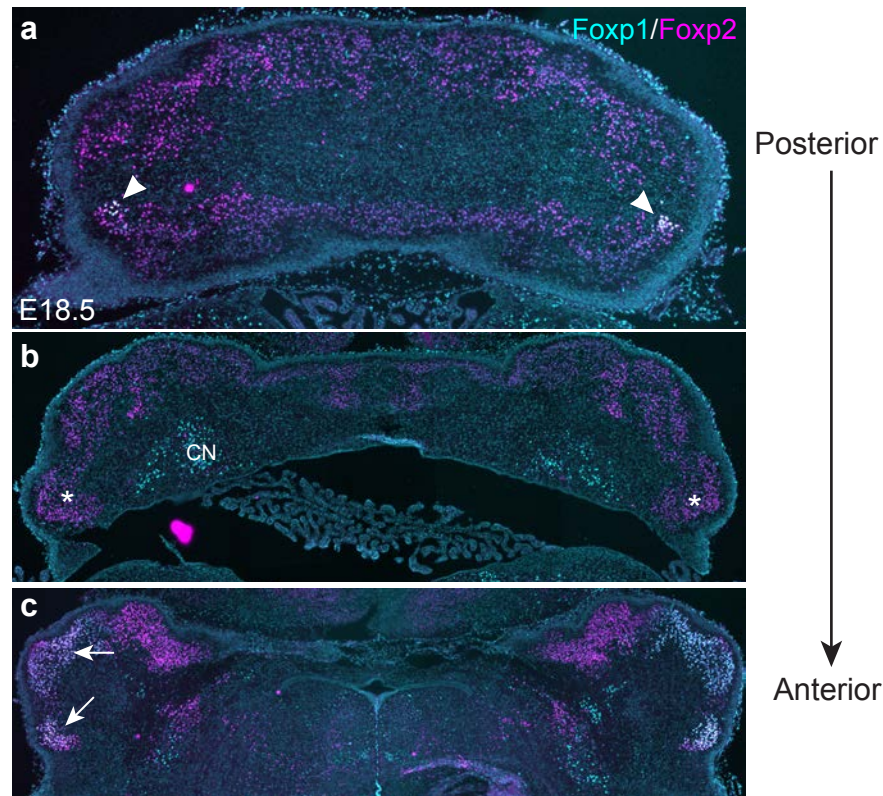
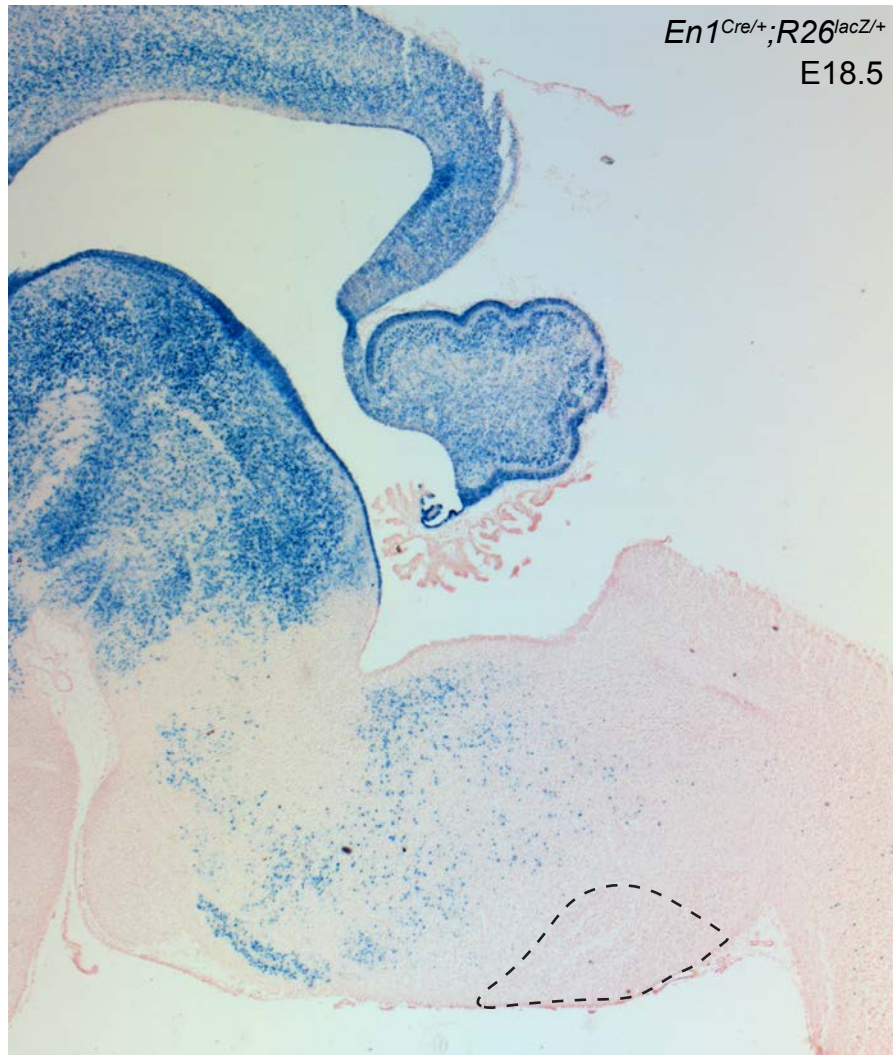

