Supplementary Figures S1-S5.

Urinary microbiome of reproductive-age healthy European women

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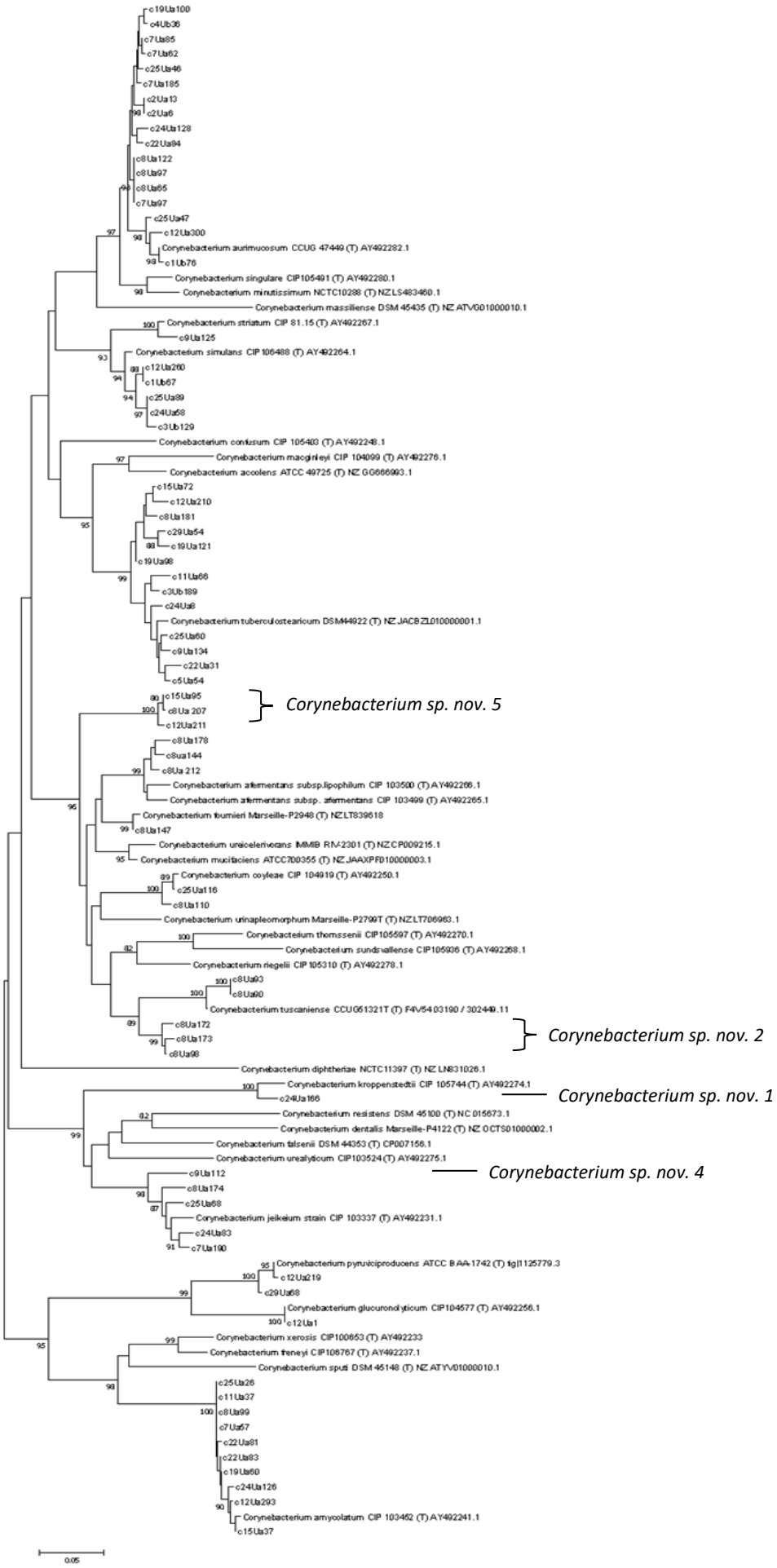
A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c22Ua94
c8Ua122
c8Ua97
c8Ua65
c7Ua97
c25Ua47
c12Ua300
Corynebacterium aurimucosum CCUG 47449 (T) AY492282.1
c1Ub76
Corynebacterium singulare CIP105491 (T) AY492280.1
Corynebacterium minutissimum NCTC10288 (T) NZ LS483460.1
Corynebacterium massiliense DSM 45435 (T) NZ ATVG01000010.1
Corynebacterium striatum CIP 81.15 (T) AY492267.1
c9Ua125
Corynebacterium simulans CIP 106488 (T) AY492264.1
c12Ua260
c1Ub67
c25Ua89
c24Ua58
c3Ub129
Corynebacterium confusum CIP 105403 (T) AY492248.1
Corynebacterium macginleyi CIP 104099 (T) AY492276.1
Corynebacterium accolens ATCC 49725 (T) NZ GG666993.1
c15Ua72
c12Ua210
c8Ua181
c29Ua54
c19Ua121
c19Ua98
c11Ua66
c3Ub189
c24Ua8
Corynebacterium tuberculostearicum DSM44922 (T) NZ JACBZL010000001.1
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c22Ua31
c5Ua54
c15Ua95
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Corynebacterium sp. nov. 5
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c8Ua 212
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Corynebacterium afermentans subsp. afermentans CIP 103499 (T) AY492265.1
Corynebacterium fournieri Marseille-P2948 (T) NZ LT839618
c8Ua147
Corynebacterium ureicelerivorans IMMIB RIV-2301 (T) NZ CP009215.1
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Corynebacterium kroppenstedtii CIP 105744 (T) AY492274.1
c24Ua166
Corynebacterium sp. nov. 1
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Corynebacterium freneyi CIP106767 (T) AY492237.1
Corynebacterium sputi DSM 45148 (T) NZ ATYV01000010.1
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c8Ua99
c7Ua67
c22Ua81
c22Ua83
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0.05

