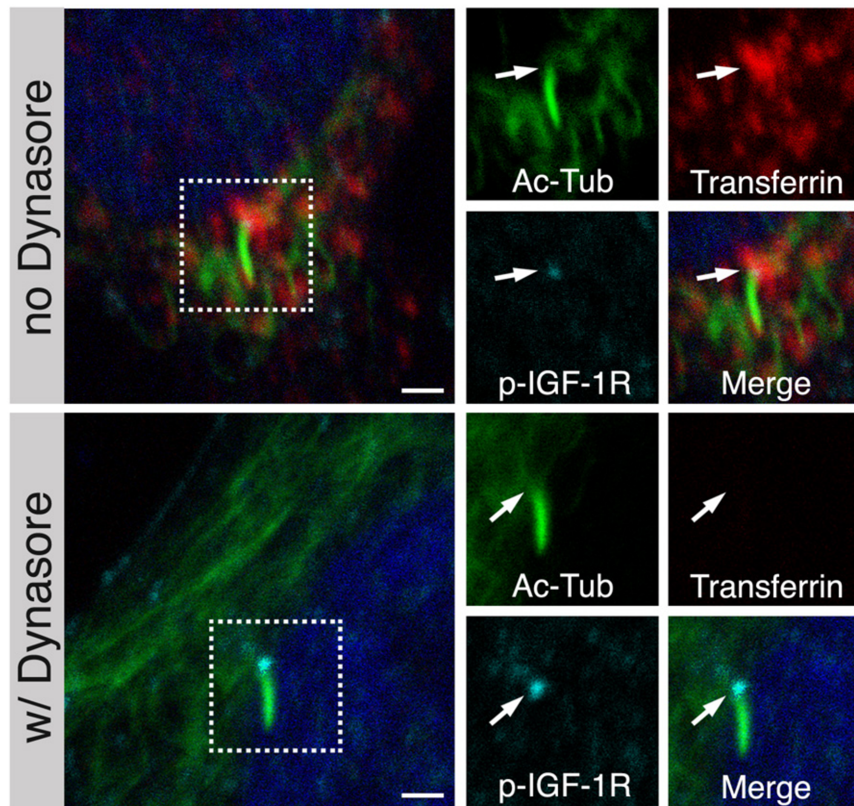
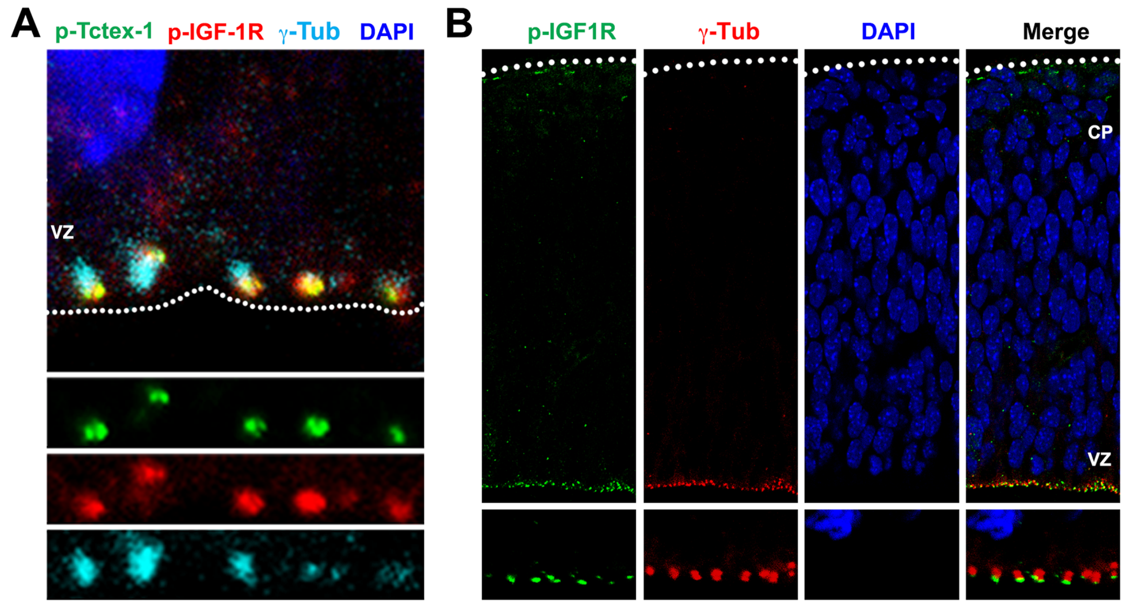
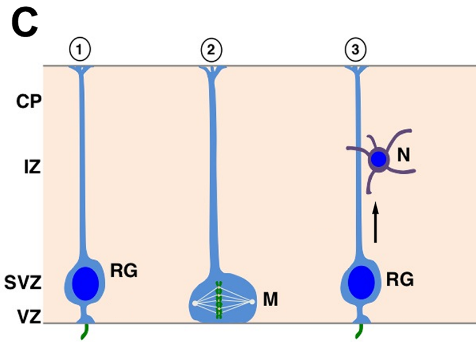
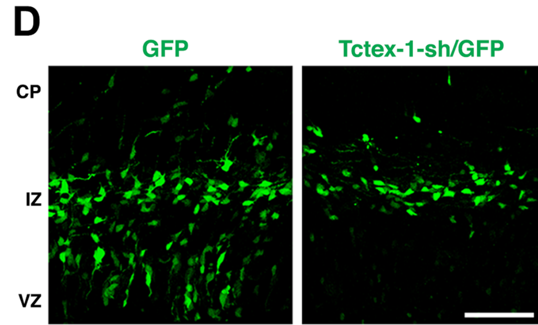
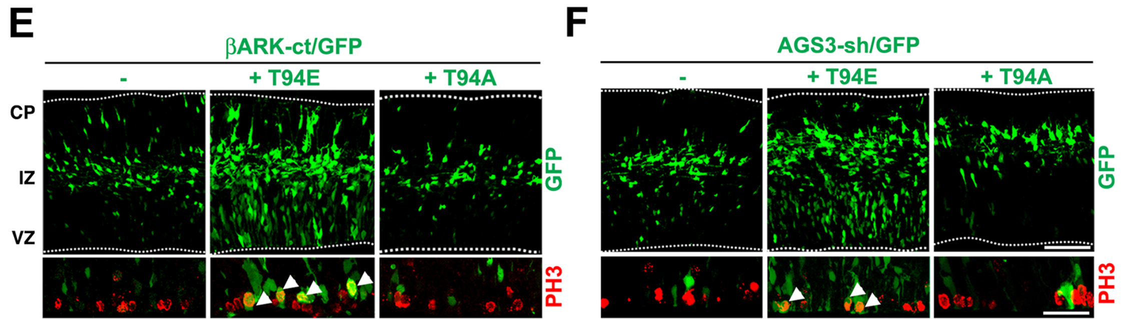


