Common regulatory targets of NFIA, NFIX and NFIB during postnatal cerebellar development.

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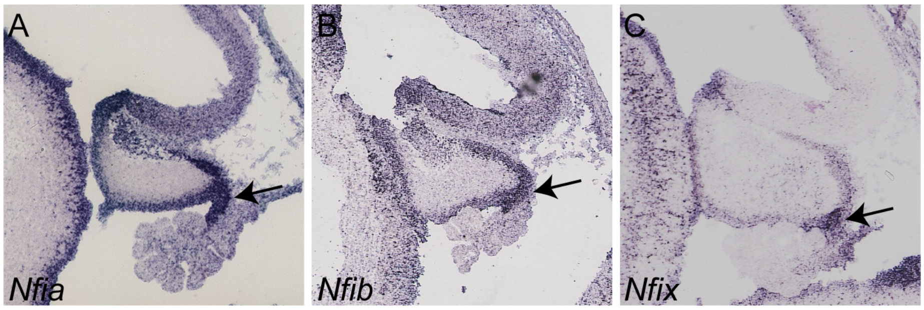
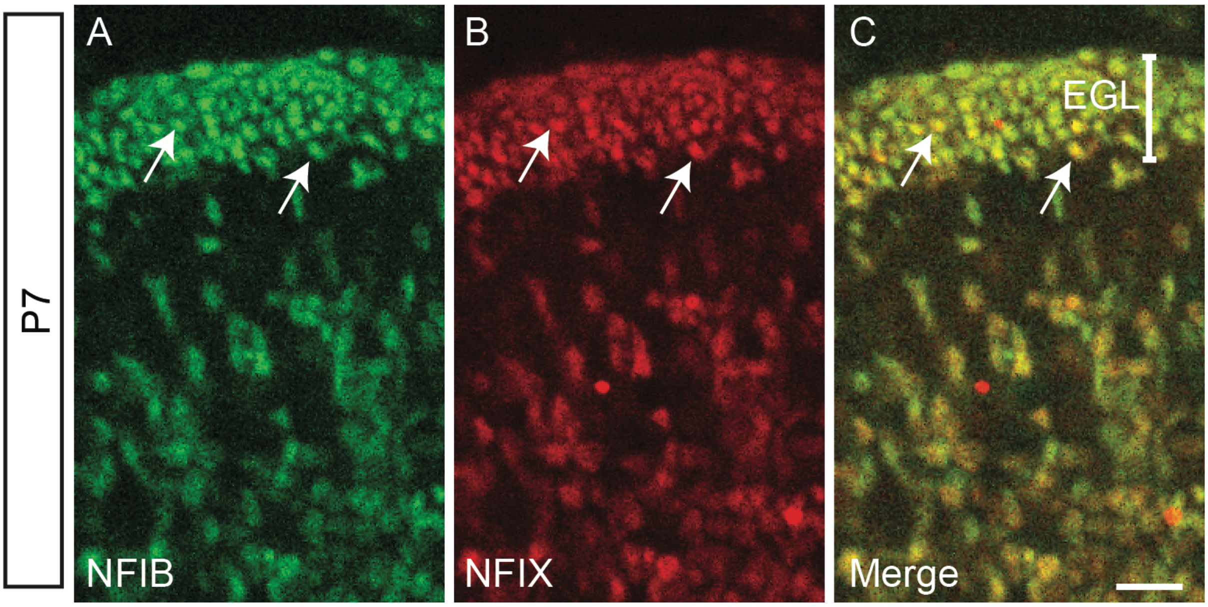


