

Table S1. Summary statistics of 16S rRNA sequencing

| Segments | N | Clean reads | Coverage range | Average of reads per sample |
|---------------------|------------|--------------------|-----------------------|------------------------------------|
| Cloaca | 43 | 2587887 | 32689 ~ 73206 | 60183 |
| Vagina | 55 | 3289560 | 38803 ~ 74390 | 59810 |
| Uterus | 54 | 3247856 | 34225 ~ 73746 | 60145 |
| Isthmus | 55 | 3114377 | 30858 ~ 71968 | 56625 |
| Magnum | 37 | 2172421 | 31774 ~ 74824 | 58714 |
| Infundibulum | 48 | 2865423 | 33766 ~ 74648 | 59696 |
| Total | 292 | 17277524 | 30858 ~ 74824 | 59170 |

Table S2. Relative abundance of the dominant microbial phyla in different segments

| Phylum | Infundibulum | Magnum | Isthmus | Uterus | Vagina | Cloaca |
|-----------------------|---------------------|---------------|----------------|---------------|---------------|---------------|
| Actinobacteria | 0.56% | 2.71% | 0.21% | 0.14% | 0.52% | 17.11% |
| Bacteroidetes | 3.86% | 3.79% | 0.13% | 0.15% | 0.52% | 1.32% |
| Firmicutes | 16.19% | 21.56% | 28.67% | 38.16% | 28.97% | 57.35% |
| Fusobacteria | 0.00% | 0.00% | 0.02% | 1.18% | 3.84% | 1.38% |
| Proteobacteria | 79.21% | 71.85% | 70.93% | 60.24% | 66.04% | 22.70% |
| Others | 0.18% | 0.09% | 0.05% | 0.14% | 0.12% | 0.14% |

Table S3. Relative abundance of microbial genera at the six anatomical segments

| Genus | Infundibulum | Magnum | Isthmus | Uterus | Vagina | Cloaca |
|---|--------------|--------|---------|--------|--------|--------|
| <i>c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces</i> | 0 | 0 | 0 | 0 | 0.02% | 3.49% |
| <i>c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium</i> | 0.09% | 0 | 0.03% | 0.03% | 0.16% | 9.77% |
| <i>c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Chryseobacterium</i> | 3.78% | 3.45% | 0.11% | 0 | 0.08% | 0.01% |
| <i>c_Bacilli;o_Bacillales;f_Planococcaceae;g_Kurthia</i> | 4.74% | 0 | 1.10% | 2.10% | 0.01% | 1.57% |
| <i>c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Aerococcus</i> | 0.42% | 3.10% | 0.13% | 2.81% | 1.08% | 1.08% |
| <i>c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus</i> | 5.25% | 7.70% | 15.43% | 23.13% | 16.18% | 28.61% |
| <i>c_Bacilli;o_Lactobacillales;f_Vagococcaceae;g_Vagococcus</i> | 1.17% | 6.64% | 1.27% | 1.64% | 1.41% | 0.10% |
| <i>c_Bacilli;o_Staphylococcales;f_Staphylococcaceae;g_Staphylococcus</i> | 4.08% | 3.53% | 9.50% | 6.56% | 4.28% | 1.87% |
| <i>c_Clostridia;o_Peptostreptococcales-Tissierellales;f_Peptostreptococcales-Tissierellales;g_Gallicola</i> | 0 | 0 | 0 | 0.56% | 1.92% | 15.86% |
| <i>c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacterium</i> | 0 | 0 | 0.02% | 1.18% | 3.84% | 1.38% |
| <i>c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas</i> | 1.83% | 6.47% | 1.84% | 1.45% | 0.93% | 0.89% |
| <i>c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Aeromonas</i> | 8.92% | 2.66% | 1.60% | 0 | 3.15% | 0.38% |
| <i>c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae;_</i> | 0.95% | 0.49% | 0.43% | 2.66% | 4.02% | 0.71% |
| <i>c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Comamonas</i> | 3.59% | 0 | 0.04% | 0.35% | 1.62% | 1.51% |
| <i>c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;_</i> | 5.94% | 10.08% | 7.16% | 1.52% | 4.16% | 0.59% |
| <i>c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Escherichia-Shigella</i> | 24.53% | 25.39% | 40.18% | 43.79% | 28.90% | 13.34% |
| <i>c_Gammaproteobacteria;o_Enterobacteriales;f_Erwiniaaceae;g_Pantoea</i> | 0.01% | 2.56% | 1.43% | 0.63% | 0.12% | 0 |
| <i>c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter</i> | 9.02% | 3.34% | 5.57% | 7.05% | 3.53% | 1.34% |
| <i>c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas</i> | 11.13% | 11.77% | 7.77% | 1.90% | 13.10% | 0.92% |
| <i>c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas</i> | 12.89% | 8.39% | 4.22% | 0.34% | 4.63% | 0.81% |
| Others | 1.64% | 4.41% | 2.20% | 2.28% | 6.87% | 15.77% |

