## Supplementary Information

**Supplemental Table 1.** Heritability estimates for predominant taxa by self-reported ancestry in women below the average age of menopause onset (< 51 years old).

| Taxa | Ancestry | Component | Standardized Estimate | Unstandardized Estimate | 95% LI | 95% UI |
|---|---|---|---|---|---|---|
| *Lactobacillus crispatus* | African | A | 0.2707 | 0.0794 | -0.0635 | 0.2483 |
| | | E | 0.7293 | 0.2141 | 0.1161 | 0.4130 |
| | European | A | 0.3731 | 0.1602 | 0.0596 | 0.2813 |
| | | E | 0.6269 | 0.2691 | 0.1943 | 0.3819 |
| *Lactobacillus iners* | African | A | 0.1527 | 0.0454 | -0.0993 | 0.2108 |
| | | E | 0.8473 | 0.2516 | 0.1393 | 0.4697 |
| | European | A | 0.0798 | 0.0205 | -0.0385 | 0.0824 |
| | | E | 0.9202 | 0.2369 | 0.1762 | 0.3258 |
| *Gardnerella vaginalis* | African | A | 0.1073 | 0.0094 | -0.0323 | 0.0550 |
| | | E | 0.8927 | 0.0780 | 0.0445 | 0.1428 |
| | European | A | -0.1730 | -0.0169 | -0.0432 | 0.0076 |
| | | E | 1.1730 | 0.1143 | 0.0842 | 0.1580 |

LI = Lower Interval; UI = Upper Interval; A = additive genetic component; E = unique environmental component

**Supplemental Table 2a.** Model fit statistics for *L. crispatus* in the European American sample.

| Model | Comparison | Parameters | -2*Log Likelihood | DF | AIC | Log Likelihood Difference | DF Difference | P-value |
|---|---|---|---|---|---|---|---|---|
| ACE | - | 4 | 461.544 | 240 | -18.456 | NA | NA | NA |
| AE | ACE | 3 | 463.562 | 241 | -18.438 | 2.018 | 1 | 0.155 |
| CE | ACE | 3 | 467.132 | 241 | -14.868 | 5.588 | 1 | 0.018 |
| E | ACE | 2 | 474.536 | 242 | -9.464 | 12.992 | 2 | 0.002 |

**Supplemental Table 2b.** Model fit statistics for *L. iners* in the European American sample.

| Model | Comparison | Parameters | -2*Log Likelihood | DF | AIC | Log Likelihood Difference | DF Difference | P-value |
|---|---|---|---|---|---|---|---|---|
| ACE | - | 4 | 353.389 | 240 | -126.611 | NA | NA | NA |
| AE | ACE | 3 | 354.365 | 241 | -127.635 | 0.976 | 1 | 0.323 |
| CE | ACE | 3 | 354.738 | 241 | -127.262 | 1.349 | 1 | 0.245 |
| E | ACE | 2 | 355.125 | 242 | -128.875 | 1.736 | 2 | 0.420 |

**Supplemental Table 2c.** Model fit statistics for *G. vaginalis* in the European American sample.

| Model | Comparison | Parameters | -2*Log Likelihood | DF | AIC | Log Likelihood Difference | DF Difference | P-value |
|---|---|---|---|---|---|---|---|---|
| ACE | - | 4 | 131.799 | 240 | -348.201 | NA | NA | NA |
| AE | ACE | 3 | 132.421 | 241 | -349.579 | 0.622 | 1 | 0.430 |
| CE | ACE | 3 | 131.889 | 241 | -350.111 | 0.090 | 1 | 0.765 |
| E | ACE | 2 | 134.841 | 242 | -349.159 | 3.042 | 2 | 0.219 |

**Supplemental Table 2d.** Model fit statistics for *L. crispatus* in the African American sample.

| Model | Comparison | Parameters | -2*Log Likelihood | DF | AIC | Log Likelihood Difference | DF Difference | P-value |
|---|---|---:|---:|---:|---:|---:|---:|---:|
| ACE | - | 4 | 132.505 | 84 | -35.495 | NA | NA | NA |
| AE | ACE | 3 | 132.608 | 85 | -37.392 | 0.103 | 1 | 0.748 |
| CE | ACE | 3 | 132.854 | 85 | -37.146 | 0.349 | 1 | 0.555 |
| E | ACE | 2 | 133.369 | 86 | -38.631 | 0.864 | 2 | 0.649 |

