# Culturing of female bladder bacteria reveals an interconnected urogenital microbiota

Thomas-White et al.

## Supplementary Material

**Supplementary Table 1: List of the metagenomic samples and the relative coverage of the bladder culture collection**

| ENA* Identifier | Coverage by Abundance (%) | Coverage by Genera (Total) | Coverage by Genera (%) |
|---|---|---|---|
| ERS685380 [https://www.ebi.ac.uk/ena/data/view/ERS685380] | 63.9 | 6 (10) | 60.0 |
| ERS685386 [https://www.ebi.ac.uk/ena/data/view/ERS685386] | 62.8 | 6 (8) | 75.0 |
| ERS685396 [https://www.ebi.ac.uk/ena/data/view/ERS685396] | 65.9 | 7 (12) | 58.3 |
| ERS685400 [https://www.ebi.ac.uk/ena/data/view/ERS685400] | 98.2 | 2 (2) | 100.0 |
| ERS685390 [https://www.ebi.ac.uk/ena/data/view/ERS685390] | 97.1 | 3 (3) | 100.0 |
| ERS685384 [https://www.ebi.ac.uk/ena/data/view/ERS685384] | 72.4 | 6 (9) | 66.7 |
| ERS685395 [https://www.ebi.ac.uk/ena/data/view/ERS685395] | 89.3 | 2 (2) | 100.0 |
| ERS685397 [https://www.ebi.ac.uk/ena/data/view/ERS685397] | 67.1 | 11 (17) | 64.7 |
| ERS685401 [https://www.ebi.ac.uk/ena/data/view/ERS685401] | 40.9 | 9 (15) | 60.0 |
| ERS685403 [https://www.ebi.ac.uk/ena/data/view/ERS685403] | 34.9 | 9 (12) | 75.0 |
| ERS685382 [https://www.ebi.ac.uk/ena/data/view/ERS685382] | 44.5 | 7 (17) | 41.2 |
| ERS685385 [https://www.ebi.ac.uk/ena/data/view/ERS685385] | 60.0 | 7 (11) | 63.6 |

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**Supplementary Table 2: List of the publicly available genomes of vaginal strains analysed in this study**. These vaginal genomes are all publicly available, the majority of which were collected by the HMP[1]. Vaginal genomes were only included if the metadata specifically stated that the strain had been collected from the vagina ("urogenital" isolates were excluded).

| Assembly Accession | Species |
|---|---|
| GCA_001546135.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546165.1/] | *Actinomyces neuii* MJR8396A |
| GCA_000758775.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758775.1/] | *Actinomyces* sp S4-C9 |
| GCA_000758755.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758755.1/] | *Actinomyces* sp S6-Spd3 |
| GCA_001552755.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001552755.1/] | *Aerococcus christensenii* KA00635 |
| GCA_000178435.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000178435.1/] | *Aerococcus viridans* ATCC11563 |
| GCA_001546145.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546145.1/] | *Alloscardovia omnicolens* CMW7705A |
| GCA_000758765.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758765.1/] | *Anaerococcus lactolyticus* S7-1-13 |
| GCA_001546165.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546165.1/] | *Anaerococcus tetradius* MJR8151 |
| GCA_000758825.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758825.1/] | *Arcanobacterium* sp S3PF19 |
| GCA_001552785.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001552785.1/] | *Atopobium deltae* LSCR 12804 |
| GCA_000758945.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758945.1/] | *Atopobium parvulum* DNF00906 |
| GCA_000159235.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000159235.2/] | *Atopobium vaginae* DSM15829 |
| GCA_001546215.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546215.1/] | *Bacillus coagulans* GED7749B |
| GCA_001552765.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001552765.1/] | Bacteroidales bacterium KA00344 |
| GCA_001546225.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546225.1/] | *Bifidobacterium bifidum* MJR8628B |
| GCA_001546235.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546235.1/] | *Bifidobacterium breve* GED8481 |
| GCA_000466545.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000466545.1/] | *Bifidobacterium breve* JCP7499 |
| GCA_000146775.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000146775.1/] | *Bifidobacterium dentium* ATCC27679 |
| GCA_000759055.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759055.1/] | *Corynebacterium tuscaniense* DNF00037 |
| GCA_001552885.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001552885.1/] | Clostridiales bacterium KA00274 |
| GCA_000758905.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758905.1/] | Clostridiales bacterium S5-A14a |

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|---|---|
| GCA_001552965.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001552965.1/] | *Corynebacterium* sp DNF00584 |
| GCA_000194985.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000194985.1/] | *Dialister micraerophilus* DSM19965 |
| GCF_001546375.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546375.1/] | *Enterococcus faecium* MJR8396B |
| GCA_000159695.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000159695.1/] | *Finegoldia magna* ATCC53516 |
| GCA_000178895.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000178895.1/] | *Fusobacterium nucleatum* ATCC23726 |
| GCA_001546435.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546435.1/] | *Fusobacterium nucleatum* MJR7757B |
| GCA_001546445.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546445.1/] | *Gardnerella vaginalis* GED7275B |
| GCA_001546455.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546455.1/] | *Gardnerella vaginalis* GED7760B |
| GCA_001553005.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553005.1/] | *Gemella asaccharolytica* KA00071 |
| GCA_001553035.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553035.1/] | *Gemella haemolysans* DNF01167 |
| GCA_001552975.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001552975.1/] | *Lachnoanaerobaculum saburreum* DNF00896 |
| GCA_000177035.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000177035.2/] | *Lactobacillus gasseri* SV-16A-US |
| GCA_000161915.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000161915.2/] | *Lactobacillus crispatus* MV-1A-US |
| GCA_000176975.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000176975.2/] | *Lactobacillus crispatus* SJ-3C-US |
| GCA_001541385.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001541385.1/] | *Lactobacillus crispatus* VMC3 |
| GCA_001541405.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001541405.1/] | *Lactobacillus crispatus* VMC4 |
| GCA_001541515.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001541515.1/] | *Lactobacillus crispatus* VMC5 |
| GCA_001541535.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001541535.1/] | *Lactobacillus crispatus* VMC7 |
| GCA_001541585.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001541585.1/] | *Lactobacillus crispatus* VMC8 |
| GCA_000175055.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000175055.1/] | *Lactobacillus gasseri* 202-4 |
| GCA_000176995.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000176995.2/] | *Lactobacillus gasseri* SJ-9E-US |
| GCA_000185405.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000185405.1/] | *Lactobacillus iners* ATCC55195 |
| GCA_000179955.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000179955.1/] | *Lactobacillus iners* LEAF 2052A-d |
| GCA_000149145.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000149145.2/] | *Lactobacillus iners* SPIN 2503V10-d |

