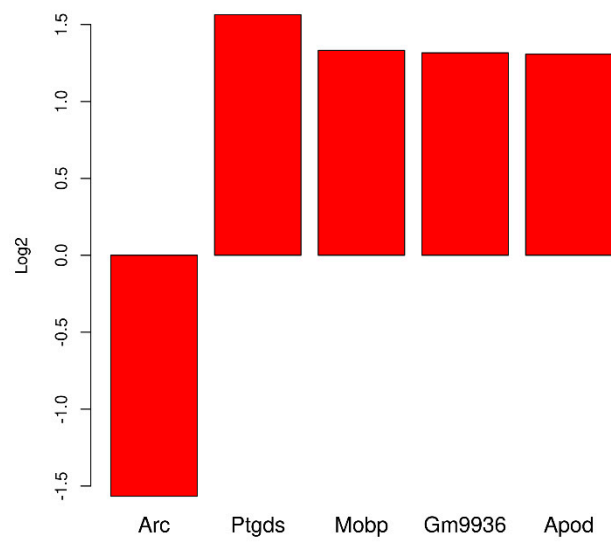
(A) CA



(B) DG

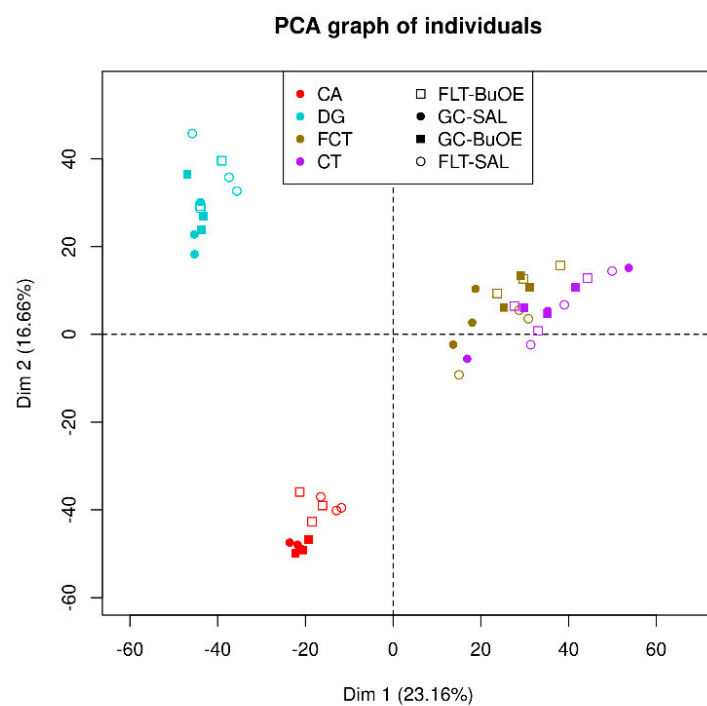


(C) FCT

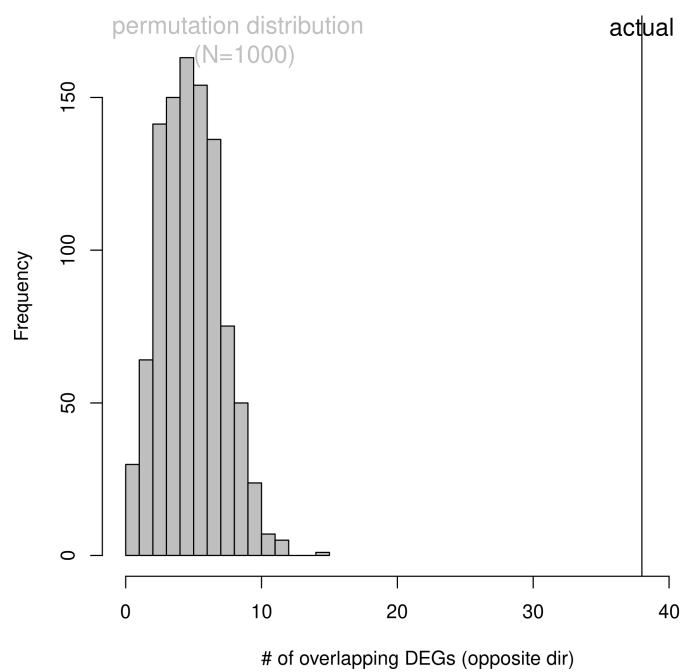


(D) CT

**Figure S2. Related to Figure 3. A-D** Barplots showing log<sub>2</sub> Fold Change values for the top 5 DEGs by magnitude of log<sub>2</sub> Fold Change for the indicated brain regions.

