Supplementary Figures 1-5

The cervical microbiome of ewe breeds with known divergent fertility following artificial insemination with frozen thawed semen

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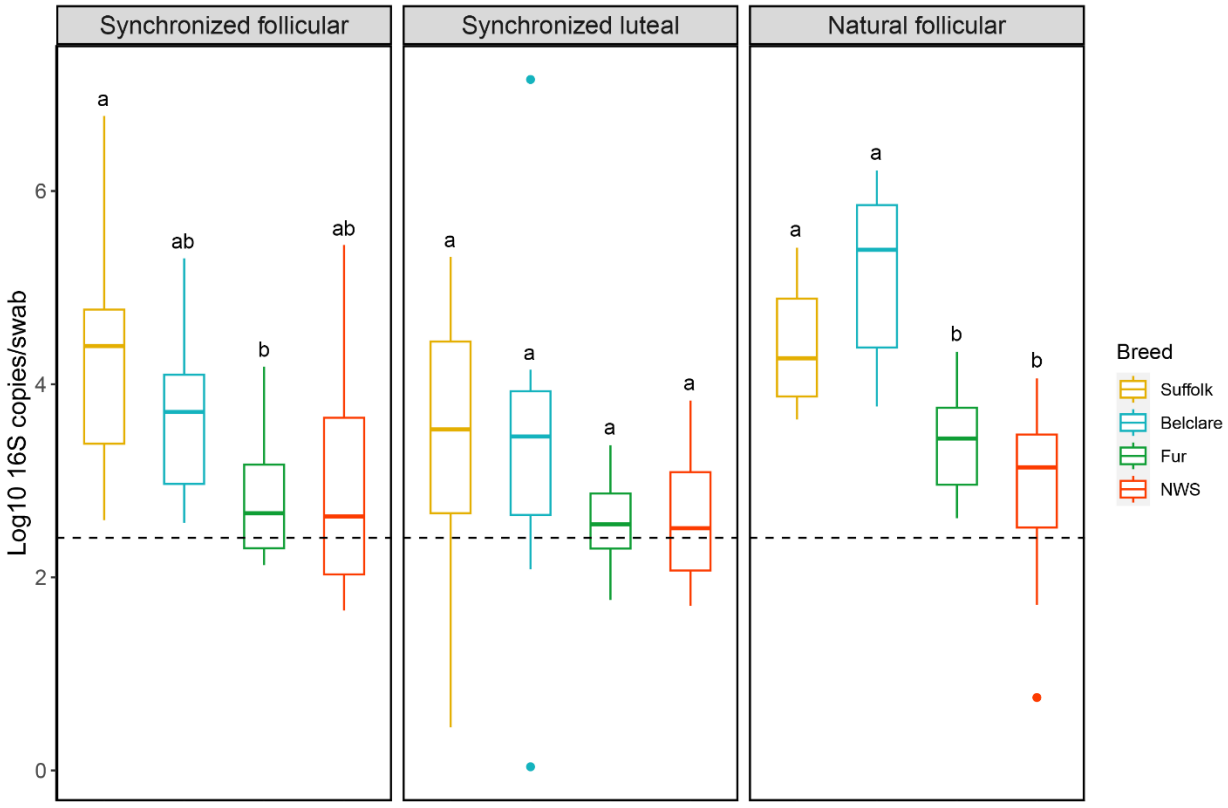
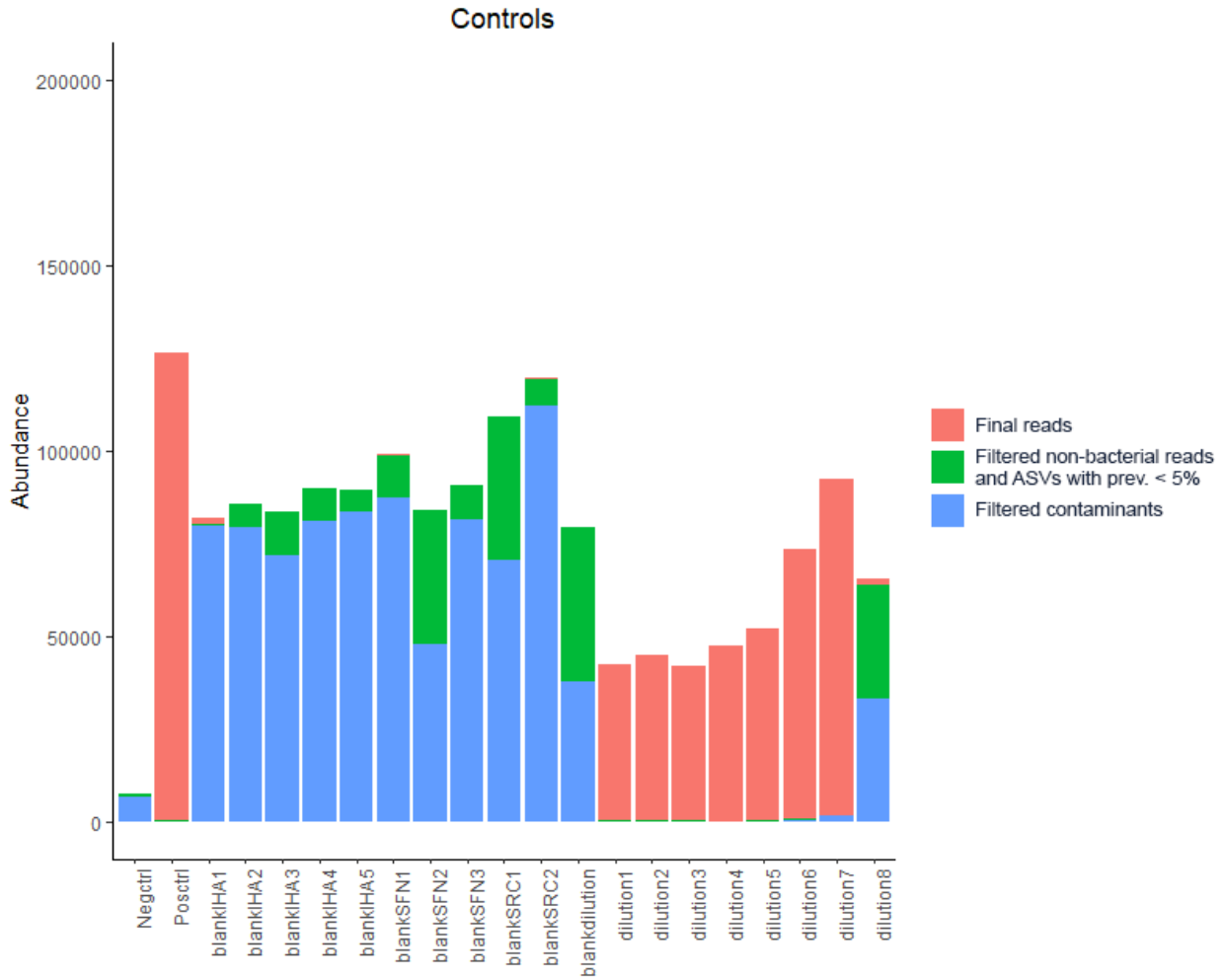
Supplementary figures

