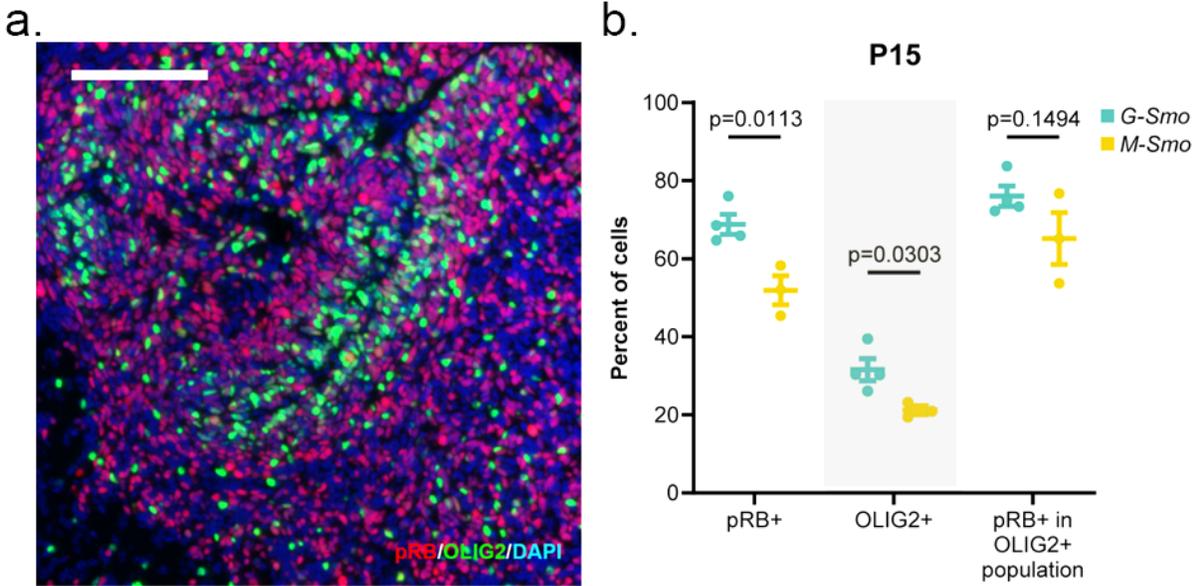# Supplementary Figures for:

Cryptic developmental events determine medulloblastoma radiosensitivity and cellular heterogeneity without altering transcriptomic profile.

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Supplementary Fig. 1 Proliferation is similar in OLIG2+ subsets of *G-Smo* and *M-Smo* tumors. (A) IHC for pRB and OLIG2 in a representative *G-Smo* tumor, including a perivascular region where OLIG2+ cells are more frequent. Scale bar = 100 µm. (B) Quantification of the fractions of pRB+ cells and OLIG2+ cells in *G-Smo* and *M-Smo* tumors, and the fraction of OLIG2+ cells that are pRB+. *G-Smo* tumors show significantly more pRB+ cells and OLIG2+ cells, but the pRB+ fraction of OLIG2+ cells is similar in both genotypes. Points represent values for individual replicates, bars indicate the means and whiskers indicate the SEM.
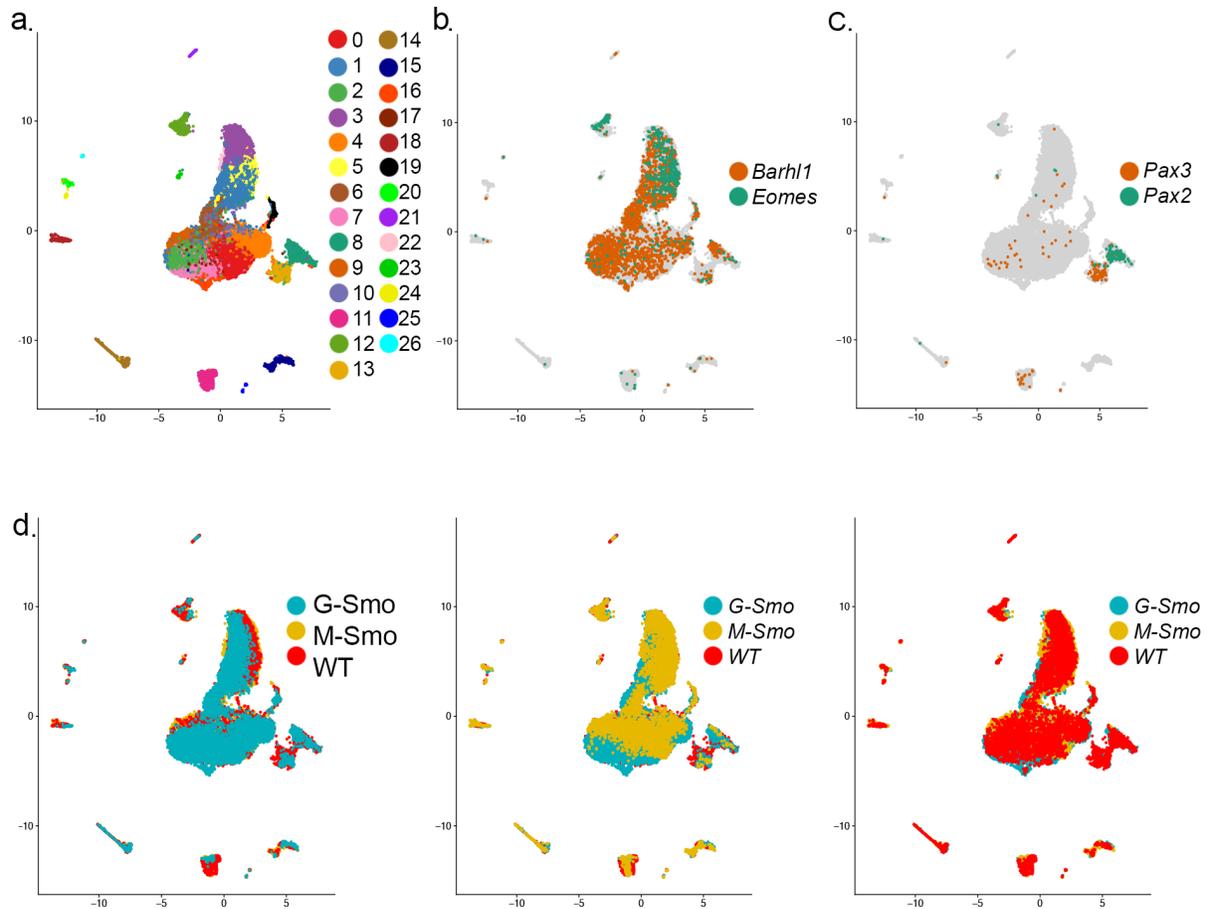
Supplementary Fig. 2 Harmony co-clusters medulloblastoma cells with P7 WT CGNPs and stromal cells from tumors and WT cerebella. (A) UMAP plot of HARMONY analysis of *G-Smo*, *M-Smo* and P7 WT cerebella, color-coded by cluster. (B) Feature plot of CGNP marker *Barhl1* and UBC marker *Eomes*, identifying the *Atoh1* lineage. (C) Feature plot of cerebellar interneuron markers *Pax3* and *Pax2* identifying the interneurons of ventricular zone lineage. (D) UMAPs as in (A), with genotype color-coded. The UMAP is reiterated with each genotype plotted on top in a separate iteration, to prevent over-plotting from obscuring each genotype.