

Author Correction: Tryptophan depletion results in tryptophan- to-phenylalanine substitutants


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In addition, we wish to clarify the filters used in the analysis of LSCC cancer proteomes (Fig. 3a and Fig. 3f). As described in the Methods section “Analysis of large-scale proteomics data of human cancer,” for intra-tumour type analysis (Fig. 3f), a filter for maximum number of samples was applied to retain peptides with higher specificity in expression. However, we would like to add that in the tumor-specific analysis (Fig. 3a) this filter was not applied for W>F substitutants both because of their exclusive significant and specific distribution (Extended Data Fig. 3, p.val 1.13E–09) and in order to optimize inclusion of signal for gene expression correlation analysis (Fig. 3c–e). Importantly, both filtering strategies indicated a similar biological conclusion, as reported in the manuscript (Fig. 3a and Fig. 3f). We apologize for this unclarity and thank Gautam Kok, Imre Schene and Sabine Fuchs for bringing it to our attention.



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