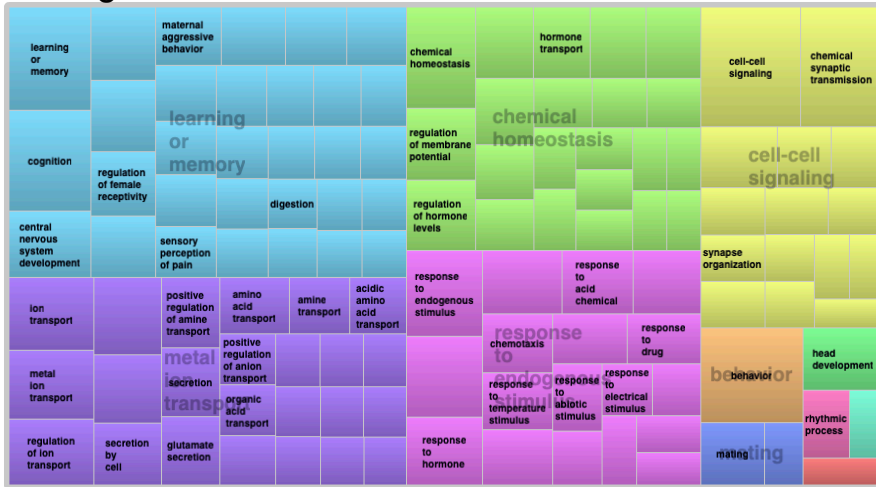
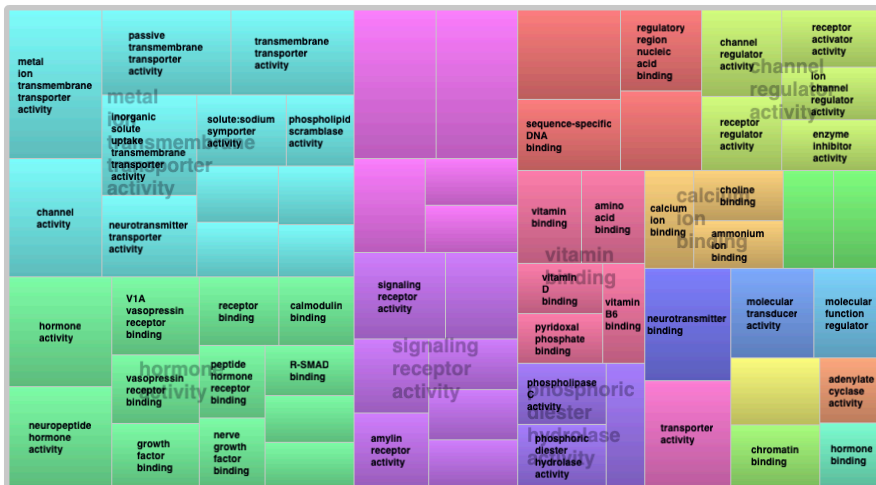


