



Figure S2. A common mouse and human ZFTA-RELA^{FUS1} ependymoma transcriptome: A. Overlap in genes upregulated specifically in two independent cohorts of human ST-EP-ZFTA^{FUS} ependymoma (Refs. 6,8). **B.** Overlap in genes upregulated in four different mouse models of ZFTA-RELA^{FUS1}-driven ependymoma relative to normal brain (Arabzade et al., Ozawa et al., and Zheng et al.,) or mNSCs (Parker et al.,). **C.** Ninety-three genes comprising the ZFTA^{FUS}-sig overlap between the 359 genes upregulated specifically in human ST-EP-ZFTA^{FUS} ependymoma from (A) and at least two mouse models in (B). **D.** Heatmap of RNAseq gene expression in the SJCRRH cohort of the 93 core gene set commonly upregulated in human and mouse ZFTA-RELA^{FUS1}-driven ependymoma in C.