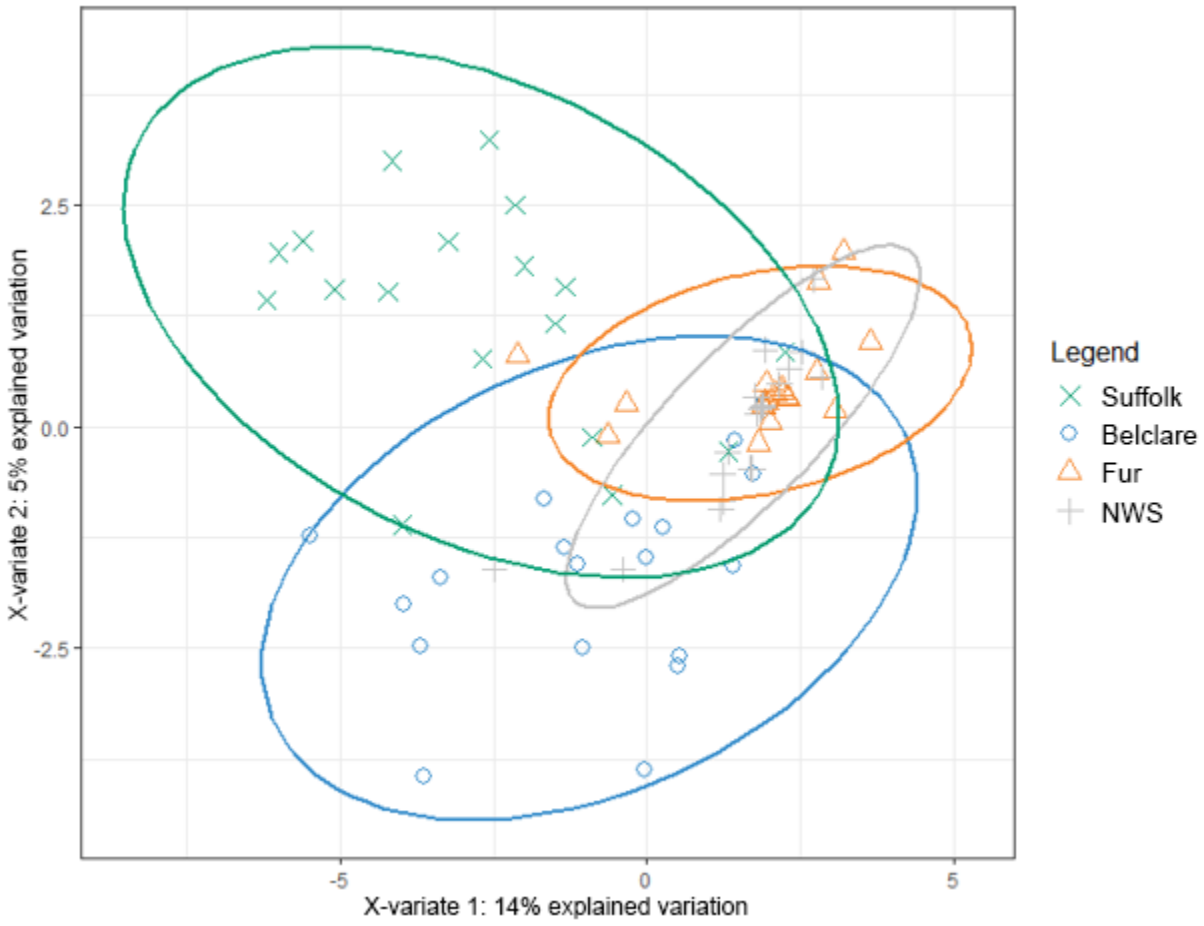
Supplementary figure 1. Median cervical bacterial abundances of Suffolk, Belclare, Fur, and Norwegian White Sheep (NWS) at the follicular (left) and luteal (center) phases of a hormonally synchronized estrus, and at the follicular phase of a natural estrus (right). Data are presented as log10 16S rRNA gene copies per sample with the dashed line indicating the median bacterial abundance levels in the blank extraction controls. [ab]Different superscripts differ significantly between ewe breeds within each phase of the cycle ($P<0.05$).