B

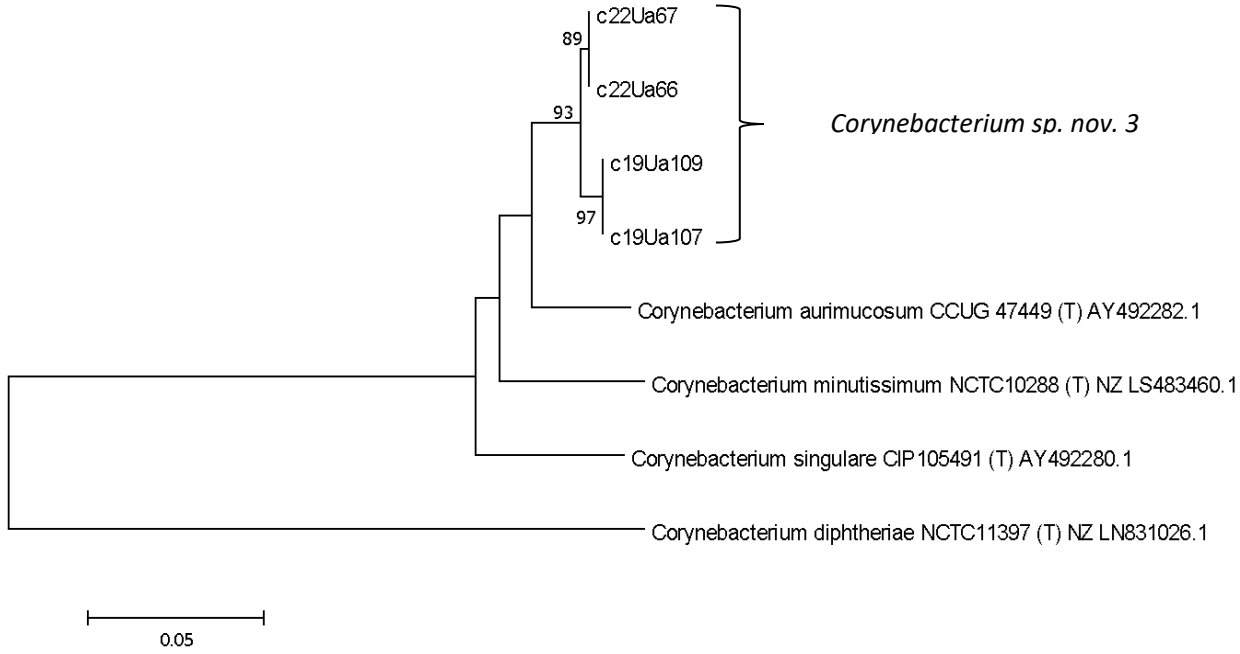


Figure S1. *Corynebacterium* putative novel species 1-5. Neighbor-joining tree based on *rpoB* gene sequences showing the phylogenetic relationships between *Corynebacterium* selected closely related type strains and putative novel species. Nucleotide sequences were extracted from draft/complete genomes obtained from the NCBI Assembly Database, for which the accession numbers are shown next to the strain designation. Bootstrap percentages (based on 1000 replications) are shown at nodes. Only values above 80% are shown. Bar, 0.05 substitutions per nucleotide position. Figure S1A represents isolates sequenced with primers F- CGWATGAACATYGGBCAGGT and R- TCCATYTCRCCRAARCGCTG with ~450 bp amplicon, while figure S1B includes isolated sequenced with primers F- CNTCBCACTAYGGNCGNATG and R- GAVCGNGCGTGRATCTTYTC with ~1700 bp amplicon.

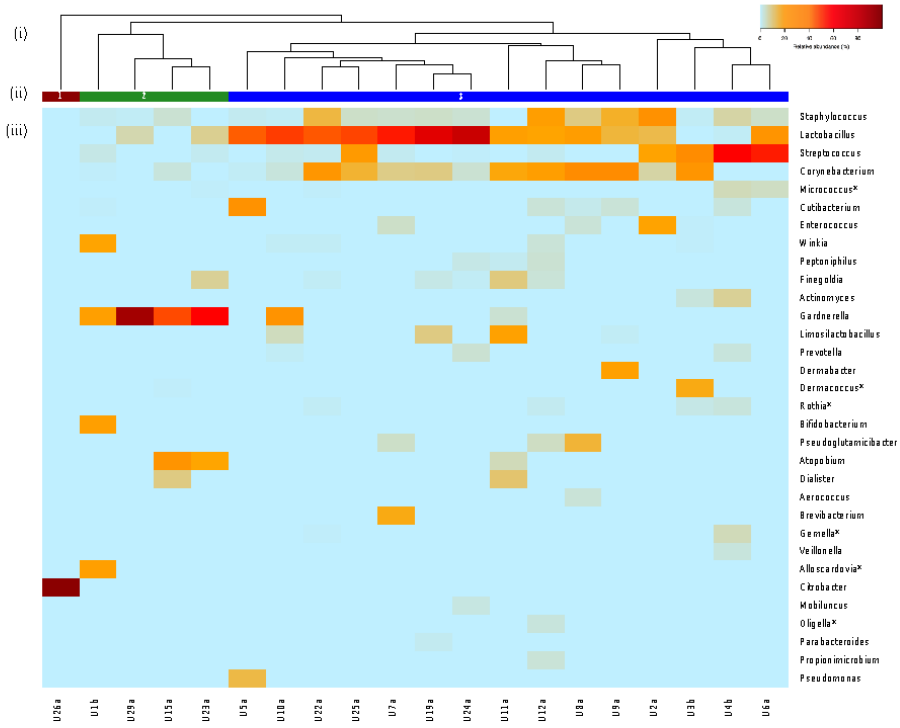


Figure S2. Genus-level community structure types of healthy FUM by culturomics.