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|---|---|
| GCA_000162435.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000162435.1/] | *Lactobacillus jensenii* 115-3-CHN |
| GCA_000162335.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000162335.1/] | *Lactobacillus jensenii* SJ-7A-US |
| GCA_000175035.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000175035.1/] | *Lactobacillus jensenii* 269-3 |
| GCA_000180015.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000180015.1/] | *Lactobacillus oris* PB013-T2-3 |
| GCA_000699985.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000699985.1/] | *Lactobacillus rhamnosus* 51B |
| GCA_000179475.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000179475.1/] | *Lactobacillus salivarius* ACS-116-V-Col5a |
| GCA_000159435.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000159435.1/] | *Lactobacillus vaginalis* ATCC49540 |
| GCA_001546855.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546855.1/] | *Megasphaera* sp MJR8396C |
| GCA_000146285.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000146285.1/] | *Mobiluncus curtisii* Subsp curtisii ATCC35241 |
| GCA_000185445.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000185445.1/] | *Mobiluncus curtisii* Subsp holmesii ATCC35242 |
| GCA_000146895.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000146895.1/] | *Mobiluncus mulieris* ATCC35239 |
| GCA_000164135.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000164135.1/] | *Mycobacterium parascrofulaceum* BAA614 |
| GCA_001553055.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553055.1/] | *Olsenella* sp DNF00959 |
| GCA_001553085.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553085.1/] | *Parvimonas* sp KA00067 |
| GCA_001553115.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553115.1/] | *Peptoniphilus* coxii DNF00729 |
| GCA_000146345.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000146345.1/] | *Peptoniphilus* duerdenii BAA-1640 |
| GCA_001546555.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546555.1/] | *Peptoniphilus* harei CMW7756A |
| GCA_001553125.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553125.1/] | *Peptoniphilus* sp DNF00840 |
| GCA_001553145.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553145.1/] | *Peptostreptococcus anaerobius* KA00810 |
| GCA_000758885.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758885.1/] | *Peptostreptococcus* sp MV1 |
| GCA_000759315.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759315.1/] | *Prevotella amnii* DNF00058 |
| GCA_001553225.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553225.1/] | *Prevotella amnii* DNF00307 |
| GCA_000759045.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759045.1/] | *Prevotella bivia* DNF00188 |
| GCA_000759245.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759245.1/] | *Prevotella bivia* DNF00320 |

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|---|---|
| GCA_000759165.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759165.1/] | *Prevotella bivia* DNF00650 |
| GCA_001546565.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546565.2/] | *Prevotella bivia* GED7760C |
| GCA_001546595.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546595.1/] | *Prevotella corporis* MJR7716 |
| GCA_000759205.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759205.1/] | *Prevotella denticola* DNF00960 |
| GCA_000759225.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759225.1/] | *Prevotella disiens* DNF00882 |
| GCA_000762405.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000762405.1/] | *Prevotella timonensis* S9-PR14 |
| GCA_001546875.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546875.1/] | *Propionibacterium avidum* MJR7694 |
| GCA_001553525.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553525.1/] | *Proteus mirabilis* GED7834 |
| GCA_000759125.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759125.1/] | *Staphylococcus haemolyticus* DNF00585 |
| GCA_001546615.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546615.1/] | *Staphylococcus lugdunensis* MJR7738 |
| GCA_001546635.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546635.1/] | *Staphylococcus simulans* MJR7712 |
| GCA_000146405.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000146405.1/] | *Streptococcus equinus* ATCC700338 |
| GCA_001546795.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546795.1/] | *Streptococcus mitis* CMW7705B |
| GCA_001552895.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001552895.1/] | *Tissierella bacterium* KA00581 |
| GCA_000758845.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000758845.1/] | *Tissierella bacterium* S7-1-4 |
| GCA_001553285.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553285.1/] | *Varibaculum cambriense* DNF00696 |
| GCA_001553315.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553315.1/] | *Veillonella dispar* DNF00926 |
| GCA_000759285.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000759285.1/] | *Veillonella montpellierensis* DNF00314 |
| GCA_000215025.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000215025.2/] | *Veillonella parvula* ACS-068-V-Sch12 |
| GCA_001553345.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553345.1/] | *Veillonella* sp DNF00869 |
| GCA_001553355.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553355.1/] | Veillonellaceae bacterium DNF00626 |
| GCA_001553395.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553395.1/] | Veillonellaceae bacterium DNF00751 |
| GCA_001553405.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001553405.1/] | Veillonellaceae bacterium KA00182 |

**Supplementary Table 3: List of genomes from gastrointestinal strains analysed.** These strains were originally collected in a previous study[2].

| ENA* id | Species |
|---|---|
| ERR1022418 [https://www.ebi.ac.uk/ena/data/view/ERR1022418] | *Intestinibacter bartlettii* |
| ERR1022321 [https://www.ebi.ac.uk/ena/data/view/ERR1022321] | *Roseburia faecis* |
| ERR1022435 [https://www.ebi.ac.uk/ena/data/view/ERR1022435] | *Blautia* nov. |
| ERR1022358 [https://www.ebi.ac.uk/ena/data/view/ERR1022358] | *Bacteroides vulgatus* |
| ERR1022308 [https://www.ebi.ac.uk/ena/data/view/ERR1022308] | Lachnospiraceae nov. |
| ERR1022387 [https://www.ebi.ac.uk/ena/data/view/ERR1022387] | *Lachnoclostridium* nov. |
| ERR1022421 [https://www.ebi.ac.uk/ena/data/view/ERR1022421] | *Sarcina* nov. |
| ERR1022291 [https://www.ebi.ac.uk/ena/data/view/ERR1022291] | *Ruminococcus torques* |
| ERR1022428 [https://www.ebi.ac.uk/ena/data/view/ERR1022428] | *Dorea longicatena* |
| ERR1022370 [https://www.ebi.ac.uk/ena/data/view/ERR1022370] | *Megasphaera* nov. |
| ERR1022360 [https://www.ebi.ac.uk/ena/data/view/ERR1022360] | *Bacteroides uniformis* |
| ERR1022433 [https://www.ebi.ac.uk/ena/data/view/ERR1022433] | Lachnospiraceae nov. |
| ERR1022323 [https://www.ebi.ac.uk/ena/data/view/ERR1022323] | *Turicibacter sanguinis* |
| ERR1022329 [https://www.ebi.ac.uk/ena/data/view/ERR1022329] | *Bacteroides salyersiae* |
| ERR1022279 [https://www.ebi.ac.uk/ena/data/view/ERR1022279] | *Faecalibacterium prausnitzii* |
| ERR1022288 [https://www.ebi.ac.uk/ena/data/view/ERR1022288] | *Anaerostipes hadrus* |
| ERR1022305 [https://www.ebi.ac.uk/ena/data/view/ERR1022305] | *Lachnoclostridium* nov. |
| ERR1022450 [https://www.ebi.ac.uk/ena/data/view/ERR1022450] | *Intestinimonas butyriciproducens* |
| ERR1022307 [https://www.ebi.ac.uk/ena/data/view/ERR1022307] | *Fusicatenibacter saccharivorans* |
| ERR1022345 [https://www.ebi.ac.uk/ena/data/view/ERR1022345] | *Roseburia inulinivorans* |
| ERR1022281 [https://www.ebi.ac.uk/ena/data/view/ERR1022281] | *Parabacteroides distasonis* |
| ERR1022299 [https://www.ebi.ac.uk/ena/data/view/ERR1022299] | Ruminococcaceae nov. |

