

ERRATUM

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Erratum to: 'Integrated analysis of the local and systemic changes preceding the development of post-partum cytological endometritis'

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Unfortunately, the original version of this article [1] contained an error. The figure legends did not correspond to the correct figures, the correct version can be seen below.

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1. Foley C, Chapwanya A, Callanan JJ, Whiston R, et al. Integrated analysis of the local and systemic changes preceding the development of post-partum cytological endometritis. *BMC Genomics*. 2015;16:811.

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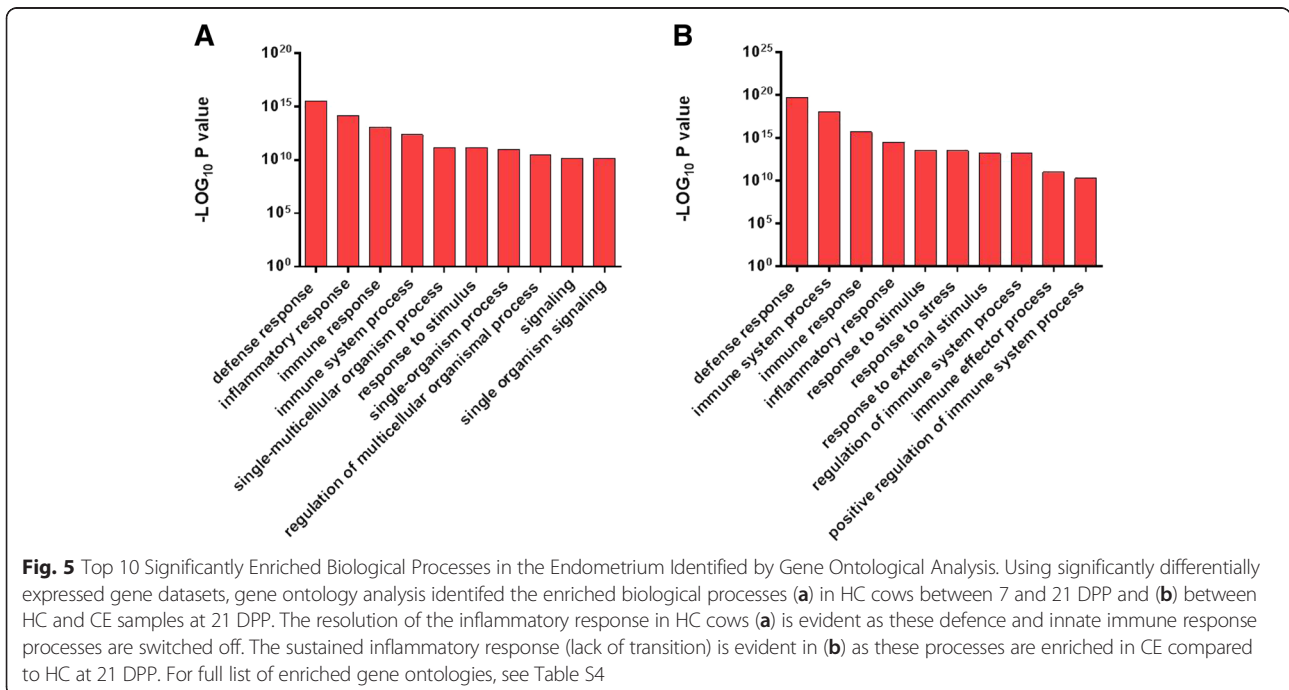
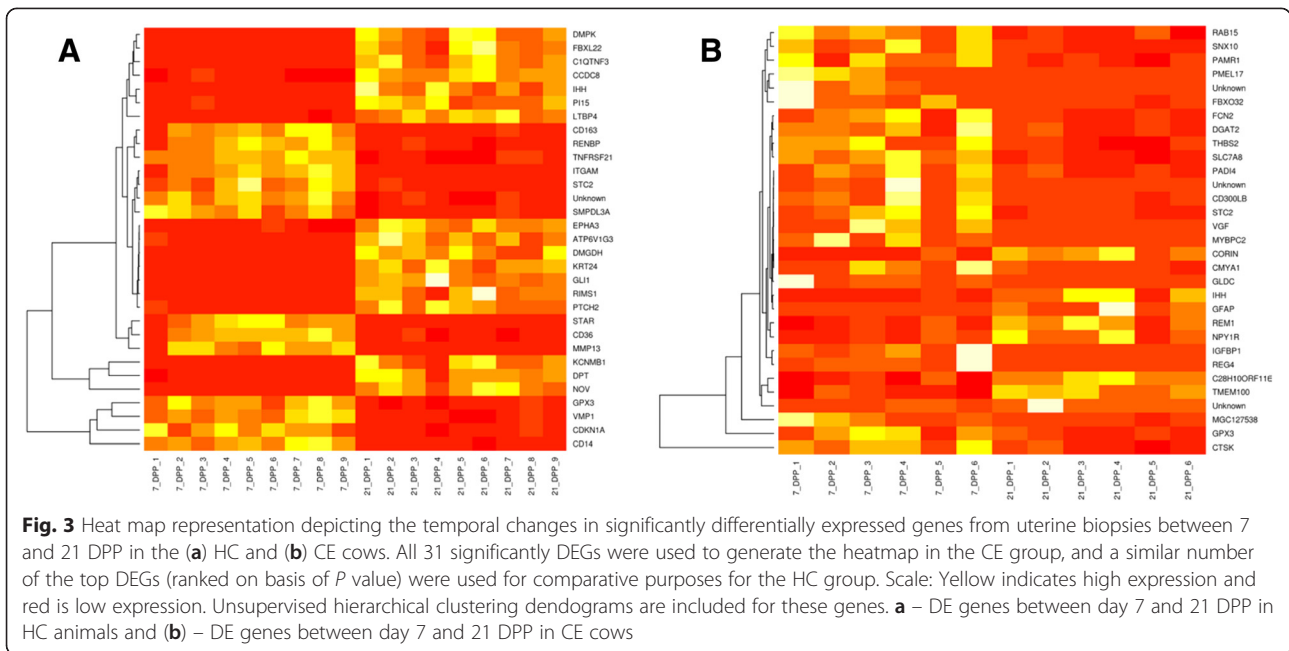
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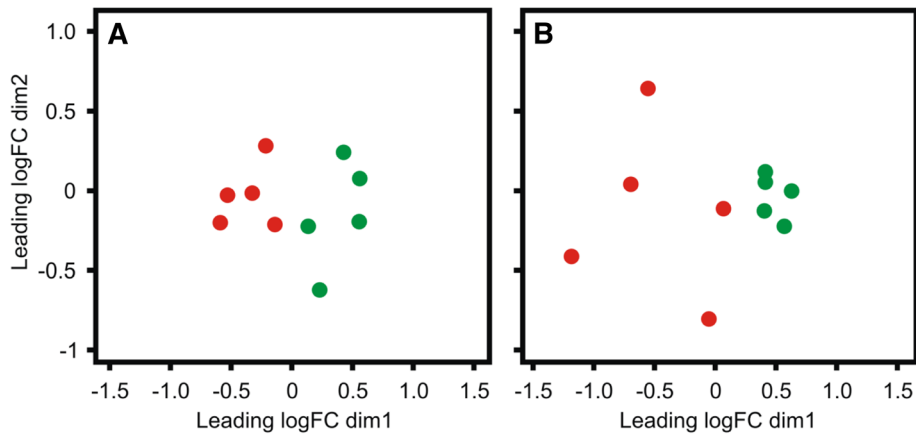