**Supplemental Table 2e.** Model fit statistics for *L. iners* in the African American sample.

| Model | Comparison | Parameters | -2*Log Likelihood | DF | AIC | Log Likelihood Difference | DF Difference | P-value |
|---|---|---:|---:|---:|---:|---:|---:|---:|
| ACE | - | 4 | 145.090 | 84 | -22.910 | NA | NA | NA |
| AE | ACE | 3 | 145.103 | 85 | -24.897 | 0.013 | 1 | 0.909 |
| CE | ACE | 3 | 145.141 | 85 | -24.859 | 0.051 | 1 | 0.822 |
| E | ACE | 2 | 145.244 | 86 | -26.756 | 0.155 | 2 | 0.926 |

**Supplemental Table 2f.** Model fit statistics for *G. vaginalis* in the African American sample.

| Model | Comparison | Parameters | -2*Log Likelihood | DF | AIC | Log Likelihood Difference | DF Difference | P-value |
|---|---|---:|---:|---:|---:|---:|---:|---:|
| ACE | - | 4 | 38.507 | 84 | -129.493 | NA | NA | NA |
| AE | ACE | 3 | 39.442 | 85 | -130.558 | 0.935 | 1 | 0.334 |
| CE | ACE | 3 | 39.778 | 85 | -130.222 | 1.271 | 1 | 0.260 |
| E | ACE | 2 | 39.894 | 86 | -132.106 | 1.386 | 2 | 0.500 |

**Supplemental Table 3a.** Expanded list of taxa in European American MZ.

| Taxa | ICC | 95% LI | 95% UI | *Cell 11 | Cell 12 | Cell 21 | Cell 22 |
|---|---:|---:|---:|---:|---:|---:|---:|
| Aerococcus.christensenii | 0.0401 | -0.1405 | 0.2182 | 39 | 21 | 14 | 10 |
| Anaerococcus.OTU145 | 0.0327 | -0.1478 | 0.2111 | 48 | 9 | 21 | 6 |
| Anaerococcus.tetradius | 0.0000 | -0.1796 | 0.1796 | 63 | 9 | 11 | 1 |
| Atopobium.vaginae | 0.3185 | 0.1473 | 0.4712 | 22 | 22 | 18 | 22 |
| Bifidobacterium.breve_cluster | 0.3262 | 0.1557 | 0.4778 | 57 | 15 | 8 | 4 |
| Clostridiales.BVAB2 | 0.0000 | -0.1796 | 0.1796 | 55 | 14 | 13 | 2 |
| Coriobacteriaceae.OTU27 | 0.0000 | -0.1796 | 0.1796 | 46 | 14 | 18 | 6 |
| Dialister.cluster51 | 0.0000 | -0.1796 | 0.1796 | 50 | 15 | 14 | 5 |