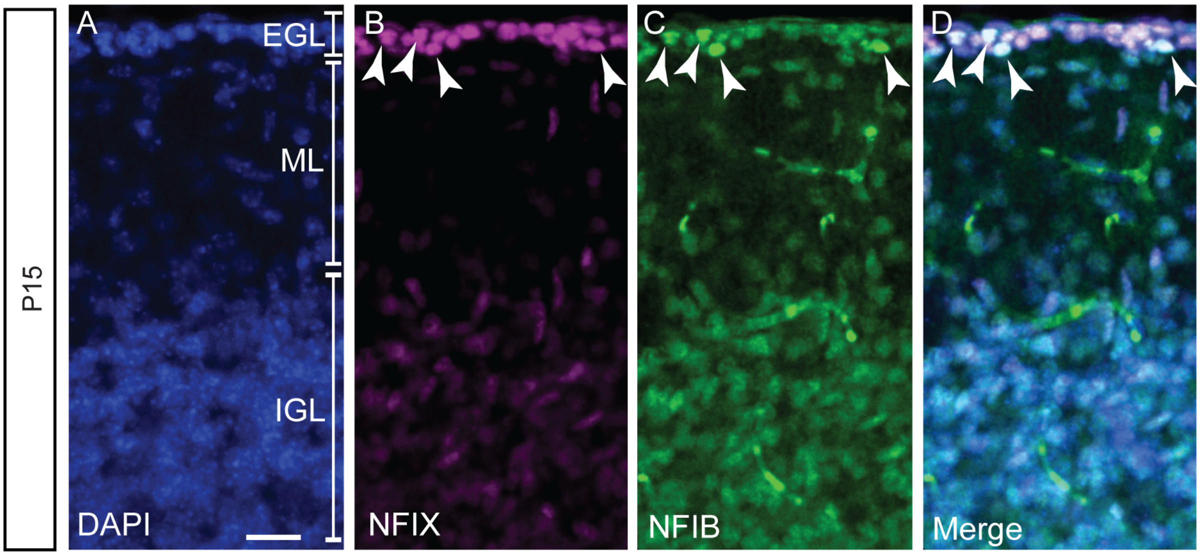
Supplementary Figure 1. Expression of *Nfia, Nfib* and *Nfix* within the embryonic rhombic lip.

Sagittal sections of E14.5 mouse brains, showing the expression of *Nfia* (A), *Nfib* (B) and *Nfix* (C) within the rhombic lip (arrows in A-C). These data are derived from the online repository, GenePaint - https://gp3.mpg.de/.



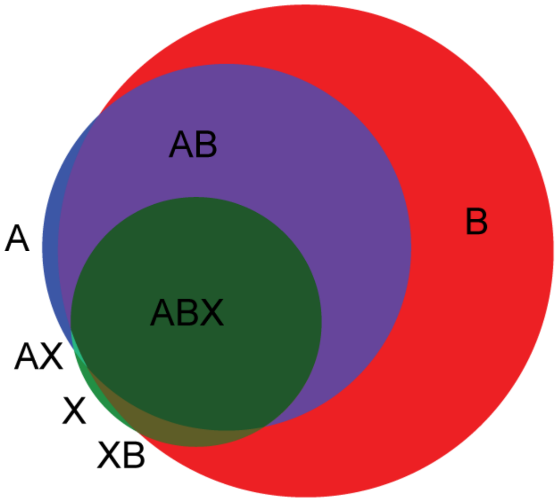
Supplementary Figure 2. NFIX and NFIB are co-expressed by GNPs within the EGL of the P7 mouse cerebellum.

Sagittal P7 cerebellar sections showing the expression of NFIB (A, green) and NFIX (B, red), with the merged channels shown in C. NFIX and NFIB are co-expressed by GNPs within the EGL at this age (arrowsin A-C). EGL = external granule layer. Scale bar (in C): 20 μm.



Supplementary Figure 3. NFIX and NFIB are co-expressed by GNPs within the EGL of the P15 mouse cerebellum.

Sagittal P15 cerebellar sections showing the nuclear marker DAPI (A, blue), NFIX (B, magenta) and NFIB (C, green), with the merged channels shown in D. NFIX and NFIB are co-expressed by GNPs within the EGL at this age (arrowheads in B-D). EGL = external granule layer; ML = molecular layer; IGL = internal granule layer. Scale bar (in A): 20 µm.



A	341
B	9,488
X	45
AB	6,514
AX	42
BX	219
ABX	5,480
Total	22,129

Supplementary Figure 4. Overlap of NFI ChIP-seq peaks in regions of accessible chromatin.

Venn diagram revealing the overlap in common binding events in regions of accessible chromatin in our NFIA-, NFIB- and NFIX-ChIPseq datasets. The Table to the right details the number of unique and shared events from the total of 22,129 sites with at least one NFI binding event associated with it.