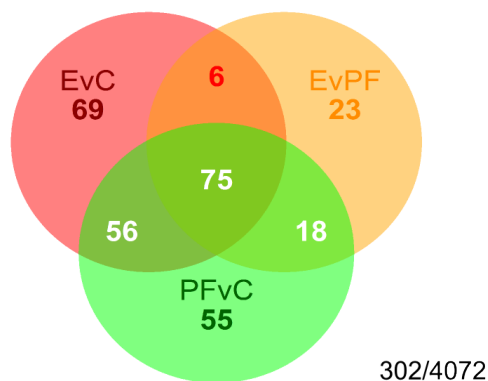
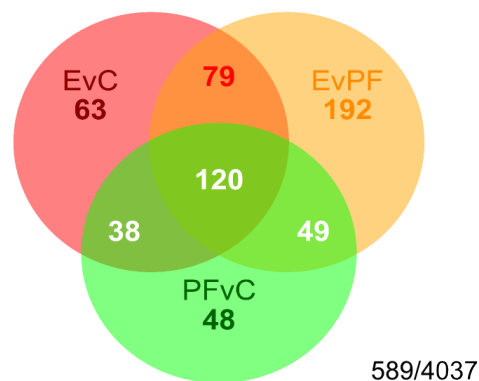


Figure S1: Plot of p-value distributions for gene expression differences among prenatal treatment groups, within the steady-state conditions, in **a)** PFC at Day 16 post-saline injection, **b)** PFC at Day 39 post-saline injection, **c)** HPC at Day 16 post-saline injection, and **d)** HPC at Day 39 post-saline injection. The greatest effects of prenatal ethanol exposure on gene expression p-values were exhibited at D16 in PFC, followed by D16 HPC, as exhibited by enrichment of p-values towards zero for the ethanol contrasts (E-C, E-PF). No change in p-values was apparent in Day 39 PFC, and only a pair-fed effect was apparent in Day 39 HPC.

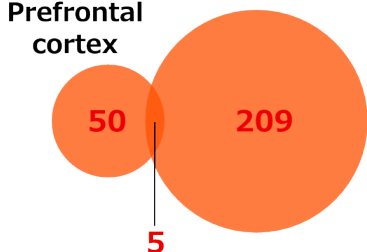
a) Prefrontal cortex



Hippocampus

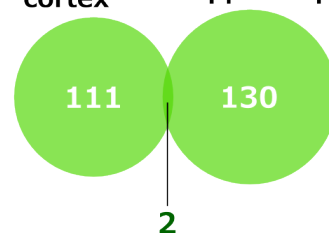


b) Prefrontal cortex



- positive regulation of neuron differentiation
- dorsal/ventral pattern formation
- circadian rhythm
- regulation of lymphocyte differentiation
- regulation of lipase activity

c) Prefrontal cortex



- negative regulation of neuron projection development
- positive regulation of epithelial cell migration

Figure S2: Venn diagrams demonstrating the number of Biological Processes significant for each contrast in Day 16 animals under steady-state conditions, and overlap of processes between different contrasts for PFC and HPC at FDR <1% **(a)**. FDR was increased to 10% to identify Biological Processes that showed overlapping changes in both tissues, specific to prenatal alcohol exposure **(b)** and pair-feeding **(c)**. FDR <10%.