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|---|---|
| ERR1022335 [https://www.ebi.ac.uk/ena/data/view/ERR1022335] | *Bifidobacterium bifidum* |
| ERR1022408 [https://www.ebi.ac.uk/ena/data/view/ERR1022408] | *Ruminococcus bicirculans* |
| ERR1022460 [https://www.ebi.ac.uk/ena/data/view/ERR1022460] | *Bacteroides caccae* |
| ERR1022381 [https://www.ebi.ac.uk/ena/data/view/ERR1022381] | Lachnospiraceae nov. |
| ERR1022320 [https://www.ebi.ac.uk/ena/data/view/ERR1022320] | *Bifidobacterium adolescentis* |
| ERR1022452 [https://www.ebi.ac.uk/ena/data/view/ERR1022452] | Ruminococcaceae nov. |
| ERR1022474 [https://www.ebi.ac.uk/ena/data/view/ERR1022474] | *Roseburia intestinalis* |
| ERR1022432 [https://www.ebi.ac.uk/ena/data/view/ERR1022432] | *Ruminococcus faecis* |
| ERR1022275 [https://www.ebi.ac.uk/ena/data/view/ERR1022275] | *Blautia* nov. |
| ERR1022422 [https://www.ebi.ac.uk/ena/data/view/ERR1022422] | *Anaerostipes hadrus* |
| ERR1022313 [https://www.ebi.ac.uk/ena/data/view/ERR1022313] | Ruminococcaceae nov. |
| ERR1022457 [https://www.ebi.ac.uk/ena/data/view/ERR1022457] | *Bacteroides fragilis* |
| ERR1022414 [https://www.ebi.ac.uk/ena/data/view/ERR1022414] | *Bacteroides cellulosilyticus* |
| ERR1022352 [https://www.ebi.ac.uk/ena/data/view/ERR1022352] | *Lachnospira pectinoschiza* |
| ERR1022391 [https://www.ebi.ac.uk/ena/data/view/ERR1022391] | *Lachnospira* nov. |
| ERR1022289 [https://www.ebi.ac.uk/ena/data/view/ERR1022289] | Lachnospiraceae nov. |
| ERR1022319 [https://www.ebi.ac.uk/ena/data/view/ERR1022319] | *Bacteroides finegoldii* |
| ERR1022325 [https://www.ebi.ac.uk/ena/data/view/ERR1022325] | *Ruminococcus torques* |
| ERR1022304 [https://www.ebi.ac.uk/ena/data/view/ERR1022304] | *Ruminococcus torques* |
| ERR1022274 [https://www.ebi.ac.uk/ena/data/view/ERR1022274] | Lachnospiraceae nov. |
| ERR1022347 [https://www.ebi.ac.uk/ena/data/view/ERR1022347] | *Sarcina* nov. |
| ERR1022478 [https://www.ebi.ac.uk/ena/data/view/ERR1022478] | Lachnospiraceae nov. |
| ERR1022394 [https://www.ebi.ac.uk/ena/data/view/ERR1022394] | *Lachnospira* nov. |
| ERR1022280 [https://www.ebi.ac.uk/ena/data/view/ERR1022280] | *Turicibacter sanguinis* |

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|---|---|
| ERR1022424 [https://www.ebi.ac.uk/ena/data/view/ERR1022424] | *Blautia* nov. |
| ERR1022353 [https://www.ebi.ac.uk/ena/data/view/ERR1022353] | Lachnospiraceae nov. |
| ERR1022405 [https://www.ebi.ac.uk/ena/data/view/ERR1022405] | *Lachnoclostridium* nov. |
| ERR1022437 [https://www.ebi.ac.uk/ena/data/view/ERR1022437] | *Fusicatenibacter saccharivorans* |
| ERR1022466 [https://www.ebi.ac.uk/ena/data/view/ERR1022466] | *Romboutsia* nov. |
| ERR1022276 [https://www.ebi.ac.uk/ena/data/view/ERR1022276] | *Lachnoclostridium* nov. |
| ERR1022480 [https://www.ebi.ac.uk/ena/data/view/ERR1022480] | Lachnospiraceae nov. |
| ERR1022458 [https://www.ebi.ac.uk/ena/data/view/ERR1022458] | *Bacteroides vulgatus* |
| ERR1022378 [https://www.ebi.ac.uk/ena/data/view/ERR1022378] | *Blautia* nov. |
| ERR1022464 [https://www.ebi.ac.uk/ena/data/view/ERR1022464] | Erysipelotrichaceae nov. |
| ERR1022380 [https://www.ebi.ac.uk/ena/data/view/ERR1022380] | Lachnospiraceae nov. |
| ERR1022339 [https://www.ebi.ac.uk/ena/data/view/ERR1022339] | *Blautia* nov. |
| ERR1022382 [https://www.ebi.ac.uk/ena/data/view/ERR1022382] | *Coprococcus comes* |
| ERR1022349 [https://www.ebi.ac.uk/ena/data/view/ERR1022349] | *Eubacterium ramulus* |
| ERR1022332 [https://www.ebi.ac.uk/ena/data/view/ERR1022332] | Erysipelotrichaceae nov. |
| ERR1022399 [https://www.ebi.ac.uk/ena/data/view/ERR1022399] | *Eubacterium* rectale |
| ERR1022361 [https://www.ebi.ac.uk/ena/data/view/ERR1022361] | *Bacteroides* nov. |
| ERR1022351 [https://www.ebi.ac.uk/ena/data/view/ERR1022351] | Lachnospiraceae nov. |
| ERR1022365 [https://www.ebi.ac.uk/ena/data/view/ERR1022365] | *Enorma massiliensis* |
| ERR1022309 [https://www.ebi.ac.uk/ena/data/view/ERR1022309] | *Dorea longicatena* |
| ERR1022455 [https://www.ebi.ac.uk/ena/data/view/ERR1022455] | Christensenellaceae nov. |
| ERR1022282 [https://www.ebi.ac.uk/ena/data/view/ERR1022282] | *Collinsella aerofaciens* |
| ERR1022371 [https://www.ebi.ac.uk/ena/data/view/ERR1022371] | *Sarcina* nov. |
| ERR1022416 [https://www.ebi.ac.uk/ena/data/view/ERR1022416] | *Collinsella aerofaciens* |

