## Correction to: Specificity of resistance and geographic patterns of virulence in a

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Correction to: BMC Evol Biol https://doi.org/10.1186/s12862-019-1406-3

vertebrate hostparasite system

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.

Received: 3 April 2019 Accepted: 3 April 2019 Published online: 13 May 2019

## Reference

 Piecyk et al. (2019) Specificity of resistance and geographic patterns of virulence in a vertebrate hostparasite system (2019) 19:80: https://doi.org/10. 1186/s12862-019-1406-3.

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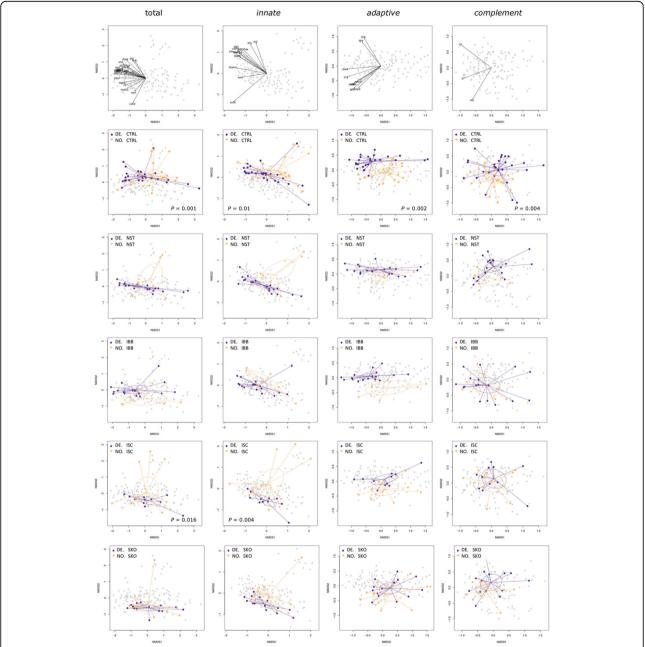


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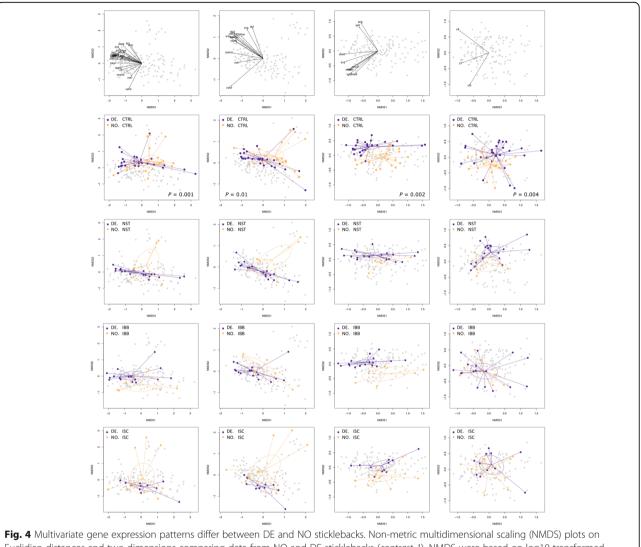
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**Fig. 4** Multivariate gene expression patterns differ between DE and NO sticklebacks. Non-metric multidimensional scaling (NMDS) plots on Euclidian distances and two dimensions comparing data from NO and DE sticklebacks (*contrast 1*). NMDS were based on log10-transformed calibrated normalized relative quantities (CNRQ values) of all 24 immune genes, twelve genes of innate immunity (*marco, mst1ra, mif, il-1β, tnfr1, saal1, tlr2, csf3r, p22<sup>phox</sup>, 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**



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* $\beta$ , tnfr1, *saal1, tlr2, csf3r, p22<sup>phox</sup>, nkef-b, sla1, cd97*), nine genes of adaptive immunity (*stat4, stat6, igm, cd83, foxp3, tgf-* $\beta$ , *il-16, mhcll, tcr-* $\beta$ ), 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])