

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)	<i>Corynebacterium</i> , <i>Lactobacillus</i> , <i>Streptococcus</i> , <i>Staphylococcus</i> , <i>Propionibacterium</i>	Men aged ≥ 18 yr with STI (n = 10)	<i>Sneathia</i> , <i>Prevotella</i> , <i>Gemella</i> , <i>Aerococcus</i> , <i>Lactobacillus</i> , <i>Streptococcus</i> , <i>Veillonella</i> , <i>Anaerococcus</i> , <i>Atopobium</i> , <i>Corynebacterium</i> , <i>Mycoplasma</i>	First-void urine	16S rRNA GS	Nelson et al. (2010) [25]
Men aged ≥ 18 yr without STI (n = 22)	<i>Lactobacillus</i> , <i>Sneathia</i> , <i>Veillonella</i> , <i>Corynebacterium</i> , <i>Prevotella</i> , <i>Streptococcus</i> , <i>Ureaplasma</i> , <i>Mycoplasma</i> , <i>Anaerococcus</i> , <i>Atopobium</i> , <i>Aerococcus</i> , <i>Staphylococcus</i> , <i>Gemella</i> , <i>Enterococcus</i> , <i>Finnegoldia</i>	Men aged ≥ 18 yr with STI (n = 10)	<i>Neisseria</i> , <i>Streptococcus</i> , <i>Corynebacterium</i> , <i>Prevotella</i> , <i>Ureaplasma</i> , <i>Lactobacillus</i> , <i>Aerococcus</i> , <i>Gemella</i> , <i>Sneathia</i> , <i>Veillonella</i> , <i>Staphylococcus</i> , <i>Propionibacterium</i> , <i>Mycoplasma</i> , <i>Ralstonia</i> , <i>Anaerococcus</i>	First-void urine	16S rRNA GS	Dong et al. (2011) [27]

STI, sexually transmitted infection; GS, gene sequencing.