| | |
|---|---|
| ERR1022412 [https://www.ebi.ac.uk/ena/data/view/ERR1022412] | *Bacteroides uniformis* |
| ERR1022316 [https://www.ebi.ac.uk/ena/data/view/ERR1022316] | *Sarcina* nov. |
| ERR1022295 [https://www.ebi.ac.uk/ena/data/view/ERR1022295] | *Blautia* nov. |
| ERR1022395 [https://www.ebi.ac.uk/ena/data/view/ERR1022395] | *Intestinibacter bartlettii* |
| ERR1022369 [https://www.ebi.ac.uk/ena/data/view/ERR1022369] | Erysipelotrichaceae nov. |
| ERR1022294 [https://www.ebi.ac.uk/ena/data/view/ERR1022294] | *Blautia* nov. |
| ERR1022411 [https://www.ebi.ac.uk/ena/data/view/ERR1022411] | *Bacteroides vulgatus* |
| ERR1022434 [https://www.ebi.ac.uk/ena/data/view/ERR1022434] | Lachnoclostridium nov. |
| ERR1022392 [https://www.ebi.ac.uk/ena/data/view/ERR1022392] | Lachnoclostridium nov. |
| ERR1022333 [https://www.ebi.ac.uk/ena/data/view/ERR1022333] | Erysipelotrichaceae nov. |
| ERR1022413 [https://www.ebi.ac.uk/ena/data/view/ERR1022413] | *Bacteroides thetaiotaomicron* |
| ERR1022463 [https://www.ebi.ac.uk/ena/data/view/ERR1022463] | *Turicibacter sanguinis* |
| ERR1022315 [https://www.ebi.ac.uk/ena/data/view/ERR1022315] | *Blautia hydrogenotrophica* |
| ERS417308 [https://www.ebi.ac.uk/ena/data/view/ERS417308] | *Bifidobacterium adolescentis* |
| ERR1022471 [https://www.ebi.ac.uk/ena/data/view/ERR1022471] | *Blautia luti* |
| ERR1022363 [https://www.ebi.ac.uk/ena/data/view/ERR1022363] | *Bacteroides uniformis* |
| ERR1022454 [https://www.ebi.ac.uk/ena/data/view/ERR1022454] | *Intestinimonas* nov. |
| ERR1022400 [https://www.ebi.ac.uk/ena/data/view/ERR1022400] | *Fusicatenibacter saccharivorans* |
| ERR1022453 [https://www.ebi.ac.uk/ena/data/view/ERR1022453] | *Anaerotruncus colihominis* |
| ERR1022465 [https://www.ebi.ac.uk/ena/data/view/ERR1022465] | *Romboutsia* nov. |
| ERR1022439 [https://www.ebi.ac.uk/ena/data/view/ERR1022439] | *Eisenbergiella tayi* |
| ERR1022423 [https://www.ebi.ac.uk/ena/data/view/ERR1022423] | *Anaerostipes hadrus* |
| ERR1022481 [https://www.ebi.ac.uk/ena/data/view/ERR1022481] | Lachnospiraceae nov. |
| ERR1022272 [https://www.ebi.ac.uk/ena/data/view/ERR1022272] | Lachnospiraceae nov. |

| | |
|---|---|
| ERR1022286 [https://www.ebi.ac.uk/ena/data/view/ERR1022286] | *Mitsuokella jalaludinii* |
| ERR1022300 [https://www.ebi.ac.uk/ena/data/view/ERR1022300] | *Collinsella aerofaciens* |
| ERR1022342 [https://www.ebi.ac.uk/ena/data/view/ERR1022342] | Lachnospiraceae nov. |
| ERR1022398 [https://www.ebi.ac.uk/ena/data/view/ERR1022398] | Lachnospiraceae nov. |
| ERR1022443 [https://www.ebi.ac.uk/ena/data/view/ERR1022443] | Ruminococcaceae nov. |
| ERR1022431 [https://www.ebi.ac.uk/ena/data/view/ERR1022431] | Lachnospiraceae nov. |
| ERR1022456 [https://www.ebi.ac.uk/ena/data/view/ERR1022456] | *Bacteroides* nov. |
| ERR1022440 [https://www.ebi.ac.uk/ena/data/view/ERR1022440] | *Ruminiclostridium* nov. |
| ERR1022318 [https://www.ebi.ac.uk/ena/data/view/ERR1022318] | *Eubacterium rectale* |
| ERR1022451 [https://www.ebi.ac.uk/ena/data/view/ERR1022451] | Ruminococcaceae nov. |
| ERR1022311 [https://www.ebi.ac.uk/ena/data/view/ERR1022311] | Ruminococcaceae nov. |
| ERR1022445 [https://www.ebi.ac.uk/ena/data/view/ERR1022445] | Ruminococcaceae nov. |
| ERR1022426 [https://www.ebi.ac.uk/ena/data/view/ERR1022426] | *Blautia* nov. |
| ERR1022344 [https://www.ebi.ac.uk/ena/data/view/ERR1022344] | *Roseburia* nov. |
| ERR1022334 [https://www.ebi.ac.uk/ena/data/view/ERR1022334] | Clostridiales incertae sedis nov. |
| ERR1022430 [https://www.ebi.ac.uk/ena/data/view/ERR1022430] | *Lachnoclostridium* nov. |
| ERR1022368 [https://www.ebi.ac.uk/ena/data/view/ERR1022368] | Erysipelotrichaceae nov. |
| ERR1022338 [https://www.ebi.ac.uk/ena/data/view/ERR1022338] | *Blautia* nov. |
| ERR1022442 [https://www.ebi.ac.uk/ena/data/view/ERR1022442] | Ruminococcaceae nov. |
| ERR1022417 [https://www.ebi.ac.uk/ena/data/view/ERR1022417] | Erysipelotrichaceae nov. |
| ERR1022357 [https://www.ebi.ac.uk/ena/data/view/ERR1022357] | *Ruminococcus torques* |
| ERR1022373 [https://www.ebi.ac.uk/ena/data/view/ERR1022373] | Clostridiaceae nov. |
| ERR1022310 [https://www.ebi.ac.uk/ena/data/view/ERR1022310] | *Ruminococcus gnavus* |
| ERR1022429 [https://www.ebi.ac.uk/ena/data/view/ERR1022429] | Lachnospiraceae nov. |

