

CORRECTION

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Correction to: Specificity of resistance and geographic patterns of virulence in a vertebrate host-parasite system



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Correction to: BMC Evol Biol

<https://doi.org/10.1186/s12862-019-1406-3>

After publication of the original article [1], the authors have notified us that the incorrect version of Fig. 4 was used. Below you can find the both incorrect and correct versions of the figure.

The original article has been corrected.

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Reference

1. Piecyk et al. (2019) Specificity of resistance and geographic patterns of virulence in a vertebrate host-parasite system (2019) 19:80: <https://doi.org/10.1186/s12862-019-1406-3>.

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Corrected figure

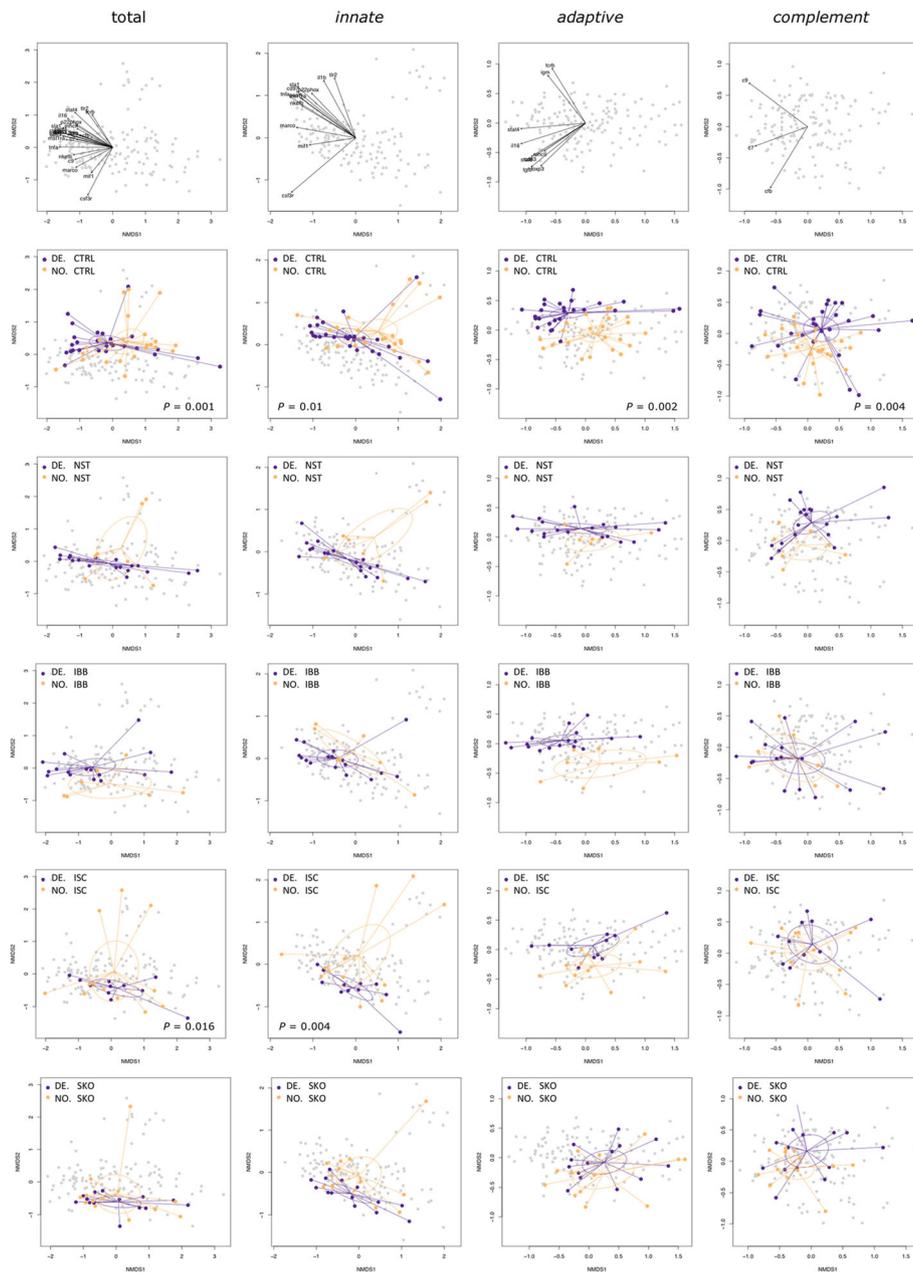


Fig. 4 Multivariate gene expression patterns differ between DE and NO sticklebacks. Non-metric multidimensional scaling (NMDS) plots on Euclidian distances and two dimensions comparing