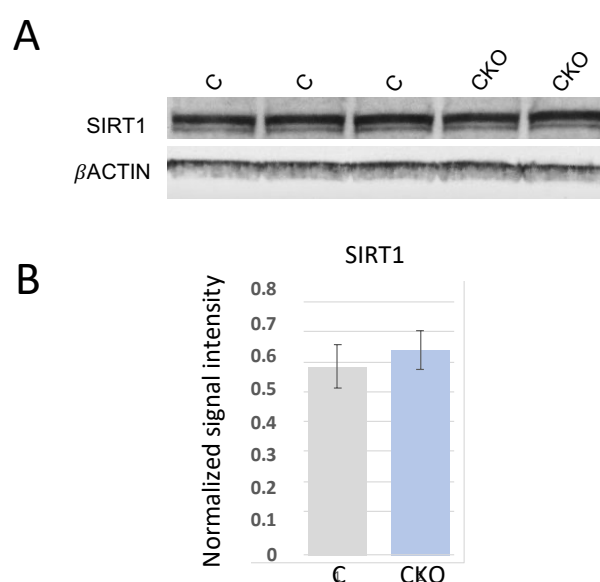
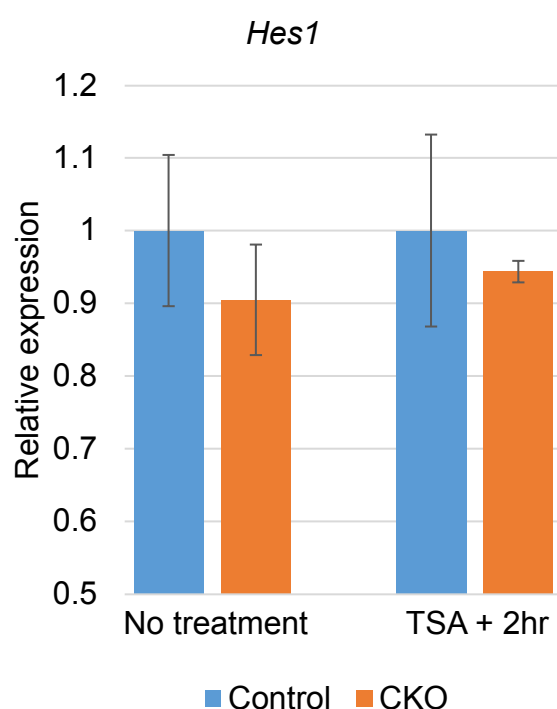


**Fig. S1. Pax3+ progenitors and TrkA+ neurons are depleted in *Wnt1-Cre; Elp1* *LoxP/LoxP* CKO embryos during development of the dorsal root ganglia.** A,B,E) E11.5. Pax3+ cells are significantly reduced in CKO embryos compared to controls. \**P* value < 0.00, n = 3 control and 3 CKO. C,D,F) E12.5. TrkA+ neurons are significantly reduced in CKO embryos compared to controls. \**P* value < 0.00, n = 3 control and 3 CKO. Scale bar = 25  $\mu$ m; error bars denote SEM. CKO, conditional knockout; DRG, dorsal root ganglion.

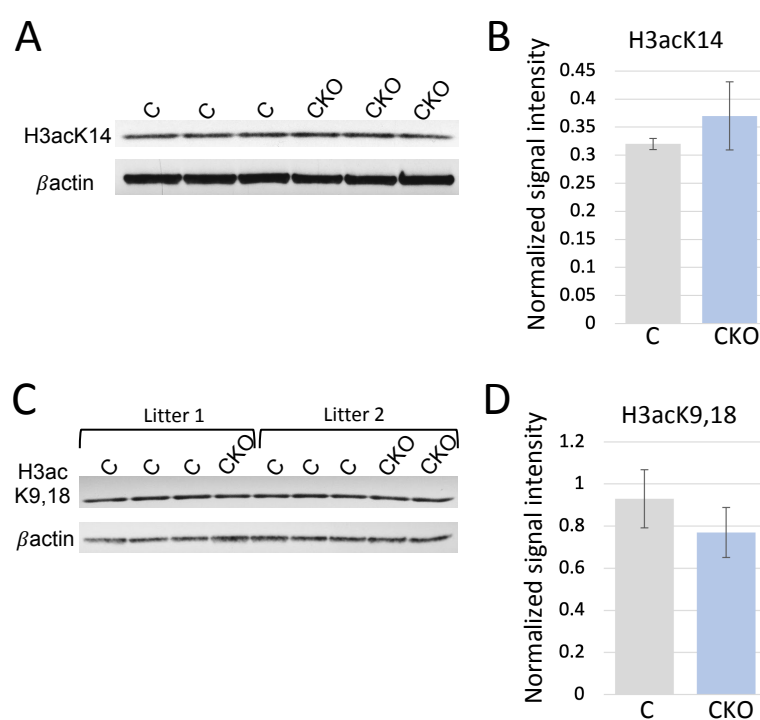


**Fig. S2. Sirtuin1 levels are normal in *Elp1* CKO embryos.**

A) E17.5. Western blots show that SIRT1 levels are the same in brain tissue from *Wnt1-Cre; Elp1<sup>LoxP/LoxP</sup>* CKO embryos and controls. B) Quantification of normalized band intensities from multiple litters. *P* value = 0.67, n = 4 control and 3 CKO.



**Fig. S3. *Hes1* transcript levels are normal in *Elp1* CKO embryos at E11.5 and are not impacted by TSA.** Quantitative RT-PCR shows that transcript levels of *Hes1* are normal in *Elp1* CKO embryos at E11.5 ( $P = 0.45$ ,  $n = 3$  control and 3 CKO) and that *Hes1* expression is not impacted by TSA ( $P = 0.53$ ).



**Fig. S4. Histone acetylation is normal in *Elp1* CKO embryos.** E17.5. A) Western blots show that levels of acetylated H3acK14 are the same in brain tissue from *Elp1* CKOs and controls. B) Quantification of normalized band intensities.  $P = 0.49$ ,  $n=3$  control and 3 CKOs from the same litter. C) Western blots show that levels of acetylated H3acK9,18 are the same in brain tissue from *Elp1* CKOs and controls. D) Quantification of normalized band intensities.  $P = 0.14$ ,  $n= 6$  control and 3 CKOs from two separate litters.

**Table S1.** H2A Histones (*Mus musculus*)

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**Table S2.** Mouse ubiquitin proteasome system genes that are misregulated in the absence of Elp1

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**Table S3.** Transcriptome results for Notch target genes (defined as genes whose expression levels have been demonstrated to change as a result of Notch signalling) (Giaimo et al., 2018; Borggreffe & Oswald, 2009).

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**Table S4.** Transcriptome z-ratio values plotted against chromosome location. Scroll right for individual z-ratios.

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