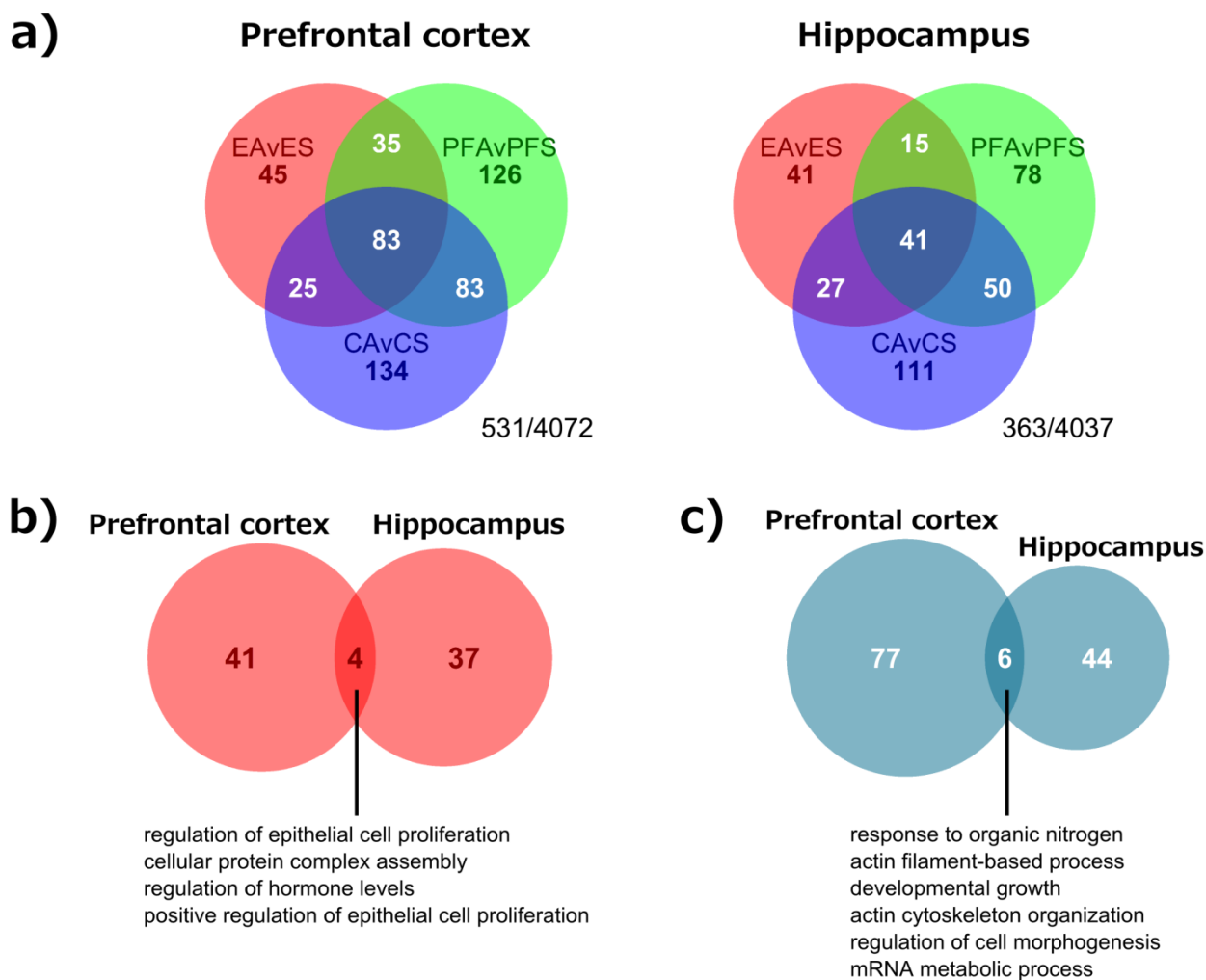


Figure S3: Venn diagrams demonstrating the number of Biological Processes significantly altered in the response to Adjuvant within each prenatal treatment group, and the overlap of processes enriched between groups **(a)**. Many Biological Processes showed changes specific to prenatal alcohol exposure, and several overlapped between tissues **(b)**. Other processes were common to the PF and C response to adjuvant, and several overlapped between tissues **(c)**. FDR <1%.

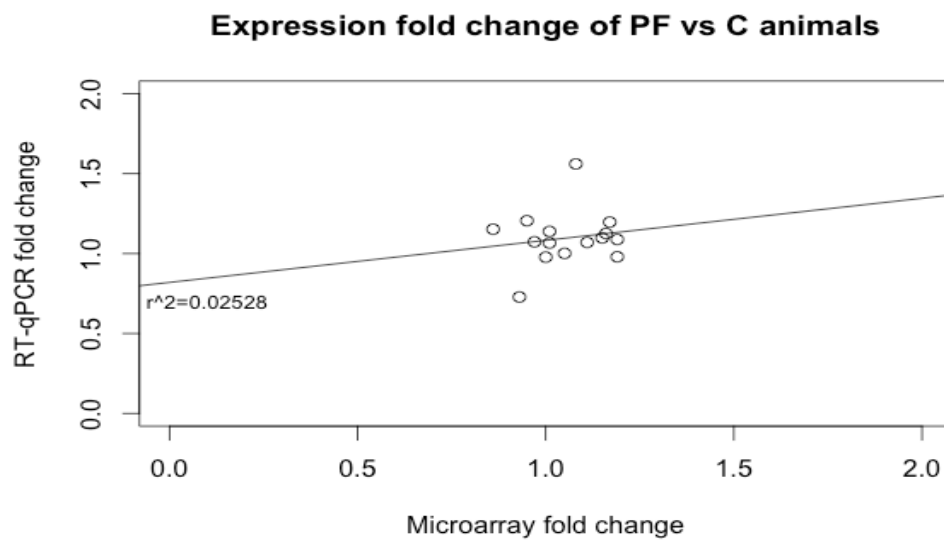


Figure S4: Fold changes in expression were not correlated between microarray and RT-qPCR results for PF vs C animals ($r^2=0.02528$, $p=0.5714$).