Fig. 6 Multi-Dimensional Scaling (MDS) Plots Generated from Endometrial microRNA-seq Data. **a** MDS-plot shown for HC cows at both 7 (red) and 21 DPP (green). Similarly, **(b)** MDS-plot shown for CE cows at both 7 (red) and 21 DPP (green). Clustering of the D7 and D21 profiles is apparent at both time points for HC and CE cows although tighter clustering of 7 DPP samples for the HC group than for the CE group (B) shows a higher degree of variation between samples at 7 DPP (B, red). Five HC (healthy control) samples at both 7 DPP (D7, red) and corresponding same animal sample at 21 DPP (D21, green) and B) five CE (cytologically endometritic) cows at the same two time points are shown

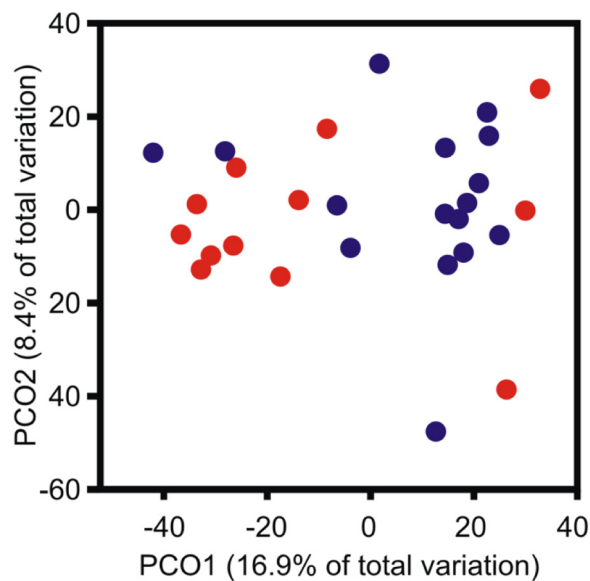


Fig. 7 Principal Coordinates Ordination of Endometrial Bacterial Communities. Bacterial community analysis, performed using culture-independent Terminal Restriction Fragment Length Polymorphism (T-RFLP), shows a significant clustering of samples according to their respective microbial communities. HC and CE cows are shown as blue and red circles, respectively