| | |
|---|---|
| ERR1022326 [https://www.ebi.ac.uk/ena/data/view/ERR1022326] | *Anaerostipes hadrus* |
| ERR1022390 [https://www.ebi.ac.uk/ena/data/view/ERR1022390] | Lachnospiraceae nov. |
| ERR1022362 [https://www.ebi.ac.uk/ena/data/view/ERR1022362] | *Bacteroides faecis* |
| ERR1022285 [https://www.ebi.ac.uk/ena/data/view/ERR1022285] | *Sarcina* nov. |
| ERR1022355 [https://www.ebi.ac.uk/ena/data/view/ERR1022355] | *Oscillibacter* nov. |
| ERR1022346 [https://www.ebi.ac.uk/ena/data/view/ERR1022346] | *Coprococcus eutactus* |
| ERR1022441 [https://www.ebi.ac.uk/ena/data/view/ERR1022441] | Ruminiclostridium nov. |
| ERR1022366 [https://www.ebi.ac.uk/ena/data/view/ERR1022366] | *Bifidobacterium adolescentis* |
| ERR1022407 [https://www.ebi.ac.uk/ena/data/view/ERR1022407] | *Oscillibacter* nov. |
| ERR1022468 [https://www.ebi.ac.uk/ena/data/view/ERR1022468] | *Sarcina* nov. |
| ERR1022415 [https://www.ebi.ac.uk/ena/data/view/ERR1022415] | *Parabacteroides distasonis* |
| ERR1022343 [https://www.ebi.ac.uk/ena/data/view/ERR1022343] | Lachnospiraceae nov. |
| ERR1022402 [https://www.ebi.ac.uk/ena/data/view/ERR1022402] | Lachnospiraceae nov. |
| ERR1022409 [https://www.ebi.ac.uk/ena/data/view/ERR1022409] | Ruminococcaceae nov. |
| ERR1022427 [https://www.ebi.ac.uk/ena/data/view/ERR1022427] | *Coprococcus comes* |
| ERR1022273 [https://www.ebi.ac.uk/ena/data/view/ERR1022273] | *Lachnoclostridium* nov. |
| ERR1022296 [https://www.ebi.ac.uk/ena/data/view/ERR1022296] | *Blautia wexlerae* |
| ERR1022449 [https://www.ebi.ac.uk/ena/data/view/ERR1022449] | Ruminococcaceae nov. |
| ERR1022379 [https://www.ebi.ac.uk/ena/data/view/ERR1022379] | *Blautia luti* |
| ERR1022278 [https://www.ebi.ac.uk/ena/data/view/ERR1022278] | *Coprococcus* nov. |
| ERR1022448 [https://www.ebi.ac.uk/ena/data/view/ERR1022448] | Ruminococcaceae nov. |
| ERR1022283 [https://www.ebi.ac.uk/ena/data/view/ERR1022283] | *Bifidobacterium adolescentis* |
| ERR1022322 [https://www.ebi.ac.uk/ena/data/view/ERR1022322] | *Bacteroides uniformis* |
| ERR1022446 [https://www.ebi.ac.uk/ena/data/view/ERR1022446] | *Flavonifractor plautii* |

| | |
|---|---|
| ERR1022419 [https://www.ebi.ac.uk/ena/data/view/ERR1022419] | Clostridiales incertae sedis nov. |
| ERR1022293 [https://www.ebi.ac.uk/ena/data/view/ERR1022293] | *Roseburia inulinivorans* |
| ERR1022447 [https://www.ebi.ac.uk/ena/data/view/ERR1022447] | *Pseudoflavonifractor capillosus* |
| ERR1022386 [https://www.ebi.ac.uk/ena/data/view/ERR1022386] | Lachnospiraceae nov. |
| ERR1022277 [https://www.ebi.ac.uk/ena/data/view/ERR1022277] | Lachnospiraceae nov. |
| ERR1022331 [https://www.ebi.ac.uk/ena/data/view/ERR1022331] | *Bacteroides thetaiotaomicron* |
| ERR1022367 [https://www.ebi.ac.uk/ena/data/view/ERR1022367] | *Turicibacter sanguinis* |
| ERR1022375 [https://www.ebi.ac.uk/ena/data/view/ERR1022375] | *Romboutsia* nov. |
| ERR1022401 [https://www.ebi.ac.uk/ena/data/view/ERR1022401] | *Lachnospira pectinoschiza* |
| ERR1022482 [https://www.ebi.ac.uk/ena/data/view/ERR1022482] | *Eubacterium rectale* |

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**Supplementary Table 4: List of strains found in female bladder but not in the vagina - from the comparison of bladder and vaginal strain collections.** For further metadata on these strains refer to Supplementary Data 1.

| Species | ENA* id | Genome size |
|---|---|---|
| *Pseudomonas aeruginosa* | ERR1045860 [https://www.ebi.ac.uk/ena/data/view/ERR1045860] | 6035570 |
| *Gordonia terrae* | ERR1203657 [https://www.ebi.ac.uk/ena/data/view/ERR1203657] | 5703010 |
| *Bacillus infantis* | ERR1203601 [https://www.ebi.ac.uk/ena/data/view/ERR1203601] | 5204484 |
| *Klebsiella pneumoniae* | ERR1045826 [https://www.ebi.ac.uk/ena/data/view/ERR1045826] | 5102152 |
| *Escherichia coli* | ERR1045836 [https://www.ebi.ac.uk/ena/data/view/ERR1045836] | 5148822 |
| *Escherichia coli* | ERR1045830 [https://www.ebi.ac.uk/ena/data/view/ERR1045830] | 5013219 |
| *Escherichia coli* | ERR1045825 [https://www.ebi.ac.uk/ena/data/view/ERR1045825] | 5000645 |
| *Bacillus idriensis* | ERR1203634 [https://www.ebi.ac.uk/ena/data/view/ERR1203634] | 4598139 |
| *Enterobacter cloacae* | ERR1939923 [https://www.ebi.ac.uk/ena/data/view/ERR1939923] | 4655730 |
| *Enterobacter cloacae* | ERR1939938 [https://www.ebi.ac.uk/ena/data/view/ERR1939938] | 4654361 |
| *Enterobacter cloacae* | ERR1203667 [https://www.ebi.ac.uk/ena/data/view/ERR1203667] | 4649113 |