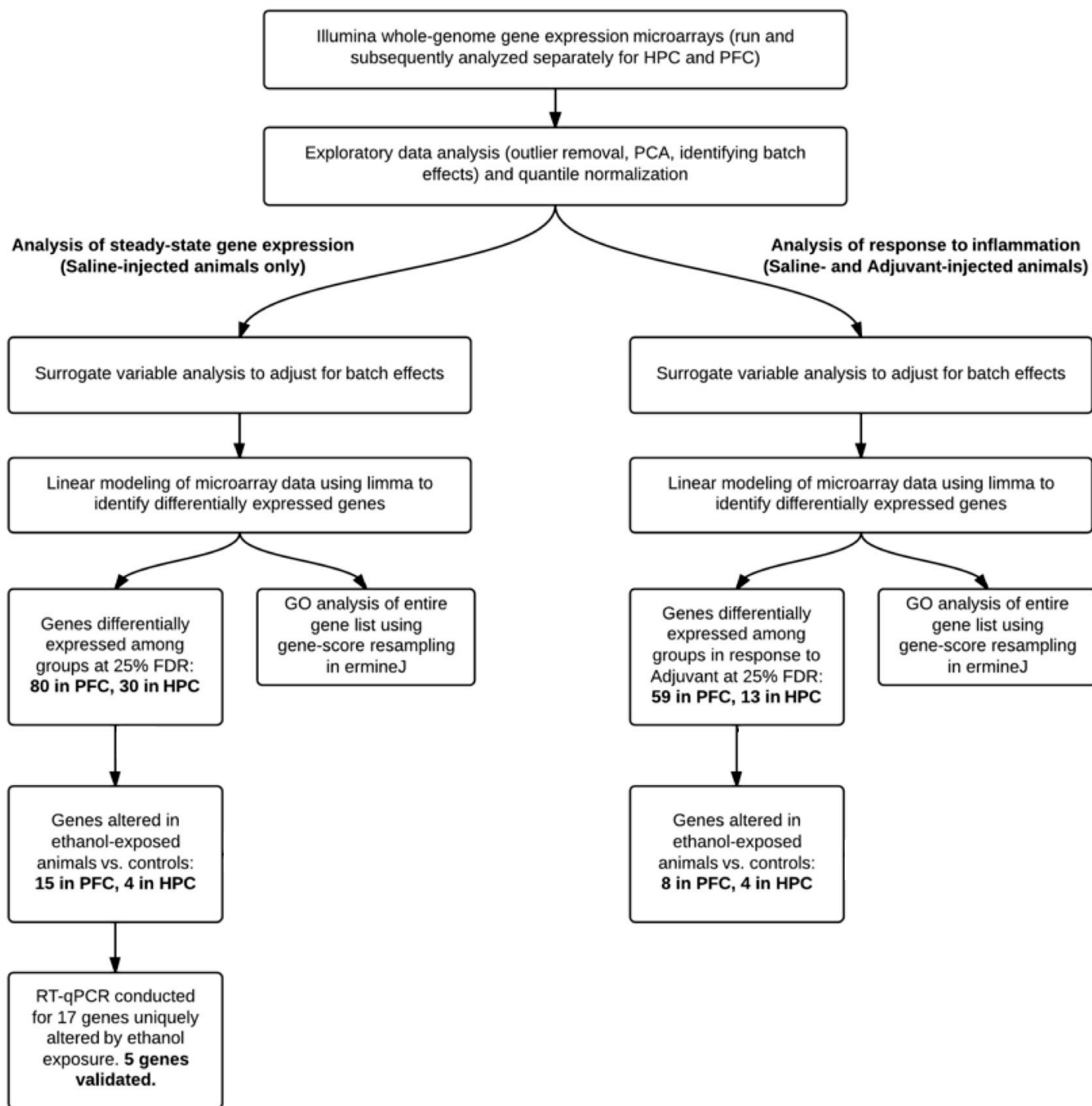


Figure S5: Overview of analyses and main findings for gene expression analysis