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Supplemental Information

**Integrative Transcriptomics Reveals Sexually
Dimorphic Control of the Cholinergic/Neurokinin
Interface in Schizophrenia and Bipolar Disorder**

Sebastian Lobentanzer, Geula Hanin, Jochen Klein, and Hermona Soreq

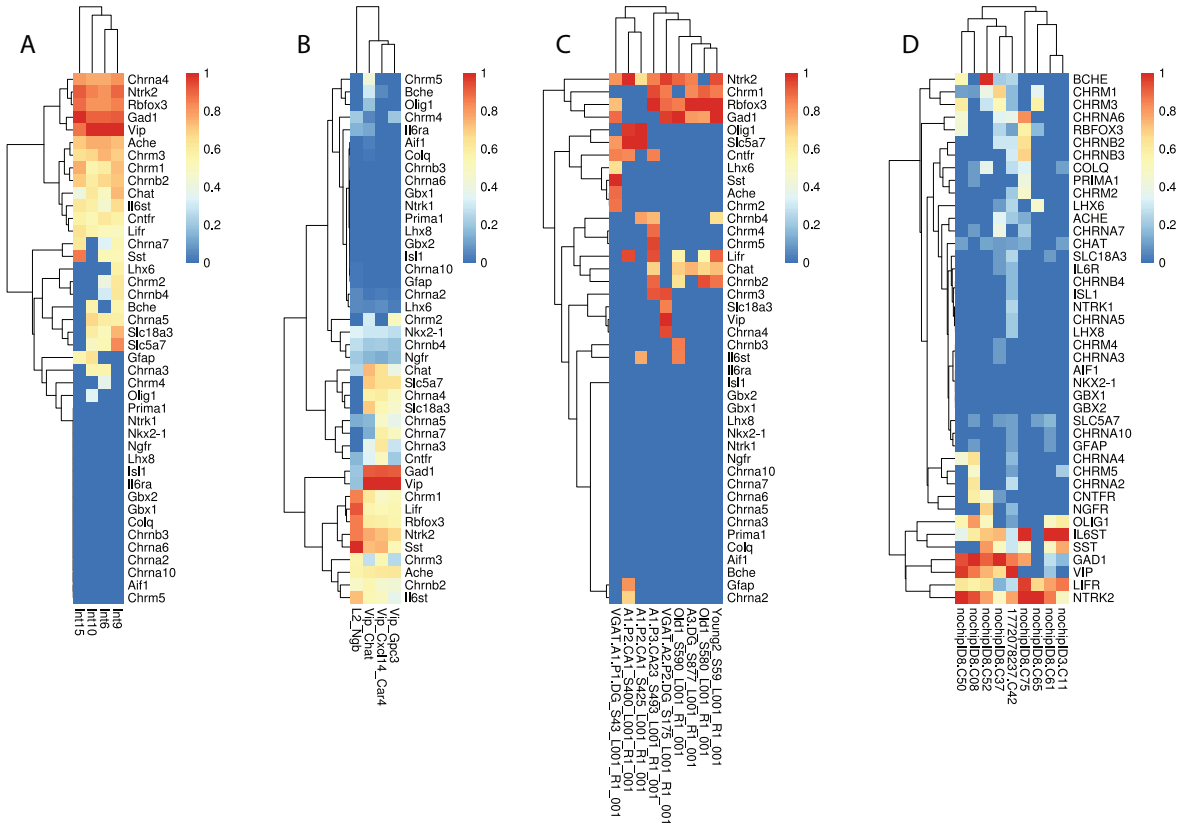


Fig. S1, Single-cell sequencing expression heatmaps with original sample annotation from (A) Zeisel et al 2015, (B) Tasic et al 2016, (C) Habib et al 2016, (D) Darmanis et al 2015, related to Figure 3.