Table S4. Spearman correlation between cloacal microbial genera

| Genus1 | Genus2 | Abundance1 | Abundance2 | Phylum1 | Phylum2 | correlation | adj_P | Direction |
|--------------------------------------|--------------------------|-------------------|-------------------|----------------|----------------|--------------------|--------------|------------------|
| <i>g_Corynebacterium</i> | <i>g_Actinomyces</i> | 10.12% | 3.70% | Actinobacteria | Actinobacteria | 0.41 | 4.70E-02 | positive |
| <i>g_Brevibacterium</i> | <i>g_Actinomyces</i> | 0.07% | 3.70% | Actinobacteria | Actinobacteria | 0.42 | 4.15E-02 | positive |
| <i>f_Aerococcaceae_</i> | <i>g_Actinomyces</i> | 0.16% | 3.70% | Firmicutes | Actinobacteria | 0.63 | 1.42E-04 | positive |
| <i>f_Aerococcaceae_</i> | <i>g_Brevibacterium</i> | 0.16% | 0.07% | Firmicutes | Actinobacteria | 0.46 | 2.03E-02 | positive |
| <i>f_Aerococcaceae_</i> | <i>g_Corynebacterium</i> | 0.16% | 10.12% | Firmicutes | Actinobacteria | 0.45 | 2.71E-02 | positive |
| <i>g_Aerococcus</i> | <i>g_Kocuria</i> | 0.99% | 1.20% | Firmicutes | Actinobacteria | 0.59 | 6.07E-04 | positive |
| <i>g_Facklamia</i> | <i>g_Actinomyces</i> | 0.76% | 3.70% | Firmicutes | Actinobacteria | -0.45 | 2.57E-02 | negative |
| <i>g_Facklamia</i> | <i>g_Turicibacter</i> | 0.76% | 1.29% | Firmicutes | Firmicutes | 0.43 | 3.31E-02 | positive |
| <i>g_Facklamia</i> | <i>g_Kocuria</i> | 0.76% | 1.20% | Firmicutes | Actinobacteria | 0.54 | 3.55E-03 | positive |
| <i>g_Facklamia</i> | <i>g_Aerococcus</i> | 0.76% | 0.99% | Firmicutes | Firmicutes | 0.56 | 2.09E-03 | positive |
| <i>g_Globicatella</i> | <i>g_Actinomyces</i> | 0.06% | 3.70% | Firmicutes | Actinobacteria | 0.50 | 1.00E-02 | positive |
| <i>g_Globicatella</i> | <i>f_Aerococcaceae_</i> | 0.06% | 0.16% | Firmicutes | Firmicutes | 0.53 | 4.24E-03 | positive |
| <i>g_Lactobacillus</i> | <i>g_Turicibacter</i> | 1.26% | 1.29% | Firmicutes | Firmicutes | 0.44 | 3.25E-02 | positive |
| <i>g_Streptococcus</i> | <i>g_Brevibacterium</i> | 0.87% | 0.07% | Firmicutes | Actinobacteria | -0.50 | 1.00E-02 | negative |
| <i>g_Streptococcus</i> | <i>g_Turicibacter</i> | 0.87% | 1.29% | Firmicutes | Firmicutes | 0.50 | 9.70E-03 | positive |
| <i>g_Streptococcus</i> | <i>g_Actinomyces</i> | 0.87% | 3.70% | Firmicutes | Actinobacteria | -0.41 | 4.57E-02 | negative |
| <i>g_Streptococcus</i> | <i>f_Aerococcaceae_</i> | 0.87% | 0.16% | Firmicutes | Firmicutes | -0.41 | 4.39E-02 | negative |
| <i>g_Staphylococcus</i> | <i>g_Kocuria</i> | 2.10% | 1.20% | Firmicutes | Actinobacteria | 0.44 | 2.80E-02 | positive |
| <i>g_Clostridium_sensu_stricto_1</i> | <i>g_Turicibacter</i> | 0.02% | 1.29% | Firmicutes | Firmicutes | 0.47 | 1.73E-02 | positive |
| <i>g_Clostridium_sensu_stricto_1</i> | <i>g_Romboutsia</i> | 0.02% | 1.15% | Firmicutes | Firmicutes | 0.49 | 1.00E-02 | positive |
| <i>g_Romboutsia</i> | <i>g_Lactobacillus</i> | 1.15% | 1.26% | Firmicutes | Firmicutes | 0.50 | 1.00E-02 | positive |
| <i>g_Romboutsia</i> | <i>g_Turicibacter</i> | 1.15% | 1.29% | Firmicutes | Firmicutes | 0.94 | 1.82E-19 | positive |
| <i>g_Romboutsia</i> | <i>g_Facklamia</i> | 1.15% | 0.76% | Firmicutes | Firmicutes | 0.50 | 9.97E-03 | positive |
| <i>g_Romboutsia</i> | <i>g_Streptococcus</i> | 1.15% | 0.87% | Firmicutes | Firmicutes | 0.44 | 3.05E-02 | positive |