| Enterobacteriaceae.cluster31 | 0.0232 | -0.1570 | 0.2020 | 50 | 10 | 13 | 11 |
| Finegoldia.magna | 0.5713 | 0.4364 | 0.6810 | 21 | 20 | 18 | 25 |
| Gardnerella.vaginalis | 0.0000 | -0.1796 | 0.1796 | 1 | 13 | 8 | 62 |
| Lactobacillus.crispatus_cluster | 0.3801 | 0.2152 | 0.5240 | 3 | 12 | 10 | 59 |
| Lactobacillus.gasseri_cluster | 0.1638 | -0.0163 | 0.3336 | 22 | 17 | 20 | 25 |
| Lactobacillus.iners | 0.1245 | -0.0564 | 0.2975 | 1 | 7 | 9 | 67 |
| Lactobacillus.jensenii | 0.0000 | -0.1796 | 0.1796 | 22 | 25 | 13 | 24 |
| Megasphaera.cluster52 | 0.0000 | -0.1796 | 0.1796 | 45 | 17 | 12 | 10 |
| Mycoplasma.hominis | 0.0172 | -0.1630 | 0.1962 | 54 | 14 | 9 | 7 |
| Parvimonas.OTU142 | 0.0000 | -0.1796 | 0.1796 | 55 | 12 | 13 | 4 |
| Peptoniphilus.indolicus | 0.2794 | 0.1051 | 0.4371 | 39 | 16 | 15 | 14 |
| Prevotella.OTU48 | 0.1578 | -0.0224 | 0.3281 | 66 | 4 | 11 | 3 |
| Prevotella.amnii | 0.0000 | -0.1796 | 0.1796 | 51 | 16 | 12 | 5 |
| Prevotella.bivia | 0.0000 | -0.1796 | 0.1796 | 29 | 18 | 22 | 15 |
| Prevotella.cluster2 | 0.0000 | -0.1796 | 0.1796 | 17 | 15 | 20 | 32 |
| Prevotella.disiens | 0.0938 | -0.0872 | 0.2689 | 50 | 13 | 16 | 5 |
| Sneathia.amnii | 0.0439 | -0.1368 | 0.2218 | 42 | 12 | 16 | 14 |
| Sneathia.sanguinegens | 0.0000 | -0.1796 | 0.1796 | 58 | 12 | 8 | 6 |
| Staphylococcus.cluster47 | 0.0104 | -0.1696 | 0.1896 | 36 | 16 | 15 | 17 |
| Streptococcus.agalactiae | 0.0041 | -0.1756 | 0.1836 | 56 | 9 | 15 | 4 |
| Streptococcus.anginosus | 0.1194 | -0.0616 | 0.2927 | 42 | 14 | 17 | 11 |
| TM7.OTU.H1 | 0.0000 | -0.1796 | 0.1796 | 59 | 9 | 12 | 4 |
| Ureaplasma.cluster23 | 0.1010 | -0.0800 | 0.2757 | 39 | 11 | 15 | 19 |
| X_Lachnospiraceae_.BVAB1 | 0.0000 | -0.1796 | 0.1796 | 23 | 22 | 18 | 21 |

