

Supplementary Figure 1:

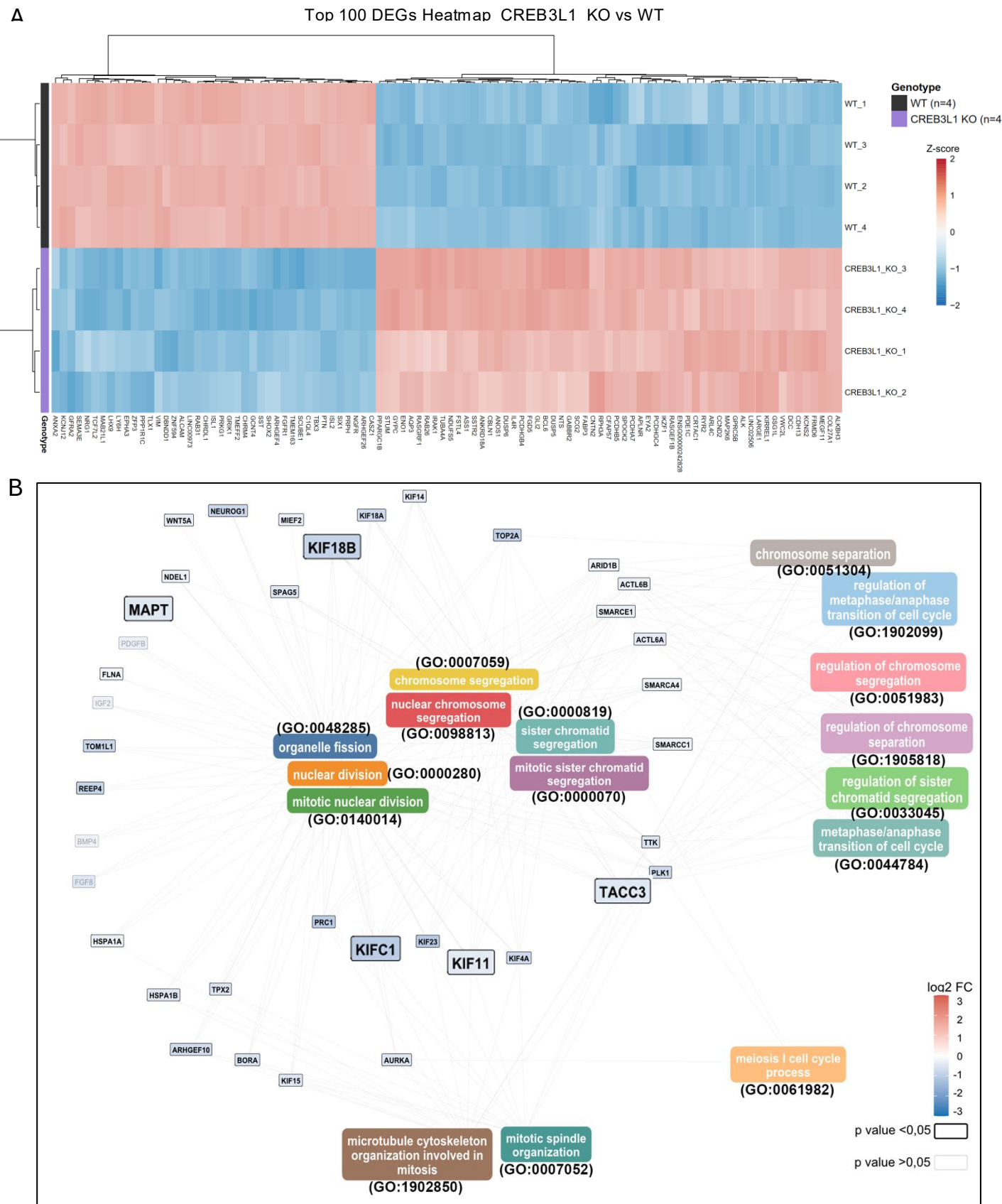


Figure S1: Differential expression profiling and gene ontology analysis of downregulated cytoskeletal genes in CREB3L1_KO i3Neurons compared to WT controls. A: Heatmap of the Top 100 Differentially Expressed Genes (DEGs) from RNA-seq analysis. **B:** Representative network image illustrating GO BP and key DEGs involved in mitotic and microtubule cytoskeleton organization. Colored nodes represent significantly enriched GO terms. Node color intensity corresponds to the expression change ($\log_2$ FC) in CREB3L1_KO i3Neurons compared to WT cells. Edges represent functional associations or shared connections between pathways and genes.