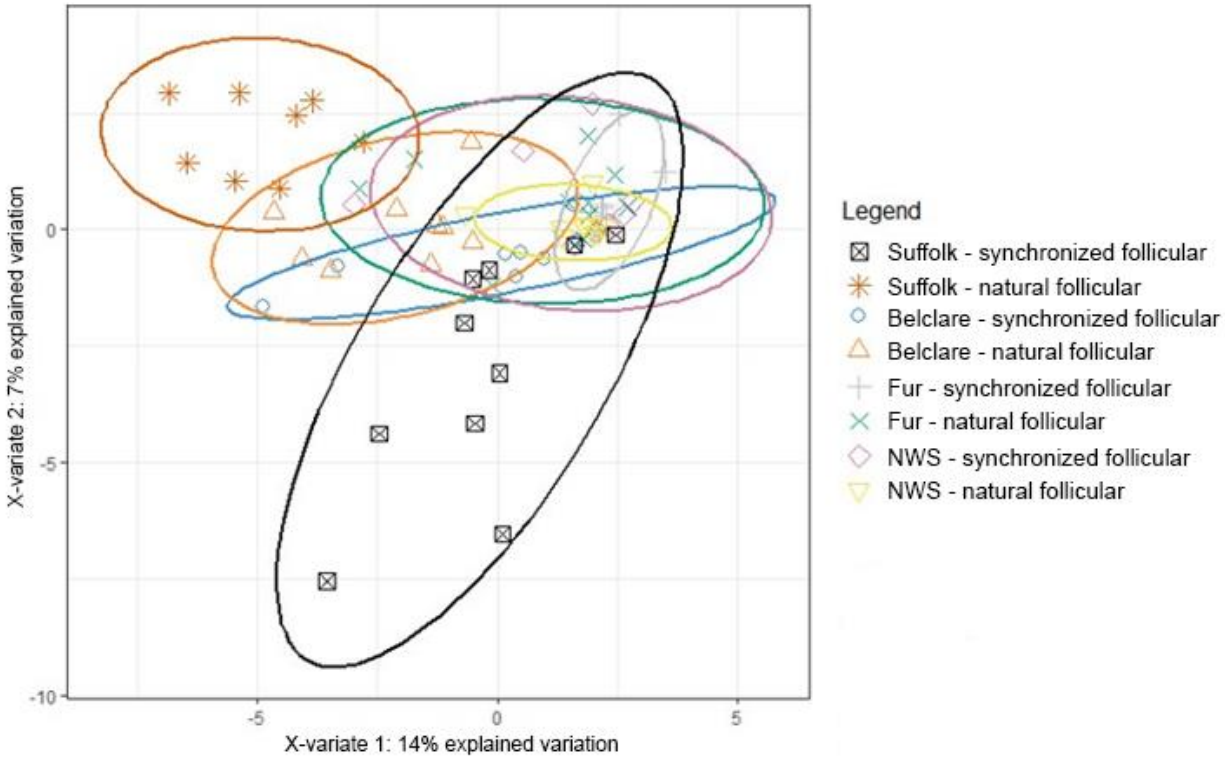
Supplementary figure 2. Bar plot showing reads classified as identified contaminant amplicon sequence variants (ASVs); ASVs filtered due to identification as Archaea, chloroplasts, mitochondria, or due to presence in less than 5% of the total number of cervical samples; and ASVs representing the mock community in the control samples.



