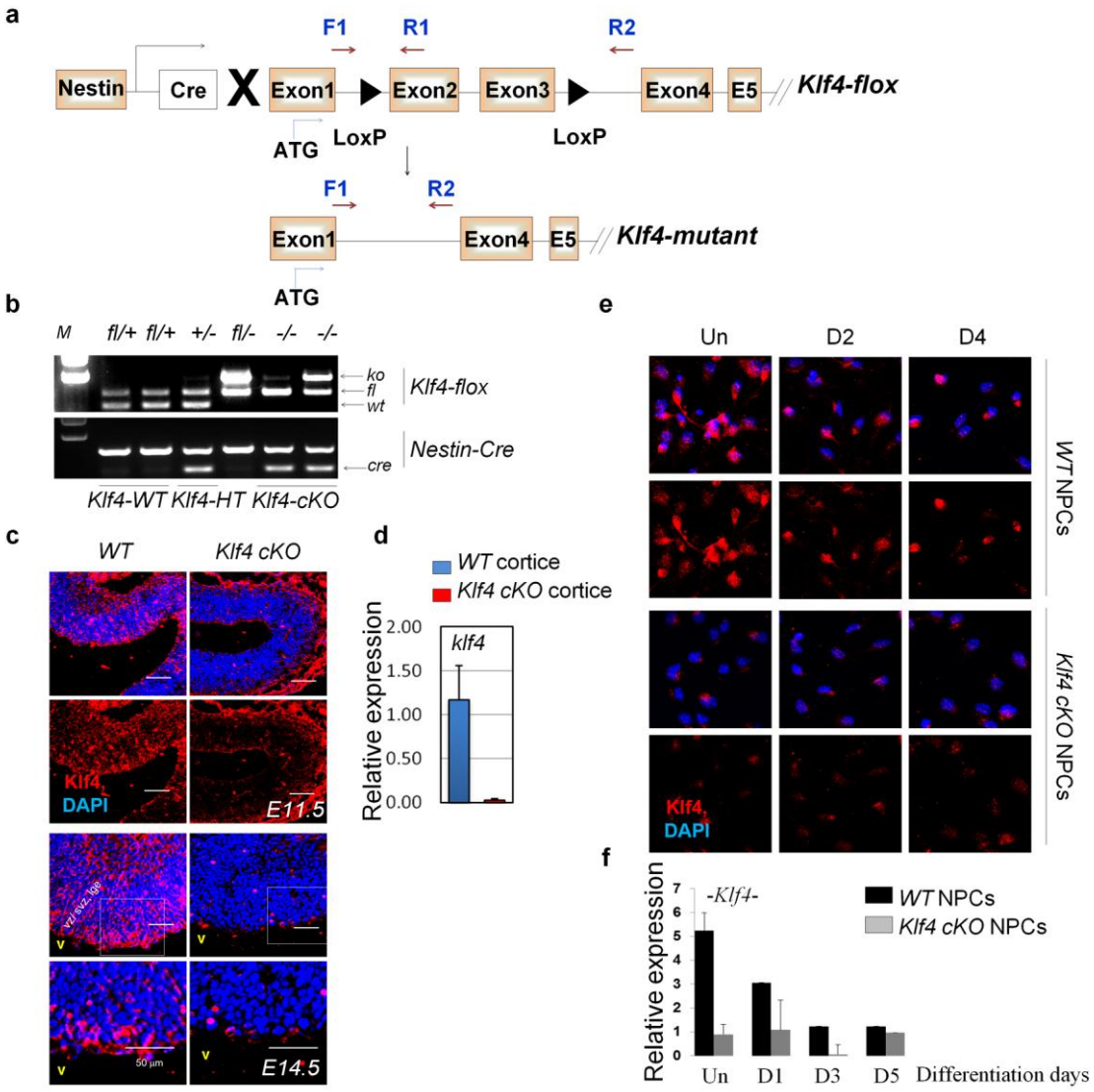
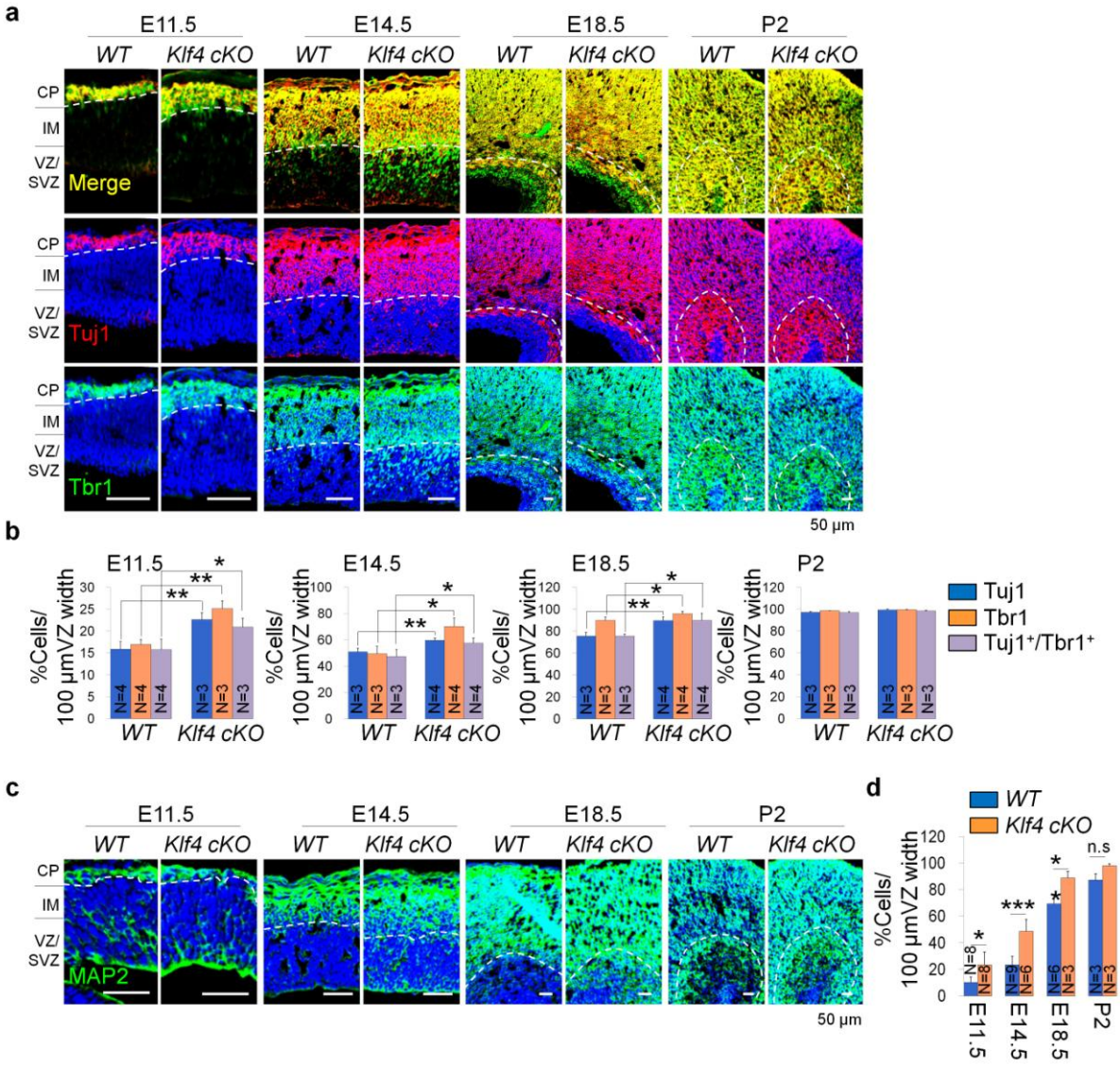
SUPPLEMENTARY FIGURE LEGENDS

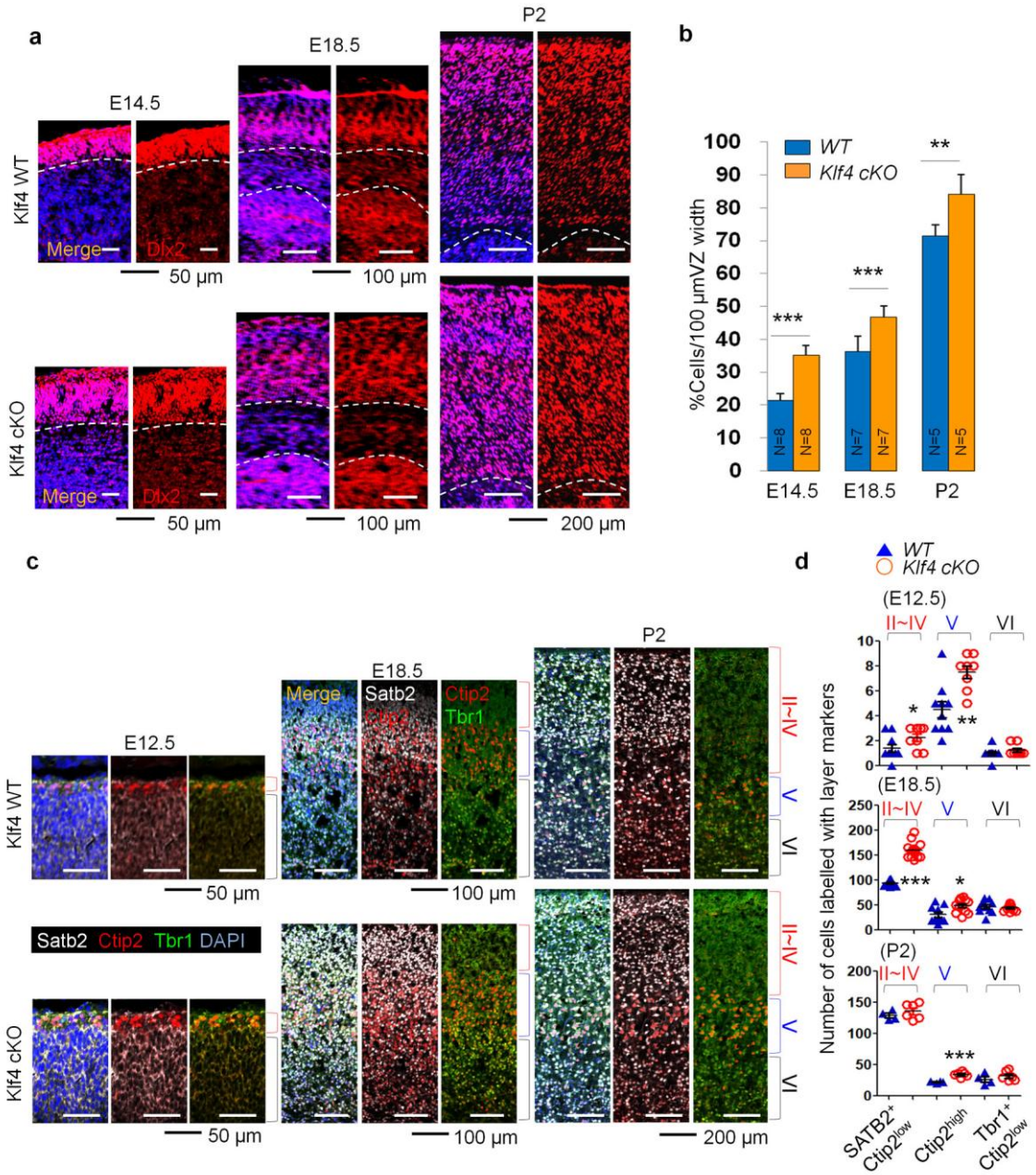


Supplementary Figure 1. Generation of Klf4 conditional knockout mice. (**a**, **b**) *Nestin-cre* mice were crossed with *Klf4*$^{fl/+}$ or *Klf4*$^{fl/fl}$ mice to generate *wild-type* and *Klf4* conditional knockout embryos. Genotyping was performed with indicated primers. (**b**) Upper band is Klf4 knockout, middle band is floxed, and lower band indicates wild-type. Left lane (*M*) indicates size

marker. (**c**) Fixed cyro-embedded coronal sections from E11.5 or E14.5 mouse forebrain stained with antibodies against Klf4 (red). DAPI (blue). Scale bars, 50 µm. (**d**) qPCR analysis of Klf4 mRNA cortices equivalent to those shown in (c, lower panel). (**e**) Immunostaining to detect Klf4 expression in *wild-type* and *Klf4 cKO NPCs*. Nuclear staining shown by DAPI (blue). Scale bar, 50 µm. (**f**) qPCR analysis of Klf4 levels in *wild-type* and *Klf4 NPCs* at indicated days (d) of differentiation (n=2-3).

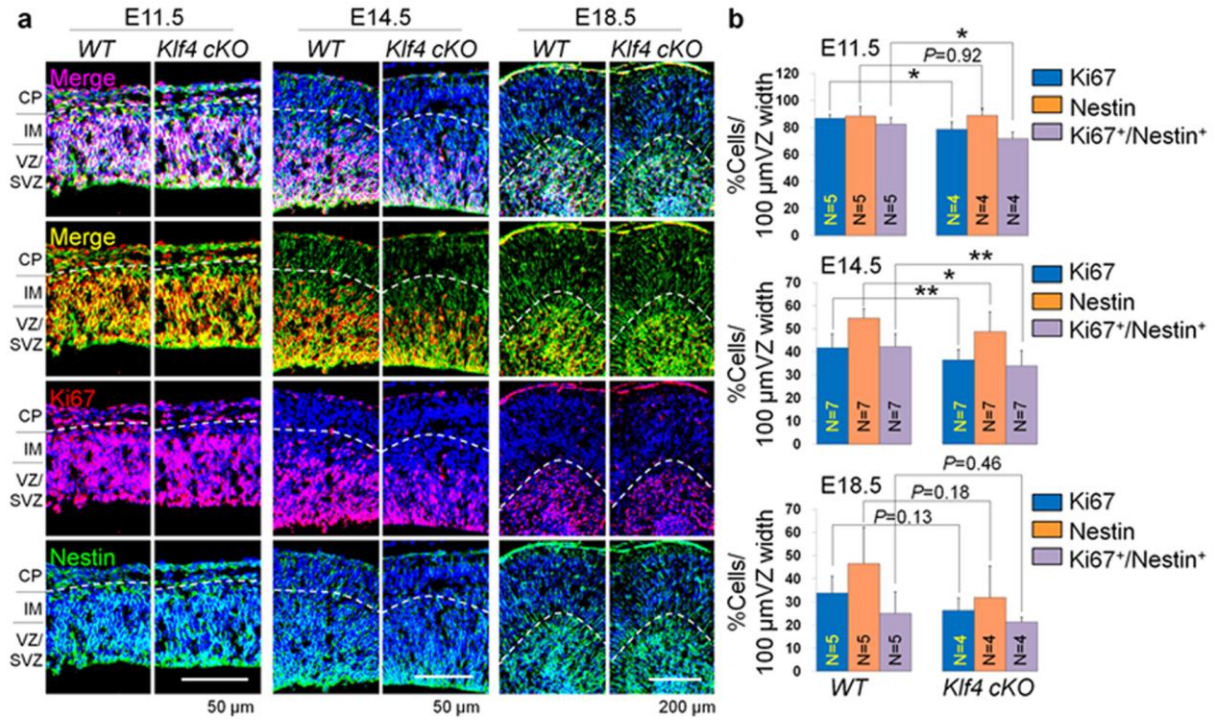


Supplementary Figure 2. Klf4 down-regulation enhances neurogenesis *in vivo.* (**a, c**) Fixed coronal sections from E11.5, E14.5, E18.5 or P2 mouse forebrain stained with antibodies against Tuj1 (red), Tbr1 (green) or Map2 (green). DAPI (blue). (**b, d**) Images shown above were quantified in cortex areas of 100 μm ventricular width extending from VZ to the pial surface (E11.5: *Klf4* $^{fl/+}$*(WT)*, n=4-8, *Klf4 cKO*, n=3-8, and E14.5: *Klf4*$^{fl/+}$ *(WT)*, n=3-9, *Klf4 cKO*, n=4-6, E18.5: *Klf4*$^{fl/+}$ *(WT)*, n=3-6, *Klf4 cKO*, n=3-4, P2: *Klf4*$^{fl/+}$ *(WT)*, n=3, *Klf4 cKO*, n=3). Scale bars, 50 μm. Values correspond to mean±SD. t-tests were performed to calculate significance (*P < 0.05, **P < 0.005, ***P < 0.0005).



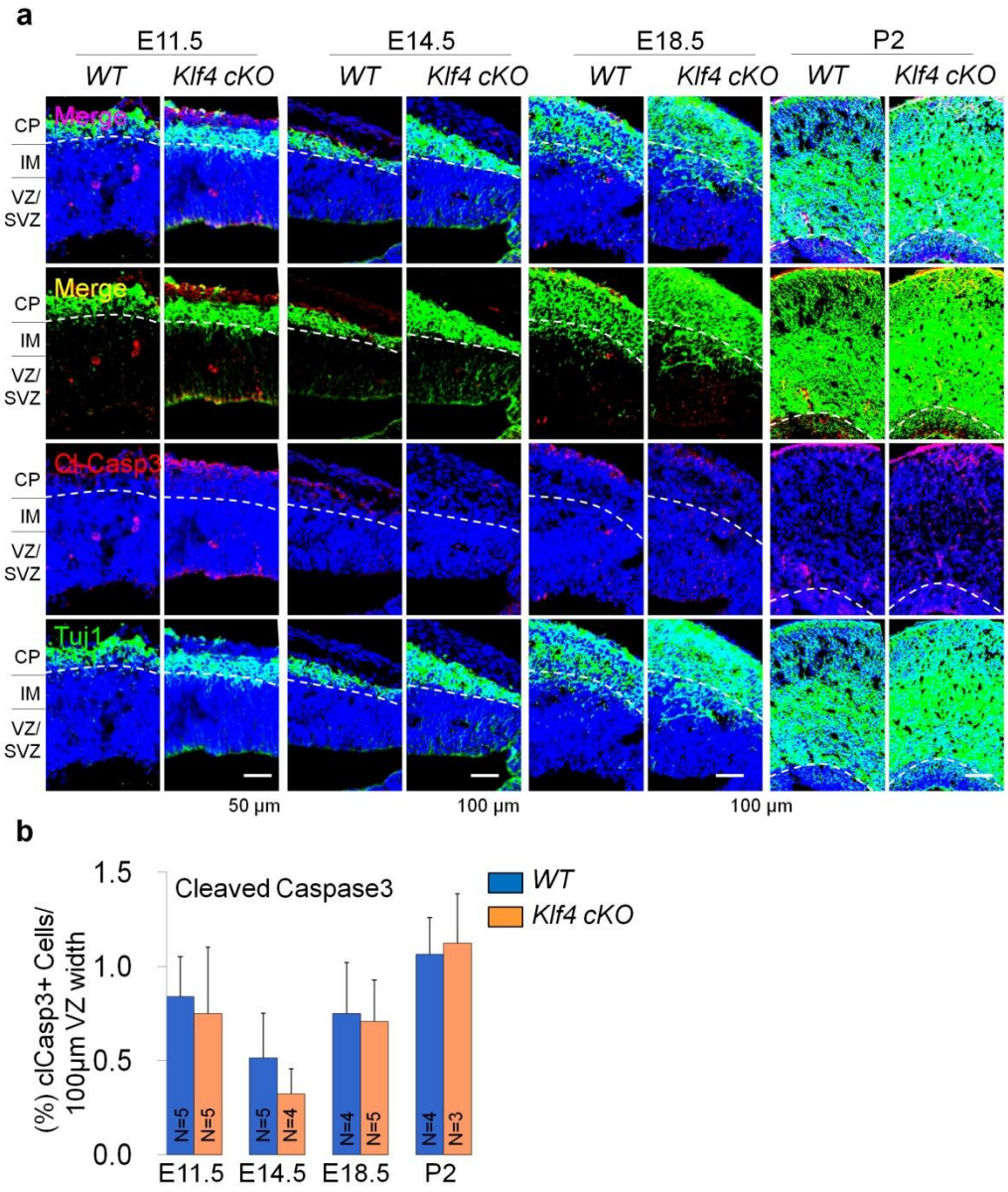
Supplementary Figure 3. Klf4 down-regulation enhances deep layer corticogenesis *in vivo*. (**a**) Fixed coronal sections from E14.5, E18.5 or P2 mouse forebrain stained with antibodies against Dlx2 (red). DAPI (blue). (**b**) Images shown in (a) were quantified in cortex in areas of 100 μm ventricular width extending from VZ to the pial surface in E14.5 (n=8/genotype), E18.5 (n=7/genotype), and P2 (n=5/genotype). (**c**) Representative immuno-labeling of E12.5, E18.5

and P2 cortical sections with indicated antibodies revealing cortical layering in *WT* and *Nestin^{cre}:Klf4 cKO* mice. (**d**) Quantification of (c) numbers over brackets denote cortical layers where the cells were counted. CTIP2^{low} (layer 6) and CTIP2^{high} (layer 5) expressing cells were used to differentiate between Tbr1^{+}/CTIP2^{low} cells of layer 5 and CTIP^{high} cells in layer 5. SATB2^{+}/CTIP2- cells were counted above layer of CTIP^{high} cells in E12.5 (n=8~10/genotype), E18.5 (n=10~12/genotype), and P2 (n=4~6/genotype). Values correspond to mean±SD. t-tests were performed to calculate significance (*P < 0.05, **P < 0.005, ***P < 0.0005).