Supplementary Figure 2:

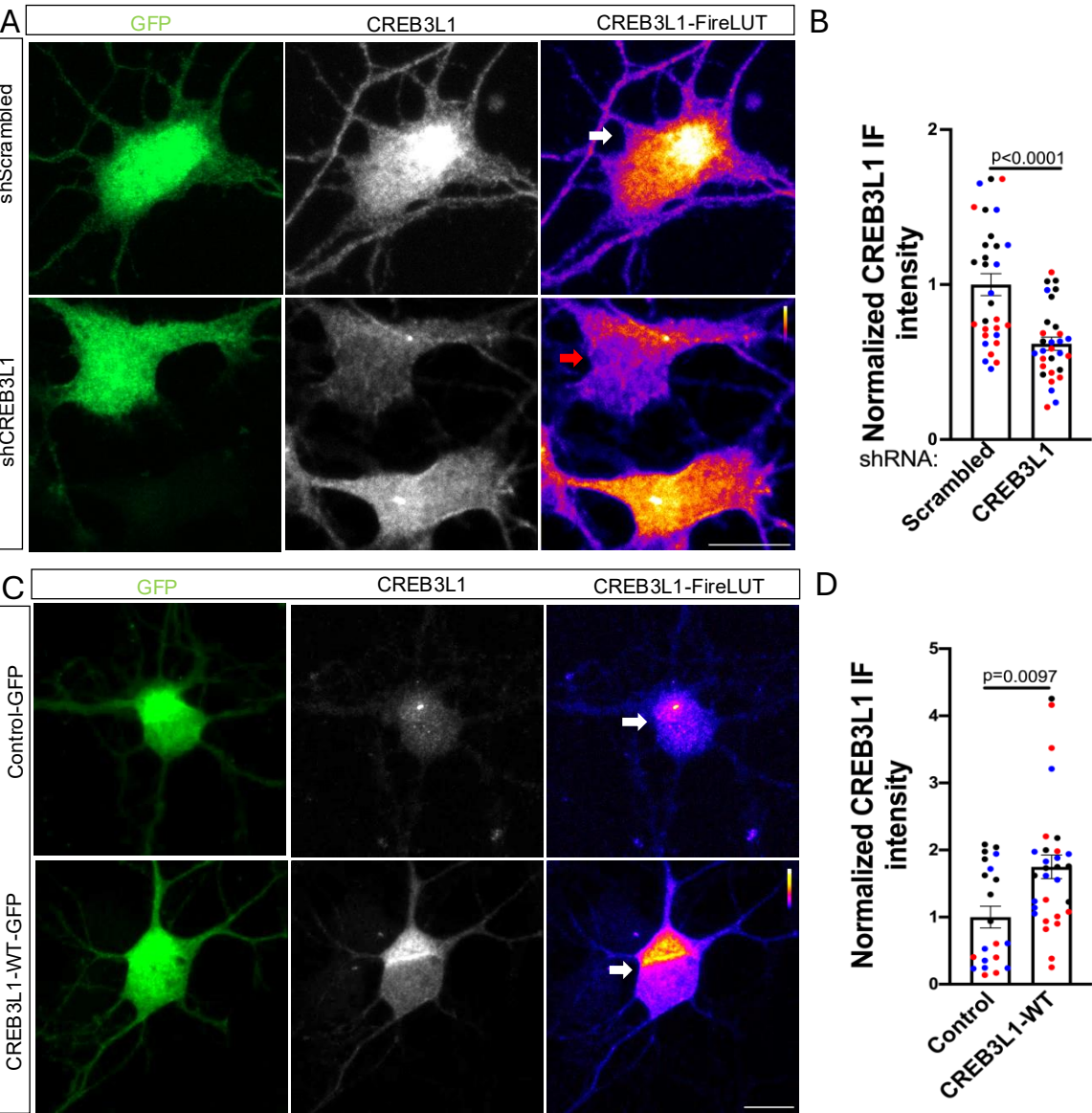


Figure S2: CREB3L1 Knockdown and overexpression efficiency in hippocampal neurons
A: Representative images of hippocampal neurons transfected with shScrambled or shCREB3L1 and immunolabeled against CREB3L1. GFP-positive cells and the CREB3L1 label are shown in Fire-LUT for better visualization. Scale bar: 10 μ m. **B:** Quantification of the normalized intensity of shCREB3L1 neurons vs. shScrambled neurons. **C:** Representative images of hippocampal neurons transfected with Control or CREB3L1-WT and immunolabeled against CREB3L1. GFP-positive cells and the CREB3L1 label are shown in Fire-LUT for better visualization. Scale bar: 10 μ m. **D:** Quantification of the normalized intensity of shCREB3L1 neurons vs. shScrambled neurons. Student's t-test, Mann-Whitney test. Results represent the mean of three independent experiments (n = 3).