(i) Hierarchical clustering of Bray-Curtis dissimilarity distance matrices on the relative proportions of CFU/ml within individual urine samples. (ii) Bars below dendrogram denote community structure types. (iii) Heatmap of relative abundances of bacterial genera within each urinary microbiota. Only genera that are at least 1% abundant in at least one sample are shown in order of decreasing prevalence (from top to bottom). Asterisk (*) denotes detection only by culturomics and not by community amplicon sequencing.

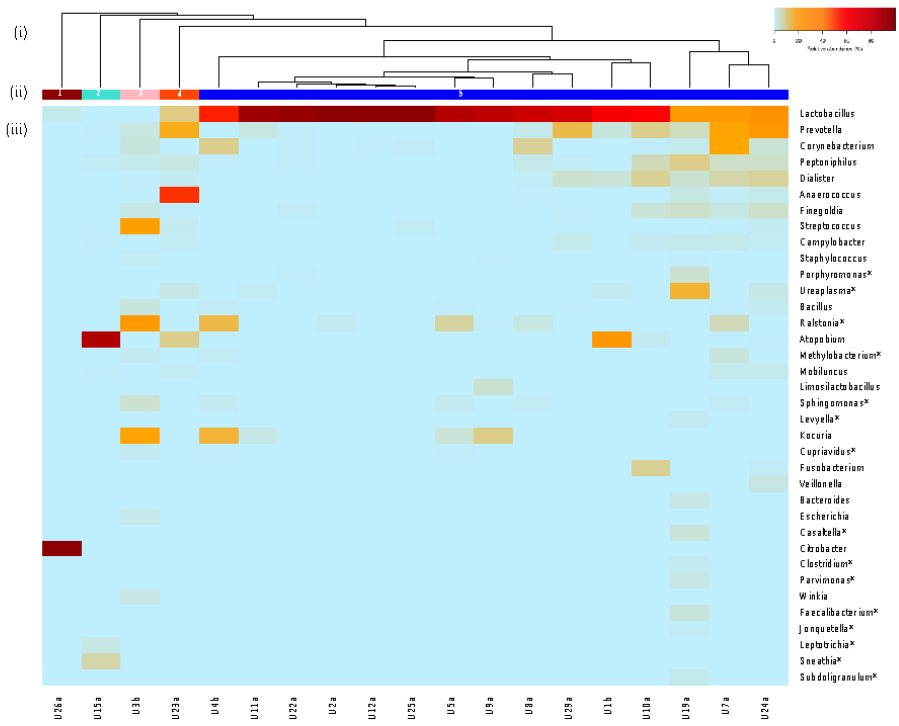


Figure S3. Genus-level community structure types of healthy FUM by community amplicon sequencing.

(i) Hierarchical clustering of Bray-Curtis dissimilarity distance matrices on the relative proportions of reads for each OTU within individual urine samples. (ii) Bars below dendrogram denote community structure types. (iii) Heatmap of relative abundances of bacterial genera within each urinary microbiota. Only genera that are at least 1% abundant in at least one sample are shown in order of decreasing prevalence (from top to bottom). Asterisk denotes detection only by community amplicon sequencing and not by culturomics.