Supplementary Figure 3. Visual comparison by supervised partial least-squares discriminant analysis (sPLS-DA) of the cervical bacterial microbiome in Suffolk (n = 18), Belclare (n = 19), Fur (n = 19) and Norwegian White Sheep (NWS; n = 20) at the follicular phase of both a natural estrus and a hormonally synchronized estrus.



Supplementary Figure 4. Visual comparison by supervised partial least-squares discriminant analysis (sPLS-DA) of the cervical bacterial microbiome in different breeds sorted by the follicular phase of either a natural or a synchronized estrus in Suffolk (natural: n = 8; synchronized: n = 10), Belclare (natural: n = 9; synchronized: n = 9), Fur (natural: n = 10; synchronized: n = 9), and Norwegian White Sheep (NWS; natural: n = 10; synchronized: n = 10).



Supplementary Figure 5. Linear discriminant analysis effect size (LEfSe)-like plot generated using mixOmics. The plot illustrates the contribution to the first component of the supervised partial least-squares discriminant analysis (sPLS-DA, SupplementaryAdditional Figure 4) for ewes sampled at the follicular phase of either natural (Nat_Fol) or synchronized (Ind_Fol) estrus, as presented in Supplementary Additional Figure 4. Suffolk (natural: n = 8; synchronized: n = 10), Belclare (natural: n = 9; synchronized: n = 9), Fur (natural: n = 10; synchronized: n = 9), and Norwegian White Sheep (NWS; natural: n = 10; synchronized: n = 10).