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**Supplementary Table 5: List of strains that are highly similar between female bladder and vagina whole genome datasets.** For further metadata on these strains, refer to Supplementary Data 1.

| Species | Bladder strain ENI* ID | Vaginal strain Assembly Accession | ANI** (%) |
|---|---|---|---|
| *Actinomyces neuii* | ERR1045850 [https://www.ebi.ac.uk/ena/data/view/ERR1045850] | GCA_001546135.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546165.1/] | 98.4717 |
| *Actinomyces neuii* | ERR1045813 [https://www.ebi.ac.uk/ena/data/view/ERR1045813] | GCA_001546135.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_001546165.1/] | 98.6541 |
| *Lactobacillus crispatus* | ERR1045852 [https://www.ebi.ac.uk/ena/data/view/ERR1045852] | GCA_000176975.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000176975.2/] | 99.2249 |
| *Lactobacillus crispatus* | ERR1045847 [https://www.ebi.ac.uk/ena/data/view/ERR1045847] | GCA_000176975.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000176975.2/] | 99.7258 |
| *Lactobacillus crispatus* | ERR1939956 [https://www.ebi.ac.uk/ena/data/view/ERR1939956] | GCA_000176975.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000176975.2/] | 99.1365 |
| *Lactobacillus gasseri* | ERR1939928 [https://www.ebi.ac.uk/ena/data/view/ERR1939928] | GCA_000175055.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000175055.1/] | 99.3113 |
| *Lactobacillus gasseri* | ERR1045824 [https://www.ebi.ac.uk/ena/data/view/ERR1045824] | GCA_000175055.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000175055.1/] | 99.4368 |
| *Lactobacillus gasseri* | ERR1939936 [https://www.ebi.ac.uk/ena/data/view/ERR1939936] | GCA_000175055.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000175055.1/] | 99.4413 |
| *Lactobacillus jensenii* | ERR1045855 [https://www.ebi.ac.uk/ena/data/view/ERR1045855] | GCA_000162335.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000162335.1/] | 99.8623 |

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**Average Nucleotide Identity

**Supplementary Table 6: Top 20 statistically enriched functional domains in the urogenital microbiota compared to the gastrointestinal microbiota**

| COG* ID | Function | Urogenital Bacteria (count) | GI Bacteria (count) | q-value |
|---|---|---|---|---|
| COG3425 | 3-hydroxy-3-methylglutaryl CoA synthase | 88 | 0 | $1.33 \times 10^{-18}$ |
| COG1780 | Protein involved in ribonucleotide reduction | 109 | 6 | $5.76 \times 10^{-16}$ |
| COG0431 | NAD(P)H-dependent FMN reductase | 104 | 5 | $6.52 \times 10^{-16}$ |
| COG4479 | Uncharacterized protein YozE, UPF0346 family | 72 | 0 | $3.45 \times 10^{-15}$ |
| COG4473 | Predicted ABC-type exoprotein transport system, permease component | 71 | 0 | $5.71 \times 10^{-15}$ |
| COG5503 | DNA-dependent RNA polymerase auxiliary subunit epsilon | 71 | 0 | $5.71 \times 10^{-15}$ |
| COG3407 | Mevalonate pyrophosphate decarboxylase | 83 | 2 | $8.15 \times 10^{-15}$ |
| COG3237 | Uncharacterized conserved protein YjbJ, UPF0337 family | 68 | 0 | $2.63 \times 10^{-14}$ |
| COG0276 | Protoheme ferro-lyase (ferrochelatase) | 67 | 0 | $4.40 \times 10^{-14}$ |
| COG4483 | Uncharacterized protein YqgQ, DUF910 family | 67 | 0 | $4.40 \times 10^{-14}$ |
| COG1577 | Mevalonate kinase | 84 | 3 | $5.84 \times 10^{-14}$ |
| COG1113 | L-asparagine transporter and related permeases | 112 | 10 | $1.40 \times 10^{-13}$ |
| COG3759 | Uncharacterized membrane protein | 64 | 0 | $2.07 \times 10^{-13}$ |
| COG1230 | Co/Zn/Cd efflux system component | 118 | 12 | $2.53 \times 10^{-13}$ |
| COG2141 | Flavin-dependent oxidoreductase, luciferase family (includes alkanesulfonate monooxygenase SsuD and methylene tetrahydromethanopterin reductase) | 70 | 1 | $2.74 \times 10^{-13}$ |
| COG4858 | Uncharacterized membrane-anchored protein | 60 | 1 | $4.26 \times 10^{-11}$ |
| COG1257 | Hydroxymethylglutaryl-CoA reductase | 78 | 5 | $5.17 \times 10^{-11}$ |
| COG1072 | Panthothenate kinase | 88 | 8 | $9.90 \times 10^{-11}$ |
| COG4835 | Uncharacterized protein | 52 | 0 | $1.19 \times 10^{-10}$ |
| COG5506 | Uncharacterized protein YueI, DUF2278 family | 52 | 0 | $1.19 \times 10^{-10}$ |

***** Clusters of Orthologous Groups of proteins

**Supplementary Table 7: Statistically enriched functional domains in the gastrointestinal microbiota compared to the urogenital microbiota**

| COG* ID | Function | GI Bacteria (count) | Urogenital Bacteria (count) | q-value |
|---|---|---|---|---|
| COG1873 | Sporulation protein YlmC, PRC-barrel domain family | 115 | 3 | $1.67 \times 10^{-21}$ |
| COG3854 | Stage III sporulation protein SpoIIIAA | 114 | 3 | $2.61 \times 10^{-21}$ |
| COG1453 | Predicted oxidoreductase of the aldo/keto reductase family | 117 | 4 | $7.85 \times 10^{-21}$ |
| COG2607 | Predicted ATPase, AAA+ superfamily | 111 | 3 | $1.01 \times 10^{-20}$ |
| COG3773 | Cell wall hydrolase CwlJ, involved in spore germination | 112 | 4 | $7.18 \times 10^{-20}$ |
| COG3546 | Mn-containing catalase (includes spore coat protein CotJC) | 121 | 7 | $7.27 \times 10^{-19}$ |
| COG3363 | Archaeal IMP cyclohydrolase | 97 | 3 | $6.47 \times 10^{-18}$ |
| COG1625 | Fe-S oxidoreductase, related to NifB/MoaA family | 94 | 3 | $2.67 \times 10^{-17}$ |
| COG2155 | Uncharacterized membrane protein YuzA, DUF378 family | 106 | 6 | $6.77 \times 10^{-17}$ |
| COG2221 | Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits | 103 | 6 | $2.54 \times 10^{-16}$ |
| COG4277 | Predicted DNA-binding protein with the Helix-hairpin-helix motif | 103 | 6 | $2.54 \times 10^{-16}$ |
| COG2198 | HPt (histidine-containing phosphotransfer) domain | 71 | 0 | $4.13 \times 10^{-16}$ |
| COG0700 | Spore maturation protein SpmB (function unknown) | 97 | 5 | $5.31 \times 10^{-16}$ |
| COG1838 | Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain | 116 | 11 | $4.30 \times 10^{-15}$ |
| COG1236 | RNA processing exonuclease, beta-lactamase fold, Cft2 family | 88 | 4 | $4.41 \times 10^{-15}$ |
| COG1803 | Methylglyoxal synthase | 132 | 16 | $7.87 \times 10^{-15}$ |
| COG1533 | DNA repair photolyase | 114 | 11 | $9.59 \times 10^{-15}$ |
| COG1149 | MinD superfamily P-loop ATPase, contains an inserted ferredoxin domain | 109 | 10 | $1.67 \times 10^{-14}$ |
| COG3581 | Predicted nucleotide-binding protein, sugar kinase/HSP70/actin superfamily | 105 | 9 | $1.89 \times 10^{-14}$ |
| COG4624 | Iron only hydrogenase large subunit, C-terminal domain | 140 | 21 | $1.44 \times 10^{-13}$ |