Fig. S1 (related to Fig. 1): RPE-1 cells were starved for 48 hr, and then treated with dynasore (100 μM, Sigma) for 2 hr before adding IGF-1 and Alexa-594 conjugated transferrin (6 μg/mL Invitrogen) for 2 additional hours. Top: In control cells (no dynasore), a subset of incorporated transferrin (red) was distributed to endosomes near the ciliary base, as previously reported (Kim et al., 2010). Bottom: Dynasore treatment effectively blocked the endocytosis of transferrin without affecting the ciliary base distribution of phospho-IGF-1R (cyan, arrows).


A
p-Tctex-1 p-IGF-1R γ-Tub DAPI
VZ
B
p-IGF1R
γ-Tub
DAPI
Merge
CP
VZ


C
1
2
3
CP
IZ
SVZ
VZ
RG
M
N
RG


D
GFP
Tctex-1-sh/GFP
CP
IZ
VZ


E
βARK-ct/GFP
-
+ T94E
+ T94A
CP
IZ
VZ
GFP
PH3
F
AGS3-sh/GFP
-
+ T94E
+ T94A
GFP
PH3

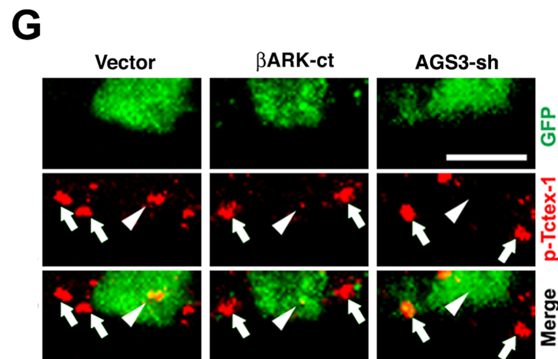

G
Vector
βARK-ct
AGS3-sh
GFP
p-Tctex-1
Merge

Fig. S2 (related to Fig. 5): (A) Confocal images of the ventricle border of a cortical slice co-labeled with phospho(T94)Tctex-1 (green), phospho-IGF-1R (red), and γ-Tub (cyan). (B) Representative confocal image of E13 cortical slice labeled with phospho-IGF-1R (green), γ-Tub (red), and DAPI (blue). The zoom-in images of the ventricle borders are also shown (bottom panels). Activated IGF-1R was especially concentrated near the basal bodies of almost all RG apical endfeet. (C) Schematic diagram of the radially elongated RG, mitotic cells (M) at ventricular border and multipolar post-mitotic neurons (N) at IZ. CP: cortical plate. (D) Cortical slices transfected with GFP or Tctex-1-sh/GFP. (E) Representative images transfected with βARK-ct alone or together with T94E, or T94A Tctex-1 (top); arrowheads point to P-H3-labeled, mitotic GFP-positive cells at the VZ (bottom). (F) Cortical slices transfected with AGS3-sh alone or together with T94E, or T94A Tctex-1 (top); P-H3-labeled, mitotic GFP-positive cells at the VZ are marked by arrowheads (bottom). (G) Representative images of the phospho(T94)Tctex-1 immunolabeling in the VZ of the cortical slices 24 hr after transfection of indicated plasmid. Arrowheads and arrows point to GFP-positive transfected cells and their neighboring non-transfected cells, respectively. Scale bars: 100 μm (D, top panel in F), 50 μm (bottom panel in F), 5 μm (G).

