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## Correction: Quantitative and Qualitative Perturbations of CD8<sup>+</sup> MAITs in Healthy *Mycobacterium tuberculosis*–Infected Individuals

## **Mikhail Pomaznoy**

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The graphs in Fig. 5F were inadvertently duplicated from Fig. 6 in the article as originally published. The corrected Fig. 5 is shown below. The figure legend was correct as published and is shown below for reference. The figure has been corrected in the online article.

Pomaznoy

Page 2



FIGURE 5. Gene expression profile and *M. tuberculosis*–specific signature of MR1tet<sup>–</sup> MAITs compared with memory CD8 T cells and MR1tet<sup>+</sup> MAITs.

(A) PCA plot illustrating differences between memory CD8 T cells and MR1tet<sup>-</sup> MAITs and between LTBI and TB neg individuals. (**B**, **D**, and **E**) Volcano plots obtained from the DEseq2 analysis showing log2 fold change versus  $-\log 10 p$  value. The differentially expressed genes are represented in black [adjusted *p* value <0.01 (B and E) and p < 0.05 (D), absolute log2 fold change >1 are indicated by dotted lines]. (B) MR1tet<sup>-</sup> cells compared with memory CD8 T cells. (C) Venn-diagram showing overlap between the 226-gene signature identified in Fig. 4B and the signature in Fig. 5B, based on hypergeometric distribution test (considering the 18,315 transcripts detected within memory CD8 T cells as the total number of genes). (D) MR1tet<sup>-</sup> cells comparing individuals with LTBI versus TB neg. (E) Volcano plot comparing MR1tet<sup>-</sup> cells with MR1tet<sup>+</sup> cells. (F) CCR1,

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Pomaznoy

CXCR4, CXCR6, TIGIT, IL-7R, and ABCB1 expression at the mRNA (upper panels: gene expression values in counts normalized by sequencing depth calculated by the DEseq2 package) and protein (lower panels: protein expression as percent frequency of subset) levels in memory CD8 T cells and MR1tet<sup>-</sup> MAITs. Gene expression data were derived from memory CD8 T cells from 17 individuals and MR1tet<sup>-</sup> cells (*n* individuals = 12) using an Illumina sequencing platform. Protein expression data were derived from memory CD8 T cells from 20 individuals and MR1tet<sup>-</sup> cells (*n* individuals = 7) using flow cytometry. Median  $\pm$  interquartile range is shown. Two-tailed Mann–Whitney *U* test.