Elongator and codon bias regulate protein levels in mammalian peripheral neurons

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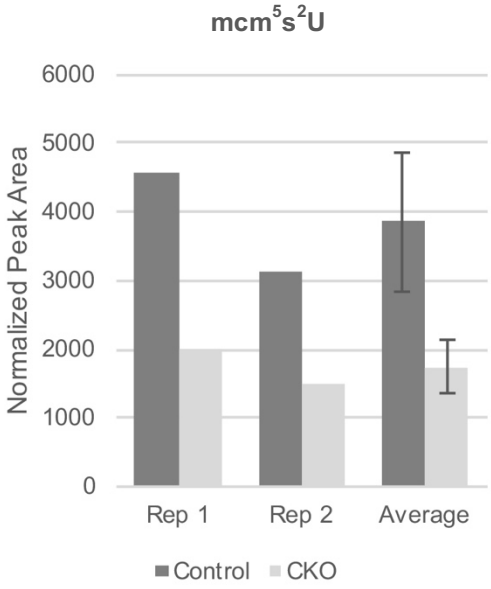
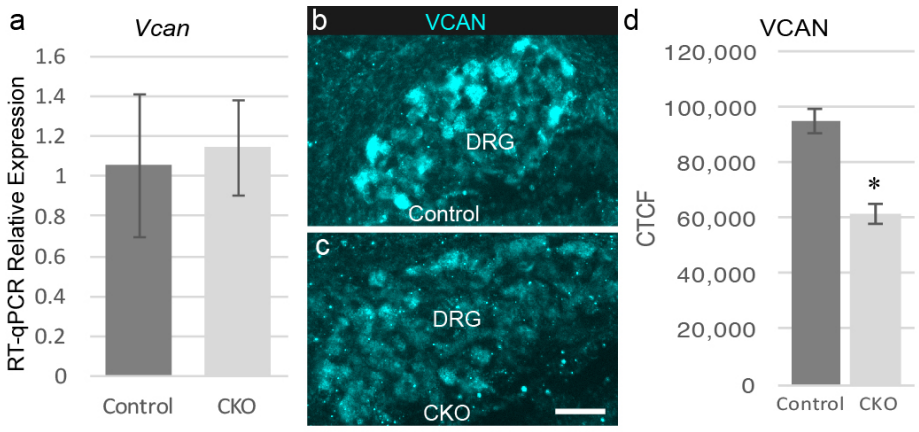
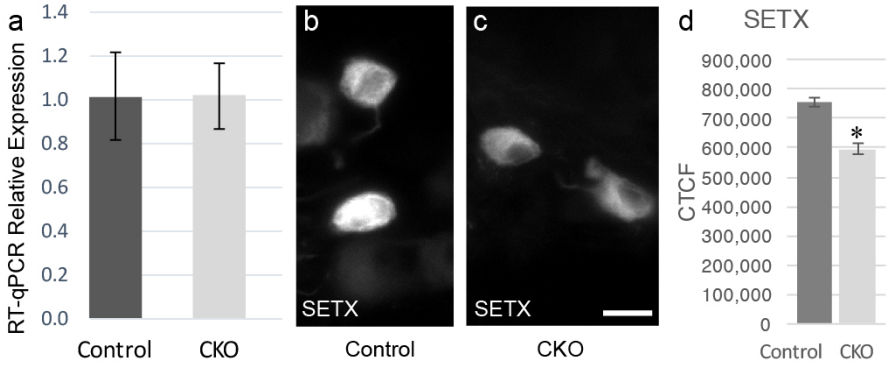