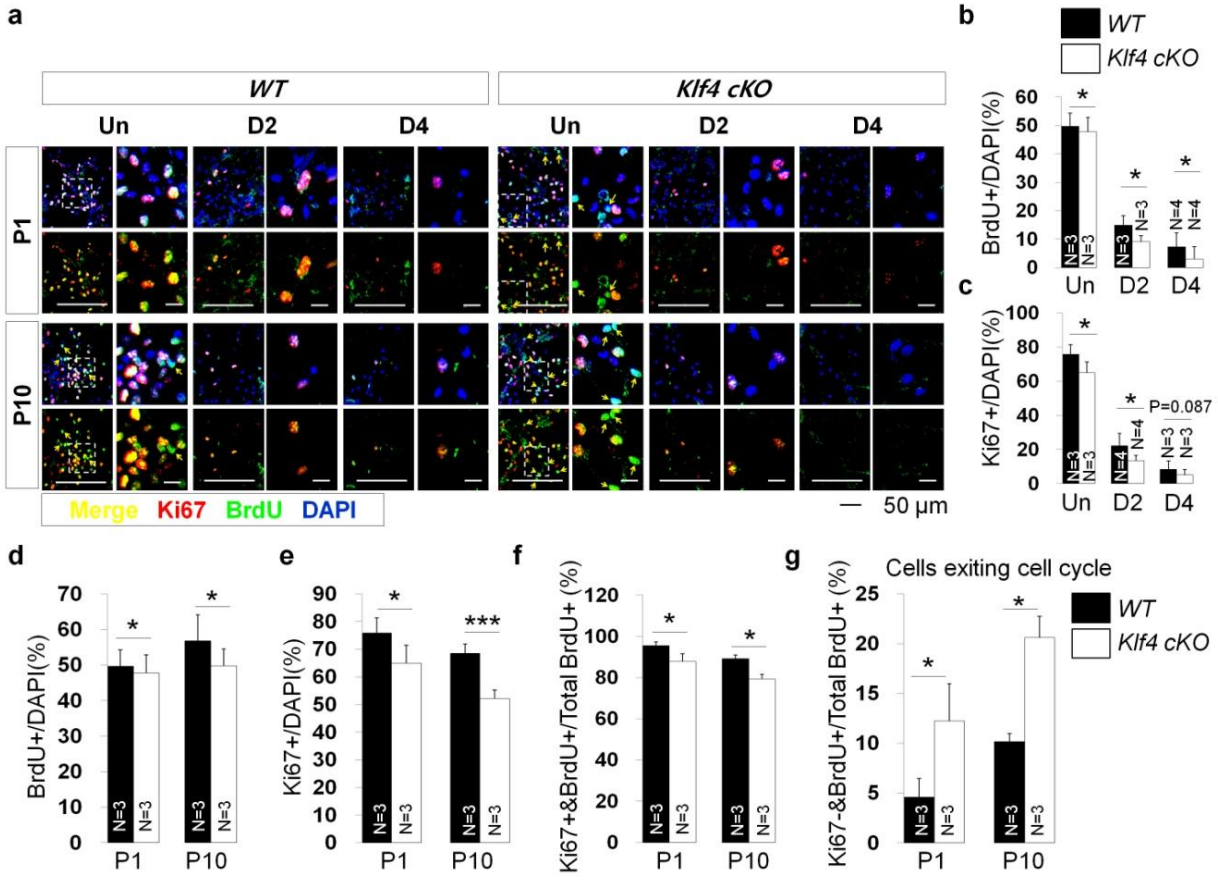
Supplementary Figure 4. Klf4 down-regulation enhances neuronal maturation and decreases proliferative neural progenitor population in developmental neocortex. (**a**) Fixed coronal sections from E11.5, E14.5, or E18.5 mouse forebrain stained with antibodies against Nestin (green) and Ki67 (red). DAPI (blue). (**b**) Images shown above were quantified in cortex

in areas of 100 μm ventricular width extending from VZ to the pial surface. Scale bars, 50 μm. Values correspond to mean±SD. *t*-tests were performed to calculate significance (*P < 0.05, **P < 0.005).



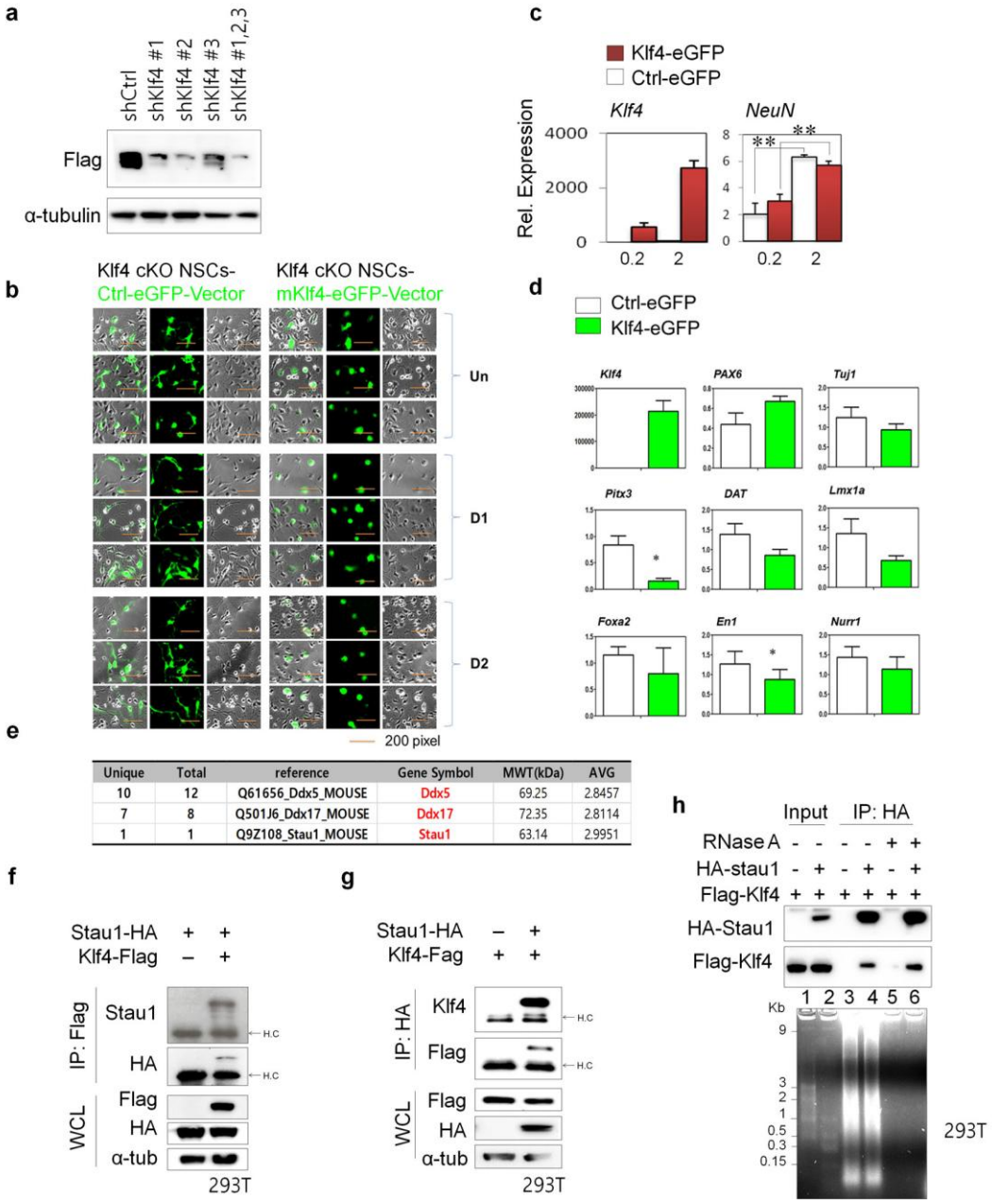
Supplementary Figure 5. Klf4 down-regulation does not change cell death of progenitors and neurons in developmental neocortex. (**a**) Representative immuno-labeling for apoptotic cells with clCasp3 and neuronal marker TuJ1 in coronal telencephalic sections from E11.5, E14.5, or P2 mice. (**b**) Apoptosis of cells were quantified in cortex in areas of 100 mm ventricular width

extending from VZ to the pial surface (E11.5: *Klf4* $^{fl/+}$*(WT)*, n=5, *Klf4 cKO*, n=5, and E14.5: *Klf4*$^{fl/+}$ *(WT)*, n=5, *Klf4 cKO*, n=4, E18.5: *Klf4*$^{fl/+}$ *(WT)*, n=4, *Klf4 cKO*, n=5, P2: *Klf4*$^{fl/+}$ *(WT)*, n=4, *Klf4 cKO*, n=3). Scale bars, 50 or 100 μm. Values correspond to mean±SD. *t*-tests were performed to calculate significance.



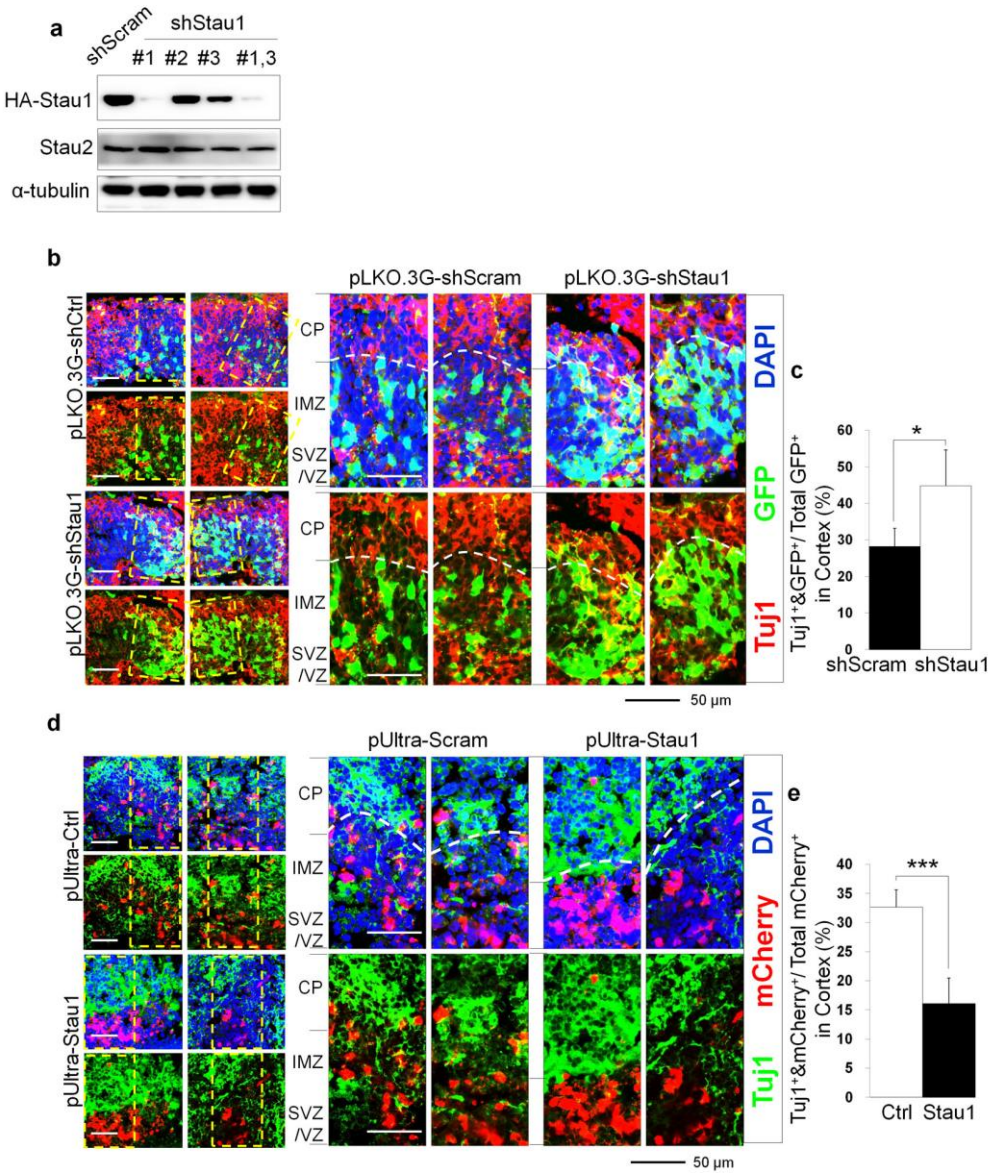
Supplementary Figure 6. Klf4 down-regulation decreases proliferative neural progenitor cells and increases cells exiting cell cycle. (**a**) Representative immuno-labeling for Ki67 and BrdU in the P1 (passage 1) or P10 (passage 10) NPCs pulsed with BrdU (30 μg/ml) for 5 hrs. The area outlined by dotted lines is magnified in the adjacent images. Un, undifferentiation; D2, differentiation 2 days *in vitro*; D4, differentiation 4 days *in vitro*. Yellow arrows indicate cells exiting cell cycle which are Ki67 negative cells incorporated BrdU in the S phase. (**b-e**) Quantification of (a). Histogram showing percent stained cells relative to the number of DAPI^{+}

nuclei. Scale bar, 50 µm. D, differentiation days *in vitro*. (**f**) Fraction of $Ki67^{+}BrdU^{+}$ cells in total $BrdU^{+}$ cell population. (**g**) Fraction of cells exiting the cell cycle defined as fraction of $Ki67^{-}$ $BrdU^{+}$ cells in total $BrdU^{+}$ cell population. Scale bars, 50 µm. Values correspond to mean±SD. *t*-tests were performed to calculate significance (*P < 0.05, **P < 0.005, ***P < 0.0005).



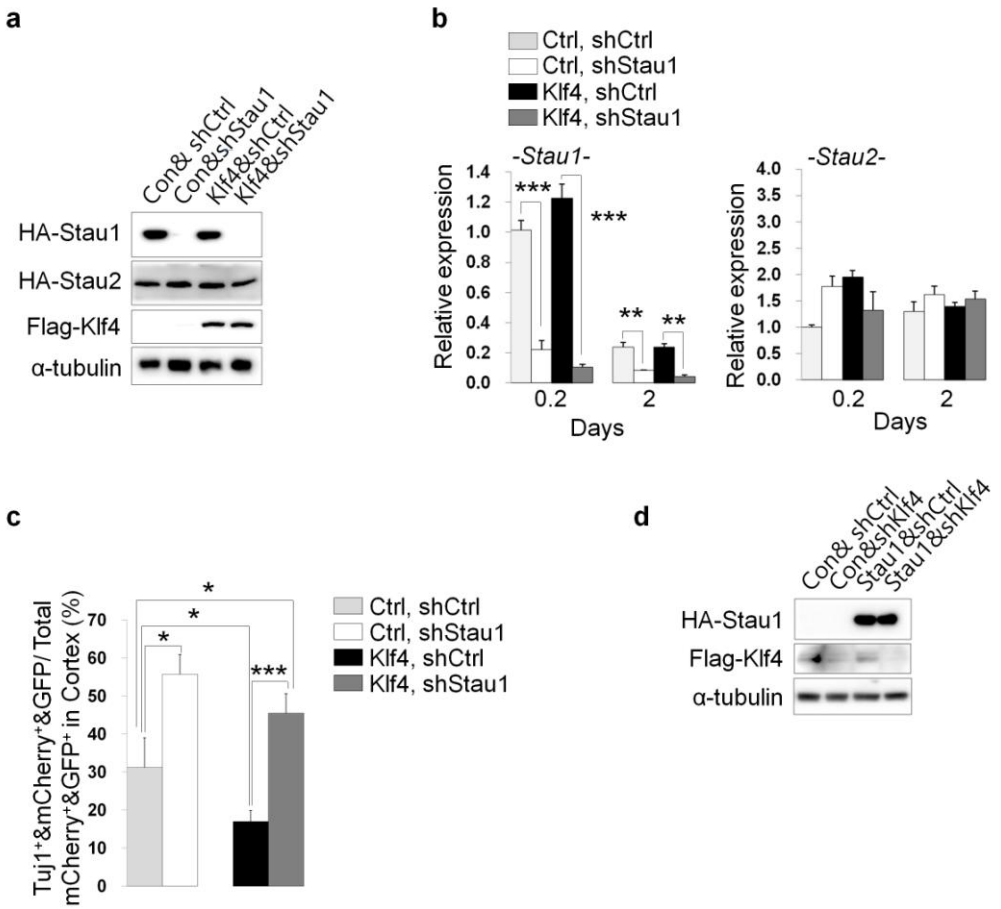
Supplementary Figure 7. Klf4 regulates NPC neuronal differentiation and interacts with post-transcriptional regulators. (**a**) NPCs expressing Flag-Klf4 were transfected with pLKO.1-

shScramble or pLKO.1-shKlf4 #1, #2, and #3, and one day later, Flag and α-tubulin in lysates were detected by immunoblotting (n=2). (**b**) *Klf4 cKO* NPCs transfected with *Control-EGFP* vector or *Klf4-EGFP* vector. GFP+ cells were assessed after 1 or 2 days of culture in N2 medium. (**c**, **d**) qPCR analysis of indicated transcripts in samples equivalent to those shown in (b) (n=3). (**e**) MS spectrometry analysis with Flag-Klf4 in NPCs (**f, g**) Co-Immunoprecipitation (co-IP) of HA-tagged Stau1 or Flag-tagged Klf4 in HEK293T cells transfected with these constructs. (**h**) (upper) Co-IP of above samples with or without RNase A (10μg/ml). Values correspond to mean±SD. *t*-tests were performed to calculate significance (*P < 0.05, **P < 0.005). (lower) Agarose gel of total RNA in above samples were sperated with standard electrophoresis procedures. We used a 7.5×10 cm mini-gel horizontal system (C.B.S. Scientific) to run a 1.5% agarose gel at 100 V (6 V/cm) for 2 h. Marker lanes (1–2) contained commercial RNA ladders (1. New England Bio Labs ssRNA ladder #No362s, 2. NEB low Range ssRNA ladder #No364s). Lane 3 and 4, total RNA in IP lysates without RNase A (10μg/ml). Lane 5 and 6, total RNA in IP lysates with RNase A (10μg/ml). RNA ladders and each total RNA samples were premixed with 2xRNA loading dye (Thermo Scientific, #Ro641). The bands were visualized using Molecular Imager® Gel Doc™ XR+ (Bio-Rad). See also Supplementary Figs. 19, 20.

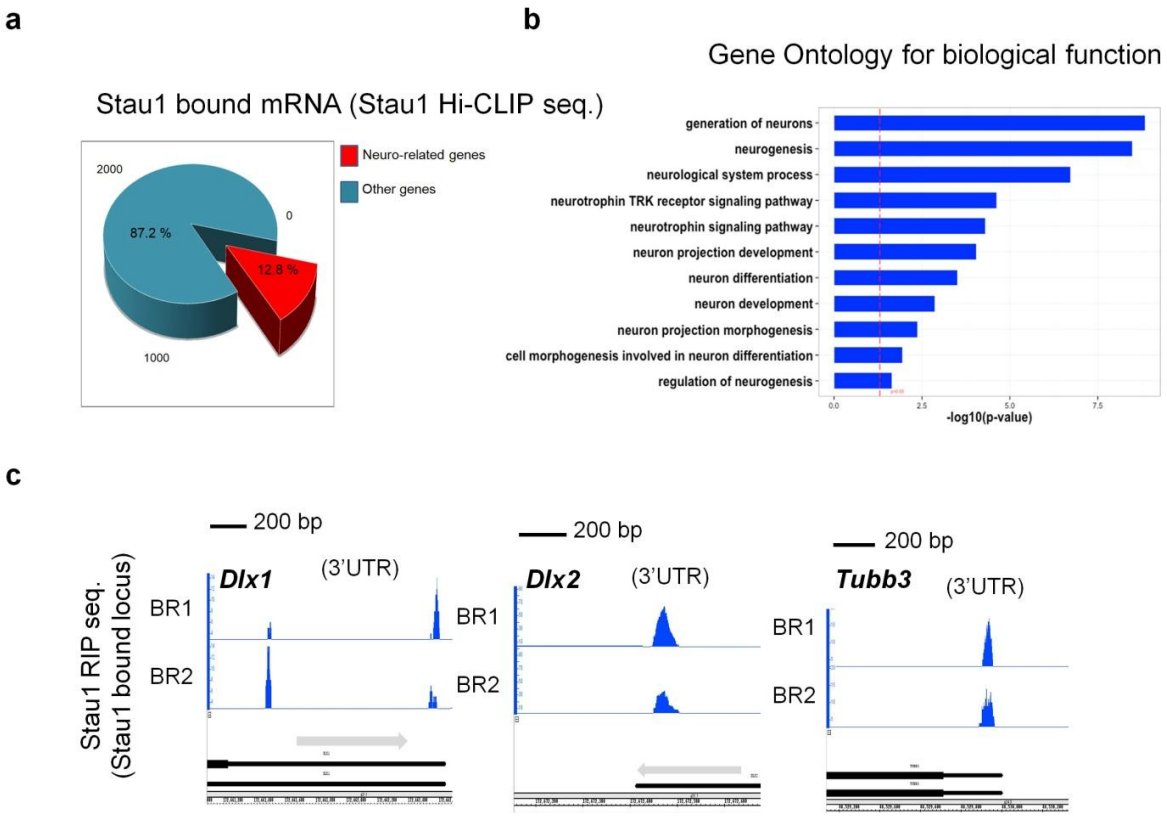


Supplementary Figure 8. Stau1 regulates NPC neuronal differentiation *in vivo*. (**a**) NPCs were infected with pLKO.1-shScramble or pLKO.1-shStau1 #1, #2, and #3, and one day later, Stau1, Stau2 and α-tubulin in lysates were detected by immunoblotting (n=2). (**b**) Effect of Stau1 knockdown on embryonic mouse cortex. Green fluorescent images indicate GFP labeled shScramble or shStau1 expression in electroporated embryo brain. CP, cortical plate; IMZ, intermediate zone; SVZ/VZ, (sub)ventricular zone. (**c**) The effect of Stau1 knockdown on

