**Supplementary Figure 1. Bioinformatic analysis of top 100 differentially expressed genes (DEG) in the USF1 KO hippocampus.**

**A)** ‘ENCODE and ChEA Consensus TFs from ChIP-X’ enrichment analysis of top 100 DEG. **B)** ‘GO Biological Process’ enrichment analysis of top 100 DEG. **C)** ‘GO Molecular Function’ enrichment analysis of top 100 DEG.