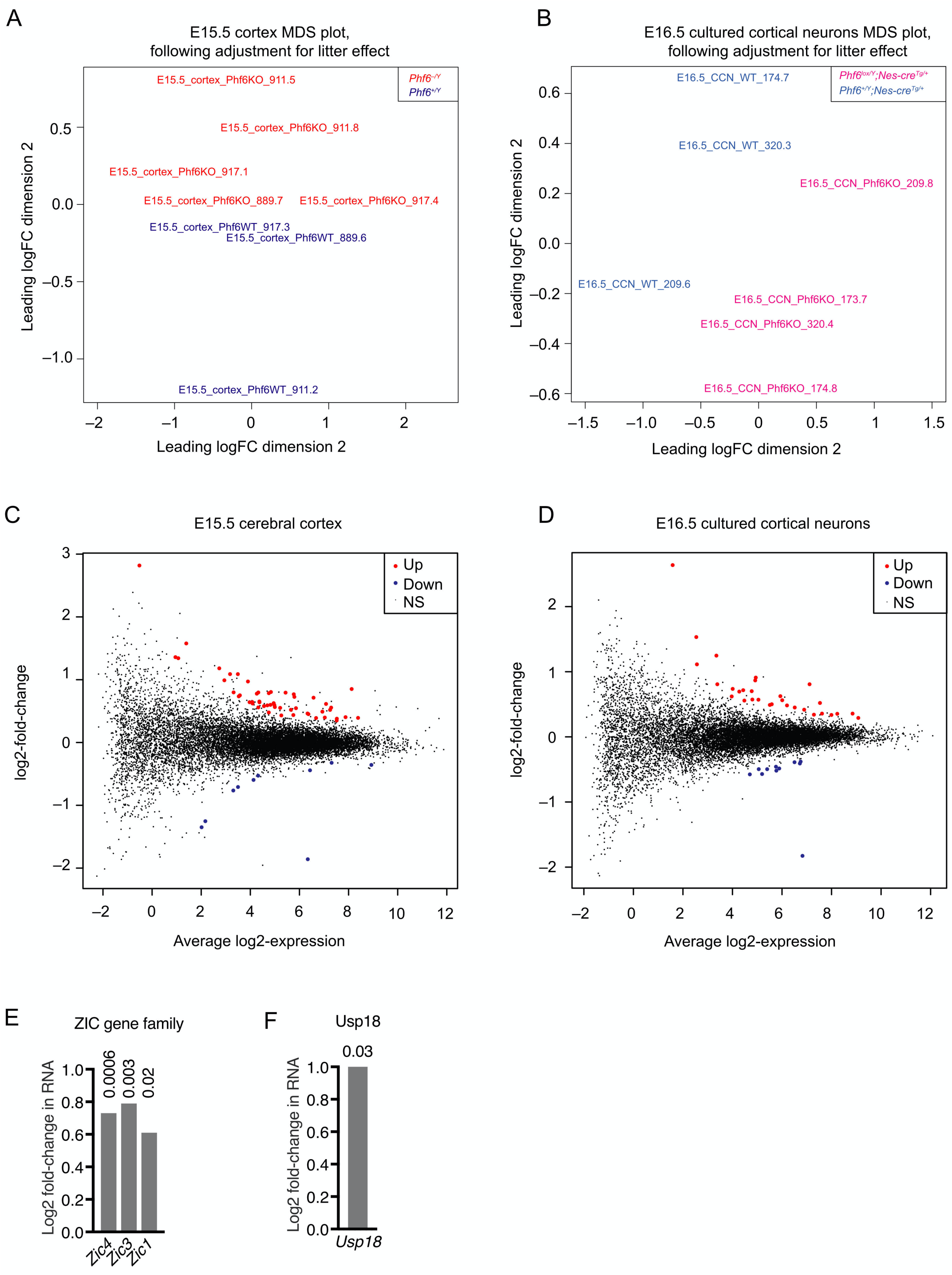

S13 Fig: RNA-sequencing analysis of *Phf6*-deleted and control E15.5 cortex and E16.5 cultured cortical neurons

(A) Multidimensional scaling (MDS) plot of N = 5 *Phf6*$^{-/Y}$ *vs.* 3 *Phf6*$^{+/Y}$ E15.5 cortices samples used for RNA-sequencing analysis, showing clustering of samples after adjustment for litter-effect; color-coded by genotype.

(B) MDS plot of N = 4 *Phf6*$^{lox/Y}$*;Nes-cre*$^{Tg/+}$ vs. 3 *Phf6*$^{+/Y}$*;Nes-cre*$^{Tg/+}$ E16.5 cortical neuron isolates used for RNA-sequencing analysis showing clustering of samples after adjustment for litter-effect; color-coded by genotype.

(C,D) Mean-difference plot for *Phf6*$^{-/Y}$ *vs.* *Phf6*$^{+/Y}$ E15.5 cortex RNA-sequencing data showing log$_2$-fold change for each gene over average log$_2$ expression (C). Mean-difference plot for *Phf6*$^{lox/Y}$;*Nes-cre*$^{Tg/+}$ vs. *Phf6*$^{+/Y}$;*Nes-cre*$^{Tg/+}$ E16.5 cultured cortical neuron RNA-sequencing data (D). Significantly up- and downregulated genes in the *Phf6* deleted samples relative to controls are coloured red and blue respectively. NS = not significant.

(E) Log$_2$ fold-change in RNA levels of ZIC family transcription factor genes in E15.5 *Phf6*$^{–/Y}$ *vs. Phf6*$^{+/Y}$ cortex.

(F) Log$_2$ fold-change in RNA levels of the *Usp18* gene in *Phf6*$^{lox/Y}$;*Nes-cre*$^{Tg/+}$ vs. *Phf6*$^{+/Y}$;*Nes-cre*$^{Tg/+}$ E16.5 cortical neurons.

RNA sequencing data were analysed as described in the methods section.