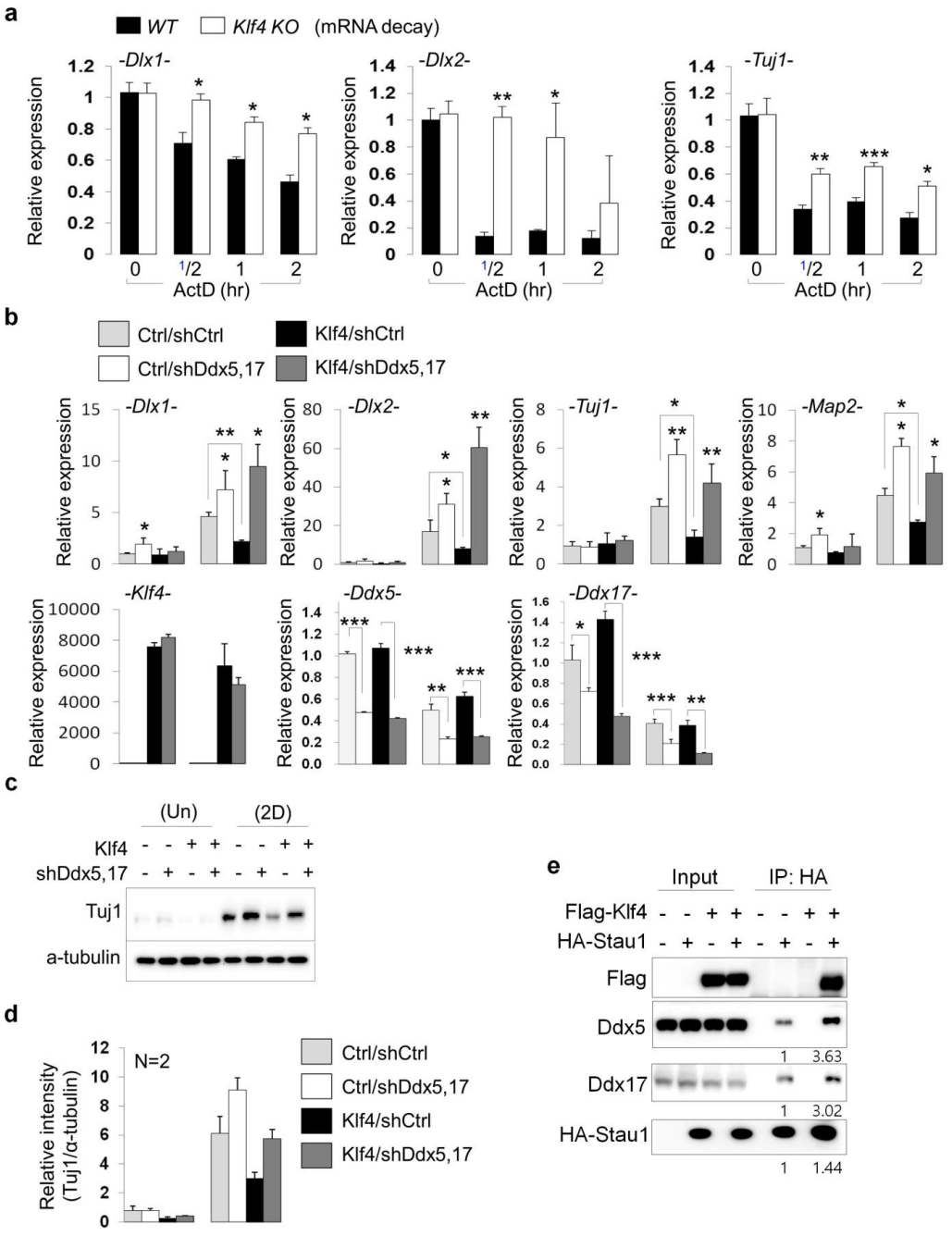
neurogenesis was evaluated by counting Tuj1 (red)/EGFP (green) double positive cells versus total EGFP-positive cells in cortex. shScramble (n=4), shStau1 (n=6). (**d**) Effect of Stau1 overexpression on embryonic mouse cortex. Red fluorescent images indicates mCherry labeled control or mStau1 expression in electroporated embryo brain. CP, cortical plate; IMZ, intermediate zone; SVZ/VZ, (sub)ventricular zone. (**e**) The effect of Stau1 overexpression on neurogenesis was evaluated by counting Tuj1(green)/mCherry(red) double positive cells versus total mCherry-positive cells in cortex. Control (n=5), Stau1 (n=7). Values correspond to mean±SD. *t*-tests were performed to calculate significance (*P < 0.05, **P < 0.005). See also Supplementary Fig. 20.



Supplementary Figure 9. Stau1 rescues defect of neurogenesis seen in Klf4 overexpression *in vivo*. (**a**) Immunoblot of indicated antibodies in Klf4-overexpressing or control NPCs infected with pLKO.1 shScramble or pLKO.1 shStau1 lentivirus (n=1-2). (**b**) RT-qPCR of indicated transcripts in samples shown in (a) (n=3). (**c**) The rescue effect of Stau1 knockdown on neurogenesis was evaluated by counting $Tuj1^{+}mCherry^{+}GFP^{+}$ triple positive cells versus total $mCherry^{+}GFP^{+}$ cells in electroporated cortex. shScramble/Control (n=3), shStau1/Control (n=3), shScramble/Klf4 (n=3), shStau1/Klf4 (n=6). (**d**) Immunoblots of indicated antibodies in Stau1-overexpressing or control NPCs infected with pLKO.1 shScramble or pLKO.1 shKlf4 lentivirus (n=1). Values correspond to mean±SD. Anova tests were performed to calculate significance (*P < 0.01, **P < 0.001, ***P < 0.0001). See also Supplementary Table 4, Supplementary Fig. 20.

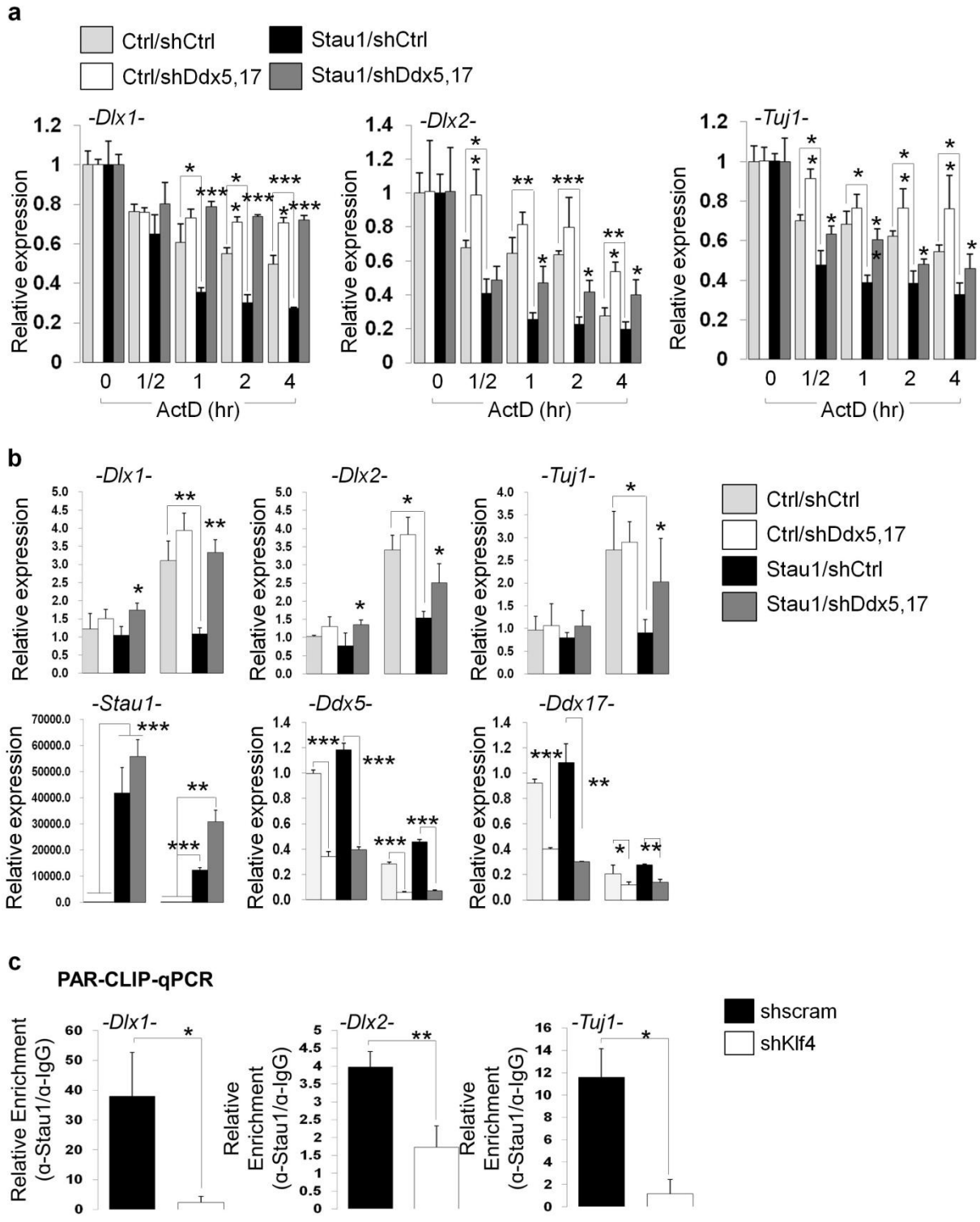


Supplementary Figure 10. Stau1 specifically binds to neurogenesis-associated mRNAs. (**a**) Stau1 hi-CLIP sequencing analysis in HEK293 cells (GSE52447)[1]. Among genes enriched by Stau1, 12.8% are neuro-related genes. (**b**) Gene ontology (GO) analysis of annotated genes at Staufen1 binding sites. (**c**) Stau1 RIP sequencing analysis[2]. Distribution of Stau1 binding peaks in HEK293 cells. Stau1 protein was highly enriched in 3'UTRs of *Dlx1*, *Dlx2* and *Tubb3* mRNAs.



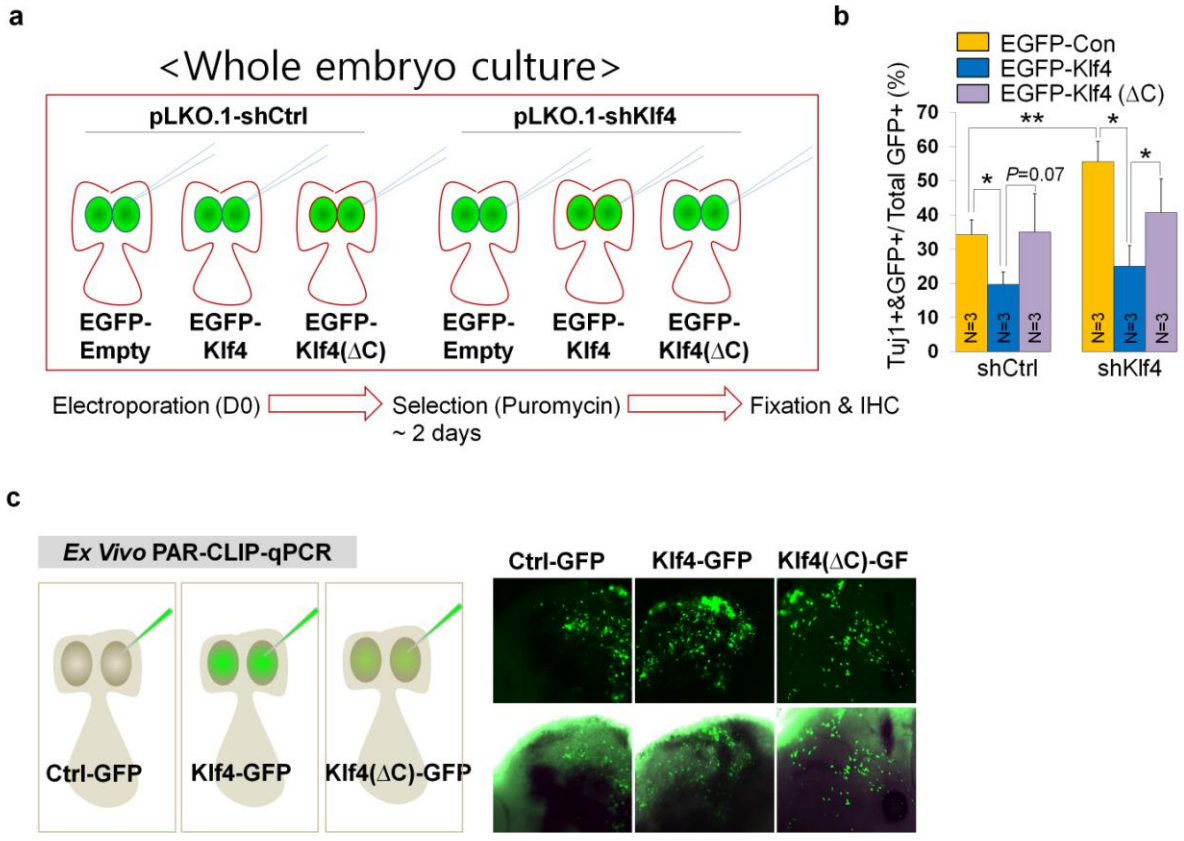
Supplementary Figure 11. Klf4 promotes mRNA decay and inhibit neurogenesis by cooperating with Stau1/Ddx5/17 complex. (**a**) Wild-type and Klf4 cKO NPCs were treated with actinomycin D (5 μg/ml) for indicated times and mRNAs were prepared for RNA stability assays (n=3). Values correspond to mean±SD. *t*-tests were performed to calculate significance

(*P < 0.05, **P < 0.005, ***P < 0.0005). (**b**) RT-qPCR of indicated transcripts in control- or Klf4-overexpressing NPCs infected with pLKO.1 shScramble or pLKO.1 shDdx5/17 lentivirus cultured for 0.2 or 2 days in differentiation conditions (n=3). Values correspond to mean±SD. Anova tests were performed to calculate significance (*P < 0.01, **P < 0.001, ***P < 0.0001). (**c**) Immunoblot of indicated antibodies in samples shown in (b) (n=2). See Supplementary Table 4. (**d**) Quantification of (c). (**e**) HEK293T cells were transfected with empty or Flag-Klf4 expression plasmids with control or HA-Stau1 vector. At 24 hours after transfection, lysates were immunoprecipitated with anti-IgG or anti-Mbd3 (n=1) and were analyzed by immunoblotting for indicated proteins. See also Supplementary Fig. 21.

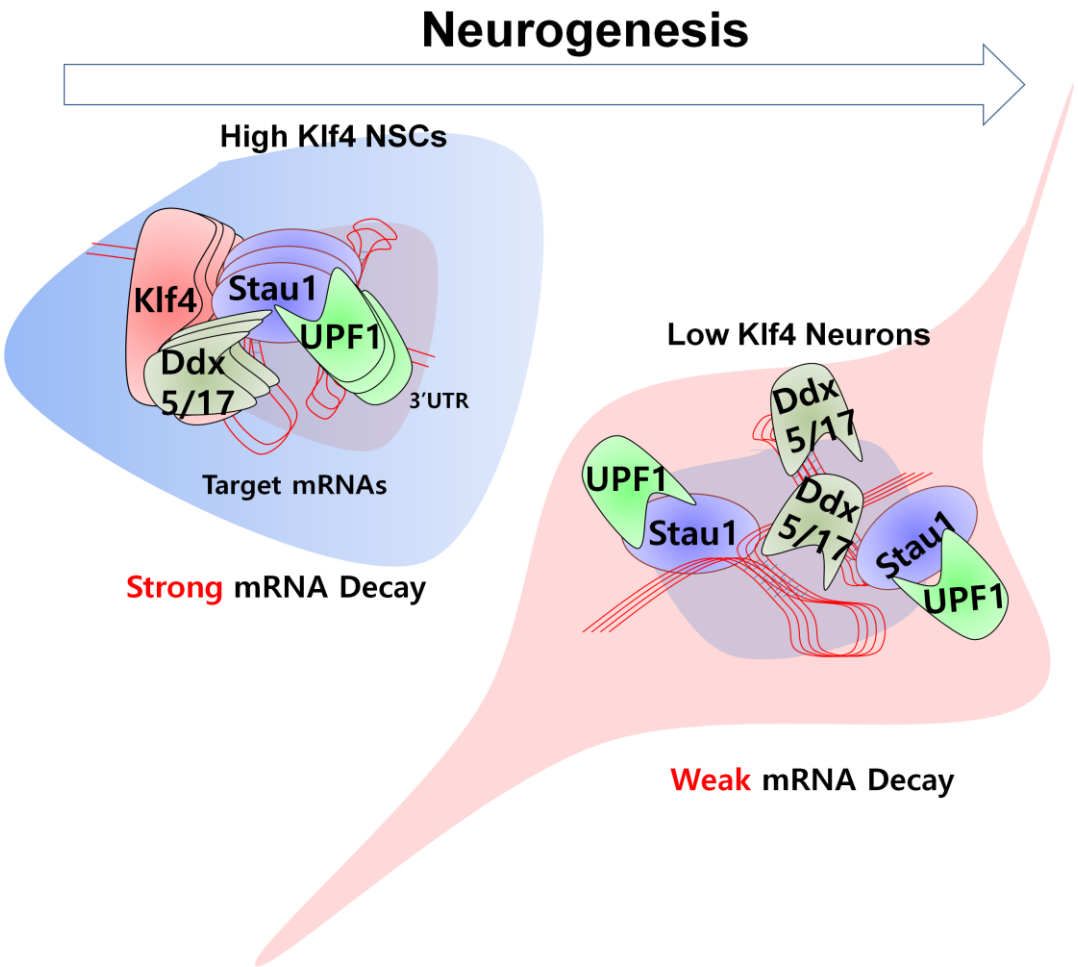


Supplementary Figure 12. Ddx5/17 double stranded RNA helicases are novel components

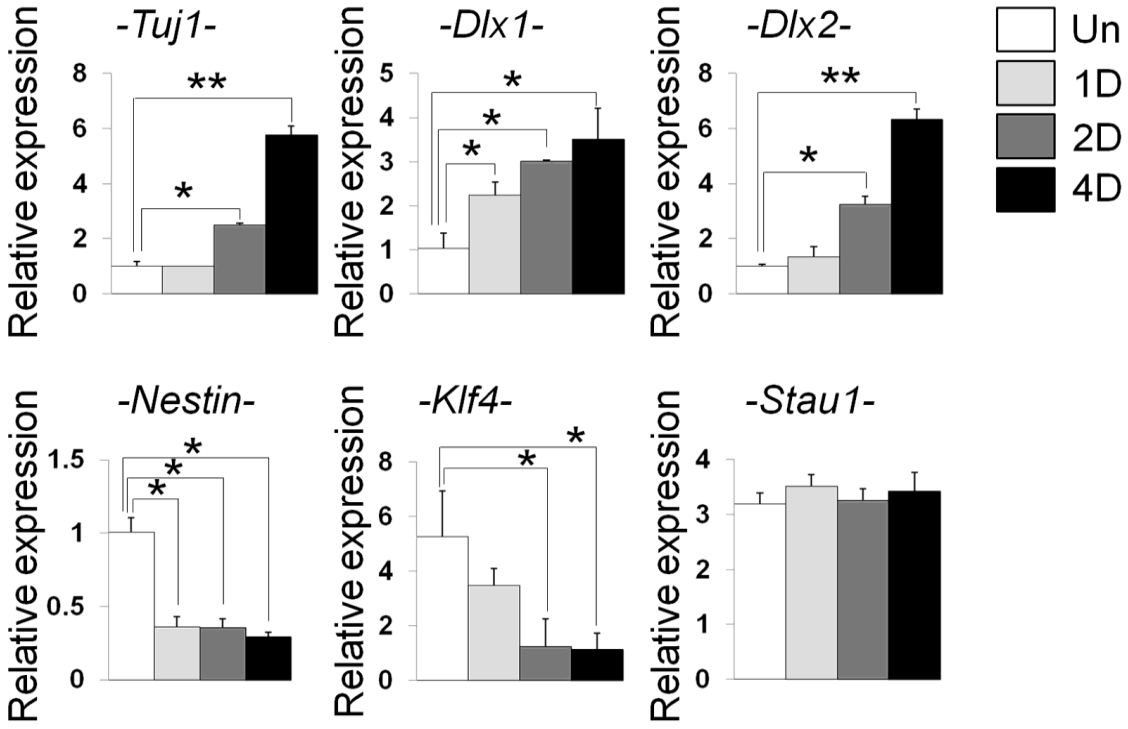
for SMD (**a**) RT-qPCR to assess the mRNA decay following Stau1 overexpression in NPCs transduced with shScramble or shDdx5/17 knockdown constructs. NPCs were treated with actinomycin D (5 μg/ml) for indicated times, and mRNAs were prepared for RNA stability assay (n=3). (**b**) RT-qPCR of indicated transcripts in control- or Stau1-overexpressing NPCs infected with pLKO.1 shScramble or pLKO.1 shDdx5/17 lentivirus cultured for 0.2 or 2 days in differentiation conditions (n=3). (**c**) PAR-CLIP qPCR to assess Stau1 enrichment on target mRNAs in NPCs transduced with shKlf4 knockdown or shScramble constructs. Each values enriched by Stau1 protein were divided by IgG control. Data is presented as mean±SD. Anova tests were performed to calculate statistical significance (*P < 0.01, **P < 0.001, ***P < 0.0001). See Supplementary Table 4.