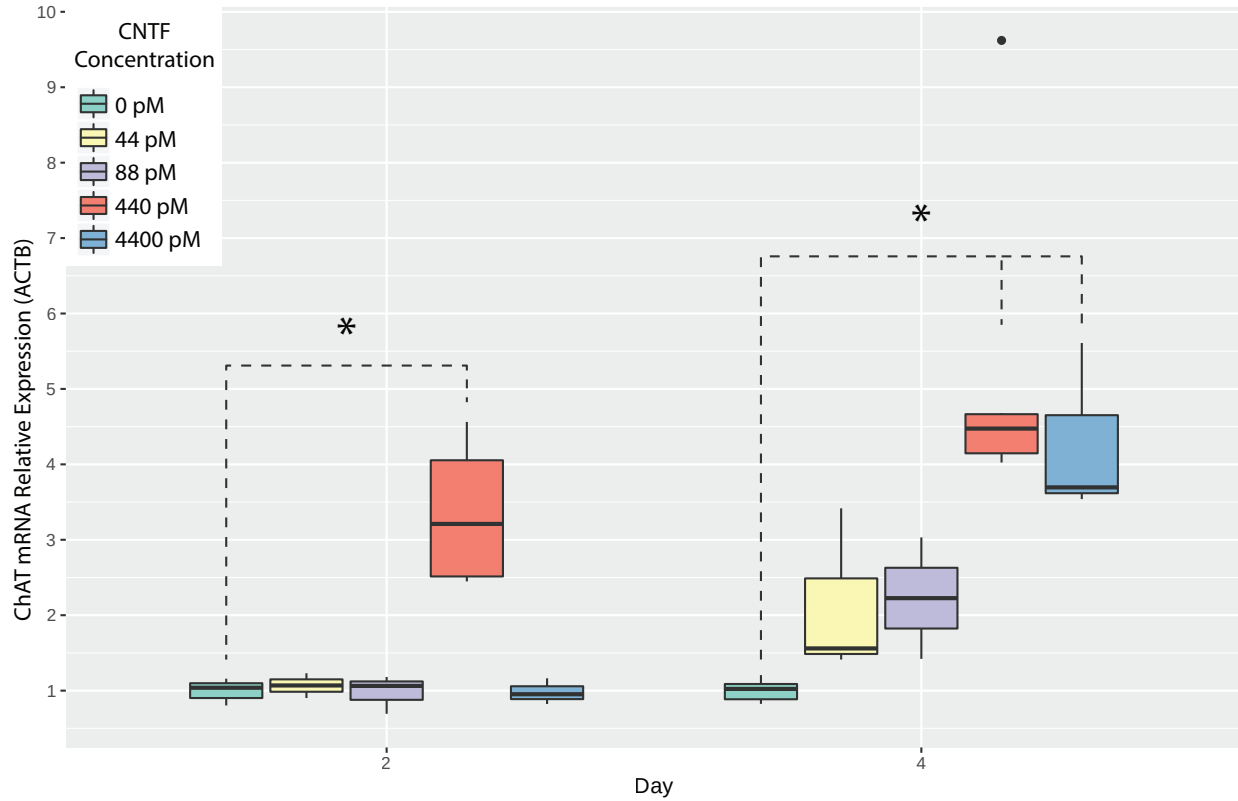


Fig. S2, Dose-response-curve of LA-N-5 during CNTF-induced cholinergic differentiation as measured by expression of CHAT mRNA relative to ACTB. Significant differences at 10 ng/ml CNTF after 2 days ($p = 0.019$) and 4 days ($p = 0.005$), and 100 ng/ml after 4 days ($p = 0.038$). Related to Figure 4.

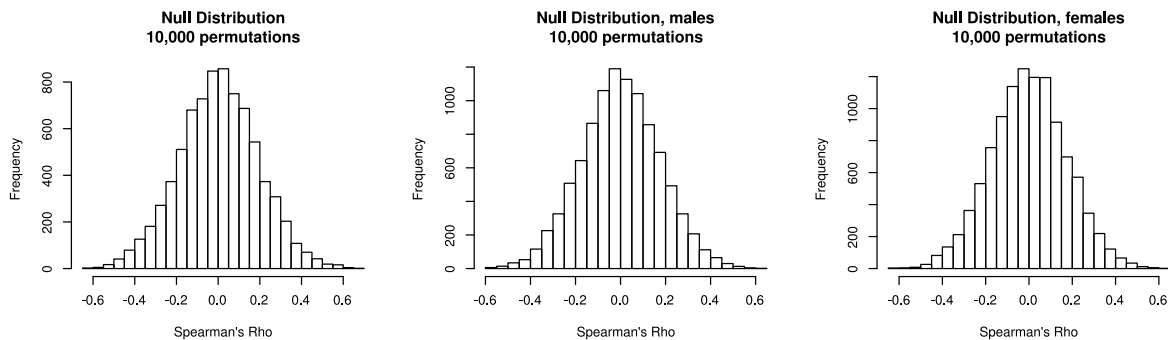


Fig. S3, Unbiased meta-analysis null distributions of Spearman's rho in sex-independent, male, and female datasets, related to STAR Methods - Whole transcriptome meta-analysis, Figure 1.