| Genus1 | Genus2 | Abundance1 | Abundance2 | Phylum1 | Phylum2 | correlation | adj_P | Direction |
|--------------------------------|--------------------------------|-------------------|-------------------|----------------|----------------|--------------------|--------------|------------------|
| <i>g_Gallicola</i> | <i>g_Enterococcus</i> | 16.34% | 29.37% | Firmicutes | Firmicutes | -0.46 | 2.20E-02 | negative |
| <i>g_Gallicola</i> | <i>g_Lactobacillus</i> | 16.34% | 1.26% | Firmicutes | Firmicutes | 0.42 | 4.31E-02 | positive |
| <i>g_Gallicola</i> | <i>g_Streptococcus</i> | 16.34% | 0.87% | Firmicutes | Firmicutes | 0.50 | 1.00E-02 | positive |
| <i>g_Helcococcus</i> | <i>f_Aerococcaceae_</i> | 0.52% | 0.16% | Firmicutes | Firmicutes | 0.68 | 1.02E-05 | positive |
| <i>g_Helcococcus</i> | <i>g_Corynebacterium</i> | 0.52% | 10.12% | Firmicutes | Actinobacteria | 0.43 | 3.31E-02 | positive |
| <i>g_Helcococcus</i> | <i>g_Actinomyces</i> | 0.52% | 3.70% | Firmicutes | Actinobacteria | 0.92 | 9.02E-17 | positive |
| <i>g_Helcococcus</i> | <i>g_Bacteroides</i> | 0.52% | 0.84% | Firmicutes | Bacteroidetes | 0.42 | 3.75E-02 | positive |
| <i>g_Helcococcus</i> | <i>g_Globicatella</i> | 0.52% | 0.06% | Firmicutes | Firmicutes | 0.50 | 1.00E-02 | positive |
| <i>g_W5053</i> | <i>g_Actinomyces</i> | 0.08% | 3.70% | Firmicutes | Actinobacteria | 0.42 | 3.83E-02 | positive |
| <i>g_W5053</i> | <i>f_Aerococcaceae_</i> | 0.08% | 0.16% | Firmicutes | Firmicutes | 0.41 | 4.39E-02 | positive |
| <i>g_W5053</i> | <i>g_Bacteroides</i> | 0.08% | 0.84% | Firmicutes | Bacteroidetes | 0.53 | 3.97E-03 | positive |
| <i>g_W5053</i> | <i>g_Helcococcus</i> | 0.08% | 0.52% | Firmicutes | Firmicutes | 0.48 | 1.27E-02 | positive |