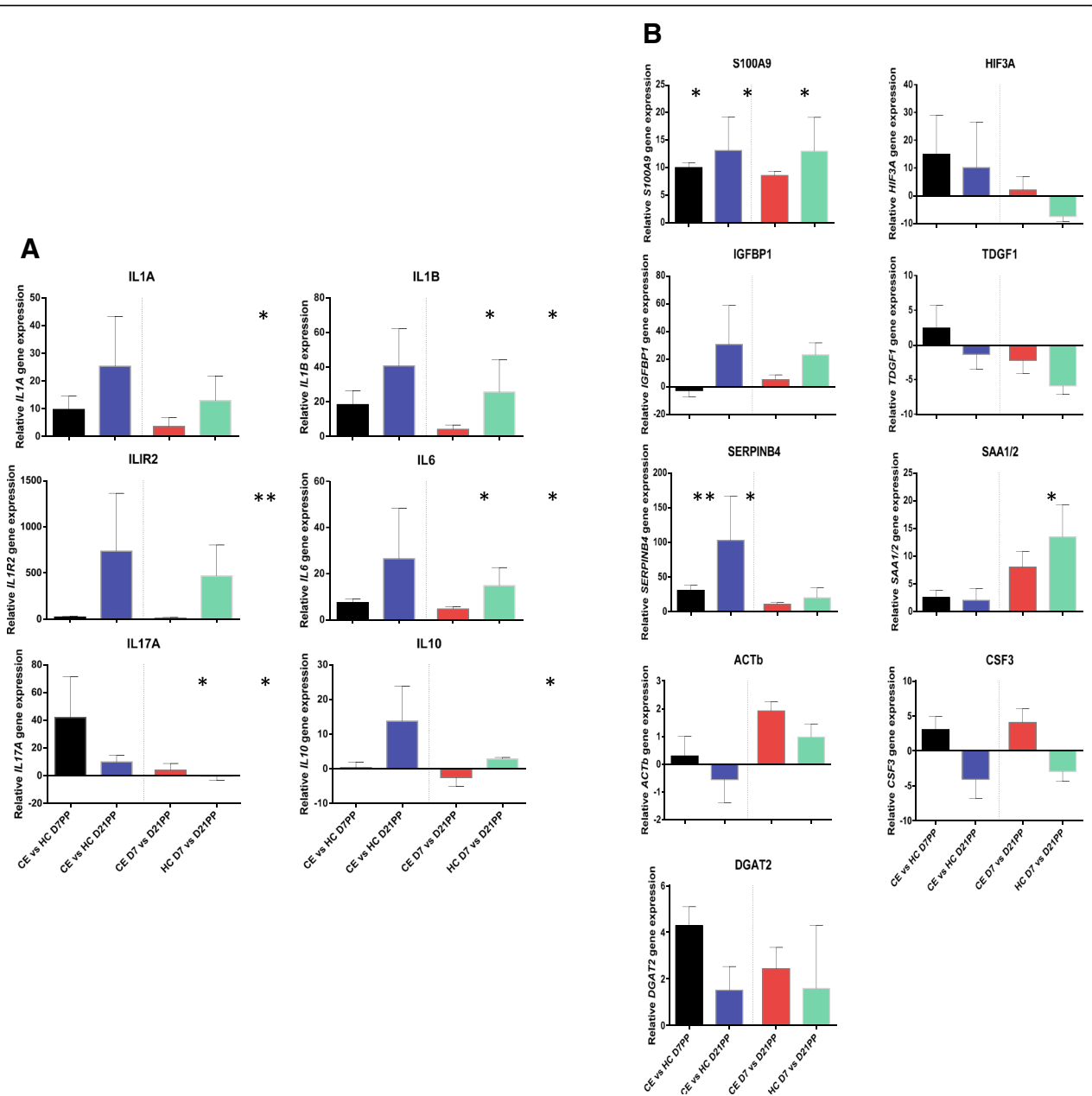


Fig. 8 RT-qPCR validation of gene expression changes detected using mRNA-seq. Confirmation of differentially expressed genes from NGS results using quantitative real-time PCR. Significant changes in gene expression of both (a) pro- and anti-inflammatory cytokines as well as other (b) effector molecules of the immune response confirmed the findings from NGS. Results are colour-coded according to comparison and levels of expression of each gene of interest was normalised to expression levels of *PPIA*; D7PP between SCE and HC cows (black), D21PP between SCE and HC (blue), between D7 and D21PP in SCE (red) and between D7 and D21PP in HC (green). Between and within group comparisons are separated by a dotted line. * $P < 0.05$; ** $P < 0.01$. $n = 5-8$ samples per time point, bars represent mean \pm SEM