Figure S1: Representation of the publication frequency of bacterial taxa

This figure represents the most frequent species found at least once in the human urinary tract. Using the online tool wordart (https://wordart.com/create), the size of the name of each 562 species is proportional to the number of times it occurs in the PubMed database according to the automatic query.

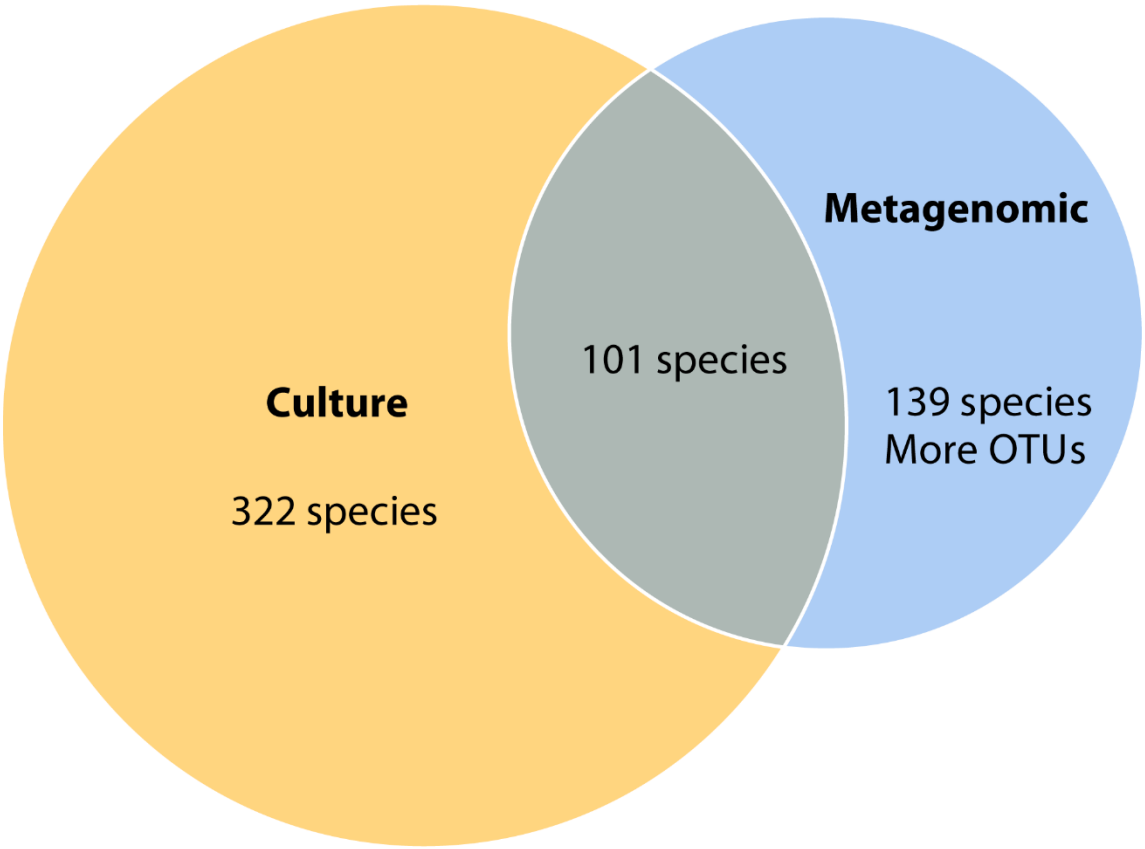

Figure S2: Venn diagram representing the proportion of bacteria found in urine by culture and metagenomics*

Venn diagram representing the bacterial taxa most commonly and uncommonly found by culture and metagenomic techniques. * All the unique and shared taxa are listed in the Dataset S2.