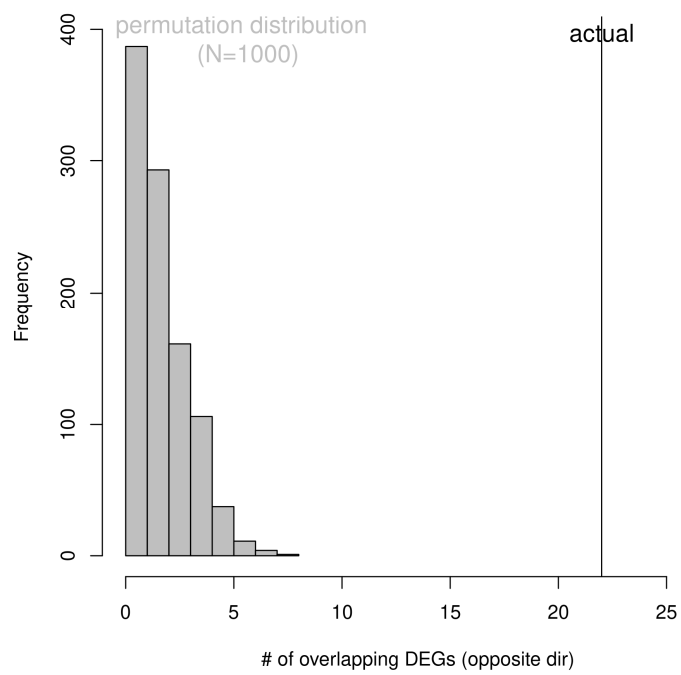


**(A)**

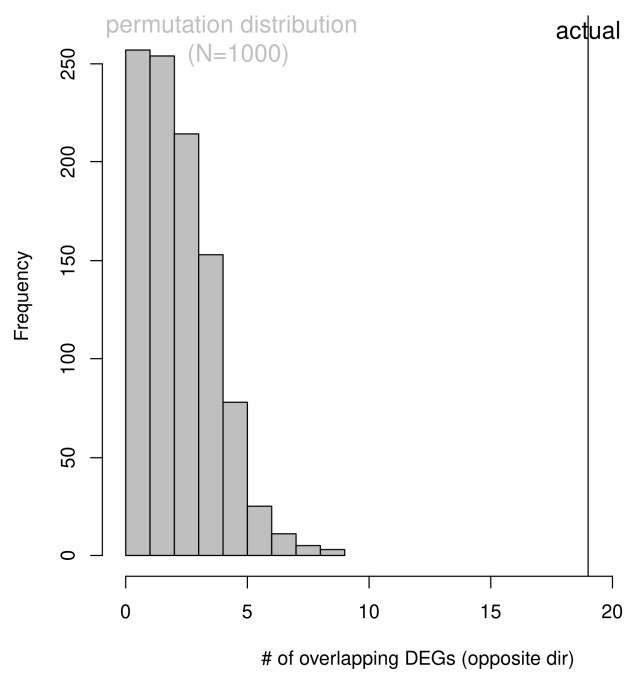


**(B) CA**

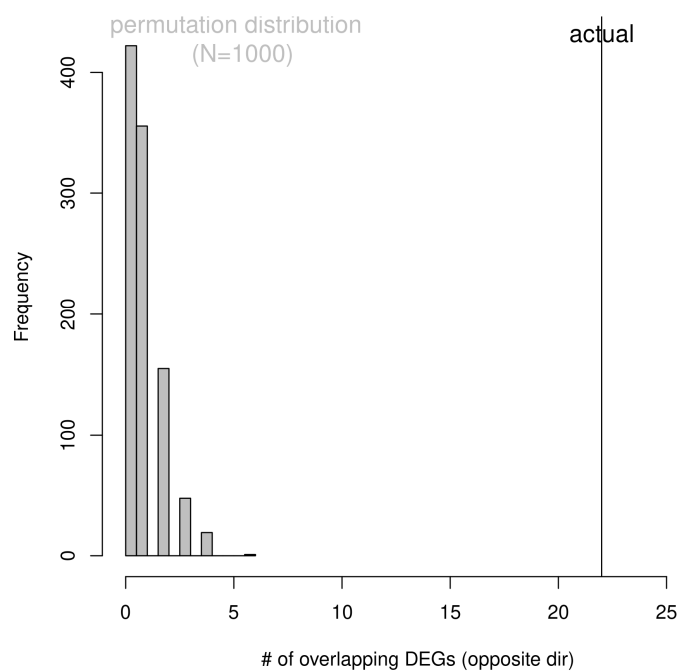




(C) DG

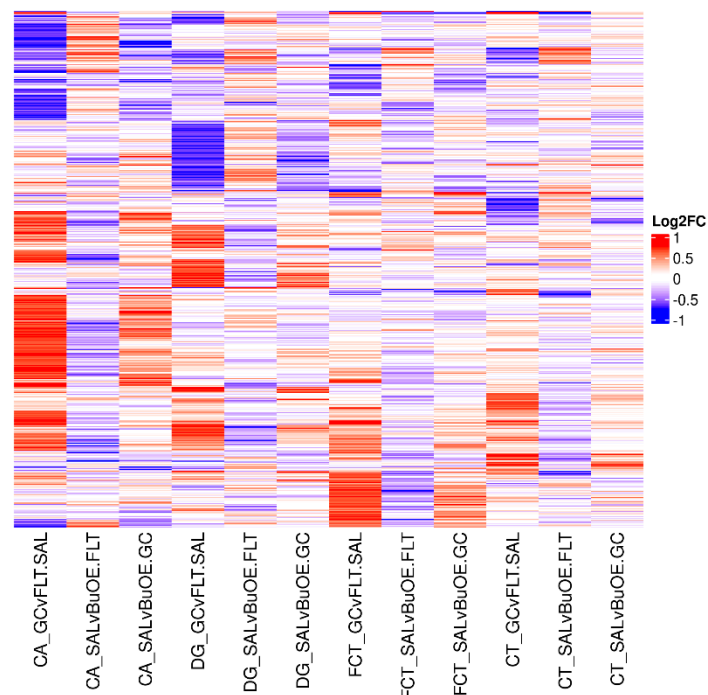


(D) FCT

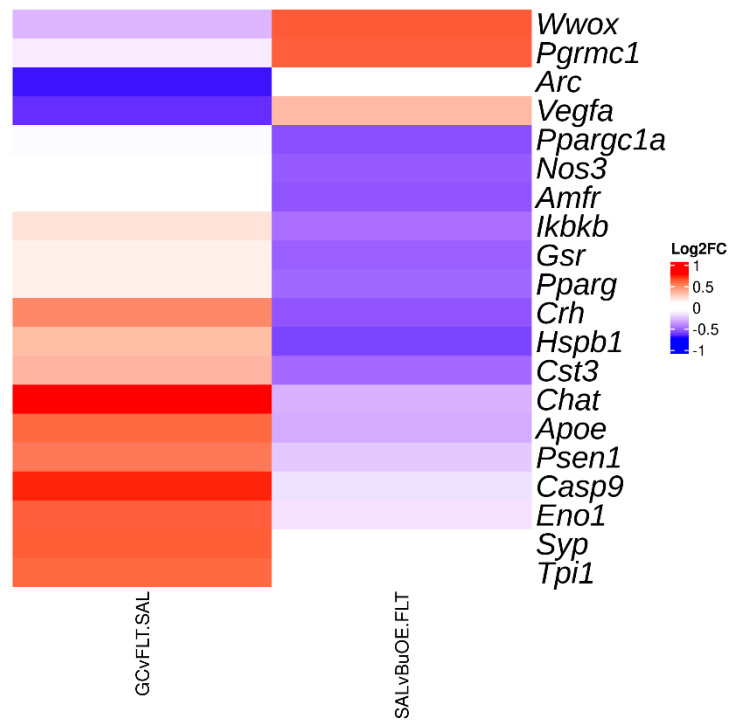


(E) CT

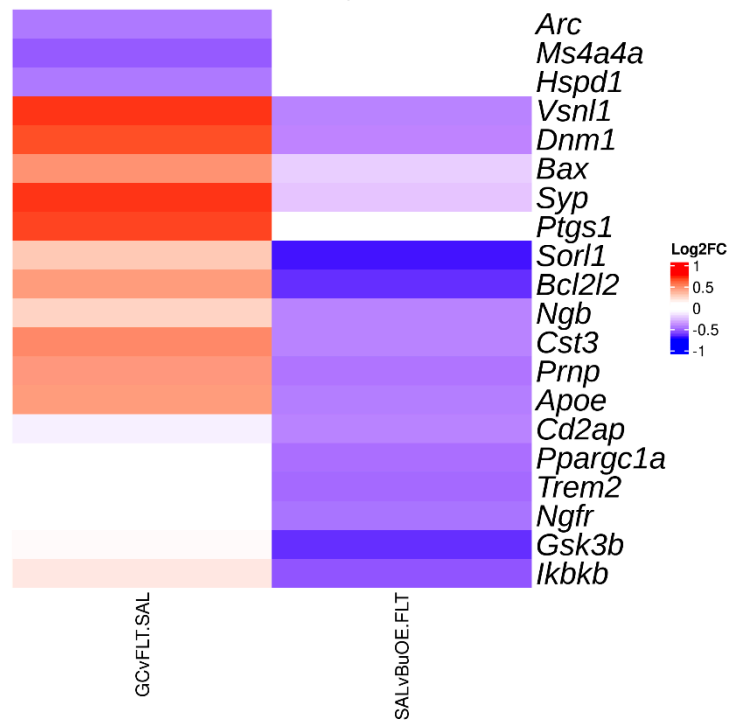
**Figure S3. Related to Figure 5.** A PCA of data from the indicated samples, with all individual replicates treated separately. **B-E** Histograms showing the distribution of the number of DEGs that change in opposite directions between GC-SAL vs. FLT-SAL and FLT-SAL vs. FLT-BuOE for the indicated regions, when randomly shuffling to select DEGs for FLT-SAL vs. FLT-BuOE. The vertical line indicates the actual number of DEGs that change in opposite directions for the two comparisons. N=1000 permutations were performed when randomly selecting FLT-SAL vs. FLT-BuOE DEGs.