***** Clusters of Orthologous Groups of proteins

**Supplementary Table 8: Metadata for strains collected from the bladder and vagina of individual women. Corresponding to isolates in Figure 3.**

**A. Assembly statistics**

| Species (Subject ID) | Location | Patient ID | Relative Abundance by EQUC | Number of Contigs | N50 | Median Contig Length | Average coverage |
|---|---|---|---|---|---|---|---|
| *E. coli* (EST08) | | | | | | | |
| ERR2092972 [https://www.ebi.ac.uk/ena/data/view/ERR2092972/] | Bladder | P1 | No info | 169 | 115344 | 1355 | 66.8 |
| ERR2092973 [https://www.ebi.ac.uk/ena/data/view/ERR2092973/] | Vaginal | P1 | No info | 117 | 107673 | 9444 | 75.7 |
| *S. anginosus* (EST14) | | | | | | | |
| ERR2092974 [https://www.ebi.ac.uk/ena/data/view/ERR2092974/] | Bladder | P2 | 100% | 53 | 116687 | 4011 | 47.5 |
| ERR2092975 [https://www.ebi.ac.uk/ena/data/view/ERR2092975/] | Vaginal | P2 | 100% | 695 | 106465 | 265 | 34.9 |
| *L. iners* (EST16) | | | | | | | |
| ERR2092976 [https://www.ebi.ac.uk/ena/data/view/ERR2092976/] | Bladder | P3 | 88% | 10 | 99769 | 11783 | 412 |
| ERR2092977 [https://www.ebi.ac.uk/ena/data/view/ERR2092977/] | Vaginal | P3 | 43% | 7 | 839239 | 99769 | 214.0 |
| *L. crispatus* (EST10) | | | | | | | |
| ERR2092980 [https://www.ebi.ac.uk/ena/data/view/ERR2092980/] | Bladder | P4 | 100% | 238 | 19090 | 4827 | 395.5 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ERR2092981 [https://www.ebi.ac.uk/ena/data/view/ERR2092981/] | Vaginal | P4 | 36% | 286 | 20244 | 2877 | 291.8 |

**B. Other isolates found in each patient**

| Patient | Age | HRQL* | Bladder | CFU/ml | Vaginal | CFU/ml |
|---|---|---|---|---|---|---|
| *E. coli* (EST08) | 76 | 27.2 | *Aerococcus urinae* | No info | *Aerococcus urinae* | No info |
| | | | *Escherichia coli* | No info | *Escherichia coli* | No info |
| | | | *Gardnerella vaginalis* | No info | *Klebsiella pneumoniae* | No info |
| | | | *Klebsiella pneumoniae* | No info | *Alloscardovia omnicolens* | No info |
| *S. anginosus* (EST14) | 63 | 85.6 | *Streptococcus anginosus* | 10 | *Actinobaculum schaalii* | 2,000 |
| | | | | | *Actinomyces neuii* | 5,000 |
| | | | | | *Alloscardovia omnicolens* | 4,000 |
| | | | | | *Candida parapsilosis* | 20,500 |
| | | | | | *Corynebacterium amycolatum* | 400 |
| | | | | | *Corynebacterium aurimucosum* | 5,333 |
| | | | | | *Corynebacterium coyleae* | 12,000 |
| | | | | | *Enterococcus faecalis* | 100 |
| | | | | | *Facklamia hominis* | 1,500 |
| | | | | | *Globicatella sulfidiciens* | 200 |
| | | | | | Gram + rods - Unknown 1 | 2,000 |
| | | | | | *Proteus mirabilis* | 250 |
| | | | | | *Streptococcus agalactiae* | 20,000 |
| | | | | | *Streptococcus anginosus* | 1,000 |
| *L. iners* (EST16) | 62 | 43.2 | *Corynebacterium amycolatum* | 10 | *Aerococcus urinae* | 100,200 |
| | | | *Corynebacterium aurimucosum* | 10 | *Alloscardovia omnicolens* | 3,600 |
| | | | *Corynebacterium imitans* | 10 | *Corynebacterium amycolatum* | 3,050 |
| | | | *Corynebacterium urealyticam* | 20 | *Corynebacterium aurimucosum* | 10,000 |
| | | | *Lactobacillus iners* | 400 | *Corynebacterium coyleae* | 1,000 |
| | | | | | *Corynebacterium simulans* | 1,000 |
| | | | | | *Corynebacterium tuscaniense* | 3,000 |
| | | | | | *Enterococcus faecalis* | 8,833 |
| | | | | | *Lactobacillus iners* | 100,000 |
| | | | | | *Staphylococcus pasteuri* | 400 |
| | | | | | *Staphylococcus pettenkoferi* | 1,000 |
| | | | | | Unknown Gram - rods | 400 |
| *L. crispatus* | 58 | 69.6 | *Aerococcus urinae* | 27 | *Aerococcus urinae* | 1,000 |
| | | | *Corynebacterium* | 10 | *Arthrobacter cumminsii* | 5,000 |

| | | | | |
|---|---|---|---|---|
| (EST10) | *coyleae* | | | |
| | *Enterococcus faecalis* | 10 | *Candida parapsilosis* | 800 |
| | *Lactobacillus crispatus* | 45 | *Corynebacterium amycolatum* | 250 |
| | *Lactobacillus gasseri* | 20 | *Corynebacterium aurimucosum* | 100 |
| | Unknown Gram + rods | 10 | *Corynebacterium coyleae* | 300 |
| | | | *Enterococcus faecalis* | 675 |
| | | | *Lactobacillus crispatus* | 125,000 |
| | | | *Lactobacillus gasseri* | 55,350 |
| | | | *Micrococcus luteus* | 500 |
| | | | *Staphylococcus epidermidis* | 133 |
| | | | *Staphylococcus simulans* | 533 |
| | | | *Streptococcus anginosus* | 10,200 |
| | | | *Facklamia hominis* | 100,000 |