| <i>g_Phascolarctobacterium</i> | <i>g_Enterococcus</i> | 0.09% | 29.37% | Firmicutes | Firmicutes | -0.41 | 4.39E-02 | negative |
| <i>g_Phascolarctobacterium</i> | <i>g_Gallicola</i> | 0.09% | 16.34% | Firmicutes | Firmicutes | 0.43 | 3.31E-02 | positive |
| <i>g_Phascolarctobacterium</i> | <i>g_W5053</i> | 0.09% | 0.08% | Firmicutes | Firmicutes | 0.49 | 1.00E-02 | positive |
| <i>g_Phascolarctobacterium</i> | <i>g_Bacteroides</i> | 0.09% | 0.84% | Firmicutes | Bacteroidetes | 0.82 | 5.13E-10 | positive |
| <i>g_Veillonella</i> | <i>g_Bacteroides</i> | 0.05% | 0.84% | Firmicutes | Bacteroidetes | 0.47 | 1.73E-02 | positive |
| <i>g_Veillonella</i> | <i>g_Lactobacillus</i> | 0.05% | 1.26% | Firmicutes | Firmicutes | 0.56 | 1.77E-03 | positive |
| <i>g_Veillonella</i> | <i>g_Phascolarctobacterium</i> | 0.05% | 0.09% | Firmicutes | Firmicutes | 0.41 | 4.39E-02 | positive |
| <i>g_Fusobacterium</i> | <i>g_Bacteroides</i> | 1.48% | 0.84% | Fusobacteria | Bacteroidetes | 0.48 | 1.45E-02 | positive |
| <i>g_Fusobacterium</i> | <i>g_Gallicola</i> | 1.48% | 16.34% | Fusobacteria | Firmicutes | 0.41 | 4.75E-02 | positive |
| <i>g_Fusobacterium</i> | <i>g_Phascolarctobacterium</i> | 1.48% | 0.09% | Fusobacteria | Firmicutes | 0.44 | 3.03E-02 | positive |
| <i>g_Escherichia.Shigella</i> | <i>g_Ralstonia</i> | 13.15% | 0.02% | Proteobacteria | Proteobacteria | -0.43 | 3.52E-02 | negative |
| <i>g_Gallibacterium</i> | <i>g_Helcococcus</i> | 0.12% | 0.52% | Proteobacteria | Firmicutes | 0.44 | 2.89E-02 | positive |
| <i>g_Gallibacterium</i> | <i>g_Actinomyces</i> | 0.12% | 3.70% | Proteobacteria | Actinobacteria | 0.46 | 1.93E-02 | positive |