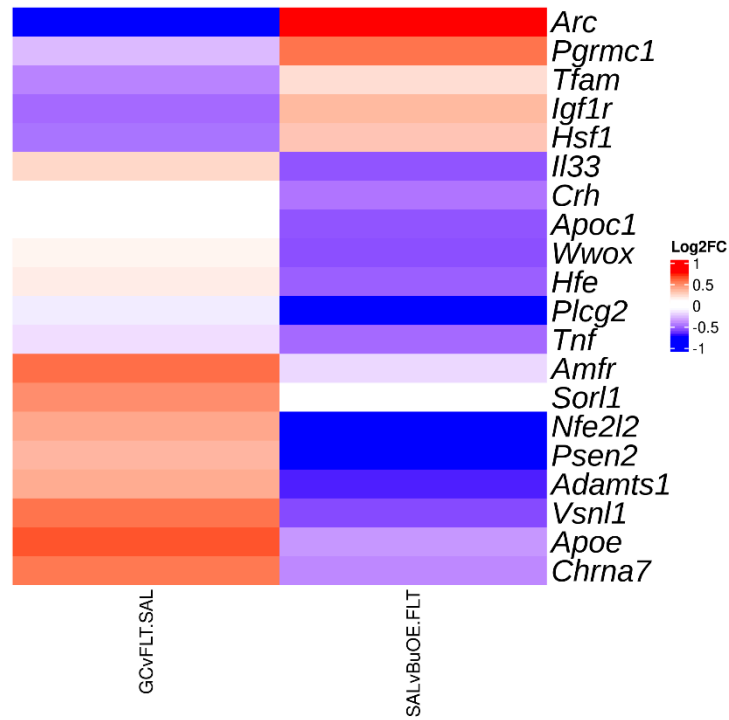
(A)



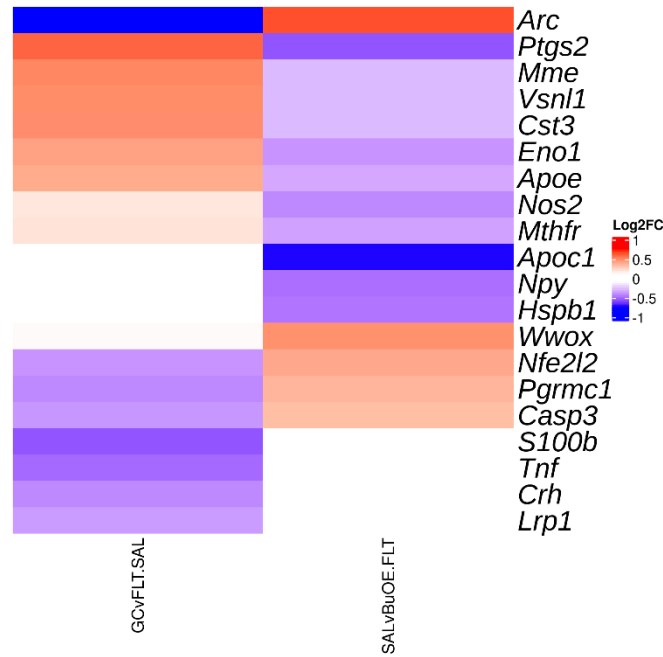
(B) AD genes in CA



(C) AD genes in DG



(D) AD genes in FCT



(E) AD genes in CT

**Figure S4. Related to Figure 6.** **A** Heatmap of log<sub>2</sub> Fold Change (FC) values from the indicated comparisons and brain regions, at the GC-SAL vs. FLT-SAL DEGs. Genes are ordered by hierarchical clustering. **B-E** Heatmaps of log<sub>2</sub> FC values from the indicated comparisons, at genes associated with Alzheimer's Disease, at the indicated brain regions. For each brain region, the top 20 genes, ordered by the maximum of the log<sub>2</sub> FC from both comparisons, are shown. Genes are ordered by hierarchical clustering. GCvFLT.SAL = GC-SAL vs. FLT-SAL; SALvBuOE.FLT = FLT-SAL vs. FLT- BuOE; SALvBuOE.GC = GC-SAL vs. GC-BuOE.