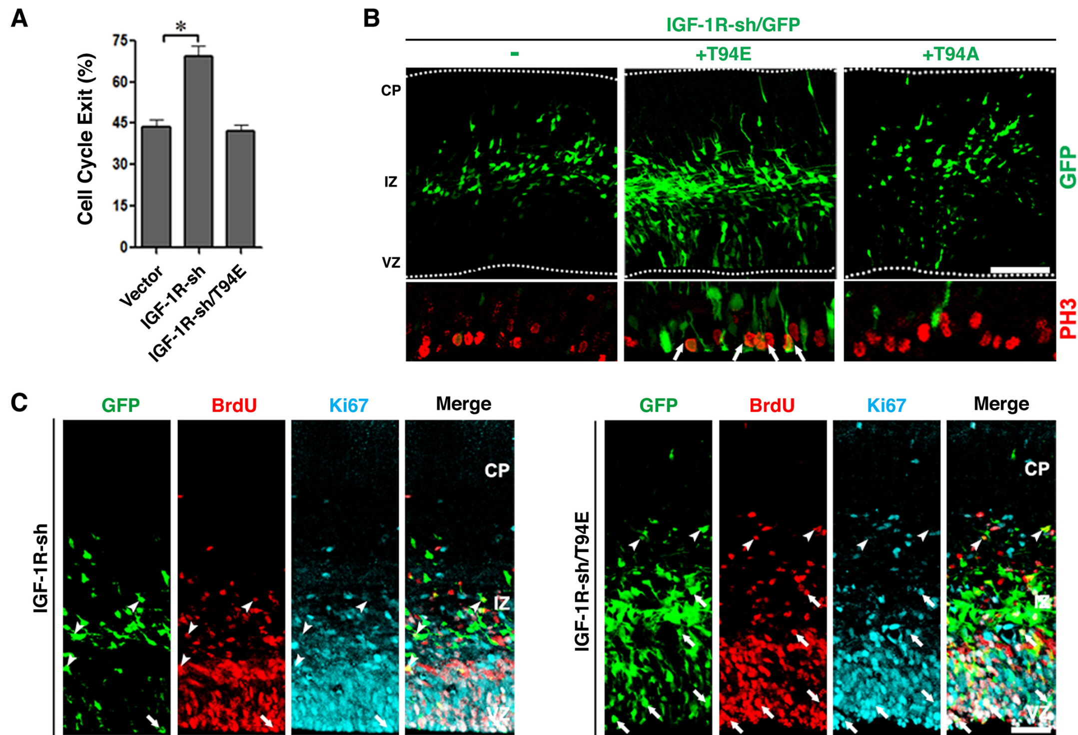


Fig. S3 (related to Fig. 5): (A) Cell cycle exit index. Fractions of GFP^+ /$BrdU^+$ /$Ki67^-$ cells out of total GFP^+ /$BrdU^+$ cells are listed as means ± SEM. Data are presented as mean ± SEM (*p<0.05; *t*- test). (B) Cortical slices transfected with IGF-1R-shRNA/GFP, with (+) or without (-) T94E or T94A plasmid were labeled with PH3 (bottom panels). Arrows point to the GFP^+ transfected cells that are also $PH3^+$. (C) Representative images of cortical slices harvested from animals subjected to the cell cycle exit assay, followed by triple labeling. Arrows point to cells that are GFP^+, $Ki67^+$, and $BrdU^+$. Arrowheads point to GFP^+ /$BrdU^+$ /$Ki67^-$ cells. Scale bars: 100 μm (B), 50 μm (C).

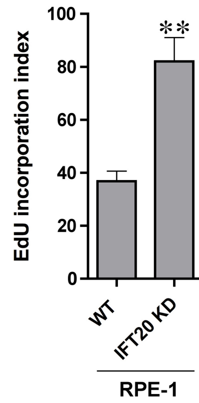


Fig. S4 (related to Fig. 3): Quantification of S phase entry, measured by the EdU incorporation of indicated cells treated with serum after 48 hr starvation. The highest % of IFT20KD EdU^+ cells (n=3) was taken to be 100%. Data are presented as mean ± SEM (**$p<0.01$; one-way ANOVA; n=3 experiments).

References

Kim, J., Lee, J.E., Heynen-Genel, S., Suyama, E., Ono, K., Lee, K., Ideker, T., Aza-Blanc, P., and Gleeson, J.G. (2010). Functional genomic screen for modulators of ciliogenesis and cilium length. Nature *464*, 1048-1051.