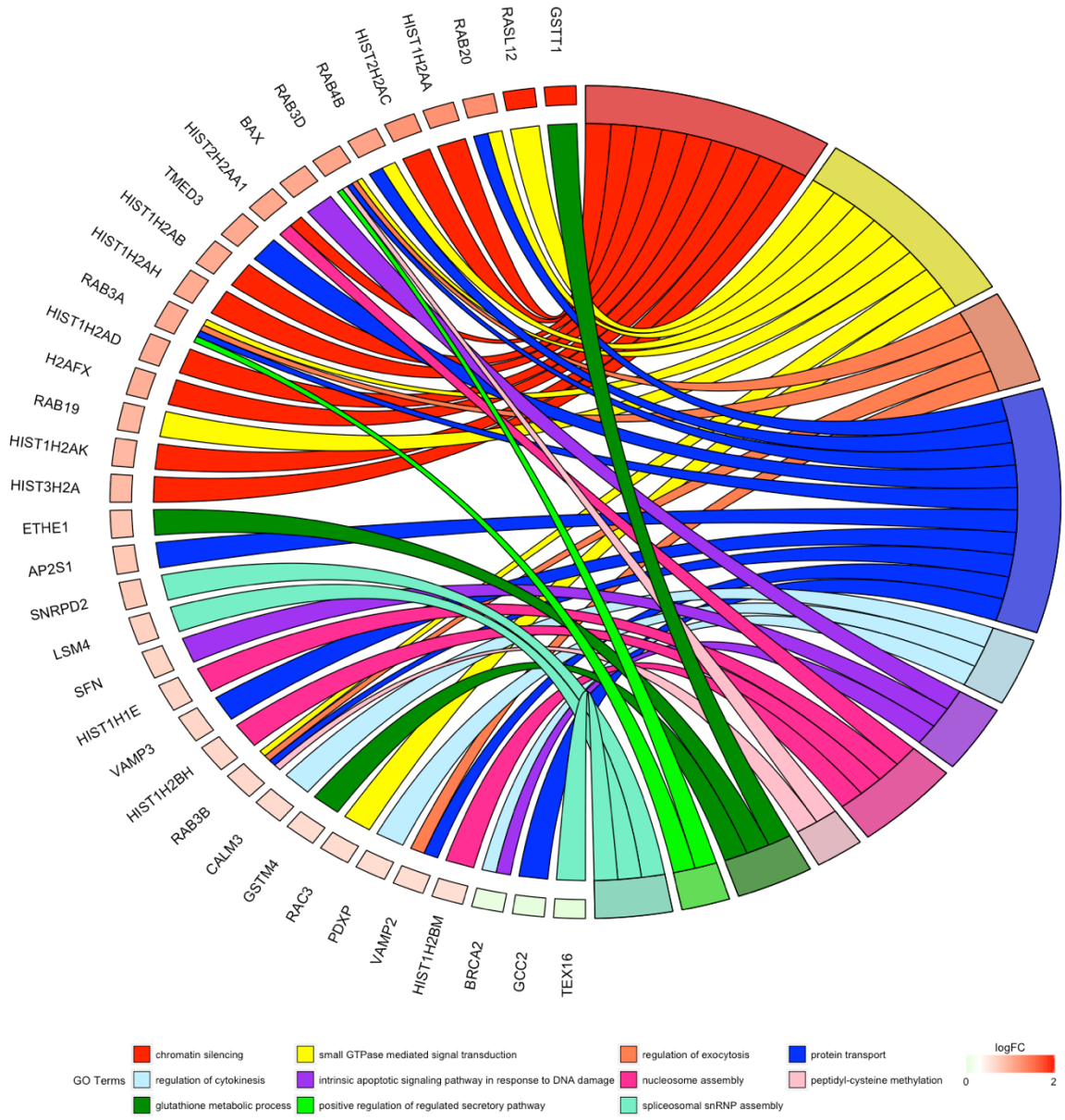
Supplementary Figure 1. Liquid chromatography-mass spectrometry (LC-MS) based tRNA modification analysis shows that mcm^5s^2-modified uridine levels are depleted in mammalian neurons in the absence of Elongator. DRG were collected and pooled from 4 control and 4 CKO embryos per biological replicate. Peak area values of mcm^5s^2U are shown normalized to the quantity of purified tRNA for each sample.



Supplementary Figure 2. Depleted levels of VCAN in Elongator CKO embryos. a) RT-qPCR confirms normal levels of *Vcan* transcript (P=0.78). b-d) Quantitative immunohistochemistry confirms decreased levels of VCAN protein (P<0.001). Error bars denote SD in a, and SEM in d. Scale bar: 40um



Supplementary Figure 3. Depleted levels of SETX in Elongator CKO embryos. a) RT-qPCR confirms normal levels of *Setx* transcript (P=1.0). b-d) Quantitative immunohistochemistry confirms decreased levels of SETX protein (P<0.001). Error bars denote SD in a, and SEM in d. Scale bar: 8um.



Supplementary Figure 4. Selected, significantly enriched GO biological processes for genes that are strong candidates for Elongator regulation (downregulated proteins encoded by genes with $\geq$ 1005 codons and an AA/AG ratio > 1.3 and upregulated proteins encoded by genes with $\leq$ 300 codons and an AA/AG ratio < 0.3). Proteins are arranged by decreasing log10 fold change from top to bottom. Ribbons connect GO terms to their associated proteins. *All genes were transcribed normally.