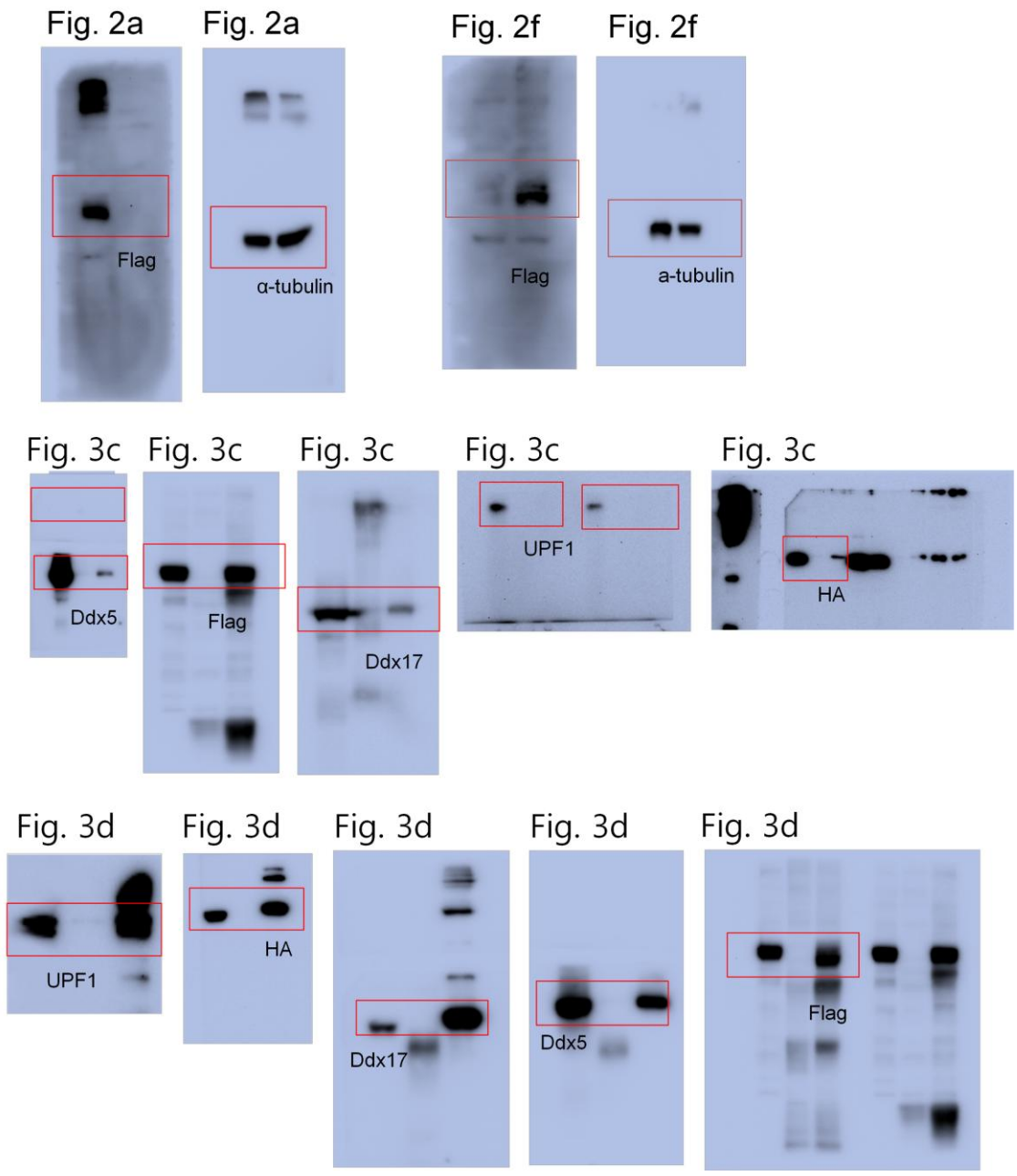
Supplementary Figure 13. Klf4 inhibits neurogenesis through formation of Klf4/Stau1 complex *ex vivo*. (**a**) Schematic of injection site (green) and experimental process for *ex utero* electroporation. pEGFP-Control, pEGFP-Klf4, or pEGFP-ΔC vectors were electroporated in mouse embryonic cortex together with shscramble or shKlf4 lentiviral vectors. (**b**) The effect of wild-type Klf4 or its mutant (ΔC) overexpression on neurogenesis was evaluated by counting Tuj1/EGFP double positive cells versus total EGFP-positive cells in VZ/SVZ/IMZ/CP compartments (n=3). (**c**) Schematic of PAR-CLIP-qPCR experiment in cortices electroporated with pEGFP-Control, pEGFP-Klf4, or pEGFP-ΔC constructs and grown in *ex vivo* condition for 2 days (2D).



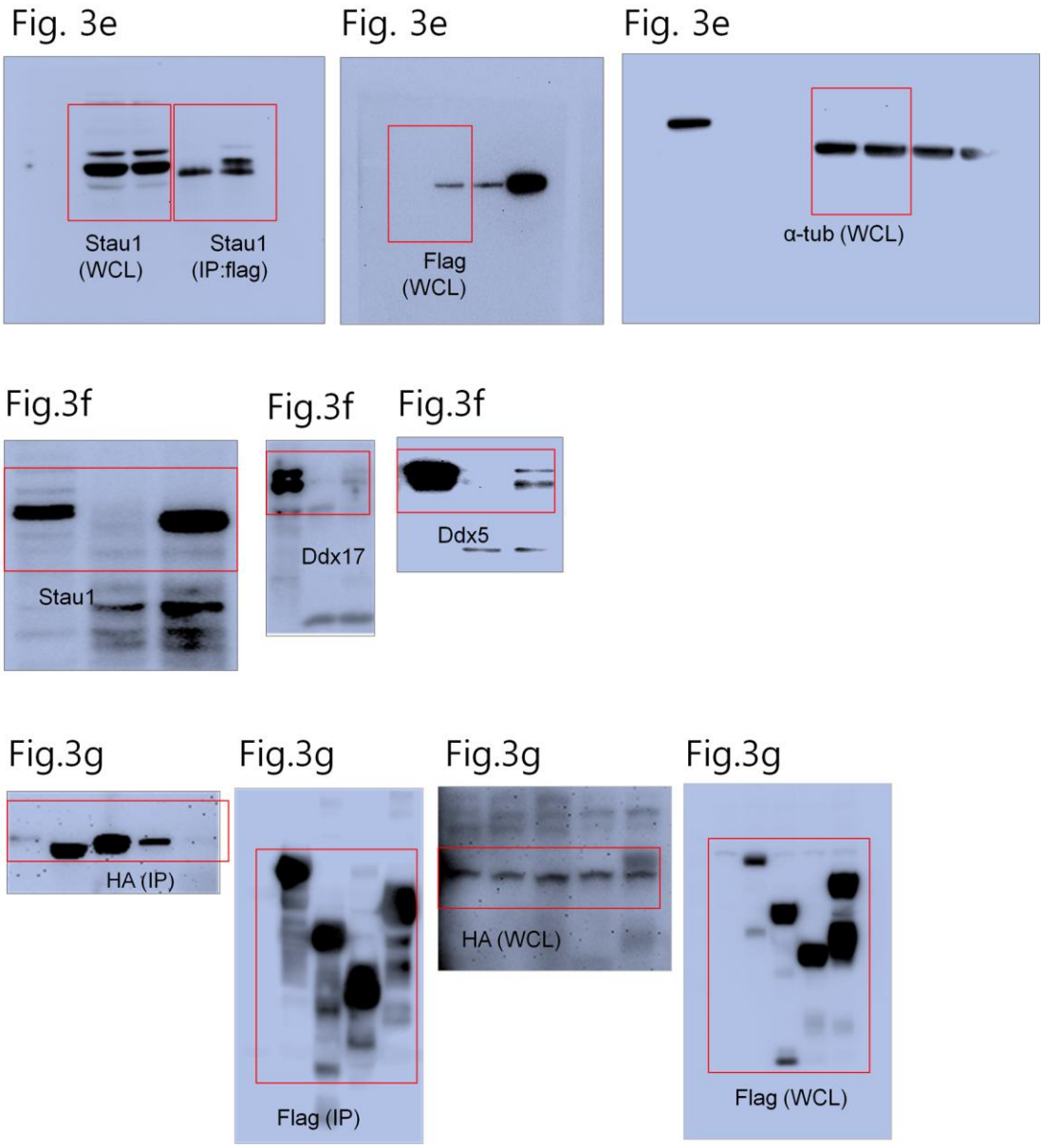
Supplementary Figure 14. Klf4/Ddx5/17 dependent Stau1 mediated mRNA decay (SMD) regulates cortical neurogenesis. A model of proposed function of the Klf4-Ddx5/17-Stau1 axis in NPC cell fate determination during neurogenesis.



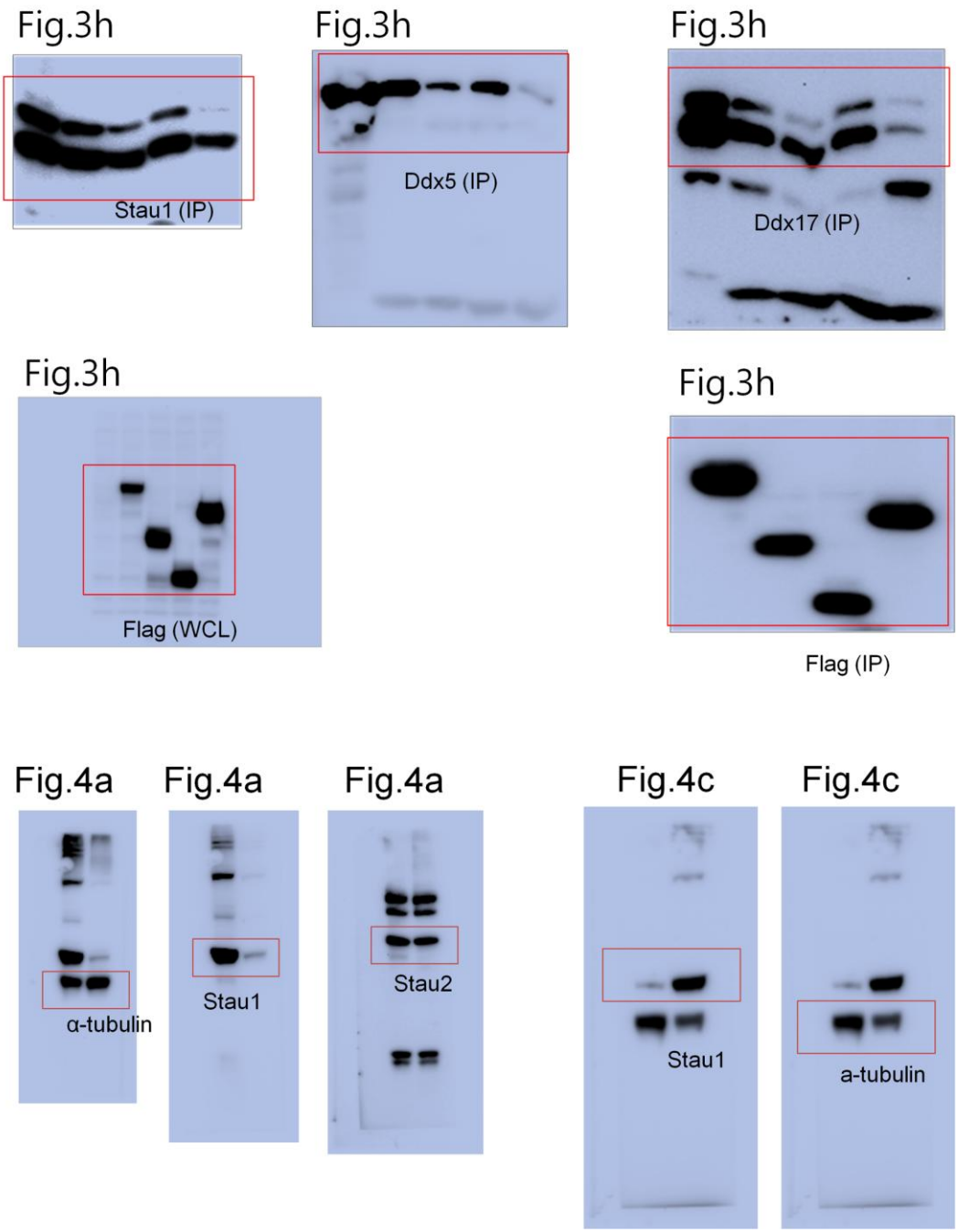
Supplementary Figure 15. *Klf4*, but not *Stau1*, decreases during neural differentiation of NPCs. qPCR analysis of indicated mRNAs. Values correspond to the mean±SD. Diff. (d), days in differentiation. Statistical t-test analysis was performed to calculate significance (*P < 0.05, **P < 0.005, ns, P > 0.05).



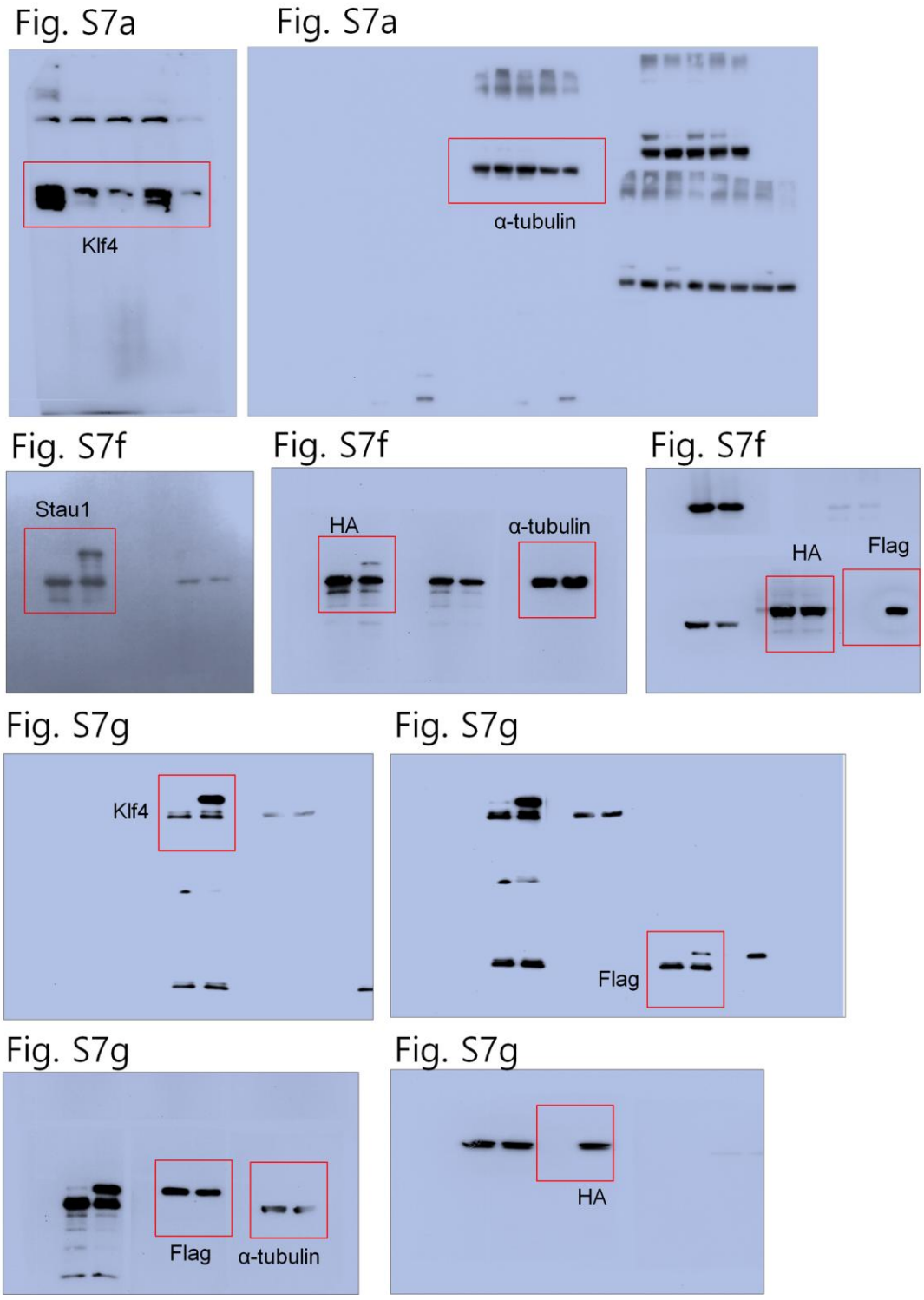
Supplementary Figure 16. Full blots from main figures. The full blots used for Figure 2a, f, 3c, d. The specific bands shown in the main figures are indicated by red boxes.



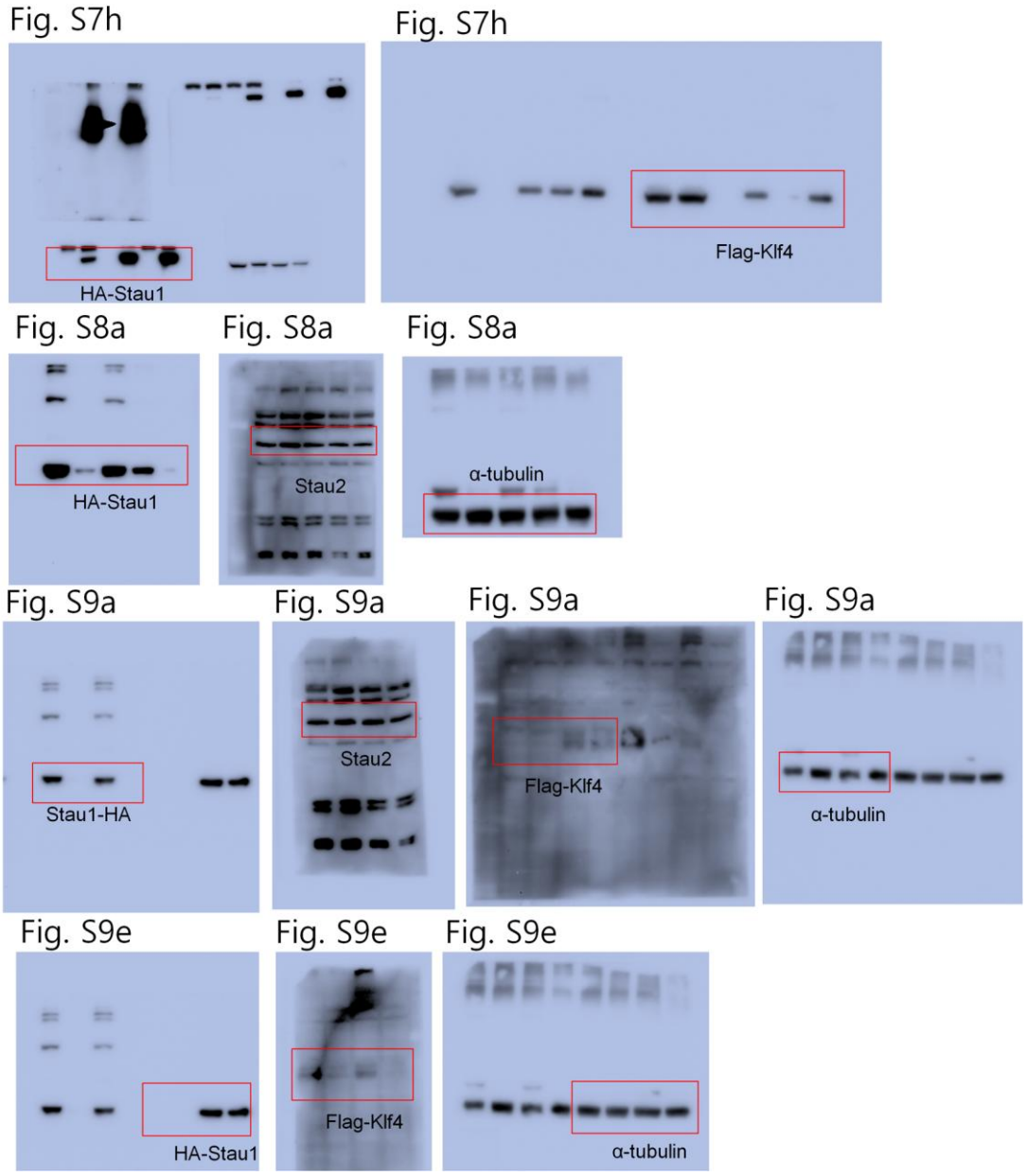
Supplementary Figure 17. Full blots from main figures. The full blots used for Figure 3e-g. The specific bands shown in the main figures are indicated by red boxes.



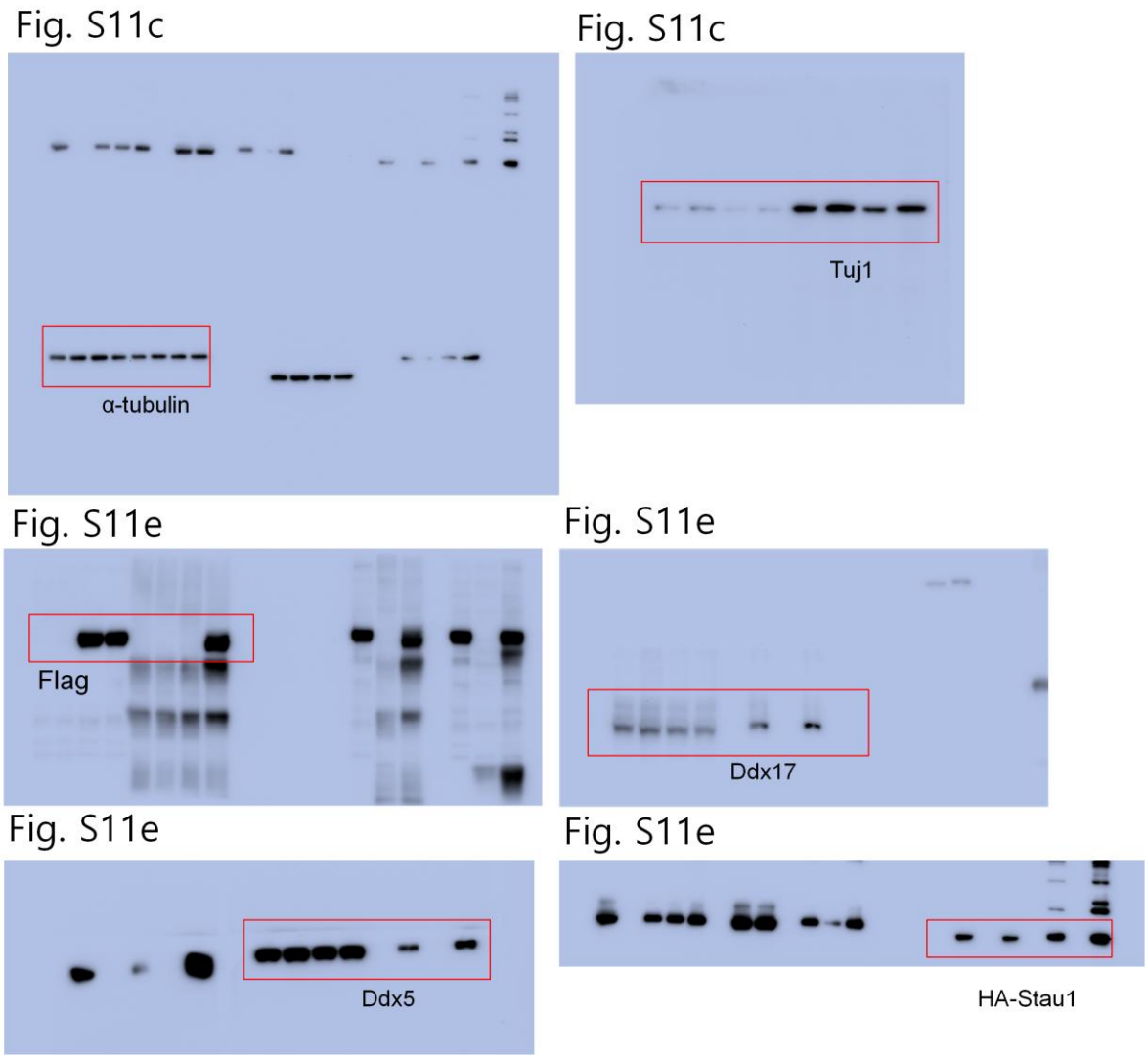
Supplementary Figure 18. Full blots from main figures. The full blots used for Figure 3h, 4a, c. The specific bands shown in the main figures are indicated by red boxes.



