doi: 10.1111/imm.12430

In Ontondo et al. 2015, errors have been identified in the Supporting Information Figure S1. The correct images of panels A and B are shown below.

We apologize for this error.

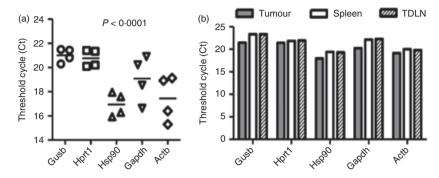


Figure S1. Expression of housekeeping genes.

Total RNA was extracted from tumours, spleens and lymph nodes and used for qRT-PCR analysis of various chemokine genes as described in the materials and methods section. (A) Expression of housekeeping genes in a tumour samples (expressed as Ct values). (B) Expression of housekeeping genes in a tumour sample compared to spleen and TDLN obtained from a tumour-bearing mouse. Gene expression is normalized to HPRT1 expression as an internal control within each tissue. One way ANOVA (Friedman test), was used for statistical analysis.

## Reference

1 Ondondo B, Colbeck E, Jones E et al. A distinct chemokine axis does not account for enrichment of Foxp3<sup>+</sup> CD4<sup>+</sup> T cells in carcinogen-induced fibrosarcomas. Immunology 2015; 145: