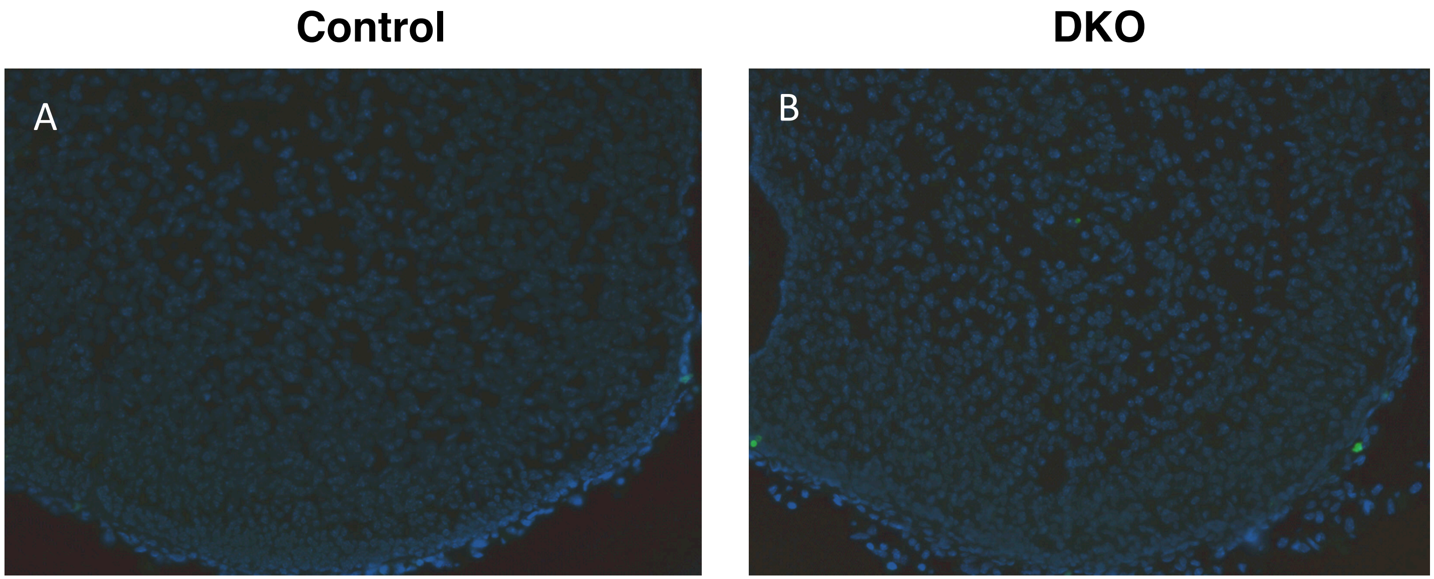
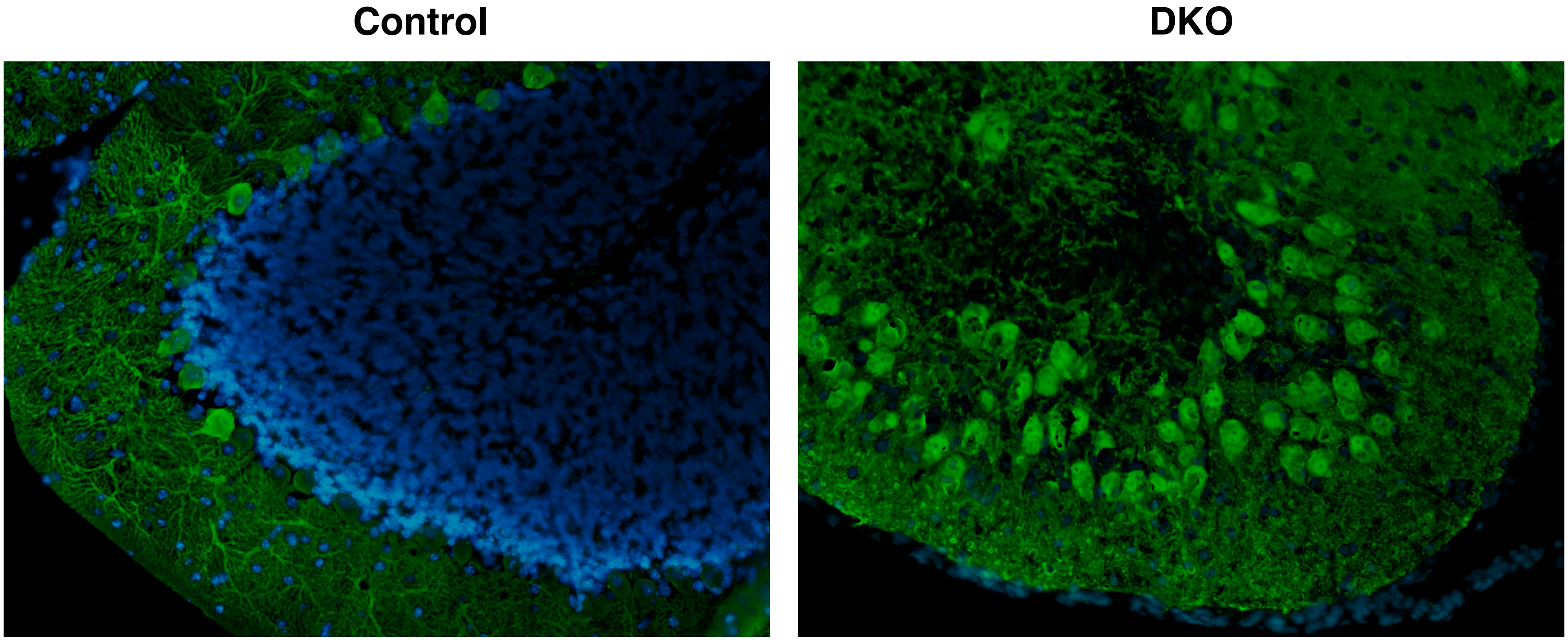

