

TEXT

1. The percentage of differentially expressed genes between B6 and CAST becomes 7% as opposed to 15%.
2. The number of differentially expressed genes between naïve and activated CD4+ T Cells in B6 changes from 2063 to 1314.
3. The number of shared up-regulated genes between B6 and CAST upon activation changes from 225 to 138; and the species-specific B6 genes falls from 96 to 38, and the CAST genes falls from 75 to 59.
4. The legend of Figure 2 has been adjusted so that the numbers are consistent with the newly generated figure.
5. The legend of Figure 3 has been changed in that the number of representative randomly sampled genes has reduced from 70 to 35.

FIGURES

Figure 1B-D and Figures 2,3 and 4 have been regenerated using the MCMC runs generated using the corrected spike-in calculation. In all four figures, the primary change is the scale on the axes. All other results remain as presented in the initial paper.

SUPPLEMENTARY MATERIAL

Figure S3, Figure S4A-F, Figure S5-S6, Figure S7A, Figure S7C-E and Figure S9 have been regenerated using the MCMC runs generated using the corrected spike-in calculation. In all cases, the primary changes are the scale on the axes. All other results remain as presented in the initial papers.

Textual changes:

1. On re-reading the Supplementary Methods, we noted that in the section where we described how the tSNE plots were generated, the following sentence “After variance decomposition, genes where less than 90% of the variability in expression levels across cells was attributed to biological factors (i.e., lowly-variable genes) were removed.” had been erroneously included in the initial submission – for completeness, we have removed this sentence in the revised supplementary material.
2. Throughout, we changed the lower bound for excluding genes for the differential testing from 50 to 1, in line with the change in scale induced by the new spike-in calculations. This has also been altered in Supplementary Figure legends as necessary.

3. Line 218: change 10% to 20% (fraction of differentially expressed genes driven by differences in the quality of the reference genome).
4. Consistent with the change in the figure, we changed the percentage of cells in which downregulated genes were expressed after activation from 18% to 23%; the percentage of cells in which upregulated genes were expressed increased from 36% to 62%. This latter change increase strengthens the conclusions drawn in the original manuscript.
5. Similar to point 4, on lines 240 and 241, percentages change from 5% to 9% and 4% to 6%.
6. Line 275: the number of up-regulated genes in B6 and CAST should read 138 instead of 225. The total number of up-regulated genes across both species (line 276) changes from 1208 to 784. On line 279, the number of B6 and CAST specific response genes falls to 38 and 59 from 96 and 75 respectively. We sampled 27 and 43 genes for visualization.
7. Fig S3E – in the legend changed 10^{-10} to 10^{-5}
8. Fig S5D; Fig 6C-F; Fig S7A numbers or percentages have been updated inline with the revised figure.