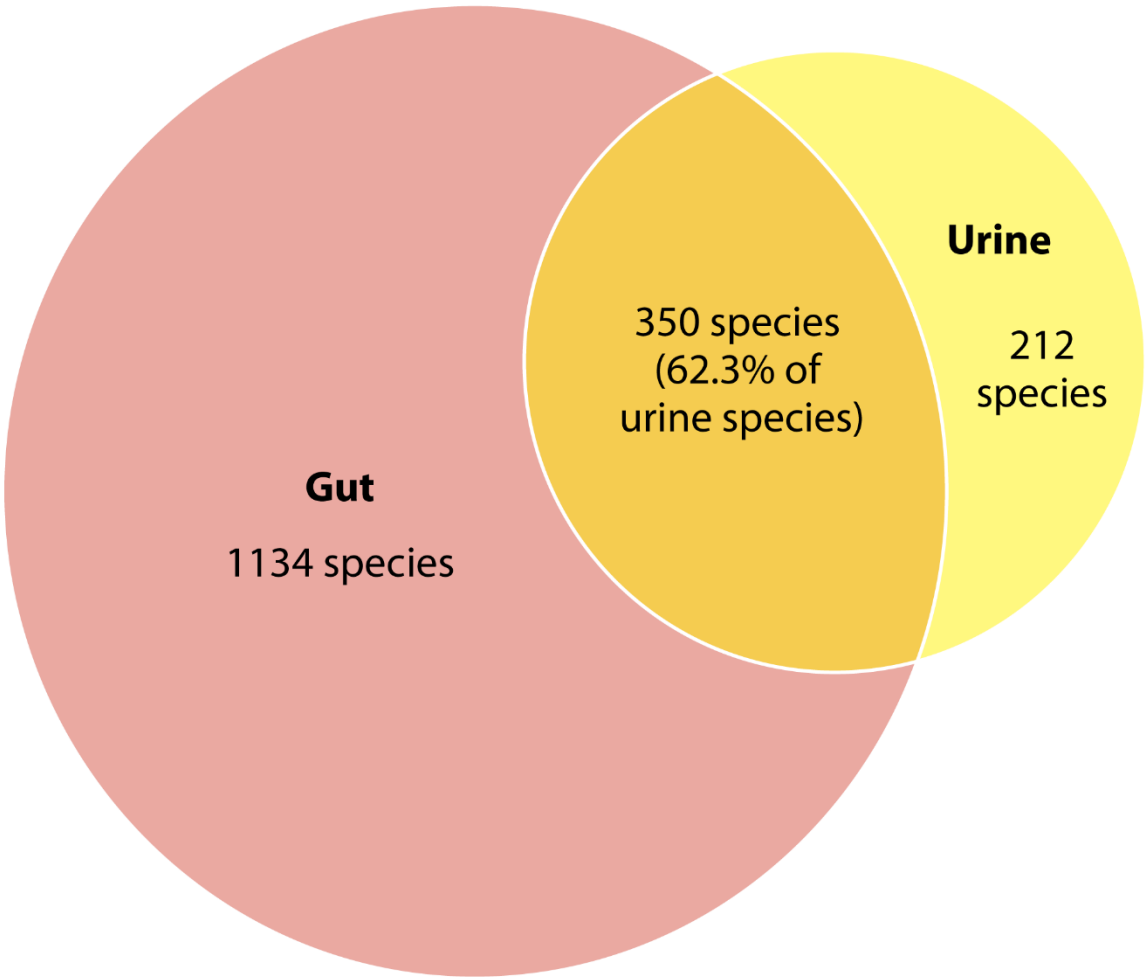

Figure S3: Venn diagram representing the proportion of common and uncommon bacteria found in the urine and gut repertoires*

Venn diagram representing the most common and uncommon species in the gut and urine repertoires. * All the unique and shared taxa are listed in the Dataset S4.

Table S1: Publication frequency of bacterial taxa	
Urine species	**Frequency**
Escherichia coli	17031
Staphylococcus aureus	4499
Pseudomonas aeruginosa	4145
Chlamydia trachomatis	4049
Neisseria gonorrhoeae	2707
Klebsiella pneumoniae	2657
Proteus mirabilis	2193
Enterococcus faecalis	1800
Streptococcus pneumoniae	1454
Mycobacterium tuberculosis	1254
Streptococcus pyogenes	966
Ureaplasma urealyticum	961
Haemophilus influenzae	933
Staphylococcus epidermidis	925
Streptococcus agalactiae	765
Serratia marcescens	662
Staphylococcus saprophyticus	632
Mycobacterium bovis	566
Salmonella typhimurium	558
Mycoplasma genitalium	523
Mycoplasma hominis	504
Acinetobacter baumannii	446
Enterobacter cloacae	437
Clostridium difficile	431
Enterococcus faecium	397
Proteus vulgaris	299
Salmonella typhi	287
Neisseria meningitidis	264
Gardnerella vaginalis	251
Citrobacter freundii	241
Leptospira interrogans	233
Clostridium perfringens	203
Bacteroides fragilis	202
Enterobacter aerogenes	188
Klebsiella oxytoca	187
Morganella morganii	184
Salmonella enteritidis	181
Moraxella catarrhalis	175
Mycobacterium terrae	173
Mycobacterium szulgai	171
Bacillus subtilis	162
Listeria monocytogenes	151
Haemophilus parainfluenzae	150
Shigella dysenteriae	141
Stenotrophomonas maltophilia	139
Providencia stuartii	137
Borrelia burgdorferi	125
Mycobacterium avium	124
Providencia rettgeri	120
Staphylococcus haemolyticus	111
Campylobacter jejuni	103

Table S1: Publication frequency of bacterial taxa

This table represents the publication frequency of the most frequent species found at least once in the human urinary tract.

Dataset S1: List of identified prokaryotic species with standing in nomenclature using LPSN (http://www.bacterio.net) and taxonomy on NCBI (http://www-ncbi-nlm-nih-gov.gate2.inist.fr/taxonomy/?term=) (20,660 bacteria and archaea on the 15th of February 2018) used for the automated search, and number of publications associated with the prokaryotic species according to the automated request.

Dataset S2: Summary of all the results obtained. Name of the bacterial species, discovery modality (metagenomic and / or culture), pathogenicity (represented according to the risk group but also according to the reported cases of human and urinary tract infections in the literature), oxygen metabolism status, taxonomic classification.

Dataset S3: Taxa repartition per Phyla and Genus

Dataset S4: Comparison of the human urinary tract repertoire, the human gut repertoire and the human global repertoire

Dataset S5: Ethnicity of study participants