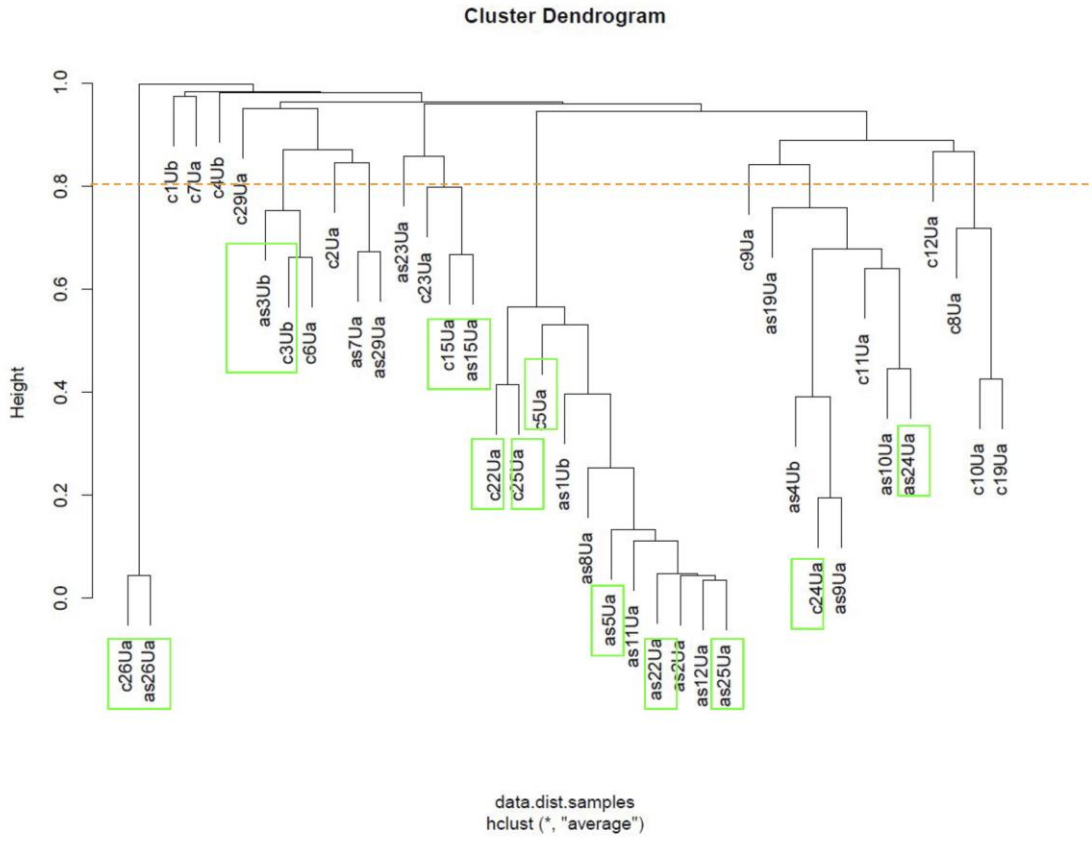