Control

DKO

Legend: TUNEL staining of E17.5 cerebellum. DAPI (Blue), TUNEL (green).

Figure S1
Wey, et al.

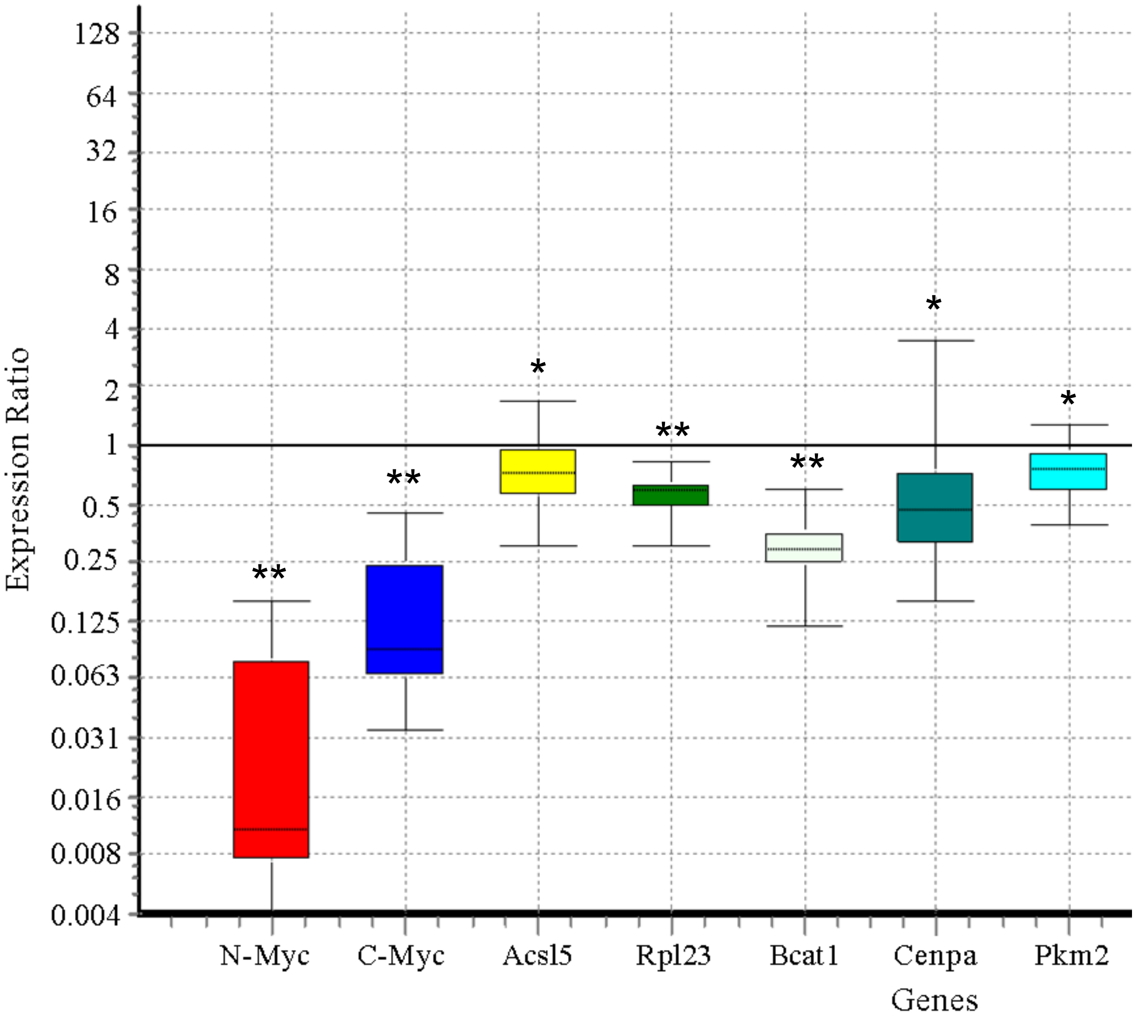


Control

DKO

Legend: BTUJ (green) staining of control and DKO mature cerebellum. Both sections were stained with DAPI (Blue), only apparent in the DKO as a putative residual EGL.

Figure S2
Wey, et al.



q RT-PCR validation of downregulated genes in the DKO cerebella. * Indicates samples are statistically significant with a $p < 0.05$, while ** Indicates samples have a $p < 0.005$. Error bars are standard deviations. Mean results are displayed from 3 (DKO) and 4 (control) biological replicates, with control values set to 1.0.

Figure S3
Wey, et al.

Down in all 3 domains

	Forebrain	Midbrain	Cerebellum
1500012F01Rik	1.953545	1.330658	1.799071
2410015N17Rik	1.380956	1.320027	1.608744
2610206B13Rik	1.68608	1.687102	1.681078
2610528E23Rik	1.389473	1.326666	1.320036
2810417H13Rik	1.832888	1.369072	2.944132
Adk	1.652339	1.4379	1.51814
AI838661	1.34915	1.571047	1.650312
Akr1c19	2.58958	2.173496	1.547631