* Cell XX denotes presence/absence of taxa in 2x2 contingency table within twin pair
1 = Absent; 2 = Present; Cell 11 = taxa absent in both members of a twin pair
ICC = Intraclass Correlation; LI = Lower Interval; UI = Upper Interval

**Supplemental Table 3b.** Expanded list of taxa in European Amerrrican DZ twins.

| Taxa | ICC | 95% LI | 95% UI | *Cell 11 | Cell 12 | Cell 21 | Cell 22 |
|---|---|---|---|---|---|---|---|
| Aerococcus.christensenii | 0.0000 | -0.2673 | 0.2673 | 15 | 10 | 8 | 5 |
| Anaerococcus.OTU145 | 0.2025 | -0.0684 | 0.4457 | 23 | 6 | 6 | 3 |
| Anaerococcus.tetradius | 0.0000 | -0.2673 | 0.2673 | 27 | 8 | 3 | 0 |
| Atopobium.vaginae | 0.0000 | -0.2673 | 0.2673 | 12 | 6 | 8 | 12 |
| Bifidobacterium.breve_cluster | 0.1026 | -0.1693 | 0.3600 | 30 | 3 | 4 | 1 |
| Clostridiales.BVAB2 | 0.0000 | -0.2673 | 0.2673 | 28 | 5 | 3 | 2 |
| Coriobacteriaceae.OTU27 | 0.0000 | -0.2673 | 0.2673 | 22 | 9 | 6 | 1 |
| Dialister.cluster51 | 0.0595 | -0.2112 | 0.3216 | 19 | 10 | 6 | 3 |
| Enterobacteriaceae.cluster31 | 0.0080 | -0.2598 | 0.2747 | 26 | 5 | 6 | 1 |
| Finegoldia.magna | 0.4875 | 0.2532 | 0.6678 | 7 | 7 | 12 | 12 |
| Gardnerella.vaginalis | 0.0000 | -0.2673 | 0.2673 | 2 | 6 | 4 | 26 |
| Lactobacillus.crispatus_cluster | 0.0000 | -0.2673 | 0.2673 | 2 | 3 | 4 | 29 |
| Lactobacillus.gasseri_cluster | 0.0000 | -0.2673 | 0.2673 | 10 | 7 | 11 | 10 |
| Lactobacillus.iners | 0.0000 | -0.2673 | 0.2673 | 1 | 4 | 3 | 30 |
| Lactobacillus.jensenii | 0.0870 | -0.1846 | 0.3462 | 8 | 8 | 8 | 14 |
| Megasphaera.cluster52 | 0.1120 | -0.1601 | 0.3682 | 20 | 8 | 5 | 5 |
| Mycoplasma.hominis | 0.0000 | -0.2673 | 0.2673 | 23 | 6 | 8 | 1 |
| Parvimonas.OTU142 | 0.0000 | -0.2673 | 0.2673 | 22 | 8 | 6 | 2 |
| Peptoniphilus.indolicus | 0.3929 | 0.1403 | 0.5974 | 14 | 8 | 12 | 4 |
| Prevotella.OTU48 | 0.0000 | -0.2673 | 0.2673 | 27 | 6 | 4 | 1 |
| Prevotella.amnii | 0.0081 | -0.2597 | 0.2748 | 28 | 4 | 3 | 3 |
| Prevotella.bivia | 0.0000 | -0.2673 | 0.2673 | 14 | 10 | 11 | 3 |
| Prevotella.cluster2 | 0.1689 | -0.1030 | 0.4173 | 13 | 4 | 6 | 15 |
| Prevotella.disiens | 0.5215 | 0.2955 | 0.6923 | 29 | 4 | 3 | 2 |
| Sneathia.amnii | 0.0000 | -0.2673 | 0.2673 | 16 | 5 | 10 | 7 |
| Sneathia.sanguinegens | 0.0752 | -0.1960 | 0.3357 | 28 | 6 | 1 | 3 |
| Staphylococcus.cluster47 | 0.4595 | 0.2192 | 0.6473 | 15 | 5 | 10 | 8 |
| Streptococcus.agalactiae | 0.0000 | -0.2673 | 0.2673 | 25 | 8 | 4 | 1 |
| Streptococcus.anginosus | 0.1691 | -0.1028 | 0.4175 | 18 | 8 | 7 | 5 |
| TM7.OTU.H1 | 0.0000 | -0.2672 | 0.2673 | 26 | 6 | 4 | 2 |
| Ureaplasma.cluster23 | 0.0024 | -0.2650 | 0.2695 | 16 | 10 | 5 | 7 |
| X_Lachnospiraceae_.BVAB1 | 0.0495 | -0.2207 | 0.3126 | 14 | 12 | 5 | 7 |

* Cell XX denotes presence/absence of taxa in 2x2 contingency table within twin pair
1 = Absent; 2 = Present; Cell 11 = taxa absent in both members of a twin pair
ICC = Intraclass Correlation; LI = Lower Interval; UI = Upper Interval