data from NO and DE sticklebacks (*contrast 1*). NMDS were based on log10-transformed calibrated normalized relative quantities (CNRQ values) of all 24 immune genes, twelve genes of innate immunity (*marco, mst1ra, mif, il-1 β , tnfr1, saal1, tlr2, csf3r, p22^{phox}, nkef-b, sla1, cd97*), nine genes of adaptive immunity (*stat4, stat6, igm, cd83, foxp3, tgf- β , il-16, mhcll, tcr- β*), or three genes of the complement system (*cfb, c7, c9*). Each dot represents one individual; colors refer to the host population. Ellipses represent 95% confidence intervals. *P*-values are shown if significant after FDR-correction. The contribution of each gene is shown in the first row. The second row shows data from sham-exposed (CTRL) sticklebacks. The third to sixth row show data from infected individuals. Function `metaMDS()` was used to plot the NMDS; the contribution of each gene was plotted by use of the `envfit()` function (both functions are implemented in R package *vegan* [74])

Incorrect figure

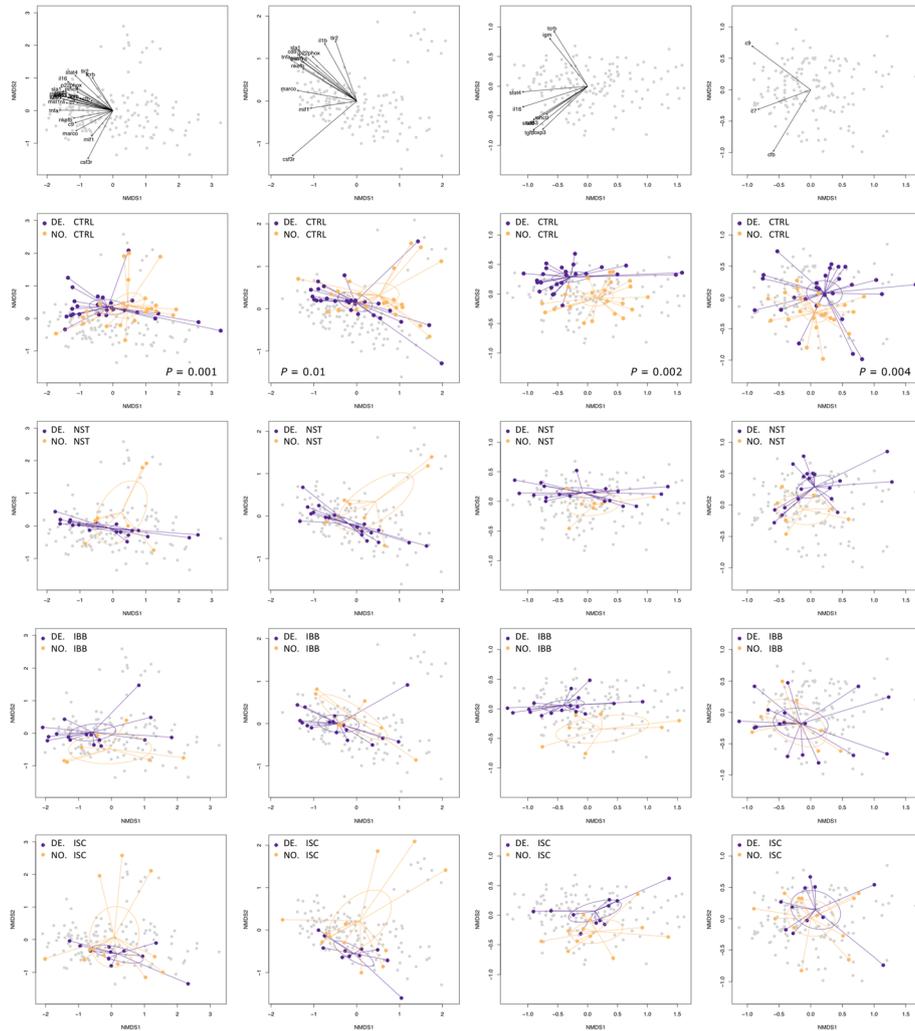


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