CORRECTION



Correction: Inflammation and neutrophil extracellular traps in cerebral cavernous malformation

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Correction to:

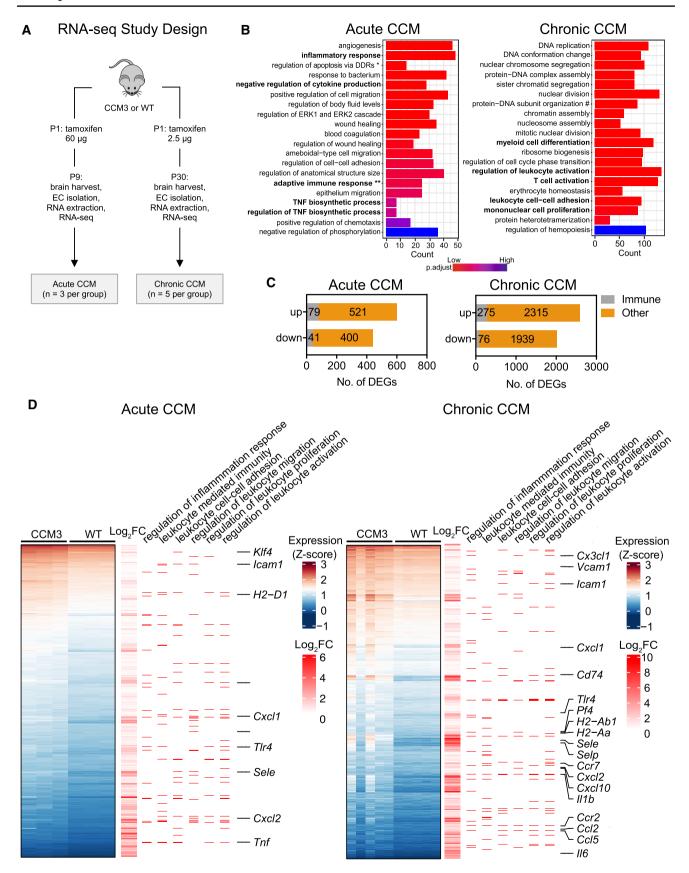
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√Fig. 1 RNA-Seq analysis showed increased expression of inflammation-related genes in brain microvascular endothelial cells from Ccm3iECKO mice (CCM3) in acute and chronic CCM. A Schematic diagram of the experimental design of the transcriptomic study in acute and chronic CCM, comparing CCM3 mice and wild-type (WT) mice (n=3 per group in acute CCM, n=5 in chronic CCM). **B** RNA-Seq gene expression analysis of up-regulated genes showing the top 20 most enriched gene ontology (GO) terms in acute (left panel) and chronic (right panel) CCM. Immune-related GO terms are given in bold. *Regulation of extrinsic apoptotic signaling pathway via death domain receptors, **adaptive immune responses based on somatic recombination of immune receptors built from immunoglobulin superfamily domains, # protein-DNA complex subunit organisation. C Bar plots for the numbers of CCM-associated immune genes that were up-regulated or down-regulated (DEGs) in acute (left) and chronic (right) CCM. For definition of immune genes, see Methods. D Heatmap showing the expression levels (Z-score of regularized log (rlog)-transformed counts) of significantly up-regulated DEGs $(p_{adi} < 0.05 \& llog_2 foldchangel > 0.5; blue: low; red: high) in both$ acute (upper panel) and chronic (lower panel) models. The first annotation column to the right indicates differential expression in log₂ fold changes (red: high; white: low). The second to seventh annotation columns indicates the DEGs associated with enriched immune-like GO terms (stated at the top of the figure) from over-representation analysis. Some of the genes labelled after annotation columns were discussed in the text

In the published article Fig. 1 contain error. The correction Fig. 1 is as follow.

The original article has been updated.

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