**Supplemental Table 3c.** Expanded list of taxa in African American MZ.

| Taxa | ICC | 95% LI | 95% UI | *Cell 11 | Cell 12 | Cell 21 | Cell 22 |
|---|---|---|---|---|---|---|---|
| Aerococcus.christensenii | 0.5498 | 0.2616 | 0.7479 | 5 | 3 | 7 | 9 |
| Anaerococcus.OTU145 | 0.0179 | -0.3205 | 0.3523 | 13 | 5 | 3 | 3 |
| Anaerococcus.tetradius | 0.1355 | -0.2106 | 0.4515 | 13 | 5 | 2 | 4 |
| Atopobium.vaginae | 0.0936 | -0.2508 | 0.4170 | 2 | 7 | 6 | 9 |
| Bifidobacterium.breve_cluster | 0.0000 | -0.3365 | 0.3365 | 13 | 3 | 7 | 1 |
| Clostridiales.BVAB2 | 0.0000 | -0.3365 | 0.3365 | 8 | 5 | 8 | 3 |
| Coriobacteriaceae.OTU27 | 0.2473 | -0.0973 | 0.5390 | 10 | 4 | 2 | 8 |
| Dialister.cluster51 | 0.0000 | -0.3365 | 0.3365 | 5 | 6 | 7 | 6 |
| Enterobacteriaceae.cluster31 | 0.0000 | -0.3365 | 0.3365 | 18 | 2 | 3 | 1 |
| Finegoldia.magna | 0.1251 | -0.2207 | 0.4430 | 11 | 1 | 4 | 8 |
| Gardnerella.vaginalis | 0.2250 | -0.1207 | 0.5220 | 0 | 2 | 0 | 22 |
| Lactobacillus.crispatus_cluster | 0.2045 | -0.1417 | 0.5062 | 3 | 1 | 7 | 13 |
| Lactobacillus.gasseri_cluster | 0.0000 | -0.3365 | 0.3365 | 6 | 8 | 8 | 2 |
| Lactobacillus.iners | 0.0946 | -0.2499 | 0.4178 | 0 | 1 | 1 | 22 |
| Lactobacillus.jensenii | 0.6247 | 0.3649 | 0.7943 | 6 | 6 | 10 | 2 |
| Megasphaera.cluster52 | 0.0000 | -0.3365 | 0.3365 | 6 | 5 | 7 | 6 |
| Mycoplasma.hominis | 0.0578 | -0.2842 | 0.3868 | 10 | 5 | 6 | 3 |
| Parvimonas.OTU142 | 0.0580 | -0.2841 | 0.3870 | 10 | 5 | 5 | 4 |
| Peptoniphilus.indolicus | 0.1152 | -0.2303 | 0.4348 | 7 | 7 | 3 | 7 |
| Prevotella.OTU48 | 0.1318 | -0.2143 | 0.4484 | 17 | 1 | 4 | 2 |
| Prevotella.amnii | 0.0000 | -0.3365 | 0.3365 | 9 | 5 | 5 | 5 |
| Prevotella.bivia | 0.1193 | -0.2263 | 0.4382 | 4 | 6 | 9 | 5 |
| Prevotella.cluster2 | 0.0737 | -0.2695 | 0.4003 | 4 | 3 | 5 | 12 |
| Prevotella.disiens | 0.0467 | -0.2944 | 0.3773 | 14 | 3 | 3 | 4 |
| Sneathia.amnii | 0.1222 | -0.2235 | 0.4406 | 7 | 5 | 5 | 7 |
| Sneathia.sanguinegens | 0.0000 | -0.3365 | 0.3365 | 9 | 3 | 6 | 6 |
| Staphylococcus.cluster47 | 0.0000 | -0.3365 | 0.3365 | 7 | 2 | 11 | 4 |
| Streptococcus.agalactiae | 0.0059 | -0.3313 | 0.3417 | 11 | 3 | 7 | 3 |
| Streptococcus.anginosus | 0.1423 | -0.2040 | 0.4569 | 10 | 4 | 7 | 3 |
| TM7.OTU.H1 | 0.0000 | -0.3365 | 0.3365 | 14 | 3 | 6 | 1 |
| Ureaplasma.cluster23 | 0.0000 | -0.3365 | 0.3365 | 3 | 4 | 6 | 11 |
| X_Lachnospiraceae_.BVAB1 | 0.0000 | -0.3365 | 0.3365 | 8 | 3 | 5 | 8 |

* Cell XX denotes presence/absence of taxa in 2x2 contingency table within twin pair
1 = Absent; 2 = Present; Cell 11 = taxa absent in both members of a twin pair
ICC = Intraclass Correlation; LI = Lower Interval; UI = Upper Interval