Supplementary Figure 19. Full blots from main figures. The full blots used for Supplementary Figure 7a, f, g. The specific bands shown in the main figures are indicated by red boxes.



Supplementary Figure 20. Full blots from main figures. The full blots used for Supplementary Figure 7h, 8a, 9a, e. The specific bands shown in the main figures are indicated by red boxes.



Supplementary Figure 21. Full blots from main figures. The full blots used for Supplementary Figure 11c, e. The specific bands shown in the main figures are indicated by red boxes.

Supplementary Table 1. Construction of pLKO3G shRNA and target sequences.

To knock down Klf4 and Stau1 expression in NSCs we generated pLKO.3G short hairpin (sh)RNA lenti-viral vector system. Target sequences of Klf4 and Stau1 were chosen using RNAi consortium shRNA library (http://www.broadinstitute.org/rnai/public/) (three clones targeting different sequences in the three coding regions of Klf4 and Stau1 gene) against Klf4 and Stau1. To generate oligos for cloning, sense and antisense sequences of chosen target sequences were ordered from IDT. Sequence-verified shRNA lentiviral plasmid vectors for mouse Klf4 and Stau1 gene were cloned into the pLKO.3G vector and knockdown efficiency were measured by western blot (see Supplementary Fig. 7a).

For gene transfections we utilized Lipofectamine 3000 and Amaxa nucleofection (Lonza, http: //www.lonzabio.com/cell-biology/transfection/) for the transfection of mouse NSCs. A range of knockdown efficiencies was observed. The shKlf4 (#1, #2 and #3) clones showed maximum efficiencies and three vectors were used for further experiments (see Fig. 2a). For shStau1 knockdown experiment, Two (we encoded it as shStau1 #1 and #3) out of three clones appeared to be efficiently knocking down Stau1 expression in NSCs (see Fig. 4a and Supplementary Fig. 8a) and both were used for further experiments. For shControl transfection, sequences were chosen based on Sigma-Aldrich shRNA products which had been previously validated as a non-target shRNA control. The plasmids containing the below sequences that does not target any gene, making it useful as a negative control in our experiments and appear no change Klf4 or Stau1 expression (see Supplementary Fig. 7a and 8a).

Gene	shKlf4 #1	Target region
Target sequence Ordered oligo	CATGTTCTAACAGCCTAAATG AATTCATGTTCTAACAGCCTAAATGCTCGAGCATTTAGGCTGTTAGAACATGTTTTTTTAT	3' UTR
Gene	shKlf4 #2	
Target sequence Ordered oligo	TTGTGGATATCAGGGTATAAA AATTTTGTGGATATCAGGGTATAAACTCGAGTTTATACCCTGATATCCACAATTTTTTTAT	3' UTR
Gene	shKlf4 #3	
Target sequence Ordered oligo	CTCTCTCACATGAAGCGACTT AATTCTCTCTCACATGAAGCGACTTCTCGAGAAGTCGCTTCATGTGAGAGAGTTTTTTTAT	CDS
Gene	shStau1 #1	
Target sequence Ordered oligo	ATTGCGCTGAAGCGGAATTTG AATTATTGCGCTGAAGCGGAATTTGCTCGAGCAAATTCCGCTTCAGCGCAATTTTTTTTAT	CDS
Gene	shStau1 #2	
Target sequence Ordered oligo	GCCAAGGGATGAATCCTATTA AATTGCCAAGGGATGAATCCTATTACTCGAGTAATAGGATTCATCCCTTGGCTTTTTTTAT	CDS
Gene	shStau1 #3	
Target sequence Ordered oligo	CCAGGGATTCCAGGTTGAATA AATTCCAGGGATTCCAGGTTGAATACTCGAGTATTCAACCTGGAATCCCTGGTTTTTTTAT	CDS

Supplementary Table 2. Primer sequences used for quantitative or RT-PCR analysis.

Genes	Primer Sequences	Tm (℃)
Nestin	5'-CCCTGAAGTCGAGGAGCTG-3'	57.4
	5'-CTGCTGCACCTCTAAGCGA-3'	57.3
Dlx1	5'-ATGCCAGAAAGTCTCAACAGC-3'	60.6
	5'-AACAGTGCATGGAGTAGTGCC-3'	62.4
Dlx2	5'-AAAGAAAGTCCGGAAACCACG-3'	60.1
	5'-TCTTCTTGAACTTGCATCGGC-3'	60.5
Tuj1	5'-TAGACCCCAGCGGCAACTAT-3'	58.2
	5'-GTTCCAGGTTCCAAGTCCACC-3'	58.0
Gad67	5'-GCCACAAACTCAGCGGCATAGAAA-3'	60.0
	5'-AGACGTCATACTGCTTGTCTGGCT-3'	60.0
NeuN	5'-GAAACCGCAAGCCCTCATTTC-3'	60.1
	5'-TTGGATGCCTCTTGGTTTGGT-3'	60
Pitx3	5'-TGCGCTGTCGTTATCGGAC-3'	62.4
	5'-GGTAGCGATTCCTCTGGAAGG-3'	61.7
Pax6	5'-AACCCACGCAAGATGGCTG-3'	62.9
	5'-GCATCCCAGTGCATAAAAACCA-3'	61.4
Dat	5'-AAATGCTCCGTGGGACCAATG-3'	63
	5'-GTCTCCCGCTCTTGAACCTC-3'	61.9
Lmx1a	5'-ACGGCCTGAAGATGGAGGA-3'	62.3
	5'-CAGAAACCTGTCCGAGATGAC-3'	60.1
Foxa2	5'-CCCTACGCCAACATGAACTCG-3'	63
	5'-GTTCTGCCGGTAGAAAGGGA-3'	61.2
En1	5'-CTAAGGCCCGATTTCGGTTG-3'	60.8
	5'-GAGTGAACGGGGTCTCTACCT-3'	62.4
Klf4	5'-GTGCCCCGACTAACCGTTG-3'	63
	5'-GTCGTTGAACTCCTCGGTCT-3'	61.2
Staufen1	5'-GGACCCTCACTCTCGGATG-3'	60.8
	5'-TTCTGGCAGGGGTTCACTCT-3'	62.7
Staufen2	*5'-AGTGACCTCTGGCACAACTCT-3'*	62.8
	5'-TGGCTTCAGCAGTAGGAGATG-3'	61.3
Gapdh	5'-AGGTCGGTGTGAACGGATTTG-3'	57.6
	5'-TGTAGACCATGTAGTTGAGGTCA-3'	55.1

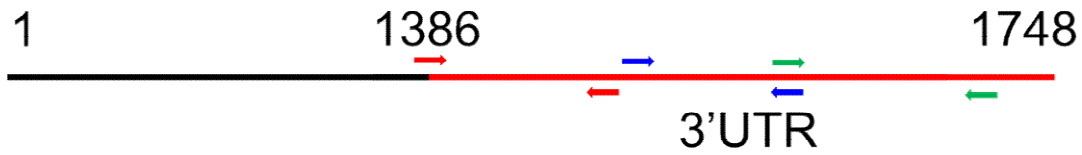
Gapdh : Glyceeraldehyde-3-phosphate dehydrogenase

Supplementary Table 3. Primer sequences used for mRNA decay and PAR-CLIP qPCR analysis.

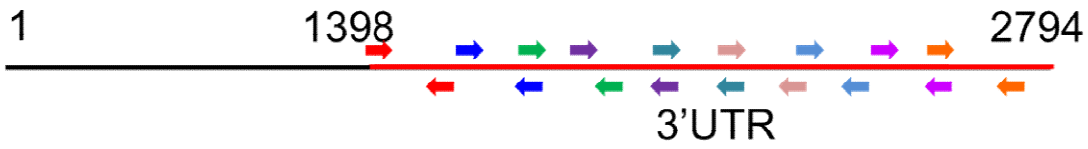
Gene	Sequence	Tm (°C)	GC (%)
mTuj1-CLIP(1-F)	AGTTGCTCGCAGCTGGGGTGT	58.2	55
mTuj1-CLIP(1-R)	AAAGCTGGGGGCAGTGTCA	59.7	57.9
mTuj1-CLIP(2-F)	CTTCTCACCAGCTCATTAGG	52.5	50
mTuj1-CLIP(2-R)	ACAGAGGTGGCTAAAATGGG	54.9	50
mTuj1-CLIP(3-F)	CCCATTTTAGCCACCTCTGT	54.9	50
mTuj1-CLIP(3-R)	CTGACAGACAGCAGTAAC	50	50
mDlx1-CLIP(1-F)	GGTTATCAGTTCGCACTCAC	53.4	50
mDlx1-CLIP(1-R)	AAGCCCTCTGCCTTCACTGTT	54	52
mDlx1-CLIP(2-F)	TGCTTCTCGGAGCCCCTAAAA	58.6	52.4
mDlx1-CLIP(2-R)	AAGATGAGAGTCTGGTCCGG	55.7	55
mDlx1-CLIP(3-F)	CCGGACCAGACTCTCATCTT	56	55
mDlx1-CLIP(3-R)	GGTCGTAGAATGAGGACAGC	55	55
mDlx1-CLIP(4-F)	CTCCAAAAAGTCACCAGGTCTG	55.7	50
mDlx1-CLIP(4-R)	TCAGCGTCAGATGAAGTCTG	54.3	50
mDlx1-CLIP(5-F)	CAGACTTCATCTGACGCTGA	54.3	50
mDlx1-CLIP(5-R)	ACTTTCCTGTCCTTGTTCCC	54.7	50
mDlx1-CLIP(6-F)	GGAACAAGGACAGGAAAG	50.3	50
mDlx1-CLIP(6-R)	CCAGGTGTTCTTGTCCAAACG	56.4	52.4
mDlx1-CLIP(7-F)	GAACACCTGGCCAAGAAG	53.5	55.6
mDlx1-CLIP(7-R)	GCCGCTGCTTGTGTCTTACT	58	55
mDlx1-CLIP(8-F)	TCGACCACAGAACACAAGTC	54.7	50
mDlx1-CLIP(8-R)	TCGGGTTTACAGCCACACAC	57.7	55
mDlx1-CLIP(9-F)	GTGTGTGGCTGTAAACCCGA	57.7	55
mDlx1-CLIP(9-R)	CTTATTTACAAAGTTCGCCCCC	54.3	45.5
mDlx2-CLIP(1-F)	TCGAGTGGACAGCGTCTGA	57.9	58.2
mDlx2-CLIP(1-R)	AGAAGTGGCTCCACGAC	54.5	58.8
mDlx2-CLIP(2-F)	GTCGTGGAGCCACTTCT	54.5	58.8
mDlx2-CLIP(2-R)	ACCCTGAGGATCACGCTGA	58.3	57.9
mDlx2-CLIP(3-F)	TCAGCGTGATCCTCAGGGT	58.3	57.9
mDlx2-CLIP(3-R)	TGGAGTAGGACCCAGGAG	55.3	61.1
mDlx2-CLIP(4-F)	ACCTCCTGGGTCCTACTCCA	59.6	60
mDlx2-CLIP(4-R)	GGTCATCCGCAAAGGCACCTA	59.8	57.1
mDlx2-CLIP(5-F)	TAGGTGCCTTTGCGGATGACC	59.8	57.1
mDlx2-CLIP(5-R)	GGGGAAATCTGCACAGACACC	53.6	52.6
mDlx2-CLIP(6-F)	GGTGTCTGTGCAGATTTCCCC	58.3	57.1

mDlx2-CLIP(6-R)	ATAGGGACTGCTGAGGTCACTG	58.2	54.5

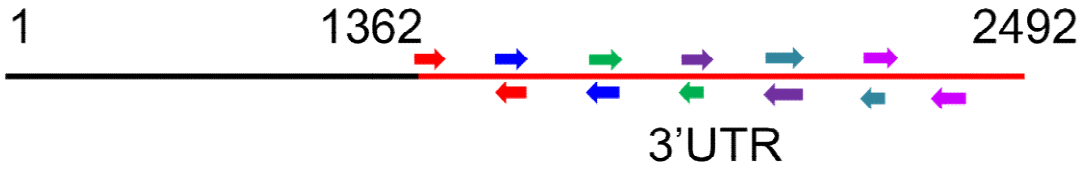
m *Tuj1*-CLIP



m *Dlx1*-CLIP



m *Dlx2*-CLIP



Supplementary Table 4. Values and parameters for the statistical comparisons shown in main and supplementary figures

Fig.1F

Klf4 gene	Table Analyzed	Data 1				
	One-way analysis of variance					
	P value	< 0.0001				
	P value summary	***				
	Are means signif. different	Yes				
	Number of groups	4				
	F	39.81				
	R squared	0.9372				
	ANOVA Table	SS	df	MS		
	Treatment (between colum	45.17	3	15.06		
	Residual (within columns)	3.020	8	0.3783		
	Total	48.2	11			
	Tukey's Multiple Comparisc	Mean Diff.	q	Significant?	Summary	95% CI of diff
	WT-Un vs cKO-Un	4.103	11.53	Yes	***	2.498 to 5.714
	WT-Un vs WT-2DIV	0.7073	1.994	No	ns	-0.9003 to 2.316
	WT-Un vs cKO-2DIV	4.294	12.09	Yes	***	2.685 to 5.902
	cKO-Un vs WT-2DIV	-3.393	9.569	Yes	***	-5.006 to -1.790
	cKO-Un vs cKO-2DIV	0.1873	0.529	No	ns	-1.420 to 1.796
	WT-2DIV vs cKO-2DIV	3.583	10.1	Yes	***	1.978 to 5.194

Dlx1 gene	Table Analyzed	Data 1				
	One-way analysis of variance					
	P value	0.0002				
	P value summary	***				
	Are means signif. differe	Yes				
	Number of groups	4				
	F	24.67				
	R squared	0.9024				
	ANOVA Table	SS	df	MS		
	Treatment (between colu	4184	3	1395		
	Residual (within columns	452.3	8	56.53		
	Total	4636	11			
	Tukey's Multiple Compari	Mean Diff.	q	Significant?	Summary	95% CI of diff
	WT-Un vs cKO-Un	-12.75	2.936	No	ns	-32.41 to 6.913
	WT-Un vs WT-2DIV	-8.856	2.04	No	*	-28.52 to 10.80
	WT-Un vs cKO-2DIV	-48.96	11.28	Yes	***	-68.64 to -29.32
	cKO-Un vs WT-2DIV	3.891	0.8962	No	ns	-15.77 to 23.55
	cKO-Un vs cKO-2DIV	-36.21	8.342	Yes	**	-55.89 to -16.57
	WT-2DIV vs cKO-2DIV	-40.12	9.243	Yes	***	-59.79 to -20.46

Dlx2 gene	Table Analyzed	Data 1				
	One-way analysis of variance					
	P value	< 0.0001				
	P value summary	***				
	Are means signif. diffe	Yes				
	Number of groups	4				
	F	130.1				
	R squared	0.9799				
	ANOVA Table	SS	df	MS		
	Treatment (between c	42130	3	14040		
	Residual (within colum	863.7	8	108		
	Total	42990	11			
	Tukey's Multiple Comp	Mean Diff.	q	Significant?	Summary	95% CI of diff
	WT-Un vs cKO-Un	-3.892	0.6487	No	ns	-31.06 to 23.28
	WT-Un vs WT-2DIV	-70.07	11.68	Yes	***	-97.24 to -42.90
	WT-Un vs cKO-2DIV	-145.4	24.24	Yes	***	-172.6 to -118.3
	cKO-Un vs WT-2DIV	-66.18	11.03	Yes	***	-93.35 to -39.01
	cKO-Un vs cKO-2DIV	-141.5	23.59	Yes	***	-168.7 to -114.4
	WT-2DIV vs cKO-2DI	-75.37	12.56	Yes	***	-102.5 to -48.20

Tuj1	Table Analyzed	Data 1				
	One-way analysis of variance					
	P value	< 0.0001				
	P value summary	***				
	Are means signif. different	Yes				
	Number of groups	4				
	F	56.19				
	R squared	0.9547				
	ANOVA Table	SS	df	MS		
	Treatment (between colum	12.43	3	4.142		
	Residual (within columns)	0.59	8	0.07375		
	Total	13.02	11			
	Tukey's Multiple Comparisc	Mean Diff.	q	Significant?	Summary	95% CI of diff
	WT-Un vs cKO-Un	-0.2157	1.375	No	ns	-0.9258 to 0.4945
	WT-Un vs WT-2DIV	-0.6953	4.433	No	*	-1.406 to 0.01424
	WT-Un vs cKO-2DIV	-2.581	16.45	Yes	***	-3.291 to -1.871
	cKO-Un vs WT-2DIV	-0.4802	3.063	No	ns	-1.190 to 0.2299
	cKO-Un vs cKO-2DIV	-2.365	15.08	Yes	***	-3.075 to -1.655
	WT-2DIV vs cKO-2DIV	-1.885	12.02	Yes	***	-2.595 to -1.175

Gad67	Table Analyzed	Data 1				
	One-way analysis of variance					
	P value	< 0.0001				
	P value summary	***				
	Are means signif. differe	Yes				
	Number of groups	4				
	F	270				
	R squared	0.9902				
	ANOVA Table	SS	df	MS		
	Treatment (between colu	22290	3	7431		
	Residual (within columns	220.2	8	27.52		
	Total	22510	11			
	Tukey's Multiple Compari	Mean Diff.	q	Significant?	Summary	95% CI of diff
	WT-Un vs cKO-Un	2.436	0.8036	No	ns	-11.28 to 16.15
	WT-Un vs WT-2DIV	-77.5	25.56	Yes	***	-91.22 to -63.78
	WT-Un vs cKO-2DIV	-91.32	30.15	Yes	***	-105.0 to -77.60
	cKO-Un vs WT-2DIV	-79.94	26.36	Yes	***	-93.65 to -66.22
	cKO-Un vs cKO-2DIV	-93.76	30.96	Yes	***	-107.5 to -80.04
	WT-2DIV vs cKO-2DIV	-13.82	4.564	Yes	*	-27.54 to -0.1045

NeuN	Table Analyzed	Data 1				
	One-way analysis of variance					
	P value	< 0.0001				
	P value summary	***				
	Are means signif. diffe	Yes				
	Number of groups	4				
	F	66.2				
	R squared	0.9613				
	ANOVA Table	SS	df	MS		
	Treatment (between c	25.8	3	8.601		
	Residual (within colum	1.039	8	0.1299		
	Total	26.84	11			
	Tukey's Multiple Comp	Mean Diff.	q	Significant?	Summary	95% CI of diff
	WT-Un vs cKO-Un	-0.7715	3.707	No	ns	-1.714 to 0.1710
	WT-Un vs WT-2DIV	-2.136	10.26	Yes	***	-3.079 to -1.194
	WT-Un vs cKO-2DIV	-3.859	18.54	Yes	***	-4.801 to -2.916
	cKO-Un vs WT-2DIV	-1.365	6.557	Yes	**	-2.307 to -0.4221
	cKO-Un vs cKO-2DIV	-3.087	14.83	Yes	***	-4.030 to -2.144
	WT-2DIV vs cKO-2DI	-1.722	8.276	Yes	**	-2.665 to -0.7798

Fig.4E

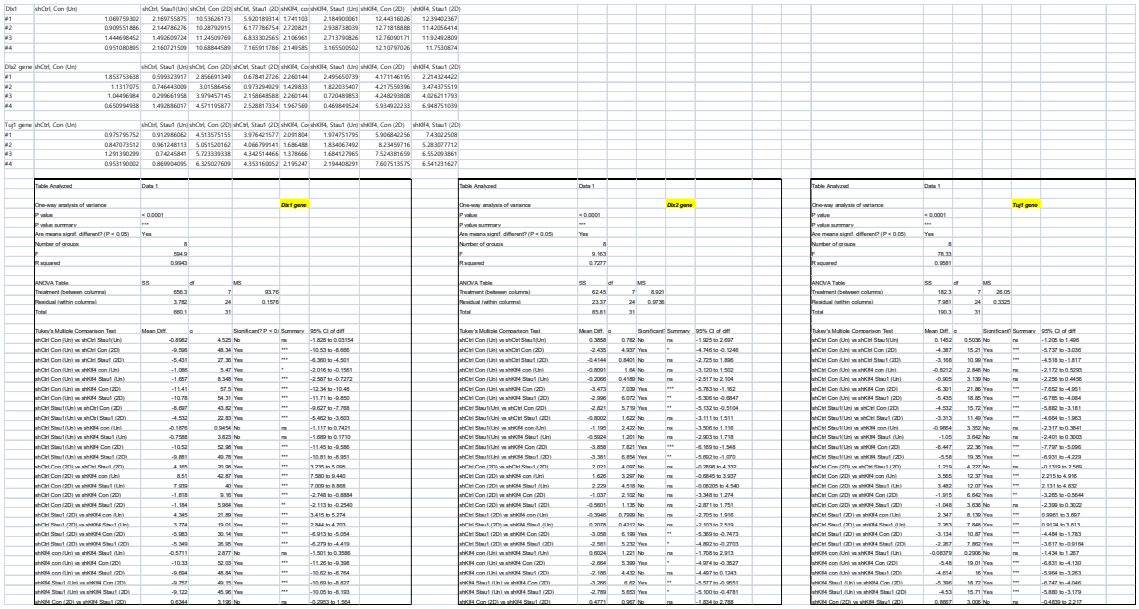
Dlx1 gene	Ctrl, shCon (Un)	Ctrl, shStau1 (Un)	Ctrl, shCon (2D)	Ctrl, shStau1 (2D)	KIf4OE, shCon (Un)	KIf4OE, shStau1 (Un)	KIf4, shCtrl (2D)	KIf4, shStau1 (2D)
#1	1.069793302	2.465821226	9.984688415	24.01666964	0.926711405	0.935002313	9.283651116	12.58654299
#2	0.909513886	2.665971592	14.00415594	24.37113339	0.827278845	0.67227884	8.74177274	15.31769964
#3	1.444698452	2.378631206	14.79526857	22.71571874	0.780657281	0.466696504	7.985835697	12.74585897
#4	0.951080895	1.248630691	15.77700645	20.42540833	1.126871669	0.881353625	8.565234904	12.0399668
Dlx2 gene	Ctrl, shCon (Un)	Ctrl, shStau1 (Un)	Ctrl, shCon (2D)	Ctrl, shStau1 (2D)	KIf4, shCon (Un)	KIf4, shStau1 (Un)	KIf4, shCtrl (2D)	KIf4, shStau1 (2D)
#1	0.965066036	2.512746642	3.635268872	8.527911457	0.34738677	0.661395462	3.017019473	4.935027906
#2	1.117285526	1.182015794	6.169280248	8.786918254	0.15617808	0.190978567	3.325672286	5.089262976
#3	1.065906349	0.449193517	6.825263311	11.87034979	1.437883091	2.497732889	4.42053774	6.905661495
#4	0.791102936	1.355638102	9.051185027	12.20749952	1.80678117	0.481787838	4.674583653	6.935232111
Tuj1 gene	Ctrl, shCon (Un)	Ctrl, shStau1 (Un)	Ctrl, shCon (2D)	Ctrl, shStau1 (2D)	KIf4, shCon (Un)	KIf4, shStau1 (Un)	KIf4, shCtrl (2D)	KIf4, shStau1 (2D)
#1	0.826743413	0.838455833	6.160350951	6.765273191	0.325433356	0.573939155	2.952918253	4.774892882
#2	0.763991016	0.975436533	6.273800936	8.328153402	0.159191056	0.587408203	3.205470808	3.837915309
#3	0.898534016	0.980976848	5.456800377	8.099558367	0.343887055	0.655208923	3.214136225	4.4862588
#4	1.101268213	1.162782891	4.82753263	7.916576262	0.297050723	0.755092594	3.082827631	4.679724648