*Supplemental Figures:*

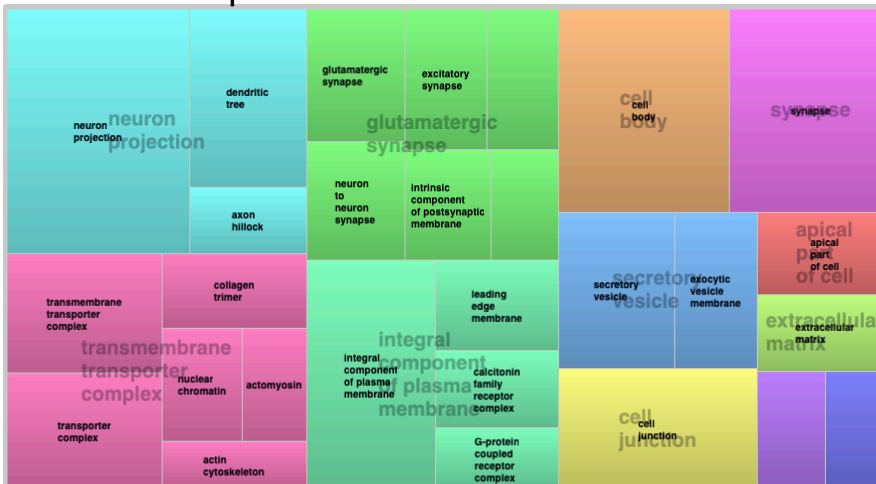
## Biological Process



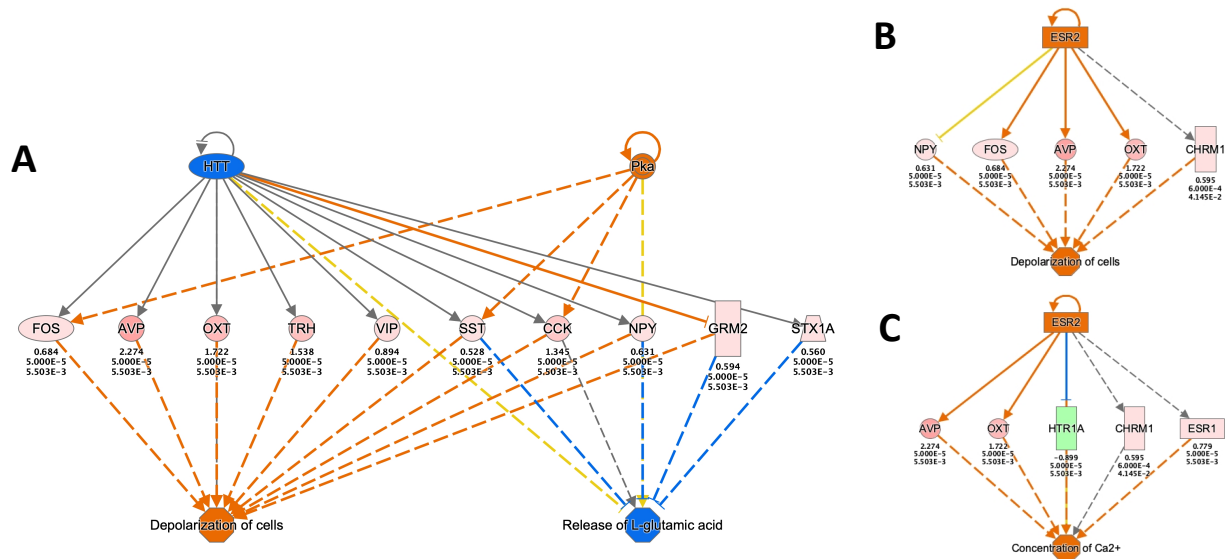
## Molecular Function



## Cellular Component

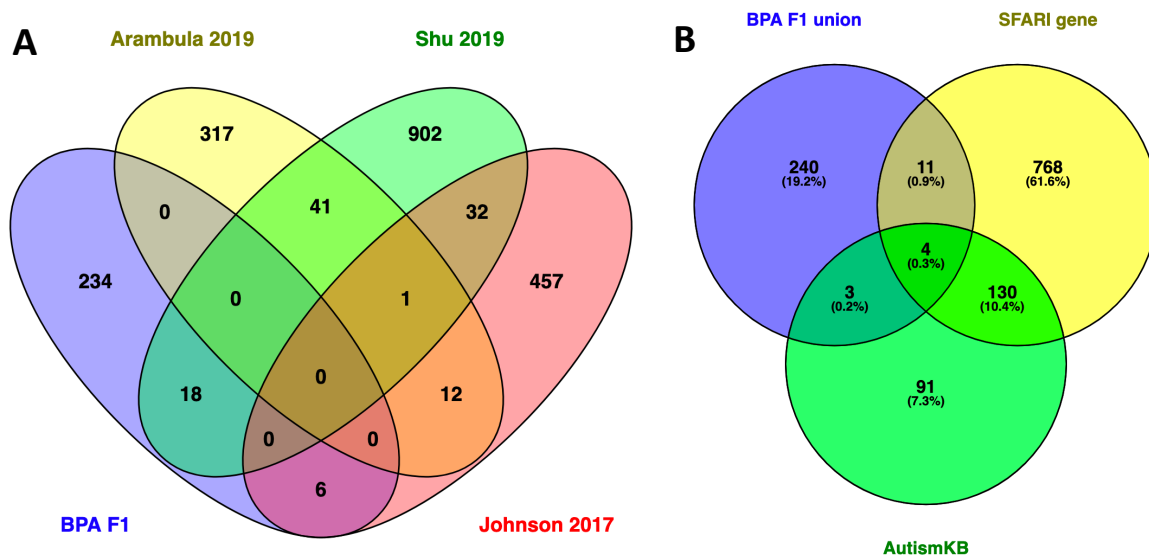


**Supplemental Figure 1: REVIGO summary of Gene Ontology analysis.** Significantly over-represented Molecular Functions, Biological Processes and Cellular Components were summarized using a sematic similarity algorithm.



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**Supplemental Figure 2: Ingenuity Pathway Analysis of top upstream regulators.** Ingenuity generates potential hypotheses for how a function or disease is regulated in the dataset by activated or inhibited upstream regulators. Orange color indicates predicted activation. Blue color indicated predicted inhibition. Genes in pink indicate upregulation while green indicated downregulation of gene expression in BPA F1 hypothalamus. Yellow lines indicate that the findings are inconsistent with the state of the downstream molecule, while grey lines indicate the effect is not predicted.



**Supplemental Figure 3: Venn Diagrams of DEGs in common published datasets.** **A.** Overlap of our DEGs (n=259 genes) with data sets published with those derived from *Mus musculus* (Shu *et al.* 2019), *Peromyscus californicus* (Johnson *et al.* 2017) and Sprague Dawley rats (Arambula *et al.* 2016); all using hypothalamus tissue. **B.** Overlap of our DEGs (n=259 genes) with two publicly available databases of genes curated from humans and animal models that are suspected to act in autism spectrum disorder: SFARI human genes and AutismKB 2.0.

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