

CORRECTION

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Correction to: Expansion and activation of distinct central memory T lymphocyte subsets in complex regional pain syndrome

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Following publication of the original article [1], the authors reported an error in Figure 4 as the wrong figure was used. In the incorrect Fig. 4, panels b-i were missing the numerical scale values. The original article has been corrected. The authors would like to apologize for this error.

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1. Russo MA, Fiore NT, van Vreden C, Bailey D, Santarelli DM, McGuire HM, Fazekas de St Groth B, Austin PJ. Expansion and activation of distinct central memory T lymphocyte subsets in complex regional pain syndrome. *J Neuroinflammation*. 2019;16:63 <https://doi.org/10.1186/s12974-019-1449-9>.

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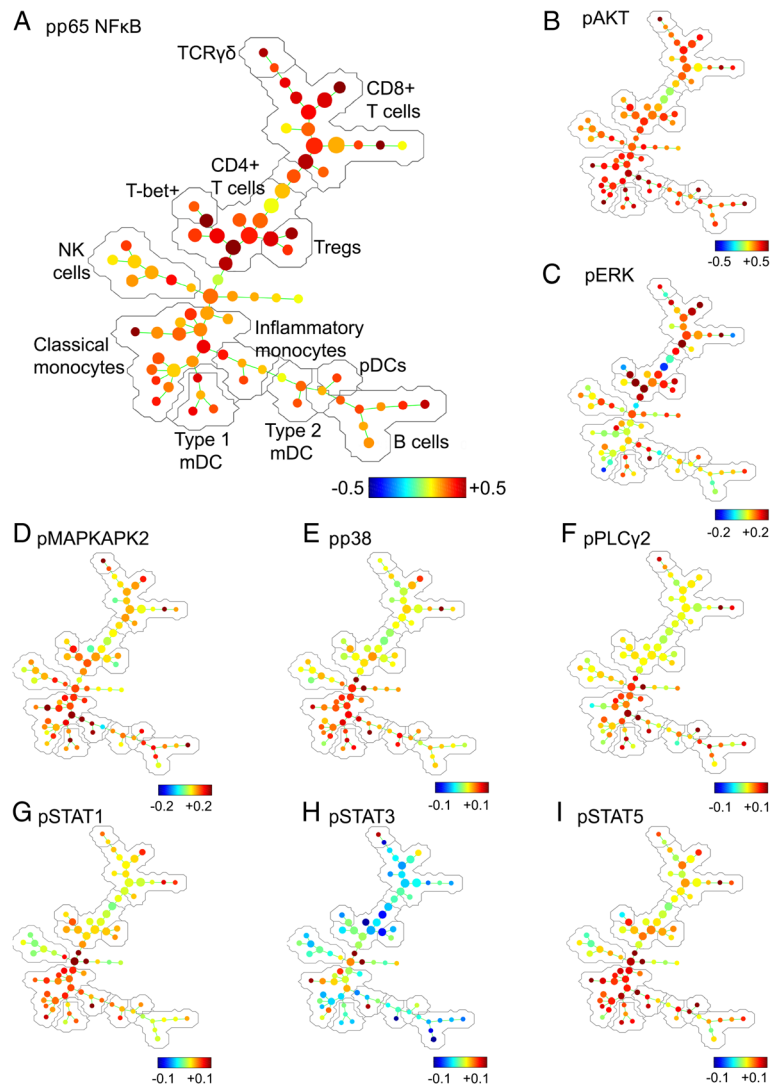


Fig. 4 Spanning tree progression of density-normalised events (SPADE) trees showing evidence of pro-inflammatory activation in distinct lymphocyte and myeloid cell populations in the blood of CRPS participants relative to healthy controls. The SPADE algorithm was run on a downsampled population of single leukocytes from all CRPS and control participants. SPADE trees were generated showing the fold-change between CRPS and control groups in the expression of phosphorylated (activated), **a** p65 NFκB, **b** AKT, **c** ERK, **d** MAPKAPK2, **e** p38, **f** PLCγ2, **g** STAT1, **h** STAT3 and **i** STAT5. The major cell populations labelled in **(a)** are representative of all SPADE trees. Note: colour scales vary for each marker