

CORRECTION

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Correction to: Repertoire analysis of $\gamma\delta$ T cells in the chicken enables functional annotation of the genomic region revealing highly variable pan-tissue TCR gamma V gene usage as well as identifying public and private repertoires

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Correction to: BMC Genomics 22, 719 (2021)
<https://doi.org/10.1186/s12864-021-08036-9>

Following publication of the original article [1], the authors identified an error in Fig. 3 and 6. In addition one of the affiliations was incorrectly assigned. The correct figures are given hereafter and the affiliation change has been implemented.

gamma V gene usage as well as identifying public and private repertoires. BMC Genomics. 2021;22(1):719. <https://doi.org/10.1186/s12864-021-08036-9>.

All the changes requested are implemented in this correction and the original article [1] has been corrected.

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Reference

1. Dixon R, Preston SG, Dascalu S, Flammer PG, Fiddaman SR, McLoughlin K, et al. Repertoire analysis of $\gamma\delta$ T cells in the chicken enables functional annotation of the genomic region revealing highly variable pan-tissue TCR

The original article can be found online at <https://doi.org/10.1186/s12864-021-08036-9>.

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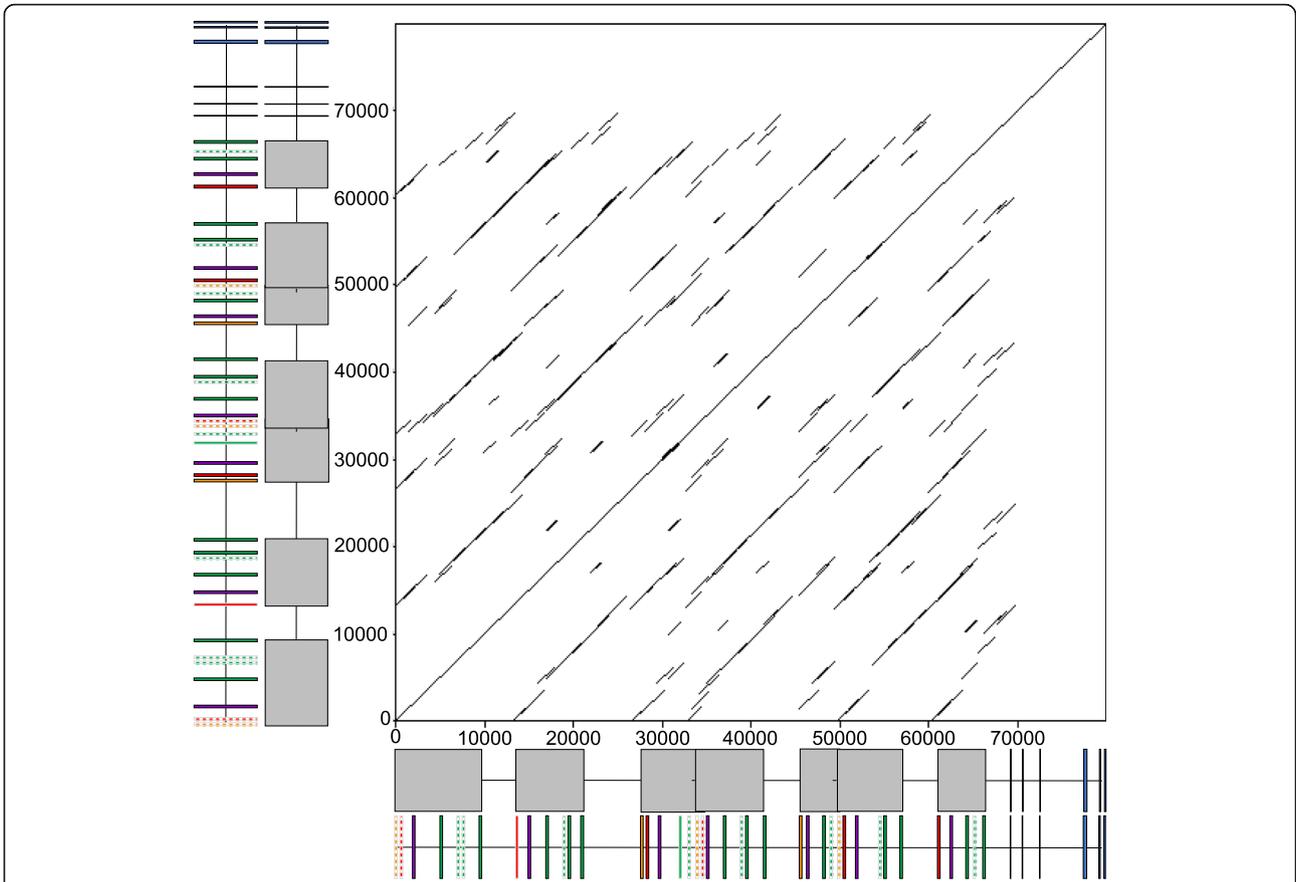


Fig. 3 Dotplot reveals that the Chicken TCR Gamma Locus Evolved via a set of Duplication Events. A comparison of sequence similarity across the TCR gamma locus using a dot plot generated with Dotmatcher, window size of 1000 and threshold of 500. The default EMBOSS matrix was used (with match = + 5 and a mismatch = - 4) and a dot plotted where the value was above the threshold. The X and Y axis include schematic representations of the chicken TCR gamma locus and an indication of potentially duplicated blocks of TRGV genes. Homologous comparison is represented by the diagonal passing through the origin and the parallel diagonal indications represent regions with high similarity hide