Table S5. Spearman correlation between vaginal microbial genera

| Genus1 | Genus2 | Abundance1 | Abundance2 | Phylum1 | Phylum2 | Correlation | adj_P | Direction |
|--------------------------------------|--------------------------|-------------------|-------------------|----------------|----------------|--------------------|--------------|------------------|
| <i>g_Turicibacter</i> | <i>g_Corynebacterium</i> | 0.21% | 0.22% | Firmicutes | Actinobacteria | 0.41 | 1.30E-02 | positive |
| <i>g_Aerococcus</i> | <i>g_Bacteroides</i> | 1.06% | 0.39% | Firmicutes | Bacteroidetes | -0.42 | 9.65E-03 | negative |
| <i>g_Enterococcus</i> | <i>g_Corynebacterium</i> | 17.48% | 0.22% | Firmicutes | Actinobacteria | 0.48 | 1.81E-03 | positive |
| <i>g_Enterococcus</i> | <i>g_Rhodococcus</i> | 17.48% | 0.04% | Firmicutes | Actinobacteria | 0.38 | 2.36E-02 | positive |
| <i>g_Lactobacillus</i> | <i>g_Turicibacter</i> | 1.02% | 0.21% | Firmicutes | Firmicutes | 0.56 | 1.22E-04 | positive |
| <i>g_Lactobacillus</i> | <i>g_Corynebacterium</i> | 1.02% | 0.22% | Firmicutes | Actinobacteria | 0.49 | 1.57E-03 | positive |
| <i>g_Streptococcus</i> | <i>g_Lactobacillus</i> | 0.43% | 1.02% | Firmicutes | Firmicutes | 0.56 | 1.21E-04 | positive |
| <i>g_Streptococcus</i> | <i>g_Turicibacter</i> | 0.43% | 0.21% | Firmicutes | Firmicutes | 0.58 | 5.38E-05 | positive |
| <i>g_Staphylococcus</i> | <i>g_Aerococcus</i> | 3.82% | 1.06% | Firmicutes | Firmicutes | 0.56 | 1.17E-04 | positive |
| <i>g_Clostridium_sensu_stricto_1</i> | <i>g_Streptococcus</i> | 0.14% | 0.43% | Firmicutes | Firmicutes | 0.41 | 1.24E-02 | positive |
| <i>g_Clostridium_sensu_stricto_1</i> | <i>g_Lactobacillus</i> | 0.14% | 1.02% | Firmicutes | Firmicutes | 0.37 | 2.83E-02 | positive |
| <i>g_Clostridium_sensu_stricto_1</i> | <i>g_Turicibacter</i> | 0.14% | 0.21% | Firmicutes | Firmicutes | 0.56 | 1.02E-04 | positive |
| <i>g_Clostridium_sensu_stricto_1</i> | <i>g_Romboutsia</i> | 0.14% | 0.36% | Firmicutes | Firmicutes | 0.50 | 9.46E-04 | positive |
| <i>g_Clostridium_sensu_stricto_1</i> | <i>g_Gallicola</i> | 0.14% | 2.11% | Firmicutes | Firmicutes | 0.39 | 2.12E-02 | positive |
| <i>g_Romboutsia</i> | <i>g_Streptococcus</i> | 0.36% | 0.43% | Firmicutes | Firmicutes | 0.58 | 4.51E-05 | positive |
| <i>g_Romboutsia</i> | <i>g_Corynebacterium</i> | 0.36% | 0.22% | Firmicutes | Actinobacteria | 0.41 | 1.38E-02 | positive |
| <i>g_Romboutsia</i> | <i>g_Turicibacter</i> | 0.36% | 0.21% | Firmicutes | Firmicutes | 0.92 | 4.84E-22 | positive |
| <i>g_Romboutsia</i> | <i>g_Lactobacillus</i> | 0.36% | 1.02% | Firmicutes | Firmicutes | 0.62 | 9.34E-06 | positive |
| <i>g_Gallicola</i> | <i>g_Bacteroides</i> | 2.11% | 0.39% | Firmicutes | Bacteroidetes | 0.37 | 3.33E-02 | positive |
| <i>g_Gallicola</i> | <i>g_Corynebacterium</i> | 2.11% | 0.22% | Firmicutes | Actinobacteria | 0.41 | 1.25E-02 | positive |
| <i>g_Fusobacterium</i> | <i>g_Bacteroides</i> | 4.62% | 0.39% | Fusobacteria | Bacteroidetes | 0.41 | 1.30E-02 | positive |
| <i>g_Fusobacterium</i> | <i>g_Gallicola</i> | 4.62% | 2.11% | Fusobacteria | Firmicutes | 0.41 | 1.38E-02 | positive |
| <i>g_Fusobacterium</i> | <i>g_Corynebacterium</i> | 4.62% | 0.22% | Fusobacteria | Actinobacteria | 0.37 | 3.34E-02 | positive |

