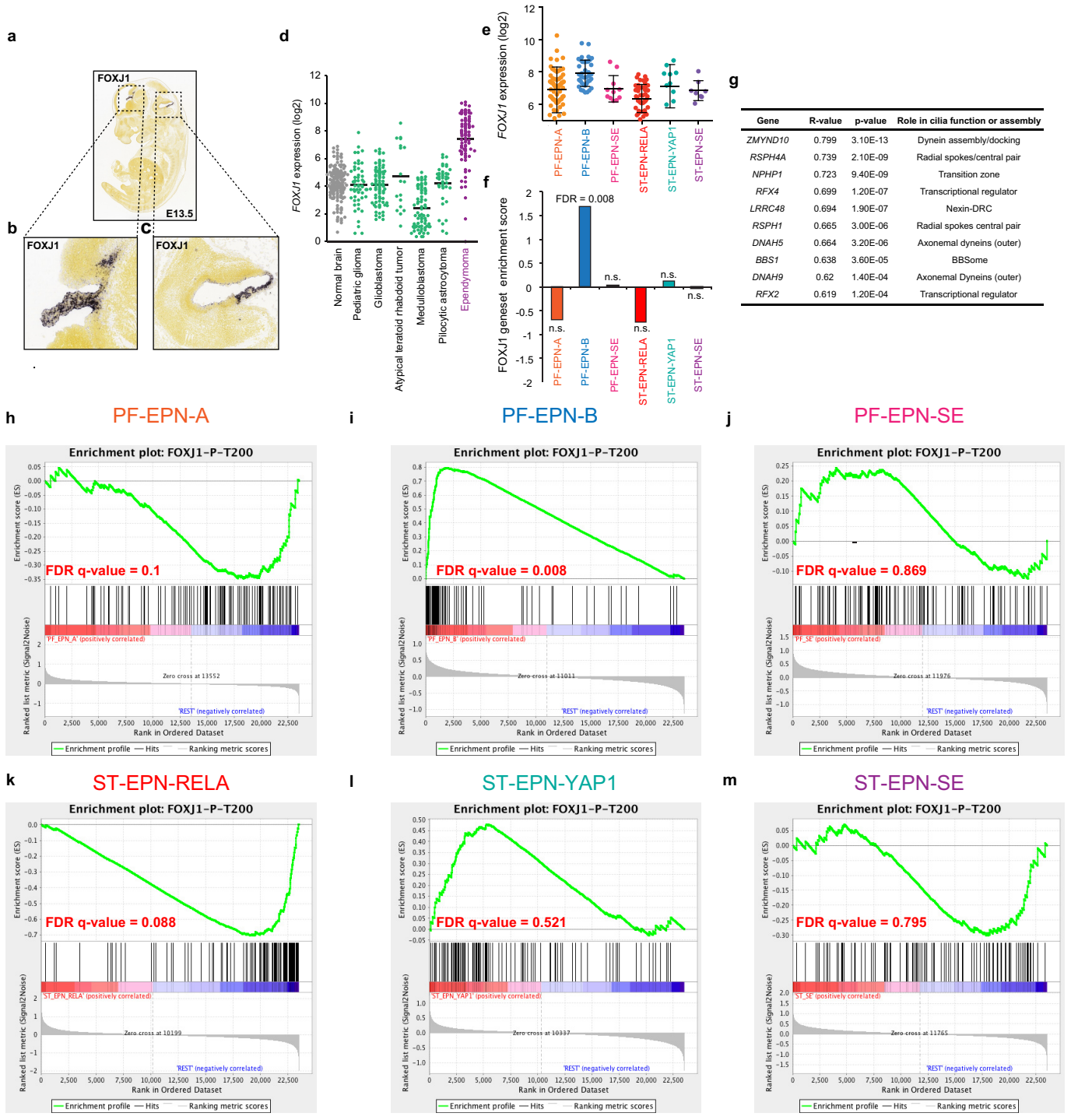

Extended Data Figure 10 | Putative cell lineage programs of origin uncovered by transcription factor mapping. a–c, Immunohistochemical staining of Foxj1 at day 13.5 of mouse embryonic development (E13.5). Staining in discrete regions encompassing the choroid plexus and ependymal layer are shown in the forebrain (**b**) and hindbrain (**c**). **d**, $\log_2$ normalized gene expression of *FOXJ1* in ependymoma ($n = 83$ independent samples) compared to independent sample cohorts of the following tissue types: normal brain ($n = 172$), paediatric glioma ($n = 53$), glioblastoma ($n = 84$), atypical rhabdoid teratoid tumours ($n = 18$), medulloblastoma ($n = 62$) and pilocytic astrocytoma ($n = 41$). Horizontal bar indicates the mean value. **e**, Subgroup-specific gene expression of *FOXJ1* derived from ref. 1 ($n = 209$ independent samples). Error bars indicate s.d. and interquartile range; horizontal bar indicates median. **f**, Gene set enrichment analysis[30] demonstrating significant enrichment of the *FOXJ1* transcriptional program derived from E14.5 mouse embryos specifically in PF-EPN-B tumours ($n = 209$ independent samples). FDR corrected significance evaluated by gene set enrichment analysis. **g**, Significant *FOXJ1* gene-expression correlations with proteins known to regulate cilia assembly and function. *P* values for significant positive or negative correlations have been corrected for multiple testing using the Bonferroni method. **h–m**, *FOXJ1* gene set enrichment plots of PF-EPN-A (**h**), PF-EPN-B (**i**), PF-EPN-SE (**j**), ST-EPN-RELA (**k**), ST-EPN-YAP1 (**l**) and ST-EPN-SE (**m**) ependymomas. FDR-corrected significance evaluated by gene set enrichment analysis, $n = 209$ independent samples.