Table Analyzed	Data 1					
				Dlx1 gene		
One-way analysis of variance						
P value	< 0.0001					
P value summary	***					
Are means signif. different? (P < 0.05)	Yes					
Number of groups	6					
F	168.4					
R squared	0.980					
ANOVA Table	SS	df	MS			
Treatment (between columns)	1855	7	265.0			
Residual (within columns)	37.84	24	1.577			
Total	1892	31				
Tukey's Multiple Comparison Test	Mean Diff.	q	Significant? P < 0.05	Summary	95% CI of diff	
Ctrl shCon (Un) vs Ctrl shStau1 (Un)	-1.080	1.745	No	ns	-4.026 to 1.845	
Ctrl shCon (Un) vs Ctrl shCon (2D)	-12.51	19.91	Yes	***	-15.49 to -9.606	
Ctrl shCon (Un) vs Ctrl shStau1 (2D)	-21.71	34.7	Yes	***	-24.73 to -18.85	
Ctrl shCon (Un) vs KIf4OE shCon (Un)	0.170	0.2839	No	ns	-2.783 to 3.119	
Ctrl shCon (Un) vs KIf4OE shStau1 (Un)	0.3541	0.5653	No	ns	-2.586 to 3.296	
Ctrl shCon (Un) vs KIf4 shCon (2D)	-7.551	12.03	Yes	***	-10.49 to -4.610	
Ctrl shCon (Un) vs KIf4 shStau1 (2D)	-12.02	19.24	Yes	***	-15.02 to -9.136	
Ctrl shStau1 (Un) vs Ctrl shCon (2D)	-11.44	18.24	Yes	***	-14.39 to -8.510	
Ctrl shStau1 (Un) vs Ctrl shStau1 (2D)	-20.65	32.96	Yes	***	-23.63 to -17.75	
Ctrl shStau1 (Un) vs KIf4OE shCon (Un)	1.251	2.023	No	ns	-1.687 to 4.214	
Ctrl shStau1 (Un) vs KIf4OE shStau1 (Un)	1.434	2.31	No	ns	-1.480 to 4.391	
Ctrl shStau1 (Un) vs KIf4 shCon (2D)	-6.470	10.28	Yes	***	-9.366 to -3.514	
Ctrl shStau1 (Un) vs KIf4 shStau1 (2D)	-10.93	17.49	Yes	***	-13.92 to -8.043	
Ctrl shCon (2D) vs Ctrl shStau1 (2D)	-9.240	14.72	Yes	***	-12.18 to -6.301	
Ctrl shCon (2D) vs KIf4OE shCon (Un)	12.72	20.27	Yes	***	9.784 to 15.67	
Ctrl shCon (2D) vs KIf4OE shStau1 (Un)	12.95	20.56	Yes	***	9.961 to 15.94	
Ctrl shCon (2D) vs KIf4 shCon (2D)	4.990	7.959	Yes	***	2.055 to 7.937	
Ctrl shCon (2D) vs KIf4 shStau1 (2D)	0.4870	0.760	No	ns	-2.473 to 3.409	
Ctrl shStau1 (2D) vs KIf4OE shCon (Un)	21.97	34.99	Yes	***	19.03 to 24.91	
Ctrl shStau1 (2D) vs KIf4OE shStau1 (Un)	22.19	35.27	Yes	***	19.20 to 25.08	
Ctrl shStau1 (2D) vs KIf4 shCon (2D)	14.24	22.69	Yes	***	11.30 to 17.18	
Ctrl shStau1 (2D) vs KIf4 shStau1 (2D)	9.717	15.47	Yes	***	6.769 to 12.65	
KIf4OE shCon (Un) vs KIf4OE shStau1 (Un)	0.1783	0.2811	No	ns	-2.764 to 3.118	
KIf4OE shCon (Un) vs KIf4 shCon (2D)	-7.720	12.3	Yes	***	-10.67 to -4.788	
KIf4OE shCon (Un) vs KIf4 shStau1 (2D)	-12.26	19.52	Yes	***	-15.20 to -9.316	
KIf4OE shStau1 (Un) vs KIf4 shCon (2D)	-7.901	12.59	Yes	***	-10.85 to -4.965	
KIf4OE shStau1 (Un) vs KIf4 shStau1 (2D)	-12.44	19.8	Yes	***	-15.37 to -9.493	
KIf4 shCon (2D) vs KIf4 shStau1 (2D)	-4.539	7.210	Yes	***	-7.469 to -1.599	

Table Analyzed	Data 1					
				Dlx2 gene		
One-way analysis of variance						
P value	< 0.0001					
P value summary	***					
Are means signif. different? (P < 0.05)	Yes					
Number of groups	8					
F	29.45					
R squared	0.8951					
ANOVA Table	SS	df	MS			
Treatment (between columns)	333.6	7	47.66			
Residual (within columns)	38.84	24	1.618			
Total	372.5	31				
Tukey's Multiple Comparison Test	Mean Diff.	q	Significant?	Summary	95% CI of diff	
Ctrl shCon (Un) vs Ctrl shStau1 (Un)	-0.3751	0.5896	No	ns	-3.354 to 2.604	
Ctrl shCon (Un) vs Ctrl shCon (2D)	-5.42	8.522	Yes	***	-8.400 to -2.441	
Ctrl shCon (Un) vs Ctrl shStau1 (2D)	-9.346	14.7	Yes	***	-12.33 to -6.370	
Ctrl shCon (Un) vs KIf4OE shCon (Un)	0.06275	0.0987	No	ns	-2.917 to 3.042	
Ctrl shCon (Un) vs KIf4OE shStau1 (Un)	-0.1376	0.2163	No	ns	-3.117 to 2.842	
Ctrl shCon (Un) vs KIf4 shCon (2D)	-2.86	4.496	No	ns	-5.839 to 0.1188	
Ctrl shCon (Un) vs KIf4 shStau1 (2D)	-4.956	7.809	Yes	***	-7.946 to -1.967	
Ctrl shStau1 (Un) vs Ctrl shCon (2D)	-5.045	7.932	Yes	***	-8.025 to -2.066	
Ctrl shStau1 (Un) vs Ctrl shStau1 (2D)	-8.971	14.11	Yes	***	-11.95 to -5.995	
Ctrl shStau1 (Un) vs KIf4OE shCon (Un)	0.4376	0.6883	No	ns	-2.542 to 3.417	
Ctrl shStau1 (Un) vs KIf4OE shStau1 (Un)	0.2372	0.3729	No	ns	-2.742 to 3.217	
Ctrl shStau1 (Un) vs KIf4 shCon (2D)	-2.485	3.908	No	ns	-5.464 to 0.4949	
Ctrl shStau1 (Un) vs KIf4 shStau1 (2D)	-4.591	7.216	Yes	***	-7.571 to -1.612	
Ctrl shCon (2D) vs Ctrl shStau1 (2D)	-3.926	6.176	Yes	**	-6.908 to -0.9431	
Ctrl shCon (2D) vs KIf4OE shCon (Un)	5.483	8.62	Yes	***	2.504 to 8.463	
Ctrl shCon (2D) vs KIf4OE shStau1 (Un)	5.283	8.305	Yes	***	2.303 to 8.262	
Ctrl shCon (2D) vs KIf4 shCon (2D)	2.561	4.026	No	ns	-0.4186 to 5.540	
Ctrl shCon (2D) vs KIf4 shStau1 (2D)	0.454	0.7137	No	ns	-2.525 to 3.433	
Ctrl shStau1 (2D) vs KIf4OE shCon (Un)	9.412	14.8	Yes	***	6.432 to 12.39	
Ctrl shStau1 (2D) vs KIf4OE shStau1 (Un)	9.211	14.48	Yes	***	6.232 to 12.19	
Ctrl shStau1 (2D) vs KIf4 shCon (2D)	6.486	10.2	Yes	***	3.510 to 9.469	
Ctrl shStau1 (2D) vs KIf4 shStau1 (2D)	4.383	6.89	Yes	**	1.403 to 7.362	
KIf4OE shCon (Un) vs KIf4OE shStau1 (Un)	-0.2006	0.3154	No	ns	-3.180 to 2.779	
KIf4OE shCon (Un) vs KIf4 shCon (2D)	-2.922	4.594	No	ns	-5.902 to 0.05701	
KIf4OE shCon (Un) vs KIf4 shStau1 (2D)	-5.026	7.901	Yes	***	-8.009 to -2.050	
KIf4OE shStau1 (Un) vs KIf4 shCon (2D)	-2.722	4.279	No	ns	-5.701 to 0.2576	
KIf4OE shStau1 (Un) vs KIf4 shStau1 (2D)	-4.826	7.591	Yes	***	-7.808 to -1.845	
KIf4 shCon (2D) vs KIf4 shStau1 (2D)	-2.107	3.312	No	ns	-5.088 to 0.8726	

Table Analyzed	Data 1					
				Tuj1 gene		
One-way analysis of variance						
P value	< 0.0001					
P value summary	***					
Are means signif. different? (P < 0.05)	Yes					
Number of groups	8					
F	206.8					
R squared	0.9837					
ANOVA Table	SS	df	MS			
Treatment (between columns)	213.1	7	30.42			
Residual (within columns)	3.53	24	0.1471			
Total	216.5	31				
Tukey's Multiple Comparison Test	Mean Diff.	q	Significant?	Summary	95% CI of diff	
Ctrl shCon (Un) vs Ctrl shStau1 (Un)	-0.09182	0.4788	No	ns	-0.9961 to 0.8064	
Ctrl shCon (Un) vs Ctrl shCon (2D)	-4.792	24.99	Yes	****	-5.680 to -3.904	
Ctrl shCon (Un) vs Ctrl shStau1 (2D)	-6.86	35.88	Yes	****	-7.778 to -5.982	
Ctrl shCon (Un) vs KIf4OE shCon (Un)	0.5662	2.953	No	ns	-0.3320 to 1.464	
Ctrl shCon (Un) vs KIf4OE shStau1 (Un)	0.2547	1.328	No	ns	-0.6406 to 1.153	
Ctrl shCon (Un) vs KIf4 shCon (2D)	-2.216	11.56	Yes	****	-3.114 to -1.318	
Ctrl shCon (Un) vs KIf4 shStau1 (2D)	-3.547	18.5	Yes	****	-4.445 to -2.649	
Ctrl shStau1 (Un) vs Ctrl shCon (2D)	-4.69	24.46	Yes	****	-5.588 to -3.792	
Ctrl shStau1 (Un) vs Ctrl shStau1 (2D)	-6.768	35.4	Yes	****	-7.666 to -5.870	
Ctrl shStau1 (Un) vs KIf4OE shCon (Un)	0.658	3.431	No	ns	-0.2402 to 1.556	
Ctrl shStau1 (Un) vs KIf4OE shStau1 (Un)	0.3455	1.807	No	ns	-0.5518 to 1.245	
Ctrl shStau1 (Un) vs KIf4 shCon (2D)	-2.124	11.08	Yes	****	-3.023 to -1.226	
Ctrl shStau1 (Un) vs KIf4 shStau1 (2D)	-3.455	18.02	Yes	****	-4.354 to -2.557	
Ctrl shCon (2D) vs Ctrl shStau1 (2D)	-2.068	10.94	Yes	****	-2.996 to -1.200	
Ctrl shCon (2D) vs KIf4OE shCon (Un)	5.348	27.89	Yes	****	4.450 to 6.246	
Ctrl shCon (2D) vs KIf4OE shStau1 (Un)	5.037	26.26	Yes	****	4.139 to 5.935	
Ctrl shCon (2D) vs KIf4 shCon (2D)	2.566	13.38	Yes	****	1.668 to 3.464	
Ctrl shCon (2D) vs KIf4 shStau1 (2D)	1.235	6.44	Yes	**	0.3367 to 2.133	
Ctrl shStau1 (2D) vs KIf4OE shCon (Un)	7.446	38.83	Yes	****	6.548 to 8.344	
Ctrl shStau1 (2D) vs KIf4OE shStau1 (Un)	7.134	37.2	Yes	****	6.236 to 8.033	
Ctrl shStau1 (2D) vs KIf4 shCon (2D)	4.634	24.32	Yes	****	3.765 to 5.562	
Ctrl shStau1 (2D) vs KIf4 shStau1 (2D)	3.333	17.38	Yes	****	2.434 to 4.231	
KIf4OE shCon (Un) vs KIf4OE shStau1 (Un)	-0.3115	1.625	No	ns	-1.210 to 0.5867	
KIf4OE shCon (Un) vs KIf4 shCon (2D)	-2.782	14.51	Yes	****	-3.681 to -1.884	
KIf4OE shCon (Un) vs KIf4 shStau1 (2D)	-4.113	21.45	Yes	****	-5.012 to -3.215	
KIf4OE shStau1 (Un) vs KIf4 shCon (2D)	-2.471	12.88	Yes	****	-3.369 to -1.573	
KIf4OE shStau1 (Un) vs KIf4 shStau1 (2D)	-3.802	19.82	Yes	****	-4.700 to -2.904	
KIf4 shCon (2D) vs KIf4 shStau1 (2D)	-1.331	6.94	Yes	**	-2.229 to -0.4326	

Fig. 4F



Dlx1	shCtrl, Con (Un)	shCtrl, Stau1(Un)	shCtrl, Con (2D)	shCtrl, Stau1 (2D)	shKif4, co	shKif4, Stau1 (Un)	shKif4, Con (2D)	shKif4, Stau1 (2D)
#1	1.069759302	2.169755875	10.53626173	5.920189314	1.741103	2.184900061	12.44316026	12.39402367
#2	0.936551886	2.144786276	10.28762915	6.177786754	2.720821	2.938738039	12.71818888	11.42056414
#3	1.444658452	1.492609724	11.24509769	6.833302565	2.106961	2.713790826	12.76090171	11.92492809
#4	0.951080895	2.160721509	10.68844589	7.165911786	2.149585	3.165500502	12.10797026	11.7530874

Dlx2 gene	shCtrl, Con (Un)	shCtrl, Stau1 (Un)	shCtrl, Con (2D)	shCtrl, Stau1 (2D)	shKif4, Co	shKif4, Stau1 (Un)	shKif4, Con (2D)	shKif4, Stau1 (2D)
#1	1.853753638	0.599323917	2.856691349	0.678412726	2.260144	2.495650739	4.171146195	2.214324422
#2	1.1317075	0.746443009	3.01586456	0.973294929	1.429833	1.822035407	4.217559396	3.474375519
#3	1.04496984	0.299641958	3.079457145	2.158648588	2.260144	0.720489853	4.248259808	4.024211793
#4	0.650994938	1.492886017	4.571195877	2.528817334	1.967569	0.469849524	5.934922233	6.948751039

Tuj1 gene	shCtrl, Con (Un)	shCtrl, Stau1 (Un)	shCtrl, Con (2D)	shCtrl, Stau1 (2D)	shKif4, Co	shKif4, Stau1 (Un)	shKif4, Con (2D)	shKif4, Stau1 (2D)
#1	0.975795752	0.912986062	4.513575155	3.976421577	2.091804	1.974751795	5.906842256	7.43022508
#2	0.847073512	0.961248113	5.051520162	4.066799141	1.684488	1.834067492	8.23459716	5.283077712
#3	1.291350299	0.742145841	5.723339338	4.342514466	1.378666	1.684127665	7.524381659	6.552893861
#4	0.953190002	0.869904095	6.325027609	4.353160052	2.195247	2.194408291	7.607513575	6.541231627

Table Analyzed	Data 1				
One-way analysis of variance				**Dlx1 gene**	
P value	< 0.0001				
P value summary	***				
Are means signif. different? (P < 0.05)	Yes				
Number of groups	8				
F	594.9				
R squared	0.9940				
ANOVA Table	SS	df	MS		
Treatment (between columns)	656.3	7	93.76		
Residual (within columns)	3.782	24	0.1576		
Total	660.1	31			

Tukey's Multiple Comparison Test	Mean Diff.	q	Significant? P < 0.05	Summary	95% CI of diff
shCtrl Con (Un) vs shCtrl Stau1(Un)	-0.8982	4.525	No	ns	-1.828 to 0.03154
shCtrl Con (Un) vs shCtrl Con (2D)	-9.586	48.34	Yes	***	-10.53 to -8.666
shCtrl Con (Un) vs shCtrl Stau1 (2D)	-5.431	27.36	Yes	***	-6.360 to -4.501
shCtrl Con (Un) vs shKif4 con (Un)	-1.086	5.47	Yes	*	-2.016 to -0.1561
shCtrl Con (Un) vs shKif4 Stau1 (Un)	-1.857	9.348	Yes	***	-2.787 to -0.7272
shCtrl Con (Un) vs shKif4 Con (2D)	-11.41	57.5	Yes	***	-12.34 to -10.48
shCtrl Con (Un) vs shKif4 Stau1 (2D)	-10.78	54.31	Yes	***	-11.71 to -9.850
shCtrl Stau1(Un) vs shCtrl Con (2D)	-8.687	43.82	Yes	***	-9.627 to -7.768
shCtrl Stau1(Un) vs shCtrl Stau1 (2D)	-4.532	22.83	Yes	***	-5.462 to -3.603
shCtrl Stau1(Un) vs shKif4 con (Un)	-0.1876	0.9454	No	ns	-1.117 to 0.7421
shCtrl Stau1(Un) vs shKif4 Stau1 (Un)	-0.7388	3.823	No	ns	-1.689 to 0.1710
shCtrl Stau1(Un) vs shKif4 Con (2D)	-10.52	52.98	Yes	***	-11.45 to -9.586
shCtrl Stau1(Un) vs shKif4 Stau1 (2D)	-9.881	49.78	Yes	***	-10.81 to -8.951
shCtrl Con (2D) vs shCtrl Stau1 (2D)	4.155	20.96	Yes	***	3.225 to 5.085
shCtrl Con (2D) vs shKif4 con (Un)	8.51	42.87	Yes	***	7.580 to 9.440
shCtrl Con (2D) vs shKif4 Stau1 (Un)	7.939	40	Yes	***	7.009 to 8.868
shCtrl Con (2D) vs shKif4 Con (2D)	-1.818	9.16	Yes	***	-2.748 to -0.8884
shCtrl Con (2D) vs shKif4 Stau1 (2D)	-1.184	5.964	Yes	**	-2.113 to -0.2540
shCtrl Stau1 (2D) vs shKif4 con (Un)	4.345	21.89	Yes	***	3.415 to 5.274
shCtrl Stau1 (2D) vs shKif4 Stau1 (Un)	3.774	19.01	Yes	***	2.844 to 4.703
shCtrl Stau1 (2D) vs shKif4 Con (2D)	-5.983	30.14	Yes	***	-6.913 to -5.054
shCtrl Stau1 (2D) vs shKif4 Stau1 (2D)	-5.349	26.95	Yes	***	-6.278 to -4.419
shKif4 con (Un) vs shKif4 Stau1 (Un)	-0.5711	2.877	No	ns	-1.501 to 0.3586
shKif4 con (Un) vs shKif4 Con (2D)	-10.33	52.03	Yes	***	-11.26 to -9.398
shKif4 con (Un) vs shKif4 Stau1 (2D)	-9.694	48.84	Yes	***	-10.62 to -8.764
shKif4 Stau1 (Un) vs shKif4 Con (2D)	-9.757	49.15	Yes	***	-10.69 to -8.827
shKif4 Stau1 (Un) vs shKif4 Stau1 (2D)	-9.122	45.96	Yes	***	-10.05 to -8.193
shKif4 Con (2D) vs shKif4 Stau1 (2D)	0.6344	3.196	No	ns	-0.2953 to 1.564

Table Analyzed	Data 1				
One-way analysis of variance				**Dlx2 gene**	
P value	< 0.0001				
P value summary	***				
Are means signif. different? (P < 0.05)	Yes				
Number of groups	8				
F	9.163				
R squared	0.7277				
ANOVA Table	SS	df	MS		
Treatment (between columns)	62.45	7	8.921		
Residual (within columns)	23.37	24	0.9736		
Total	85.81	31			