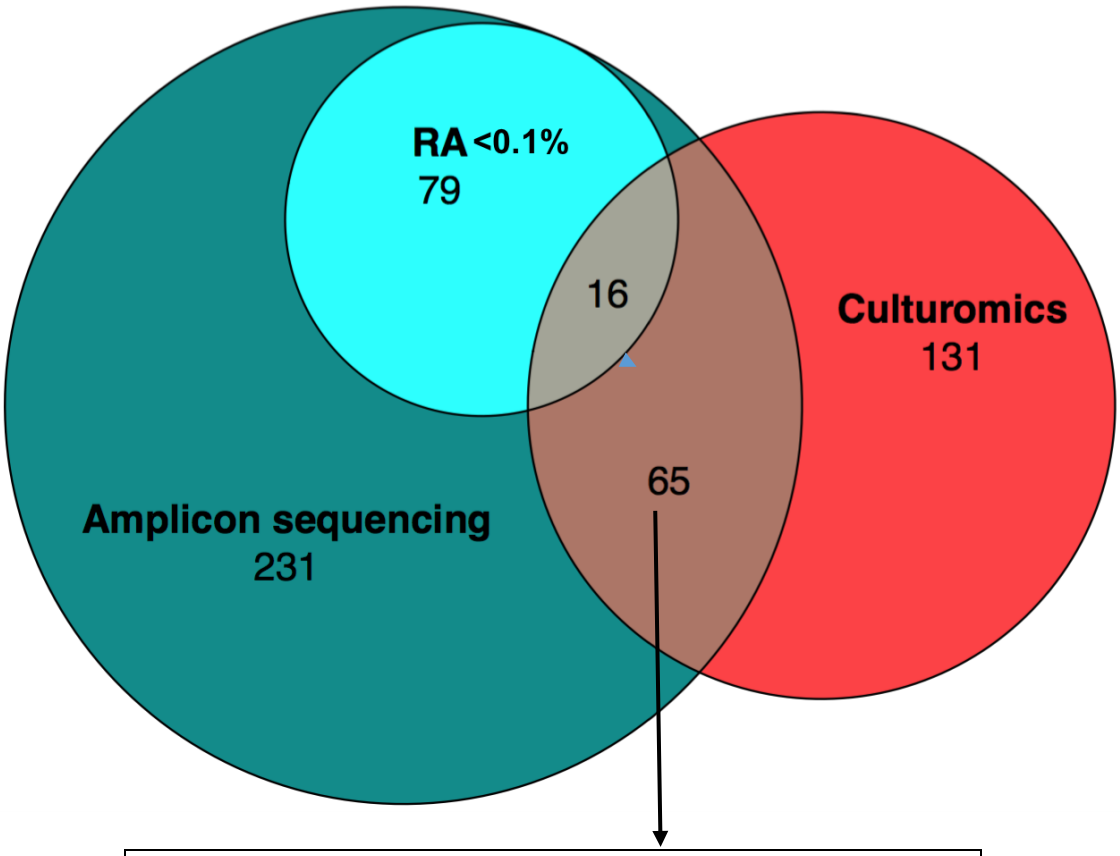