**Supplemental Table 3d.** Expanded list of taxa in African American DZ twins.

| Taxa | ICC | 95% LI | 95% UI | *Cell 11 | Cell 12 | Cell 21 | Cell 22 |
|---|---|---|---|---|---|---|---|
| Aerococcus.christensenii | 0.0000 | -0.3687 | 0.3687 | 5 | 4 | 6 | 5 |
| Anaerococcus.OTU145 | 0.0000 | -0.3687 | 0.3687 | 13 | 3 | 2 | 2 |
| Anaerococcus.tetradius | 0.0000 | -0.3687 | 0.3687 | 9 | 3 | 6 | 2 |
| Atopobium.vaginae | 0.5096 | 0.1735 | 0.7394 | 2 | 4 | 4 | 10 |
| Bifidobacterium.breve_cluster | 0.0000 | -0.3687 | 0.3687 | 16 | 2 | 1 | 1 |
| Clostridiales.BVAB2 | 0.0000 | -0.3687 | 0.3687 | 8 | 5 | 4 | 3 |
| Coriobacteriaceae.OTU27 | 0.0000 | -0.3687 | 0.3687 | 7 | 7 | 3 | 3 |
| Dialister.cluster51 | 0.0000 | -0.3687 | 0.3687 | 4 | 7 | 6 | 3 |
| Enterobacteriaceae.cluster31 | 0.0935 | -0.2851 | 0.4468 | 13 | 2 | 3 | 2 |
| Finegoldia.magna | 0.0000 | -0.3687 | 0.3687 | 6 | 6 | 5 | 3 |
| Gardnerella.vaginalis | 0.0000 | -0.3687 | 0.3687 | 0 | 3 | 2 | 15 |
| Lactobacillus.crispatus_cluster | 0.0622 | -0.3137 | 0.4213 | 3 | 2 | 5 | 10 |
| Lactobacillus.gasseri_cluster | 0.0000 | -0.3687 | 0.3687 | 6 | 5 | 2 | 7 |
| Lactobacillus.iners | 0.0304 | -0.3422 | 0.3947 | 0 | 0 | 0 | 20 |
| Lactobacillus.jensenii | 0.0000 | -0.3687 | 0.3687 | 7 | 1 | 5 | 7 |
| Megasphaera.cluster52 | 0.0000 | -0.3687 | 0.3687 | 5 | 7 | 4 | 4 |
| Mycoplasma.hominis | 0.0306 | -0.3420 | 0.3949 | 12 | 4 | 2 | 2 |
| Parvimonas.OTU142 | 0.0000 | -0.3687 | 0.3687 | 8 | 6 | 4 | 2 |
| Peptoniphilus.indolicus | 0.0243 | -0.3476 | 0.3895 | 8 | 6 | 5 | 1 |
| Prevotella.OTU48 | 0.0000 | -0.3687 | 0.3687 | 12 | 3 | 4 | 1 |
| Prevotella.amnii | 0.0000 | -0.3687 | 0.3687 | 11 | 4 | 4 | 1 |
| Prevotella.bivia | 0.1428 | -0.2385 | 0.4860 | 5 | 4 | 6 | 5 |
| Prevotella.cluster2 | 0.0000 | -0.3687 | 0.3687 | 4 | 5 | 3 | 8 |
| Prevotella.disiens | 0.0000 | -0.3687 | 0.3687 | 14 | 3 | 2 | 1 |
| Sneathia.amnii | 0.0000 | -0.3687 | 0.3687 | 6 | 9 | 2 | 3 |
| Sneathia.sanguinegens | 0.0000 | -0.3687 | 0.3687 | 6 | 6 | 5 | 3 |
| Staphylococcus.cluster47 | 0.0000 | -0.3687 | 0.3687 | 8 | 5 | 3 | 4 |
| Streptococcus.agalactiae | 0.0288 | -0.3436 | 0.3934 | 13 | 2 | 3 | 2 |
| Streptococcus.anginosus | 0.0000 | -0.3687 | 0.3687 | 12 | 5 | 3 | 0 |
| TM7.OTU.H1 | 0.0000 | -0.3687 | 0.3687 | 13 | 4 | 2 | 1 |
| Ureaplasma.cluster23 | 0.0000 | -0.3687 | 0.3688 | 8 | 1 | 5 | 6 |
| X_Lachnospiraceae_.BVAB1 | 0.1208 | -0.2595 | 0.4686 | 7 | 5 | 1 | 7 |

* Cell XX denotes presence/absence of taxa in 2x2 contingency table within twin pair
1 = Absent; 2 = Present; Cell 11 = taxa absent in both members of a twin pair
ICC = Intraclass Correlation; LI = Lower Interval; UI = Upper Interval