Tukey's Multiple Comparison Test	Mean Diff.	q	Significant?	Summary	95% CI of diff
shCtrl Con (Un) vs shCtrl Stau1(Un)	0.3858	0.782	No	ns	-1.925 to 2.697
shCtrl Con (Un) vs shCtrl Con (2D)	-2.435	4.937	Yes	*	-4.746 to -0.1246
shCtrl Con (Un) vs shCtrl Stau1 (2D)	-0.4144	0.8401	No	ns	-2.725 to 1.896
shCtrl Con (Un) vs shKif4 con (Un)	-0.8091	1.64	No	ns	-3.120 to 1.502
shCtrl Con (Un) vs shKif4 Stau1 (Un)	-0.2066	0.4189	No	ns	-2.517 to 2.104
shCtrl Con (Un) vs shKif4 Con (2D)	-3.473	7.039	Yes	***	-5.783 to -1.162
shCtrl Con (Un) vs shKif4 Stau1 (2D)	-2.996	6.072	Yes	**	-5.306 to -0.6847
shCtrl Stau1(Un) vs shCtrl Con (2D)	-2.821	5.719	Yes	**	-5.132 to -0.5104
shCtrl Stau1(Un) vs shCtrl Stau1 (2D)	-0.8002	1.622	No	ns	-3.111 to 1.511
shCtrl Stau1(Un) vs shKif4 con (Un)	-1.195	2.422	No	ns	-3.506 to 1.116
shCtrl Stau1(Un) vs shKif4 Stau1 (Un)	-0.5924	1.201	No	ns	-2.903 to 1.718
shCtrl Stau1(Un) vs shKif4 Con (2D)	-3.859	7.821	Yes	***	-6.169 to -1.548
shCtrl Stau1(Un) vs shKif4 Stau1 (2D)	-3.381	6.854	Yes	**	-5.692 to -1.070
shCtrl Con (2D) vs shCtrl Stau1 (2D)	2.021	4.097	No	ns	-0.3098 to 4.352
shCtrl Con (2D) vs shKif4 con (Un)	1.626	3.297	No	ns	-0.6845 to 3.937
shCtrl Con (2D) vs shKif4 Stau1 (Un)	2.229	4.518	No	ns	-0.08205 to 4.540
shCtrl Con (2D) vs shKif4 Con (2D)	-1.037	2.102	No	ns	-3.348 to 1.274
shCtrl Con (2D) vs shKif4 Stau1 (2D)	-0.5601	1.135	No	ns	-2.871 to 1.751
shCtrl Stau1 (2D) vs shKif4 con (Un)	-0.3946	0.7998	No	ns	-2.705 to 1.916
shCtrl Stau1 (2D) vs shKif4 Stau1 (Un)	0.2076	0.4210	No	ns	-2.103 to 2.519
shCtrl Stau1 (2D) vs shKif4 Con (2D)	-3.058	6.199	Yes	**	-5.369 to -0.7473
shCtrl Stau1 (2D) vs shKif4 Stau1 (2D)	-2.581	5.232	Yes	*	-4.892 to -0.2703
shKif4 con (Un) vs shKif4 Stau1 (Un)	0.6024	1.221	No	ns	-1.708 to 2.913
shKif4 con (Un) vs shKif4 Con (2D)	-2.664	5.399	Yes	*	-4.974 to -0.3527
shKif4 con (Un) vs shKif4 Stau1 (2D)	-2.186	4.432	No	ns	-4.497 to 0.1343
shKif4 Stau1 (Un) vs shKif4 Con (2D)	-3.266	6.62	Yes	**	-5.577 to -0.9551
shKif4 Stau1 (Un) vs shKif4 Stau1 (2D)	-2.789	5.653	Yes	*	-5.100 to -0.4781
shKif4 Con (2D) vs shKif4 Stau1 (2D)	0.4771	0.967	No	ns	-1.834 to 2.788

Table Analyzed	Data 1				
One-way analysis of variance				**Tuj1 gene**	
P value	< 0.0001				
P value summary	***				
Are means signif. different? (P < 0.05)	Yes				
Number of groups	8				
F	76.33				
R squared	0.9581				
ANOVA Table	SS	df	MS		
Treatment (between columns)	182.3	7	26.05		
Residual (within columns)	7.981	24	0.3325		
Total	190.3	31			

Tukey's Multiple Comparison Test	Mean Diff.	q	Significant?	Summary	95% CI of diff
shCtrl Con (Un) vs shCtrl Stau1(Un)	0.1452	0.5036	No	ns	-1.205 to 1.496
shCtrl Con (Un) vs shCtrl Con (2D)	-4.387	15.21	Yes	***	-5.737 to -3.036
shCtrl Con (Un) vs shCtrl Stau1 (2D)	-3.168	10.99	Yes	***	-4.518 to -1.817
shCtrl Con (Un) vs shKif4 con (Un)	-0.8212	2.848	No	ns	-2.172 to 0.5208
shCtrl Con (Un) vs shKif4 Stau1 (Un)	-0.905	3.139	No	ns	-2.256 to 0.4456
shCtrl Con (Un) vs shKif4 Con (2D)	-6.301	21.86	Yes	***	-7.652 to -4.951
shCtrl Con (Un) vs shKif4 Stau1 (2D)	-5.435	18.85	Yes	***	-6.785 to -4.084
shCtrl Stau1(Un) vs shCtrl Con (2D)	-4.532	15.72	Yes	***	-5.882 to -3.181
shCtrl Stau1(Un) vs shCtrl Stau1 (2D)	-3.313	11.49	Yes	***	-4.664 to -1.963
shCtrl Stau1(Un) vs shKif4 con (Un)	-0.9954	3.352	No	ns	-2.317 to 0.3641
shCtrl Stau1(Un) vs shKif4 Stau1 (Un)	-1.05	3.642	No	ns	-2.401 to 0.3003
shCtrl Stau1(Un) vs shKif4 Con (2D)	-6.447	22.36	Yes	***	-7.797 to -5.096
shCtrl Stau1(Un) vs shKif4 Stau1 (2D)	-5.58	19.35	Yes	***	-6.931 to -4.229
shCtrl Con (2D) vs shCtrl Stau1 (2D)	1.219	4.227	No	ns	-0.1193 to 2.585
shCtrl Con (2D) vs shKif4 con (Un)	3.585	12.37	Yes	***	2.213 to 4.956
shCtrl Con (2D) vs shKif4 Stau1 (Un)	3.482	12.07	Yes	***	2.131 to 4.832
shCtrl Con (2D) vs shKif4 Con (2D)	-1.915	6.642	Yes	**	-3.265 to -0.5644
shCtrl Con (2D) vs shKif4 Stau1 (2D)	-1.048	3.636	No	ns	-2.399 to 0.3022
shCtrl Stau1 (2D) vs shKif4 con (Un)	2.367	8.139	Yes	***	0.9951 to 3.697
shCtrl Stau1 (2D) vs shKif4 Stau1 (Un)	2.263	7.848	Yes	***	0.9134 to 3.613
shCtrl Stau1 (2D) vs shKif4 Con (2D)	-3.134	10.87	Yes	***	-4.484 to -1.783
shCtrl Stau1 (2D) vs shKif4 Stau1 (2D)	-2.267	7.862	Yes	***	-3.617 to -0.9164
shKif4 con (Un) vs shKif4 Stau1 (Un)	-0.08379	0.2906	No	ns	-1.434 to 1.267
shKif4 con (Un) vs shKif4 Con (2D)	-5.48	19.01	Yes	***	-6.831 to -4.130
shKif4 con (Un) vs shKif4 Stau1 (2D)	-4.614	16	Yes	***	-5.964 to -3.263
shKif4 Stau1 (Un) vs shKif4 Con (2D)	-5.396	18.72	Yes	***	-6.747 to -4.046
shKif4 Stau1 (Un) vs shKif4 Stau1 (2D)	-4.53	15.71	Yes	***	-5.880 to -3.179
shKif4 Con (2D) vs shKif4 Stau1 (2D)	0.8657	3.006	No	ns	-0.4839 to 2.215

Fig. 6B

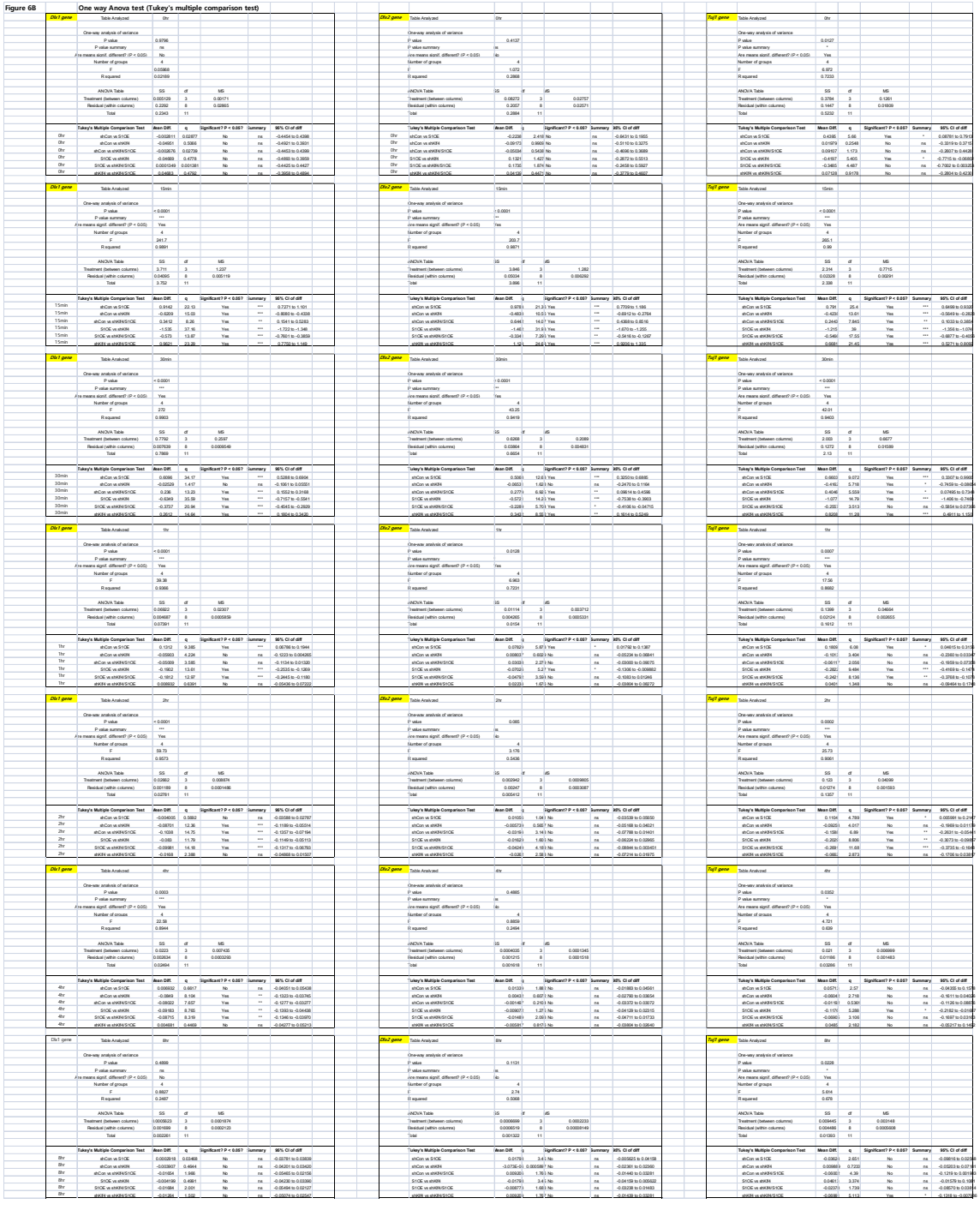


Figure 6B
One way Anova test (Tukey's multiple comparison test)
Dlx1 gene
Dlx2 gene
Tuj1 gene
Table Analyzed
0hr
15min
30min
1hr
2hr
4hr
One-way analysis of variance
P value
P value summary
Are means signif. different? (P < 0.05)
Number of groups
F
R squared
ANOVA Table
SS
df
MS
Treatment (between columns)
Residual (within columns)
Total
Tukey's Multiple Comparison Test
Mean Diff.
q
Significant? P < 0.05?
Summary
95% CI of diff
ctrCon vs S1CE
ctrCon vs ctrKN
ctrCon vs ctrKN/S1CE
S1CE vs ctrKN
S1CE vs ctrKN/S1CE
ctrKN vs ctrKN/S1CE

Fig. 6C

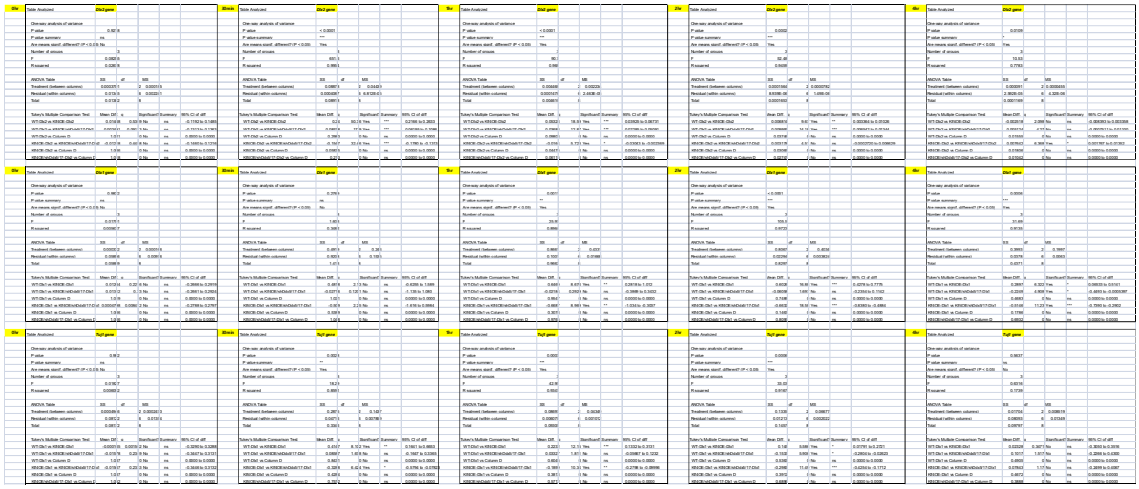


Fig. 7A

Table Analyzed	Data 1				
One-way analysis of variance					
P value	< 0.0001				
P value summary	***				
Are means signif. different? (P < 0.05)	Yes				
Number of groups	6				
F	17.49				
R squared	0.862				
ANOVA Table	SS	df	MS		
Treatment (between columns)	8065	5	1613		
Residual (within columns)	1291	14	92.21		
Total	9355	19			

Tukey's Multiple Comparison Test	Mean Diff.	q	Significant?	Summary	95% CI of diff
Klf4KONSC GFP-control (Un) vs Klf4KONSC GFP-mKlf4(Un)	29.87	6.222	Yes	**	7.599 to 52.15
Klf4KONSC GFP-control (Un) vs Klf4KONSC GFP-dC(Un)	12.71	2.647	No	ns	-9.566 to 34.98
Klf4KONSC GFP-control (Un) vs Klf4KONSC GFP-control (2D)	52.16	10.06	Yes	***	28.10 to 76.22
Klf4KONSC GFP-control (Un) vs Klf4KONSC GFP-mKlf4(2D)	49.66	9.576	Yes	***	25.60 to 73.72
Klf4KONSC GFP-control (Un) vs Klf4KONSC GFP-dC(2D)	48.35	8.223	Yes	***	21.07 to 75.63
Klf4KONSC GFP-mKlf4(Un) vs Klf4KONSC GFP-dC(Un)	-17.17	3.575	No	ns	-39.44 to 5.108
Klf4KONSC GFP-mKlf4(Un) vs Klf4KONSC GFP-control (2D)	22.29	4.297	No	ns	-1.771 to 46.34
Klf4KONSC GFP-mKlf4(Un) vs Klf4KONSC GFP-mKlf4(2D)	19.79	3.816	No	ns	-4.271 to 43.84
Klf4KONSC GFP-mKlf4(Un) vs Klf4KONSC GFP-dC(2D)	18.48	3.143	No	ns	-8.799 to 45.76
Klf4KONSC GFP-dC(Un) vs Klf4KONSC GFP-control (2D)	39.45	7.607	Yes	**	15.39 to 63.51
Klf4KONSC GFP-dC(Un) vs Klf4KONSC GFP-mKlf4(2D)	36.95	7.125	Yes	**	12.89 to 61.01
Klf4KONSC GFP-dC(Un) vs Klf4KONSC GFP-dC(2D)	35.65	6.062	Yes	**	8.367 to 62.92
Klf4KONSC GFP-control (2D) vs Klf4KONSC GFP-mKlf4(2D)	-2.499	0.4508	No	ns	-28.22 to 23.22
Klf4KONSC GFP-control (2D) vs Klf4KONSC GFP-dC(2D)	-3.806	0.6141	No	ns	-32.56 to 24.95
Klf4KONSC GFP-mKlf4(2D) vs Klf4KONSC GFP-dC(2D)	-1.307	0.2109	No	ns	-30.06 to 27.45

Fig.7B

Dlx1	Con-GFP (Un)	Klf4-GFP (Un)	Klf4(dC)-GFP (Un)	Con-GFP (2D)	Klf4-GFP (2D)	Klf4(dC)-GFP (2D)
#1	1.063181427	1.159388847	1.079743708	4.715546079	2.248161856	3.053965623
#2	0.97286996	1.064555289	0.985695169	4.825178117	2.93434501	3.823184385
#3	1.00672099	0.822600863	0.933405183	5.821571039	3.12124418	3.962168841
Dlx2	Con-GFP (Un)	Klf4-GFP (Un)	Klf4(dC)-GFP (Un)	Con-GFP (2D)	Klf4-GFP (2D)	Klf4(dC)-GFP (2D)
#1	1.580623248	1.23410714	1.887443338	7.676026815	1.932785564	3.944571212
#2	0.62585646	0.61705357	0.36538448	10.15292219	2.148768113	4.881520628
#3	0.916726256	1.151462677	0.877895082	7.022123894	2.571121961	6.523077157
Tuj1	Con-GFP (Un)	Klf4-GFP (Un)	Klf4(dC)-GFP (Un)	Con-GFP (2D)	Klf4-GFP (2D)	Klf4(dC)-GFP (2D)
#1	0.943198633	1.343447853	0.979410077	1.151606585	0.628564116	1.461071135
#2	1.355111055	0.687222757	1.059884505	1.298430184	0.842810928	1.285802098
#3	0.811788701	1.073481696	1.069578947	1.714672977	0.791026804	1.519104916

			0.943198633	1.343447853	0.97941	1.151607	0.628564	1.261071
0.943198633	1.355111055	0.811788701	1.355111055	0.687222757	1.059885	1.29843	0.842811	1.285802
1.343447853	0.687222757	1.073481696	0.811788701	1.073481696	1.069579	1.714673	0.791027	1.519105
0.979410077	1.059884505	1.069578947						
1.151606585	1.298430184	1.714672977						
0.628564116	0.842810928	0.791026804						
1.261071135	1.285802098	1.519104916						

	Data 1				
One-way analysis of variance					
P value	< 0.0001				
P value summary	***				
Are means signi	Yes				
Number of group	6				
F	61.99				
R squared	0.9627				
ANOVA Table	SS	df	MS		
Treatment (betw	44.41	5	8.883		
Residual (within	1.719	12	0.1433		
Total	46.13	17			
Tukey's Multiple	Mean Diff.	q	Significant? P <	Summary	95% CI of diff
Con-GFP (Un) v	-0.001258	0.005754	No	ns	-1.040 to 1.037
Con-GFP (Un) v	0.01464	0.067	No	ns	-1.024 to 1.053
Con-GFP (Un) v	-4.107	18.79	Yes	***	-5.145 to -3.068
Con-GFP (Un) v	-1.754	8.024	Yes	**	-2.792 to -0.7153
Con-GFP (Un) v	-2.599	11.89	Yes	***	-3.637 to -1.561
Klf4-GFP (Un) v	0.0159	0.07275	No	ns	-1.022 to 1.054
Klf4-GFP (Un) v	-4.105	18.78	Yes	***	-5.144 to -3.067
Klf4-GFP (Un) v	-1.752	8.018	Yes	**	-2.791 to -0.7141
Klf4-GFP (Un) v	-2.598	11.89	Yes	***	-3.636 to -1.559
Klf4(dC)-GFP (U	-4.121	18.86	Yes	***	-5.159 to -3.083
Klf4(dC)-GFP (U	-1.768	8.091	Yes	**	-2.807 to -0.7300
Klf4(dC)-GFP (U	-2.613	11.96	Yes	***	-3.652 to -1.575
Con-GFP (2D) v	2.353	10.77	Yes	***	1.315 to 3.391
Con-GFP (2D) v	1.508	6.899	Yes	**	0.4693 to 2.546
Klf4-GFP (2D) v	-0.8452	3.867	No	ns	-1.884 to 0.1931

Table Analyzed	Data 1				
One-way analysis of variance					
P value	< 0.0001				
P value summary	***				
Are means signif.	Yes				
Number of groups	6				
F	29.25				
R squared	0.9242				
ANOVA Table	SS	df	MS		
Treatment (betwe	133.8	5	26.75		
Residual (within c	10.98	12	0.9146		
Total	144.7	17			
Tukey's Multiple C	Mean Diff.	q	Significant? P <	Summary	95% CI of diff
Con-GFP (Un) vs	0.04019	0.07279	No	ns	-2.583 to 2.663
Con-GFP (Un) vs	-0.002506	0.004538	No	ns	-2.626 to 2.621
Con-GFP (Un) vs	-7.243	13.12	Yes	***	-9.866 to -4.619
Con-GFP (Un) vs	-1.176	2.131	No	ns	-3.800 to 1.447
Con-GFP (Un) vs	-4.075	7.381	Yes	**	-6.699 to -1.452
Klf4-GFP (Un) vs	-0.0427	0.07733	No	ns	-2.666 to 2.581
Klf4-GFP (Un) vs	-7.283	13.19	Yes	***	-9.906 to -4.660
Klf4-GFP (Un) vs	-1.217	2.204	No	ns	-3.840 to 1.407
Klf4-GFP (Un) vs	-4.116	7.454	Yes	**	-6.739 to -1.492
Klf4(dC)-GFP (Ur	-7.24	13.11	Yes	***	-9.863 to -4.617
Klf4(dC)-GFP (Ur	-1.174	2.126	No	ns	-3.797 to 1.449
Klf4(dC)-GFP (Ur	-4.073	7.376	Yes	**	-6.696 to -1.450
Con-GFP (2D) vs	6.066	10.99	Yes	***	3.443 to 8.689
Con-GFP (2D) vs	3.167	5.736	Yes	*	0.5440 to 5.791
Klf4-GFP (2D) vs	-2.899	5.25	Yes	*	-5.522 to -0.2755