| Genus1 | Genus2 | Abundance1 | Abundance2 | Phylum1 | Phylum2 | Correlation | adj_P | Direction |
|-------------------------------|-------------------------------|-------------------|-------------------|----------------|----------------|--------------------|--------------|------------------|
| <i>g_Fusobacterium</i> | <i>g_Lactobacillus</i> | 4.62% | 1.02% | Fusobacteria | Firmicutes | 0.51 | 7.82E-04 | positive |
| <i>g_Brevundimonas</i> | <i>g_Corynebacterium</i> | 0.77% | 0.22% | Proteobacteria | Actinobacteria | 0.38 | 2.76E-02 | positive |
| <i>g_Brevundimonas</i> | <i>g_Lactobacillus</i> | 0.77% | 1.02% | Proteobacteria | Firmicutes | 0.43 | 9.65E-03 | positive |
| <i>g_Ralstonia</i> | <i>g_Corynebacterium</i> | 0.01% | 0.22% | Proteobacteria | Actinobacteria | 0.52 | 4.53E-04 | positive |
| <i>g_Ralstonia</i> | <i>g_Rhodococcus</i> | 0.01% | 0.04% | Proteobacteria | Actinobacteria | 0.67 | 3.23E-07 | positive |
| <i>g_Escherichia.Shigella</i> | <i>f_Enterobacteriaceae._</i> | 30.10% | 4.12% | Proteobacteria | Proteobacteria | -0.60 | 2.17E-05 | negative |
| <i>g_Acinetobacter</i> | <i>g_Escherichia.Shigella</i> | 4.20% | 30.10% | Proteobacteria | Proteobacteria | -0.48 | 1.83E-03 | negative |
| <i>g_Acinetobacter</i> | <i>f_Enterobacteriaceae._</i> | 4.20% | 4.12% | Proteobacteria | Proteobacteria | 0.45 | 5.23E-03 | positive |
| <i>g_Pseudomonas</i> | <i>g_Escherichia.Shigella</i> | 12.91% | 30.10% | Proteobacteria | Proteobacteria | -0.51 | 7.54E-04 | negative |

Table S6. The difference of eggshell color-L value between the birds with the highest and lowest vaginal *Staphylococcus* abundance.

| Age (weeks) | The highest abundance | The lowest abundance | adj_ <i>P</i> |
|-------------|-----------------------|----------------------|---------------|
| 36 | 56.89 ± 1.76 | 59.31 ± 2.23 | 0.015 |
| 56 | 58.00 ± 1.63 | 60.72 ± 1.90 | 0.003 |
| 72 | 58.85 ± 2.70 | 61.91 ± 2.86 | 0.029 |
| 80 | 60.55 ± 2.81 | 61.42 ± 3.23 | 0.528 |
| 90 | 54.47 ± 2.59 | 57.86 ± 3.70 | 0.039 |

Table S7. The difference of eggshell color-L value between the birds with the highest and lowest vaginal *Ralstonia* abundance.

| Age (weeks) | The highest abundance | The lowest abundance | adj_ <i>P</i> |
|-------------|-----------------------|----------------------|---------------|
| 36 | 56.95 ± 3.01 | 59.13 ± 1.56 | 0.057 |
| 56 | 58.49 ± 2.58 | 60.89 ± 2.09 | 0.035 |
| 72 | 59.23 ± 2.65 | 62.06 ± 1.94 | 0.014 |
| 80 | 58.41 ± 2.38 | 61.51 ± 2.43 | 0.010 |
| 90 | 53.62 ± 3.35 | 57.95 ± 3.79 | 0.015 |

Table S8. The difference of egg number between the birds with the highest and lowest vaginal *Romboutsia* abundance.

| Age (weeks) | The highest abundance | The lowest abundance | adj_ <i>P</i> |
|-------------|-----------------------|----------------------|---------------|
| 36 | 108.9 ± 7.34 | 115.8 ± 6.56 | 0.040 |
| 56 | 238.5 ± 9.88 | 247.6 ± 5.74 | 0.021 |
| 72 | 340.4 ± 12.44 | 352.2 ± 6.8 | 0.017 |
| 80 | 390.1 ± 15.02 | 402.5 ± 7.93 | 0.033 |
| 90 | 446.6 ± 19.84 | 460.5 ± 11.15 | 0.069 |