Arbp	1.45569	1.39505	1.414541
Atp6v1d	1.487886	1.354029	1.306473
C77032	1.453379	1.30675	1.431214
Fbxl3a	1.75876	1.573825	1.556751
Ldh1	1.374228	1.361858	1.505528
LOC544988	2.659666	2.932711	1.993356
LOC545007	2.632969	2.267968	2.147624
LOC545013	2.181864	2.174951	1.502957
Mapk8	1.389015	1.352758	1.304919
Picalm	1.914126	1.923121	1.581222
Pkm2	1.998208	1.608084	1.756061
Ptpre	1.517021	1.394027	1.513023
Rcl1	1.411821	1.358058	1.420385
S100a8	1.359795	1.41392	2.362404
Usp29	1.540584	2.214131	1.464458

Up in all 3 domains

	Forebrain	Midbrain	Cerebellum
1700009P17Rik	0.70	0.76	0.69
4933427D14Rik	0.60	0.47	0.73
Atbf1	0.75	0.69	0.69
BC065120	0.61	0.53	0.65
Cap1	0.61	0.57	0.59
Col1a2	0.73	0.68	0.54
Cops8	0.50	0.49	0.48
D14Ertd449e	0.57	0.59	0.49
Esd	0.72	0.62	0.70
H2afj	0.72	0.65	0.72
LOC73072	0.56	0.43	0.60
Mrc1	0.77	0.71	0.52
Ptprt	0.73	0.76	0.76
Rgs5	0.56	0.60	0.57
Wnt5a	0.67	0.76	0.55
Zcchc3	0.70	0.71	0.73
Zfp330	0.67	0.62	0.71

Mean array data (Control/DKO ratio) for annotated genes with expression changes in fore and midbrain as well as cerebellum.

Figure S4
Wey, et al.