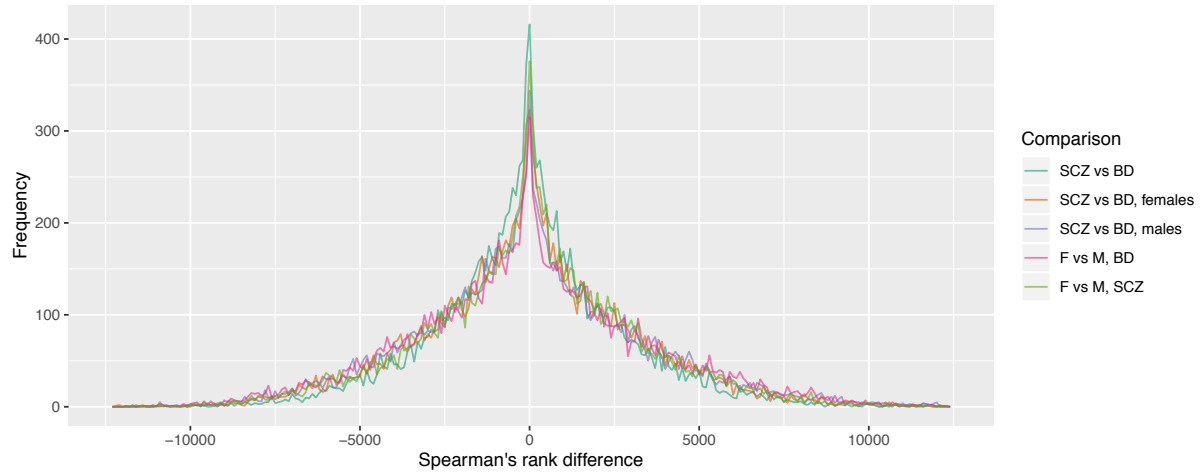


Fig. S4, Spearman rank-differences between any two compared conditions in the GO-enrichment of beta-values from unbiased meta-analysis, related to STAR Methods - Whole transcriptome meta-analysis, Figure 1.

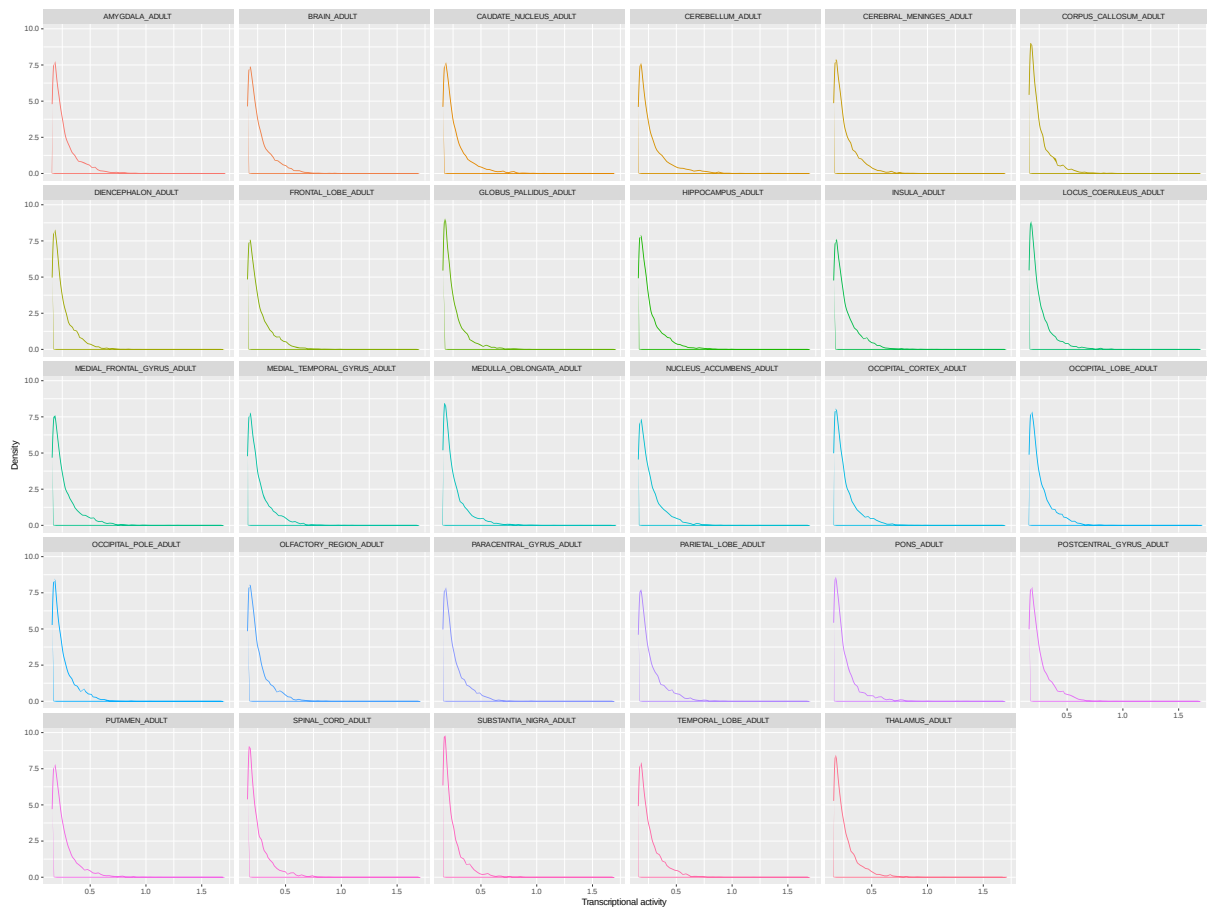


Fig. S5, Density plots of transcriptional activities in analysed CNS brain regions derived from the dataset of Marbach et al 2016 (top 1% most active transcription factors in each brain region), related to STAR Methods - miR-gene-TF targeting.