**Supplementary Table 1. Urinary microbiome in patients with STI [24]**

| Control individuals | Main bacterial taxa found in controls | Patients | Main bacterial taxa found in patients | Sample collection | Technique used | Reference |
|---------------------|---------------------------------------|----------|--------------------------------------|------------------|---------------|-----------|
| Men aged ≥ 18 yr without STI (n = 9) | *Corynebacterium*, *Lactobacillus*, *Streptococcus*, *Staphylococcus*, *Propionibacterium* | Men aged ≥ 18 yr with STI (n = 10) | *Sneathia*, *Prevotella*, *Gemella*, *Aerococcus*, *Lactobacillus*, *Streptococcus*, *Veillonella*, *Anaerococcus*, *Atopobium*, *Corynebacterium*, *Mycoplasma* | First-void urine | 16S rRNA GS | Nelson et al. (2010) [25] |
| Men aged ≥ 18 yr without STI (n = 22) | *Lactobacillus*, *Sneathia*, *Veillonella*, *Corynebacterium*, *Prevotella*, *Streptococcus*, *Ureaplasma*, *Mycoplasma*, *Anaerococcus*, *Atopobium*, *Aerococcus*, *Staphylococcus*, *Gemella*, *Enterococcus*, *Finegoldia* | Men aged ≥ 18 yr with STI (n = 10) | *Neisseria*, *Streptococcus*, *Corynebacterium*, *Prevotella*, *Ureaplasma*, *Lactobacillus*, *Aerococcus*, *Gemella*, *Sneathia*, *Veillonella*, *Eggerthella*, *Propionibacterium*, *Mycoplasma*, *Ralstonia*, *Anaerococcus* | First-void urine | 16S rRNA GS | Dong et al. (2011) [27] |

STI, sexually transmitted infection; GS, gene sequencing.