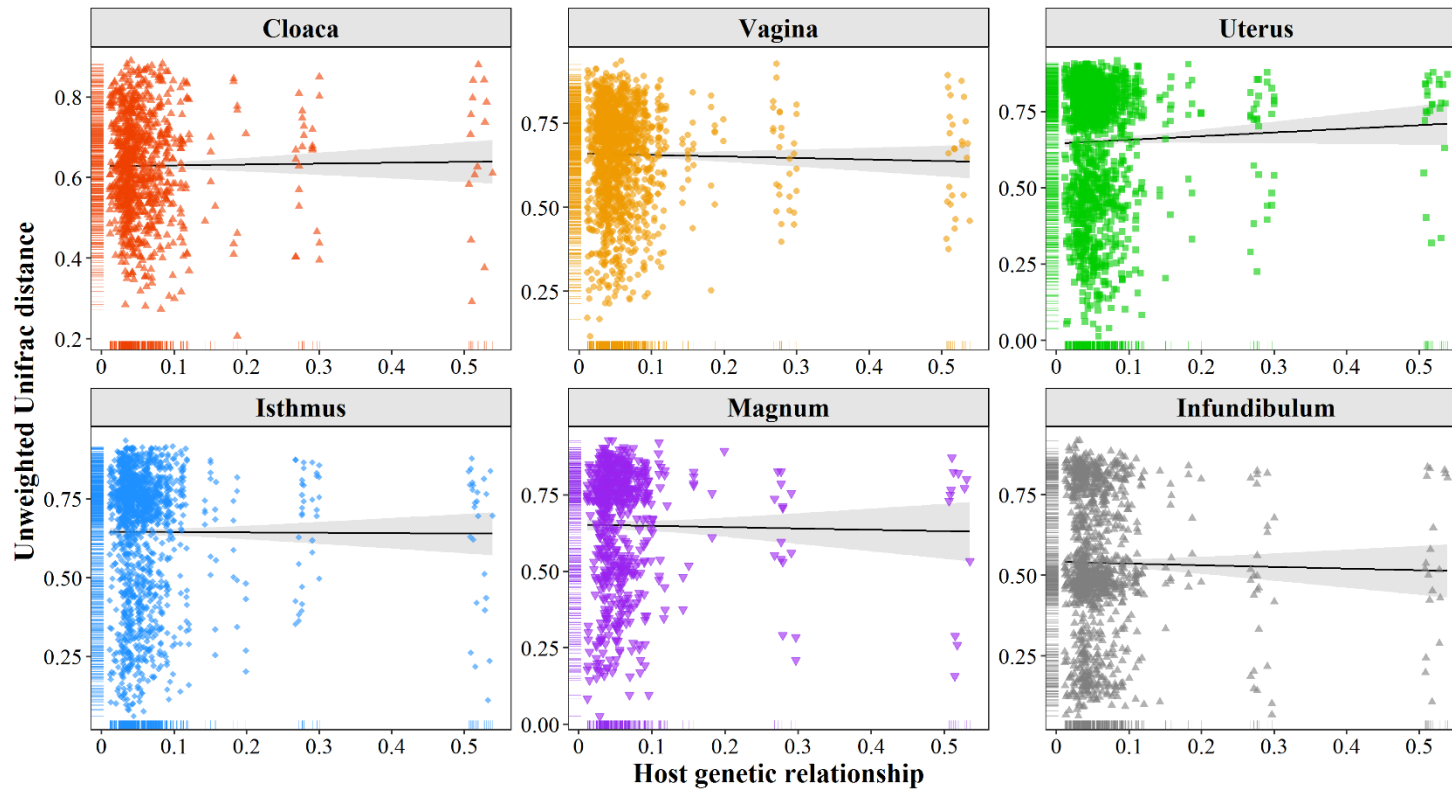


Figure S1. Relationship between host genetic relationship and unweighted UniFrac distance on the six segments of reproductive tract.