



S14 Fig: Additional assessment of the expression of selected genes identified as differentially expressed between *Phf6* deleted and control samples by RNA-sequencing

(A) RT-qPCR of *Phf6*^{lox/Y}; *Nes-cre*^{Tg/+} vs. *Phf6*^{+/Y}; *Nes-cre*^{Tg/+} E15.5 cortex.

As in the RNA-sequencing dataset, mRNA levels for the selected genes were higher in the *Phf6*^{lox/Y}; *Nes-cre*^{Tg/+} vs. *Phf6*^{+/Y}; *Nes-cre*^{Tg/+} cortex.

(B) Representative images of RNA/RNA whole mount in situ hybridisation of E15.5 *Phf6*^{lox/Y}; *Nes-cre*^{Tg/+} vs. *Phf6*^{+/Y}; *Nes-cre*^{Tg/+} brains using RNA probes as indicated.

N = 5-8 tissue samples per genotype. Data are presented as mean \pm sem (A). Data from individual foetuses are represented as open circles (A). Data were analysed by two-way ANOVA (A).