Figure S4. Species-level hierarchical clustering including 19 samples characterized by culturomics (c) and amplicon sequencing (as). Hierarchical clustering was based on Bray-Curtis dissimilarity distance matrices, for which all species detected were included. A cutoff value of 0.8 was used to define the clusters (dashed orange line). Samples clustered into the same CST by both methodologies are shown in green boxes.



Species detected by both methodologies		
*Abiotrophia defectiva**	*Corynebacterium tuberculostearicum*	*Peptoniphilus coxii*
Acinetobacter spp.*	*Cutibacterium acnes*	*Peptoniphilus duerdenii*
Actinomyces europaeus	*Dermabacter* spp.*	*Peptoniphilus lacrimalis*
Actinomyces spp.*	*Dialister micraerophilus*	*Prevotella bivia*
*Actinomyces urogenitalis**	*Dialister propionicifaciens*	*Prevotella corporis*
*Actinomyces viscosus**	*Enterococcus faecalis*	*Prevotella disiens*
Actinotignum schaalii	*Escherichia coli*	*Propionimicrobium lymphophilum*
Anaerococcus tetradius	*Facklamia hominis*	*Pseudoclavibacter* spp.*
Atopobium minutum	*Fannyhessea vaginae*	*Rhizobium radiobacter**
*Bacillus simplex**	*Finegoldia magna*	*Slackia exigua**
Bacillus spp.	*Fusobacterium nucleatum*	*Staphylococcus aureus**
Bacteroides vulgatus	*Granulicatella adiacens**	*Staphylococcus epidermidis*
Bifidobacterium spp.*	*Lactobacillus crispatus*	*Staphylococcus haemolyticus*
Campylobacter ureolyticus	*Lactobacillus delbrueckii*	*Staphylococcus hominis*
Citrobacter koseri	*Lactobacillus gasseri*	*Staphylococcus lugdunensis**
Collinsella aerofaciens	*Lactobacillus iners*	*Staphylococcus* spp.
Corynebacterium aurimucosum	*Lactobacillus jensenii*	*Streptococcus agalactiae*
Corynebacterium coyleae	*Limosilactobacillus mucosae*	*Streptococcus anginosus*
Corynebacterium jeikeium	*Limosilactobacillus vaginalis*	*Streptococcus gordonii**
Corynebacterium riegelii	*Mobiluncus curtisii*	*Streptococcus* spp.
Corynebacterium simulans	*Moraxella* spp.*	*Veillonella parvula*
	Peptoniphilus asaccharolyticus	*Winkia neuii*
* species detected by amplicon sequencing in relative abundance < 0.1%		

Figure S5. Venn-Euler diagram showing the number of species (N = 297) detected by culturomics and/or amplicon sequencing. The size of the circles and intersections is proportional to the number of species detected. Species detected by both methodologies are listed in alphabetical order. (RA, relative abundance)