* Health Related Quality of Life

**Supplementary Table 9: A list of the publicly available reference genomes used for comparison, downloaded from NCBI**

| Species | Strain | Accession |
|---|---|---|
| *Escherichia coli* | BL21 | GCA_000009565.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000009565.1/] |
| *Escherichia coli* | K12_MG1655 | GCA_000005845.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000005845.2/] |
| *Escherichia coli* | O83:H1_NRG857C | GCA_000183345.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000183345.1/] |
| *Escherichia coli* | UPEC_CFT073 | GCA_000007445.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000007445.1/] |
| *Lactobacillus crispatus* | FB077 | GCA_000301135.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000301135.1/] |
| *Lactobacillus crispatus* | CTV-05 | GCA_000165885.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000165885.1/] |
| *Lactobacillus crispatus* | FB049-03 | GCA_000301115.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000301115.1/] |
| *Lactobacillus crispatus* | JV V01 | GCA_000160515.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000160515.1/] |
| *Lactobacillus crispatus* | 125-2-CHN | GCA_000162255.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000162255.1/] |
| *Lactobacillus crispatus* | 214-1 HMP | GCA_000177575.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000177575.1/] |
| *Lactobacillus crispatus* | ST1 | GCA_000091765.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000091765.1/] |
| *Lactobacillus iners* | DSM1335 | GCA_000160875.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000160875.1/] |
| *Lactobacillus iners* | ATCC55195 | GCA_000185405.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000185405.1/] |
| *Lactobacillus iners* | LactinV11V1-d | GCA_000149065.2 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000149065.1/] |
| *Lactobacillus iners* | AB1 | GCA_000177755.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000177755.1/] |
| *Streptococcus anginosus* | C1051 | GCA_000463465.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000463465.1/] |
| *Streptococcus* | C238 | GCA_000463505.1 |

| | | |
|---|---|---|
| *anginosus* | | [https://www.ncbi.nlm.nih.gov/assembly/GCF_000463505.1/] |
| *Streptococcus anginosus* | MAS624 | GCA_000478925.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000478925.1/] |
| *Streptococcus anginosus* | SA1_831165 | GCA_000831165.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000831165.1/] |
| *Streptococcus anginosus* | SK1138 | GCA_000287595.1 [https://www.ncbi.nlm.nih.gov/assembly/GCF_000287595.1/] |

**Supplementary Table 10: Table of Average Nucleotide Identity (ANI) values for *E. coli* isolates and reference strains**

| | ERR2092972 | *E. coli* BL21 | *E. coli* K12 MG1655 | *E. coli* O83H1 NRG857C | *E. coli* UPEC CFT073 |
|---|---|---|---|---|---|
| ERR2092973 | 99.72% | 98.43% | 98.56% | 96.50% | 96.45% |
| ERR2092972 | --------- | 98.33% | 98.56% | 96.45% | 96.43% |
| *E. coli* BL21 | | ---------- | 98.16% | 96.37% | 96.26% |
| *E. coli* K12 MG1655 | | | ---------- | 96.26% | 96.17% |
| *E. coli* UPEC CFT073 | | | | ---------- | 97.31% |

**Supplementary Table 11: Table of Average Nucleotide Identity (ANI) values for *S. anginosus* isolates and reference strains**

| | ERR2092975 | *S. ang* C1051 | *S. ang* C238 | *S. ang* MAS624 | *S. ang* SA1 | *S. ang* SK1138 |
|---|---|---|---|---|---|---|
| ERR2092974 | 99.77% | 95.32% | 93.91% | 93.55% | 93.70% | 93.06% |
| ERR2092975 | --------- | 95.25% | 94.0% | 93.53% | 93.70% | 93.11% |
| *S. ang* C1051 | | --------- | 94.05% | 94.09% | 93.62% | 93.58% |
| *S. ang* C238 | | | --------- | 97.66% | 93.19% | 92.62% |
| *S. ang* MAS624 | | | | ---------- | 92.97% | 92.62% |
| *S. ang* SA1 | | | | | --------- | 94.79% |

**Supplementary Table 12: Table of Average Nucleotide Identity (ANI) values for *L. iners* isolates and reference strains**

| | ERR2092976 | *L. iners* LactinV11V1d | *L. iners* DSM13335 | *L. iners* AB1 | *L. iners* ATCC 55195 |
|---|---|---|---|---|---|
| ERR2092977 | 99.99% | 97.29% | 97.88% | 97.80% | 97.49% |
| ERR2092976 | --------- | 97.29% | 97.89% | 97.81% | 97.51% |

| | | | | |
|---|---|---|---|---|
| *L. iners* LactinV11V1d | ---------- | 97.56% | 97.46% | 97.23% |
| *L. iners* DSM13335 | | ---------- | 99.95% | 97.75% |
| *L. iners* AB1 | | | --------- | 97.52% |
| *L. iners* ATCC 55195 | | | | ---------- |

**Supplementary Table 13: Tables of Average Nucleotide Identity (ANI) values for *L. crispatus* isolates and reference strains**

| | ERR 2092980 | *L. crisp* ST1 | *L. crisp* 2141 | *L. crisp* JVV01 | *L. crisp* FB049 | *L. crisp* FB077 | *L. crisp* CT05 |
|---|---|---|---|---|---|---|---|
| ERR2092981 | 99.80% | 96.71% | 98.28% | 97.99% | 98.94% | 99.23% | 99.08% |
| ERR2092980 | --------- | 96.57% | 98.42% | 98.18% | 98.99% | 99.28% | 99.25% |
| *L. crisp* ST1 | | --------- | 96.06% | 96.0% | 96.24% | 96.27% | 96.35% |
| *L. crisp* 2141 | | | --------- | 98.88% | 98.36% | 98.17% | 98.11% |
| *L. crisp* JVV01 | | | | --------- | 98.16% | 97.93% | 97.82% |
| *L. crisp* FB049 | | | | | --------- | 98.88% | 98.34% |
| *L. crisp* FB077 | | | | | | --------- | 98.51% |

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