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Correction to: C3aR signaling and gliosis in response to neurodevelopmental damage in the cerebellum



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Correction to: J Neuroinflammation https://doi.org/10.1186/s12974-019-1530-4

Following publication of the original article [1], the authors noticed missing labels in Fig. 1a. The bar graph contains the labels C3, C2, C1ql2, C1ql1, C1qb, GFAP, and VGF. However, the labels should be C3, C4b, C2, C3aR1, C1ql2, C1ql4, C1ql1, C1qa, C1qb, C1qc, GFAP, USP18, and VGF. The correct version of Fig. 1a is published in this Erratum.

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Published online: 23 January 2020

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 Young KG, Yan, K, Picketts DJ. C3aR signaling and gliosis in response to neurodevelopmental damage in the cerebellum. J Neuroinflammation. 2019;16:135. https://doi.org/10.1186/s12974-019-1530-4.

The original article can be found online at https://doi.org/10.1186/s12974-019-1530-4

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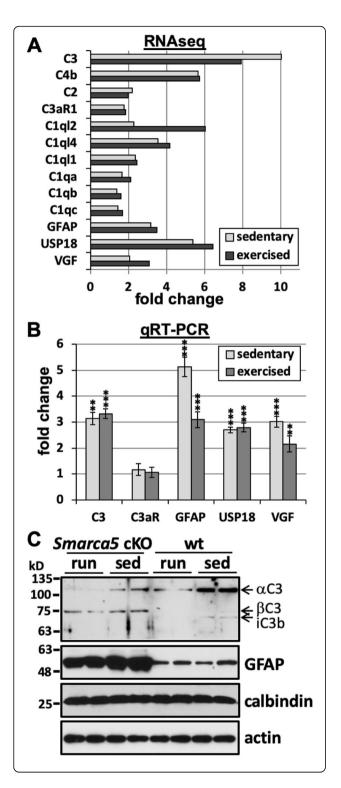


Fig. 1 Altered C3 complement protein expression in the Smarca5 cKO cerebellum of exercised and sedentary mice. Increases in mRNA transcripts coding for complement, complement-related proteins, and inflammation-related proteins in the Smarca5 cKO cerebellum, as indicated by RNAseq analysis (a). Fold changes are shown for the Smarca5 cKO groups (sedentary or exercised) relative to corresponding wild-type groups. qRT-PCR analysis confirmed the increases in C3, GFAP, USP18, and VGF (b), though the magnitudes of these increases varied from the RNAseq data set. Shown are the fold changes in the Smarca5 cKO cerebellum relative to wild-type littermates (n = 3 in each of the four groups of wild-type exercised (run) or sedentary (sed), and mutant exercised or sedentary animals; differences relative to wild-type littermates are noted with **p < 0.005 and ***p < 0.001). No increase was observed for the C3a receptor, C3aR. Protein analysis demonstrated a clear increase in GFAP expression in *Smarca5* cKO cerebellum samples (c). C3 protein expression was also altered in the Smarca5 cKO cerebellum. The C3a chain was less prominent relative to the C3β chain in Smarca5 cKO cerebellum samples compared to wild-type samples. Blotting results are representative of similar results from four mice/group