***FOXP* genes regulate Purkinje cell diversity and cerebellar morphogenesis**

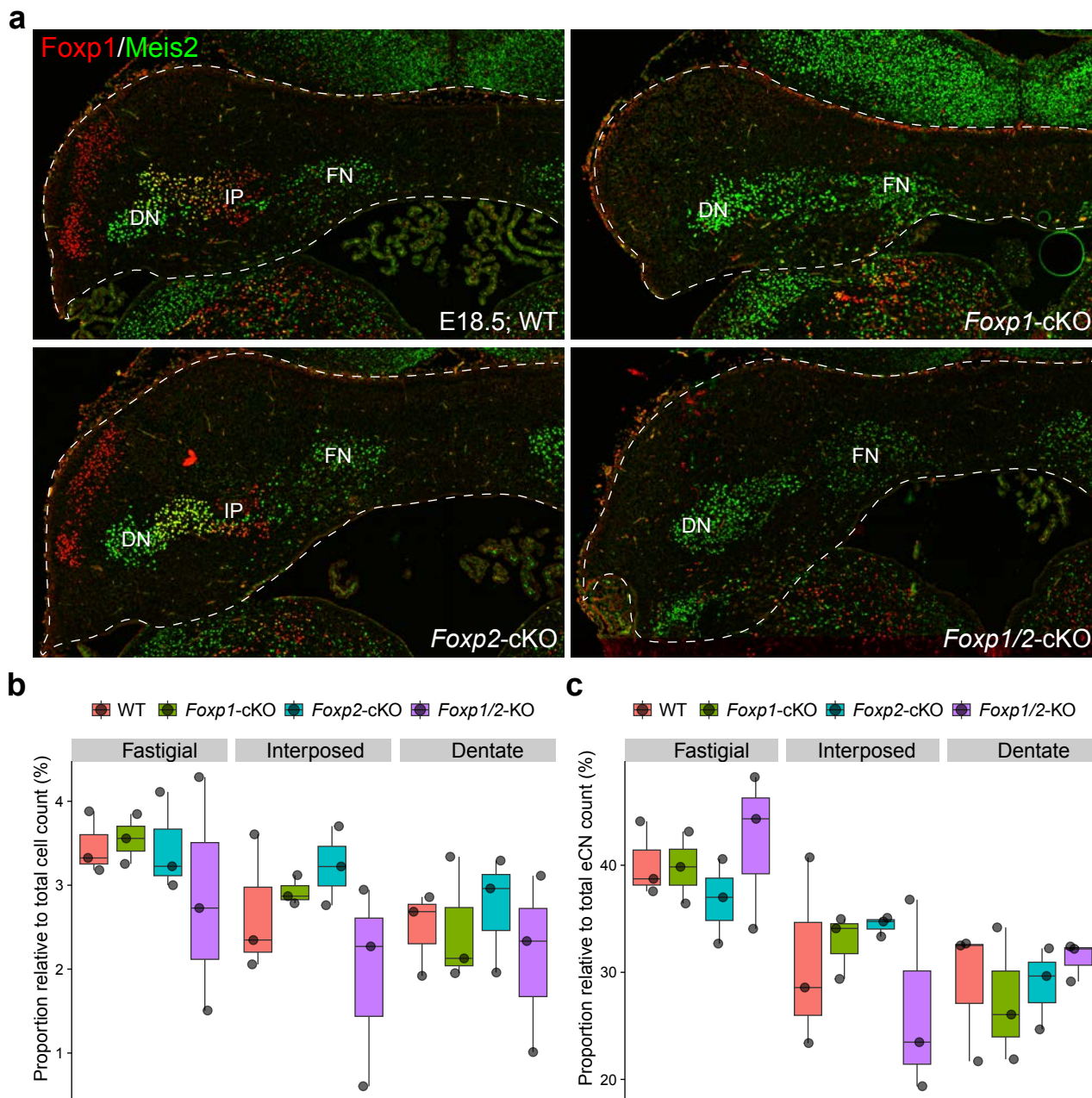
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authors and unedited



Supplementary Figure S1. Foxp1-expressing PCs occupy the lateral-most part of the cerebellum. a-c, Immunofluorescence (IF) for Foxp1 and Foxp2 in three coronal sections of the E18.5 cerebellum corresponding to different AP positions (x = 3 samples). Arrowheads and arrows indicate Foxp1+ PCs in the lateral end of lobe X and the hemisphere, respectively. The asterisk denotes the absence of Foxp1+ PCs in the intervening section.



Supplementary Figure S2. *En1*^{cre} drives recombination in the cerebellum and mid-brain, but not in the inferior olive. X-gal histochemistry in a sagittal section of the E18.5 mouse brain (n = 3 samples). The dashed line demarcates the inferior olive in the medulla. Note that the X-gal+ cells are uniformly distributed in the brain region derived from the mesencephalon and rhombomere 1.



Supplementary Figure S3. Analysis of excitatory cerebellar nuclei in Foxp1/2 mutant cerebella.

a, Immunofluorescence for Meis2 and Foxp1 in coronal sections of E18.5 cerebella ($n = 3$ samples/genotype). **b,c**, Box plots showing the proportion of fastigial, interposed, and dentate nuclei relative to the total cerebellar cell population (**b**) or total excitatory nuclear neurons (**c**) across different genotypes. Individual data points ($n = 3$ per genotype) are overlaid to illustrate variability within each group. Statistical analysis using two-way ANOVA revealed a significant main effect of cell type for both (**b**) ($F(2, 24) = 3.927$, $p = 0.0335$) and (**c**) ($F(2, 24) = 12.624$, $p = 0.000179$), but no significant main effect of genotype ($F(3, 24) = 1.915$, $p = 0.1541$ for **b**; $F(3, 24) = 0.000$, $p = 1.000$ for **c**) or interaction between cell type and genotype ($F(6, 24) = 0.191$, $p = 0.9764$ for **b**; $F(6, 24) = 0.952$, $p = 0.477460$ for **c**).