Table Analy	Data 1				
One-way analysis of variance					
P value	0.0279				
P value sun	*				
Are means	Yes				
Number of	6				
F	3.762				
R squared	0.6105				
ANOVA Tal	SS	df	MS		
Treatment (	0.9535	5	0.1907		
Residual (w	0.6083	12	0.05069		
Total	1.562	17			
Tukey's Mul	Mean Diff.	q	Significant?	Summary	95% CI of diff
Con-GFP (l	0.001982	0.01525	No	ns	-0.6156 to 0.6196
Con-GFP (l	0.0004082	0.00314	No	ns	-0.6172 to 0.6180
Con-GFP (l	-0.3515	2.704	No	ns	-0.9691 to 0.2660
Con-GFP (l	0.2826	2.174	No	ns	-0.3350 to 0.9001
Con-GFP (l	-0.3853	2.964	No	ns	-1.003 to 0.2323
Klf4-GFP (l	-0.001574	0.01211	No	ns	-0.6192 to 0.6160
Klf4-GFP (l	-0.3535	2.72	No	ns	-0.9711 to 0.2641
Klf4-GFP (l	0.2806	2.159	No	ns	-0.3370 to 0.8982
Klf4-GFP (l	-0.3873	2.979	No	ns	-1.005 to 0.2303
Klf4(dC)-GI	-0.3519	2.707	No	ns	-0.9695 to 0.2656
Klf4(dC)-GI	0.2822	2.171	No	ns	-0.3354 to 0.8997
Klf4(dC)-GI	-0.3857	2.967	No	ns	-1.003 to 0.2319
Con-GFP (2	0.6341	4.878	Yes	*	0.01652 to 1.252
Con-GFP (2	-0.03376	0.2597	No	ns	-0.6513 to 0.5838
Klf4-GFP (2	-0.6679	5.138	Yes	*	-1.285 to -0.05028

Fig. S9B

Stau1	Con/shcon(Un)	Con/shStau1(Un)	Klf4/shcon(Un)	Klf4/shStau1(Un)	Con/shcon(2D)	Con/shStau1(2D)	Klf4/shcon(2D)	Klf4/shStau1(2D)
	1.00521214	0.195128985	1.111493876	0.124136562	0.251157919	0.078563336	0.228062318	0.038875364
	0.964263938	0.304075187	1.199555576	0.102237757	0.261823531	0.078020659	0.273099769	0.026923317
	0.984525173	0.165224553	1.294594249	0.111878134	0.195693354	0.083620472	0.228062318	0.044041274
	1.1076484	0.224144344	1.303598864	0.07588718	0.244289992	0.085971364	0.223368863	0.050942021
Stau2	Con/shcon(Un)	Con/shStau1(Un)	Klf4/shcon(Un)	Klf4/shStau1(Un)	Con/shcon(2D)	Con/shStau1(2D)	Klf4/shcon(2D)	Klf4/shStau1(2D)
	0.993092495	1.84889932	2.034959384	1.342572503	1.510472586	1.652900636	1.349570179	1.711190051
	0.952637998	1.967913307	2.077718207	1.664397469	1.399585866	1.596596773	1.387511761	1.618884433
	1.028113827	1.501772904	1.885569072	0.837987135	1.121166078	1.419123356	1.497441871	1.419123356
	1.049716684	1.761331747	1.796264746	1.459020344	1.176906737	1.808758755	1.349570179	1.399585866

Table Analyzed	Data 1				
		Stau1 gene			
One-way analysis of variance					
P value	< 0.0001				
P value summary	***				
Are means signif. different? (P < 0.05)	Yes				
Number of groups	8				
F	377.7				
R squared	0.991				
ANOVA Table	SS	df	MS		
Treatment (between columns)	5.863	7	0.8376		
Residual (within columns)	0.05323	24	0.002218		
Total	5.916	31			
Tukey's Multiple Comparison Test	Mean Diff.	q	Significant? P < 0.(	Summary	95% CI of diff
Con/shcon(Un) vs Con/shStau1(Un)	0.7933	33.69	Yes	***	0.6830 to 0.9036
Con/shcon(Un) vs Klf4/shcon(Un)	-0.2119	8.999	Yes	***	-0.3222 to -0.1016
Con/shcon(Un) vs Klf4/shStau1(Un)	0.9119	38.73	Yes	***	0.8016 to 1.022
Con/shcon(Un) vs Con/shcon(2D)	0.7772	33.01	Yes	***	0.6669 to 0.8875
Con/shcon(Un) vs Con/shStau1(2D)	0.9339	39.66	Yes	***	0.8236 to 1.044
Con/shcon(Un) vs Klf4/shcon(2D)	0.7773	33.01	Yes	***	0.6670 to 0.8876
Con/shcon(Un) vs Klf4/shStau1(2D)	0.9752	41.42	Yes	***	0.8649 to 1.086
Con/shStau1(Un) vs Klf4/shcon(Un)	-1.005	42.69	Yes	***	-1.115 to -0.8949
Con/shStau1(Un) vs Klf4/shStau1(Un)	0.1186	5.037	Yes	*	0.008317 to 0.2289
Con/shStau1(Un) vs Con/shcon(2D)	-0.0161	0.6837	No	ns	-0.1264 to 0.09419
Con/shStau1(Un) vs Con/shStau1(2D)	0.1406	5.971	Yes	**	0.03031 to 0.2509
Con/shStau1(Un) vs Klf4/shcon(2D)	-0.01601	0.6797	No	ns	-0.1263 to 0.09429
Con/shStau1(Un) vs Klf4/shStau1(2D)	0.1819	7.727	Yes	***	0.07166 to 0.2922
Klf4/shcon(Un) vs Klf4/shStau1(Un)	1.124	47.73	Yes	***	1.013 to 1.234
Klf4/shcon(Un) vs Con/shcon(2D)	0.9891	42.01	Yes	***	0.8788 to 1.099
Klf4/shcon(Un) vs Con/shStau1(2D)	1.146	48.66	Yes	***	1.035 to 1.256
Klf4/shcon(Un) vs Klf4/shcon(2D)	0.9892	42.01	Yes	***	0.8789 to 1.099
Klf4/shcon(Un) vs Klf4/shStau1(2D)	1.187	50.42	Yes	***	1.077 to 1.297
Klf4/shStau1(Un) vs Con/shcon(2D)	-0.1347	5.721	Yes	**	-0.2450 to -0.02441
Klf4/shStau1(Un) vs Con/shStau1(2D)	0.02199	0.9339	No	ns	-0.08830 to 0.1323
Klf4/shStau1(Un) vs Klf4/shcon(2D)	-0.1346	5.717	Yes	**	-0.2449 to -0.02432
Klf4/shStau1(Un) vs Klf4/shStau1(2D)	0.06334	2.69	No	ns	-0.04695 to 0.1736
Con/shcon(2D) vs Con/shStau1(2D)	0.1567	6.655	Yes	**	0.04641 to 0.2670
Con/shcon(2D) vs Klf4/shcon(2D)	0.00009288	0.003944	No	ns	-0.1102 to 0.1104
Con/shcon(2D) vs Klf4/shStau1(2D)	0.198	8.411	Yes	***	0.08775 to 0.3083
Con/shStau1(2D) vs Klf4/shcon(2D)	-0.1566	6.651	Yes	**	-0.2669 to -0.04631
Con/shStau1(2D) vs Klf4/shStau1(2D)	0.04135	1.756	No	ns	-0.06894 to 0.1516
Klf4/shcon(2D) vs Klf4/shStau1(2D)	0.198	8.407	Yes	***	0.08766 to 0.3082

Table Analyzed	Data 1				
			Stau2 gene		
One-way analysis of variance					
P value	< 0.0001				
P value summary	***				
Are means signif. different? (P < 0.05)	Yes				
Number of groups	8				
F	10.4				
R squared	0.7521				
ANOVA Table	SS	df	MS		
Treatment (between columns)	2.452	7	0.3503		
Residual (within columns)	0.8082	24	0.03368		
Total	3.261	31			
Tukey's Multiple Comparison Test	Mean Diff.	q	Significant?	Summary	95% CI of diff
Con/shcon(Un) vs Con/shStau1(Un)	-0.7641	8.328	Yes	***	-1.194 to -0.3343
Con/shcon(Un) vs Klf4/shcon(Un)	-0.9427	10.27	Yes	***	-1.373 to -0.5130
Con/shcon(Un) vs Klf4/shStau1(Un)	-0.3201	3.489	No	ns	-0.7499 to 0.1097
Con/shcon(Un) vs Con/shcon(2D)	-0.2961	3.228	No	ns	-0.7259 to 0.1336
Con/shcon(Un) vs Con/shStau1(2D)	-0.6135	6.686	Yes	**	-1.043 to -0.1837
Con/shcon(Un) vs Klf4/shcon(2D)	-0.3901	4.252	No	ns	-0.8199 to 0.03965
Con/shcon(Un) vs Klf4/shStau1(2D)	-0.5313	5.79	Yes	**	-0.9611 to -0.1015
Con/shStau1(Un) vs Klf4/shcon(Un)	-0.1786	1.947	No	ns	-0.6084 to 0.2511
Con/shStau1(Un) vs Klf4/shStau1(Un)	0.444	4.839	Yes	*	0.01421 to 0.8738
Con/shStau1(Un) vs Con/shcon(2D)	0.4679	5.1	Yes	*	0.03817 to 0.8977
Con/shStau1(Un) vs Con/shStau1(2D)	0.1506	1.642	No	ns	-0.2791 to 0.5804
Con/shStau1(Un) vs Klf4/shcon(2D)	0.374	4.076	No	ns	-0.05582 to 0.8037
Con/shStau1(Un) vs Klf4/shStau1(2D)	0.2328	2.537	No	ns	-0.1970 to 0.6626
Klf4/shcon(Un) vs Klf4/shStau1(Un)	0.6226	6.786	Yes	**	0.1929 to 1.052
Klf4/shcon(Un) vs Con/shcon(2D)	0.6466	7.047	Yes	***	0.2168 to 1.076
Klf4/shcon(Un) vs Con/shStau1(2D)	0.3293	3.589	No	ns	-0.1005 to 0.7591
Klf4/shcon(Un) vs Klf4/shcon(2D)	0.5526	6.023	Yes	**	0.1228 to 0.9824
Klf4/shcon(Un) vs Klf4/shStau1(2D)	0.4114	4.484	No	ns	-0.01835 to 0.8412
Klf4/shStau1(Un) vs Con/shcon(2D)	0.02396	0.2611	No	ns	-0.4058 to 0.4537
Klf4/shStau1(Un) vs Con/shStau1(2D)	-0.2934	3.197	No	ns	-0.7231 to 0.1364
Klf4/shStau1(Un) vs Klf4/shcon(2D)	-0.07003	0.7632	No	ns	-0.4998 to 0.3598
Klf4/shStau1(Un) vs Klf4/shStau1(2D)	-0.2112	2.302	No	ns	-0.6410 to 0.2186
Con/shcon(2D) vs Con/shStau1(2D)	-0.3173	3.458	No	ns	-0.7471 to 0.1125
Con/shcon(2D) vs Klf4/shcon(2D)	-0.09399	1.024	No	ns	-0.5238 to 0.3358
Con/shcon(2D) vs Klf4/shStau1(2D)	-0.2352	2.563	No	ns	-0.6649 to 0.1946
Con/shStau1(2D) vs Klf4/shcon(2D)	0.2233	2.434	No	ns	-0.2065 to 0.6531
Con/shStau1(2D) vs Klf4/shStau1(2D)	0.08215	0.8953	No	ns	-0.3476 to 0.5119
Klf4/shcon(2D) vs Klf4/shStau1(2D)	-0.1412	1.539	No	ns	-0.5710 to 0.2886

Fig. S9D

shCon&Con OE

	mCherry&	Tuj1&mCherry&GFP	Tuj1&mCheery&GFP/mCherry&GFP
	5	2	**40**
	4	1	**25**
	7	2	**28.57143**

shStau1&Con OE

4	2	**50**
7	4	**57.14286**
5	3	**60**

shCon&Klf4 OE

7	1	**14.28571**
6	1	**16.66667**
5	1	**20**

shStau1&Klf4 OE

10	4	**40**
6	3	**50**
7	3	**42.85714**
4	2	**50**
5	2	**40**
4	2	**50**

	shCon&Con OE	shStau1&Con OE	shCon&Klf4 OE	shStau1&Klf4 OE
#1	25	50	14.28571429	40
#2	28.57142857	57.14285714	16.66666667	50
#3	40	60	20	42.85714286
#4				50
#5				40
#6				50

Table Analyzed	Data 1				
One-way analysis of variance					
P value	< 0.0001				
P value summary	***				
Are means signif. different? (P < 0.05)	Yes				
Number of groups	4				
F	31.19				
R squared	0.8948				
ANOVA Table	SS	df	MS		
Treatment (between columns)	2727	3	908.9		
Residual (within columns)	320.6	11	29.14		
Total	3047	14			
Tukey's Multiple Comparison Test	Mean Diff.	q	Significant?	Summary	95% CI of diff
shCon&Con OE vs shStau1&Con OE	-24.52	7.868	Yes	**	-40.74 to -8.311
shCon&Con OE vs shCon&Klf4 OE	14.21	4.558	No	ns	-2.007 to 30.42
shCon&Con OE vs shStau1&Klf4 OE	-14.29	5.293	Yes	*	-28.33 to -0.2447
shStau1&Con OE vs shCon&Klf4 OE	38.73	12.43	Yes	***	22.52 to 54.94
shStau1&Con OE vs shStau1&Klf4 OE	10.24	3.793	No	ns	-3.803 to 24.28
shCon&Klf4 OE vs shStau1&Klf4 OE	-28.49	10.56	Yes	***	-42.53 to -14.45

Fig. S11B

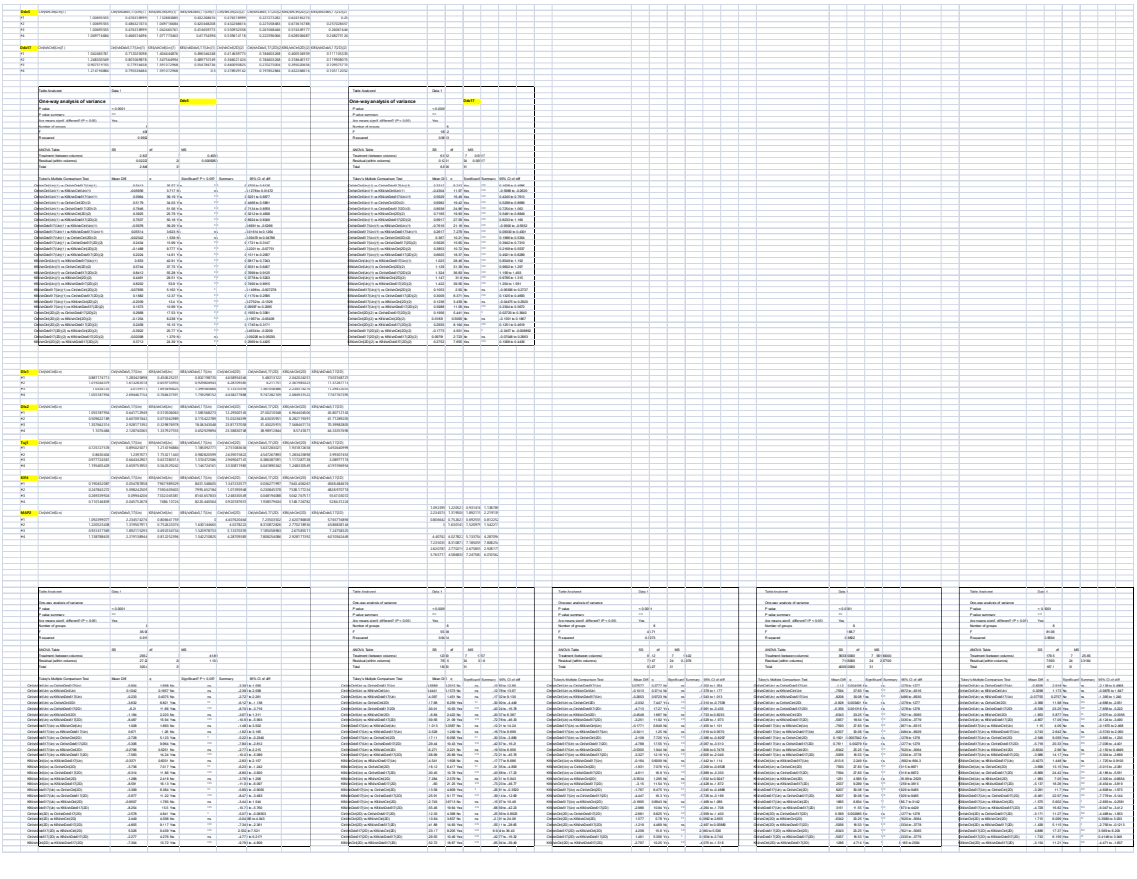


Fig. S12A

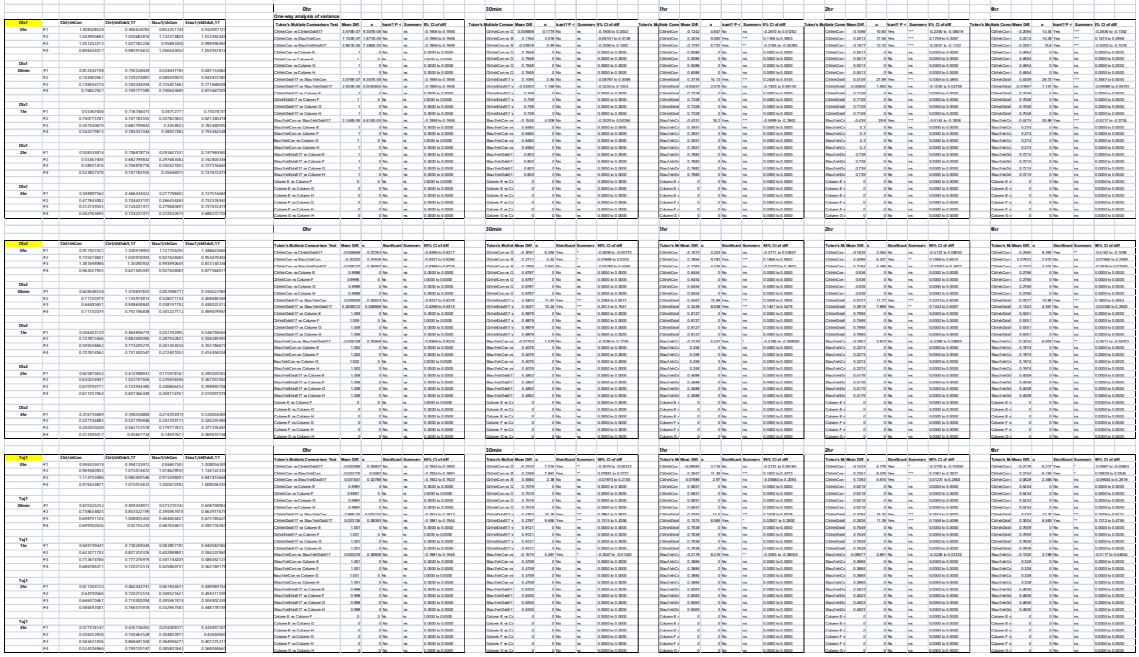
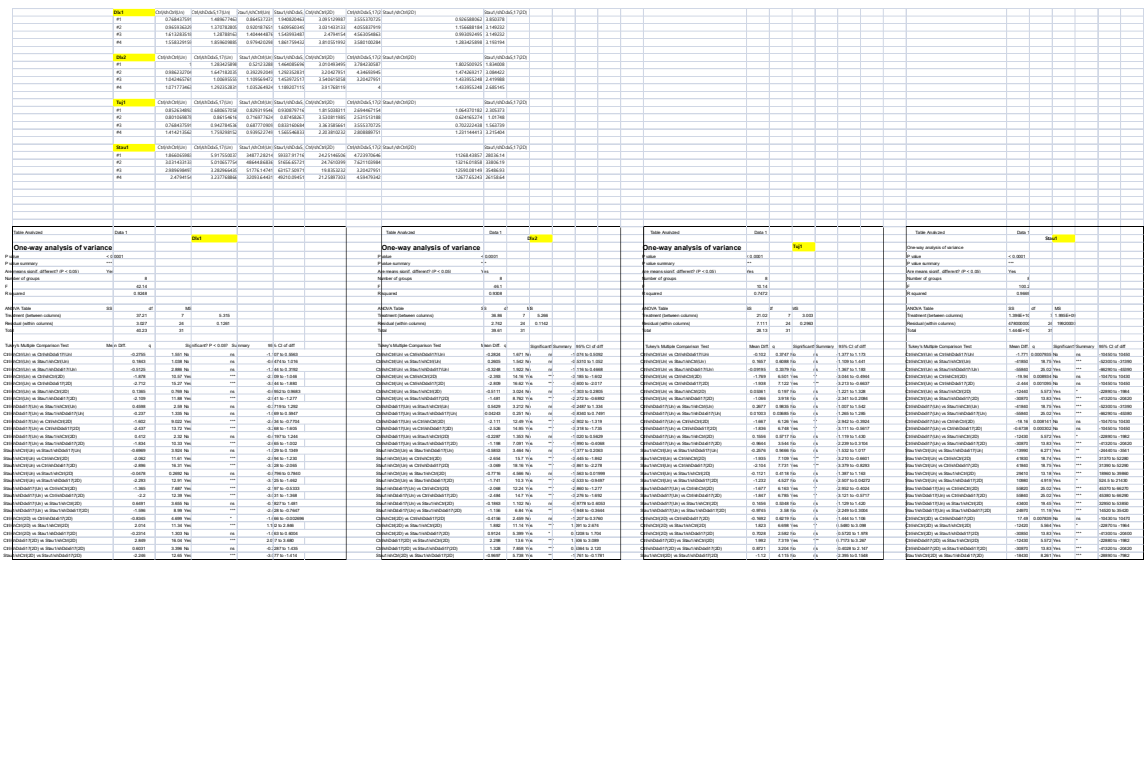


Fig. S12B



Supplementary References

1. Sugimoto, Y. *et al.* hiCLIP reveals the in vivo atlas of mRNA secondary structures recognized by Staufen 1. *Nature* **519**, 491-494 (2015).
2. Ricci, E.P. *et al.* Staufen1 senses overall transcript secondary structure to regulate translation. *Nat. Struct. Mol. Biol.* **21**, 26-35 (2014).